

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
Q8WWQ8	STAB2_HUMAN	Homo sapiens	Stabilin-2	27.26403	S35;T38	S2497	31492838	MMLQHLVIFCLGLVVQNFCSPAETT GQARRCDRKSLLTIRTECRSCALNL GVKCPDGYTMITSGSVGVRDCRYTF EVRTYLSLPGCRHICRKYDLPQPRCC PGRWGPDCIECPGGAGSPCNGRGS CAEGMEGNGTCSCEQEGFGGTACET CADDNLFGPSVCSSVCNVCVHVCNS GLDGDGTCECYSAYTGPKCDKPIPEC AALLCPENSRCSPSTEDENKLECKC LPNYRGDGKYCDPINPCLRKICHPH AHCTYLGPNRHSCTCQEGYRGDGGQ VCLPVDPCQINFGNCPTKSTVCKYD GPGQSHCECKEHEYQNFVPGVGCMS TDICKSDNPCHRNANCTTVAPGRTE CICQKGYVGDGLTCYGNIMERLREL NTEPRGKWQGRLLTSFISLLDKAYAW PLSKLGPFTVLLPTDKGLKGFNVNE LLVDNKAQYFVKLHIIAGQMNIIEY MNNNDMFYTLTGKSGEIFNSDKDN QIKLKLHGGKKVKIQQDIIASNGLL HILDRAMDKLEPTFESNNEQTIMTM LQPRYSKFRSLLEETNLGHALDEDEG VGGPYTIFVFNNEALNNMKDGTLDY LLSPEGRKLELVRYHIVPFTQLEV ATLISTPHIRSMANQLIQFNTTDNGQ ILANDVAMEIEITAKNGRIYTLTGVL IPPSIVILPHRCDETKREMKGTCV SCSLVYWSRCPANSEPTALFTHRCV YSGRFGSLKSGCARYCNATVKIPKCC KGFYGPDCNQCPGGFSNPSGNGQ CADSLGGNGTCICEEGFQGSQCQFC SDPNKYGPRCNKKCLCVHGTENNRI DSDGACLTGTCRDGSAGRLCDKQTS ACGPYVQFCHIHATCEYSNGTASCIC KAGYEGDGTLCSEMDPCTGLTPGGC SRNAECIKTGTGTHTCVCQQGWG NGRDCSEINNCLLPSAGGCHDNAS CLYVGPQNECECKKGFGRNGIDCE PITSCLEQTGKCHPLASCQSTSSGV WSCVCQEGYEGDGFCLCYGNAAVEL SFLSEAAIFNRWINNASLQPTLSATS NLTVLVPSQQATEDMDQDEKSFWL SQSNIPALIKYHMLLGTyrVADLQTL SSSDMLATSLQGNFLHAKVDGNIT IEGASIVDGDNAATNGVIHINKVLVP QRRLTGSLPNLLMRLEQMPDYSIFR GYIIQYNLANAIEAADAYTFVAPNNN AIENYIREKKVLSLEEDVLRHVHVVLE EKLLKNDLHNGMHRETMLGFSYFL SFFLHNDQLYVNEAPINYTNVATDK GVHGLGKVLQKNCNDNDTTIIR GRCRTCSSELTCPFGTKSLGNEKRR CIYTSYFMGRRTLFIGCQPKCVRTVI TRECCAGFFGPQCQPCPGNAQNV FGNGICLDGVNGTGVCEGEGFSGT ACETCTEGKYGIHCDQACSCVHGRC NQGPLGDGSCDCDVGWRGVHCDN ATTEDNCNGTCHTSANCLTNSDGT ASCKCAAGFQNGTICTAINACEISN GGCSAKADCKRTPGRRVCTCKAGY TGDGIVCLEINPCLENHGGCDKNAE CTQTGPNQAAACNCLPAYTGDGKVCT LINVCLTKNGGCSEFAICNHTGQVE RTCTCKPNYIGDFTCRGSIYQELPK NPKTSQYFFQLQEHFVKDLVGPFPF TVFAPLSAAFDEEARVKDWDKYGLM PQVLRVHVVAACHQLLENLKLISNA TSLQGEPIVISVSQSTVYINNKAIISS DIISTNGIVHIIDKLLSPKNLLITPKDN SGRILQNLTLATNNGYKFSNLIQD SGLLSVITDPIHTPVTLFWPTDQALH ALPAEQDDFLFNQDNKDKLKEYLKF HVIRDAKVLAVDLPSTAWKTLOGS ELSVKCGAGRDIGDLFLNGQTCRIV QRELLFDLGVAYGIDCLLIDPTLGG	True	True	4.548	1.923	1.611	1.699	1.108	5.0	2.234

CDTFTTFDASGECGSCVNTPSCPRW
SKPKGVKQKCLYNLPFKRNLEGCRE
RCSLVIQIPRCCKGYFGRDCQACPGG
PDAPCNRGVCCLDQYSATGEKCN
TGFNGTACEMCWPGRFGPDCLPCG
CSDHGQCDDGITSGQCLCETGW
GPSCDTQAVLPAVCTPPCSAHATCK
ENNTCECNLDYEGDGITCTVVD
QDNGGCAKVARCSQKGTKVS
KGYKGDGHSCTEIDPCADGLNGGC
HEHATCKMTGPGKHKCECKSHYVG
DGLNCEPEQLPIDRCLQDNGQCHA
DAKCVDLHFQDTTVGVFHLRSPLGQ
YKLTFDKAREACANEAATMATYNQL
SYAQKAKYHLCSAGWLETGRVAYPT
AFASQNCGSGVVGIVDYGPRPNKSE
MWDVFCYRMKDVNCTCKVGYVGD
GFSCSGNLLQVLMSPSLTNFLTEV
LAYSNSARGRAFLHLDLSIRGTL
FVPQNSGLGENETLSGRDIEHHLAN
VSMFFYNDLVNGTTLQTRLGSKLLIT
ASQDPLQPTETRFVDGRILQWDIFA
SNGIIHVISRPLKAPPVTLTHTGLG
AGIFFAILVTGAVALAAYSFRINRR
TIGFQHFSEEDINVAALGKQOPENI
SNPLYESTTSAPPEPSYDPFTDSEER
QLEGNDPLRTL