



TATTAGACTATGAACAGCTCAGAAGAGAAAATGAAGACTTGAAATTGAAATTTAAAAGAAAAAATGAGTT  
 AGAGGAATTTGAGCTTCTAGAACAAAAAGAAGAAAGAGATCAAGAGATGCAACTAATGCATGAAGTTTCC  
 AACTTAAAGAATTTAATTAACACGCAGAGAATATAATCAAGACCTTGAGAATGACCTAAGTTCAAAG  
 TGAAGCTTCTTAAAGAAAAAGAGGAGCAGATTAAGAACCTGCAGGAATACATAGATGCCCAGAAGTCAGA  
 AAAGATGAAGATAGACCTGTCATACACATCGGACGCCACTGAAGACCTGAAACAGGCGATGCGCACCCCTG  
 TCTGATTTGGACACAGTGGCCCTTGACGCTAAGAAAAGAGTCAGCCTTCTTGAAGTGAAGTCTGGAGC  
 TGAAGGAGAAAAATTAATGAACTTTCGGATTCCCGTAAGCAAATGGAAAGTGACATTCAGATGTATCAACG  
 CCAACTGGAAGCAAAAAAGAAAAATGCAAACTGATCTGGATAAGGAATTACAGTTGGCTTTTCAAGAAATA  
 TCAAAACTCAGCGCCCTGGTAGATGGCAAAGGTTTACTGTCTAATTTGGAATTGGAGAAAAGGATTACTG  
 ATCTCCAAAAAGAACTAAATAAAGAAGCTGAAGAAAAACAACTTTGCAAGAAGAAGTTAACTTGTGTGTC  
 GGAGTTGAAATCTTTACCGTCTGAGGTGGAAACGCTGAGGAGAGAGCTGTATGAGAAATCTGAAGAGCTC  
 CATATAATAACCCACAGAAAGAGAGAACTGTTTTCTGAAATGGCTATAAAGACAGTAGGATTCAAGGTT  
 TACTTGAGGAAATGGAAACACTAGAGATGACCTTGCCACTTCCCAGCTGAGTCGGAGGGGCAGTGATGG  
 AGAATGGCAAGCCCTGGAAAGCCTGCACGCAGAGCTGGAGCACAGACACGCGGGGGTCTGGAGGAGAGA  
 GAGAGGCTGAAGCAGGAGATTGGGGCTCTCTCAAAGAAGCAGAAAGCCTGGCTTTCAGTTTGGATTCCG  
 TGAAGGCCGAGCTTTCTACAAGACTCAAGAGCTTGAGCAGAAAAACAGTTGAGGGTCAAGAAAGGCTAAA  
 TAAATGGAGGCGCTGAGAGAAGAGTTAGAAAAGCAGAGACTCCAGCTGCAGTCTGTAGAGAAGGAGAAA  
 GTCCTGCTCACTGAGAAGCTGCAGCAAGCCTTGAAGGAAGTAAAAGCCTTAACCCAGAAAAAGAAAAACC  
 TGAAGCAGCTCCAGGAGAGCCTGCAAACTGAGAGAGACCAACTCAGAAGTGACATTCAGGACACTGTGAA  
 CATGAACATAGATACTCAAGAGCAGTTACTAAATGCTCTGGAGTCTCTGAAACAACCAAGAAACAATT  
 AACATGCTGAAAAATGAAAGCTGCTGAGGAACTATCCGATAATTTGCATGTAAAGGACAGGGGAGGAGCTA  
 GAGATGAAGCTCAGCAAAAGATGGATGGCATAGATGAACAGAATGAGAGTGCCACACATTTGCTTGGTGG  
 TGTAAGGACAATGAGGTAACTGAGGAACAGAGGAAAAATCGACTCTAATGCAGGAGAAATAGCCGACTC  
 CAACAGACACTGGAAGTGTAGAGCAGAAAAGGAACTGAAGATGGAGCTAAAGGAAAAATATCGAAA  
 TGAGTATTGAAAACAGGAAGAGTTAAGAATCTTAGAGATGAACTGAAAAGACAACAAGAGGTAGCTGC  
 ACAGGAAAAGGATCATGCCACCGAGAAGACCCAGGAGCTCTCCAGGACGCAGGAAAGATTGGCAAAAAACA  
 GAAGAGAAGTTAGAGGAAAAGAACCAGAACTCCAAGAGACACAGCAGCAACTTCTTAGTACACAAGAAG  
 CTATGAGTAAGCTGCAGGCAAAGGTGATTGACATGGAAAGCTTACAGAATGAATTCAGGAACCAAGGATT  
 GGCATTGGAGCGTGTGGAGACAGAGAACTGGAGTTAGCTCAGAGACTTCATGAAAGTTATGAGGAGGTG  
 AAATCTATAACCAAGAAAGAAATGATCTAAAGGAATTGCAGGAGTCATTTGAAATAGAGAAGAAGCAAC  
 TTAAGAATATGCAAGGAAATAGAAGCCGCGGGCCTACAAACAAAAGAAGAACTAAACATTGCCACGC  
 GAATCTAAAAGAGTACCAGGAAATCATCACAGAGCTAAGAGGAAGCATTCTGAAAACGAAAGCACAAGGA  
 GCAAGCACCCAGGACACGGCAAAAAGCGCCCTGAGCTACAAGGAGAGGTTCCAGAGCAAGAGCTGCTTC  
 CTGTTGTCAAAGAAGCCAGGCACAGTGCAGAAAAAGTGAACGGACTGGAGCCAGTGGGAGCACATTTCCAG  
 AACAGTGCCTCCATGACAATGGAGGCGATAGAAAATAGAAAACCTCAGGCTGACCAAGAACTTGAAGAA  
 AGTCAGATGGAGATCAGCTGTCTACTAGAGAGAGAGAAGACCTGAGAAGGACACAGGAAACACTTCAGG  
 TCGAATGTACCCAGCTGAAAGAAGATGCCAGAAGAACTTTGGCTAATCATCTAGAACTGAAGAGGAACT  
 TAACCTTGCTCGTTGTTGCCGTAAGAGCAGGAGAACAAGATTGACACCCTAATAACGAGCCTCTCGCAG  
 AGGGAACCTGAGCTGTCCAGTGTGCGAGGACAAGTACTGCTGACTACTGCTGAACTGGAGAGAAAGGTTT  
 AAGAACTCTGTGAGAAACAGGAAGAACTTACTAGGAAAAGAACTAGCGAGGCTCAAGGGAAGATGAGTGA  
 ACTAGAGCAACTCAGGGAGCTGTGCTTGGCCAGGCTCGGCACTGCAGAACGCAGAGAGTGACAGGCTG  
 CGGCTGAATACACAAGTGAAGAAAAGTCAAGAGGAAATGAAAACCTAAGGGAGGAAAGAGAAGAGCTGA  
 GAAGAATGCAAGAGGCTTTCACGTGGAAGTGTGAGCAGCAGAAAAGAAAGCATGAAGGAAATCAGCTCAAA  
 ACTCCAAGAACTACAGAACAAGAGTATGAATGTCTTGAATGAAGACTATTAATGAGACTCAAGGAAGC  
 AGATGTGAAATGGACCACTTGAACAGCAGCTGGAGGCCAGAAAGTCAACTCTGGAAAAGGTGGAGATGG  
 AGAATGTAACCTTGACTCAAAGACTTCATGAGACCCTTGAGGAAATGAGATCTGTAGCAAAAAGAAAGAGA  
 TGAGCTTTGGAGCATGGAGGAGCGCTCACAGTAGAGAGAGACCAACTGAAGAAGAGCCTTGAAGAAACA  
 GTAACATAAGGTATGAAAAAGAGGAAGAGCTAAGAGTTGCGCATGTGCATCTGGAAGAGCACCAGGAAA  
 CTATCAACAAGCTCAGAAAGATGGTGTCTGACTACACAGATGAAATATCACATACTCAAGGGGACCTAAA  
 GCACACAAATGCCGTTGTAGAAGCTCAGAACCAAGATCTCCGGGAAAAAGAACATCAACTTTCTCAAGTA  
 AAAGCTGATCTCAGAGAAACCGTGGATCAAATGGAGCAACTGAAGAAGAAGCTCGAAGCCAGAGTTCTGA  
 CTCTAGAAAGCAGAGAAATAGAGAAGTTAGAATTGACTCAGCAACTTAAACGAAAACCTTAAAAAATAAC

ACTTGTCTACTAAGGAAAATGATAGCCTAAAAATTATGGATGAAGCCCTCAGGGAAGAACGAGACCAGCTA  
CGGAAAAGTCTTCAGCAAACAGAGGCAAGGGATCTGAAAATCAAGAGAACTAAGAATTGCTCACATGA  
ATCTAAAAGAGCACCAGAACTATTGACCGACTCATGGAGACTATGCTGAGAAGACAGAGGAAAATATC  
AAATATGAAAATGGAGTTAGAAAATGTAACATGAAATTAACAAGAAAAGTTCAAGAACTTAAGACAAGT  
GAGCGTCAACGTGTTAAGTTAAAAGCAGATGCCAGTGAAGCCAAGAAGGAGCTCAAGGAGCAGGGCTTAA  
CTCTGAGTAAGATAGAGATGGAGAACTTAAATCTCGCTCAGAAGATTCATGAGAACCTTGAAGAAAATGAA  
ATCTGTAAAGAAAAGAAAGAGATGATCTAAAGAACTTGAGGAGATACTCAGAATGGAGAGAGACCAGCTC  
AAGGACAACCTGAGAGAAGCCATGCTTAAAGGCCACCAGAACCATGAAGAGACAATGAAATGTGGAAAGG  
GGTACTGTGTGCTGGAGAATACTGTACAGGAAGACTTCGAGAAAAGTGCTTCAGGATAGAAAACTCCT  
GAAAAGATACTCAGAAATGGCTAATGATTATGAGTGCTTGAATAAAGTCTCTCTTGACTTGGAGAGAGAA  
ACTAAAACCCAAAAGAGCTGTGAGTTACTGTAAGAACAAGCTCTCACTTCCGCACACACAGACCAAAG  
AGATGGAAAAGCTTCTGACTGCAAACCAGAGATGTTCCCTGGAGTTCACAGAGCCCTCAAGAGACTTAA  
GTACGTGTTAAGCTCCATTGCGAGGATAAAGGAAGAGCAGCATGAGTCCATCAATAAACGTGAAATGGCT  
TTTATTCAGGAAGTGGAAAAGCAGAATGAACTGCAGATTCAAATCCAGAGCCTTTCACAGACTTACCGTA  
TTCCAGCCAGAGACTTACAGATCAAAGTGCAGGAGATGGACCTCCATATTGAGGAAAATGCTCAAAGA  
TTTTTCAGAAAATGATTTCTCACCATAAAAACTGAAAGTCCAACAAGTATTAATAATAGAAAAGAAATA  
ACTGAGTTTTTGGAAAATGGCTAAATACTCTTTTTGATACAGAAAATCTTAAGAGCACCATCCAGAAAAG  
AAAACAAAAGCATTGGGCTCGTGAATAACTTCTATCACAGCAGAACTACTGCCATGATAAATGAATCAAC  
GGAGTTTGAGGAAAGAAGTGCTACCAGATCCAAAGACTTGGATCAGTACCTGAAGTCACTGAAAAGAAACA  
ACTGAGCAACTGTCTGAAGTCTACCAGACACTGACCGCTCCCAGTCTGTTGTGCATCTCCATCTACCG  
TGCAGCCTTCCACACGGGACAGTGAGCGTCTCAGGCTGCATCAGGAGCTGAACAACCTGACCTCAAAGAA  
CAAAATTGCTTTAGGAGCTGTCCCTATAAAGAAGAAAATGAGGATCTCAAAATGCAGCTGGTGAAGAGT  
GACCTAGAGAAGAAGGCGACCGCCAAGGAATTCGATAAGAAAATCTCTCTCTAAAAGCCACTGTTGAAC  
ATCAAGAAGAAAATGATAAGGCTACTGAGAGAAAATCTTAGAGGACATCAACAGGCCCAGGATACCTCAAT  
GATCTCAGAACAAGACTCTCAGCTTCTGAGTAAACCTCTAACCTGTGGAGGTGGCAGTGGAAATGTACAA  
AGCACAAAAGCTCTTATTTTAAAAGTGAATATAAAAAGGATGGGAAGTGAGATTTCTAAGTTAAAGCAGC  
AAAATGAGCAGCTAAGAAAGCAAATAATCAACTATTAAGTGATAACTCTCAACTCTCCAATGAGGTTAA  
AACCTGGGAGGAAAGAACTCTTAAAAGAGACAGTTACAGAGAAACAACCTTGTGAGAATTTCTCAAAGTCT  
CCTAAAGTGACTCGACAGATTCTAAAAGGAGACAGAACACAACCTTCTCAGTGCAGGGCACAAAATCTCC  
AGGATCTGTGCCAAAAGATTCCCAAAATCATGGTTTTTGTATAACCGGTCAAAGTCTCTTCCAGCACC  
TCACCCGATCCGCTATTTTGACAACTCCAGTCTAGGGCTGTGCCAGAACCAGATGACGTAGAGAATGTG  
GAGCCTAAGACAGACCTCTGCCAAGCCTCTTGGAAAAGATGTGTCCAGTGAAGACGCAG

ACGCGTACGCGGCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

Protein Sequence: >MR219176 representing NM\_173762  
 Red=Cloning site Green=Tags(s)

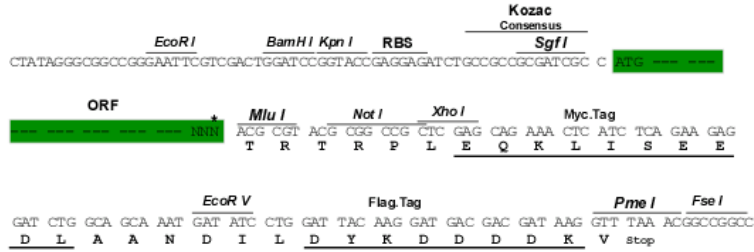
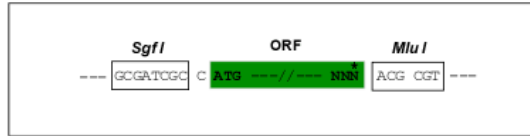
M A E E A S V A V C V R V R P L N S R E E E L G E A T H I Y W K T D K N A I Y Q S D G G K S F Q F D R V F D S N E T T K N V Y E E I A V P I  
 I S S A I Q G Y N G T I F A Y G Q T A S G K T H T M M G S E D C L G V I P R A I H D I F Q R I K K F P E R E F L L R V S Y M E I Y N E T I T  
 D L L C N A Q K M K P L I I R E D T N R T V V Y S D L T E E V V Y T A E M A L K W L A T G E K N R H Y G I T K M N Q R S S R S H T I F R M I  
 L E S R E K A E P S N C D G S V K V S H L N L V D L A G S E R A A Q T G A E G V R L K E G C F I N R N L F I L G Q V I K K L S D G Q V G G F  
 I N Y R D S K L T R I L Q N S L G G N A K T R I I C T I T P A S L D E T L T L Q F A S T A K Y M K N T P Y V N E V S N D E A L L K R Y R R  
 E I A D L R K Q L E E V N T K T R A Q E M E K D Q L A Q L L D E K D L L Q K V Q D E K I N N L K R M L V T S S S I A L Q Q E L E I K R K R R  
 V T W C Y G K M K D S N Y E K E F K V P T S I T T R K R K T S V T S L R E N S L M K F G E S A A S S E F E M L N N T L E S L A E V E W S S A  
 T T L L S E E N V E S E L N S L N A Q Y N D L V L D Y E Q L R R E N E D L K L K E K N E L E E F E L L E Q K E E R D Q E M Q L M H E V S  
 N L K N L I K H A E E Y N Q D L E N D L S S K V K L L K E K E E Q I K N L Q E Y I D A Q K S E K M K I D L S Y T S D A T E D L K Q A M R T L  
 S D L D T V A L D A K K E S A F L R S E N L E L K E K I N E L S D S R K Q M E S D I Q M Y Q R Q L E A K K M Q T D L D K E L Q L A F Q E I  
 S K L S A L V D G K G L L S N L E L E K R I T D L Q K E L N K E A E E K Q T L Q E E V N L L S E L K S L P S E V E T L R R E L Y E K S E E L  
 H I I T T E R E K L F S E M A H K D S R I Q G L L E E I G N T R D D L A T S Q L S R R G S D G E W Q A L E S L H A E L E H R H A G V L E E R  
 E R L K Q E I G A L S K E A E S L A F S L D S V K A E L S H K T Q E L E Q K T V E G Q E R L N K M E A L R E E L E S R D S S L Q S V E K E K  
 V L L T E K L Q Q A L K E V K A L T Q E K K N L K Q L Q E S L Q T E R D Q L R S D I Q D T V N M N I D T Q E Q L L N A L E S L K Q H Q E T I  
 N M L K M K A A E E L S D N L H V K D R G G A R D E A Q Q K M D G I D E Q N E S A H T L L G G G K D N E V T E E Q R K I D S L M Q E N S G L  
 Q Q T L E S V R A E K E Q L K M D L K E N I E M S I E N Q E E L R I L R D E L K R Q Q E V A A Q E K D H A T E K T Q E L S R T Q E R L A K T  
 E E K L E E K N Q K L Q E T Q Q Q L L S T Q E A M S K L Q A K V I D M E S L Q N E F R N Q G L A L E R V E T E K L E L A Q R L H E S Y E E V  
 K S I T K E R N D L K E L Q E S F E I E K K Q L K E Y A R E I E A A G L Q T K E E L N I A H A N L K E Y Q E I I T E L R G S I S E N A E Q G  
 A S T Q D T A K S A P E L Q G E V P E Q E L L P V V K E A R H S A E K V N G L E P V G A H S R T V H S M T M E G I E I E N L R L T K K L E E  
 S Q M E I S C L T R E R E D L R R T Q E T L Q V E C T Q L K E D A R R T L A N H L E T E E E L N L A R C C L K E Q E N I D T L I T S L S Q  
 R E T E L S S V R G Q L A L T T A E L E R K V Q E L C E K Q E E L T R K E T S E A Q G K M S E L Q L R E L L A Q A S A L Q N A E S D R L  
 R L N T Q L E E S Q E E M K T L R E E R E E L R R M Q E A L H V E S E Q Q K E S M K E I S S K L Q E L Q N K E Y E C L A M K T I N E T Q G S  
 R C E M D H L N Q Q L E A Q K S T L E K V E M E N V N L T Q R L H E T L E E M R S V A K E R D E L W S M E E R L T V E R D Q L K K S L E E T  
 V T K G M E K E E E L R V A H V H L E E H Q E T I N K L R K M V S D Y T D E I S H T Q G D L K H T N A V V E A Q N Q D L R E K E H Q L S Q V  
 K A D L R E T V D Q M E Q L K K K L E A Q S S T L E S R E I E K L E L T Q Q L N E N L K K I T L V T K E N D S L K I M D E A L R E E R D Q L  
 R K S L Q Q T E A R D L E N Q E K L R I A H M N L K E H Q E T I D R L M E T M S E K T E E I S N M K M E L E N V N M K L Q E K V Q E L K T S  
 E R Q R V K L K A D A S E A K K E L K E Q G L T L S K I E M E N L N L A Q K I H E N L E E M K S V R K E R D D L K K L E E I L R M E R D Q L  
 K D N L R E A M L K A H Q N H E E T M K C G K G L L C A G E Y C T G R L R E K C F R I E K L L K R Y S E M A N D Y E C L N K V S L D L E R E  
 T K T Q K E L S V T V R T K L S L P H T Q T K E M E K L L T A N Q R C S L E F H R A L K R L K Y V L S S I A R I K E E Q H E S I N K R E M A  
 F I Q E V E K Q N E L Q I Q I Q S L S Q T Y R I P A R D L Q I K L S Q E M D L H I E E M L K D F S E N D F L T I K T E V Q Q V L N N R K E I  
 T E F L G K W L N T L F D T E N L K S T I Q K E N K S I G L V N N F Y H S R I T A M I N E S T E F E E R S A T R S K D L D Q Y L K S L K E T  
 T E Q L S E V Y Q T L T A S Q S V V H L H P T V Q P S T R D S E R P Q A A S G A E Q L T S K N K I A L G A V P Y K E E I E D L K M Q L V K S  
 D L E K K A T A K E F D K K I L S L K A T V E H Q E E M I R L L R E N L R G H Q Q A Q D T S M I S E Q D S Q L L S K P L T C G G G S G I V Q  
 S T K A L I L K S E Y K R M G S E I S K L K Q Q N E Q L R K Q N N Q L L S D N S Q L S N E V K T W E E R T L K R D S Y R E T T C E N S P K S  
 P K V T R T D S K R R Q N T T S Q C R A Q N L Q D P V P K D S P K S W F F D N R S K S L P A P H P I R Y F D N S S L G L C P E P D D V E N V  
 E P K T D L C Q A S L E K D V S Q C K T Q

TRTRPLEQKLISEEDLAANDILDYKDDDDKV

Restriction Sites: Sgfl-MluI

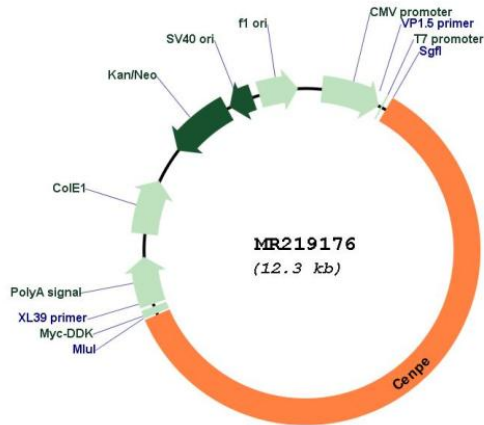
Cloning Scheme:

Cloning sites used for ORF Shuttling:



\* The last codon before the Stop codon of the ORF

Plasmid Map:



ACCN: NM\_173762

ORF Size: 7413 bp

<b>OTI Disclaimer:</b>	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. <a href="#">More info</a>
<b>OTI Annotation:</b>	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
<b>Components:</b>	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.</li> </ol>
<b>RefSeq:</b>	<a href="#">NM_173762.4</a> , <a href="#">NP_776123.3</a>
<b>RefSeq Size:</b>	7813 bp
<b>RefSeq ORF:</b>	7416 bp
<b>Locus ID:</b>	229841
<b>UniProt ID:</b>	<a href="#">Q6RT24</a>
<b>Cytogenetics:</b>	3 62.55 cM
<b>MW:</b>	286.2 kDa

**Gene Summary:**

Microtubule plus-end-directed kinetochore motor which plays an important role in chromosome congression, microtubule-kinetochore conjugation and spindle assembly checkpoint activation. Drives chromosome congression (alignment of chromosomes at the spindle equator resulting in the formation of the metaphase plate) by mediating the lateral sliding of polar chromosomes along spindle microtubules towards the spindle equator and by aiding the establishment and maintenance of connections between kinetochores and spindle microtubules. The transport of pole-proximal chromosomes towards the spindle equator is favored by microtubule tracks that are detyrosinated. Acts as a processive bi-directional tracker of dynamic microtubule tips; after chromosomes have congressed, continues to play an active role at kinetochores, enhancing their links with dynamic microtubule ends. Suppresses chromosome congression in NDC80-depleted cells and contributes positively to congression only when microtubules are stabilized (By similarity). Plays an important role in the formation of stable attachments between kinetochores and spindle microtubules (PubMed:12925705). The stabilization of kinetochore-microtubule attachment also requires CENPE-dependent localization of other proteins to the kinetochore including BUB1B, MAD1 and MAD2. Plays a role in spindle assembly checkpoint activation (SAC) via its interaction with BUB1B resulting in the activation of its kinase activity, which is important for activating SAC (PubMed:12361599). Necessary for the mitotic checkpoint signal at individual kinetochores to prevent aneuploidy due to single chromosome loss (PubMed:12925705).[UniProtKB/Swiss-Prot Function]