>MOUSE Histone acetyltransferase KAT2B OS=Mus musculus OX=10090 GN=Kat2b PE=1 SV=2

MAEAGGAGSPALPPAPPHGSPRTLATAAGSSASCGPATAVAAAGTAEGPGGGGSARIAVK

KAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTPPRGDLQQIIVSLTESCRS

CSHALAAHVSHLENVSEEEMDRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSI

LQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKERQTTIELAKMFLNRINYW

HLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTKVFGRTLLRSVFTI

MRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSP

LGIQTVISPPVTGTALFSSNSTSHEQINGGRTSPGCRGSSGLEANPGEKRKMNNSHAPEE

AKRSRVMGDIPVELINEVMSTITDPAGMLGPETNFLSAHSARDEAARLEERRGVIEFHVV

GNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGIC

FRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHEILNFLTYADEYAIGYFKK

QGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPQIPYTEFSVIIKKQKEIIKKLIERKQA

QIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPKDPEQLYSTLKNILQQV

KNHPNAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLRNRYYVSKKLFMADLQRVFTNC

KEYNPPESEYYKCASILEKFFFSKIKEAGLIDK

>HUMAN Histone acetyltransferase KAT2B OS=Homo sapiens OX=9606 GN=KAT2B PE=1 SV=3

MSEAGGAGPGGCGAGAGAGAGPGALPPQPAALPPAPPQGSPCAAAAGGSGACGPATAVAA

AGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTP

PRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQ

NSPIWDQDFLSASSRTSQLGIQTVINPPPVAGTISYNSTSSSLEQPNAGSSSPACKASSG

LEANPGEKRKMTDSHVLEEAKKPRVMGDIPMELINEVMSTITDPAAMLGPETNFLSAHSA

RDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSK

EPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNR

YYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>MUNMU Histone acetyltransferase OS=Muntiacus muntjak OX=9888 GN=FD754\_004887 PE=3 SV=1

MGPGTARVAGASGIWLFLSESLMDGPRGCSLGLWYQSGGHTAHVSHLENVSEEEMNRLLG

IVLDVEYLFTCVHREEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQ

GVNNFVQYKFSHLPPKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYT

RWLCYCNVPQFCDSLPRYETAQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLIL

THFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTVSYNSSSTSL

EQQNGGSTSPSCRGASGLETNPGEKRKMNDSHVLEETKKPRVMGDIPLELIHEVMSTITD

PAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLSQKPNKKVLMWLVGLQNVFS

HQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVK

GYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGA

TLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESI

PGIRETGWKPSGREKSKEARDPEQLYSTLRSILQQVKSHQSAWPFMEPVKRTEAPGYYEV

IRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSK

IKEAGLIDK

>tr|D2HXC4|D2HXC4\_AILME Histone acetyltransferase (Fragment) OS=Ailuropoda melanoleuca OX=9646 GN=PANDA\_017267 PE=3 SV=1

AEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRL

LGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKEN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSNSS

SLEQPNGGSTSPSCKGSSGLEANPGEKRKMNDSHAMEEAKKPRVMGDIPMELIDEVMSTI

TDPAAMLRPETNLLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKEKSKEPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFF

SKIKEAGLIDK

>tr|A0A2K5VBM7|A0A2K5VBM7\_MACFA Histone acetyltransferase OS=Macaca fascicularis OX=9541 GN=KAT2B PE=3 SV=2

MNCDKSGLPSPSPPPLWDKNFPALPGAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTES

CRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLR

KSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKERQTIVELAKMFLNRI

NYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSV

FTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSR

TSHHLTPSSPFARAVISPPPVAGTISYNSTSSSLEQSNAGSSSPACKRKMTDSHVLEEAK

RPRVMGDIPMELINEVMSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGN

SLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFR

MFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQG

FSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQI

RKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPRDPDQLYSTLKSILQQVKS

HQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKE

YNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A7N5KJV9|A0A7N5KJV9\_AILME Lysine acetyltransferase 2B OS=Ailuropoda melanoleuca OX=9646 GN=KAT2B PE=4 SV=1

GFLSGPWGRVAAGAFERVRLSHGQGPSCVPGTSGQSGLSPWPALWMRPLGTDHSVDICWG

HGTKGHWSAAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLEN

VSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEK

KPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPN

DDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKD

KLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTAGTISYNSN

SSSLEQPNGGSTSPSCKGSSGLEANPGEKRKMNDSHAMEEAKKPRVMGDIPMELIDEVMS

TITDPAAMLRPETNLLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQ

NVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSN

EQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKD

YEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIP

IESIPGIRETGWKPSGKEKSKEPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPG

YYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKF

FFSKIKEAGLIDK

>tr|A0A6J2M6I0|A0A6J2M6I0\_9CHIR Histone acetyltransferase OS=Phyllostomus discolor OX=89673 GN=KAT2B PE=3 SV=1

MSEAGGVALGSGAGAGAGAGAGLGALPPQPPAPPPLPPQGSPCAAAAGGSGSCGPATAVA

AAGTAEGPGGSGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPT

PPRADLQQMIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEE

DADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPPK

ERQTIMELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLP

RYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYS

QNSPIWDQDFLSASSRTSQLGIQTVINPPPVAGTISYNSNSSSLEHLNGGSTSPSSKGSS

GLEANPGEKRKMNDCHVLEEAKKPRVMGDIPMELITEVMSTITDPAVMVGPENNFLSAHS

ARDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVF

DPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEFHIK

HDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPQIPYTEF

SVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKQSGKEKS

KEPKDSDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKN

RYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A5F9D1K3|A0A5F9D1K3\_RABIT Histone acetyltransferase OS=Oryctolagus cuniculus OX=9986 PE=3 SV=1

LGHPPLHSLATAESWPGRGATGTESGAPTGTRTRCAGAARRRISLVSRGAEESCKCNGWK

NPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLF

TCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYK

FSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVP

QFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSM

LEEEVYSQNSPIWDQDFLSASSRISQLGIQTVINPPPVARTVSYNSNSSSLEQPNGGSSS

PACKAASGLEANPGEKRKMNDSHVLEEAKKPRVMGDIPMELIHEVMSTITDPAAMLGPET

NFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKRILMWLVGLQNVFSHQLPRMPKE

YITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNH

LKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKAKYVGYIKDYEGATLMGCELNP

RIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGISMYRPS

FKSEEPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSER

LKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|G3RKM2|G3RKM2\_GORGO Histone acetyltransferase OS=Gorilla gorilla gorilla OX=9595 GN=KAT2B PE=3 SV=1

PAPPQGSPCAAAAGGSGACGPATAVAAAGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEK

LGVYSACKAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENV

SEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKK

PPFEKPSIEQGVNNFVQYKFSHLPAKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPND

DISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDK

LPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTVINPPPVAGT

ISYNSTSSSLEQPNAGSSSPACKASSGLEANPGEKRKMTDSHVLEEAKKPRVMGDIPMEL

INEVMSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKILM

WLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVF

CAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKY

VGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKD

GVRQIPIESIPGIRETGWKPSGKEKSKEPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVK

RTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCA

NILEKFFFSKIKEAGLIDK

>tr|A0A6P4UYN5|A0A6P4UYN5\_PANPR Histone acetyltransferase OS=Panthera pardus OX=9691 GN=KAT2B PE=3 SV=1

MLFLVFTGPSQLQWKAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHALAAH

VSHLENVSEEEMNRLLGIVLDVEYLFTCVHREEDADTKQVYFYLFKLLRKSILQRGKPVV

EGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKERQTIVELAKMFLNRINYWHLEAPSQR

RLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQ

ARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTVIS

PPPVAGTISYNSNSSSLEQPNGGSTSPSCKGSSGLEANPGEKRKMNDSHALEEAKKPRVM

GDIPMELIDEVMSTITDPAAMLGPETNLLSAHSARDEAARLEERRGVIEFHVVGNSLNQK

PNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQ

GFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEI

KIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYP

GLSCFKDGVRQIPIESIPGIRETGWKPSGREKSKEPKDPDQLYSTLKSILQQVKSHQSAW

PFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPE

SEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A6P5KCW8|A0A6P5KCW8\_PHACI Histone acetyltransferase OS=Phascolarctos cinereus OX=38626 GN=KAT2B PE=3 SV=1

MSEAGGAGPAGGGGGGGGGGGGGAGGQQQPPPPPPQPPPPPVPLPPPPPPPQGSPATGGG

PARAAASAAAAAAAAPAAAVPAPVPAGPGPAASSGPASAESPGVGSGASTARIAVKKAQL

RSAPRAKKLEKLGVYSSCKAEESCKCNGWKNPNPPPTPPRADVQQIIVSLTESCRSCSHT

LATHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMG

KPVVEGSLESPPFEKPSIEQGVNNFVHYKFSHLPSKERQTIVELAKMFLNRINYWHLETP

SQRRLRAPNDDVAGYKVNYTRWLCYCHVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQL

LEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQSSPIWDQDFLAASSHSGQLGIQT

VINPPPVARTVSYNGSPSSLEQPIGGSMSPACKVSSGLEGNRGEKRKMNDLHSLEEAKRP

RVVGDIPIELINEVMSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSL

NQKPNKKIMMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMF

PSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHSILNFLTYADEYAIGYFKKQGFS

KDIKVPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRK

VYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKERGKEPKDPDQLYSTLKNILQQVKSHQ

SAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYN

PPESEYYKCANILEKFFFTKIKEAGLIDK

>tr|A0A3Q7WQF9|A0A3Q7WQF9\_URSAR Histone acetyltransferase OS=Ursus arctos horribilis OX=116960 GN=KAT2B PE=3 SV=1

MSEAGGAGPGGGGAGAGAGAGLGALPPQPSAPPPAPPQGSPCAAAAGGSGACGPATAVAA

AGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTP

PRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQ

NSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSNSSSLEQPNGGSASPSCKGSSG

LEANPGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETSLLSAHSA

RDEAARLEERRGVIEFHVVGNSLSQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSK

EPKDPDQLYSTLKSVLQQSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYY

VSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A3P4RFU7|A0A3P4RFU7\_GULGU N-acetyltransferase domain-containing protein OS=Gulo gulo OX=48420 GN=BN2614\_LOCUS3 PE=4 SV=1

MNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFE

KPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISG

YKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLE

KRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYN

SNSSSLEQPNGGSTSPSCKGSSGLEANPGEKRKMNDSHALEEAKKPRVMGDIPMELIDEV

MSTITDPAAMLGPETNLLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVG

LQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVT

SNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYI

KDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQ

IPIESIPGIRETGWKPSGKEKSKEPKDPDQLYSTLKSILQQVKI

>tr|A0A091CQ82|A0A091CQ82\_FUKDA Histone acetyltransferase OS=Fukomys damarensis OX=885580 GN=H920\_18822 PE=3 SV=1

MGLCVLGAVELLESLARTQPEELQWAAPALMVARWVEAEESCKCNGWKNPNPSPTPPRAD

LQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTK

QVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKERQTI

VELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETT

QVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPI

WDQDFLSVSSRTSQLGIQTVISPPPVAGTVSYNSNSSSLEQPNGGSSSPACKASSGLEAN

SGEKRKMNDSHVLEEPKRPRVMGDIPMELISEVMSTITDPAAMLGPETNFLSAHSARDEA

ARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHK

TLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILN

FLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIK

KQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKSSGKDKSKEPKD

PDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVS

KKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A7K7HSQ8|A0A7K7HSQ8\_9PASS Histone acetyltransferase (Fragment) OS=Rhegmatorhina hoffmannsi OX=468512 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAGVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQPNTGNMSPACKVSSALDPNSGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K6ZV93|A0A7K6ZV93\_9AVES Histone acetyltransferase (Fragment) OS=Nothoprocta pentlandii OX=2585814 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRADLQQAVVSLTEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPIVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAEYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSTSRTGQMGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSVLDPNLGDKRKNNEPYSLEDAKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A091J555|A0A091J555\_EGRGA Histone acetyltransferase (Fragment) OS=Egretta garzetta OX=188379 GN=Z169\_16255 PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAVVSLAEPCRSCSHALATHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRAGQLGIQTVINPPPVARSVSYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVIGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L3SJJ0|A0A7L3SJJ0\_RISTR Histone acetyltransferase (Fragment) OS=Rissa tridactyla OX=75485 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHPLAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLECPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L1RVA9|A0A7L1RVA9\_9PASS Histone acetyltransferase (Fragment) OS=Locustella ochotensis OX=187437 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVIGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|M7C1B7|M7C1B7\_CHEMY Histone acetyltransferase OS=Chelonia mydas OX=8469 GN=UY3\_00796 PE=3 SV=1

MLVSVKNKSASPDKLDICGLPDTGVYSGIFLMPRLHLPGVQCAAIDVSVVDLAGLVKTPL

NLPQITLLLTPVLHLNEKKSREFDGLQSTSHSVDPAAEESCKCNGWKNPNPPPTPPRADL

QQTIVSLTEPCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQ

VYFSLFKLLRKCILQMGKPVVEGSLESPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVE

LAKMFLNRINYWHLETPLQRKLRSPNDDIAGYKVNYTRWLCYCNVPQFCDSLPRYETTQV

FGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTLILTHFPKFLSMLEEEVYSQNSPIWD

QDFMVSSSRTGQLGIQTVISPPPVARSVSYNASPSSLEQPNSGSMSPACKVSSCHDPALG

EKRKNTEPYSQEDSKRPRVVGDIPIELINEVMSTITDPAAMLGPETNFLSAHSARDEAAR

LEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTL

ALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHNILNFL

TYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQ

KEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKDRGKEPKDPD

QLYSTLKTILQQVKGSHGFTGNVPASPLRAVDYAWSLAMNLKTMSERLKNRYYVSKKLFM

ADLQRVFTNCREYNPPESEYYKCANILEKFFYTKIKEAGLIDK

>tr|A0A7K6UB61|A0A7K6UB61\_9AVES Histone acetyltransferase (Fragment) OS=Aegotheles bennettii OX=48278 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAVVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDTAEYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVINPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPCSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K6PYK7|A0A7K6PYK7\_9CORV Histone acetyltransferase (Fragment) OS=Ifrita kowaldi OX=461245 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGSMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L2WK14|A0A7L2WK14\_PANHA Histone acetyltransferase (Fragment) OS=Pandion haliaetus OX=56262 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFETPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVINPPPVARTVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLID

>tr|A0A7L0QA67|A0A7L0QA67\_SETKR Histone acetyltransferase (Fragment) OS=Setophaga kirtlandii OX=298831 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L3DEJ8|A0A7L3DEJ8\_PLUSO Histone acetyltransferase (Fragment) OS=Pluvianellus socialis OX=227228 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAASLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVINPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K5M3S6|A0A7K5M3S6\_CARCD Histone acetyltransferase (Fragment) OS=Cardinalis cardinalis OX=98964 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L0X9W0|A0A7L0X9W0\_TYRSA Histone acetyltransferase (Fragment) OS=Tyrannus savana OX=137541 GN=Kat2b PE=3 SV=1

AEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHTLAAHVSHLENVSEEEMNRL

LGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSIE

QGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVNY

TRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTLI

LTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPSS

LEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTIT

DPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNVF

SHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQV

KGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYEG

ATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIES

IPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYYE

VIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFYT

KIKEAGLIDK

>tr|A0A7K5G475|A0A7K5G475\_9AVES Histone acetyltransferase (Fragment) OS=Chunga burmeisteri OX=1352770 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAGVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSQTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDAKKPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K8M648|A0A7K8M648\_9CORV Histone acetyltransferase (Fragment) OS=Ptilorrhoa leucosticta OX=449384 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSVEDSKRLRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K9JWB3|A0A7K9JWB3\_9PASE Histone acetyltransferase (Fragment) OS=Dicaeum eximium OX=667154 GN=Kat2b PE=3 SV=1

AEESCKCNGWKNPNPPPTPPRAELQQAAASLGEPCRSCSHALAAHVSHLENVSEEEMNRL

LGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSIE

QGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVNY

TRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTLI

LTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPSS

LEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTIT

DPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNVF

SHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQV

KGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYEG

ATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIES

IPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYYE

VIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFYT

KIKEAGLIDK

>tr|A0A7L0S1K4|A0A7L0S1K4\_GLABR Histone acetyltransferase (Fragment) OS=Glaucidium brasilianum OX=78217 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLSEPCRSCNHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKMN

YTRWLCYCNVPQFCDSLPRYETTQIFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNTGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L0U5W8|A0A7L0U5W8\_CHOAC Histone acetyltransferase (Fragment) OS=Chordeiles acutipennis OX=118183 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCNHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPEQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L3UWG1|A0A7L3UWG1\_MOLAT Histone acetyltransferase (Fragment) OS=Molothrus ater OX=84834 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPTAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K5SKQ9|A0A7K5SKQ9\_9FRIN Histone acetyltransferase (Fragment) OS=Urocynchramus pylzowi OX=571890 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAVVLWVLSVAFYKFEFLFCLAAHVSHLENVSEE

EMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFE

KPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAG

YKVNYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQE

KRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPIARSVAYS

ASPSSLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEV

MSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVG

LQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVT

SNEQVKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYI

KDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQ

IPIESIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEA

PGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILE

KFFYTKIKEAGLIDK

>tr|A0A7K5D950|A0A7K5D950\_9TYRA Histone acetyltransferase (Fragment) OS=Pachyramphus minor OX=369605 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHTLAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQPNSGNMSPACKVSSSLDPNLGEKRKNNEPYSVEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERSKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A2D4Q039|A0A2D4Q039\_MICSU Histone acetyltransferase (Fragment) OS=Micrurus surinamensis OX=129470 PE=3 SV=1

LQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVT

SNEQVKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYI

KDYEGATLMGCELNPKIPYTEFSVIIKKQKEIIKKLIERKQSQIQKVYPGLSCFKDGVRQ

IPIESIPGIRETGWKPNNKEKSKEPKDLDQLYSTLKNILQQVKSHQSAWPFMEPVKRTEA

PGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADMQRVFTNCREYNPPESEYYKCANILE

KFFYTKIKEAGLIDK

>tr|A0A7K4U3J0|A0A7K4U3J0\_9PASS Histone acetyltransferase (Fragment) OS=Sinosuthora webbiana OX=337173 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEECRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K7D1Q0|A0A7K7D1Q0\_PHEME Histone acetyltransferase (Fragment) OS=Pheucticus melanocephalus OX=371919 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRKLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K8K4S1|A0A7K8K4S1\_9GRUI Histone acetyltransferase (Fragment) OS=Lophotis ruficrista OX=172689 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAVVSLAEGCRSCGHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPSGGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVIGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L3X519|A0A7L3X519\_9GRUI Histone acetyltransferase (Fragment) OS=Atlantisia rogersi OX=2478892 GN=Kat2b PE=3 SV=1

AEESCKCNGWKNPNPPPTPPRAELQQAVVSLAEPCRSCSHALAAHVSHLENVSEEEMNRL

LGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSIE

QGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVNY

TRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTLI

LTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPSS

LEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTIT

DPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNVF

SHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQV

KGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYEG

ATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIES

IPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYYE

VIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFYT

KIKEAGLIDK

>tr|A0A6J3CGL3|A0A6J3CGL3\_AYTFU Histone acetyltransferase OS=Aythya fuligula OX=219594 GN=KAT2B PE=3 SV=1

GGPQQGSPAAGGVAAAAGPARTAADSPAGPGSARTAGKKAQLRAAPRAKKLEKLGVYSAC

KAEESCKCNGWKNPNPPPTPPRADLQQTVVSLTEPCRSCSHTLAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSPNSPIWDQDFIVSTSRTGQLGIQTVINPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSVLDPNLGEKRKNNEPYSLEDSKRPRIVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A093P9P0|A0A093P9P0\_PYGAD Histone acetyltransferase (Fragment) OS=Pygoscelis adeliae OX=9238 GN=AS28\_14257 PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQHAVVSLAEPCRSCSHALATHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K9QGJ4|A0A7K9QGJ4\_IRECY Histone acetyltransferase (Fragment) OS=Irena cyanogastra OX=175120 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHTLAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L4IQ14|A0A7L4IQ14\_9PASS Histone acetyltransferase (Fragment) OS=Pomatorhinus ruficollis OX=932028 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K6IRE7|A0A7K6IRE7\_9CORV Histone acetyltransferase (Fragment) OS=Machaerirhynchus nigripectus OX=1160894 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPIVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPTLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L2PRX8|A0A7L2PRX8\_9PASS Histone acetyltransferase (Fragment) OS=Hypocryptadius cinnamomeus OX=589841 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNTGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGITGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYYEV

IRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFYTK

IKEAGLIDK

>tr|A0A7K9P1L9|A0A7K9P1L9\_9CORV Histone acetyltransferase (Fragment) OS=Edolisoma coerulescens OX=2585810 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELPQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L3LQE2|A0A7L3LQE2\_9CHAR Histone acetyltransferase (Fragment) OS=Turnix velox OX=2529409 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKSPNPPPTPPRAELQQVAVSLAEPCRSCSHPLAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIADYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPSSGNMSPACKVASALDPNLGNKRKNNEPYSLEDSKRLRVVGDIPIELINEVMSTI

ADPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K4Y1K8|A0A7K4Y1K8\_REGSA KAT2B acetyltransferase (Fragment) OS=Regulus satrapa OX=13245 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQVAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPIVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSAAYSASPS

SLEQSNSGNMSPACKVSSALDPNLGEKRKNNEPYSVEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPM

>tr|A0A0A0APF7|A0A0A0APF7\_CHAVO Histone acetyltransferase (Fragment) OS=Charadrius vociferus OX=50402 GN=N301\_05246 PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAASLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVINPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L0ND56|A0A7L0ND56\_9PASS Histone acetyltransferase (Fragment) OS=Formicarius rufipectus OX=1118560 GN=Kat2b PE=3 SV=1

AEESCKCNGWKNPNPPPTPPRAELQQVAVSLAEPCRSCSHALAAHVSHLENVSEEEMNRL

LGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSIE

QGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVNY

TRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTLI

LTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPSS

LEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTIT

DPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNVF

SHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQV

KGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYEG

ATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIES

IPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYYE

VIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFYT

KIKEAGLIDK

>tr|A0A7K9MSR8|A0A7K9MSR8\_HYDTY Histone acetyltransferase (Fragment) OS=Hydrobates tethys OX=79633 GN=Kat2b PE=3 SV=1

QAEDSCKCNGWKNPNPPPTPPRAELQQAVVSLAEPCRSCSHALATHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRQRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVINPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDSNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A5F9CZ50|A0A5F9CZ50\_RABIT Histone acetyltransferase OS=Oryctolagus cuniculus OX=9986 PE=3 SV=1

LGHPPLHSLATAESWPGRGATGTESGAPTGTRTRCAGAARRRISLVSRGAEESCKCNGWK

NPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLF

TCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYK

FSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVP

QFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSM

LEEEVYSQNSPIWDQDFLSRERYLSFISLLPQMPTTASYGPELNSGSWNSIRVPHMAARY

LSEKRKMNDSHVLEEAKKPRVMGDIPMELIHEVMSTITDPAAMLGPETNFLSAHSARDEA

ARLEERRGVIEFHVVGNSLNQKPNKRILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHK

TLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILN

FLTYADEYAIGYFKKQGFSKEIKIPKAKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIK

KQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPKD

PDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVS

KKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|F7CX59|F7CX59\_ORNAN Histone acetyltransferase OS=Ornithorhynchus anatinus OX=9258 GN=KAT2B PE=3 SV=3

MAEPGGAGPGAPPSSPAAGGSSSSSSSSSSAAPEGPGGGAGSARIAAKKAQLRSAPRPKK

LQKLGVYSACKAEESCKCNGWKNPNPPPTPPRADLQQTIVNLTESCRSCSHALAAHVSHL

ENESEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSL

ESPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSP

NDDIAGYKVNYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEK

DKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFMASSSRVGQLGIQTVISPPPPV

ARTVAYSGSPSSLEQPSGGNMSPACKVSSGLESNLGEKRKIIDPHSLEEAKKPRVVGDIP

IELINEVMSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKK

IMMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTE

IVFCAVTSNEQVKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPK

AKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSC

FKDGVRQIPIESIPGIRETGWKPSGKERGKEPKDPDQLYSTLKNILQQVKSHQSAWPFME

PVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYY

KCANILEKFFFTKIKEAGLIDK

>tr|A0A2U3VRS8|A0A2U3VRS8\_ODORO Histone acetyltransferase OS=Odobenus rosmarus divergens OX=9708 GN=KAT2B PE=3 SV=1

MSEAGGAGPGGGGAGAGAGAGLGALPLQPPAPPPAPPQGSPCAAAAGGSGACGPATAVAA

AGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTP

PRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQ

NSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSNSSSLEQPNGGSTSPSCKGSSG

LEANPGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETNLLSAHSA

RDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSK

EPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNR

YYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A6J3AET1|A0A6J3AET1\_VICPA Histone acetyltransferase OS=Vicugna pacos OX=30538 GN=KAT2B PE=3 SV=1

MVGMLSWEQVLKNMASETFPVSKETTAACYLILLLSLFILQAEESCKCNGWKNPNPSPTP

PRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETAQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYNQ

NSPIWDQDFLSASSRTSQLGIQTVINPPPVAGTISYNSNASSLEQPNGGGPSPSCKGASG

LEANPGEKRKMNDSHAVEEAKKPRVMGDIPLELIHEVMSTITDPAAMLGPETNFLSAHSA

RDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSK

EPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNR

YYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A1S3A6A0|A0A1S3A6A0\_ERIEU Histone acetyltransferase OS=Erinaceus europaeus OX=9365 GN=KAT2B PE=3 SV=1

MTLFVKLGGLIQAEESCKCNGWKNPNPTPTPPRADLQQIIVSLSESCRSCSHALAAHVSH

LENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGS

LEKKPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNQINYWHLEAPSQRRLR

PPSDDVSGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQ

EKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTVINPPP

VAGTISYNSNSSSIEQPNGGNASPSCKASSGLEANPGEKRKMNDSHVLEEAKKPRVMGDI

PMELINEVMSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLKQKPNK

KMLMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFT

EIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIP

KTKYVGYIKDYEGATLMGCELNPQIPYTEFSVIVKKQKEIIKKLIERRQAQVRKVYPGLS

CFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPKDPDQLYSTLKSILQQVKSHQSAWPFM

EPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEY

YKCANILEKFFFSKIKEAGLIDK

>tr|A0A6J3H091|A0A6J3H091\_SAPAP histone acetyltransferase KAT2B isoform X2 OS=Sapajus apella OX=9515 GN=KAT2B PE=4 SV=1

MSEAGGAGPGGCGAGAGAGAGPGALPPQPAALPPAPPQGSPCAAAAGGSGACGPATAVAA

AGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTP

PRADLQQIFVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQ

NSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSTSSSLEQPNAGSSSPVCKASSG

LEANPGEKRKMTDSHILEEAKKPRVMGDIPMELINEVMSTITDPAAMLGPETNFLSAHSA

RDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSK

EPKDPDQLYSTLKSILQQVKI

>tr|G1P979|G1P979\_MYOLU Histone acetyltransferase OS=Myotis lucifugus OX=59463 GN=KAT2B PE=3 SV=1

AEESCKCIGWKNPDRSPTPPRADLQQKIVSLTDSCRGCNHALAAHVSHLEDLSEEEMNRL

LGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKTILQRGKPVVEGSLEKKPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKEN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFPASSRTSQLGIQTVINPPPVAGTISYSSNSSS

LEQPNGGSSSPSGKGSSGLEANPGEKRKMNDSHVLEEAKKPRVMGDIPMELIHEVMSTIT

DPAVMVGPENNLLSAHSARDEAARMEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVF

SHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQV

KGYGTHLMNHLKEFHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEG

ATLMGCELNPQIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIES

IPGIRETGWKQSGKEKSKEPKDSDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYE

VIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFS

KIKEAGLIDK

>tr|A0A5F9DT50|A0A5F9DT50\_RABIT Histone acetyltransferase OS=Oryctolagus cuniculus OX=9986 PE=3 SV=1

WFTLQWPPWPARCSRPTYPGLPWGAGPKDLGHPPLHSLATAESWPGRGATGTESGAPTGT

RTRCAGAARRRISLVSRGAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHAL

AAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGK

PVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAP

SQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQL

LEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRISQLGIQT

AVGYISMCCTFLCLKPYFFPFIFITIGEKRKMNDSHVLEEAKKPRVMGDIPMELIHEVMS

TITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKRILMWLVGLQ

NVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSN

EQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKAKYVGYIKD

YEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIP

IESIPGIRETGWKPSGKEKSKEPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPG

YYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKF

FFSKIKEAGLIDK

>tr|A0A452UVV1|A0A452UVV1\_URSMA Histone acetyltransferase OS=Ursus maritimus OX=29073 GN=KAT2B PE=3 SV=1

PWGRVAAGAFERARHSHGQGPSCVPGTSEQSGLSPWPALWMRPLGTDHSAEESCKCNGWK

NPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLF

TCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYK

FSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVP

QFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSM

LEEEVYSQNSPIWDQDFLSKADVVSDSRDSTVISVTKVVTQLSFGLVGMYLPALCLRSSI

VCPFILIITGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETSLLS

AHSARDEAARLEERRGVIEFHVVGNSLSQKPNKKILMWLVGLQNVFSHQLPRMPKEYITR

LVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEY

HIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPY

TEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGK

EKSKEPKDPDQLYSTLKSVLQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSER

LKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A2K6K9U4|A0A2K6K9U4\_RHIBE Histone acetyltransferase OS=Rhinopithecus bieti OX=61621 GN=KAT2B PE=3 SV=1

MVRGCGAGLGGCGEEPGQGPGGALPPQPVALPPRPAAPLARLPAGGSGACGPATAVVQRD

GRRSGRRWLAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTPPRADLQQIIV

SLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYL

FKLLRKSILQRGKPVVEGSLEKKPPFENLGVNNFVQYKFSHLPAKERQTIVELAPSQRRL

RSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQAR

QEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTVISPP

PVAGTISYNSTSSSLEQSNAGSSSPACKASSGLEANPGEKRKMTDSHVLEEAKRPRVMGD

IPMELINEVMSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPN

KKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGF

TEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKI

PKAKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGL

SCFKDGVRQIPIESIPGISTYRPSFKKPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKR

TEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCAN

ILEKFFFSKIKEAGLIDK

>tr|A0A452UVU2|A0A452UVU2\_URSMA Histone acetyltransferase OS=Ursus maritimus OX=29073 GN=KAT2B PE=3 SV=1

MFFYHISSGQLLLLLQVFVLLPLSQKGLLKIADSILPSPNPPLPISSSFFSIALSLSNIL

YNLLFGVACLPQPSPPQGQDLYLFTSIPSKSTQHRAEESCKCNGWKNPNPSPTPPRADLQ

QIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQV

YFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVE

LAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQV

FGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWD

QDFLSASSRTSQLGIQTVISPPPVAGTISYNSNSSSLEQPNGGSASPSCKGSSGLEANPG

EKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETSLLSAHSARDEAAR

LEERRGVIEFHVVGNSLSQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTL

ALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFL

TYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQ

KEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPKDPD

QLYSTLKSVLQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKK

LFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A6J3H0V8|A0A6J3H0V8\_SAPAP Histone acetyltransferase OS=Sapajus apella OX=9515 GN=KAT2B PE=3 SV=1

MSEAGGAGPGGCGAGAGAGAGPGALPPQPAALPPAPPQGSPCAAAAGGSGACGPATAVAA

AGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTP

PRADLQQIFVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQ

NSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSTSSSLEQPNAGSSSPVCKASSG

LEANPGEKRKMTDSHILEEAKKPRVMGDIPMELINEVMSTITDPAAMLGPETNFLSAHSA

RDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSK

EPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNR

YYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A667GWM7|A0A667GWM7\_LYNCA Histone acetyltransferase OS=Lynx canadensis OX=61383 PE=3 SV=1

RARALPPQPPAPPPAPPQGSPCAAAAAAGGSGACGPATAVAAAGTAEGPGGGGSARIAVK

KAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTPPRADLHCSHSRTFAVSSS

RVTYVPSILSSAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVTGKKTQTPNKFISIYLR

KSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKERQTIVELAKMFLNRI

NYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSV

FTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSR

TSQLGIQTVISPPPVAGTISYNSNSSSLEQPNGGSTSPSCKGSSGLEANPGEKRKMNDSH

ALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETNLLSAHSARDEAARLEERRGVIE

FHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVI

GGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIG

YFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIE

RKQAQIRKVYPGLSCFKDGVRQIPIESIPGISIKEPKDPDQLYSTLKSILQQVKSHQSAW

PFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPE

SEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A7E6E582|A0A7E6E582\_9CHIR Histone acetyltransferase OS=Phyllostomus discolor OX=89673 GN=KAT2B PE=3 SV=1

MSEAGGVALGSGAGAGAGAGAGLGALPPQPPAPPPLPPQGSPCAAAAGGSGSCGPATAVA

AAGTAEGPGGSGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPT

PPRADLQQMIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEE

DADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPPK

ERQTIMELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLP

RYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYS

QNSPIWDQDFLSASSRTSQLGIQTGEKRKMNDCHVLEEAKKPRVMGDIPMELITEVMSTI

TDPAVMVGPENNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEFHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYE

GATLMGCELNPQIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKQSGKEKSKEPKDSDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFF

SKIKEAGLIDK

>tr|A0A7E6E621|A0A7E6E621\_9CHIR histone acetyltransferase KAT2B isoform X3 OS=Phyllostomus discolor OX=89673 GN=KAT2B PE=4 SV=1

MSEAGGVALGSGAGAGAGAGAGLGALPPQPPAPPPLPPQGSPCAAAAGGSGSCGPATAVA

AAGTAEGPGGSGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPT

PPRADLQQMIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEE

DADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPPK

ERQTIMELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLP

RYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYS

QNSPIWDQDFLSASSRTSQLGIQTVINPPPVAGTISYNSNSSSLEHLNGGSTSPSSKGSS

GLEANPGEKRKMNDCHVLEEAKKPRVMGDIPMELITEVMSTITDPAVMVGPENNFLSAHS

ARDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVF

DPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEFHIK

HDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPQIPYTEF

SVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKQSGKEKS

KEPKDSDQLYSTLKSILQQVKI

>tr|A0A6P6H161|A0A6P6H161\_PUMCO Histone acetyltransferase OS=Puma concolor OX=9696 GN=KAT2B PE=3 SV=1

MAKAPAVFQVPQESGLLPQALLDSLRRPLHGHLLGAMAEESCKCNGWKNPNPSPTPPRAD

LQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHREEDADTK

QVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKERQTI

VELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETT

QVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPI

WDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSNSSSLEQPNGGSTSPSCKGSSGLEAN

PGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETNLLSAHSARDEA

ARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHK

TLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILN

FLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIK

KQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGREKSKEPKD

PDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVS

KKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A5F9C2L4|A0A5F9C2L4\_RABIT Histone acetyltransferase OS=Oryctolagus cuniculus OX=9986 PE=3 SV=1

LGHPPLHSLATAESWPGRGATGTESGAPTGTRTRCAGAARRRISLVSRGAEESCKCNGWK

NPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLF

TCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYK

FSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVP

QFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSM

LEEEVYSQNSPIWDQDFLSASSRISQLGIQTVTTKSNGSRGSPGRMGGRQSHISGCEVLP

AGSEKMNDSHVLEEAKKPRVMGDIPMELIHEVMSTITDPAAMLGPETNFLSAHSARDEAA

RLEERRGVIEFHVVGNSLNQKPNKRILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKT

LALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNF

LTYADEYAIGYFKKQGFSKEIKIPKAKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKK

QKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPKDP

DQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSK

KLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A384DRV1|A0A384DRV1\_URSMA Histone acetyltransferase OS=Ursus maritimus OX=29073 GN=KAT2B PE=3 SV=1

MPNHTCWELWQGFKKAGYSPASEAPAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESC

RSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRK

SILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRIN

YWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVF

TVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRT

SQLGIQTVISPPPVAGTISYNSNSSSLEQPNGGSASPSCKGSSGLEANPGEKRKMNDSHA

LEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETSLLSAHSARDEAARLEERRGVIEF

HVVGNSLSQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIG

GICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGY

FKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIER

KQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPKDPDQLYSTLKSVL

QQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVF

TNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A452UVR3|A0A452UVR3\_URSMA Histone acetyltransferase OS=Ursus maritimus OX=29073 GN=KAT2B PE=3 SV=1

GKQGEKNCDQRCNTKPRHKYLCNLFSDLQQIIVSLTESCRSCSHALAAHVSHLENVSEEE

MNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKGVNNFVQYKFSHLPSKERQTIVELA

KMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFG

RTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQD

FLSASSRTSQLGIQTAGTISYNSNSSSLEQPNGGSASPSCKGSSGLEANPVGLVGMYLPA

LCLRSSIVCPFILIITGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLG

PETSLLSAHSARDEAARLEERRGVIEFHVVGNSLSQKPNKKILMWLVGLQNVFSHQLPRM

PKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHL

MNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCE

LNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRET

GWKPSGKEKSKEPKDPDQLYSTLKSVLQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMD

LKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGL

IDK

>tr|A0A3Q7UVM1|A0A3Q7UVM1\_URSAR Histone acetyltransferase OS=Ursus arctos horribilis OX=116960 GN=KAT2B PE=3 SV=1

MSEAGGAGPGGGGAGAGAGAGLGALPPQPSAPPPAPPQGSPCAAAAGGSGACGPATAVAA

AGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTP

PRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQ

NSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSNSSSLEQPNGGSASPSCKGSSG

LEANPGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPETSLLSAHSA

RDEAARLEERRGVIEFHVVGNSLSQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSK

EPKDPDQLYSTLKSVLQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNR

YYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A452UVX4|A0A452UVX4\_URSMA Histone acetyltransferase OS=Ursus maritimus OX=29073 GN=KAT2B PE=3 SV=1

GKQGEKNCDQRCNTKPRHKYLCNLFSDLQQIIVSLTESCRSCSHALAAHVSHLENVSEEE

MNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFE

KPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISG

YKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLE

KRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTIISPPPVAGTISYNSNSSSLE

QPNGGSASPSCKGSSGLEANPGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDP

AAMLGPETSLLSAHSARDEAARLEERRGVIEFHVVGNSLSQKPNKKILMWLVGLQNVFSH

QLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKG

YGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGAT

LMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIP

GIRETGWKPSGKEKSKEPKDPDQLYSTLKSVLQQVKSHQSAWPFMEPVKRTEAPGYYEVI

RFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKI

KEAGLIDK

>tr|A0A452UW13|A0A452UW13\_URSMA Histone acetyltransferase OS=Ursus maritimus OX=29073 GN=KAT2B PE=3 SV=1

CVHEIANFLSFAGFLSGPWGRVAAGAFERARHSHGQGPSCVPGTSEQSGLSPWPALWMRP

LGTDHSAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVSE

EEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPP

FEKPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDI

SGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLP

LEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTGKFLFQPNGGSA

SPSCKGSSGLEANPGEKRKMNDSHALEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPE

TSLLSAHSARDEAARLEERRGVIEFHVVGNSLSQKPNKKILMWLVGLQNVFSHQLPRMPK

EYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMN

HLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELN

PRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGISIKEP

KDPDQLYSTLKSVLQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYY

VSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|L5L144|L5L144\_PTEAL Histone acetyltransferase OS=Pteropus alecto OX=9402 GN=PAL\_GLEAN10016025 PE=3 SV=1

MVTGWPSRISCRKEGRNMKEIPIQAVEGARCATERVSLLVHGAELQLESWNHQGSPVARD

PAVFQGPQESGLSLSRWTSLELSTPWTFAWGSGTEAEESCKCNGWKNPNPSPTPPRADLQ

QIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQV

YFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPSKERQTIVE

LAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQV

FGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWD

QDFLSASSRTSQLGIQTVINPPPVAGTISYNSNSSSLEQPNGGSTSPSCKGSSGLEANPG

EKRKMNDTHVLEEAKKPRVMGDIPMELIDEVMSTITDPAAMLGPEKPNKKILMWLVGLQN

VFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNE

QVKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKEIKIPRTKYVGYIKDY

EGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPI

ESIPGIRETGWKPSGKEKSKEPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGY

YEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFF

FSKIKEAGLIDK

>tr|G1SQ72|G1SQ72\_RABIT Histone acetyltransferase OS=Oryctolagus cuniculus OX=9986 PE=3 SV=2

LEPAAAPAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVS

EEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKP

PFEKPSIEQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDD

ISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKL

PLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSRERYLSFISLLPQMPTTASYGPE

LNSGSWNSIRVPHMAARYLSEKRKMNDSHVLEEAKKPRVMGDIPMELIHEVMSTITDPAA

MLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKRILMWLVGLQNVFSHQL

PRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYG

THLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKAKYVGYIKDYEGATLM

GCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGI

RETGWKPSGKEKSKEPKDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRF

PMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKE

AGLIDK

>tr|A0A2I3LWZ8|A0A2I3LWZ8\_PAPAN Histone acetyltransferase OS=Papio anubis OX=9555 GN=KAT2B PE=3 SV=1

MSEAGGAGPGGCGAGAGAGAGPGALPPQPVVLPPAPPQGSPCAAAAGGSGACGPATAVAA

AGTAEGPGGGGSARIAVKKAQLRSAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTP

PRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEED

ADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKE

RQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPR

YETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQ

NSPIWDQDFLSASSRTSQLGIQTVISPPPVAGTISYNSTSSSLEQSNAGSSSPACKASSG

LEANPGEKRKMTDSHVLEEAKRPRVMGDIPMELINEVMSTITDPAAMLGPETNFLSAHSA

RDEAARLEERRGVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFD

PKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKH

DILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFS

VIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGISTYRPSFKSEIFYK

EPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNR

YYVSKKLFMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A5F9CW25|A0A5F9CW25\_RABIT Histone acetyltransferase OS=Oryctolagus cuniculus OX=9986 PE=3 SV=1

LGHPPLHSLATAESWPGRGATGTESGAPTGTRTRCAGAARRRISLVSRGAEESCKCNGWK

NPNPSPTPPRADLQQIIVSLTESCRSCSHALAAHVSHLENVSEEEMNRLLGIVLDVEYLF

TCVHKEEDADTKQVYFYLFKLLRKSILQRGKPVVEGSLEKKPPFEKPSIEQGVNNFVQYK

FSHLPSKERQTIVELAKMFLNRINYWHLEAPSQRRLRSPNDDISGYKENYTRWLCYCNVP

QFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPLEKRTLILTHFPKFLSM

LEEEVYSQNSPIWDQDFLSASSRISQLGIQTATMAGAAPIRSQEPGVSSGSPTGVQGPSE

KRKMNDSHVLEEAKKPRVMGDIPMELIHEVMSTITDPAAMLGPETNFLSAHSARDEAARL

EERRGVIEFHVVGNSLNQKPNKRILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLA

LIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLT

YADEYAIGYFKKQGFSKEIKIPKAKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQK

EIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRETGWKPSGKEKSKEPKDPDQ

LYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKL

FMADLQRVFTNCKEYNPPESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A7N9IDA6|A0A7N9IDA6\_MACFA Lysine acetyltransferase 2B OS=Macaca fascicularis OX=9541 GN=KAT2B PE=4 SV=1

MSEAGGAGPGGCGAGAGAGPGPGRCPAARGAAALAAAGTAEGPGGGGSARIAVKKAQLRS

APRAKKLEKLGVYSACKAEESCKCNGWKNPNPSPTPPRADLQQIIVSLTESCRSCSHALA

AHVSHLENVSEEEMNRLLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKSILQRGKP

VVEGSLEKKPPFEKPSIEQGVNNFVQYKFSHLPAKERQTIVELAKMFLNRINYWHLEAPS

QRRLRSPNDDISGYKENYTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLL

EQARQEKDKLPLEKRTLILTHFPKFLSMLEEEVYSQNSPIWDQDFLSASSRTSQLGIQTV

ISPPPVAGTISYNSTSSSLEQSNAGSSSPACKASSGLEANPGEKRKMTDSHVLEEAKRPR

VMGDIPMELINEVMSTITDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLN

QKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFP

SQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSK

EIKIPKTKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKV

YPGLSCFKDGVRQIPIESIPGISTYRPSFKSEIFYKEPRDPDQLYSTLKSILQQVKSHQS

AWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNP

PESEYYKCANILEKFFFSKIKEAGLIDK

>tr|A0A7L0M6S8|A0A7L0M6S8\_9PSIT Histone acetyltransferase (Fragment) OS=Amazona guildingii OX=175529 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAVVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVMGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERSKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L4D8M5|A0A7L4D8M5\_9AVES Histone acetyltransferase (Fragment) OS=Eurystomus gularis OX=325343 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAASLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKISSALDSNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K7WFH5|A0A7K7WFH5\_9AVES Histone acetyltransferase (Fragment) OS=Nothocercus julius OX=2585813 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRADLQQTVASLTEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAEYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSTSRTGQLGIQTVISPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSVLDPNLGEKRKNNEPYSLEDSKRPRIVGDIPIELINEVMSTI

TDPTAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7K8G1L7|A0A7K8G1L7\_ORTSP Histone acetyltransferase (Fragment) OS=Orthonyx spaldingii OX=38397 GN=Kat2b PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAAVSLAEPCRSCSHALAAHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPS

SLEQSNSANMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKEAKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A093IAQ4|A0A093IAQ4\_EURHL Histone acetyltransferase (Fragment) OS=Eurypyga helias OX=54383 GN=N326\_05116 PE=3 SV=1

QAEESCKCNGWKNPNPPPTPPRAELQQAVVSLAEPCRSCSHALATHVSHLENVSEEEMNR

LLGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSI

EQGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVN

YTRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTL

ILTHFPKFLSMLEEEVYSQNSPIWDQDFMVTTSQTGQLGIQTVINPPPVARSVSYSASPS

SLEQPNSGNMSPACKVSSSLDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTI

TDPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNV

FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQ

VKGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYE

GATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIE

SIPGIRETGWKPSGKERGKESKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYY

EVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFY

TKIKEAGLIDK

>tr|A0A7L2KZW4|A0A7L2KZW4\_9PASS Histone acetyltransferase (Fragment) OS=Zosterops hypoxanthus OX=2485327 GN=Kat2b PE=3 SV=1

AEESCKCNGWKNPNPPPTPPRAELQQAGVSLGEPCRSCSHALAAHVSHLENVSEEEMNRL

LGIVLDVEYLFTCVHKEEDADTKQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSIE

QGVNNFVQYKFSHLPSKERQTIVELAKMFLNRINYWHLETPSQRRLRSPNDDIAGYKVNY

TRWLCYCNVPQFCDSLPRYETTQVFGRTLLRSVFTVMRRQLLEQARQEKDKLPQEKRTLI

LTHFPKFLSMLEEEVYSQNSPIWDQDFMVSSSRTGQLGIQTVISPPPVARSVAYSASPSS

LEQPNSGNMSPACKVSSALDPNLGEKRKNNEPYSLEDSKRPRVVGDIPIELINEVMSTIT

DPAAMLGPETNFLSAHSARDEAARLEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNVF

SHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQV

KGYGTHLMNHLKEYHIKHNILNFLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYEG

ATLMGCELNPRIPYTEFSVIIKKQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIES

IPGIRETGWKPSGKERGKEPKDPDQLYSTLKTILQQVKSHQSAWPFMEPVKRTEAPGYYE

VIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFYT

KIKEAGLIDK

>tr|A0A670K3M7|A0A670K3M7\_PODMU Histone acetyltransferase OS=Podarcis muralis OX=64176 GN=KAT2B PE=3 SV=1

FFLAAPPPLPAVGGGGGGNGGGGNGALQQGSPAAGGLAACGPSPAATAAAAAAAGGGGGG

GPGSGGPGSARVVGKKAQLRAAPRAKKLEKLGVYSACKAEESCKCNGWKNPNPPPTPPRA

ELQQAVVSLNEPCRSCNHALAAHVSHLENVSEDEMNRLLGIVLDVEYLFACVHKEEDADT

KQVYFYLFKLLRKCILQMGKPVVEGSLESPPFEKPSIEQGVNNFVQYKFSHLPSKERQTI

VELAKMFLNRINYWHLETPSQRRQRSPNDDIASYKVNYTRWLCYCNVPQFCDSLPRYETT

QVFGRTLLRSVFTVMRRQLLEHARQEKDKLPPEKRTLILTHFPKFLSMLEEEVYSQSSPI

WDPDFIASSSRSAQLGIQTVISRPPVVRSVPYSASPSSLEQPSGGSMSPACKAASSLDPN

LGEKRKSNEPYSVEDAKKPRVVGDIPIELINEVMSTITDPAAMLGPETNFLSAHSARDEA

ARMEERRGVIEFHVVGNSLNQKPNKKIMMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHK

TLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHNILN

FLTYADEYAIGYFKKQGFSKDIKVPKAKYVGYIKDYEGATLMGCELNPRIPYTEFSVIIK

KQKEIIKKLIERKQAQIRKVYPGLSCFKDGVRQIPIESIPGIRDTGWKPSSKEKGKEPKD

PDQLYSTLKNILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVS

KKLFMADLQRVFTNCREYNPPESEYYKCANILEKFFYTKIKEAGLIDK