

UniprotKB ID	Entry name	organism	full name	oglcnaScore	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q8R4U0	STAB2_MOUSE	Mus musculus	Stabilin-2	40.575542	S1845	S2503	40997131;40885482;29187734	MARSKLLLGKLLPLILIFLGLLVQNA CSFTEAPELTKRCDKKSFLTITKTECO SCSVNIAVKCPDGYKITNGTVGVVD CRYSLKIQSYVLDIPGCRHICRKDYL QPQCCPGHWGPDCEMCPGGARAPC GGRGVCDEGMEGTGSCSCRAGFRG TACENCAAEDVFGPNC SAVCSCVH GVCNSGISGDGTCECLSAYRGRCD KPIPECAALLCPENSRCSPSSKDETK LQCKCLPSYKGDGQTCCKPINPCKN VCHPHASCSYLGPNRHSCVCQKGY QGDGQVCLPVDPCQTSYGNCPKST VCRYDGPQSHCECKEHYRNFVPG VGCSTMDICESKNPCHKNANCSTVS PGQTQCTCQKGYVGDGLNCYGNIM QRLRELNTEPRGMWQGQLTFSISIL DRTYAWPLSNLGPFTVLLPSDKGLK GVDVKELMDKEAARYFVKLHIIAG QMSTEQMYNLDTFYLTGKSGEIIH KDKDNQLKLYGSKIVQIIQGNIVA SNGLVHLLDRAMDKIEPTLESNPQQ TIMTMLQPRYGKFRSLEKTNVGOA LEKGGIDEPYTFIVPSNEALSNTAG VLDYLLSPEGSRKLELVRYHIVAF QLEVATLVSTLHIRSMANQITFNIS KGQILANNVADETEVAAKNGRIYTL TGVLI PPSILPILPHRCNETKREMKL GTCVRCFMKNWSKCPNTNSEPTAIFT NKCFYGSRAWNLKIGCARYCDVTV IPRCCKGFFGPD CNPCPGGFMNPCS GNGQCIDGLGGNGTCICEDFGQSSR CQFCSPNRYGPQCNRTCQCVHGIC DNRLDSGSCLPGTCREGTAGRFCD KQTSACGPYMQFCHIHATCEYSNET ASCVCNDGYEGDGLCSKDPCLGS TSRGGCSPNAECIQASTGTYSVCVQ RGWTGNGRDCVEINSCLLPSSGGC HDNATCLYVGGQNECECKKGFGRG NGIDCEPIHSCLEQIEKCHPLATCQYT LSGVVSCVCQEGYEGNGLCYGNV LMELSFLEAAVFYQWINNASLQSM LSATSNTLVVPSLQAIKMDQNEK SFWLSRNNIPALIKYHTLLGTYYRAD LQTLPSHMLATSLQGSFLRLDKAD GNITIEGASFVDGDNAAATNGVVHII KVLIPQRGLTGSLSLLRLEQMPDY SIFRGYIIHYNLASEAADAYTVFVP NNEAIESYIREKKATSLKEDILQYHV VLGEKLLRNDLHNGMHRETMLGFS YLLAFFLHNDQLYVNEAPINYNVA TDKGVHGLEKVLKIKNRCDNNDT IIVRGKCKGCSQTLCPLETKPLSET RKCISYVYFMGKRSIFIGCQLQCVRTI ITSACCAGFFGQPCQACPGKQNVV SGNGFCLDGVNGTGTCECEQGFNG TACETCTEGKYGIHCDQACSCVHGR CNQGPSGDGSCDCDVGWRGVKCD EITTDNCNGTCHTSANCLLDPDGA SCKCAAGFQNGTVCTAINACEISN GGCSAKADCKRTIPGSRVVCVKAGY TGDGIVCLEINPCLENHGGCDRHA CTOTGPNQAVCNCLPKYTGDKVCT LINVCLTNNGGCSPFACNHTEQDQ RTCTCKPDYTG DGIVCRGSIHSELPK NPSTSQYFFQLQEHAVQELAGP TVFVPSDSFNSSEKLVVWQKGL MSQILRYHVACQQLLENLKVITSA TTLQGEPISSVQD TVLINKKAKVLS SDIISTNGVIHVIDTLLSPQNLITPK GASGRVLLNLTVAANHGTYKFSKLI QDSGLLKVITDPMHTPVTLFWPTDK ALQALPQEQDQDFLNEDNKDKLKAY LKFHVIRDTMALASDLPRASWKT QGSELSVRCGTGSDV GELFLNGQM CRIIQRLLFDGGVAYGIDCLLMDPT EGGRCDFTTFNIPGEGSCFSTPR CPLQSKPKGVRKKCIYNLPFRRDVE GCQNLCTLVVHVPRCCSGYFMPDC QACPGGPDTPCNRNRMCMYDQYKPT GQCQCHTGFNGTACELCLPGRFGP	False	True	3.041	1.889	1.56	1.481	0.955	4.721	2.927

DCQPCGCSEHGQCDEGITGSGQCLC  
EAGWTGRFCDAPTIVIPVPCIPACSM  
HATCMENNTCVCNLNYEGDGITCT  
VVDfCKQNNGGCAKVAKCSQKGTQ  
VSCSCQKGYKGDGHSCTEIDPCANG  
VNGGCHEHATCRMTGPGKQKCECK  
SHYVGDGRDCEPEQLPLDRCLQDN  
GQCHPDANCVDLHFQDTTVGVFHL  
RSPLGQYKLTFFDKAKEACAKEAASIA  
TYNQLSYAQKAKYHLCsAGWLESGR  
VAYPTIYASKKCANIVGIVDYGTRTN  
KSEMWDVFCYRMKDVNCTCKAGYV  
GDGFSCNGNLLQVLMsFPsLTNFLT  
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LITSSQDLHQEARFVDGRAILQWDI  
IASNGVLHIIEPLKAPPTAATAAHSG  
LGTGIFCAVVLVTGAIALAAYSFRNLN  
QRTTGFRFFEEDDIDALAFGKQQP  
ESITNPLYETSTPAAPEPSCDPFTDS  
GERELENSDPLGALRS