	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	P0DSP1	SORL_RAT	Rattus norvegicus	Sortilin-related receptor	36.238305	NaN	S114;S2207	18683930;30625365	MATRSSRRESRLPFLFTLVALLPPGA LGGGWTQRLHGGGAPLPQDRGFFV VQGDPHELRLGTHGDAWGASPAAR KPLRTRRSAALQPQPIQVYGQVSLND SHNQMVVHWAGEKSNVIVALARDS LALTRPKSSDVYVSYDYGKSFNKISE KLNFGVGNSSEAVISQFYHSPADNK RYIFVDAYARYLWITFDFGSTIHGFSI PFRAADLLLHSKASNLLLGFDSSHP NKQLWKSDDFGQTWIMIQEHVKSF SWGIDPYDQPNTIYIERHEPFGFSTV FRSTDFFQSRENQEVILEEVRDFQL RDKYLFATKVVHLPGSQQQSSVQLW VSFGRKPMRAAQFVTKHPINEYYIAD ASEDQVFVCVSHSNNSTNLYISEAE GLKFSLSLENVLYYSPGGAGSDTLVR YFANEPFADFHRVEGLQGVYIATLIN GSMSEENMRSVITFDKGGTWEFLQ APAFTGYGEKINCELSQGCSLHLAQ RLSQLLNLQLRRMPILSKESAPGLIIA TGSVGKNLASKTNVYISSSAGARWR EALPGPHYYTWGDHGGIIMAIAQGM ETNELKYSTNEGETWKTFVFSEKPV FVYGLLTEPGEKSTVFTIFGSNKESV HSWLILQVNATDALGVPCTENDYKL WSPSDERGNECLLGHKTVFKRRTP HATCFNGEDFDRPVVVSNCSCTRED YECDFGFKMSEDISLEVCVPDPEFS GKPYSPPVPCPVGSSYRRTRGYRKIS GDTCSGGDVEARLEGELVPCPLAEE NEFILYAMRKSIYRYDLASGATEQLP LSGLRAAVALDFDYEHNCLYWSDLA LDTIQRLCLNGSTGQEVIINSGLETV EALAFEPLSQLLYWVDAGFKKIEVA NPDGDFRLTIVNSSVLDRPRALVLVP QEGVMFWTDWGDLKPGIYRSNMD GSAAYRLVSEDVKWPNGISVDGHWI YWTDAYLDCIERITFSGQQRSVILDN LPHPYAIAVFKNEIYWDDWSQLSIFR ASKYSRSQVETLASQLTGLMDMKIF YKGKNAGSNACIPQPCSLLCLPKAN NSKSCRCPEGVASSVLPSGYLMCDC PQGYERKNNTCVKEENTCLRNQYH CSNGNCINSIWWCDFDNDCGDMS DERNCPTTICDADTQFRCQESGTCIP LSYKCDLEDDCGDNSDESHCEMHQ CRSDEFNCSSGMCIRSSWVCDGDN DCRDWSDEANCTAIYHTCEASNFQ CHNGHCIPQRWACDGDADCQDGSD EDPISCEKKCNGFHCPNGTCIPSSK HCDGLRDCPDGSDEQHCEPFCTRF MDFVCKNRQQCLFHSMVCDGIIQC RDGSDEDATFAGCSQDPEFHKECD EFGFQCQNGVCISLIWKCDGMDDC GDYSDEANCENPTEAPNCSRYFQFH CENGRCIPNRWKCDRENDCGDWS DEKDCGDSHIFPSPTPGPSTCLPNYF RCSSGACVMGTWVCDGYRDCADGS DEEACPSLANSTAASTPTQLGQCDR FEFECRQPKKCIPNWKRCDGHQDC QDGQDEANCPTHSTLTCMSREFKC EDGEACIVLSERCDGFLDCSDESDE KACSDELTVYKVQNLQWIADFSGDV TLTWTRPKKMPSASCVYNVYYRVVG ESIWKTLETHSNKTSTVLKVLKPDTT YQVKVQVHCLSKVHNTNDFVTLRTP EGLPDAPRNLQLSLNSEEEGVILGH WAPPVHTHGLIREYIVEYSRSGSKM WASQRAASNSTEIKNLLLNALYTVR VAAVTSRGIGNWSDSKSITTTKGKVI QAPNIHIDSYDENSLSFTLTMDGDIK VNGYVVNLFWSFDAHKQEKKTLNF RGGSSLSHKVSNLTAHTSYEVSAWA KTDLGDSPLAFEHILTRGISPPAPSLK AKAINQTAVECIWTGPKNVVYGIFYA TSFLDLYRNPKSLTTSLHNKTVIVSK	None	None	None	None	None	None	None	None	None

									DEQYLFLVRVLIPYQGPSSDYVVVKM IPDSRLPPRHLHAVQIGKTSAVIKWE SPYDSPDQDLFYAIAVKDLIRKTDRS YKVRSRNSTVEYSLSKLEPGGKYHII VQLGNMSKDSSIKITTVSLSAPDALK IITENDHVLLFWKSLALKEKQFNETR GYEIHMFDSAVNLTAYLGNTTDNFF KVSNLKMGHNYTFTVQARCLFGSQI CGEPAVLLYDELSSGGDATVVQTAR STDVAAVVVPILFLILLSLGVGFAVLY TKHRRLQSSFTAFANSHYSSRLGSAI FSSGDDLGEDDEDAPMITGFSDDVP MVIA									