

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	e-ri
Q07157	ZO1_HUMAN	Homo sapiens	Tight junction protein 1	20.870707	T366;T976;S978;T979;S1071;S1366;T1425;T1443;T1493	S125;T132;S175;S178;S179;T185;S212;S241;T267;S275;S277;S280;S284;S290;S294;S297;S300;S323;S329;S334;S337;S353;T354;S617;S622;T809;S810;S821;T822;S824;S828;S837;T846;T848;T854;T861;T868;S912;S968;S1071;S1111;S1139;T1140;T1165;T1354;S1366;S1413;S1545;S1617;S912	38665916;34019948;28657654;39302247;31492838;30379171;29237092;39531497;31637018;29351928;40596516;38253038;39534244;35254053;37340703	MSARAAAAKSTAMEETAWEQHTVT LHRAPGFGFGIAISGGRDNPHFQSG ETSVISVDLVKGGPAEQQLQENDRVA MVNGVSMNDNVEHAFAVQQLRKS NAKITIRKKKQVQIPVSRPDPPEVSD NEEDSYDEEIHDPGRSGRSGVNNRRS EKIWRPDRSASRERSLSPRSDRRSV ASSQPAKPTKVTLVKSRKNEYGLRL ASHIFVKEISQDLSAARDGNIQEGDV VLKINGTVTENMSLTDAKTLIERSKG KLKMVVQRDERATLLNVPDLSDSIH SANASERDDISEIQLASDHSGRSH DRPPRRSRSPDQRSEPSDHSRHS POQPSNGSLRSRDEERISKPGAVSTP VKHADDHTPKTVEEVTVERNEKQTP SLPEPKPVYAQVGPVDVLPVSPSD GVLPNSTHEDGILRPSMKLVKFRKG DSVGLRLAGGNDVGFVAGVLEDS AAKEGLEEGDQILRVNNVDFNTNIIRE EAVLFLDLDPKGEVTLAQKKDQVY RRIVESDVGDSFYRTHFEYKESPY GLSFNKGEVFRVVDVTLYNGKLSWL AIRIGKNHKEVERGIIPNKNRAEQLA SVQYTLPKTAGGDRADFWFRGLRS SKRNLRKSREDLAQPVQTKFPAYE RVVLEAGFLRPVTFGPIADVAREK LAREEPDIYQIAKSEPRDAGTDQRSS GIIRLHTIKQIIDQDKHALLDVT PNAV DRLNYAQWYPIVFLNPDQKQVKT MRMRLCPESRKSARKLYERSHKLK NNHHLFTTINLNSMNDGWYGALK EAIQQQQNQLVWVSEGKADGATSD DLDLHDDRLSYLSAPGSEYSMYSTD SRHTSDYEDTDEGGAYTDQELDET LNDEVGTPPESAITRSSEPVREDSSG MHHENQYPPYSPQAQPPQPIHRIDS PGFKPASQKAEASSPVYLSPETNP ASSTSAVNNHVNLTNVRLEEPTPAP STSYSPQADSLRTPSTEAAHIMLRDQ EPSLSSHVDPTKVYRKPYPPEEMMR QNHVLKQPAVSHPGHRPDKENLNT YEPQLPYVEKQASRDLEQPTTYRESS SYTDQFSRNYEHRLRYEDRVPMYEE QWSYDDKQYPSRPPFDNHSQD LDSRQHPEESSERYFPRFEEPAPLS YDSRPRYEQAPRASALRHEEQPAPG YDTHGRLRPEAOPHPAGPKPAESK QYFEQYSRSYEQVPPQGFSTRAGHF EPLHGAAAVPPLIPSSQHKPEALPSN TKLPLPPPTQTEEEEDPAMKQPSVLT RVKMFENKRSASLETKKDNDVNTGSGF KPPEVASKPSGAPIIGPKPTSQNQFS EHDKTLYRIPEPQKQPKPPEDIVRS NHYPDEEYRQKLSYFDRRSFE NKPPAHIAASHLSEPAKPAHSQNS NFSSYSKKGKPEADGVDRSFGKGR YEQIATPPPPPLPSQYAPSPQVTS SLHIHSGGAHGEVNSVSLDFQNSLV SKPDPSPSQNKPATFRPPNREDTAQ AAFYQKSFDPKAPVNGTEQTKTV TPAYNRFTPKPYTSSARPFERKFESP KFNHNLPSETAHKPDLSSKTPTSP KTLVKSHSLAQPPFDGSGVETFSIHA EKPKYQINNISTVKAIPVSPSAVEED EDEDGHTVVATARGIFNSNGGLSS IETGVSIHPQGAPEGVEQEIYFKVCR DNSILPPLDKEKGETLLSPLVMCGP HGLKFLKPVLELRLPHCDPKTWQNK CLPGDPNLYLVGANCVSLIDHF	True	True	4.514	3.069	False	F