## Phylogeny

• Orthologs curated in UniProt/Ensembl exist for human, mouse, rat, zebrafish, Drosophila and C. elegans, demonstrating broad conservation of SBK1 (brenes2019theencyclopediaof pages 2-3).  
• Kinome placement (Manning 2002 framework): Group – CaMK; Family – SBK-related CAMK; Sub-family – SBK1 (johnson2023anatlasof pages 9-10, brenes2019theencyclopediaof pages 2-3).  
• Closest human paralogues by sequence/motif clustering are CAMK1G and CAMK2G within the CaMK group (johnson2023anatlasof pages 9-10).

## Reaction Catalyzed

ATP + protein-L-Ser/Thr ⇌ ADP + protein-L-Ser/Thr-phosphate (reveguk2024classifyingproteinkinase pages 1-2).

## Cofactor Requirements

Mg²⁺ is required, coordinated by the Asp of the DFG motif (reveguk2024classifyingproteinkinase pages 1-2).

## Substrate Specificity

Not experimentally determined; SBK1 lacks an assigned consensus motif in the current substrate-specificity atlas (johnson2023anatlasof pages 4-5).

## Structure

• Single canonical protein-kinase catalytic domain (~250 aa) with no auxiliary domains (reveguk2024classifyingproteinkinase pages 2-4).  
• No crystal structure; high-confidence AlphaFold2 model AF-Q52WX2-F1 included in structural survey (reveguk2024classifyingproteinkinase pages 1-2, 10-12).  
• Conserved motifs: VAIK Lys (β3) for ATP anchoring, HRD Asp (catalytic loop), DFG Asp-Phe-Gly initiating the activation loop; both DFG-in and DFG-out conformations observed in clustering (reveguk2024classifyingproteinkinase pages 4-5).  
• Regulatory architecture: αC-Glu/Lys salt bridge present in active state; hydrophobic spine residues at positions 120 & 142 align with canonical active packing (reveguk2024classifyingproteinkinase pages 10-12).  
• No unique insertions or ligand-bound complexes reported (reveguk2024classifyingproteinkinase pages 2-4).

## Regulation

• Post-transcriptional: cytoplasmic ceRNA axis with lncRNA DRAIC; DRAIC sponges miR-92a-1-5p, limiting miRNA repression of SBK1 (alhammad2024dysregulationofthe pages 7-10).  
• Post-translational: no experimentally mapped phosphorylation, ubiquitination or other modification sites reported (reveguk2024classifyingproteinkinase pages 1-2).  
• Allosteric/conformational controls specific to SBK1 have not been described (johnson2023anatlasof pages 4-5).

## Function

• Localisation: predominantly cytoplasmic (alhammad2024dysregulationofthe pages 7-10).  
• Cancer-linked expression:  
– Up-regulated in ovarian cancer; promotes cell survival and apoptosis resistance (alhammad2024dysregulationofthe pages 7-10).  
– Down-regulated in lung and oesophageal cancers; low expression associates with poor overall survival in LUAD/LUSC (alhammad2024dysregulationofthe pages 7-10).  
– Classified as a dark kinase; gene-dependency in 56/990 cancer lines and over-expressed in KIRC, LGG, LIHC, THYM (unknownauthors2021integrativeanalysisof pages 97-102).  
• No experimentally validated interacting partners, upstream regulators or downstream substrates are reported in the cited sources (johnson2023anatlasof pages 4-5).

## Other Comments

• Disease associations: combined low DRAIC/SBK1 predicts poor prognosis in non-small-cell lung cancer; SBK1 amplification/over-expression occurs in multiple tumour types (alhammad2024dysregulationofthe pages 7-10, unknownauthors2021integrativeanalysisof pages 97-102).  
• No peer-reviewed germline/somatic mutations or selective inhibitors have been reported; no PDB structures are available (unknownauthors2021integrativeanalysisof pages 97-102).

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