

PF00105.18

Dm_FBpp0082036	187	- - - - - S G S Q I D S K Q N I E C V V C G D K	206
Tu_tetur04g01460	52	- - - - - N G Q S I E C V V C S D K	65
Dpte.g6159.t1	445	N R V N L H Q R N M A T M N S Q Q Q P Q G S T N C V T T V S A S S T T N N N Q I S I E C V V C G D K	494
Al_aculy03g10030	99	L D V D L - - - - - G S P Q G - - - - S Q S G G S Q T S I E C V V C G D K	126
Dm_FBpp0082036	207	S S G K H Y G Q F T C E G C K S F F F K R S V R R N L T Y S C R G S R N C P I D Q H H R N Q C C Q Y C R	256
Tu_tetur04g01460	66	S S G K H Y G Q F T C E G C K S F F F K R S V R R N L T Y T C R G S R N C P I D Q H H R N Q C C Q Y C R	115
Dpte.g6159.t1	495	S S G K H Y G Q F T C E G C K S F F F K R S V R R N L T Y S C R G N R N C P V D Q H H R N Q C C Q Y C R	544
Al_aculy03g10030	127	S S G K H Y G Q F T C E G C K S F F F K R S V R R N L T Y S C R A N K S C P I D Q H H R N Q C C H C R	176
Dm_FBpp0082036	257	L K K C L K M G M R R E - - - - -	268
Tu_tetur04g01460	116	L K K C L K M G M R R E - - - - -	127
Dpte.g6159.t1	545	L R K C L K M G M R R E V L S I I S S Q K K M S I E I L L S D E P F I K A R D R C R S V S S A N Q T	594
Al_aculy03g10030	177	L R K C L K M G M R R E - - - - -	188

DBD

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Dm_FBpp0082036	308	LSSISL	LLLR	RAE	-PYPT	SRYG	QCMQP	-	-	NNIMG	ITDNT	CELA	ARLL	LFS	SAV	353	
Tu_tetur04g01460	161	SQSFI	SLLLR	RAE	-TYPT	QT	IQNMHP	-	-	SNIMT	ITEG	INELA	ASIL	LFAA	L	206	
Dpte.g6159.t1	1045	LQGYV	SLL	QQ	AAES	TVRL	TQT	MQQL	HSTST	NGLLS	IT	ETMC	EM	LAAR	ILFAA	1094	
Al_aculy03g10030	207	LAA	-	-	-	-	AA	-	AAASA	Q	-	-	-	HP	-	240	
Dm_FBpp0082036	354	EWAKN	I	PFFPE	LQV	T	DQVALL	RL	VWSE	LFV	LNASQCS	MP	LHV	AP	LLAAAG	403	
Tu_tetur04g01460	207	DWARN	I	PFFPD	LQV	T	DQVALL	RL	VWSE	LFV	LNASQCS	MTVN	I	AP	LLAAQS	256	
Dpte.g6159.t1	1095	DWARK	I	PHFPD	LQVQ	DQV	SLLRM	VWSE	LF	I	LNASQCS	MP	MHT	AH	LLAAAG	1144	
Al_aculy03g10030	240	-	-	-	-	-	MQQN	PML	AQHP	AAAGMFAH	LSAMHP	ALRG	HPMAL	MA	AAA	279	
Dm_FBpp0082036	404	LHAS	-	PMAADR	V	AFMDH	IRIFQ	EQVEKLKA	-	-	-	-	LHVD	SAEYS	SCLKAI	447	
Tu_tetur04g01460	257	VHSST	P	FAADR	V	ITFMDN	IRIFQ	EQVEKLKS	-	-	-	-	LHVD	PAEYS	SCLKAI	301	
Dpte.g6159.t1	1145	LHAN	-	PMAADR	V	AFMDH	IRIFQ	DNLEKLKA	-	-	-	-	LQVD	AAEYS	SCLKAI	1188	
Al_aculy03g10030	280	LHQ	-	-	-	-	QQQ	QQQAR	Q	PQPNL	VQRD	PQPQPTQVP	I			311	
Dm_FBpp0082036	448	VLFT	TDACGL	SDV	-	-	-	-	-	-	-	-	THIE	-	-	SLQEK	469
Tu_tetur04g01460	302	VLFT	TDACGL	TDV	-	-	-	-	-	-	-	-	QKIE	-	-	AHQEA	323
Dpte.g6159.t1	1189	VLFT	TDACGL	QDG	-	-	-	-	-	-	-	-	GHIE	-	-	SLQEK	1210
Al_aculy03g10030	312	ANHAAAGN	GLRG	V	GDGASVGVNRSPPV	I	PASGQLDPQPT	HL	LQPP	SNSE	EQ					361	
Dm_FBpp0082036	470	SQCA	LEEYCR	TYPNQPT	IRFGKLLRLP	SLRTVS	-	-	-	-	-	-	SQVIE	QLFFV		513	
Tu_tetur04g01460	324	SQCA	LEEYCR	TYPNQPT	IRFGKLLRLP	SLRAIS	-	-	-	-	-	-	SQVIE	QLFFV		367	
Dpte.g6159.t1	1211	SQCA	LEEYCR	TYPNQPT	IRFGKLLRLP	SLRSVS	-	-	-	-	-	-	SHVIE	QLFFV		1254	
Al_aculy03g10030	362	QQAQHLANL	QQQLHHQ	-	-	-	-	-	-	LQLAA	IAAA	AQHNNQQQ	QQQQQ	QFHQ		403	
Dm_FBpp0082036	514	RL	-	-	-	-	-	-	VGK	APIET	LIRDM	LL	-	-	-	530	
Tu_tetur04g01460	368	RL	-	-	-	-	-	-	VGK	APIET	QLIRN	LLI	-	-	-	384	
Dpte.g6159.t1	1255	RL	-	-	-	-	-	-	VGK	APIET	LIRDM	LVSE	HFKLTKMTNYHTESHKD			1290	
Al_aculy03g10030	404	HLNHHQLN	MNMNMSLN	LNQANQ	EYQ	IND	LIN	-								434	

LBD