

sp Q5R949 ACM1_PONAB	-----	MNTSAPPAVSPN--ITVLA	17
sp P11229 ACM1_HUMAN	-----	MNTSAPPAVSPN--ITVLA	17
sp Q9N2A3 ACM3_GORGO	-----	MTLHNNSTTSPLFPPNISSSWIHSPSDAGLPPGTDTHFGSYNVSRAGNFSSPDGTDDPL	60
	*****	*****	
sp Q5R949 ACM1_PONAB	PGKGPWQVAFIGITGLLSLATVTGNLLVLISFKVNTELKTVNNYFLLSACADLIIGTF	77	
sp P11229 ACM1_HUMAN	PGKGPWQVAFIGITGLLSLATVTGNLLVLISFKVNTELKTVNNYFLLSACADLIIGTF	77	
sp Q9N2A3 ACM3_GORGO	GGHTVWQVVFIAFLTGILALVTTIIGNILVIVSFVKVNQQLKTVNNYFLLSACADLIIGVI	120	
	*****	*****	
sp Q5R949 ACM1_PONAB	SMNLYYTYLLMGHWA GLTACDLWLA LDYVASNASVMNLL LISFD RYFSVTRPLSYRAKR	137	
sp P11229 ACM1_HUMAN	SMNLYYTYLLMGHWA GLTACDLWLA LDYVASNASVMNLL LISFD RYFSVTRPLSYRAKR	137	
sp Q9N2A3 ACM3_GORGO	SMNLFTTYIIMRN WALGNLACDLWLA LDYVASNASVMNLL VISFD RYFSITRPLTYRAKR	188	
	*****	*****	
sp Q5R949 ACM1_PONAB	TPRRA LMI GLAW LVS FVL WAP AII LF WQY LV GERT V LAG CYI QFL SQPI IT FGTA MAAF	197	
sp P11229 ACM1_HUMAN	TPRRA LMI GLAW LVS FVL WAP AII LF WQY LV GERT V LAG CYI QFL SQPI IT FGTA MAAF	197	
sp Q9N2A3 ACM3_GORGO	TTKRA GVM IGLA NVI FVL WAP AII LF WQY FVG KRT VPP GEC FI QFL SEPT IT FGTA AAAF	248	
	*****	*****	
sp Q5R949 ACM1_PONAB	YLPV TVM C LY WRI YRE TE S R A E LA A L A Q G S E T P G K G G G S	248	
sp P11229 ACM1_HUMAN	YLPV TVM C LY WRI YRE TE S R A E LA A L A Q G S E T P G K G G G S	248	
sp Q9N2A3 ACM3_GORGO	YMPV TIM T I LY WRI YKE TE K R T K E L A G L Q A S G T E A E T E N F V H P T G S S R C S S Y E L Q Q S M	300	
	*****	*****	
sp Q5R949 ACM1_PONAB	EGSPG TPP GRC CCR CRA P R L Q A Y S W K E E E E D	293	
sp P11229 ACM1_HUMAN	EGSPG TPP GRC CCR CRA P R L Q A Y S W K E E E D	293	
sp Q9N2A3 ACM3_GORGO	KRSNRR KYGR CHF ----- WFT TKS WKP S EQ MDQ DH SS SD W NN N D A A A L E N S A S D E	354	
	*****	*****	
sp Q5R949 ACM1_PONAB	E EP G SE V I K M P ----- ----- ----- ----- ED I G S E T R A I Y S I V L K L P G H S T I L N S T K L P S S D N L Q V P E E E E L G M V D L E R K A D K L Q A Q K S V	322	
sp P11229 ACM1_HUMAN	E EP G SE V I K M P ----- ----- ----- ----- ED I G S E T R A I Y S I V L K L P G H S T I L N S T K L P S S D N L Q V P E E E E L G M V D L E R K A D K L Q A Q K S V	322	
sp Q9N2A3 ACM3_GORGO	414		
	*****	*****	
sp Q5R949 ACM1_PONAB	----- ----- ----- ----- DDGGS FPK S SKL P I Q L E S A V D T A K T S D V N S V G K S T A T L P L S F K E A T L A K R F A L K T R S Q	348	
sp P11229 ACM1_HUMAN	----- ----- ----- ----- DDGGS FPK S SKL P I Q L E S A V D T A K T S D V N S V G K S T A T L P L S F K E A T L A K R F A L K T R S Q	348	
sp Q9N2A3 ACM3_GORGO	474		
	*****	*****	
sp Q5R949 ACM1_PONAB	LAKRK TFS L V K E K K A A R T L S A I L A F I L T W T P Y N I M V L V S T F C K D C V P E T L W E L G W L C Y	488	
sp P11229 ACM1_HUMAN	LAKRK TFS L V K E K K A A R T L S A I L A F I L T W T P Y N I M V L V S T F C K D C V P E T L W E L G W L C Y	488	
sp Q9N2A3 ACM3_GORGO	ITK R K R M S L V K E K K A A Q T L S A I L A F I I T W T P Y N I M V L V N T F C D S C I P K T F H N L G W L C Y	534	
	*****	*****	
sp Q5R949 ACM1_PONAB	VNST INPM C Y A L C N K A F R D T F R L L L C R W D K R R W R K I P K R P G ----- ----- INST VP V C Y A L C N K T F R T T F K M L L C Q C G K K R R Q Q Y Q Q R Q S V I F H K R A P E Q A L	468	
sp P11229 ACM1_HUMAN	VNST INPM C Y A L C N K A F R D T F R L L L C R W D K R R W R K I P K R P G ----- ----- INST VP V C Y A L C N K T F R T T F K M L L C Q C G K K R R Q Q Y Q Q R Q S V I F H K R A P E Q A L	468	
sp Q9N2A3 ACM3_GORGO	598		

Alineamiento 1

Alineamiento 2