## Phylogeny

TEX14 orthologs have been cloned in Homo sapiens, Mus musculus, Xenopus laevis and Gallus gallus, demonstrating conservation across vertebrates (iwamori2010tex14interactswith pages 2-4).  
Comparative sequence analysis shows that placental mammalian orthologs retain three N-terminal ankyrin repeats, a central pseudokinase fold and a C-terminal CEP55-binding segment, whereas distal C-terminal residues diverge more rapidly (greenbaum2011germcellintercellular pages 13-14).  
No TEX14 counterparts have been reported in invertebrate genomes, indicating a vertebrate-specific emergence (iwamori2010tex14interactswith pages 2-4).  
Within the human kinome TEX14 clusters with atypical pseudokinases outside the conventional kinase groups defined by the Manning 2002 classification owing to loss of the canonical catalytic triad (unknownauthors2019tracingtheevolution pages 160-165).  
Relationship to other pseudokinases such as TRIB and STRAD is limited to the shared absence of VAIK, HRD and DFG motifs, placing TEX14 in its own sub-family (unknownauthors2019tracingtheevolution pages 160-165).

## Reaction Catalyzed

No ATP-dependent phosphotransfer reaction has been detected for TEX14, confirming enzymatic inactivity in vitro (mondal2012tex14aplk1regulated pages 12-15).

## Cofactor Requirements

Because the active site is inactive, TEX14 function does not require divalent metal cofactors such as Mg²⁺ or Mn²⁺ (mondal2012tex14aplk1regulated pages 22-26).

## Substrate Specificity

Systematic kinase-substrate profiling has not identified a consensus recognition motif for TEX14, consistent with its classification as a pseudokinase (mondal2012tex14aplk1regulated pages 12-15).

## Structure

TEX14 is a 1,450-residue protein with three N-terminal ankyrin repeats that mediate protein-protein interactions (greenbaum2006tex14isessential pages 3-4).  
The central region (~residues 350–650) adopts a protein kinase-like bilobal fold but lacks the canonical VAIK, HRD and DFG catalytic motifs, accounting for loss of catalytic activity (greenbaum2006tex14isessential pages 3-4).  
Five polo-box docking motifs located between residues 581 and 875 recruit PLK1 to kinetochores in a Cdk1-primed manner (mondal2012tex14aplk1regulated pages 2-4).  
An APC/CCdc20-recognised D-box (residues 527-535, RxxLxxxxN) directs proteasomal degradation during metaphase (mondal2012tex14aplk1regulated pages 8-9).  
The extreme C-terminus contains a conserved GPPX₃Y motif that binds CEP55 with high affinity, underpinning abscission blockade (iwamori2010tex14interactswith pages 1-2).  
TEX14 self-associates and forms an inner ring within the midbody matrix together with centralspindlin components (greenbaum2007conversionofmidbodies pages 3-4).  
No experimental structure is available, but AlphaFold model AF-Q8IWB6-F1 predicts a classical kinase architecture lacking the catalytic spine (unknownauthors2022novelmissensetex15 pages 40-41).

## Regulation

Cdk1 phosphorylates TEX14 in early mitosis, creating priming sites that enable binding of the PLK1 polo-box domain (mondal2012tex14aplk1regulated pages 2-4).  
PLK1 subsequently phosphorylates Ser431 during prometaphase and metaphase (mondal2012tex14aplk1regulated pages 22-26).  
Ser431 phosphorylation promotes APC/CCdc20 recognition of the D-box and ubiquitin-mediated proteasomal degradation of TEX14 (mondal2012tex14aplk1regulated pages 22-26).  
Mutation of Ser431 or the D-box stabilises TEX14 at kinetochores and delays the metaphase-to-anaphase transition (mondal2012tex14aplk1regulated pages 8-9).  
During cytokinesis TEX14 binds CEP55 via the GPPX₃Y motif, competitively blocking CEP55 interaction with ALIX and TSG101 and thereby inhibiting abscission (iwamori2010tex14interactswith pages 1-2).

## Function

TEX14 is strongly expressed in testicular tissue, including Sertoli cells, spermatogonia, spermatocytes and spermatids (bellil2021humantestisexpressed(tex) pages 7-9).  
Male mice lacking TEX14 fail to form stable intercellular bridges, exhibit spermatogenic arrest beyond the first meiotic division and are sterile (greenbaum2006tex14isessential pages 3-4).  
TEX14 converts midbodies into intercellular bridges by binding CEP55 and blocking abscission in germ cells (iwamori2010tex14interactswith pages 1-2).  
In somatic mitosis TEX14 is recruited to prophase kinetochores by PLK1 and is required for the assembly of outer-kinetochore complexes MIS12 and NDC80 (mondal2012tex14aplk1regulated pages 9-11).  
TEX14 depletion reduces kinetochore-microtubule attachment, decreases intra-kinetochore tension and weakens spindle assembly checkpoint signalling via BubR1, Mad2 and Mps1 (mondal2012tex14aplk1regulated pages 7-8).  
PLK1-dependent degradation of TEX14 during metaphase is necessary for timely anaphase onset (mondal2012tex14aplk1regulated pages 22-26).  
TEX14 interacts with MKLP1 in the midbody matrix, further stabilising the intercellular bridge architecture (greenbaum2007conversionofmidbodies pages 3-4).

## Other Comments

Frameshift, nonsense, splice-site and partial deletion mutations in TEX14 segregate with non-obstructive azoospermia, maturation arrest and Sertoli-cell-only phenotypes in men (bellil2021humantestisexpressed(tex) pages 10-12).  
A ten-base-pair deletion producing a premature stop codon was identified in two infertile brothers, leading to severe testicular hypoplasia and absent spermatogenesis (bellil2021humantestisexpressed(tex) pages 12-13).  
TEX14 is genomically amplified and overexpressed in a subset of breast tumours, linking aberrant dosage to chromosomal instability (mondal2012tex14aplk1regulated pages 11-12).

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