



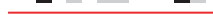






— PF00105.18

Dm_FBpp0074915	200	AVVPADSRPQTPEYIKSYPVMDTTVASSVKG	EPELN	IEFDGTTVLCRVCG	249	
Tu_tetur19g00650	23	-----	SSFKDSELK	IEFDGTTVLCRVCG	46	
Dpte.g6820.t1	82	-----	DRCKDLDLK	IEFDGTTVLCRVCG	105	
Al_aculy01g02260.1	41	-----	-----	IEFDGSAILCQVCG	55	
						
Dm_FBpp0074915	250	DKASGFHYGVHSCGCKGFFRRS	IQQKIQYRPCTKNQQCS	ILRINNRRCQ	299	
Tu_tetur19g00650	47	DASGFHYGVHSCGCKGFFRRS	IQQKIQYRPCTKNQQCS	ILRINNRRCQ	96	
Dpte.g6820.t1	106	DKASGFHYGVHSCGCKGFFRRS	IQQKIQYRPCTKNQQCS	ILRINNRRCQ	155	
Al_aculy01g02260.1	56	DKASGFHYGVHSCGCKGFFRRS	IQQKIQYRPSKNQQCP	IMRVNNRRCQ	105	
						
Dm_FBpp0074915	300	YCRLKKCI	AVGMSRD	-----	314	
Tu_tetur19g00650	97	YCRLKKCI	AVGMSRD	-----	111	
Dpte.g6820.t1	156	YCRLKKCI	AVGMSRDE	FTFLSLVLSQKEKSNI	IREKKT	205
Al_aculy01g02260.1	106	YCRLKKCI	AVGMSRD	-----	120	
						

DBD

— PF00104.30

Dm_FBpp0074915	388	YSMPTLLACPLNPAPELQS-----EQEFSORFAHVIIRGVIDFAGM	427
Tu_tetur19g00650	184	YARCPSTMACPLNPLPP-NGIENGPGEGILENFSERFSPAIRGVVEFAKR	232
Dpte.g6820.t1	599	YAQCQPQ-MTCLNPLPAQNQIDSNR---LMEDFSERFSPAIRGVVEFAKR	644
Al_aculy01g02260.1	184	-----HSLSGGGGGG-----	194
			
Dm_FBpp0074915	428	IPGFQLLTQDDKFTLLKAGLFDALFVRLICMFDSSINSIICLNGQVMRRD	477
Tu_tetur19g00650	233	IPGFAYLSQDDQVFTLLKAGVFEVLLVRLACMFDKTSNSMICLNGMVLKRE	282
Dpte.g6820.t1	645	IPGFSLLAQEDQVFTLLKAGVFEVLLVRLACMFDSTNSMICLNGLSLRD	694
Al_aculy01g02260.1	194	-AGGASVTASTQM-----ETTTDQMNQLQDNQTNDE	224
			
Dm_FBpp0074915	478	AIQ-----NGANA	485
Tu_tetur19g00650	283	SLH-----SQSSA	290
Dpte.g6820.t1	695	SLH-----SASNA	702
Al_aculy01g02260.1	225	NHHYHQHHHQEQQKLKSALMRHHQHQHQQQQQRERERELELELEEQNQ	274
			
Dm_FBpp0074915	486	RFLVDSTFNFAERMNSMNLTDAEIGLFCALVLIPTDRPGLRNLELIEKMY	535
Tu_tetur19g00650	291	RFLLDSMFGFAEMLNALNLTDHEIALFCALVLIPTDRPGLRNIDLIGKIN	340
Dpte.g6820.t1	703	RFLLDSMFEFAERLNSLRLTDNELGLFCALVVLIPTDRPGLRNIDLVQKIN	752
Al_aculy01g02260.1	275	R-----EHLNQLQLNDSLEALLCSSVVVATDQAGLKNAELVGKIS	314
			
Dm_FBpp0074915	536	SRLKGCQLQY--IVAQNRPDQ-----PE-----	555
Tu_tetur19g00650	341	RKLVDLLDK--LVTSNHSDN-----PG-----	360
Dpte.g6820.t1	753	KRLLEEILQK--AIATNHHQQNLSTTES---AVAAAAQAANQ-----	788
Al_aculy01g02260.1	315	EKLQSLNRRNAVNTDNTNNNNISSIQANQRQEVSNPAINLNQQQQRHQH	364
			
Dm_FBpp0074915	555	-----FLAKLLETMPDLRTLSTLHTEKLVVFRTEHKELLRQQMWS--	595
Tu_tetur19g00650	360	-----LFSSLVNKIPDLRTLNTLHSEKLLAYKMG-----	389
Dpte.g6820.t1	788	-----LFQELIRKIPDLRTLNALHSDKLGLGKSFGGLEQPQQSMNSA	830
Al_aculy01g02260.1	365	QPEQKDELLLAELMRKVPELR-----RERLIAALAEERDSILAAD----	403
			

LBD