	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q92673	SORL_HUMAN	Homo sapiens	Sortilin-related receptor	26.147272	T1727	S114;S2206	39531497	MATRSSRRESRLPFLFTLVALLPPGA LCEVWTQRLHGGSAPLPQDRGFLVV QGDPRELRLWARGDARGASRADEK PLRRKRSAALQPEPIKVYGQVSLNDS HNQMVVHWAGEKSNVIVALARDSL ALARPKSSDVYVSYDYGKSFKKISDK LNFGLGNRSEAVIAQFYHSPADNKR YIFADAYAQYLWITFDFCNTLQGFSI PFRAADLLLHSKASNLLLGFDRSHP NKQLWKSDDFGQTWIMIQEHVKSF SWGIDPYDKPNTIYIERHEPSGYSTV FRSTDFFQSRENQEVILEEVRDFQL RDKYMFATKVVHLLGSEQQSSVQL WVSFGRKPMRAAQFVTRHPINEYYI ADASEDQVFVCVSHSNNRTNLYISE AEGLKFSLSLENVLYYSPGGAGSDTL VRYFANEPFADFHRVEGLQGVYIATL INGSMNEENMRSVITFDKGGTWEF LQAPAFTGYGEKINCELSQGCSLHL AQRLSQLLNLQLRRMPILSKESAPG LIIATGSVGKNLASKTNVYISSSAGAR WREALPGPHYYTWGDHGGIITAIAQ GMETNELKYSTNEGETWKTFIFSEK PVFVYGLLTEPGEKSTVFTIFGSNKE NVHSWLILQVNATDALGVPCTENDY KLWSPSDERGNECLLGHKTVFKRRT PHATCFNGEDFDRPVVVSNCSCTRE DYECDFGFKMSEDLSLEVCVPDPEF SGKSYSPPVPCPVGSTYRRTRGYRKI SGDTCSGGDVEARLEGELVPCPLAE ENEFILYAVRKSIYRYDLASGATEQL PLTGLRAAVALDFDYEHNCLYWSDL ALDVIQRLCLNGSTGQEVIINSGLET VEALAFEPLSQLLYWVDAGFKKIEVA NPDGDFRLTIVNSSVLDRPRALVLVP QEGVMFWTDWGDLKPGIYRSNMD GSAAYHLVSEDVKWPNGISVDDQWI YWTDAYLECIERITFSGQQRSVILDN LPHPYAIAVFKNEIYWDDWSQLSIFR ASKYSGSQMEILANQLTGLMDMKIF YKGKNTGSNACVPRPCSLLCLPKAN NSRSCRCPEDVSSSVLPSGDLMCDC PQGYQLKNNTCVKQENTCLRNQYR CSNGNCINSIWWCDFDNDCGDMS DERNCPTTICDLDTQFRCQESGTCIP LSYKCDLEDDCGDNSDESHCEMHQ CRSDEYNCSSGMCIRSSWVCDGDN DCRDWSDEANCTAIYHTCEASNFQ CRNGHCIPQRWACDGDTDCQDGSD EDPVNCEKKCNGFRCPNGTCIPSSK HCDGLRDCSDGSDEQHCEPLCTHF MDFVCKNRQQCLFHSMVCDGIIQC RDGSDEDAAFAGCSQDPEFHKVCD EFGFQCQNGVCISLIWKCDGMDDC GDYSDEANCENPTEAPNCSRYFQFR CENGHCIPNRWKCDRENDCGDWS DEKDCGDSHILPFSTPGPSTCLPNYY RCSSGTCVMDTWVCDGYRDCADGS DEEACPLLANVTAASTPTQLGRCDR FEFECHQPKTCIPNWKRCDGHQDC QDGRDEANCPTHSTLTCMSREFQC EDGEACIVLSERCDGFLDCSDESDE KACSDELTVYKVQNLQWTADFSGDV TLTWMRPKKMPSASCVYNVYYRVV GESIWKTLETHSNKTNTVLKVLKPD TTYQVKVQVQCLSKAHNTNDFVTLR TPEGLPDAPRNLQLSLPREAEGVIVG HWAPPIHTHGLIREYIVEYSRSGSKM WASQRAASNFTEIKNLLVNTLYTVR VAAVTSRGIGNWSDSKSITTIKGKVIP PPDIHIDSYGENYLSFTLTMESDIKV NGYVVNLFWAFDTHKQERRTLNFR GSILSHKVGNLTAHTSYEISAWAKTD LGDSPLAFEHVMTRGVRPPAPSLKA	True	True	2.73	4.576	1.995	5.0	5.0	5.0	5.0

									KAINQTAVECTWTGPRNVVYGIFYAT SFLDLYRNPKSLTTSLHNKTVIVSKD EQYLFLVRVVVPYQGPSSDYVVVKMI PDSRLPPRHLHVVHTGKTSVVIKWE SPYDSPDQDLLYAVAVKDLIRKTDRS YKVKSRNSTVEYTLNKLEPGGKYHII VQLGNMSKDSSIKITTVSLSAPDALK IITENDHVLLFWKSLALKEKHFNES RGYEIHMFDSAMNITAYLGNTTDNF FKISNLKMGHNYTFTVQARCLFGNQ ICGEPAILLYDELGSGADASATQAAR STDVAAVVVPILFLILLSLGVGFAILY TKHRRLQSSFTAFANSHYSSRLGSAI FSSGDDLGEDDEDAPMITGFSDDVP MVIA								