

AAD01930.1	HS_PhLP1	- - - - - EGISVNT GPKGVI NDWRRFKQLETEQREEQCR
AAA36210	HS_PHD	- - - - - EGQATH TGPKGVI NDWRKFK-LESQDSDSIPP
tre29008		ELKLPPASFDSGRST GVKGV IADARSYESARKT-KWRSRA
XP_384281.1	GZ	EIKLPPVSFDNGRAT GVKGV IADARNYEAAARKN-KWRHRV
XP_359577.2	MG	MGGLNSGAT TDKSESGGSADEHDD DADGEFLQQW
AAF26212.1	CP_BDM-1	PVQLPPASFDAGRAT GVKGV IADARSFEKAKKSSKWGEKM
XP_956705	NC	EIRLPPAGFDAGAAT GVKGV IADARAYENAKRSAKWKNRV
XP_657686.1	AN	SYTVPNTRFEAN- - TGPKGVI ADAQA FERARRT -NFRKSF
Q71A39	Dd_PhLP1	- - - QQEPKIKSGGNT GVKGV LSDYAEHREKQKQKYLQKKY