

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9UGU0	TCF20_HUMAN	Homo sapiens	Transcription factor 20	19.474911	S220;S237;S238;S240;S241;S242;S243;S244;S245;S246;T336;S368;T385;S559;S686;T693;S694;T696;S699;S701;S704;S1474	S419;S430;S538;S559;S574;S583;S640;S871;S966;S1005;S1053;S1305;S1335;S1361;S1522;S1669;T1671;T1762;T1764	30379171;32574038;29237092;31492838;34846842;35254053;29351928;27114449;33214551;35132862;30059200;28411811;35289036;34019948	MQSFREQSSYHGNQQSYPQEVHGS SRLEEFSPRQAQMFQNFGGTGGSS GSSGSGSGGGRRGAAAAAAMASET SGHQYQGFKEAGDFYYMAGNKD PVTTGTTPQPPQRRRPSGPVQSYGPPQ GSSFGNQYSGSEGHVGFQAQHSGL GGVSHYQQDYTGPFSPGSAQYQQQA SSQQQQQQVQQLRQQLYQSHQPLP QATGQPASSSSHLQPMQRPSTLPSS AAGYQLRVGQFGQHYQSSASSSSSS SFPSPQRFSQSGQSYDGSYNVNAGS QYEGHNVGSNAQAYGTQSNYSYQP QSMKNFEQAKIPQGTQQGQQQQQP QQQOHPHQHVMQYTNAAATKLPQS QVGOYNQPEVPVRSMPQFHQNFSP SNPSPAASVVQSPSCSSTPSPMLQT GENLQCGQGSVPMGSRNRILQLMP QLSPTPSMMPSPNSHAAGFKGFGL GVPEKRLTDPGLSSLSALSTQVANLP NTVQHMLLSDALTPQKKTSKRPSSS KKADSCNTSEGSSQPEEQLKSPMAE SLDGGCSSSESDQGERVRLSGQST SSDTTYKGGASEKAGSSPAQGAQNE PPRLNASPAAREEATSPGAKDMPLS SDGNPKVNEKTVGVIVSREAMTGRV EKPGGQDKGSQEDDPAATQRPPSN GGAKETSHASLPQPEPPGGGSKGN KNGDNNSNHNGEGNGQSGHSAAG PGFTSRTEPSKSPGSLRYSYKDSFGS AVPRNVSGFPQYPTGQEKGDFTGHG ERKGRNEKFPDLLQEVLOGYHHHP DRRYSRSTQEHQGMAGSLEGTRTP NVLVSQTNELASRGLLNKSGSLE NPHWGPWERKSSSTAPEMKQINLT DYPIPRKFEIEPQSSAHEPQGSLSER RSVICDISPLRQIVRDPGAHSLGHMS ADTRIGRNDRLNPTLSQSVILPGLV SMETKLKSQSQIKEEDFEQSKSQA SFNNKKSQGDHCHPPSIKHESYRGNA SPGAATHDSLSDYGPQDSRPTPMRR VPGRVGGREGMRGRSPSQYHDFAE KLMSPGRSRGPGGDPHMMNPHM TFSERANRSSLHTPFSPNSETLASAY HANTRAHAYGDPNAGLNSQLHYKR QMYQQQPEEYKDWSSGSAQGVIAA AQHRQEGPRKSPRQQQFLDRVRSPL KNDKDGMMYGPVGTYHDPQAQEA GRCLMSSDGLPNKGMELKHGSQKL QESCWDLRQTSQPAKSSGPPGMSS QKRYGPPHETDGHGLAEATQSSKPG SVMLRRLPGQEDHSSQNPLIMRRRV RSFISPIPSKRQSQDVKNSSSTEDKGR LLHSSKEGADKAFNSYAHLSHSQDI KSIPKRDSSKDLPSRNCPAVTLT SPAKTKILPPRKGRGLKLEAIVQKITS PNIRRSASSNSAEAGDVTVLLDILS LKSGPPEGGSVAVQDADIEKRKGEV ASDLVSPANQELHVEKPLPRSSEEW RGSVDDKVKTTETHAETVTAGKEPPG AMTSTTSQKPGSNQGRPDGSLGGTA PLIFPDSKNVPPVILAPEANPKAEE KENDTVTISPKQEGFPPKGYFPPSGKK KGRPIGVSNNKQKQQQPPPPPPQPP

QIPEGSADGEPKPKKQRRRERRKP GAQPRKRRTKQAVPIVEPQEPEIKLK YATQPLDKTDAKNKSFYPIHVVNK CELGAVCTIINAEEEEQTKLVRGRKG QRSLTPPPSSTESKALPASSFMLQGP VVTESVVMGHLVCCCLCGKWASYRN MGDLFGPFYQDYAATLPKNPPPKR ATEMQSKVKVRHKSASNGSKTDTEE EEEEQQQQKEQRSLAAHPRFKRRH RSEDCGGGPRSLRGLPCKKAATEG SSEKTVLDKPSVPTTSEGGPELELQ IPELPLDSNEFWVHEGCILWANGIYL VCGRLYGLQEALEIAREMKCCHCQE AGATLGCYNKGCSPFRYHYPCAIDAD CLLHEENFSVRCPKHKPPPLPCPLPPL QNKTAKGSLSTEQSERG
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