intry	
Mtype	PRT
Class	STANDARD 100K_RAT
Seglen	1005_84
Ac	
<ul> <li>Entry Mod</li> </ul>	
	01-NOV-1997
Rel	35
Type	Created
	01-NOV-1997
Rel	35 Last sequence update
Date Rel	15-JUL-1999 38
	Last annotation update
Descr	100 KDA PROTEIN (EC 6.3.2)
Species	Rattus norvegicus (Rat)
<ul><li>Org</li><li>Entry</li></ul>	Eukaryota
	Metazoa
	Chordata
<ul> <li>Entry</li> </ul>	Craniata
<ul> <li>Entry</li> </ul>	Vertebrata
<ul> <li>Entry</li> </ul>	Euteleostomi
	Mammalia
	Eutheria
<ul> <li>Entry</li> </ul>	Rodentia
<ul> <li>Entry</li> </ul>	Sciurognathi
<ul> <li>Entry</li> </ul>	Muridae
	Murinae
• Entry	Rattus
• Num	1
Pos	SEQUENCE FROM N.A
Comr	nent ntry STRAIN=WISTAR
	intry TISSUE=TESTIS
Db	MEDLINE
	neid 92253337
Autho	or Intry Mueller D
	intry Rehbein M
• E	Intry Baumeister H
	intry Richter D
Cite	Nucleic Acids Res. 20:1471-1475(1992)
• Num	2
Pos	ERRATUM ment
Db	
Medli	
Autho	or Intry Mueller D
	intry Rehbein M
· E	Intry Baumeister H
	intry Richter D
Cite	Nucleic Acids Res. 20:2624-2624(1992)

Embl	
	c Id CAA45756
Prir	m Id X64411
	ıtus
Interpre	
Sec     Prin	c Id
	c Id
Pfam	TIME TO THE TOTAL THE TOTAL TO THE TOTAL TOT
<ul> <li>Sta</li> </ul>	itus 1
	total HECT
	m Id   PF00632
• <u>Sta</u>	itus 1 c Id PABP
Prir	10 FABE m Id PF00658
Keywor	
• Ent	try Ubiquitin conjugation
	try Ligase
Feature	
	main
•	From 77
	To
	Descr Fature 1
	• Entry
•	From 127 To 150
	Descr
	- Entry
	From   420
•	To 439
	Descr
	• Entry
•	From 448 To 457
	Descr
	• Entry
•	From 485
	To 514 Descr
	• Entry
	From   579
	To 590
	Descr • Entry
•	From   786
	To 889 Descr
	• Entry
•	From 827 To 847
	Descr
	• Entry
Bin	ding
	From 858 To 858
	Descr UBIQUITIN (BY SIMILARITY)
Sig	nal
Cha	ain
	ulfid
	n Ter
	d Res nflict
	rbohyd
	Bind Bind
	nilar

Pir	
Mendel	
Hssp	
Prosite	
Gene	
Prints	
Flybase	
Maizedb	
viaizeub	
Wormpe	
Mtype	PRT
Class	STANDARD
Id	104K_THEPA
Seglen	924
Ac	
<ul> <li>Entry</li> </ul>	
Mod	,
<ul> <li>Date</li> </ul>	01-APR-1990
Rel	
Type	Created
	01-APR-1990
Rel	14
Type	Last sequence update
	L
	01-AUG-1992
Rel	
	Last annotation update
Descr	104 KDA MICRONEME-RHOPTRY ANTIGEN
Species	Theileria parva
Org	
<ul> <li>Entry</li> </ul>	Eukaryota
<ul> <li>Entry</li> </ul>	Aiveolata
• Entry	Apicomplexa
<ul> <li>Entry</li> </ul>	Piroplasmida
<ul> <li>Entry</li> </ul>	Theileriidae
F., 4	The Hart
	Theileria
Ref	
• Num	
Pos	SEQUENCE FROM N.A
Com	ment
•	Entry
Db	MEDLINE
MedI	ineid 90158697
Auth	
	Entry lams K.P
	nuy pans K.F
	Entry Young J.R
•	entry Nene V
•	Entry Desai J
	Entry Webster P
•	entry   webster P
	Entry Ole-Moiyoi O.K
•	Entry Musoke A.J
Cite	Mol. Biochem. Parasitol. 39:47-60(1990)
Embl	
	d AAA18217
	d M2954
Statu	IS
Interpro	
Pfam	
Keyword	
<ul> <li>Entry</li> </ul>	Antigen
	. •

Entry Sporozoite
Entry Repeat

Feature	
	main
•	From 1
	To 19
	Descr
	• Entry
•	<u>From</u> <u>905</u>
	To 924
	Descr
	• Entry
	nding
	nal
Ch	
Dis	sulfid
	n Ter
Mo	d Res
Co	nflict
	rbohyd
Np	Bind
	nilar
Pir	
	c Id   <mark>A44945_</mark>
Pri	m Id <mark>A44945</mark>
Mendel	
Hssp	
Prosite	
Gene	
Prints	
Flybase	
Maized	
Wormp	ep
Mtype	PRT
Class	STANDARD
Id	108_LYCES
Seqlen	102
Ac	
• En	try
Mod	
	te 15-JUL-1999
	1 <mark>38                                   </mark>
Ту	pe Created
• Da	te 15-JUL-1999
Re	
	pe Last sequence update
ı yı	pe Last sequence upuate
• Da	te   15-JUL-1999
Re	
	pe Last annotation update
Descr	PROTEIN 108 PRECURSOR
Species	
Org	
<ul> <li>Ent</li> </ul>	try Eukaryota
• En	try Viridiplantae
• En	try Empryonhyta
	try Embryophyta
• En	try
• En	
<ul><li>En</li></ul>	try   Tracheophyta try   Spermatophyta
<ul><li>Ent</li><li>Ent</li><li>Ent</li></ul>	try

Entry euasterids I
Entry Solanales
Entry Solanaceae
Entry Solanum

Ref	f	
•	Num	1
	Pos	SEQUENCE FROM N.A
	Comment	
	<ul> <li>Entry</li> </ul>	STRAIN=CV. VF36
	<ul> <li>Entry</li> </ul>	TISSUE=ANTHER
	Db	MEDLINE
		94143497
	Author	
	<ul> <li>Entry</li> </ul>	Chen R
	<ul> <li>Entry</li> </ul>	Smith A.G
		Plant Physiol. 101:1413-1413(1993)
Em		
•	Sec Id C	
	Prim Id Z	14088
Last	Status erpro	
Pfa		
	yword	
	Entry	
Fea	atures	
	Domain	
	Binding	
	Signal From	
	То	
		POTENTIAL
	Chain	
	<ul> <li>From</li> </ul>	
	То	
	Descr	PROTEIN 108
	From	las
		77
		BY SIMILARITY
	• From	
	To	
		BY SIMILARITY
	• From To	
		BY SIMILARITY
	• From	
	To	
	Non Ter	BY SIMILARITY
	Mod Res	
	Conflict	
	Carbohyd	
	Np Bind	
Di-	Similar	
Pir	ndel	
IVIC	Status 1	133
	Sec Id L	
_	Prim Id 8	
Hss		
	site	
Ger		
Pri	base	
	izedb	
	rmpep	
Mty		ANDARD
Id		KD_VIGUN
Sec	qlen 75	
Ac		
•	Entry	

Mod	Mod	
•	• Date 01-NOV-1990	
	Rel 16	
	Type Created	
	Date 01-NOV-1990	
	Rel 16	
	Type Last sequence update	
•	• Date 01-FEB-1995	
	Rel 31	
Dag	Type Last annotation update	
	Descr 10 KDA PROTEIN PRECURSOR (CLONE PSAS10)  Species Vigna unguiculata (Cowpea)	
	Org	
•	• Entry Viridiplantae	
	Entry Embryophyta	
•	Entry Tracheophyta	
	Entry Spermatophyta	
•	Entry Magnoliophyta	
	Entry eudicotyledons	
	Entry Rosidae	
	Entry eurosids I	
	Entry Fabales	
•	• Entry Fabaceae	
,	Entry Papilionoideae	
	Entry Vigna	
	Ref	
•	Num 1 Pos SEQUENCE FROM N.A	
	Comment	
	• Entry	
	Db MEDLINE	
	Medlineid 91355865	
	Author	
	Entry Ishibashi N	
	Entry Yamauchi D	
	Entry Miniamikawa T	
	Cite Plant Mol. Biol. 15:59-64(1990)	
	Embl	
	000 14 07410 1700	
	Prim Id X16877	
	Status	
nte	Interpro	
,	• Sec Id -	
Dfc	Prim Id IPR002118	
rid	Pfam	

Status 1
Sec Id Gamma-thionin
Prim Id PF00304

Entry GerminationEntry Signal

Keyword

Features
Domain
Binding
Signal
From 1
<u>To ? </u>
Descr POTENTIAL
Chain
• From ? To 75
Descr 10 kDa PROTEIN
Disulfid
• From 31
To 75
Descr BY SIMILARITY
Francisco
• From 42 To 63
Descr BY SIMILARITY
• <u>From <mark>48</mark></u>
To <mark>69</mark>
Descr BY SIMILARITY
• From   52
To 71
Descr BY SIMILARITY
Non Ter
Mod Res
Conflict
Carbohyd
Np Bind Similar
Pir
- Sec Id S11156
Prim Id S11156
Mendel
Hssp
Sec Id 1CHL
Prim Id P45639
Prosite
Status 1
Sec Id GAMMA_THIONIN Prim Id PS00940
Gene Gene
Prints
Flybase
Maizedb
Wormpep
Mtype PRT
Class STANDARD
Id 110K PLAKN
Seqlen 296
Ac
• Entry
Mod
- <u>Date 01-JAN-1990</u>
Rel 13
Type Created
• Date 01-JAN-1990
Rel 13
Type Last sequence undate

Plasmodium knowlesi

Date 01-FEB-1994
Rel 28
Type Last annotation update
Descr 110 KDA ANTIGEN (PK110) (FRAGMENT)
Plasmodium knowlesi

Org	ו	
•	Entry Euk	aryota
•	Entry Alv	
•	Entry Api	complexa
•	Entry Had	emosporida
•	Entry Pla	smodium
Ret		
•	Num	1
	Pos	SEQUENCE FROM N.A
	Comment Db	MEDLINE
		88039002
	Author	86037002
	Entry	Perler F.B
		Moon A.M
	<ul> <li>Entry</li> </ul>	Qiang B.Q
	• Entry	Meda M
	<ul> <li>Entry</li> </ul>	Dalton M
	<ul> <li>Entry</li> </ul>	Card C
		Schmidt-Ullrich R
		Wallach D
		Lynch J
		Donelson J.E
	Cite	Dorickson 3.2.  Mol. Biochem. Parasitol. 25:185-193(1987)
Em		mor. bodiem. rarastor. 20:100 170(1707)
•	Sec Id A	AA29471
	Prim Id N	119152
	Status	
	erpro	
Pfa		
· Ke	yword Entry <mark>Ma</mark> l	orlo
٠		
•	Entry Ant	igen
	Entry Rep	neat .
Fea	atures	
	Domain	
	<ul> <li>From</li> </ul>	
	То	296
	Descr	
		ntry 13.5 X 12 AA TANDEM REPEATS OF E-E-T-Q-K-
	• E	ntry T-V-E-P-E-Q-T
	Binding	
	Signal	
	Chain	
	Disulfid Non Ter	
	From	1
	To	1
	Mod Res	
	Conflict Carbohyd	
	Np Bind	
	Similar	

Sec Id A54527 Prim Id A54527

Mendel
Hssp
Prosite
Gene
Prints

Flybase Maizedb

-		
1	Wormp	ep
.	Mtype	PRT
	Class	STANDARD
	ld	11S3_HELAN
	Seglen	493
	Ac • En	
_	Mod	uyi .
_	• Da	te 01-NOV-1990
	Re	
		De Created
	• Da	te 01-NOV-1990
	Re	
		be Last sequence update
	• Da Re	te 30-MAY-2000
		Last annotation update
Ī	Descr	11S GLOBULIN SEED STORAGE PROTEIN G3 PRECURSOR (HELIANTHININ G3)
	Species	
	Org	
	• En	try Eukaryota
	• En	try   Viridiplantae
	• En	try Embryophyta
	• En	try Tracheophyta
	- En	try Spermatophyta
	• En	try Magnoliophyta
	• En	try eudicotyledons
		try Asteridae
	• En	ry euasterids II
	• Fn	try Asterales
	• En	try Asteraceae
	• En	try Asteroideae
		try Heliantheae
-		try Helianthus
	Ref	
	• Nu Po:	
		s jeducitec i row w.a
	Db	
		dlineid 89232734
	Au	thor
	•	Entry Vonder Haar R.A
		Entry Allen R.D
	•	Entry Cohen E.A
	•	Entry Nessler C.L
		Entry Thomas T.L
	Cit	
Ī	Embl	
-	• Se	c Id AAA33374
		m Id M28832
-		tus
-	Interpr	o cid <mark></mark>
		m Id   IPR000459
-		

Pfam • Stat

 Status
 1

 Sec Id
 Seedstore\_11s

 Prim Id
 PF00190

Keyword
Entry   Seed storage protein
Entry Multigene family
- Entry Signal
Features
Domain
• From 23
To 35
Descr  • Entry
·
• From 111
To   127
Descr
• Entry
• From 191
To 297
Descr
• Entry
Binding
Signal
From 1
<u>To 20                                   </u>
Descr
Chain  • From 21
• From 21 To 305
Descr ACIDIC CHAIN
• From 306
To 493
Descr BASIC CHAIN
Disulfid  From 103
• From 103 To 312
Descr Interchain (acidic-basic) (potential)
Non Ter
Mod Res
Mod Nes Conflict
Carbohyd
Np Bind
Similar
Pir
• <u>Sec Id</u> <u>JA0089</u>
Prim Id JA0089
Mendel
Hssp
Prosite . Status 1
• Status 1 Sec Id 11S_SEED_STORAGE
Prim Id PS00305
Gene HAG3
Prints
Sec Id 11SGLOBULIN
Prim Id PR00439
Flybase
Maizedb
Wormpep

Mtype PRT
Class STANDARD
Id 115B\_CUCMA
Seqlen 480
Ac
• Entry

Mo	d	
•		01-JAN-1990
		13
	Type	Created
	Date	01-JAN-1990
	Rel	13
	Type	Last sequence update
	Date	01-NOV-1990
	Rel	16
		Last annotation update
Des		11S GLOBULIN BETA SUBUNIT PRECURSOR
	ecies	Cucurbita maxima (Pumpkin) (Winter squash)
Org		Eukaryota
•	Entry	Viridiplantae
•	Entry	Embryophyta
	Entry	Tracheophyta
•	Entry	Spermatophyta
•	Entry	Magnoliophyta
	Entry	eudicotyledons
•	Entry	Rosidae
•	Entry	eurosids I
	Entry	Cucurbitales
•		Cucurbitaceae
•		Cucurbita
Ref		
•	Num	1 SEQUENCE FROM N A
•	Num Pos	SEQUENCE FROM N.A
•	Num Pos Comr	
•	Pos Comr • E Db	nent ntry MEDLINE
•	Pos Comr • E Db Medli	nent ntry  MEDLINE neid 88166744
•	Pos Comr • E Db Medli	nent ntry  MEDLINE neid 88166744 or
•	Num Pos Comr • E Db Medli Autho	nent htty  MEDLINE neid 88166744 or htty Hayashi M
•	Num Pos Comr • E Db Medli Autho	nent ntry  MEDLINE neid 88166744 or
•	Num Pos Comr • E Db Medli Autho • E	nent htty  MEDLINE neid 88166744 or htty Hayashi M
•	Num Pos Comr • E Db Medli Autho • E	nent ntry   Mori H ntry   Nishimura M
•	Pos Comr • E Db Medli Autho • E • E	nerst htry MEDLINE neidi 88166744  or htry Hayashi M htry Mori H htry Nishimura M htry Akazawa T
•	Num Pos Comm Bob Medli Author E E E E E E E E E E E E E E E E E E E	nent Intry   MEDLINE   Media
	Num Pos Comr Db Medli Autho E E E E E Cite	nent ntry MEDLINE neid 88166744 or ntry Hayashi M ntry Mori H ntry Nishimura M ntry Akazawa T ntry Hara-Nishimura I Eur. J. Blochem. 172:627-632(1988)
	Num Pos Comr Db Medli Autho E E E E Num	nent Intry   MEDLINE   MED
	Num Pos Comr Db Medli Autho E E E E Num Pos	nent htry MEDLINE heid 88166744  or htry Hayashi M htry Mori H htry Nishimura M htry Akazawa T htry Hara-Nishimura I Eur. J. Biochem. 172:627-632(1988)  2 SEQUENCE OF 22-30 AND 297-302
	Num Pos Comm	nent htry MEDLINE heid 88166744  or htry Hayashi M htry Mori H htry Nishimura M htry Akazawa T htry Hara-Nishimura I Eur. J. Biochem. 172:627-632(1988)  2 SEQUENCE OF 22-30 AND 297-302
	Num Pos Comr Db Medli Autho E E E E Num Pos	nent ntry MEDLINE neid 88166744  or ntry Hayashi M ntry Mori H ntry Nishimura M ntry Akazawa T ntry Hara-Nishimura I Eur. J. Biochem. 172:627-632(1988)  2 SEQUENCE OF 22-30 AND 297-302 nent
	Num Pos Commedia Autho E E E E E Num Pos Comm Db Medii Autho	nent ntry MEDLINE neid 88166744  or ntry Hayashi M ntry Mori H ntry Nishimura M ntry Akazawa T ntry Hara-Nishimura I Eur. J. Biochem. 172:627-632(1988)  2 SEQUENCE OF 22-30 AND 297-302 nent neid
	Num Pos Commedia Autho E E E E E Num Pos Comm Db Medii Autho	ment Intry   MEDLINE   MED
	Num Pos Comr  E B B Medli Author  E Cite Num Pos Comr Db Medli Author  E Cite Num Comr Db Medli Author  E E E E E E E E E E E E E E E E E E	nent ntry MEDLINE neid 88166744  or ntry Hayashi M ntry Mori H ntry Nishimura M ntry Akazawa T ntry Hara-Nishimura I Eur. J. Biochem. 172:627-632(1988)  2 SEQUENCE OF 22-30 AND 297-302 nent neid
	Num Pos Comri  E Db Medli Autho  E Cite Num Pos Comr Db Medli Autho  E Cite  Num Pos Comr Db Medli Autho  E E E E E E E E E E E E E E E E E E	nent ntry   MEDLINE   neid   88166744   ntry   Hayashi M   ntry   Mori H   ntry   Akazawa T   ntry   Hara-Nishimura I   Eur. J. Biochem. 172:627-632(1988)   2   3   SEQUENCE OF 22-30 AND 297-302   nent   neid   nrtry   Ohmiya M   ntry   Hara I
	Num Pos Comri  E Db Medli Autho  E Cite Num Pos Comr Db Medli Autho  E Cite  Num Pos Comr Db Medli Autho  E E E E E E E E E E E E E E E E E E	ment ment ment ment ment ment ment ment
·	Num Pos Comr Db Medlii Autho E E Cite Num Pos Comr Db Medlii Autho E E E Cite L E Cite Num E E Cite Num E E Cite Num E E Cite Num E E Cite L E Cite L E E E E E E E E E E E E E E E E E E	ment http:    MEDLINE     meid   88166744     mitry   Hayashi M     mitry   Akazawa T     mitry   Hara-Nishimura I     Eur. J. Blochem. 172:627-632(1988)     2     SEQUENCE OF 22-30 AND 297-302     ment     meid     mitry   Ohmiya M     mitry   Ohmiya M     mitry   Hara I     mitry   Mastubara H     Plant Cell Physiol. 21:157-167(1980)
• • • • • • • • • • • • • • • • • • •	Num Pos Comr  b B Medli Autho Com Com E E E E E E E E E Cite Num Pos Com D Medli Autho Com E E E E E E E E E E E E E E E E E E E	ment   MEDLINE
_	Num Pos Comr Db Medli Autho E E E E E E E E E E E E E E E E E E E	ment http:    MEDLINE     meid   88166744     mtry   Hayashi M     mtry   Mori H     mtry   Nishimura M     mtry   Hara-Nishimura I     Eur. J. Biochem. 172:627-632(1988)     2     SEQUENCE OF 22-30 AND 297-302     ment     mtry   Hara I     mtry   Hara I     mtry   Hara I     mtry   Mastubara H     Plant Cell Physiol. 21:157-167(1980)     mtry   Mastubara H     plant Cell Physiol. 21:157-167(1980)     mtry   Mastubara H     plant Cell Physiol. 21:157-167(1980)     mtry   Mastubara H     mtry   Mastubara H     plant Cell Physiol. 21:157-167(1980)     mtry   Mastubara H     plant Cell Physiol. 21:157-167(1980)
•	Num Pos Comr Db Medli Autho E E E Cite Num Pos Comr Db Medli Autho E E Cite Sec Ic Cite Sec Ic Sec I	ment http:    MEDLINE     meid   88166744     mtry   Hayashi M     mtry   Mori H     mtry   Nishimura M     mtry   Hara-Nishimura I     Eur. J. Biochem. 172:627-632(1988)     2
•	Num Pos Comr Db Medli Autho E E E E E E E E E E E E E E E E E E E	ment ment ment ment ment ment ment ment

eyword
Entry Seed storage protein
Entry Signal
Ethres Ethres
Domain
Binding
Signal
From 1 To 21
To 21 Descr
Chain
• From 22
To 480
Descr 11S GLOBULIN BETA SUBUNIT
• From 22
To 296
Descr GAMMA CHAIN (ACIDIC)
• From 297
To 480
Descr DELTA CHAIN (BASIC)
Disulfid
From 124 To 303
Descr INTERCHAIN (GAMMA-DELTA) (POTENTIAL)
Non Ter
Mod Res
From 22
To 22
Descr PYRROLIDONE CARBOXYLIC ACID
Conflict  From 27
To 27
Descr S -> E (IN REF. 2)
• From 30
To 30
Descr E -> S (IN REF. 2)
Carbohyd
Np Bind
Similar
ir Sec Id FWPU1B
Prim Id S00366
lendel
SSP
rosite
Status 1
Sec Id         11S_SEED_STORAGE           Prim Id         PS00305
ene Print to produce to the control of the control
rints
Sec Id 11SGLOBULIN
Prim Id PR00439
lybase
laizedb (Armon
Vormpep
Itype PRT
lass STANGARD
d 120K_RICRI eqlen 1300
eqlen <mark>1300</mark> c
Entry

Мо	d
•	Date 01-APR-1990
	Rel 14
	Type Created
	Date   01-FEB-1996
•	Rel 33
	Type Last sequence update
•	Date 01-FEB-1996
	Rel 33
D -	Type Last annotation update  scr 120 KDA SURFACE-EXPOSED PROTEIN
Des	cci 120 KDA SURFACE-EXPOSED PROTEIN  ccies Rickettsia rickettsii
Org	
•	Entry Bacteria
•	Entry Proteobacteria
	Entry alpha subdivision
•	Entry Rickettsiales
•	Entry Rickettsiaceae
	Entry Rickettsieae
٠	
<u>•</u>	Entry Rickettsia
Ref	
•	Num 1
	Pos SEQUENCE FROM N.A Comment
	• Entry
	Db MEDLINE
	Medlineid 90136087
	Author
	• Entry Gilmore R.D. Jr
	• Entry Joste N
	• Entry McDonald G.A
_	Cite Mol. Microbiol. 3:1579-1586(1989)
Em	Sec Id CAA34402
•	Prim Id X16353
	Status
Int	erpro
Pfa	
Key	word
•	Entry Antigen
	Entry Glycoprotein
<u>.</u>	Entry S-layer
Fea	atures
	Domain Northean
	Binding Signal
	ospria. Chain
	Disulfid
	Non Ter
	Mod Res
	Conflict
	Carbohyd
	• <u>From 7</u>
	To 7
	Descr POTENTIAL
	• From 66
	To <mark>66</mark>
	Descr POTENTIAL DESCRIPTION OF THE POTENTIAL

 From
 86

 To
 86

 Descr
 POTENTIAL

•	From	
	To	103
	Descr	POTENTIAL
•	From	147
	То	147
	Descr	POTENTIAL
	From	268
	To	268
	Descr	POTENTIAL
	From	330
	То	330
		POTENTIAL
•	From To	3/5
	Descr	POTENTIAL
•	From To	415
	Descr	POTENTIAL
٠	From	
		POTENTIAL
	Desci	POTENTIAL
•	From	
	То	
		POTENTIAL
•	From	436
	То	
	Descr	POTENTIAL
•	From	444
	To	
	Descr	POTENTIAL
•	From	515
	То	515
	Descr	POTENTIAL
	From	547
	То	
		POTENTIAL
	Descr	
	From	593
•	From To	593
•	From To	
	From To Descr	POTENTIAL
	From To	593 POTENTIAL 655
	From Descr From To	593 POTENTIAL 655
	From To Descr From To Descr	593 POTENTIAL 655 655 POTENTIAL
	From Descr From To	593 POTENTIAL 655 655 POTENTIAL 698
	From To Descr From To Descr From To	593 POTENTIAL 655 655 POTENTIAL 698
	From To Descr From To Descr From To Descr From To Descr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL
	From To Descr From To Descr From To Descr From To From To To Descr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710
	From To Descr From To Descr From To Descr From To To To	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710
	From To Descr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL
	From To Descr From To Descr From To Descr From To Descr From To From From	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799
	From To Descr From To Descr From To Descr From To Descr From To To Descr From To To	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799 799
	From To Descr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799 799 POTENTIAL
	From To Descr From From To To Descr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799 799 POTENTIAL
	From To Descr From To To Descr From To	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 POTENTIAL 779 779 POTENTIAL 800 800
	From To Descr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 POTENTIAL 799 799 POTENTIAL 800 800 POTENTIAL
	From To Descr Fr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 POTENTIAL 779 799 POTENTIAL 800 800 POTENTIAL 826
	From To Descr From To	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799 799 POTENTIAL 800 800 POTENTIAL 826 826
	From To Descr Fr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 POTENTIAL 799 799 POTENTIAL 800 800 POTENTIAL 826 826 POTENTIAL
	From To Descr Fr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799 799 POTENTIAL 800 800 POTENTIAL 826 826 POTENTIAL
	From To Descr Fr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799 799 POTENTIAL 800 800 800 800 POTENTIAL 826 826 POTENTIAL 844 844
	From To Descr Fr	593 POTENTIAL 655 655 POTENTIAL 698 698 POTENTIAL 710 710 POTENTIAL 799 799 POTENTIAL 800 800 POTENTIAL 826 826 POTENTIAL

• From 861	
To 861	
Descr POTENTI	AL.
Desci POTENTI	AL
• From 879	
To 879	
Descr POTENTI	AL
Desci FOILINI	AL .
• From 920	
To 920	
Descr POTENTI	ΔΙ
Descript O'LLIVII	
• From 926	
To 926	
Descr POTENTI	ΔΙ
Descript O'LLIVII	· · ·
• From 1116	
To 1116	
Descr POTENTI	AL
• From 1128	
To 1128	
Descr POTENTI	AL
• From 1140	
To 1140	
Descr POTENTI	AL
E   4444	
• From 1146	
To 1146	
Descr POTENTI	AL
• From 1211	
110111 1211	
To 1211	<del></del>
D DOTENTI	
Descr POTENTI	AL
Np Bind	AL
Np Bind Similar	AL
Np Bind Similar Pir	AL
Np Bind Similar  Pir  Sec Id S07575	AL
Np Bind   Similar   Pir   Sec Id   S07575   Prim Id   S07575	AL
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel	AL
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel	AL .
Np Bind Similar  Pir Sec Id S07575 Prim Id S07575 Mendel Hssp	AL CONTRACTOR OF THE PROPERTY
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575 Mendel Hssp Prosite	AL
Np Bind Similar Pir Sec Id S07575 Prim Id S07575 Mendel Hssp Prosite Gene P120	AL CONTRACTOR OF THE PROPERTY
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel  Hssp Prosite Gene P120  Prints	AL CONTRACTOR OF THE PROPERTY
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase	AL CONTRACTOR OF THE PROPERTY
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb	AL CONTRACTOR OF THE PROPERTY
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase	AL CONTRACTOR OF THE PROPERTY
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep	AL CONTRACTOR OF THE PROPERTY
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT	AL .
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMi	
Np Bind Similar  Pir Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROME Seglen 368	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROME Seqlen 368 Ac	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROME Seqlen 368 Ac  Entry	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seglen 368 Ac  Entry Mod	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMS Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created  Date 01-OCT-1993 Rel 27	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U DROME Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created  Date 01-OCT-1993 Rel 27 Type Last sequence	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMS Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created  Date 01-OCT-1993 Rel 27 Type Last sequence  Date 01-FEB-1996	
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROME Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created  Date 01-OCT-1993 Rel 27 Type Last sequence  Date 01-FEB-1996 Rel 33	update
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Malzedb Wormpep  Mtype PRT Class STANDARD Id 128U_DROMI Seglen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created  Date 01-OCT-1993 Rel 27 Type Created  Date 01-OCT-1993 Rel 27 Type Last annotation  Date 01-FEB-1996 Rel 33 Type Last annotation	update
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U DROME Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created  Date 01-FEB-1996 Rel 33 Type Last sequence  Date 01-FEB-1996 Rel 33 Type Last annotatic Descr GTP-BINDING	u update S PROTEIN 128UP
Np Bind Similar  Pir  Sec Id S07575 Prim Id S07575  Mendel Hssp Prosite Gene P120 Prints Flybase Maizedb Wormpep  Mtype PRT Class STANDARD Id 128U DROME Seqlen 368 Ac  Entry Mod  Date 01-OCT-1993 Rel 27 Type Created  Date 01-FEB-1996 Rel 33 Type Last sequence  Date 01-FEB-1996 Rel 33 Type Last annotatic Descr GTP-BINDING	update

Org	
	try Eukaryota
• En	ntry Metazoa
• En	try Arthropoda
• En	try Tracheata
• En	try Hexapoda
• En	try Insecta
• En	try Pterygota
• En	try Neoptera
• En	try Endopterygota
• En	try Diptera
	try Brachycera
• En	try Muscomorpha
• En	try Ephydroidea
• En	try Drosophilidae
• En	try Drosophila
Ref	
• Nu	m 1
Po	SEQUENCE FROM N.A
Po	S SEQUENCE FROM N.A summent
Po Co •	SEQUENCE FROM N.A  mment  Entry  MEDLINE
Po Co • Db	SEQUENCE FROM N.A  mment  Entry  MEDLINE edilineid 94166747
Po Co • Db	SEQUENCE FROM N.A  mment  Entry  MEDLINE  edilineid 94166747  ithor
Po Co • Db	SEQUENCE FROM N.A  mment Entry  MEDLINE edilineid 94166747  Ithor Entry Sommer K.A
Po Co Db Me Au	SEQUENCE FROM N.A  mment  Entry  D  MEDLINE Edilineid 94166747  ithor  Entry   Sommer K.A  Entry   Petersen G
Po Co • Db	SEQUENCE FROM N.A  mment Entry  MEDLINE edlineid 94166747  ithor Entry   Sommer K.A Entry   Petersen G  Entry   Bautz E.K.F
Po Co Co Dbb Me Au • • • Cit Embl	SEQUENCE FROM N.A  mment Entry O MEDLINE Editined   94166747  Ithor Entry   Sommer K.A  Entry   Petersen G  Entry   Bautz E.K.F  Ide   Mol. Gen. Genet. 242:391-398(1994)
Pool Color Dbb Mee Au Cit Embl	SEQUENCE FROM N.A  Interpretation of the control of
Po Co Co Db Me Au	SEQUENCE FROM N.A
Dbb Me Au  Cit Embl  Embl Sta	SEQUENCE FROM N.A  mment Entry O MEDLINE delineid 94166747  ithor Entry   Petersen G Entry   Bautz E.K.F  te   Mol. Gen. Genet. 242:391-398(1994)  C Id   CAA50701   Im Id   X71866   atus   South of the control of the
Po Co	SEQUENCE FROM N.A  mment Entry  MEDLINE edilineid 94166747  ithor Entry   Petersen G Entry   Bautz E.K.F  Mol. Gen. Genet. 242:391-398(1994)  c Id CAA50701 im Id X71866  atus  c Id   CAA50701
Pool Cool Cool Cool Cool Cool Cool Cool	SEQUENCE FROM N.A  mment Entry O MEDLINE delineid 94166747  ithor Entry   Petersen G Entry   Bautz E.K.F  te   Mol. Gen. Genet. 242:391-398(1994)  C Id   CAA50701   Im Id   X71866   atus   South of the control of the
Pro Co	SEQUENCE FROM N.A  mment Entry  MEDLINE collineid 94166747  withor Entry   Petersen G Entry   Bautz E.K.F  te   Mol. Gen. Genet. 242:391-398(1994)  cc   Id   CAA50701   Im   Id   IPR000765  atus   1
Pool Cool Cool Cool Cool Cool Cool Cool	SEQUENCE FROM N.A  mment Entry Do MEDLINE Collineid 94166747  ithor Entry Sommer K.A Entry Petersen G Entry Bautz E.K.F  Ide Mol. Gen. Genet. 242:391-398(1994)  Cold CAA50701 Imid M X71866  atus  To Cold Cold Cold Cold Cold Cold Cold Col
Pool Co	SEQUENCE FROM N.A
Pool Cool Cool Cool Cool Cool Cool Cool	SEQUENCE FROM N.A

Features
Domain
Binding
Signal
Chain
Disulfid
Non Ter
Mod Res
Conflict
Carbohyd
Np Bind
• From 71
To 78
Descr GTP (BY SIMILARITY)
• From 117 To 121
Descr GTP (BY SIMILARITY)
Desd  GIP (BY SIMILARITY)
• From 248
To 251
Descr GTP (BY SIMILARITY)
Similar
Pir
• Sec Id S33467
Prim Id   S33467
• Sec Id S42582
Prim Id S42582
Mendel
MENDE MEDICAL
Prosite
Status 1
Sec Id GTP1_OBG
Prim Id PS00905
Gene 128UP OR GTP-BP
Prints
Sec Id GTP10BG
Prim Id PR00326
Flybase
Sec Id 128up
Prim Id FBgn0010339
Maizedb
Wormpep

	Mty	no	PRT
	Clas		STANDARD
	Id		12AH_CLOS4
	Seql	len	29
	Ac		
		Entry	
	Mod		
	•	Date	01-AUG-1991
			19
		Type	Created
		Date	01-AUG-1991
		Rel	
	i	Type	Last sequence update
			01-AUG-1991
			19 Last annotation update
	Des		12-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.176) (FRAGMENT)
	Spe		Clostridium sp. (strain C 48-50)
	Org		Good and in Sp. (Strain 6-46-50)
	•	Entry	Bacteria
			Firmicutes
		Entry	Bacillus/Clostridium group
	•	Entry	Clostridiaceae
		Entry	Clostridium
	Ref		
		Num	1
		Pos	SEQUENCE
		Comn	
		Db	MEDITOR .
		Autho	neid 91177018
		• E	ntry Braun M
		• E	ntry Luensdorf H
		• F	ntry Bueckmann A.F
	i	Cite	Eur. J. Blochem. 196:439-450(1991)
	Emb		
	Inte	rpro	
	Pfan		
		word	
	•	Entry	Oxidoreductase
		Entry	NADP
		tures	
,		Doma	in
		Bindir	
		Signa	
		Chain	
		Disulf	
		Non T	
		T	rom <mark>29</mark> po <mark>29</mark>
	i	Mod F	
		Confli	
		Carbo	
		Np Bi	nd
		Simila	r
	Pir		
			1 \$14099
			d <mark>S14099</mark>
	Men		
	Hssp	p	
	Gen		
	Prin		
	Flyb		

Maizedb Wormpep

. 1	Иtype	PRT
	Class	STANDARD
	d	12KD_FRAAN
	Seqlen	111
-	Ac Entry	
_	Mod Elling	
		01-0CT-1996
	Rel	34
		Created
	Data	01-0CT-1996
	Rel	34
	Type	Last sequence update
•	Rel	01-NOV-1997 35
		Last annotation update
Ī	Descr	AUXIN-REPRESSED 12.5 KDA PROTEIN
	Species	Fragaria ananassa (Strawberry)
(	Org	
•	Entry	Eukaryota
•	Entry	Viridiplantae
	Entry	Embryophyta
	Entry	Tracheophyta
	Entry	Spermatophyta
•	Entry	Magnoliophyta
•	Entry	eudicotyledons
•	Entry	Rosidae
•	Entry	eurosids I
•	Entry	Rosales
•	Entry	Rosaceae
	Entry	Fragaria
F	Ref	
•		1
	Pos	SEQUENCE FROM N.A
	Com	nent Entry   STRAIN=CV. OZARK BEAUTY
		INTRO TISSUE=FLOWER
	Db "	MEDLINE
		ineid 91329668
	Auth • I	or Entry Reddy A.S.N
		Entry Poovaiah B.W
	Cite	Plant Mol. Biol. 14:127-136(1990)
_	cite	PIBITE MOI. 14:127-130(1990)

Embl

Interpro Pfam Keyword

Sec Id CAA36676
Prim Id X52429
Status

Sec Id AAA73872
Prim Id L44142
Status

Features
Domain
• From 43
To <mark>57</mark>
Descr
• Entry
Binding
Signal
Chain
Disulfid
Non Ter
Mod Res
Conflict
Carbohyd
Np Bind
Similar
Pir
Mendel
Hssp
Prosite
Gene
Prints
Flybase
Maizedb
Wormpep

	log .
Mtype	
Id	JAMUSHU MYCSM
Segle	
Ac	
• E Mod	intry
• D	Date 01-NOV-1995
R	Rel 32
Т	Type Created
• D	Date 01-NOV-1995
R	Rel 32
Т	Type Last sequence update
• D	oate   01-NOV-1995
	Rel 32
	Type Last annotation update 12 KDA PROTEIN (FRAGMENT)
Descr	
Org	cs [mycooacterium sineginatis
• E	ntry Bacteria
• E	intry Firmicutes
	Actinobacteria Actinobacteria
• E	intry Actinobacteridae
• E	ntry Actinomycetales
	Entry Corynebacterineae
• E	Intry Mycobacteriaceae
• E	ntry Mycobacterium
Ref	
	olum 1 Pos SEQUENCE
	Comment
D	ob
	Medlineid Medlineid
<u>A</u>	Author Entry Pahl A
•	
•	
Embl	
Interp	
Pfam	
Keyw	
Featu	ores Domain
	zoniani Binding
S	ignal .
	Chain
	Disulfid Ion Ter
11	From 24
_	To 24
100	Mod Res
	Conflict Carbohyd
	lp Bind
S	Similar
Pir	
Mend	
Hssp Prosit	
Gene	
Prints	5
Flyba	
Maize	
Mtype	e PRT

Class	STANDARD
Id	12S1_ARATH
Seglen	472
Ac	
<ul> <li>Ent</li> </ul>	ry
Mod	
	le <mark>01-APR-</mark> 1990
Rel	
Тур	De Created Created
<ul> <li>Dat</li> </ul>	e 01-APR-1990
Rel	
Тур	Last sequence update
<ul> <li>Dat</li> </ul>	te 15-DEC-1998
Rel	
Тур	Last annotation update
Descr	12S SEED STORAGE PROTEIN PRECURSOR
Species	Arabidopsis thaliana (Mouse-ear cress)
Org	al Edwards
• Ent	ry Eukaryota
<ul> <li>Ent</li> </ul>	ry   Viridiplantae
. Ent	ry Embryophyta
<ul> <li>Ent</li> </ul>	ry   Tracheophyta
• Ent	ry   Spermatophyta
• Ent	ry Magnoliophyta
<ul> <li>Ent</li> </ul>	ry eudicotyledons
	ry Rosidae
<ul> <li>Ent</li> </ul>	ry eurosids II
• Ent	ry Brassicales
• Ent	ry Brassicaceae
<ul> <li>Ent</li> </ul>	ry Arabidopsis
Ref	
• Nur	
Pos	
· Cor	nment Entry
Db	
	dlineid
Aut	hor
•	Entry Pang P.P
	Entry Pruitt R.E
•	Entry Meyerowitz E.M
Cité	Plant Mol. Biol. 11:805-820(1988)
• Nur	
Pos	SEQUENCE OF 420-472 FROM N.A
	nment
- Dh	Entry
Db	dlineid
	hor
	Entry Raynal M
•	Entry Grellet F
•	Entry Laudie M
	Entry Moyor V
•	Entry Meyer Y
	Entry Meyer Y  Entry Cooke R

Embl
Sec Id AAA32777
Prim Id M37247
Status
• Sec Id CAA32493
Prim Id X14312
Status
• Sec Id CAA79005
Prim Id Z17590
Status St
Interpro
• Sec Id - Prim Id IPR000459
Pfam Pfam
· Status 1
Sec Id Seedstore_11s
Prim Id PF00190
Keyword
Entry   Seed storage protein
Entry Multigene family
• Entry Signal
Features
Domain
Binding
Signal From 1
From 1
Descr POTENTIAL
Chain
• From 25
To 282
Descr ACIDIC CHAIN (BY SIMILARITY)
• From 283
To 472
Descr BASIC CHAIN (BY SIMILARITY)  Disulfid
• From 112
To 289
Descr INTERCHAIN (ALPHA-BETA) (POTENTIAL)
Non Ter
Mod Res Conflict
Carbohyd
Np Bind
Similar
Pir
• Sec Id S08509 Prim Id S08509
Mendel
Hssp
Prosite
• Status 1
Sec Id 11S_SEED_STORAGE
Prim Id   PS00305   Gene   CRA1   CRA
Prints
Sec Id 11SGLOBULIN
Prim Id PR00439
Flybase Mainadh
Maizedb Wormpep
Mtype PRT
Class STANDARD Id 12S2_ARATH
Seqlen 455
AC
• Entry

Mod	
•	Date 01-APR-1990
	Rel 14
	Type Created
•	Date 01-APR-1990
	Rel 14
	Type Last sequence update
	Date 15-DEC-1998
	Rel 37
	Type Last annotation update
Des	
	cies Arabidopsis thaliana (Mouse-ear cress)
Org	
•	Entry Eukaryota
•	Entry Viridiplantae
•	Entry Embryophyta
•	Entry Tracheophyta
	Entry Spermatophyta
•	Entry   Magnoliophyta
	Entry eudicotyledons
•	Entry Rosidae
•	Entry eurosids II
	Entry Brassicales
•	Entry Brassicaceae
•	Entry Arabidopsis
Ref	
•	Num 1
	Pos SEQUENCE FROM N.A
	Comment  • Entry
	Db Db
	Medlineid
	Author
	• Entry Pang P.P
	Entry Pruitt R.E
	Entry Meyerowitz E.M
	Cite Plant Mol. Biol. 11:805-820(1988)
•	Num 2
	Pos SEQUENCE OF 240-360 FROM N.A
	Comment
	• Entry
	Db Medlineid
	Author
	Entry Raynal M
	• Entry Grellet F
	• Entry Laudie M

Entry Meyer YEntry Cooke R

• Entry Delseny M
Cite Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases

Embl
Sec Id
Prim Id M37248
Status
• Sec Id CAA32494
Prim Id X14313
Status
• Sec Id CAA79024 Prim Id Z17654
Status
States   Sta
• Sec Id •
Prim Id IPR000459
Pfam
- Status 1
Sec Id Seedstore_11s Prim Id PF00190
Feyword
Entry Seed storage protein
• Entry Multigene family
• Entry Signal
Features
Domain
Binding
Signal From 1
To 24
Descr POTENTIAL
Chain
• From 25
To 269
Descr ACIDIC CHAIN (BY SIMILARITY)
• From 270
To 455
Descr BASIC CHAIN (BY SIMILARITY)
Disulfid
• From 106
To 276  Descr INTERCHAIN (ALPHA-BETA) (POTENTIAL)
Non Ter
Mod Res
Conflict
Carbohyd
Np Bind
Similar
Pir           • Sec Id         S08510
Prim Id   508510
Mendel
Hssp
Prosite
• Status 1
Sec Id 115_SEED_STORAGE
Prim Id PS00305  Gene CRB
Prints
Sec Id 11SGLOBULIN
Prim Id PR00439
Flybase
Maizedb
Wormpep
Mtype PRT
Class STANDARD
Class STANDARD Id 1431_ENTHI
Class         STANDARD           Id         1431_ENTHI           Seqlen         239
Class STANDARD Id 1431_ENTHI

Mod
• Date 01-NOV-1995
Rel 32
Type Created
• <u>Date 01-NOV-1995</u>
Rel 32
Type Last sequence update
• Date 01-NOV-1997
Rel 35
Type Last annotation update
1ye (1-3-3 POTEIN 1 (14-3-3-1)
Species Entamosh histolytica
Org
Entry Eukaryota
Entry Entamoebidae
• Entry Entamoeba
Ref
• Num   1
Pos SEQUENCE FROM N.A
Comment
• Entry
Db
Medlineid
Author
Entry Samuelson J
• Entry Shen P
• Entry Meckler G
Entry Descoteaux S
• Entry Fu H
Entry Lohia A
Entry Conia A
Cite Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
Cite Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases Embl
Cite Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases  Embl  Sec Id AAA80185
Cite Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases  Embl  Sec Id AAA80185 Prim Id U13418
Cite Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases  Embl  Sec Id AAA80185 Prim Id U13418 Status
Cite   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
Cite   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
Cite         Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases           Embl         • Sec Id         AAA80185           Prim Id         U13418         Status           Interpro         • Sec Id         -           Prim Id         IPR000308         -
Cite   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
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Mtype PRT
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Id 1431\_LYCES
Seqlen 249

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		36 Last sequence update
•		<u>15-JUL-</u> 1998
		36 Last annotation update
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Org	1	
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•		
•	Entry	Tracheophyta
	Entry	Spermatophyta
•		Magnoliophyta
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•		euasterids I
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	• E	ntry TISSUE=LEAF
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	Medli	
	Autho	
		ntry Roberts M.R
		ntry Bowles D.J
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•	Sec I	1 -
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		d   1433_1   d   PS00796
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	1 433ZETA
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Flybase Maizedb	
Wormpep	
Mtype	PRI
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Ac	lee.
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Rel	33
Type	Last sequence update
Date	01-OCT-1996
Rel	34
	Last annotation update
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Entry	Magnoliophyta
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Entry	Poales
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Db	MEDLINE
Medli	neid 95148741
Autho	r
• E	ntry de Vetten N.C
• E	ntry Ferl R.J
Cite	Plant Physiol. 106:1593-1604(1994)
Embl	
	d AAB33304
	ld <u>\$77133</u>
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• Sec I	
Prim	d IPR000308
Pfam	
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Pir	
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Gene

TFT1

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Prim Id PS00797  Gene GRF1
Prints
Sec Id 1433ZETA
Prim Id PR00305 Flybase
Maizedb
Sec Id -
Prim Id 65832
Wormpep
Mtype PRT
Class STANDARD
Id         1431_SCHMA           Seqlen         252
Ac
• Entry
Mod - Date 15-JUL-1998
Rel 36
Type Created
• <u>Date</u> 15-JUL-1998
Rel 36
Type Last sequence update
• Date 15-JUL-1998
Rel 36
Type Last annotation update
Descr 14-3-3 PROTEIN HOMOLOG 1 Species Schistosoma mansoni (Blood fluke)
Org
Entry Eukaryota
Entry Metazoa
Entry Neodermata
Entry Trematoda
Entry Digenea
Entry Strigeidida
Entry Schistosomatoidea
• Entry Schistosomatidae
• Entry Schistosoma
- Emy peristosoma
• Num 1
Pos SEQUENCE FROM N.A
Comment  • Entry
Db MEDLINE
Medlineid 96123403
Author  • Entry Schechtman D
• Entry Ram D
Entry Torrah Hazdai D

Entry Arnon R

• Entry Schechter I
Cite Mol. Biochem. Parasitol. 73:275-278(1995)

Embl
• Sec Id   AAC46983
Prim Id U24281
Status Status
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· Sec Id ·
Prim Id IPR000308
Pfam
Status 1
Sec Id 14-3-3
Prim Id PF00244
Keyword
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• Status 1
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Prim Id PS00797
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Prim Id PR00305
Flybase
Maizedb
Wormpep
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Rel 32
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Rel 32
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Rel 35
Type Last annotation update
Descr 14-3-3 PROTEIN 2 (14-3-3-2)
Species Entamoeba histolytica

Org

Entry Entamoebidae

Entry Entamoeba

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•	Num	1		
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	Comme			
	• Enti			
	Db			
	Medline	id		
	Author			
	• Enti	y Samuelson J		
	• Enti	y Shen P		
	• Enti	y Meckler G		
	• Enti	y Descoteaux S		
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Org
Entry Eukaryota
Entry Viridiplantae
• Entry Embryophyta
Entry Tracheophyta
Entry   Spermatophyta
Entry Magnoliophyta
Entry eudicotyledons
Entry Asteridae
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Entry Bowles D.J
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• Sec Id
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Keyword
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Dec	Type	ast annotation update 4-3-3-LIKE PROTEIN GF14-12		
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Org		ca mays (waize)		
•		ukaryota		
•	Entry V	/iridiplantae		
•	Entry E	imbryophyta		
•		racheophyta		
•	Entry S	permatophyta		
		// Agnoliophyta		
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•	Entry L	iliopsida		
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KeywordEntryFeaturesPirSec Id

Sec Id JQ1680 Prim Id JQ1680

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Prim Id PS00796
• Status 1
Sec Id 1433_2 Prim Id PS00797
Gene GRF2
Prints
Sec Id 1433ZETA
Prim Id PR00305
Flybase
Maizedb
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Prim Id 65832 Wormpep
wormpep
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Id 1432_SCHMA
Seqlen 214
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Mod
Date 15-JUL-1998
Rel 36
Type Created
• Date 15-JUL-1998
Rel 36
Type Last sequence update
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Type Last annotation update
Descr. 14.3.3 PROTEIN HOMOLOG 2 (14.3.3.2) (FRACMENT)
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry Eukaryota
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry   Eukaryota  Entry   Metazoa
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry Eukaryota
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  • Entry Eukaryota  • Entry Metazoa  • Entry Platyhelminthes
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry Eukaryota  Entry Metazoa  Entry Platyhelminthes  Entry Neodermata
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry Eukaryota  Entry Platyhelminthes
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry   Eukaryota  Entry   Metazoa  Entry   Platyhelminthes  Entry   Neodermata  Entry   Trematoda
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry Eukaryota  Entry Metazoa  Entry Platyhelminthes  Entry Neodermata  Entry Trematoda  Entry Digenea
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry   Eukaryota  Entry   Metazoa  Entry   Platyhelminthes  Entry   Neodermata  Entry   Trematoda
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry Eukaryota  Entry Metazoa  Entry Platyhelminthes  Entry Neodermata  Entry Trematoda  Entry Digenea  Entry Strigeidida
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry   Eukaryota  Entry   Metazoa  Entry   Platyhelminthes  Entry   Neodermata  Entry   Trematoda  Entry   Digenea  Entry   Strigeidida  Entry   Schistosomatoidea
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry Eukaryota  Entry Metazoa  Entry Platyhelminthes  Entry Neodermata  Entry Trematoda  Entry Digenea  Entry Strigeidida
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke) Org  Entry   Eukaryota  Entry   Metazoa  Entry   Platyhelminthes  Entry   Neodermata  Entry   Trematoda  Entry   Digenea  Entry   Strigeidida  Entry   Schistosomatoidea  Entry   Schistosomatidae  Entry   Schistosoma
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  Entry   Eukaryota  Entry   Metazoa  Entry   Platyhelminthes  Entry   Neodermata  Entry   Trematoda  Entry   Digenea  Entry   Strigeidida  Entry   Schistosomatoidea  Entry   Schistosomatidae  Entry   Schistosomate
Descr 14-3-3 PROTEIN HOMOLOG 2 (14-3-3-2) (FRAGMENT)  Species Schistosoma mansoni (Blood fluke)  Org  • Entry Eukaryota  • Entry Metazoa  • Entry Platyhelminthes  • Entry Neodermata  • Entry Trematoda  • Entry Digenea  • Entry Strigeidida  • Entry Schistosomatoidea  • Entry Schistosomatidae  • Entry Schistosomatidae  • Entry Schistosoma  Ref  • Num 1
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Species Caenorhabditis elegans

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-	Entry E	ıkaryota
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Keyword Features Pir

Sec Id -Prim Id IPR000308

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Sec Id 14-3-3
Prim Id PF00244

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Status		
	<u>1 1433_2</u>	
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