

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q96T58	MINT_HUMAN	Homo sapiens	Msx2-interacting protein	38.808385	S2092;T2460;T2471;T2476;T2496;T2499;S2512;T2513;S2515;T2522;S2525;T2529;S2530;S2531;S2532;T2533;S2548;T2550;T2586;T2591;S2594;T2619;S2620;S2623;S2681;S2684;T2810;S2811;S2818;S2820;T2862;S2864;S2868;T2882;S2908;S2918;S2920;T2921;T2924;T2928;T2965;T2981;T3012;S3034;S3035;S3040;S3043;S3044;T3045;S3047;T3048;S3207;T3273;T3284;T3290;S3298;S3299;S3389;T3426;S3436;S3446;T3461;T3462;S3463;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	23301498;29351928;27114449;33214551;30059200;30620550;21158410;29237092;28314751;35254053;28657654;34725712;20068230;32574038;30379171;31492838;34846842;32119511;35289036;35132862;34019948	MVRETRHLWVGNLPENVREEKIEHFKRYGRVSEVKILPKRGSEGGVAAFVDFVDIKSAQKAHNSVNMGMGDRDLR TDYNEPGTIPSAARGLDDTVSIASRS REVSGFRGGGGGPPAYGPPPSLHARE GRYERRLDGASDNRRERAYEHSAYG HHERGTGGFDRTRHYDQDYRDPRE RTLQHGGLYASRSRSPNRFDAHDP RYEPREAREQFTLPSVVHRDIYRDDIT REVRGRRPERNYQHSRSRSPHSSQS RNQSPQRLASQASRPTRSPSGSGSR SRSSSSDSISSSSSTSSDSSDSSSSSS DDSPARSVQSAAVPAPTSQLLSSLEK DEPRKSFQIKVQNLVPRSTDTSLKD GLFHEFKKFGKVTSVQIHGTSEERY GLVFFRQQEDQEALASKGKLLFFG MQIEVTAWIGPETESENEFRPLDERI DEFHPKATRTLFIGNLEKTTTYHDLR NIFQRFGEIVDIDIKKVNQVGPQYAF LQYCDIASVCKAIKKMDGEYLGNNRL KLGFGKSMPTNCVWLDGLSSNVSD QYLTRHFRCRYGPVVKVVFDRKGMALVLYNEIEYAQAQAVKTKGRKIGGNK IKVDFANRESQLAFYHCMEEKSGQDI RDFYEMLAERREERRASYDYNQDRT YYESVRTPGTYPEDSRRDYPARGREF YSEWETYQGDYYESRYDDPREYRD YRNDPYEQDIREYSYRQREERERE RFESDRDRDHERRPIERSQSPVHLR RPQSPGASPSQAERLPSDSERRLYSR SDRSGSCSSLPPRYEKLDKSRLER YTKNEKTDKERTFDPERVERERLIR KEKVEKDKTDKQKRKGKVVHSPSSQS SETDQENEREQSPEKPRSCNKLRE KADKEGIAKNRLELMPCVLTVRKE KEGKVIDHTPVEKLIKALDNDTVKS SALDQKLQVSQTEPAKSDLSKLESV RMKVPKEKGLSSHVEVEKEGRLKAR KHLKPEQPADGVS AVDLEKLEARK RRFADSNLKAQKQKPEVKKSSPEME DARVLSKKQPDVSSREVILLREGAE RKPVRKEILKRESKKIKLDRLNTVAS PKDCQELASISVSGSRPSSDLQARL GELAGESVENQEVQSKKPIPSKPQL KQLQVLDQGPREDVRKNYCSLR DETPERKSGQEKSHSVNTEEKIGIDI DHTQSYRKQMEQSRKQMEMEIA KSEKFGSPKKDVDEYERRSLVHEVG KPPQDVTDSPPSKKRMDHVDFDI CTKRERNYRSSRQISEDSERTGGSPS VRHGSFHEDEDPIGSPRLLSVKGSP KVDEKVLPSYNTITVREESLKFNPYDS SRREQMADMAKIKLSVLNSEDELN RWDSQMKQDAGRFDVFPNSIHKRD SLRKRSVRDLEPGEVPSDSEDEGEH KSHSPRASALYESSRSLFLLRDREDK LRERDERLSSSLERNKFYSFALDKTI TPDTKALLERAKLSSSSREENWSFL DWDSRFANFRNNDKKEKVD SAPRPI PSWYMKKKKIRTDSGKMDKKED HKEEQERQELFASRFLHSSIFEQD SKRLQHLERKEEDSDFISGRYGGKQT

SEGANSTTDSIQEPVVLFHRSRMELE
TRMQQKEKEKDQPKPEVEKQEDTE
NHPKTPESAPENKDSSELKTPPSVGP
PSVTVVTTLESAPSALKTGDKTVEA
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APVEQLEQVDLPPGADPDKEAAMM
PAGVEEGSSGDQPPYLDKPPTPGA
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SEEANEPKAEKPDATADAEPDANQK
AEAAPESQPPASEDLEVDPPVAAKD
KKPNKSKRSKTPVQAAAVSIVEKPV
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VGPQIGVKESMPEKAAEEEGSEQ
KRDRKDAAGTDKNPPETAPVEVVEK
PAPEKNSKSKRGRSRNSRLAVDKSA
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VAVSPKESSEPKEDGLSSQLKSDP
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KQMELEQAVEHIAKLAEASASAAYK
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TPTKASVPPDLPPPPQAPVDEEPQA
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VTAAKLSPPVASGGIPHQSPPTKVTE
WITRQEEPRAQSTPSPALPPDTKASD
VDTSSSTLRKILMDPKYVSATSVTST
SVTTAIAEPVSAAPCLHEAPPPVDS
KKPLEEKTAPPVTNNSEIQASEVLVA
ADKEKVAPVIAPKITSVISRMPVSI
ENSKITLAKPAPQTLTGLVLSALTGL
VNVSLVPVNAKGPVKGSVTTLKSL
VSTPAGPVNVLKGPNVLTGPNVNL
TTPVNATVGTVNAAPGTVNAASAV
NATASAVTVTAGAVTAASGGVTATT
GTVTMAGAVIAPSTKCKQRASANEN
SRFHGSMPIVDRPADAGSGAGLR
VNTSEGVLLSYSGQKTEGPQRISAK
ISQIPPASAMDIEFQQSVSKSQVKPD
SVTASQPPSKGPQAPAGYANVATHS
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KPEPIHLSVSTPVTQGGTVKVLTOGI
NTPPVLVHNQLVLTSPSIVTNNKKLAD
PVTLKIETKVLQPANLGSLLTPHHP
ALPSKLPTEVNHVPSGSPADRTVS
HLAAAKLDAHSRPSGPGPSSFPRA
SHPSSTASTALSTNATVMLAAGIPVP
QFISSIHPEQSVIMPPHSITQTVSLSH
LSQGEVRMNTPTLPSITYSIRPEALH
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AGVPALASQHPPEEVHYHLPVARA
TAPVQSEVLVMQSEYRLHPYTVPRD
VRIMVHPHVTAVSEQPRAADGVVKV
PPASKAPQQPGKEAAKTPDAKAAPT

								TPAPVPVPVPLPAPAPAPHGEARILT VTPSNLQQLPLTPPVVTHGVQIV HSSGELFQEYRYGDIRTYHPPAQLT HTQFPAASSVGLPSRTKTAAGPPPE GEPLQPPQPVQSTQPAQPAPPCPPS QLGQPGQPPSSKMPQVSQEAKGTQT GVEQPRLPAGPANRPPEPHTQVQRA QAETGPTSFPSVSVSMKPDLPVSLP TQTAPKQPLFVPTTSGPSTPPGLVLP HTEFQPAPKQDSSPHLTSQRPVDMV QLLKKYPIVWQGLLALKNDTAAVQL HFVSGNNVLAHRSLPLSEGGPPLRI AQRMRLEATQLEGVARRMTVETDY CLLLALPCGRDQEDVVSQTESLCAA FITYLQAKQAAGIINVPNPGSNQPAY VLQIFPPCEFSEHLSRLAPDLLASIS NISPHLMIVIASV
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