

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O15021	MAST4_HUMAN	Homo sapiens	Microtubule-associated serine/threonine-protein kinase 4	8.666114	NaN	S206;S213;S270;S914;S1292;S1370;S1384;S1397;S1419;S1467;S1523;S1779;S1822;S1909;S2442;S2520;S2552	35254053	MGEKVSEAPEPVPRGCSGHGSRTPA SALVAASSPGASSAESSSGSETLSEE GEPGGFSREHQPPPPPLGGTLGAR APAAWAPASVLLERGVLALPPPLPGG AVPPAPRGSSASQEEQDEELDHILSP PPMPFRKCSNPDVASGPGKSLKYKR QLSEDGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVRMRSQA LGQSAPSLTASLKELSLPRRGSFCRT SNRKSLIGNGQSPALPRPHSPLSAH AGNSPQDSPRNFSASAHFSFARR TDGRRWSLASLPSSGYGTNTPSSTV SSSCSSQEKLHQLPYQPTPELHFL SKHFCTTESIATENRCRNTPMRPRS RSLSPGRSPACCDHEIIMMNHVYKE RFPKATAQMEERLKEIITSYSPDNVL PLADGVLSFTHHQIIEIARDCLDKSH QGLITSRYFLELQHKLDKLLQEAHD RSESGELAFIKQLVRKILIVARPARL LECLEFDPEEFYLLLEAAEGHAKEG QGIKTDIPRYIISQLGLNKDPLEEMA HLGNYDSGTAETPETDESVSASNAS LKLRRKPRESDFETIKLISNGAYGAV YFVRHKE SRQRFAMKKINKQNILR NQIQQAFVERDILTFAENPFVSMY CSFETRRHLCMVMEYVEGGDCATL MKNMGPLPVDMARMYFAETVLAL YLHNYGIVHRDLKPDNLLVTSMGHI KLTDFGLSKVGLMSMTTNLYEGHIE KDAREFLDKQVCGTPEYIAPENVILRQ GYGKPVDDWAMGIILYEFVLCVVPF FGDTPEELFGQVISDEINWPEKDEA PPPDAQDLITLLLRQNPLERLGTGGA YEVKQHRFFRSLDWNSSLRQKAEFI PQLESEDDTSYFDTRSEKYHHMETE EEDDTNDEDFNVEIRQFSSCSHRFS KVFSSIDRITQNSAEKEDSVDKTKS TTLPSTETLSWSSEYSEMQLSTSN SSDTESNRHLKSSGLLPKLAISTEGE QDEAASCPCGDPHEEPGKPALPPEEC AQEEPEVTTTASTISSSTLSVGSFSE HLDQINGRSECVDSTDNSSKPSSEP ASHMARQRLESTEKKISGKVTKSL SASALSLMIPGDMFAVSPLGSPMSP HLSDDPSSSRDSSPSRDSSAASASP HQPIVIHSSGKNYGFTIRAIRVYVGD SDIYTVHHIVWNVEEGSPACQAGLK AGDLITHINGEPVHGLVHTEVIELLL KSGNKVSITTPFENTSIKTGPARRN

SYKSRMVRRS KSKKESLERRRSL
FKKLAKQPSPLLHTSRFSCLNRSL
SGESLPGSPTHLSLSPRSPTPSYRSTP
DFPSGTNSSQSSSPSSAPNSPAGS
GHIRPSTLHGLAPKLGGRYRSGRR
KSAGNIPLSPLARTPSPTPQPTSPQR
SPSPLLGHSLGNSKIAQAFPSKMHS
PPTIVRHIVRPKSAEPPRSPLLKRVQS
EEKLSPSYGSDKKHLCSRKHSLEVT
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PPLSRARPVEQGCLKRPVSRKVGRO
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KQESHQKSHGPGSDLENFALFKLEE
REKKVYPKAVERSSTFENKASMQEA
PPLGSLLDALHKQASVRASEGAMS
DGRVPAEHRQGGDFRRAPAGTL
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KELLRCEKLDKLANIDYLRKKMSL
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HAAQMSAVSFVPLKALTGRVDSGTE
KPGLVAPESPVRKSPSEYKLEGRSVS
CLKPIEGTLDIALLSGPQASKTELPSP
ESAQSPSPSGDVRASVPPVLPSSSGK
KNDTTSARELSPSSLKMNKSYLLEP
WFLPPSRGLQNSPAVSLPDPEFKRD
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ERGPPTARSERSAARADTCREPSME
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PLQRHPSSIPPPPLTAKDLSSPAARQ
HCSSPSHASGREPGAKPSTAEPSSSP
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PPKTKHPDRSLSSQKPSVGATKKE
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ATPGSQNKASDGIGQEGGSPVPLH
TDRAPLDAKPQPTSGGRPLEVLEKPV
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AERPAAGVGKGFPEARARGKGPQKP
PTEADKPNGMKRSPSATGQSSFRST
ALPEKSLSCSSSPETRAGVREASAA
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LPLESHHPDPNTMGGASHDRALS

VTATVGETKGGDPAPAQPPARKQN
VGRDVTKPSAPNTDRPISLSNEKDF
VVRQRRGKESLRSSPHKKAL