

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9EPQ8	TCF20_MOUSE	Mus musculus	Transcription factor 20	29.840855	S233;S252;S254;T725	S447;S458;S567;S588;S603;S612;S669;S900;S994;S1033;S1081;S1333;S1363;S1389;S1550;S1697;T1699;T1790;T1792	22645316;36852467;21606357	MQSFREQSSYHGNQQSYQPQEVHSS SRIEEFSPRQAQMFQNFQGGAGGGSS GTGSSSSGRRGTAAAAAMASETSG HQGYQGFRKEAGDFYYMAGNKDTV AAGTPQPPQRRPSGPPVQSYGPPQGS SFGNQYASEGHVSQFQAQHSALGG VSHYQQDYTGPFSPGSAQYQQQASS QQQQQQQQQQQQQQQQQQQQVQQ LRQQLYQSHQPLPQTGQPASGSSH LQPMQRPSTLPSSAGYQLRVGGFGQ HYQSSASSSSSSFFSPQRFSSQSGQS YDGSYSVNAGSQYEGHNVGSNAQA YGTQSNYSYQPQSMKNFEQAKIPPG NQQGQQQQQQPQPQQQQPQQQQ QQQQQQQHPPQHVMQYTNAAATKM PLQSQVGQYNQPEVPVRSMPQFHQ NFSPISNPSAASVVQSPSCSSTPSP LMQSGENLQCGQGNVPMSSRNRL QLMPQLSPTPSMMPSPNSHAAGFK GFGLEGVPEKRLTDPGLSSLALSSQ VANLPNTVQHMLLSDALTPQKKTSK RPSSSSKKADSCCTNSEGSSQPEEQL KSPMAESLDGGCSSSSEDQGERVR QLSGQSTSSDTTYKCGASEKAGSSPT QGAQNEAPRLSTSPATRDEAASPGA KDTLSSEGN TKVNEKTVGVIVSREA MTGRVEKSGGQDKGSQEDDPAASQ RPPNSGVKEISHTSLPQDPGPGGS KGNKNGDNNSSNHNGEGNGPSSH SAVGPSFTGRTEPSKSPGSLRYSYKE SFGSAVPRNVSGYPQYPSGQEKGDF GSHGERKGRNEKFPPLLQEVLQGY HHHPDRRYPRSAQEHQGMASGLEG TARPNILVSQTNELASRGLLNKSIGS LLENPHWGPWERKSSSTAPEMKQI NLSDYPIPRKFEIEPPSSAHEPGGSL SERRSVICDISPLRQIVRDPGAHSLG HMGTDARIGRNERLNPSLSQSVILP GGLVSMETKLSQSGQIKEEDFEQS KSQASFNKKSGDHCHPTSIKHETYR GNASPGAAAHSISDYGPQDSRSTP MRRVPGRVGSRETMRGRSSSQYHD FAEKLKMSPGRSRGPGGDPHMMNP HMTFSEANRSSLHAPFSPNSES LA SAYHTNTRAHAYGDPNTGLNSQLHY KRQMYQQQEEYKDWASSSAQVI AAAQHRQEGPRKSPRQQFLDRVR SPLKNDKDGMMYGPVGTYHDPST QEAGRCLMSSDGLPAKSMELKHSS QKLESCWDLRQTSAPAKSSGPPG MSNQKRYGPPHEPDGHGLAESAQ SKPSNVMLRRLPGQEDHSSQNPLIM RRRVRSFISPIPSKRQSDVKNSNAD DKGRLLHPSKEGADKAYNSYSHLSH SQDIKSIPKRDSSKDLNPNDRNCP AVTLTSPAKTKILPPRKGRLKLEAIV QKITSPNIRRSASANS AEAAGDVTTL

								DDILSLKSGPPEGTVATQEAEMEK RKCEVVSDLVSVTNQESNVEKPLPG PSEEWKRGSGDDKVKTEAHVETASTG KEPSGTMTSTASQKPGGNQGRPDG SLGGAAPLIFPDSKNVAPVIGILAPEA NPKAEEKENDTVMISPKQESFPPKG YFPSGKKKGRPIGSVNKQKKQQQP PPPPQPPQMPEGSADGEPKPKKQRO RRERRKPGAQPRKRKTKQAVPIVEP QEPEIKLYATQPLDKTDANKSFFP YIHVVKCELGAVCTIINAEEMEQTK LVRSRKGQRSLTPPPSSTESKLPAS SFMLQGPVVTESSVMGHLVCCLCG KWASYRNMGDLFGPFYPQDYAATLP KNPPPKRSSEMQSKVKVRHKSASN GSKTDTEEMEEQQQKEQRSLAHP RFKRRHRSEDCGGGPRSLRGLPCK KAATEGSSEKTVSDTKPSVPTTSEGG PELELQIPELPLDSNEFWVHEGCIL WANGIYLVCGRLYGLQEALAIAREM KCSHCQEAGATLGCYNGCSFRYHY PCAIDADCLLHEENFSVRCPKHKPP LPCPLPPLQNKTAKGSLSTEQSERG
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