

A

	10	20	30	40	50	60	70	80
TaPAPhy_a1	mwmwrgs111111aaavaaaAEPASTLTGSPRPVTVALREDRGHAVDLPDTDPVRORRATGWAPEQIAVALSAAPTSAW							
TaPAPhy_a2p-.....E.....P.....V.....							
TaPAPhy_b1p-.....E.....P.....V.....							
TaPAPhy_b2mp-.....p-a.v.....E.....P.....V.....							
	90	100	110	120	130	140	150	160
TaPAPhy_a1	VSWITGEFQMGGTVKPLDPTGTVGVSVRYGLAADS LVRQASGDALVYSQLYPFEGLQnytSGIHHVRLQGLEPATKYYYQ							
TaPAPhy_a2D.....A.....E.....T.....E.....G.....							
TaPAPhy_b1D.....A.....A.E.T.E.....I.L.....G.....							
TaPAPhy_b2D.....A.....E.T.....G.....							
	170	180	190	200	210	220	230	240
TaPAPhy_a1	CGDPALPGAMSAVHAFRTMPAVGPRSYPGRIAVVGDGLTYnttSTVDHMASNRPDVLLVGDVCYANMYLTngtGADCY							
TaPAPhy_a2I.....							
TaPAPhy_b1I.....D.....E.....Q.....L.....S.....L.....T.....							
TaPAPhy_b2S.I.....E.....Q.....L.....S.....L.....T.....							
	250	260	270	280	290	300	310	320
TaPAPhy_a1	SCAFGKSTPIHETYQPRWDYWGRYMEAVTSGTPMMVVEGNHEIEEQIGnktFAAYRSRFAPSTESGSFSPFYYSFDAGG							
TaPAPhy_a2S.A.....P.....S.....Q.....S.A.....M.E.....							
TaPAPhy_b1S.A.....P.....S.....Q.....S.A.....M.E.....							
TaPAPhy_b2S.A.....P.....S.....Q.....S.A.....M.E.....							
	330	340	350	360	370	380	390	400
TaPAPhy_a1	IHFLMLGAYADYGRSGEQYRWLEKDLAKVDRSVTPWLAVGWHAPWYTTYKAHYREVECMRVAMEELLHSHGLDIAFTGHV							
TaPAPhy_a2Y.....							
TaPAPhy_b1I.....A.....SK.....Y.....S.....A.....Y.Y.....V.....							
TaPAPhy_b2I.....A.....SK.....S.....A.....Y.Y.....V.....							
	410	420	430	440	450	460	470	480
TaPAPhy_a1	HAYERSNRVfnytlDPCGAVHISVGDGGNREKMATTHADEPGHCPDPRPKNAFIGGFASnftSGPAAGRFCWDROPDY							
TaPAPhy_a2D.....R.....E.MST.D.M.....F.....S.....							
TaPAPhy_b1D.....R.....E.MST.D.M.....F.....S.....							
TaPAPhy_b2D.....R.....E.MST.D.M.....F.....S.....							
	490	500	510	520	530	540	550	
TaPAPhy_a1	SAYRESSFGHGILEVKnethALWRWHRNQDHYG-SAGDEIYIVREPHRC LHKHnssRPAHGRSnttRESGG							
TaPAPhy_a2M.....t.....0.....							
TaPAPhy_b1Y.....K.....L.QGAV.....E.....L.SSIAAYF-----							
TaPAPhy_b2K.....L.QGAV.....E.....L.SSIAAYF-----							

