

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	ex re
P11881	ITPR1_MOUSE	Mus musculus	Inositol 1,4,5-trisphosphate-gated calcium channel ITPR1	36.620756	T2477	S1588;S1755	33300544;40885482;34105348;37507081;40997131	MSDKMSSFLHIGDICSLYAEGSTNG FISTLGLVDDRCVVQPEAGDLNPP KKFRDCLFKLCPMNRYSAQKQFWK AAKPGANSTTDAVLLNKLHHAADLE KKQNETENRKLKLTGTVIQYGNVIQLL HLKSNKYLTVNKRLPALLEKNAMRV TLDEAGNEGSWFYIQPFYKLRISIGDS VVIGDKVVLNPNVAGQPLHASSHQL VDNPGCNEVNSVNCNTSWKIVLFM KWSDNKDDILKGGDVVRLFHAEQE KFLTCDEHRKKQHVFRLTTGRQSAT SATSSKALWEVEVVQHDPCRGGAGY WNSLFRFKHLATGHYLAAEVDPDFE EECLEFQPSVDPDQDASRSRLRNAQ EKMVYSLVSVPEGNDISSIFELDPTT LRGGDSLVRNSYVRLRHLCTNTWV HSTNIPIDKEEEKPVMLKIGTSPLKE DKEAFAIVPVSFAEVRDLDFANDASK VLGSIAGKLEKGTITONERRSVTKLL EDLVYFVTGGTNSGQDVLEVVFVSKP NREROKLMREQNILKQIFKLLQAPF TDCGDGPMRLREELGDRHAPFRHI CRLCYRVLRHSQDYRKNQEIYAKQ FGFMQKQIGYDVAEDTITALLHNN RKLEKHITAAEIDTFVSLVRKNREP RFLDYLSDLCVSMNKSIPVTQELICK AVLNPTNADILIIETKLVLSRFEFEGV STGENALEAGEDEEEVWLVWRDSN KEIRSKSVRELAQDAKEGQKEDRDIL SYRYQLNLFARMCLDRQYLAINIS GQLDVLILRCMSDENLPYDLRAS CRLMLMHVDRDPQEQVTPVKYAR LWSEIPSEIAIDDYSSGTSKDEIKER FAQTMFVVEEYLRDVCORFPFSDK EKNKLTFFEVNLRNLIYFGFYNFS DLLRLTKILLAILDCVHVTTFIPISKM TKGEENKGSNVMRSIHVGELMTQ VVLRRGGFLPMPMAAAPEGVNKVQ AEPEKEDIMVMDTKLKHIELQFILNV RLDYRISCLLCIFKREFDESNSQSSE TSSGNSSQEGPSNVPALDFEHIEE QAEFIGGSEENTPLDLDHGGRTF LRVLLHLMHDYPLVSGALQLLFR HFSQRQEVLAQAFKQVQLLVTSDVD NYKQIKQDLQLRVIVEKSELWVYK GQGPDEPMDGASGENEHKTEEGT SKPLKHESTSSYNRVVKEILIRLSKL CVQESASVRKSRKQQRLLRNMG HAVVLELLQIPYEKAEDTKMQEIMR LAHEFLQNFCAAGNQNALHKKHI NLFLNPGILEAVTMQHIFMNNFQLC SEINERVVQHFVHCIEHGRNVQYI KFLQTIKAEKGFKIKCQDMVMAEL VNSGEDVLVFNDRASFOTLIQMM RSEDRMDENSPLMYHIHLVELLAV CTEGKNVYTEIKCNLPLDDIVRVV THEDCIPEVKIAYINFLNHCYVDTEV EMKEIYTSNHMVKLFENFLVDICRA CNNTSDRKHADSIKEYVTEIVMSIV TTFSSPFSQSTTLQTRQPVFVQLL QGVFRVYHCNWLMPQKASVESC RVLSDVAKSRAIAPVDLDSQVNNLF LKSHNIVQKTALNWRLSARNAARRD SVLAASRDYRNIIERLQDIVSALEDRL RPLVQAEVSLVDVLRPELFPENT DARRKCESGGFICKLIKHTKQLEEN EEKLCIKVLQTLREMMTKDRGYGEK QISIDSENAELPQAPAEANSTEQEL EPSPLRQLEDHKKRGEALRQILVNR YYGNIRPSGRRESLTSFGNGPLSPGG PSKPGGGGGPGSSSTSRGEMSLAE VQCHLDKEGASNLVIDLIMNASSDR VFHESILLAIALLEGGNTTIQHSFFC RLTEDKKSEKFFKVFYDRMKVAQQE IKATVTVNTSDLGNKKKDDDEVDRDA PSRKKAKEPTTQITEEVRDQLEASA ATRKAFITFRREADPDDHYQSGET QATTDKAKDDLEMSAVITIMQPILRF LQLLCENHNRDLQNFRLRCQNNKTN YNLVCETLQFLDCICGSTTGGLGLL	True	True	3.071	5.0	3.04	5.0	2.205	3.007	2.

LYINEKNVALINQTLLESLTEYQCGPC  
HENQNCIATHESNGIDIITLILNDIN  
PLGKRMMDLVLELKNNAKLLLAIM  
ESRHDSENAERILYNMRPKELVEVI  
KKAYMQGEVEFEDGENGEDGAASP  
RNVGHNIYLAHQARHNKELOTML  
KPGGQVDGDEALEFYAKHTAQIEVR  
LDRIMEQIVFPVPSICEFLTKEKSLRI  
YYTTERDEQGSKINDFFLRSEDLFN  
EMNWQKKLRAQPVLVWCARNMSF  
WSSISFNLAFLMNLVAVFFYPFKGV  
RGGTLEPHWSGLLWTAMLISLAIVIA  
LPKPHGIRALIASTILRLIFSVGLOPTL  
FLLGAFNVCNKIIFLMSFVGNCGTF  
TRGYRAMVLDVEFLYHLLYLLICAM  
GLFVHEFFYSLLFDLVYREETLLNV  
IKSVTRNGRSILTAVLALILVYLFISV  
GYLFFKDDFILEVDRLPNETAVPETG  
ESLANDFLYSDVCRVETGENCTSPA  
PKEELLPAEETEODKEHTCETLLMC  
IVTVLSHGLRSGGGVGDVLRKPSKE  
EPLFAARVIYDLLLLFFMVIIHVLNFIG  
VIIDTFADLRSEKQKKEEILKTTFCIF  
GLEDRKFDNKTVTFEEHKEEHNM  
WHYLCFIVLVKVDSTEYTGPESYVA  
EMIRERNLDWFFRMRAMSLVSSDS  
EGEQNELRNLEKLESTMKLVTNLS  
GQSELKQMTQQRKQQRIGLLG  
HPPHMNVNPQQA