

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondri
Q9BTC0	DIDO1_HUMAN	Homo sapiens	Death-inducer obliterator 1	29.486749	T79;S489;T603;S606;T927;S941;S947;S952;S955;T959;T960;T962;S964;S981;T1004;S1005;S1277;S1285;T1288;T1291;T1292;S1297;T1298;S1301;T1303;S1308;S1510;S1541;S1547;S1552;S1788	S60;S114;T151;S152;S154;S523;S805;S809;S889;S898;S1019;S1030;S1040;T1244;T1256;S1260;S1312;S1456;T1469;S1522;S1714	34725712;38665916;33214551;30379171;39302247;25367160;39531497;32574038;39534244;35254053;31492838;27114449;32119511;21740066;34019948;29237092;35132862;30397120;40596516;28510447;37340703;35289036;30059200;20305658;35138101;29351928;36240223	MDDKGDPSNEEAPKAIKPTSKEFRK TWGFRRTTIKREAGADAEADPLEP PPPQQQLGLSLRRSGRQPKRTERVE QFLTIARRRGRSRMPVLESDSSEPTS CPATDAETASEGSVESASETRSGPQS ASTAVKERPASSEKVKGGDDHDDTS DSDSDGLTLKELQNLRRKREQEPT ERPLKGIQSRLRKKRREEGPAETVGS EASDTEGVLPSKQEPENDQGVVSQ AGKDDRESKLEKAAQDIKDEEPPGD LGRPKPECEGYDPNLYCICRQPHN NRFMICCDRCEEWFHGDGCVGISEA RGRLLERNGEDYICPNCTILQVODET HSETADQOEAKWRPGDADGTDCTSI GTIEQKSSDQGIKGRIEKAANPSGK KKLKIFQPVIEAPGASKCIGPGCCHV AQPDSVYCSNDCILKHAATMKFLS SGKEQKPKPEKMKMKPEKPSLPKC GAQAGIKISSVHKRPAPEKKETTIVK AVVVPARSEALGKEAACESSTPSWA SDHNYNAVKPEKTAAPSPSLLYKST KEDRRSEKAAAMAASKTAPPGSA VGKQAPARNLVPKSSFANVAAATP AIKPPSFGFKGTIPKRPWLSATPSSG ASAARQAGPAPAAATAASKKFPGSA ALVGAVRKPVPVSPMASPAPGRLG AMSAAPSQPNQIRQNRRLKKEIL WKRVNDSDDLIMTENEVKIALHIE KEMFNLFQVTDNRYKSKYRSIMFNL KDPKNQGLFHRVLRREISLAKLVRL KPEELVSKELSTWKEPARPSVMESR TKLHNESKKTAPRQEAIPDLEDSPPV SDSEEQESARAVPEKSTAPLLDVF SMLKDTTSQHRAHLFDLNCIKICTGQ VPSAEDPAPKKOKLSASVKKEDLK SKHDSSAPDPAPDSADEVMPEAVPE VASEPGLSASHPNVDRTYFPGPPG DGHPEPSPLEDLSPCASCSSGVVTV TVTSGRDPRTAPSSSCTAVASAASR PDSTMVPEARQDVPKPVLTSMVMVPK SILAKPSSSPDPRYLSVPPSPNISTSE SRSPPEGDTTLFLSRLSTIWKGFINM QSVAKFVTKAYPVSGCFDYLSEDLPD TIHGGRIAPKTVWDYVGKLSKSSVK ELCLIRFHPATEEEEVAYISLYSYFSS RGRFGVVANNNRHVKDLYLIPLSAQ DPVPSKLLPFEGPGLSEPRNIIIGLV ICQKIKRPANSGELDKMDEKRRTRLQ PEEADVPAYPKVATVPSSEKPKSKYP LCSADAAVSTTPPGSPPPPPLPEPP VLKVLSSLKPAAPSPATAATTAASAS TAASSTASSASKTASPLEHILQTLFG KKKSFDPASAREPPGSTAGLPQEPKTT AEDGVAPLLDPVIVQFQGFQSKDK ALEEEEEDDRPYDPEEYDPERAFDT QLVERGRRHEVERAPEAAAAEREV AYDPEDETILEEAKVTVDLPLNRM ADVRRNSVERPAEPVAGAATPSLVE QQKMLEELNKQIEEQKQKLEEQEE ALRQRAAVGVSMHAFSVSDALMS PPPKSSLKPAELFQEQQSADKPASL PPASQASNHRDPRQARRLATETGEG EGEPLSRLSARGAQGALPERDASRG GLVQAPMPVPEEKEPASSPWASGE KPPAGSEQDGWKAEPGEGRPATV DSSARPARVLLTPPCGALQPGFPL QHDGERDPFTCPGFASQDKALGSAQ YEDPRNLHSAGRSSSAGETEGDRE PQARPGEGTAPLPPGQKVGGSQPP FQGQREPGPHALGMSGLHGNFPG PRGPAPPPEENIASNDGPRGPPPAR FGAQKGPISLFSGQHGPPPYGDSR GPSPSYLGGRGVAPSQFEERKDPH GEKREFQDAPYNEVTGAPAQFEGTE QAPFLGSRGAPFQFGQRRPILLSQ LKGPRGGPPPSQFGGQRPVPPGHFV GPRGPHPSQFETARGPHNPQFEGPR GQAPNFMGPRGIQPPQFEDQRVH SPPRFTNQRAPAPLQFGGLRGSAPP SEKNEQTPSRFHFQOGAPQVMKPG	True	False	2.524	4.513	False

								PRLLELP SHPPQHRKDRWEEAGPP					
								SALSSSAPGQGPEADGQWASADFRE					
								GKGHEYRNQTFEGRQRERFDVGP					
								EKPLEEPDAQGRASEDRRERERGR					
								NWSREPDWDRPREWDRHRDKDSS					
								RDWDRNRERSANRDREADRGKE					
								WDRSRERSRNRERDRRRDRDRS					
								RSRERDRDKARDREGRDRKDRSK					
								SKESARDPKPEASRASDAGTASQA					