	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasm memb
0	Q14571	ITPR2_HUMAN	Homo sapiens	Inositol 1,4,5-trisphosphate-gated calcium channel ITPR2	43.046987	S1687;T1789	S937;S1160;S1709;T2607;S2633;S2636	29351928;41350704	MTEKMSSFLYIGDIVSLYAEGSVNGF ISTLGLVDDRCVVHPEAGDLANPPK KFRDCLFKVCPMNRYSAQKQYWKA KQAKQGNHTEAALLKKLQHAAELE QKQNESENKKLLGEIVKYSNVIQLL HIKSNKYLTVNKRLPALLEKNAMRV SLDAAGNEGSWFYIHPFWKLRSEGD NIVVGDKVVLMPVNAGQPLHASNIE LLDNPGCKEVNAVNCNTSWKITLF MKYSSYREDVLKGGDVVRLFHAEQE KFLTCDEYEKKQHIFLRTTLRQSATS ATSSKALWEIEVVHHDPCRGGAGQ WNSLFRFKHLATGNYLAAELNPDYR DAQNEGKNVRDGVPPTSKKKRQAG EKIMYTLVSVPHGNDIASLFELDATT LQRADCLVPRNSYVRLRHLCTNTWV TSTSIPIDTDEERPVMLKIGTCQTKE DKEAFAIVSVPLSEVRDLDFANDAN KVLATTVKKLENGTITQNERRFVTKL LEDLIFFVADVPNNGQEVLDVVITKP NRERQKLMREQNILAQVFGILKAPF KEKAGEGSMLRLEDLGDQRYAPYKY MLRLCYRVLRHSQQDYRKNQEYIAK NFCVMQSQIGYDILAEDTITALLHN NRKLLEKHITAKEIETFVSLLRRNRE PRFLDYLSDLCVSNTTAIPVTQELICK FMLSPGNADILIQTKVVSMQADNPM ESSILSDDIDDEEVWLYWIDSNKEP HGKAIRHLAQEAKEGTKADLEVLTY YRYQLNLFARMCLDRQYLAINQIST QLSVDLILRCVSDESLPFDLRASFCR LMLHMHVDRDPQESVVPVRYARLW TEIPTKITIHEYDSITDSSRNDMKRKF ALTMEFVEEYLKEVVNQPFPFGDKE KNKLTFEVVHLARNLIYFGFYSFSEL LRLTRTLLAILDIVQAPMSSYFERLSK FQDGGNNVMRTIHGVGEMMTQMV LSRGSIFPMSVPDVPPSIHPSKQGSP TEHEDVTVMDTKLKIIEILQFILSVRL DYRISYMLSIYKKEFGEDNDNAETSA SGSPDTLLPSAIVPDIDEIAAQAETMF AGRKEKNPVQLDDEGGRTFLRVLIH LIMHDYPPLLSGALQLLFKHFSQRA EVLQAFKQVQLLVSNQDVDNYKQIK ADLDQLRLTVEKSELWVEKSSNYEN GEIGESQVKGGEEPIEESNILSPVQD GTKKPQIDSNKSNNYRIVKEILIRLSK LCVQNKKCRNQHQRLLKNMGAHS VVLDLLQIPYEKNDEKMNEVMNLA HTFLQNFCRGNPQNQVLLHKHLNL FLTPGLLEAETMRHIFMNNYHLCNE ISERVVQHFVHCIETHGRHVEYLRFL QTIVKADGKYVKKCQDMVMTELING GEDVLIFYNDRASFPILLHMMCSER DRGDESGPLAYHITLVELLAACTEGK NVYTEIKCNSLLPLDDIVRVVTHDDC IPEVKIAYVNFVNHCYVDTEVEMKEI YTSNHIWKLFENFLVDMARVCNTTT DRKHADIFLEKCVTESIMNIVSGFFN SPFSDNSTSLQTHQPVFIQLLQSAFR IYNCTWPNPAQKASVESCIRTLAEVA KNRGIAIPVDLDSQVNTLFMKSHSN MVQRAAMGWRLSARSGPRFKEALG GPAWDYRNIIEKLQDVVASLEHQFS PMMQAEFSVLVDVLYSPELLFPEGS DARIRCGAFMSKLINHTKKLMEKEE KLCIKILQTLREMLEKKDSFVEEGNT LRKILLNRYFKGDYSIGVNGHLSGAY SKTAQVGGSFSGQDSDKMGISMSDI QCLLDKEGASELVIDVIVNTKNDRIF SEGIFLGIALLEGGNTQTQYSFYQQL HEQKKSEKFFKVLYDRMKAAQKEIR STVTVNTIDLGNKKRDDDNELMTSG PRMRVRDSTLHLKEGMKGQLTEAS SATSKAYCVYRREMDPEIDIMCTGPE AGNTEEKSAEEVTMSPAIAIMQPILR FLQLLCENHNRELQNFLRNQNNKT NYNLVCETLQFLDCICGSTTGGLGLL GLYINEKNVALVNQNLESLTEYCQG PCHENQTCIATHESNGIDIIIALILND	False	True	2.344	2.111	2.356	4.237	1.362	4.737

									INPLGKYRMDLVLQLKNNASKLLLAI MESRHDSENAERILFNMRPRELVD VMKNAYNQGLECDHGDDEGGDDG VSPKDVGHNIYILAHQLARHNKLLQ QMLKPGSDPDEGDEALKYYANHTA QIEIVRHDRTMEQIVFPVPNICEYLT RESKCRVFNTTERDEQGSKVNDFFQ QTEDLYNEMKWQKKIRNNPALFWF SRHISLWGSISFNLAVFINLAVALFY PFGDDGDEGTLSPLFSVLLWIAVAIC TSMLFFFSKPVGIRPFLVSIMLRSIYT IGLGPTLILLGAANLCNKIVFLVSFVG NRGTFTRGYRAVILDMAFLYHVAYV LVCMLGLFVHEFFYSFLLFDLVYRE ETLLNVIKSVTRNGRSIILTAVLALIL VYLFSIIGFLFLKDDFTMEVDRLKNR TPVTGSHQVPTMTLTTMMEACAKE NCSPTIPASNTADEEYEDGIERTCDT LLMCIVTVLNQGLRNGGGVGDVLRR PSKDEPLFAARVVYDLLFYFIVIIIVLN LIFGVIIDTFADLRSEKQKKEEILKTT CFICGLERDKFDNKTVSFEEHIKSE HNMWHYLYFIVLVKVKDPTEYTGPE SYVAQMIVEKNLDWFPRMRAMSLV SNEGDSEQNEIRSLQEKLESTMSLV KQLSGQLAELKEQMTEQRKNKQRL GFLGSNTPHVNHHMPPH								