

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						
Q2VIS4	FILA2_MOUSE	Mus musculus	Filaggrin-2	29.185005	NaN	S1198;S1204;S1205;S1278;S1284;S1285;S1356;S1362;S1363;S1438;S1439;S1510;S1516;S1517;S1590;S1596;S1597;S1744;S1750;S1751;S1824;S1830;S1831;S1902;S1908;S1909;S1980;S1986;S1987;S2104	22645316	MAYLLRSVVTIDVFYKYTKQDEECG TL SKDELKELLEKEFRPILKNPDDPD TVDVMHMLDRDRRDLDFTEFIL MIFKLALACNKVLGKEYCKASGSK HRRGHQHQQEESSETEEEETPRQK SGFRFSSWSEGEHGHSSGGSRGP AKHRRGSNSKRLERQDELSSSEESR KKHHSIFGHSWSSNKEKDGSRSE ELGEGDKSYDPSRESEEEYESGY RLNHQGREHSGLSGLEKNKYEL NYIQLRKGGEQKLGYNSSSGNSKI QSHVYGFNSNSGCCRPKNASSSCQA SRSQGGNQS CRTQSNCSGTSGG QGYGCVSEGGSSRCCQPKRSCSQS SSQRGYGSKQCGQPONCGRQORMG SSHSSCCGPGYSGGATQSSGCGQOR MSSCGHSSSHQKGCSSNGFSKGD QRASGSGHSSCCEQHGTNSSQSSG FKQHGHEGQSCCGQHGHTASSQSS GYSOHRVSGQSCHYGHGSSSGQ SSSGRHSGSGQSSSRHRNRSGSS QSSGLEEHGSSSHQSHSSGHHGSG SRQSSGSEQHGAVSGQSSGSGKHET GPSQSSSGHHGSGSQHGGGSGGQ STGFGEHSSSGHSSSGQHRSGSR HSSGSGKHESGRSQSSGSHHGSG SQQHGGGSGNSTGFGEHSSSHPL PSSGQNESSGQSSRERHGTGSGQ SSGFGQHGSGSHQSSSGHNEYGS GQTSSSWPHGKSGQESGYGEQES GHGQSSSSWQHGTGPGQSSSSSEE ESRPGQSSSSWQHKGKSGQESGYG QEAGHGQSSSSWQHGTGAGNQSS GYGEHKSQPSHSSRSWHHGTGSGQ SLGFGQHKGSHQSESSGHYESVSE PSSSSWQHNGSGESYGYGEHESG HGQSSSAWNHGNESGQSNGYGEH ESGHGQSSSAWNHGNESGQSNGF GENESGRDQEGYQRESFHGQHRH PLSQHEQHSQFQYGRSPRSPVHPES SEGEEHVVPRRYSYGHGQAG HQRESGYGQRGRPQGPSQDSSRQ PQAGHGQPSQSGYGRSPRSPVHPE YSEGEAHSEVSQRHSGSSHCHCHC HGQARHQRESVHGQRGRPQGPSQ DSSRHPQAGPQPSQSGSRRSPRSQ PVHPESSEGEHVVPRHSGSGH GHGQGGQAGHQRESVHGQOGR PQGPSQDSSRQPQAGQGPSQSGS GRSPRSPVHPESSEGEHVVPR HSGSGHGHGQGGQAGHQQRE SVHGQRSPQGPQDSSRQPQAGQ GPSQSGSRRSPRSPVHPESSEGE EHSVPRHSGSGHGHGQGGQAG HQRESVHGQVPRPEVPTQDSSRQP QAGQGPSQSGSRRSPRSPVHPES SEGEEHVVPRNSCHCHCHDQ AGHQRESVHGQRGRPQGPSQDSS RHPQAGPQPSQSGSRRSPRSPVH PESSEGEHVVPRHSGSGHGHG QGQAGHQQRESVHGQRGRPQGP TQDSSRQPQAGQGPSQSGSRRSP RSPVHPESSEGEHVVPRHSGSG HGHGHGQGGQAGHQQRESVHGQ RGRPQGPSQDSSRQPQAGQGPSQ SSGSRRSPRSPVHPESSEGEHVV PQRYSGSGHGHGQGGQAGHQQRESV HGQRGRPQGPSQDSSRQPQAGQGPSQ SSGSRRSPRSPVHPESSEGEH SVIPQRHSGSGSHGQGVHAEHQ QRESVHGQRGRPQGPSQDSSRQPQ AGQGPSLSGSGSRRSPRSPVHPES SEGEHVVPRHSHSESGHGHGQ QGQAGHQQRESVHGQRGRPQGPSQ DSSRQPQAGQGPSQSGSRRSPRSP VHPESSEGEHVVPRHSGSGHGHG QGGQAGHQQRESVHGQRGRPQGPSQ DSSRQPQAGQGPSQSGSRRSPRSP RSPRSPVHPESSEGEHVVPRHSGSGHGHGQGGQAGHQQRESVH	None	None	None	None	None	None	None	None	None	None	None	None	None	None	None

GQPVRPQGPSQDSSSQPQASQGQPS
QSGSGRSPRRSPVHPESSEGEHSV
VPQRHSGSGHGHGQGGQAGHQ
RESLHGQRGRSQSPFHPSHSIHQ
SKCTISKSSRLSGHYGRNHQSTIS
GNQYDSSQSSRHGSGYQDYDYGQ
SGYGPSGRLRSNSQSSIPFSSAHRAT
NMEVLPQGQSFSPSDHVGTKANEQI
GELVFKYRESETPDQSVDYNNLTE
SNSTTRGHEC SHGHSVVVPEHSDD
SDFNYGHSYNGKQIQSQSPTVQSC
FDDSQYILFQKHLESFSGNQSGFS
PNERQLYTCNESIDSYHLSSDSNRR
NQIYSSNNSFPNLYCIGTEQCIYLP
ATLGEGETEGQEPGYTQPGTICKYNQ
FLDGRKSRTRGNHETGKMKSGSAY
LDSNTPLYTYVQE QKSYFFE