

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
Q15911	ZFHX3_HUMAN	Homo sapiens	Zinc finger homeobox protein 3	26.112264	S219;S353;T354;S363;T547;S571;S574;S3677	S426;T428;S533;S571;S1197;S1204;S1590;S2625;S2786;S2795;S2892;S2896;S3409;S3418;S3432;S3593;S3677	34019948;35132862;35254053;29237092;30059200;35289036;37340703;29351928;34846842;21606357;31492838;32574038;30379171	MEGCDSPVVSCKDNGCGIPQHQQW TELNSTHLPDKPSMSMEQSTGESHGP LDSLRAFNERLAESTASAGPPSEPA SKEVTCNECSASFASLQTYMEHHCP SARPPPPLREESASDTGEEGDEESD VENLAGEIVYQPDGSAYIVESLSQLT QGGGACGSGSGGSLPLSLFLNSLPG AGGKQGDPSCAAPVYPQIINTFHAS SFGKWFEGPDQAFPNTSALAGLSPV LHSFRVFDVRHKSNDYLNSDGSAK SSCVSKDVPNNVDLSKFDGFVLYGK RKPILMCFCLKLSFGYVRSFVTHAV HDHRMTLSEDERKILSNKNISAIHQG IGKDKPLVSLFLEPKNKNFQHPVLS TANLIGPGHSFYGKFSGIRMEGEEA LPAGSAAGPEQPQAGLLTPSTLLNLG GLTSSVLKTPITSVPLGPLASSPTKSS EGKDSGAAEGEKQEVGDGDCFSEK VEPAEEEEEEEEEEEEEEEEEEEE EEEEEEEEDEGCKGLFPELDEELED RPHEEPGAAAGSSSKDLALSNOQIS NSPLMPNVLQTLRGTASTSSNSAS SFVVFDDGANRRNRSLFNSEGVAN VAEGGRRLDFADESANKDNATAPEP NESTEGDDGGFVPHHQHAGSLCEL GVGECPSGSGVECPKCDTVLGSSRS LGGHMTMMHSRNSCKTLKCPKCN WHYKYQQTLEAHMKEKHPEPGGSC VYCKSGQPHPRLARGESYTCGYKPF RCEVCNYSTTTKGNLSIHMQSDKHL NNMQNLQNGGGEQVFSHTAGAAA AAVAAAAAANISSSCGAPSPKPKT KPTWRCEVCDYETNVARNLRHMTS EKHMHNMMLLQONMTQIQHNRH LGLGSLPSPAEELYQYYLAQNMINL PNLKMDAASDAQFMMSGFQLDPA GPMAAMTPALVGGIPLDMRLGGG QLVSEELMNLGESFIQTNDPSLKL QCAVCNKFTTDNLDMLGLHMNVER SLSEDEWKAVMGDSYQCKLCRYNT QLKANFQLHCKTDKXVQKYLVAHI KEGGKANEWRLKCAIGNPVHLKC NACDYNTNSLEKRLRLHTVNSRHEAS LKLYKHLQQHESGVEGESCYHCVL CNYSTKAKLNLIQHVRSMKHORSES LRKLQRLQKGLPEDEDLGQIFIRR CPSTDPEEAIEDVEGPSETAADPEEL AKDQEGGASSQAEEKELTDSPATSK RISFPGSSSPLSSKRPKTAEEIKPEQ MYQCPYCKYSNADVNRLRVHAMTQ HSVQPMRLRCPQLCQDMLNKKIHLQL HLTHLHSVAPDCVEKLIMTVTTPEM VMPSSMFLPAAVPDRDGNSNLEEA GKQPETSEDLGKNILPSASTEQSGDL KPSADPGSVREDSGFICWKKGCNQ VFKTSAALQTHFNEVHAKRPQLPVS DRHVYKYRCNQCSLAFKTIEKLQLH SQYHVIRAATMCCLCQRSFRTFQAL KKHLETSHLELSEADIQQLYGGLLA NGDLLAMGDPTLAEDHTIIVEEDKE EESDLEDKQSPGSDSGSVQEDSGS EPKRALPFRKGNFTMEKFLDPSRP YKCTVCKESFTQKNILLVHYNVSH

LHKLKRALQESATGQPEPTSSPDNK  
PFKNCNTCNVAYSQSSTLEIHMRSVL  
HQTKARAAKLEAASGSSNGTGNSSS  
ISLSSSTPSPVSTSGSNTFTTNSPSSA  
GIAPSSNLLSQVPTESVGMPLGNPI  
GANIASPSEPKEANRKKLADMIA SR  
QQQQQQQQQQQQQQQQQQQAQTL  
AQAAQVQAHLQQELQQQAALIQSQ  
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LLFPFYIPSAEFQLNPEVSLPVTSGAL  
TLTGTGPGLLEDLKAQVQVPQQSHQ  
QILPQQQNQLSIAQSHSALLQPSQ  
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PGGGSEPSMLPPRIASDARGNATKA  
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PPLPAAPPQASTPAIPASAPPITSPTI  
APAQPSVPLTQLSMPMELPIFSPMLM  
MQTMPLQTLPAQLPPQLGPVEPLPA  
DLAQLYQHQLNPTLLQQQNKRPTR  
ITDDQLRVLRQYFDINNSPSEEQIKE  
MADKSGLPQKVIKHWFRNTLTKER  
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PPSPEPPKQEWGSKRSSRTRFTDY  
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SLPQPPQAPPQCPLPQSSPSPSQL  
SHLPLKPLHTSTPQQLANLPPQLIPY  
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SAQNQFIHPQFLDRSLDMPFMLFDP  
SNPLLASQLLSGAIPQIPASSATSPST  
PTSTMNTLKRKLEEKASASPGENDS  
GTGGEEPQRDKRLRRTTITPEQLEILY  
QKYLDSNPTRKMLDHAHEVGLKK  
RVVQVWFQNTARERKQGFRVGP  
AQAHRRCPFCRALFKAKTALEAHIR  
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QGVPLSPVSKTMELSPRTLLSPSSIK  
VEGIEDFESPSMSSVNLNFDQTKLD  
NDDCSSVNTAITDTTGTGDEGNADND  
SATGIATETKSSSAPNEGLTKAAMM  
AMSEYEDRLSSGLVSPAPSFYSKEYD  
NEGTVDYSETSSLADPCSPSPGASGS  
AGKSGDSGDRPGQKRFRMQMTNLQ  
LKVLKSCFNDRTPMLECEVLGND  
IGLPKRVVQVWFQARAKEKSKLS  
MAKHFGINQTSYEGPKTECTLCGIK  
YSARLSVRDHIFSQQHISKVKDTIGS  
QLDKEKEYFDPATVRQLMAQQELDR  
IKKANEVGLAAQQQGMFDNTPLOA  
LNLPTAYPALQGIPPVLLPGLNSPSL  
PGFTPSNTALTSPKPNLMGLPSTTVP  
SPGLPTSGLPNKPSASLSSPTPAQA  
TMAMGPQQPPQQQQQQQQPQVQQ  
PPPPAAQPPPTPLPLQQQQQRKD

									KDSEKVKKEKAHKKGELPVPKK EKGEAPTATAATISAPLPTMEYAVDP AQLQALQAALTSPTALLTSQFLPYF VPGFSPYYAPQIPGALQSGYLQPMYG MEGLFPYSPALSQALMGLSPGSLLO QYQQYQQSLQEAIQQQQRQLQQQ QQQKVQQQPKASQTPVPPGAPSPD KDPAKESPKPEEQKNTPREVSPLLPK LPEEPEAESKADSLYDPFIVPKVQY KLVCRKCQAGFSDEEAARSHKSLC FFGQSVVNLOEMVLHVPTGGGGGG SGGGGGGGGGGGGGGYHCLACES ALCGEEALSQHLESALHKHRTITRA ARNAKEHPSLLPHSACFPDPSTAST SQSAAHSNDSPPPSAAAPSSASPH ASRKSWPQVVSRSAAKPPSFPLSS SSTVTSSSCSTSGVQPSMPTDDYSEE SDTDLSQKSDGPASPVEGPKDPSCP KDSGLTSVGTDTFRL
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