

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
Q05793	PGBM_MOUSE	Mus musculus	Basement membrane-specific heparan sulfate proteoglycan core protein	41.854276	T847;S3622	NaN	22645316;34418053;36288343;22517741;33300544	MGQRAVGSLLLGLLLHARLLAVTHG LRAVDGLSLPEDTETVTASRYGWTYS YLSDDDELLADDASGDGLGSGDVGS GDFQMVFYFRALVNFTRSIIEYSPQLE DASAKEFREVSEAVVEKLEPEYRKIP GDQIVSVVFIKELDGVVVELDVGS EGNADGSQIQEVLHTVVSSGSIGPYV TSPWGFKFRRLGTVPQFPRVCTETE FACHSYNECVALEYRCDRRPPDCRD MSDELNCEEPVPELSSSTPAVGKVS PLPLWPEAATTPPPVTHGPOFLLPS VPGPSACGPQEASCHSGHCIPRDYL CDGQEDCRDGSDELGCASPPPCEPN EFACENGHCALKLWRCGDGDFDCED RTDEANCSVKQFGEVCGPTHFQCVS TNRCIPASFHCDEESDCPDRSDEFG CMPPQVVTTPPQQSIQASRGQTVTFT CVATGVPTPIINWRLNNGHIPAHPR VTMTSEGGRTLIIRDVKEADQGAYT CEAMNSRGMVFGIPDGVLELVPOR GPCPDGHFYLEDASCLPCFCFGVT NVCQSSLRFRDQIRLSFDQPNDFKG VNVTMPSPQGVPPLSSTQLQIDPAL QEFQLVDSLRRFLVHDAFWALPKQF LGNKVDSYGGFLRYKRYELARGML EPVQKPDVILVGAGYRLHSRGHTPT HPGTLNQRQVQLSEEHVWHESGRP VQRAEMLQALASLEAVLLQTVYNTK MASVGLSDIVMDTTVTHTIHGRAH SVEECRCPIGYSGLSCESCDAHFTRV PGGPLYGTCSGCNCNGHASSCDPVY GHCLNCQHNTGEPQCDKCKPGFFG DATKATATACRPPCPYIDASRRFSD TCFLDTDGQATCDACAPGYTGRRCE SCAPGYEGNPIQGGKCRPTTQEIIVR CDERGLGTSGETCRCKNNVVGRLC NECSDGSFHLKQNPDPGCLKCFM GVSRQCSSSSWSRAQVLGASEQPSQ FSLSNAAGTHTTSEGVSPPAGELSF SSFHLLSEPYFWSLPAFRGDKVT SYGGELRFTVMQRPRPSSAPLHRQP LVVLQGNVILEHHSRDPSPCQPS NFIVPFQEQAWQRPDGPATREHLL MALAGIDALLIQASYTQPAESRLSG ISMVAVPENTGQDSAREVEQCTCP PGYRGPSQCDCDTGYTRVPSGLYLG TCERCNCHGHSETCEPETGACQSC QHHTEGASCEQCOPGYGDAQRGT PQDCQPCPCYGAPAAGQAAHTCFLD TDGHPTCDSCSPGHSGRHCERCAP GYYGNPSQGPCHRDGQVPEVLGC GCDPHGSISSQCDAAAGQCCKAQVE GRSCSHCRPHHFHLSASNPEGCLP CFCMGTQQCASSYSRQLISTHFA PGDFQGFALVNPQRNSQLTGGFTVE PVHDGARLSFNFHLAGQESFYWQ LPEIQGDKVAAYGGKLRYLTYTAG PQGSPLLDPIQITGNMMLVASQPA LQGPERRSYEIIIFREEFWRPDPQPA TRELHLLMALADLDELLVRATFSSVP RAASISAVSLEGAQPGSSGPRALEV EECRCPPGYVGLSCDCAAPGYTRTG SGLYLGQCELCECNGHSDLCHPETG ACSRQCQHNNTAGEFCELCATGYGDA TAGTPEDCQPCACPLTNPENMFRT CESLGAGGYRCTACEPGYTGYQCEQ CAPGYEGDPNVQGGRCQPLTKESLE VQIHPSRSVVPQGGPHSLRCQVSGS PPHYFYWSREDGRPLPSSAQRHQ GSELHFPSVQPSDAGVYICTRNLH TSNSRAELLVAEAPSKPIMVTEEQR SQSVRPGADVTFICTAKSKSPAYTLV WTRLHNGKLPSTRAMDFNGILTIRNV QPSDAGTYVCTGSMFMAMDQGTAT LHVQVSGTSTAPVASIHPPQLTVQPG QQAEFRCSATGNPTMLEWIGGPGS QLPAKAIHNGILRLPAIEPSDQGGY LCRALSSAGQHVARAMLQVHGGSG PRVQVSPERTQVHEGRTVRLYCRAA GVPSASITWRKEGGLPFRHQAHGS	None	None	None	None	None	None	None	

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