

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q96T58	MINT_HUMAN	Homo sapiens	Msx2-interacting protein	32.135447	S2092;T2496;T2499;S2512;T2513;T2522;S2525;T2529;S2530;S2531;S2532;T2533;T2586;T2591;S2594;T2619;S2620;S2623;S2684;T2810;S2811;S2818;S2820;T2862;S2868;S2908;S2918;S2920;T2921;T2924;T2928;T2965;T2981;T3012;S3034;S3035;S3040;S3043;S3044;T3045;S3047;T3048;T3273;T3284;T3290;S3298;S3299;T3461;T3462;T3467	S99;S188;S190;S309;S623;S725;S727;S736;S740;S770;S830;S833;S847;S1062;T1140;S1168;S1194;S1222;S1252;S1261;S1268;S1278;S1283;S1287;S1333;S1380;S1382;T1439;T1441;T1619;T1633;T1826;S1897;S1918;T1947;S2101;S2120;S2126;S2159;T2163;S2366;T2393;T2421;S2452;S2456;T2460;S2481;S2486;S2493;T2938;T2950;S3433	30379171;33214551;20068230;27114449;31492838;32119511;30059200;28657654;32574038;29351928;28314751;29237092;34019948;21158410;30620550;23301498	MVRETRHLWVGNLPENVREEKIEHFKRYGRVSEVKILPKRGSEGGVAAFVDFVDIKSAQKAHNSVNMKGDRDLR TDYNEPGTIPSAARGLDDTVSIIASRS REVSGFRGGGGGPPAYGPPPSLHARE GRYERRLDGASDNRERAYEHSAYG HHERGTGGFDRTRHYDQDYTRDPR ERTLQHGGLYASRSRSPNRFDAHDP RYEPAREQFTLPSVVHRDIYRDDIT REVRGRRPERNYQHSRSRSPHSSQS RNQSPQRLASQASRPTRSPSGSGSR SRSSSSDSISSSSSTSSDSSDSSSSSS DDSPARSVQSAAVPAPTSQLLSSLEK DEPRKSFQIKVQNLVPRSTDTSLKD GLFHEFKKFGKVTSVQIHGTSEERY GLVFFRQQEDQEKALTASKGKLLFFG MQIEVTAWIGPETESENEFRPLDERI DEFHPKATRTLFIGNLEKTTTYHDLR NIFQRFGEIVDIDIKKVNQVGPQYAF LQYCDIASVCKAIKKMDGEYLGNNRL KLGFGKSMPTNCVWLDGLSSNVSD QYLTRHFRCRYGPVVKVVFDRKGMALVLYNEIEYAQAQAVKTKGRKIGGNK IKVDFANRESQLAFYHCMEEKSGQDI RDFYEMLAERREERRASYDYNQDRT YYESVRTPGTYPEDSRRDYPARGREF YSEWETYQGDYYESRYDDPREYRD YRNDPYEQDIREYSYRQRERERERE RFESDRDRDHERRPIERSQSPVHLR RPQSPGASPSQAERLPSDSERRLYSR SSDRSGSCSSLPPRYEKLDKSRLER YTKNEKTDKERTFDPERVERERLIR KEKVEKDKTDKQKRKGKVVHSPSSQS SETDQENEREQSPEKPRSCNKL SRE KADKEGIKRNLELMPVVLTRVKE KEGKVIDHTPVEKLAKLDNDTVKS SALDQKLQVSQTEPAKSDLSKLESV RMKVPKEKGLSSHVEVEKEGRLKAR KHLKPEQPADGVS AVDLEKLEARK RRFADSNLKAQKQKPEVKKSSPEME DARVLSKKQPDVSSREVILLREGEAE RKPVRKEILKRESKKIKLDRLNTVAS PKDCQELASISVSGSRPSSDLQARL GELAGESVENQEVQSKKPIPSKPQL KQLQVLDQGPREDVRKNYCSLR DETPERKSGQEKSHSVNTEEKIGIDI DHTQSYRKQMEQSRKQMEMEIA KSEKFGSPKKDVDEYERRSLVHEVG KPPQDVTDDSPSKKKRMDHVD FDI CTKRERNYRSSRQISED SERTGGSPS VRHGSFHEDDPIGSPRLLSVKGSP KVDEKVLPSYNTVREESLKFN PYDS SRREQMADMAKIKLSVLNSEDELN RWDSQMKQDAGRFDV SFPNSIIKRD SLRKRSVRDLEPGEVPSDSDE DGEH KSHSPRASALYESSRLSFLLRDRE DK LRERDERLSSSLERNKFYSFALDKTI TPDTKALLERAKLSSSSREENWSFL DWDSRFANFRNNDKKEKVD SAPRPI PSWYMKKKKIRT DSEGKMDKKED HKEEQERQELFASRFLHSSIFEQD SKRLQHLERKEEDSDFISGRY GYKQT

SEGANSTTDSIQEPVVLFHRSRMELE  
TRMQQKEKEKDQPKPEVEKQEDTE  
NHPKTPESAPENKDSSELKTPPSVGP  
PSVTVVTTLESAPSALKTGDKTVEA  
PLVTEEKTVEPATVSEEAKPASEPAP  
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SVTTAIAEPVSAAPCLHEAPPPVDS  
KKPLEEKTAPPVTNNSEIQASEVLVA  
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TTPVNATVGTVNAAPGTVNAASAV  
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LSQGEVRMNTPTLPSITYSIRPEALH  
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CLLLALPCGRDQEDVVSQTESLCAA  
FITYLQAKQAGIINVPNPGSNQPAY  
VLQIFPPCEFSHLSRLAPDLLASIS  
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