

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	gol app
Q811L6	MAST4_MOUSE	Mus musculus	Microtubule-associated serine/threonine-protein kinase 4	48.917875	S2165	S204;S211;S268;S912;S1290;S1368;S1382;S1395;S1417;S1465;S1521;S1776;S1819;S1906;S2439;S2517;S2549	26192747;22517741;23443134;22645316	MGEKVVSEAPEVPRGCSGHGARTLVSSAAAVSSEGASSAESSSGSETLSEE GEPSTRFSCRSQPPRPPGGALGTRLPA AWAPARVALERGVPTLPLPHPGGAV LPVPQVSSASQEEQDELDHILSPPP MPFRKCSNPDVACGLGKSLKYKROL SEDGKQLRRGSLGGALTGRYLLPNP VAGQAWPASAETSNLVLRMRSQLG QSAPSLTASLKELSLPRRGLSCLRTSN RKSLIGNGQSPALPRPHSPLSAHAG NSPQDSPRNFSASAHFSFARRTD GRRWLSLASLPSGGYGTNTPSSTVSSS CSSQEKLHQLPYQPTPDELHFLSKH FCTTESIATENRCRNTPMRPRSRL SPGRSPACCDHEIIMMNHVYKERFP KATAQMEERLKEIITSYSPDHVLP DGVLSFTHHQIELARDCLDKSHQG LITSRYFFELQHKLDKLLQEAHDRSE SGELAFIKQLVRKILVIARPARLLEC LEFDPEEFYLLAEAEGHAKEGQGIK TDIPRYIISQLGNKDPLEEMAQLGN YDSRTAETPEMDESVSSTSLRLR RKPRESDFETIKLISNGAYGAVYFVR HKESRQRFAAMKINKQNLILRNOIQ QAFVERDILFAENPFVVMYCSFET RRHLKCMVMEYVEGGDCATLMKNM GPLPVDMARMYFAETVLALEYLHNY GIVHRDLKPDNLLVTSMGHIKLTDF GLSKVGLMSMTNLYEGHIEKDARE FLDKQVCGTPEYIAPVILRQYGGK VDWWAMGIIYEFYLVGCVFFGDT EELFGQVISDEINWPEKDEAPPPDA QELITLLLQONPLERLGTGGAYEVKQ HRFFRSLDWNLSLRQKAEFIPQLES EDDTSYFDTRSEKYHHMETEEEDDT NDEDFTEIRQFSSCSRFSKVFSSI DRITQNSGEDKDDSEDKTKSTLPS TETLSWSSEYSEMQLSTNSSDTE SNRCKLSSGLLPKLAISTDGEQDEAV PCSGDPREEPEKPVPPSEECTQEEP EVTTPASTISSSTLSVGSFSEHLDQIN GRSECVDSTDNSSKPSSEPTSHVAR QRLESTEKKKISGKVTKSLASALS MIPGDMFAVSPGSPMSPHLSDDP SSSRDSSPSRDSSAASAPHQPIVH SSGKNYGFTRAIRVYVGDSDIYTVH HIVWVVEEGSPAYQAGLKAGDLITHI NGEPVHGLVHTEVIELLLKSGNKVSI TTTFFENTSIKTGPARRNSYKGRMV RRSKKSKKESLERRRSLFKKLAKQ PSPLLHTRSFSCLNRSLSSGESLPG SPTHLSLSPRSTPSYRSTPDFPSTGN SSQSSSPSSAPNSPAGSGHIRPSTL HGLAPKLSGQRYRSGRKKSAGSIPLS PLARTPSPTPQPTSPQRSPLLGH LGNAKITQAFPSKMHSPPTIVRHIVR PKSAEPPRSLKRVQSEELKSPSYG SDKLLCSRKHSLEVTQEEVQREQC QREVTLSLEENVCDAVSLSRARPV EQGCKRVPVSRKVGROESVDDLDRD KLKAKVVVKPEEKHESHQPHSLG GDESYALFRLEEREKKVYSKGLERS GHFENTSaelpsvgsllkdtlhkqa SVRASEGVTSDGAACSLTPGEHSQS LGDFKRASASGILHDSVCPISDRPAP GKVEYSEKASQAKELLRSEKLDLKL ANIDYLRKKMSLDDKDDSHCAILKP KITSSAHECLPGNPIRPMAGQETPP ASENRAFINSTHTPQMSAVSFVPLK ALAGRVENGGKAGLAAPESPVRKS PSEYKLEGRSVCLKPIEGTLDIALLS GPHASKTELLSPEPAQSPSPGINVGP CVPLALPGSSGKGDSTSLREPSSA NLKVNKSYLLEPRFLPPSRALQDSL ASGPEPKSKPERKLIHPSARSPTVT ESNLQKKEGPATHQDRSTDTRNL PGPGQTLHNVDLPRCLTRAPLPEEG TPAKEPKCLKEPSAKVKEWAVRD DGHDRDPAKLCPAETGKASDSSKPL PSGGRTQPDFYKQTQTSKAWAHAK	None	None	None	None	None	None	None

TNPKDSQDEVKSLAREDSASLLYEK
EIGRARKGPEPKPEVPATRCPPQPPG
IEGKREKLSAAPSLQKQAPKEPDRK
EQTSORPGSGPQPPPTKELNSA
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GHSDCSSHKARPGDPSPSKSKHQD
RSLSSQKLSAGSAGKKEPVTQPLGG
SIREGKGGSGPVDTFSAVLTQGKA
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KNTNGGCPPEMQAKHPPRQGHLE
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DYPSLCRQTDSPSHQATTGDRKAE
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TVQSSLRSAAPPEKSLSYSASFPEAQ
PGVREVPAANSSPSSAKATGGTSEFP
APSSRDHRKLRGGDGRSQMKSDDS
LPSFRLSTSALESHPDQVPIASGH
RGRALSVAATGEPKGRELAQPPV
RKQNACREATRAPASTDRSLPLSS
EKDFVVRQRRKELRSPSKKAS