## Phylogeny

* Assigned to the CAMK-Unique subgroup within the NKF1 clade together with SBK and SgK069, and referenced as STK33 in early kinome surveys (hanks2003genomicanalysisof pages 4-5).
* Comparative genomic analysis in the same survey indicates orthologous sequences in mouse, rat, zebrafish, Drosophila and yeast, although specific identifiers were not provided (hanks2003genomicanalysisof pages 5-6).
* Kinome-wide substrate-preference clustering places SBK3 within an AGC-like group, highlighting a classification discrepancy relative to sequence-based assignments (johnson2023anatlasof pages 4-4).

## Reaction Catalyzed

* ATP + protein-Ser/Thr → ADP + protein-Ser/Thr-phosphate (unknownauthors2021integrativeanalysisof pages 102-108).

## Cofactor Requirements

* Requires divalent metal ions; Mg²⁺ was included in purification and in-vitro assay buffers for recombinant SBK3 (johnson2023anatlasof pages 9-10).
* No additional cofactors have been reported (unknownauthors2021integrativeanalysisof pages 102-108).

## Substrate Specificity

* A comprehensive phosphopeptide screen did not identify a consensus phosphorylation motif for SBK3; substrate preference remains unreported (johnson2023anatlasof pages 4-4).

## Structure

* Contains a single serine/threonine kinase catalytic domain with conserved VAIK (subdomain II), HRD (subdomain VIB) and DFG (subdomain VII) motifs characteristic of ePKs (hanks1995theeukaryoticprotein pages 15-16).
* No experimentally determined 3D structure is available; structural information is limited to predicted models such as those generated by AlphaFold (unknownauthors2021integrativeanalysisof pages 45-52).
* Activation loop boundaries, hydrophobic spine configuration and αC-helix orientation have not been experimentally validated (unknownauthors2021integrativeanalysisof pages 102-108).

## Regulation

* Post-translational modifications, regulatory binding partners and allosteric mechanisms specific to SBK3 have not been reported (unknownauthors2021integrativeanalysisof pages 102-108).

## Function

* Successfully expressed as a His₆-GST fusion protein and purified for biochemical assays, demonstrating enzymatic activity under standard kinase assay conditions (johnson2023anatlasof pages 9-10).
* Identified as a dark kinase with limited functional annotation in large-scale multi-omics screens (unknownauthors2021integrativeanalysisof pages 97-102).
* Publications referring to PNCK as SBK3 report elevated expression in hepatocellular and nasopharyngeal carcinoma and link depletion to reduced proliferation, indicating potential cancer relevance, though nomenclature ambiguity exists (unknownauthors2021integrativeanalysisof pages 130-134).
* Inclusion in the Clinical Kinase Index dataset signifies availability of transcript-level information in public cancer and normal tissue resources, but detailed expression patterns were not described (essegian2020theclinicalkinase pages 14-15).

## Other Comments

* Recognized as an understudied (dark) kinase lacking detailed structural, regulatory and functional data, representing a gap in the human kinome knowledge base (unknownauthors2021integrativeanalysisof pages 97-102).
* Nomenclature conflicts persist: SBK3 is equated with STK33 in early kinome surveys and with PNCK in some cancer studies, necessitating careful gene identifier verification in future work (hanks2003genomicanalysisof pages 4-5, unknownauthors2021integrativeanalysisof pages 130-134).

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