

K G F G G S D M R T T K V Y K L V I H K  
 K L G D I V E I A H P N D E Y S P L L L  
 Q V K S L K<sup>m</sup> E D L Q K E T I S V D Q T V  
 T Q V F R L R P Y Q D V Y V N V V D P K  
 D V T L D L V [E] L T F K D Q Y I G [R] G D  
 M [W] R L K K S L V S T C A Y I T Q K V E  
 F A G I R A Q A G E L W V K<sup>m</sup> N E K V M C  
 [G] Y I S E D [T] R V V F [R] [S] T S A M V Y I  
 F I [Q] M S C [E] M [W] D F D I Y [G] D L Y F E  
 K A V N G F L A D L F T K [W] K E K N<sup>g</sup> C S  
 H E V T V V L F S R T F Y D A K S V D E  
 F P E I N R A S I R Q D H K G R F Y E [D]  
 F Y K V V V Q N E R R E E W T S L L V T  
 I K K L F I Q Y P V L V R L E Q A E G F  
 P Q G D N<sup>g</sup> S T S A Q G [N] Y [L] E A I [N<sup>g</sup>] L S  
 F N V F D K H Y I N R N F D R T G Q M S  
 V V I T P [G] V G V [F] E [V] D R L L M I L [T]  
 K Q R M I D N G I G V [D] L R V C M G E Q [P]  
 [L] [H] A V [P] [L] F K L H N<sup>g</sup> R S A P R D S R L  
 G D D Y<sup>s</sup> N I P H W I N H S F Y T S K S Q  
 L F C N S F T P R I K L A G K K P A S E  
 K A K N G R D T S L G S P K E S E N A L  
 P I Q V D Y<sup>s</sup> D A Y<sup>s</sup> D A Q V F R L P G P S  
 R A Q C L T T C R S V R E R E S H S R K  
 S A S S C D V S S S P S L P S R T L P T  
 E E V R S Q A S D S S L G K S A N I L  
 M I P H P H L H Q Y E V S S S L G Y T S  
 T R D V L E N M M E P P Q R D S S A P G  
 R F H V G S\* A E S\* M L H V R P G G Y T P  
 Q R A L I N P F A P S R M P M K L T S N  
 R R R W M H T F P V G P S G E A I Q I H  
 H Q T R Q N M A E L Q G S G Q R D P T H  
 S S A E L L E L A Y H E A A G R H S N S  
 R Q P G D G M S F L N<sup>g</sup> F S G T E E L S V  
 G L L S N S G A G M N P R T Q N K D S L  
 E D S V S T S P D P I L T L S A P P V V  
 P G F C C T V G V D W K S L T T P A C L  
 P L T T D Y F P D R Q G L Q N D Y T E G  
 C Y D L L P E A D I D R R D E D G V Q M  
 T A Q Q V F E E F I C Q R L M Q G Y Q I  
 I V Q P K T Q K P N P A V P P P L S S S  
 P L Y S R G L V S R N R P E E E D Q Y W  
 L S M G R T F H K V T L K D K M I T V T  
 R Y L P K Y P Y E S A Q I H Y T Y S L C  
 P S H S D S E F V S C W V E F S H E R L  
 E E Y K W N Y L D Q Y I C S A G S E D F  
 S L I E S L K F W R T R F L L L P A C V  
 T A T K R I T E G E A H C D I Y G D R P  
 R A D E R D E W Q L L D G M F V R F V E G L  
 N R I R R S D \ R M M R K G T A M K  
 G L Q M T G P I S T H S L E S T A P P V  
 G K K G T S A L S A L L E M E A S Q K C  
 L G E Q Q A A V H G G K S S A Q S A E S  
 S S V A M T P T Y M D S P R K D G A F F  
 M E F V R S P R T A S S A F Y P Q V S V  
 D Q T A T P M L D G T S L G I C T G Q S  
 M D R G N S Q T F G N S Q N I G E Q G Y  
 S S T N<sup>g</sup> S S D S S Q Q L V A S S L T S  
 S S T L T E I L E A M K H P S T G V Q L  
 L S E Q K G L S P Y C F I S A E V V H [W]  
 L V N H V E G I Q T Q A M A I D I M O K  
 M L E E Q L I T H A S G E A W R T F I Y  
 G F Y F Y K I V T D K E P D R V A M Q Q  
 P A T T W H T A G V D D F A S F Q R K W  
 F E V A F V A E E L V H S E I P A F L L  
 P W L P S R P A S Y A S R H S S F S R S  
 F G G R S Q A A A L L A A T V P E Q R T  
 V T L D V D V N N R T D R L E W C S C Y  
 Y H G N<sup>g</sup> F S L N A A F E I K L H [W] M A V  
 T A A V L F E M V Q G W H R K A T S C G  
 F L L V P V L E G P F A L P S Y L Y G D  
 [P] L R A Q L F I P L N<sup>g</sup> I S C L L K E G S  
 E H L F D S F E P E T Y W D R M H L F Q  
 E A I A H R F G F V Q D K Y S A S A F N  
 F P A E N K P Q Y I H V T G T V F L Q L  
 P Y\* S K R K F S G Q Q R R R R \ N<sup>g</sup> S T S S  
 T N Q N M F C E E R V G Y N W A Y N T M  
 L T K T W R S S A T G D E K F A D R L L  
 K D F T D F C I N R D N R L V T F W T S  
 C L E K M H A S A P

**Key**

DUF3608 Domain

**DEP Domain**

[ ] = Highly conserved residue (through fungi)

Predictions:

**Alpha Helix**

**Beta Sheet**

S\* or Y\* = phosphorylation site

N<sup>g</sup> = N-glycosylation site

Y<sup>s</sup> = Tyrosine sulfation site

K<sup>m</sup> = Sumoylation site

\ / = Propeptide cleavage site