

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
P09547	SWI1_YEAST	Saccharomyces cerevisiae	SWI/SNF chromatin-remodeling complex subunit SWI1	24.475439	NaN	NaN	33229814	MDFFNLNNNNNNNTTTTTTTN NNNTNNNTNNNNPANNTNNN NSTGHSSNTNNNTNNNTNGAS GVDDFQNFDPKPFQNLDSNNNN SNSNNNDNNNSNTVASSTNFTSPT AVVNAAPANVTGGKAANFIQNPSP QFNSPYDSNNSNTNLNLSLSPQAILA KNSIIDSSNLPQAQQQLYGGNNNN NSTGIANDNVITPHFITNVQISONS SSSTPNTNSSTPNANQQFLPFNNS ASNNGNLTSNQLISNYAASNSMDR SSSASNEFVPNTSDNNNNNSNNHN MRNNSNNKTSNNNNVTAVPAATPA NTNNSTSNANTVFSERAAMFAALQ QKQQRFQALQQQQQQQOQQOQ NQQPQQQQQQQNPKFLQSQRQQ QQRSLQSLNPALQEKISTELNNKQY ELFMKSLIENCKRRNMPLOSIPEIG NRKINLFYLYMLVQKFGGADQVTRT QQWSMVAQRLQISDYQQLESIYFRIL LPYERHMISQEGIKETAQRIFLQF LQELLKKVQQQQAALANANNNI NSASSAPTPAAPGASVPATAAPGTEA GIVPVSANTPKSLNSNINNVNNNNI GQQQVKPRKQVKKTKKELELER KEREDFQKRQKLEDDQQRQKLL LETKLRQQYEIELKLPKVYKRSIVR NYKPLINRLKHYNGYDINYISKIGEKI DSNKPIFLFAPELGAINLHALSMSLQ SKNLGEINTALNTLLVTSADSNLKIS LVKYPELLDSLAILGMNLLSNLSQN VVPYHRNTSDYIEDAGSNQYVYVQ HDKMVDKIFEKVNNNATLTPNSDN DEKVTILVDSLTCGNQLPTPTPEMEP DLDTFCFISMQSTSPAVKQWDLLE PIRFLPNQFPLKIHRTPYLTSKKIKD EIDDPFTKINTRGAEDPKVLINDQLS TISMILRNISFSDNNSRMSRNFYK RFISDLLWLVLIHPENFTCNRKILNF KKDLVIVLSNISHLLEIASSIDCLLILI LVISFGQPKLNPMASSSFSGESLTF NEFQLQWQGYQTFGVDILAKLFSLE KPNLNYFKSILLNKNTGNNLYDRNS NNNHKDKLLRLLNLYNDNNKN NNNRHLLNDVVSFLFSAIPLQOVL SQSADPSSLIDQFSPVISQSLTSILVIV QKILPLSNEVFEISENNSDSNSNNN GNKDSSEFNFNKLPFVWLSSEENIG SGLLKLSEIHLNINNSTSKNTLLQQQ NYSKVLPSINISCVLIKCLVEKSIC FENCLNNDPEILKKIASIPNLFPTDL EIFQLFTNPSVDIQIINQQLLYNLKN DILTLE	None	None	None	None	None	None	None		

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