

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	e: r:
Q14643	ITPR1_HUMAN	Homo sapiens	Inositol 1,4,5-trisphosphate-gated calcium channel ITPR1	32.665341	NaN	S1598;S1764	33214551;28510447;35083852;18077693;39302247	MSDKMSSFLHIGDICSLYAEGSTNG FISTLGLVDDRCVQPETGDLNPP KKFRDCLFKLCPMNRYSAQKQFWK AAKPGANSTTDAVLLNKLHHAADLE KKQNETENRKLLGTVIQYGNVIQLL HLKSNKYLTVNKRPLALLEKNAMRV TLDEAGNEGSWFYIQPFYKLSIGDS VVIGDKVVLNFPVNAQOPLHASSHQL VDNPGCNEVNSVNCNTSWKIVLFM KWSDNKDDILKGGDVVRLFHAEQE KFLTCDEHRKKQHVFLRTTGRQSAT SATSSKALWEVEVVQHDPCRGGAGY WNSLFRFKHLATGHYLAEEVDPDFE EECLEFQPSVDPDQDASRSRLRNAQ EKMVVSLVSVPEGNDISSIFELDPTT LRGGDSLVRPNYSVRLRHLCTNTWV HSTNIPIDKEEEKPVMLKIGTSPVKE DKEAFAIVPVSPAIEVRDLDFANDASK VLGSIAGKLEKGTITQNERRSVTKLL EDLVYFVTGGTNSGQDVLVVFVSKP NRERQKLMREQNILKQIFKLLQAPF TDCGDGPMRLREELGDQRHAPFRHI CRLCYRVLRHSQQDYRKNQEIYAKQ FGFMQKIQIGYDVLAEITITALLHNN RKLLKHTAAEIDTFVSLVRKNREP RFLDYLSDLCVSMNKSIPVTQELICK AVLNPTNADILIETKLVLSRFEFEGV SSTGENALEAGEDEEEVWLFWRDS NKEIRSKSVRELAQDAKEGQKEDRD VLSYYRYQLNLFARMCLDRQYLAIN EISGQLDVLILRCMSDENLPYDLRA SFCRLMLMHVDRDPQEQVTPVKY ARLWSEIPSEIAIDYSSGASKDEIK ERFAQTMEFVEEYLRDVCQRFPFS DKEKNKLTFEVVNLARNLIYFGFYN FSDLLRLTKILLAILDCVHVTTIFPISK MAKGEENKGNNDVEKLSNVMR SIHGVEGELMTQVVLRRGGGFLPMT MAAAPEGNVQAEPEKEDIMVMDT KLKIHILQFILNVRLDYRISCLLCIFK REFDESNSQTSSETSSGNSSQEGPSN VPGALDFEHIEEQAEGIFGSEENTP LDLDDHGGRTFLRVLHLTMHDYPP LVS GALQLLFRHFSORQEVLQAFKQ VQLLVTSQDVDNYKQIKQDLQLRSI VEKSELWVYKGGQPDDETMDGASGE NEHKKTEEGNNKPKHHESTSSNY RVVKEILIRLSKLCVQESASVRKSRK QQQRLLRNMGAHAVVLELLQIPYEK AEDTKMQEIMRLAHEFLQNFCAAGN QQNQALLHKHINLFLNPGILEAVTM QHIFMNNFQLCSEINERVVQHFVH CIETHGRNVQYIKFLQITVKAEGKFIK KCQDMVMAELVNSGEDVLVYFYNDR ASFQTLIQMMRSERDRMDENSPLM YHIHLVELLAVCTEGKNVYTEIKCNS LLPLDDIVRVVTHEDCIPEVKIAYINF LNHCYVDTEVEMKEIYTSNHMWKL FENFLVDICRACNNTSDRKHADSIL EKYVTEIVMSIVTTFSSPFSQSTTL QTRQPVFVQLLQGVFRVYHCNWLW PSQKASVESCIRVLSVAKSRAIAPV DLDSQVNNLFLKSHSIVQKTAMNW RLSARNAARRDSVLAASRDYRNIIER LQDIVSALEDRLRPLVQAELSVLVDV LHRPELLFPENTDARRKCESGGFIC KLIKHTKQLEENEKLCIKVLQTLR EMMTKDRGYGEKLISIDELDNAELP PAPDSENATEELESPPLRQLEDHK RGEALRQVLVNRYYGNVRPSGRRES LTSFGNGPLSAGGPGKPGGGGGGGG SSSMSRGEMLAEVQCHLDKEGAS NLVIDLIMNASSDRVFHESILLAIAL EGGNTTIQHSFFCRLTEDKSEKFF KVFYDRMKVAQEQEIKATVTVNTSDL GNKKKDDVEVDRDAPSRKKAKEPTTQ ITEEVRDQLEASAATRKATFTFRRE ADPDDHYQPEGGTQATADKAKDDL EMSAVITIMQPIRLFLQLLNCENHNR DLQNFRLCQNNKTNYNLVCETLQF	False	True	3.151	3.612	3.043	5.0	2.216	4.565	2.

LDCICGSTTGGLGLLYNEKNVAL
INQLESLTEYCQPCHEHQNCIAT
HESNGIDIITALLNDINPLGKRRMD
LVLELKNASKLLLAIMESRHDSN
AERILYNMRPKELVEVIKKAYMQGE
VEFEDGENGEDGAASPRNVGHNIYI
LAHQRLARHNKELQSMKPGGQVDG
DEALEFYAKHTAQIEIVRLDRIMEQI
VFPVPSICEFLTKEKSLRIYYTTERDE
QGSKINDFFLRSEDLFNEMNWWQKK
LRAQPVLYWCARNMSFWSSISFNLA
VLMNLLVAFFYPFKGVRGGTLEPHW
SGLLWTAMLISLAIVIALPKPHGIRAL
IASTILRLIFSGLQPTLFLGAFNVC
NKIIFLMSFVGNCGTFFTRGRAMVL
DVEFLYHLLYLVICAMGLFVHEFFYS
LLLFDLVYREETLLNVKSVTRNGRS
IILTAVLALILVYLFVIVGYLFFKDDFI
LEVDRLPNETAVPETGESLASEFLFS
DVCRVESGENCSPAPREELVPAEE
TEQDKEHTCETLLMCIVTVLSHGLR
SGGGVGDVLRKPSKEEPLFAARVIYD
LLFFFVMIIVLNLFVGIIDTFADLRS
EKQKKEEIKTTCFICGLERDKFDNK
TVTFEEHIKEEHNMMWHYLCFIVLVK
VKDSTEYTCPEHYVAEMIKERNLDW
FPRMRAMSLVSSDSEGEQNELRNL
QEKLESTMKLVNLSGQSELKDQ
MTEQRKQKQRIGLGLGHPHMNVNP
QQPA