

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
Q5T1R4	ZEP3_HUMAN	Homo sapiens	Transcription factor HIVEP3	26.862484	T516;T531;S763;S766;T1006;T1008;S1075;S1076;S1077;S1080;S1089;S1094;T1401;S1409;S1570;S1919	NaN	35254053;37340703;31492838;29351928;28657654	MDPEQSVKGTKKAEGSPRKRLTKGE AIQTSVSSSVYPGSGTAATQESPAQ ELLAPQFPFGPSSVLRREGSQEKTGQ QQKPPKRPPIEASVHISQLPQHPLTP AFMSPGKPEHLLLEGSTWQLVDPMR PGPSGSFVAPGLHPQSQLLPSHASII PPEDLPGVPKVFVPRPSQVSLKPTEE AHKKERKPQKPGKYICQYCSRCAK PSVLQKHRSHTGERPYPCGPGCFSF KTKSNLYKHRKSHAHRKAGLASGM GGEMYPHGLEMERIPGEEFEETEG ESTDSEETSATSGHPAELSPRPKQP LLSSGLYSSGSHSSSHERCSLSQSST AQSLDPPPFVPEPSSEHPLSHKPEDT HTIKQKLALRLSERKKVIDEQAFSLP GSKGSTESGYFSRSESAEQQVSPPN TNAKSYAEIIFGKCGRIGQRTAMLTA TSTQPLLPLSTEDKPSLVPLSVPRTO VIEHITKLITINEAVVDTSEIDSVKPR RSSLSRRSSMESPKSSLYREPLSSH EKTKEQSLLSLQHPSTAPPVPLLR SHSMPSAACTISTPHHPFRGSYSFD DHITDSEALSHSSHVFTSHPRMLKR QPAIELPLGGEYSSEEPGSSKDTAS KPSDEVPEKESELTKTKKGLKTKG VIYECNICGARYKKRDNYEAHKKYC SELQIAKPISAGTHTSPEAEKSQIEH EPWSQMMHYKLGTTLELTPLRKRR KEKSLGDEEPPAFESTKSQFGSPG PSDAARNLPLESTKSPAEPSKSVPSL EGPTGFQPRTPKPGSGSESGKERRT TSKEISVIQHTSSFESDSLEQPSGL EGEDKPLAQFPPPPAPHGRSAHSL QPKLVRQPNIQVPEILVTEEPDRPDT EPEPPPKEPEKTEEFQWPQRSQTLA QLPAEKLPKPKRLRLAEMAQSSGE SSFESSVPLSRSPSQESNVLSGSSR SASFERDDHGKAEAPSPSSDMRPKP LGTHMLTVPSHHPHAREMRRSASE QSPNVSHSAHMTETRSKSFYDGSLS LTGPSAPAVAPPARVAPPERRKCFL VRQASLSRPESELEVAPKGRQESE EPQPSSSKPSAKSSLSQISSAATSHG GPPGGKGGQDRPPLGPTVPYTEAL QVFHHPVAQTPLHEKPYLPPVSLFS FQHLVQHEPGQSPEFFSTQAMSSLL SSPYSMPPLPPLSFQAPPLPLQPTVL HPGQLHLPQLMHPANIPFRQPPSF LPMPYPTSSALSSGFFLPLQSQFALQ LPGDVESHLPQIKTSLAPLATGSAGL SPSTEYSSDIRLPPVAPPASSSAPSA PPLALPACPDTMVLVVPVRVQTNM PSYGSAMYTTLSQILVTQSQGSSATV ALPKFEEPPSKGTTVCADVHEVGP GPSGLSEEQSRAPPTPYLRVPVTLPE RKGTSLSSESILSLEGSSSTAGGSKR VLSPAGSLELTMETQQQKRVKEEEA

SKADEKLELVKPCSVVLTSTEDGKRP
EKSHLGNQGGRRLEMLSSLSDD
PSDTKEIPPLPHPALSHGTAPGSEAL
KEYPQPSGKPHRRGLTPLSVKKEDS
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SQEGTDSKKVLQFPSLHTTTNVSWC
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LYNPNLPGVSTKAALSLLRSKQKVS
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CQETGVLEEEAEEGTSDDLFQDSE
GREGSEAVEEHQFSDLESDSDSDL
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GPPHALRADSSPILGPQPPDAPASGT
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KPVSPRRPWSPEAGSRPPLARKH
SLTKNDSSPQRCSAREPQASAPSP
GLHVDPGRGMGALPCGSPRLQLSPL
TLCPLGRELAPRAHVLSKLEGTDDPG
LPRYSPTRRWSPGQAESPPRSAPP
KWALAGPGSPSAGEHGPGLGLDPRV
LFPPAPLPHKLLSRSPETCASPWQKA
ESRSPSCSPGAHPLSSRPFSALHDF
HGHILARTEENIFSHLPLHSQHLTR
APCPLIPGGIQMVQARPGAHTLLP
GPTAAWVSGFSGGSDLTGAREAQE
RGRWSPTESSASVSPVAKVSKFTLS
SELEGGDYPKERERTGGGPGRPPDW
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