

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	end retic
Q92545	TM131_HUMAN	Homo sapiens	Transmembrane protein 131	9.876938	S906;S912;S913;T914	S803;S1322;S1342;S1375;S1863;S1871	33214551;37340703;34019948;35289036;37217939;38665916	MGKRAGGGATGATTAAVVSTASAGAGLEPAAARSGGPRSAAGALLGALHLVMTLVVAAAARAEKEAFVQSESIIEVLRFDGGLLQTEITLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMPKMEKVYLHNPSSEETITLVISATTSHFHASFFQNRKILPGGNTSFDVVFLARVVGVENTLFINTSNHGVFTYQVFGVGNPNPYRLRPFGLGARVPVNSSFSPIIHNPHEPQLQVEMYSGGDLHLELPTGQQGTRKLEWIPPYETKGVMRASFSSREADNHTAFIRIKTNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKVLNLHLLNSGTKDVPITSVRPTPONDAITVHFKPITLKASESKYTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEVLDGYLGFDHAATLPHIRDSPADPVERPIYLTNTFSFAILHLDVLLPEEAKTMFKVHNFSKPVILIPNESGYIFLLFMPSTSSMHIDNNILLITNASKFHLPVVRVYTFGLDYFVLPKIEERFIDFGVLSATEASNILFAINSNPIELAIKSWHIIIGDGLSELVAVERNRTTIHSSLPFEKSSLSQSSVTLASGYFAVFRVKLTAKKLEGIHDGAIQITTDYEILTIPKAVIAVGS�LTCFPKHVVLPSPFPGKIVHQSLNIMNSFSQKVKIQIRSLSEDRVRFYKRLRGNKEDLEPGKSKIANIYFDPLQCGDHCVGLPFLSKSEPKVQPGVAMQEDMWDADWDLHQSLFKGWTGIKENSNGHRLSAIFEVNTDLQKNIISKITAEELSWPILSSPRHLKFPPLTNTNCSSEETLENPADVPVYVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRLEFQVFRNSAHPLOSSTGFMEGLSRHLILNLILKPGEEKSVKVKFTPVHNRIVSSLIHVRNNTVMDAVMVQGGQTENLRVAGKLPGPGSSLRFKITEALLKDCDLSLKLREPNTLKRFTKVENTGQLQIHIEIEISGYSCGYGFKVVNCQEFLLSANASRDIIILFTPDTASRVIRELKFITTSGESEFVFNLSLPYHMLATCAEALPRPNWELALYIIISGIMSALFLLVIGTAYLEAQQIWEPPRRRLSFEASNPFFDVGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSAGSHKCCGSPVHPHSSHNRNSADVENVRANKSSSTTSRTSAQAASSOSANKTSLVLDSENTVTQGHAGRKSKGAKQSQHGSQHHAHSPLAQHPQPPLPPVPVPPQEPQPERLSPAPLAHPSHPERASARHSSSESDITSLEAMDKDFDHHDSPALEVFTQPPSPLPKSKGKGKPLQRKVKPPKKQEEKEKKKGKQPQEDLKDLSLADDDSSSTTTTETSNDPTEPLLKEDTEKQKQKQAMPEKHESEMSQVKQKSKKLLNIKKEIPTDVKPSSLELYTPPLESKQRRNLPKSKIPLTAMTSGSKSRNAOKTKGTSKLVNDRPPALAKFLPNSQELGNTSSSEGEKDSPPPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSPTPASPPAAPCPFVARGSYSSIVNSSSSDPKIQPNQNGSKHLTKAASLPGKNGNPTFAAVTAGYDKSPGGNGFAKVVSNKTGFSSSLGISHPAVSDGSDSSGLWSPVSNPSSPDTPLNSFSAFGNSFNLTGEVFSKGLSRSCNOASQRSWNEFNNGPSYLWESPATDPSPSWPASSGSPHTHTATSLVGNSTGLWSTTPFSSSIWSSNLSSALPFTTPANTLASIGLMTENSPAPHAPSTSSPADDLGQTYNPRWISPTIGRRSSDPWSNSHFPHEN	False	False	0.888	1.2	1.11	1.14