

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q8TD84	DSCL1_HUMAN	Homo sapiens	Cell adhesion molecule DSCAML1	27.979371	S426;S1629	NaN	38253038;29351928	MWLVTFLLLLDSLHKARPEVDVGTSL YFVNDSLQVTFSSSVGVVPCPAA GSPSAAALRWYLATGDDIYDVPHIRHV HANGTLQLYFPSPSAFNSFIHDNDY FCTAENAAGKIRSPNIRVKAVFREPY TVRVEDQRSMRGNVAVFKCLIPSSV QEYVSVVSWEKDTSIPEHRFFITY HGGLYISDVQKEDALSTYRCITKHKY SGETRQSNGARLSVTDPAESIPTILD GFHSQEVWAGHTVELPCTASGYPIP AIRWLKDRPLPADSRWTKRITGLTI SDLRTEDSGTYICEVNTFGSAEATG ILMVIDPLHVTLTPKCLKTGIGSTVIL SCALTGSPFTIRWYRNTELVLVPEA ISIRGLSNETLLITSAQKSHSGAYQCF ATRKAQTAQDFAIHALEDGTPRIVSSF SEKVVNPGEQFSLMCAAKGAPPTV TVALDDEPIVRDGSHRITNQYMSD GTTISHMNVTPQIRDGGVYRCTAR NLVGSAEYQARINVRGPPSIRAMRNI TAVAGRDTLINCVRVIGYPYYSIKWYK DALLLPDNRQVVFENGTLKLDVQ KGMDEGEYLCSVLIQPLSISQSVHV AVKVPPLIQPFEPASIGQLLYPCV VSSGDMPIRITWRKDGQVIISGSGVT IESKEFMSSLISSVSLKHNGNYTCI ASNAAAVTSRERQLIVRPPRFVVQP NNQDGIYKAGVLNCSVDGYPPPKV MWKHKAGSGNPQQYHPVPLTGRIQI LPNSSLLIRHVLEEDIGYLLCQASNG VGTDISKSMFLTVKIPAMITSHPNNTI AIKGHAKELNCTARGERPIIRWEKG DTVIDPDRVMRYAIATKDNQDEVVS TLKLPADRGSVFFSCHAINSYPGE DRGLIQLTVQEPPDPELEIREVKAR SMNLRWTRQFRDGNISITGFDIEYKN KDSWDFKQSTRNISPTINQANIVDL HPASVYSIRMYSFNKIGRSEPSKELT ISTEEAAPDGPPMDVTLQPVTSSQSIQ VTWKAPKKELOQNGVIRGYQIGYREN SPGNSGQYSIVEMKATGDSEVYTLT NLKKFAQYGVVVQAFNRAGTGPSSS EINATTLEDVPSQPPENVRALSITS VAVISWSEPPRSTLNGVLKGYRVIFW SLYVDGEWGEQONITTRERVELRG MEKFTNYSVQVLAYTQAGDGVRRSSV LYIQTKEVPGPPAGIKAVPSSASSV VSWLPPTKPNVIRKYTIFCSSPGSG QPAPSEYETSPEQLFYRIHLNRGQ QYLLWVAAVTSAGRGSSEKVTIEP AGKAPAKIISFGGTVITPVMKDVRLP CNSVGDPAVAVKWTKDSSESAIPVS MDGHRLIHTNGTLLRAVKAEDSGY YTCTATNTGGFDTHVNLVQVPPDQ PRLTVSKTSASSITLTWIPGDNNGSSI RGFVLQYSVDNSEEWKDVFISSSER SFKLDSLKCGTWYKVKLAAKNSVGS GRISEIIEAKTHGREPSFSKQHLFT HINSTHARLNQGWNNGGCPITAV LEYRPGKTAWWQGLRANSSGEVFLT ELREATWYELRMACNSAGCGNET AQFATLDYDGSSTIPPIKSAQEGDDV KKLFTIGCPVILATLGVALLFIVRKKR KEKRLKRLRDAKSLAEMLSKNRNS FDPVVKGPPQGPLRHIDIPRVQLLIE DKEGKQLGDDKATIPVTDAEFSQAV NPQSFCTGVSLHHPTLIQSTGLIDM SDIRPGTNPVSRKNVKSASSTRNRY SSQWTLTKCQASTPARTLSDWRTV GSQHGVVTVESDSYASLSQDTDKG RNSMVSTESASSTYEELARAYEHAK LEEQLQHAKFEITECFISDSSSDQMT TGTNENADSMSTSMSTPSEPGICRFT ASPPKQDADRGNVAVPIPHRANK SDYCNLPLYAKSEAFFRKADGREPC PVPPPREASIRNLARTYHTQARHLTL DPASKSLGLPHPGAPAAASTATLPQR TLAMPAPPAGTAPPAPGPTPAEPPTA PSAAPPAPSTPPRAGGPHTKMGGS RDSLLEMSTSGVGRSQKQAGAGAYSK	None	None	None	None	None	None	None	None	

