		10	20	30
HSAP: ENSP00000356555 (PHAR2)	LSTIGWRKI	KK TSDKFRET	SA VLERKIS	TRO SREELI
AMEL:GB19764-PA	FSALGWKRI	_		
DMEL: CG32264 - PD	LSALGWRRI			
AAED: AAEL012182-RA	FSAFGWRRI			
AGAM: ENSANGP00000028141	FSAFGWRRI			
TCAS:GLEAN 04309	EYKYGLEF			
TNIG: GSTENP00005041001	EADAGLELI			
GGAL: ENSGALP00000020495	EAADGLEVI			
MDOM: ENSMODP0000001615	EAVDGLEMI	_		
HSAP: ENSP00000266087	ESVEGLET	_		
MMUS: ENSMUSP00000001837 (Fbx07)	ETEDGLET	LY OSAGCSNI	SD ALIVLVE	
PRIOD: ENDRIODE COORDINATE (FEREIT)				
MENOP: EMSMOPPOVOUUULES? (FEMAU?)	40 	50 	60	70
HSAP: ENSP00000356555 (PHAR2	1	50 L A S S R P K Q T V F	GAEEQN PL EI	QC
	L	50 L A S S R P K Q T V F	GAEEQN PL EI	QC
HSAP: ENSP00000356555 (PHAR2	RRGL PDQ QKGL PVII	50 		QC
HSAP: ENSP00000356555 (PHAR2 AMEL: GE19764 - PA	RRGL PDQ QKGL PVII	50 	PGAEEQNPLEIC	Q Q C
HSAP: ENSP00000356555 (PHAR2 AMEL: GB19764 - PA DMEL: CG32264 - PD	R R G L	50 	C	D Q C I I I I I I I I I I I I I I I I I I
HSAP: ENSP00000356555 (PHAR2 AMEL: GB19764 - PA DMEL: CG32264 - PD AAED: AAEL:012182 - RA AGAM: ENSANGP00000028141 TCAS: GLEAN_04309	R R G L P D Q Q R G L P V I I Q K G M P E S Q K G L P E S E M N L P E A	50 A S R P K Q T V E R T C V T F L L E E P N G S L L G G V E P N S S V L G G T A P G A V L P G G G G		D Q C S K I I P L A S G S Q S I R I
HSAP: ENSP00000356555 (PHAR2 AMEL: GB19764 - PA DMEL: CG32264 - PD AAED: AAEL012182 - RA AGAM: ENSANGP00000028141 TCAS: GLERN_04309 TNIG: GSTENP00005041001	R R G L P D Q Q R G L P V I I Q K G M P E S Q K G L P E S E M N L P E A R P Q G M P A G G	50 A S S R P K Q T V F R T C V T F L L E F P N G S L L G G V F P G G G T A P C G G V F C W S V R S F K V V A V S L R V F K	P G A E E Q N P L E I E N S L Q Y P R I S S H S Q S A P E P P I G Q A L A S G M G G G S G A L A S G D S V A P P E I L I E D Q V A Y P E L L I	D Q C S K I L L S G S Q S L R I L L L L L L L L L L L L L L L L L
HSAP: ENSP00000356555 (PHAR2 AMEL: GB19764 - PA DMEL: CG32264 - PD AAED: AAEL012182 - RA AGAM: ENSANGP00000028141 TCAS: GLEAN_04309 TNIG: GSTENP00005041001 GGAL: ENSGALP00000020495	R R G L P D Q Q R G L P V I I Q K G M P E S I Q K G L P E S I Q K G L P E S I Q K G L P E S I Q K G L P E A I P Q G M P A G I P Q G M P A G I P Q G M P E K I	50 A S S R P K Q T V F R T C V T F L L E F R R R R R R R R R R R R R R R R R R		0 Q C S K I L S G S C S C S C S C R I R I R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R I L R V L R R I L R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V L R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R R V R V R R V R V R R V R R V R V R R V R V R V R R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V R V
HSAP: ENSP00000356555 (PHAR2 AMEL: GB19764-PA DMEL: CG32264-PD AAED: AAEL012182-RA AGAM: ENSANGP00000028141 TCAS: GLEAN_04309 TNIG: GSTENP00005041001 GGAL: ENSGALP00000020495 MDOM: ENSMODP00000001615	R R G L P D Q I Q K G L P V I Q K G M P E S Q K G L P E S Q K G L P E S Q K G L P E S Q K G L P E S Q G M P A G Q G M P A G Q G M P E K Q D G M P E K Q D L G M P E N Q G M P E K Q D L G M P E N Q G M P E K Q D L G M P E N Q G M P E K Q D L G M P E N Q G M P E K Q D L G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q G M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M P E N Q M	50		C C C C C C C C C C C C C C C C C C C
HSAP: ENSP00000356555 (PHAR2 AMEL: GB19764 - PA DMEL: CG32264 - PD AAED: AAEL012182 - RA AGAM: ENSANGP00000028141 TCAS: GLEAN_04309 TNIG: GSTENP00005041001 GGAL: ENSGALP00000020495	R R G L P D Q Q Q K G L P V I I Q K G M P E S Q K G L P E S Q K G L P E S Q K G L P E S Q K G L P E S Q K G L P E S Q K G L P E S Q K G L P E S Q K G L P E S Q K G L P E S Q G M P A G Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q G M P E K Q Q Q G M P E K Q Q Q G M P E K Q Q Q G M P E K Q Q Q M P E K Q Q Q Q M P E K Q Q Q Q M P E K Q Q Q Q M P E K Q Q Q M P E K Q Q Q Q M P E K Q Q Q Q Q M P E K Q Q Q Q Q Q Q Q Q Q Q M P E K Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	50 A S S R P K Q T V F R T C V T F L L E E P N G S L L G G V F P N S S V L G G T A P G A V L P G G G G V T C M S V R S F K V V A V S L R V F K V T C V P L R L F K V T C V P L R L F K		D Q C C C C C C C C C C C C C C C C C C

Additional data file 7. Alignment of Fbox7 proteins (below the black line) and Phosphatase and actin regulators PHAR2 (above the black line). Tribolium Glean_04309 is more similar to vertebrate Fbox7 proteins than to insect proteins.