```
#ID   DESC  POS   SEQ   FND

sp:F181A_HUMAN    [Q8N9Y4] RecName: Full=Protein FAM181A;>rs:NP_612353
[NP_612353] protein FAM181A isoform 1 [Homo sapiens].191..205
      MPLEERRSSGERNDAAPTNHRRPGEKRASTAKQVSSVPFLGAAGHQQSLPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPRRLLLD
LGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPETTLVSMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWRKSPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
      PMRKRQLPASFWEEP

sp:F181B_BOVIN    [A7MB34] RecName: Full=Protein FAM181B;>rs:NP_001094693
[NP_001094693] protein FAM181B [Bos taurus].>gp:BC151312_1 [BC151312]
LOC613623 protein [Bos taurus]     214..228
      MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALEKGCCFEDEETGTPAGALLAGAESGDAREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPSSPGAADTPAKRPLAGAQTVPVPVPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGADPAGVAEAVPAAGLVRGDAAGSAGGPAVPGARKVPLRARN
LPPSFFTEPSRAGGCVCGPSGPGVSLGDLEKGSEAAEFFELLGPDYGAGTEAGALLAAEPLDVFPAGAAVLRGPP
ELEPGLFDPQPAMVGSLLYPEPWSAPGGPATKKPPLPAPGGGLTLNEPLRSVYPAAADSPGGDDGPGLLASFTPF
FSDCALPPAPPPQQVSYDYSAGYSRTAFAGLWRPDGAWEGAPGEEGAPRD   PLRARNLPPSFFTEP

sp:F181B_HUMAN    [A6NEQ2] RecName: Full=Protein FAM181B;>rs:NP_787081
[NP_787081] protein FAM181B [Homo sapiens].    221..235
      MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGEVAAPAAGLGGAGTGGAGGDVAGPAGATAIPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCSPTKKSPLTAPRGGLTLNEPLSPLYPAAADSPGGEDGRGH
LASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD  PLRARNLPPSFFTEP

sp:F181B_MOUSE    [Q80VF6] RecName: Full=Protein FAM181B;>gp:BC043329_1
[BC043329] family with sequence similarity 181, member B [Mus musculus]
      215..229
      MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGASAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPRPASPSAADAPAKRPPGAPTVATPAHCKAAP
RREATQAAAAASLQSRSLAALFDSLRHIPGGAETAGGAEAVSVPGLGAASAVGDGAGTAVSSVAPGTRKVPLRAR
NLPPSFFTEPSRVGCGGASGVPSGQGVSLGDLEKGAEAVEFFELLAPDFGSGNDSGVLMAADPLDPFPAGATVLR
GPLELESGPFEQPAMVGNLLYPEPWNTPSCPQTKKPPVAGVRGGVTLNEPVRLLYPTALDSPGGEDAPALSSFTP
FFPDCALPPPHQVSYDYSAGYSRAVYPSLWRPDGVWEGASGEEGGHPD     PLRARNLPPSFFTEP

sp:YAP1A_XENLA    [D6C652] RecName: Full=Transcriptional coactivator YAP1-
A; Short=Yes-associated protein 1-A; Short=xYAP
{ECO:0000303|PubMed:21687713}; AltName: Full=Protein yorkie homolog-A;
AltName: Full=Yes-associated protein YAP65 homolog A;>rs:NP_001233236
[NP_001233236] transcriptional coactivator YAP1-A [Xenopus
laevis].>gp:FJ979828_1 [FJ979828] yes-associated protein 65 [Xenopus
laevis]     54..68
      MEPGSQQQPSAPAQQPPPVGHQVVHVRTDSETDLEALFNAVMNPKNANLPQTLPMRMRKLPDSFFKQPQ
PEAKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLAAVSPGALSPQGVVTGLAPPSAPHLRQSSYEIPDDVPLP
PGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTGPLPDGWEQALTPEGEAYFIN
HKNKSTSWLDPRLDPRFAMNQQRLSQNAPVKAPPALPPPSPQTGVLGSGGNQQMRLQQLQMEKERLRLKHQELLR
QVRPQELALRSQIPPMEQDGGTQNPVCTTGISQELRTMTMNSSDPFLNSGTYHSRDESTESGLSMSSYSVPRTPD
DFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMETV
LAATKLDKESFLTWL   PMRMRKLPDSFFKQP

sp:YAP1B_XENLA    [Q32NJ6] RecName: Full=Transcriptional coactivator YAP1-
B; Short=Yes-associated protein 1-B; AltName: Full=Protein yorkie homolog-
B; AltName: Full=Yes-associated protein YAP65 homolog B;>rs:NP_001167495
[NP_001167495] transcriptional coactivator YAP1-B [Xenopus
```

laevis].>gp:BC108591_1 [BC108591] Unknown (protein for MGC:131098) [Xenopus laevis] 54..68
MEPGSQQQPSAPGQQPPPVGHQIVHVRTDSETDLETLFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPE
PKSHSRHVDQTTTWQDPRKAMLSQINITAPTSPPVQQNIMTPTAMNQQRLSQSAPVKSPPALQPQSPPSGVLGSG
GNQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQIPPMEQDSGPPNPVCSSGISQELRTMTMNSSDPFLNS
GTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAM
NVEGEELMPSLQEALSSDILNDMETVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

sp:YAP1_CHICK [P46936] RecName: Full=Transcriptional coactivator YAP1; Short=Yes-associated protein 1; AltName: Full=65 kDa Yes-associated protein {ECO:0000303|PubMed:8035999}; Short=YAP65 {ECO:0000303|PubMed:8035999}; AltName: Full=Protein yorkie homolog;>rs:NP_990574 [NP_990574] transcriptional coactivator YAP1 [Gallus gallus].>gp:X76483_1 [X76483] Yes-associated protein (65kDa) [Gallus gallus] 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAGSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRS
QLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDT
GDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKPDKESF
LTWL PMRLRKLPDSFFKPP

sp:YAP1_DANRE [Q1L8J7] RecName: Full=Transcriptional coactivator YAP1; Short=Yes-associated protein 1; Short=zYAP {ECO:0000303|PubMed:21687713}; AltName: Full=Protein yorkie homolog; AltName: Full=Yes-associated protein YAP65 homolog;>rs:NP_001132952 [NP_001132952] transcriptional coactivator YAP1 [Danio rerio].>gp:CR762425_2 [CR762425] novel protein similar to vertebrate Yes-associated protein 1, 65kDa (YAP1)(si:ch211-181p1.5) [Danio rerio] 45..59
MDPNQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRLRKLPDSFFTPPEPKSHSRQAS
TDAGTAGTVTPHHVRAHSSPASLQLGAVSPGALTSMGPANAPPQHLRQSSYEIPDDMPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFAMNQQRISQSAPVKQGSQLPSSPQSGVMSGNNPIRLQQIHIEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGP
GSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRLRKLPDSFFTPP

sp:YAP1_DROME [Q45VV3] RecName: Full=Transcriptional coactivator yorkie {ECO:0000305}; AltName: Full=Protein yorkie {ECO:0000303|PubMed:16096061}; AltName: Full=Transcriptional coactivator YAP1 homolog {ECO:0000305};>rs:NP_726414 [NP_726414] yorkie, isoform G [Drosophila melanogaster].>rs:NP_001036568 [NP_001036568] yorkie, isoform F [Drosophila melanogaster]. 65..79
MLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPLRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPIAAIPQLQIQPSPQHSRLAIHHSRAR
SSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAPASSAIDLDAMNTCMSQDIPMSMQ
TVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQILMAERIKQNDVL
QTTKQTTTSTIANNLGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQSGLSVLDCPDNLVSSLQIEDNLCSN
LFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

sp:YAP1_HUMAN [P46937] RecName: Full=Transcriptional coactivator YAP1; Short=Yes-associated protein 1; AltName: Full=Protein yorkie homolog; AltName: Full=Yes-associated protein YAP65 homolog;>rs:XP_024110885 [XP_024110885] transcriptional coactivator YAP1 isoform X4 [Pongo abelii].>rs:XP_001151467 [XP_001151467] transcriptional coactivator YAP1 isoform X4 [Pan troglodytes]. 85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP

TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

sp:YAP1_MOUSE [P46938] RecName: Full=Transcriptional coactivator YAP1; Short=Yes-associated protein 1; AltName: Full=Protein yorkie homolog; AltName: Full=Yes-associated protein YAP65 homolog;>rs:NP_001164618 [NP_001164618] transcriptional coactivator YAP1 isoform 1 [Mus musculus].>gp:BC014733_1 [BC014733] Yap1 protein [Mus musculus] 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLE
GDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

sp:YAP1_ORYLA [H2LBU8] RecName: Full=Transcriptional coactivator YAP1 {ECO:0000250|UniProtKB:P46937}; Short=Yes-associated protein 1 {ECO:0000250|UniProtKB:P46937}; AltName: Full=Protein hirame {ECO:0000303|PubMed:25778702}; AltName: Full=Protein yorkie homolog {ECO:0000250|UniProtKB:P46937}; AltName: Full=Yes-associated protein YAP65 homolog {ECO:0000250|UniProtKB:P46937}; 45..59
MDPSQHNPPVGHQIVHVRGDSETDLEALFNAVMNPKGAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHIDQTTTWQDPRKALLQLNQATPPSTVPVQQQNLLSPASGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
ETRYALNQQRITQSAPVKQGGPLPPNPHGGVMGGNNQMRLQQMEKERIRLKQQELLRQSQRPQIDLQPSTANQDA
EHCDELALRNQLPTSMDQDGSSNPVSSPMAQDARTMTANSNDPFLNSVSSGTYHSRDESTDSGLSMSSYSVPRTP
DDFLNSVDEMDTGDPLAPSMATQPSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESV
LAATKIDKESFLTWL PMRMRKLPDSFFKPP

sp:YAP1_RAT [Q2EJA0] RecName: Full=Transcriptional coactivator YAP1; Short=Yes-associated protein 1; AltName: Full=Protein yorkie homolog; AltName: Full=Yes-associated protein YAP65 homolog;>rs:XP_006242555 [XP_006242555] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Rattus norvegicus].>gp:DQ376007_1 [DQ376007] yes-associated protein [Rattus norvegicus] 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQEAL
SSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023971110 [XP_023971110] transcriptional coactivator YAP1 isoform X8 [Physeter catodon].>rs:XP_004283403 [XP_004283403] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Orcinus orca].>rs:XP_019779332 [XP_019779332] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Tursiops truncatus]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP

FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_028276091   [XP_028276091] LOW QUALITY PROTEIN: protein **FAM181**B
[Parambassis ranga].   247..261
MQVVGHKQRVKXPALPLPLLFDVLTSLVLPPERSPRFSSEPLTSTLECLQQLDEQHQHRVCVKRNETCS
EEKTFASGNTVDATGVAAGLSRVMAVQAAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLL
SFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNVAETPGKRQGSPLTQPSPLQSKTLPKRDGV
QASLQSKSLAALFSPVKDIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGP
DYSNMVSDQDLYQSMPLRGQPELGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKAGESLRSGPAQPPVYCQSEA
ASGPIEDNALCTLAFPSFFTDCSIPQVTYDLSGGYNRANYSSL   PLRHRNLPPSFFTEP

rs:XP_028339764   [XP_028339764] protein **FAM181**A [Physeter catodon].
204..218
MSVPRPRTLSRAEGCCGEDHCLQPCGLWGGLSVVAQRDANGCCVPPGQLGALPWSRQPPAEPPSSWKAP
CSGPLAMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRRAEPHLK
SGSEDRPGRLPLDSGHRPSPSGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQSPHPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_028370338   [XP_028370338] transcriptional coactivator YAP1 isoform
X6 [Phyllostomus discolor].   85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
ISPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_028322905   [XP_028322905] transcriptional coactivator YAP1-like
isoform X1 [Gouania willdenowi].   46..60
MDAHHAAPPAGQQIVHVRGDSQTELEALFSAVMNPSKAARAPNSLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDMPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLAHLQSAVAQHPIPGPPGHAHSLSNPAPNTQPQNITPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPS
LVQKMNPGILGIAMQQRQEKERLRFKQGIPQQTTPQEAARRNQMPGGMDHDRSAQTLVPNLDVRIRASNQEPTLN
GAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDVGEPPSMVLQDTMSVLPMSEGDELMPCIPEGLSSDLLMD
METVLSGSHMDKDSLLTWL   PMRMRKLPDSFFRQP

rs:XP_028251966   [XP_028251966] protein **FAM181**A [Parambassis ranga].
100..114
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEHRC
AKPVGTVHQIMTASEKANSHAQDVDSVEQVPMRKRQLPASFWEEPKLTQTKREHQHLGSKRSPVVTCEGSESEKR
KKCYDEDTKASMSASSRRSSSDKEMLKLDLTTHRCVSVCGCCPFHYHGHQVLHSHIVVPHPPLALWSKAAGTETE
RFDPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_028372536   [XP_028372536] protein **FAM181**B [Phyllostomus discolor].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGTEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAASPGPSSPGAADTPAKRALGAPSAQTVALPVHGK
AAPRRDASQAATAASLQSRSLAALFDSLRHIPAAADSAGGSVAAPTVGLGGAGAGGAVGDAAGPAGVSALAGSRK
VPLRARNLPPSFFTEPRASGGGCGPSGPCLSLCDLEKGSENLEFFELLGPDYGAGTEAGVLLAAEPLDVFPTGTT
VLRGPPEMEPGLFEPPPAMVGSLLYPETWSASACPPTKKPSLATPRGGSTLNEPLRRLYPATVDSPGGEDGPGLL
ASFSPFFSDCALPPPPPPPPHQVSYEYSAGYGRTPYSSLWRPDGVWEGGPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_028422539   [XP_028422539] protein **FAM181**A [Perca flavescens].
104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYGC

AKPVGTVHQSVNATEKASSDSRCVENVGSAVEQVPMRKRQLPASFWEEPKLTQTKMEHSHLGRKKNPASTPEGSE
NEKRKRSYDDDDAKATLSASSRRSSADKETLKLDLTSHHCVSVCGCCPFQYHGHQVLHSHIVVPHPPLGLWSKTA
ETERPEHHYGQKIHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_028357417 [XP_028357417] transcriptional coactivator YAP1 isoform X12 [Physeter catodon].>rs:XP_004283404 [XP_004283404] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Orcinus orca].>rs:XP_019779336 [XP_019779336] PREDICTED: transcriptional coactivator YAP1 isoform X12 [Tursiops truncatus]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELA
LRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDE
MDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDK
ESFLTWL PMRLRKLPDSFFKPP

rs:XP_028430162 [XP_028430162] transcriptional coactivator YAP1 [Perca flavescens]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVTGLSGMPPPGAAPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYFLN
HIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNIMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRLDP
RFALNQQRISQSAPVKQGGQLPPGIMGGNNQMRLQQIEKERLRLKQQELLRQRPQELAIRNQLPTSMDQDGSTNP
VSSPMAQDARTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLPPSMATQPSRF
PDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMETVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_028370335 [XP_028370335] transcriptional coactivator YAP1 isoform X3 [Phyllostomus discolor]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
LGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_028363788 [XP_028363788] protein **FAM181**A [Phyllostomus discolor].
129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGPEPHLK
RGPEDRPGRLPLDAGPDASAAGGGDCKEKALGNPYGVECLSKEQALQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGVLGPREGLPCEGKKHCKGLELLGPEMALVPMSPRAPGEKEPPKMPGVALVGRVNAWSCCPFQYH
GQPVYPGPPGALPQGPIPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_028451826 [XP_028451826] transcriptional coactivator YAP1-like isoform X1 [Perca flavescens]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKSSRQPPSLPMRMRKLPDSFFRQPDSRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAAIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWHDP
RLSQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQNINPETGPLPEGWEKAVTADGEVYYIDHINKTTAWVDPRLA
QKMNPGILGLALQQRQEKERLRCKQGLPQQITQEAGGRNQMPGGMDHDRNTQTLVPSLDVRIRASNHEPTLNGAH
SRNESTDSGLSVSSLPRTSDHVLSSVDHMDTGDSGDTSSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMET
VLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_028357414 [XP_028357414] transcriptional coactivator YAP1 isoform X10 [Physeter catodon].>rs:XP_012393541 [XP_012393541] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Orcinus orca].>rs:XP_019779334 [XP_019779334] PREDICTED: transcriptional coactivator YAP1 isoform X10 [Tursiops truncatus]. 86..100

MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMR
NINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSS
YSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSD
ILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023971106   [XP_023971106] transcriptional coactivator YAP1 isoform X4 [Physeter catodon].>rs:XP_004283402 [XP_004283402] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Orcinus orca].>rs:XP_019779328 [XP_019779328] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Tursiops truncatus].   86..100

MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL

PMRLRKLPDSFFKPP

rs:XP_028178224   [XP_028178224] transcriptional coactivator YAP1-like isoform X1 [Ostrinia furnacalis].   44..58

MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQPQPLHHQHAKHRSYDVGSHLQDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVASSVQHQSAETLLPQPASAPAITPAATPAAKSTSSNTTTDP
LGPLPEGWEQATTPEGETYFINHAARTTSWFDPRIPQHLQRTPAANAGAAGGGWANASLQACQQKIRLQSLQLER
DRLKQRQQEIRLQQELMARQSSSIMSSLASSAGAAASTDLSLDPFLSGLSEHQRQESADSGLGMAVPRVGEGDGL
FSIPHTPEDFLAGMDDRMDCSSEAGANMDSADMAIGDNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPD
NVLTWL   PLRMRQLPKSFFNPP

rs:XP_028370339   [XP_028370339] transcriptional coactivator YAP1 isoform X7 [Phyllostomus discolor].   85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_028322906   [XP_028322906] transcriptional coactivator YAP1-like isoform X2 [Gouania willdenowi].   46..60

MDAHHAAPPAGQQIVHVRGDSQTELEALFSAVMNPSKAARAPNSLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDMPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLAHLQSAVAQHPIPGPPGHAHSLSNPAPNTQPQNITPETVQKMNPGILGIAMQQRQEKERLRFKQGIPQQTT
PQEAARRNQMPGGMDHDRSAQTLVPNLDVRIRASNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDT
GDVGEPPSMVLQDTMSVLPMSEGDELMPCIPEGLSSDLLMDMETVLSGSHMDKDSLLTWL

PMRMRKLPDSFFRQP

rs:XP_023971108   [XP_023971108] transcriptional coactivator YAP1 isoform X6 [Physeter catodon].>rs:XP_012393539 [XP_012393539] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Orcinus orca].>rs:XP_019779330 [XP_019779330] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Tursiops truncatus].   86..100

MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP

PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_028277482   [XP_028277482] transcriptional coactivator YAP1-like
isoform X2 [Parambassis ranga].   42..56
MDAPPAGQQIVHVRGDSQTELEALFSAVMNPSKAARQPQSLPMRMRKLPDSFFRQPDPRGHSRQASSDG
GPCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLEKTTTWHDPRL
SQLQSAAAQHPITGTPVHAHSLSNPAPTTQPQNINPETAQKMNPGNLGLAMLQRQEKERLRCKQGLPQLTPQDAG
GRNQIPSGMDHDRSAQTHVPSLDVRIRGSNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGD
APSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL   PMRMRKLPDSFFRQP

rs:XP_028138151   [XP_028138151] transcriptional coactivator YAP1-A-like
isoform X1 [Diabrotica virgifera virgifera].   41..55
MALNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATGATSVNSVPLQTAHHRAHSSPASLQQTYAVGQQQAPVHHIKQRSYDVASKSEDNTPLPPGWEQAR
TPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAQQHQSAEQLLTSHQLSHPQSPNSNTTAKVNTDVDLGPLPEGWEQ
AQTPEGEIYFINHQTRTTSWFDPRIPTHLQQRTSGGNIIGSNWHSPTLSSSPAKAQQIRLQQLQMERERLKQRQQ
EIRRQQEIMMRSSSDLPVMDPFLSSLTDHSRQESGDSGLGMGTTYSMPHTPEDFLANMDDNMDVGSESHTMDTPD
ISTLSDNIDSTDDLVPTLQLGEEEFPMLDVQSLINPPTTRPDNVLIWL   PWSMRKLPDSFFNPP

rs:XP_028393807   [XP_028393807] uncharacterized protein LOC114518090
[Dendronephthya gigantea].   106..120
MAEIINEDKLTVTNDDQDKDFNQWRQPKTPESPKTPEEIKSNSPEHSSVQNKSLCGVKDLSRLSRKRRT
ILSVKGARICSRKRSEDKPFGSGHDSKPRTSKKEPLPMKQRSLPQSFWLQPNSIKSSSMAQNTYSRLPPLFPEDH
NPDKELMERPVTPPEERREHQPRPPKRVVTSEPDTELLFSLFKAVTGNPLEKKLIKRGRPKKIHSEKLPIVSHED
DPCMVENLTGRLFPQLSLENHHRSADARLASLTVHAGNHCIQLPTLAVDNNYPQMLSQLAQVL
PMKQRSLPQSFWLQP

rs:XP_028138152   [XP_028138152] transcriptional coactivator YAP1-like
isoform X2 [Diabrotica virgifera virgifera].   41..55
MALNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATGATSVNSVPLQTAHHRAHSSPASLQQTYAVGQQQAPVHHIKQRSYDVASKSEDNTPLPPGWEQAR
TPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAQQHQSAEQLLTSHQLSHPQSPNSNTTTHLQQRTSGGNIIGSNWH
SPTLSSSPAKAQQIRLQQLQMERERLKQRQQEIRRQQEIMMRSSSDLPVMDPFLSSLTDHSRQESGDSGLGMGTT
YSMPHTPEDFLANMDDNMDVGSESHTMDTPDISTLSDNIDSTDDLVPTLQLGEEEFPMLDVQSLINPPTTRPDNV
LIWL PWSMRKLPDSFFNPP

rs:XP_028320858   [XP_028320858] transcriptional coactivator YAP1 [Gouania
willdenowi].   45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSAGVLTPHHVRAHSSPASLQLGAVSAGSLSGMAPAGASPQHLRQSSYEIPDDVPLPAGWEMAKTASGQRYF
LNHIEQTTTWQDPRKALLQMNQAAPASTVPVQQQNLMNPTNGALPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRITQSAPGKQGQLPPHSGVMGGNNQMRLPQLEKDRLRMKPQELLRQRPQELALRNQLPTSMEQDGG
TNPVSSPMAQDARTMTANSNDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSMATQP
SRFPDYLDAIPGTDVDLGTLESESMVVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_028357415   [XP_028357415] transcriptional coactivator YAP1 isoform
X11 [Physeter catodon].>rs:XP_012393542 [XP_012393542] PREDICTED:
transcriptional coactivator YAP1 isoform X7 [Orcinus orca].>rs:XP_019779335
[XP_019779335] PREDICTED: transcriptional coactivator YAP1 isoform X11
[Tursiops truncatus].   86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRP
QELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLN

SVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAAT
KLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_028357413 [XP_028357413] transcriptional coactivator YAP1 isoform
X9 [Physeter catodon].>rs:XP_012393540 [XP_012393540] PREDICTED:
transcriptional coactivator YAP1 isoform X5 [Orcinus orca].>rs:XP_019779333
[XP_019779333] PREDICTED: transcriptional coactivator YAP1 isoform X9
[Tursiops truncatus]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRP
QAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGL
SMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEA
LSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023971104 [XP_023971104] transcriptional coactivator YAP1 isoform
X2 [Physeter catodon].>rs:XP_012393538 [XP_012393538] PREDICTED:
transcriptional coactivator YAP1 isoform X1 [Orcinus orca].>rs:XP_019779326
[XP_019779326] PREDICTED: transcriptional coactivator YAP1 isoform X2
[Tursiops truncatus]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_028293640 [XP_028293640] protein **FAM181**A [Gouania willdenowi].
99..113
MAHADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVTRYHRSAEYRCTK
PVVTTTVPSMTGSSGAQEAETVGGAAVEQVPMRKRQLPASFWEEPRLIENKKDNSVPGLKGRPEAPPEATETTKRR
GNFNDPKAPIGAPTRRSPEAKETLKLDLSSHHCLSMYGCCPCQYHGHQVLHSHIIVPHLPVGLWSKAVETETERA
EHIYGPKFHTHVVVKPIPTKPSSHSSIYSVFGFI PMRKRQLPASFWEEP

rs:XP_028370333 [XP_028370333] transcriptional coactivator YAP1 isoform
X1 [Phyllostomus discolor]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
LGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNISPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023971107 [XP_023971107] transcriptional coactivator YAP1 isoform
X5 [Physeter catodon].>rs:XP_019779329 [XP_019779329] PREDICTED:
transcriptional coactivator YAP1 isoform X5 [Tursiops
truncatus].>rs:XP_026943624 [XP_026943624] transcriptional coactivator YAP1
isoform X5 [Lagenorhynchus obliquidens]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMT

TNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNV
DLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_028321398   [XP_028321398] protein **FAM181**B [Gouania willdenowi].
156..170
MAVQTAIMNPQFMNFCFPASVMEYEVEKSLDGSLLAEAETDEEYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIIAPGNVAEAPVKRHGSSPPAQPSFLQSKTLPKRDGIQANLQSKSLAALFSPV
KDVRGEKTKKPPLRHRNLPPSFFTEPAKCPKVSSTSGMTLKDLERGNPEAVDFFELLGPDYSNMVSEQDFYQNSS
SGRVQPELGGPDPASYDIHHLASGLLYAESWTNCSGTAKKLEESLSAGSAQPPLYCQAETSSSPMDDSLAFPHFF
TDCSIPQVTYDGGYNRATYSSL PLRHRNLPPSFFTEP

rs:XP_023971103   [XP_023971103] transcriptional coactivator YAP1 isoform
X1 [Physeter catodon].>rs:XP_019779325 [XP_019779325] PREDICTED:
transcriptional coactivator YAP1 isoform X1 [Tursiops
truncatus].>rs:XP_026943620 [XP_026943620] transcriptional coactivator YAP1
isoform X1 [Lagenorhynchus obliquidens]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQ
NPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQ
QNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_028451827   [XP_028451827] transcriptional coactivator YAP1-like
isoform X2 [Perca flavescens].   46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKSSRQPPSLPMRMRKLPDSFFRQPDSRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAAIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWHDP
RLSQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQNINPETAQKMNPGILGLALQQRQEKERLRCKQGLPQQITQE
AGGRNQMPGGMDHDRNTQTLVPSLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHVLSSVDHMDTGDS
GDTSSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_028178226   [XP_028178226] transcriptional coactivator YAP1-like
isoform X3 [Ostrinia furnacalis]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQPQPLHHQHAKHRSYDVGSHLQDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVASSVQHQSAETLLPQPASAPAITPAATPAAKSTSSNTTTDP
LGPLPEGWEQATTPEGETYFINHAARTTSWFDPRIPQHLQRTPAANAGAAGGGWANASLQACQQKIRLQSLQLER
DRLKQRQQEIRLQQELMARQSSSIMSSLASSAGAAASTDLSLDPFLSGLSEHQRQESADSGLGMAVPRVGEGDGL
FSIPHTPEDFLAGMDDRMDCSSEAGANMDSADMAIGDNLDSTDDLLNEFTNDILLDDVQSLINSTPSKPDNVLTW
L   PLRMRQLPKSFFNPP

rs:XP_028370336   [XP_028370336] transcriptional coactivator YAP1 isoform
X4 [Phyllostomus discolor]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
LGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_028178225   [XP_028178225] transcriptional coactivator YAP1-like
isoform X2 [Ostrinia furnacalis]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQPQPLHHQHAKHRSYDVGSHLQDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVASSVQHQSAETLLPQPASAPAITPAATPAKSTSSNTTTDPL
GPLPEGWEQATTPEGETYFINHAARTTSWFDPRIPQHLQRTPAANAGAAGGGWANASLQACQQKIRLQSLQLERD

RLKQRQQEIRLQQELMARQSSSIMSSLASSAGAAASTDLSLDPFLSGLSEHQRQESADSGLGMAVPRVGEGDGLF
SIPHTPEDFLAGMDDRMDCSSEAGANMDSADMAIGDNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDN
VLTWL PLRMRQLPKSFFNPP

rs:XP_023971109 [XP_023971109] transcriptional coactivator YAP1 isoform
X7 [Physeter catodon].>rs:XP_019779331 [XP_019779331] PREDICTED:
transcriptional coactivator YAP1 isoform X7 [Tursiops
truncatus].>rs:XP_026943627 [XP_026943627] transcriptional coactivator YAP1
isoform X7 [Lagenorhynchus obliquidens]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_028370334 [XP_028370334] transcriptional coactivator YAP1 isoform
X2 [Phyllostomus discolor]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
LGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNISPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023971105 [XP_023971105] transcriptional coactivator YAP1 isoform
X3 [Physeter catodon].>rs:XP_019779327 [XP_019779327] PREDICTED:
transcriptional coactivator YAP1 isoform X3 [Tursiops
truncatus].>rs:XP_026943622 [XP_026943622] transcriptional coactivator YAP1
isoform X3 [Lagenorhynchus obliquidens]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_028429740 [XP_028429740] protein **FAM181**B [Perca flavescens].
153..167
MAVQTAIMNPQFMNFCFPCSVMEYEVEKSLDGSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGNITPGNVAEVPVKRQGSPLAQPLQSKTLPKRDGVQANLQSKSLAALFSPVKDI
RGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSDQDLYQSMPVRV
QPEMGGPDPASYDAHHLVGGLLYSEPWTSCSVPTKKVGENLRTGPTQPPVYCHSEAASGSIEDNALCTLAFPNFF
TDCSIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_028370337 [XP_028370337] transcriptional coactivator YAP1 isoform
X5 [Phyllostomus discolor]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNISPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_028178227 [XP_028178227] WW domain-containing transcription regulator protein 1-like isoform X4 [Ostrinia furnacalis]. 44..58

MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQPQPLHHQHAKHRSYDVGSHLQDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVASSVQHQSAETLLPQPASAPAITPAATPAAKSTSSNTTTDP
LGPLPEGWEQATTPEAQHLQRTPAANAGAAGGGWANASLQACQQKIRLQSLQLERDRLKQRQQEIRLQQELMARQ
SSSIMSSLASSAGAAASTDLSLDPFLSGLSEHQRQESADSGLGMAVPRVGEGDGLFSIPHTPEDFLAGMDDRMDC
SSEAGANMDSADMAIGDNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_007119750 [XP_007119750] protein **FAM181**B [Physeter catodon].>tr:A0A2Y9FCD7_PHYCD [A0A2Y9FCD7] SubName: Full=protein **FAM181**B {ECO:0000313|RefSeq:XP_007119750.2}; 221..235

MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDEETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAASAQTVPVQAHGK
AVPRREASQAAAAASLQSRSLAALFDSLSHVPGAGDPAGSAEAAPAAGLVGAGAGGVGGDAAGAAGGPAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAAEFFELLGPDYGAGTEAGVLLAAEPLDVLLTGA
AVLRGPPELEPGLFEPSPVMGGSLLYPEPWSAPGGPTTKKSPLAAPRGGLTLNEPLRPLYPAAADSPGGDDGPGL
LASFTPFFSDCALPPPPPPPQVSYDYSAGYSRTAYASLWRPDGIWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_028275188 [XP_028275188] transcriptional coactivator YAP1 [Parambassis ranga]. 45..59

MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKGSIMPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSMSGLAPAGASPQHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHIEQTTTWQDPRKALLMNQPPPPSSVPVQQQNLMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRLE
PRYALNQRGITQSAPVKPLPPGPHSGVMGGNSQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQDGST
NPVSSPMGQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPTSMATQPS
RFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_028370340 [XP_028370340] transcriptional coactivator YAP1 isoform X8 [Phyllostomus discolor]. 85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGNSNQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_028277481 [XP_028277481] transcriptional coactivator YAP1-like isoform X1 [Parambassis ranga]. 42..56

MDAPPAGQQIVHVRGDSQTELEALFSAVMNPSKAARQPQSLPMRMRKLPDSFFRQPDPRGHSRQASSDG
GPCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLEKTTTWHDPRL
SQLQSAAAQHPITGTPVHAHSLSNPAPTTQPQNINPETGPLPEGWEQAVTADGEVYYIDHINKTTAWVDPRLAQK
MNPGNLGLAMLQRQEKERLRCKQGLPQLTPQDAGGRNQIPSGMDHDRSAQTHVPSLDVRIRGSNHEPTLNGAHSR
NESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGDAPSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVL
SGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_028145773 [XP_028145773] transcriptional coactivator YAP1-like [Diabrotica virgifera virgifera]. 36..50

MALNKSEVVTVDPEKDLQALFDSVLKPDSKRNVQVPWHKRRLPDSFFNPPTTGSKSINHSRDSSVDSSC
GSNTSTTSVSSACTIPIHQRAHSSPASFQETYMEQQPLQHMKQKSHDVSKKSKVKNRLPSGWEQGRTRDGKIYYI
NHNTRTTTWDHPTNSLAAQTASKKHHSAEQLLSTRQLSSNPFYYNTVVQNRNLEHLPDGWEQARTSEGEIYFMNH
KTRTTSWEDPRISSRQSTSDGKYALPELSRALLKQKHQNVLRQHEDSISSLDPRIITPTHFQQPSSEENGNEFSS
QLPSAQQLRLQELYLERERLRQRHEYIREQENMMTALVHSFLPDITDRPEKEDIRGAVPPVSEALQPIMDVSREC
QNMDSFDIPMLEDDVSSTDDLEPTFRPNEEVSMTNVVDAKSYLWL PWHKRRLPDSFFNPP

rs:XP_016416304 [XP_016416304] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Sinocyclocheilus rhinocerous].45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLSSMVPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISHSAPVKQGSQLPSSPQSGVLGGNNQIRLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPSMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDSLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_016416306 [XP_016416306] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Sinocyclocheilus rhinocerous].45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLSSMVPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASAMNQQRISHSAPVKQGSQLPSSPQSGVLGGNNQI
RLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQNPVSSPSMGQDARNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDSLGPSSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_016420209 [XP_016420209] PREDICTED: protein **FAM181**A [Sinocyclocheilus rhinocerous]. 111..125
MASSDSEVKTLLNFVNLASSDIKAALDRSAPCRRSVDHRKYLQKQLKRFSHRYAKMPRCHSHRNGDSAP
AKLSEDQAPPGTGTGSGREERLNAEDGARSGQGQGQGQAPMPMRKRQLPASFWKEPQSSSGSRERLERFLQSGHV
RPPAVNGERSTTVFEDLNANPLLSGRAACACSCCSLPYRFLLPHADAPLSSRAHVVIKPIPTKPSSSSSSSSSSV
FSVFGFI PMRKRQLPASFWKEP

rs:XP_016431451 [XP_016431451] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Sinocyclocheilus rhinocerous]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAISPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVSPGTLSSMVPANPQPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPMQQQNIMNPASGPVPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQIRLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_016431452 [XP_016431452] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Sinocyclocheilus rhinocerous]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAISPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVSPGTLSSMVPANPQPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPMQQQNIMNPASAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQI
RLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGPSSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_008216287 [XP_008216287] PREDICTED: transcriptional coactivator yorkie isoform X1 [Nasonia vitripennis].>tr:K7J1R3_NASVI [K7J1R3] SubName: Full=Uncharacterized protein {ECO:0000313|EnsemblMetazoa:NV15294-PA};
52..66
MALNQDVAEPGSGAAGAKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTG
SKSPSISHSRENSADSAFGAGGGGLVNGGGAATPGGNGSGGTTSPGAQPSGAAQVPQGLTVAHPRAHSSPASLQQ
TYASAQQQSQHAPQHNSARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAA
AASVAAVAAAVESGKAAATPGQAGSNALGPLPDGWEQARTPEGEIYFINHQARTTSWFDPRIPSHLQRAPTSGAM
LPQNWQIQQQGAAGIQSSQTLQACQQKLRLQSLQMERERLKQRQQEIIRQVSSQELMLRQSTTDAAMDPFLSGIN
EQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSEGAPMETPDLSSLSDNIDSTDDLVPLQLGEEFSSD
ILEDVQSLIDPVGNPTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_008216288 [XP_008216288] PREDICTED: transcriptional coactivator yorkie isoform X2 [Nasonia vitripennis]. 52..66

MALNQDVAEPGSGAAGAKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTG
SKSPSISHSRENSADSAFGAGGGGLVNGGGAATPGGNGSGGTTSPGAQPSGAAQVPQGLTVAHPRAHSSPASLQQ
TYASAQQQSQHAPQHNSARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAA
AASVAAVAAAVESGKAAATPGQAGSNALGPLPDGWEQARTPEGEIYFINHQARTTSWFDPRIPSHLQRAPTSGAM
LPQNWQIQQQGAAGIQSSQTLQACQQKLRLQSLQMERERLKQRQQEIIRQVSSQELMLRQSTTDAAMDPFLSGIN
EQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSGAPMETPDLSSLSDNIDSTDDLVPLQLGEEFSSDI
LEDVQSLIDPVGNPTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_001604094 [XP_001604094] PREDICTED: transcriptional coactivator yorkie isoform X3 [Nasonia vitripennis]. 52..66

MALNQDVAEPGSGAAGAKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTG
SKSPSISHSRENSADSAFGAGGGGLVNGGGAATPGGNGSGGTTSPGAQPSGAAQVPQGLTVAHPRAHSSPASLQQ
TYASAQQQSQHAPQHNSARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAA
AASVAAVAAAVESGKAAATPGQAGSNALGPLPDGWEQARTPEGEIYFINHQARTTSWFDPRIPSHLQRAPTSGAM
LPQNWQIQQQGAAGIQSSQTLQACQQKLRLQSLQMERERLKQRQQEIIRQQELMLRQSTTDAAMDPFLSGINEQH
ARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSEGAPMETPDLSSLSDNIDSTDDLVPLQLGEEFSSDILE
DVQSLIDPVGNPTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_016135139 [XP_016135139] PREDICTED: uncharacterized protein LOC107590746 [Sinocyclocheilus grahami]. 232..246

MAASVIRTLSNLGLAKPFPPCFFPVEDEEETEEEYEEELREDSLEEEEDAVASESQEEEPWSFDSSPNN
AEMTNQLLRMAASVIRTLSNLGLAKPFPPCFFPVEDEEETEEEYEEELREDSLEEEEDAVASESQEEEPWSFDSS
PNNAEMTNQLLRFAELISSDVQRYFGRSQDPDACDIYAEKPCPKVGGRQRYYADFIKVASSGQGEEPESLGPLAE
LFQDAQRKGRGLPMSQRRLPVSFWTEPFAQQLDMLGDTSMQDNSLSMSNTSESSININTSLSMFSNSSVCTMTSS
SISGTLSSSSTPDFSDLLAHWAMDRENPNEFNCDYPLS PMSQRRLPVSFWTEP

rs:XP_016138714 [XP_016138714] PREDICTED: protein **FAM181**B [Sinocyclocheilus grahami]. 157..171

MAVQAAIMNSQFLNFCFPGSVMDYEVEKGLEGGLLGEEVDCGGDFKETTRDLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGIISPGTTPVQEPCKRQGSPQTPTSNLSGKTPPKKDGMQASLQSKSLAALFNS
AKDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAAEFFELLGPDYSNMVSEQDLFHTA
PIRIQQEVTVGPEPYDSHHFVSGGFLYTEPWGTCSGTSKKSGDMRTVPVQPNLYTHTDLSGSVPVEQSSPCALTF
SNFFTDCSAPPVSYDLVNGYNRGNFSSL PLRHRNLPPSFFTEP

rs:XP_018619362 [XP_018619362] PREDICTED: protein **FAM181**B [Scleropages formosus].>tr:A0A1W5AUZ7_9TELE [A0A1W5AUZ7] SubName: Full=protein **FAM181**B {ECO:0000313|RefSeq:XP_018619362.1}; 230..244

MDHTLKGRDYTPSHCKQLSKGFEGEERGRGALPSPSKRSPSVQLGGVQKCPCQWQDQGFAHLPPEQEDA
ACFCEAPPPGTAVDAVGEGAGCDAVMAVQAALMTPQSLLGEGACEGDFREATRDLLSFIDSASSNIKLALDKPVK
SRRKVNHRKYLQKQIKRCAGIAGTLGAAQDSGKRPGSSPPTHPGGCVPARPPSKRDGLQANLQSRSLAALFEPMR
DARXXXXXXXPLRQRNLPPSFFTEPAHCARVTSTSGVTLKDLERGNPEAADFLELLGPDYSGMLMEQDVGRTAPA
SNTRNQLVVRHPCGLFEVCNLIVTDKILSMSGGVDLEGIRLLDRERTLKELTGPLRQRNLPPSFFTEP

rs:XP_018620303 [XP_018620303] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Scleropages formosus].>tr:A0A1W5B304_9TELE [A0A1W5B304] SubName: Full=transcriptional coactivator YAP1 isoform X1 {ECO:0000313|RefSeq:XP_018620303.1}; 45..59

MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAIVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGSLTPQHVRAHSSPASLQLGAVSPASMASMTPPGGPPQHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHLEQSTTWQDPRKTMLQMNTSPNSSVSVQQGIMGTASGPLPEGWEQAVTTDGEIYYINHKNKTTSWLDPRLDP
RYALNQQRIGQSATVKQAPALPSSPQGGVMGGGGSQLRLQQLQMEKERVRLKQQELLRQRPQELPLRTQVPTSME
QDGSTQNNISSPGVAQDVRTMTSNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLGP
ASMATQPSRFPDYLDTIPGTNVDLGTLESDSMAVEGEELMPSLQEALSSEILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_018620312 [XP_018620312] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Scleropages formosus].>tr:A0A1W5AY12_9TELE [A0A1W5AY12] SubName: Full=transcriptional coactivator YAP1 isoform X2 {ECO:0000313|RefSeq:XP_018620312.1}; 45..59

MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAIVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGSLTPQHVRAHSSPASLQLGAVSPASMASMTPPGGPPQHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHLEQSTTWQDPRKTMLQMNTSPNSSVSVQQGIMGTASGPLPEGWEQAVTTDGEIYYINHKNKTTSWLDPRLDP
RYALNQQRIGQSATVKQAPALPSSPQGGVMGGGGSQLRLQQLQMEKERVRLKQQELLRQRPQVPTSMEQDGSTQN
NISSPGVAQDVRTMTSNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLGPASMATQP
SRFPDYLDTIPGTNVDLGTLESDSMAVEGEELMPSLQEALSSEILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_005957321 [XP_005957321] PREDICTED: protein **FAM181**A [Pantholops hodgsonii]. 130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRPLPLESGHGSSPSGGGGYKEKALGNPDREESLSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPIYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_006621320 [XP_006621320] PREDICTED: yorkie homolog [Apis dorsata].
46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAAAAAAAVGGGGPTPGGNATGTPATGAAGAATGGSGNSAGSGSNAAGAAAAGLTVAHPRA
HSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTW
EDPRKTAAAANVAAVAAAVDNGNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPQ
NWLQQQQPTGGGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIIRQQELMLRQSTTDAAMDPFLSGINEQHAR
QESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSEDFSSDILD
DVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_017767514 [XP_017767514] PREDICTED: transcriptional coactivator yorkie [Eufriesea mexicana]. 46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAAAAAAAVGGGGPAPGGNATGTPATGAAGAATGGSGNSAGSGSNAAGAAAAAVAAAAAAG
LTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLN
HLTRTTTWEDPRKTAAAANVAAVAAAVDNGKSTTGATNTLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIP
THLQRAPTSGAMLPQNWLQQQPTGGGIQSNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQSTTDAA
MDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVP
SLQLSEDFSSDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_017779527 [XP_017779527] PREDICTED: transcriptional coactivator YAP1-A-like isoform X1 [Nicrophorus vespilloides]. 41..55
MALNQDESKQVVRVDQDSETGLQALFDSVLKPDSKRPLQVPWKLRKLPDSFFNPPSTGTKSINHSRENS
VDSAFGSSSGGGGGGGGGSSNGGGTSTTPVNTVPLQTTHHRAHSSPASLQQTYAVGQQQQTTPTHHHMKQRSYDV
ASKTEDNTPLPPGWEQARTPEGQVYYLNHTTRTTTWEDPRKTTLASQVAAQQHQSAEQLLTTHQVVTPSQTQSPS
TTCTGAKTSSDVDLGPLPEGWEQSQTSDGELYFINHQTRTTSWFDPRIPTHLQRSPGSTLILPQTWHSTGNPLSP
QSSSAKSQQMRLHLLQLERDKLKMRQQEIRQQEMRRQLMVRSSSSDLPNMDPFMPNLSDHSRQESADSGLGMGTT
YSVPHTPEDFLNMDDNMEVGSESHTMDTPDMSSLTDNIDPTDDLVPTLQLCEEFPMLSDVQNIIDPPTTKPDNVL
VWL PWKLRKLPDSFFNPP

rs:XP_017779528 [XP_017779528] PREDICTED: WW domain-containing transcription regulator protein 1-like isoform X2 [Nicrophorus vespilloides]. 41..55
MALNQDESKQVVRVDQDSETGLQALFDSVLKPDSKRPLQVPWKLRKLPDSFFNPPSTGTKSINHSRENS
VDSAFGSSSGGGGGGGGGSSNGGGTSTTPVNTVPLQTTHHRAHSSPASLQQTYAVGQQQQTTPTHHHMKQRSYDV
ASKTEDNTPLPPGWEQARTPEGQVYYLNHTTRTTTWEDPRKTTLASQVAAQQHQSAEQLLTTHQVVTPSQTQSPS
TTCTATHLQRSPGSTLILPQTWHSTGNPLSPQSSSAKSQQMRLHLLQLERDKLKMRQQEIRQQEMRRQLMVRSSS
SDLPNMDPFMPNLSDHSRQESADSGLGMGTTYSVPHTPEDFLNMDDNMEVGSESHTMDTPDMSSLTDNIDPTDDL
VPTLQLCEEFPMLSDVQNIIDPPTTKPDNVLVWL PWKLRKLPDSFFNPP

rs:XP_007447169 [XP_007447169] PREDICTED: yorkie homolog isoform X1 [Lipotes vexillifer].>tr:A0A340WJ71_LIPVE [A0A340WJ71] SubName: Full=yorkie homolog isoform X1 {ECO:0000313|RefSeq:XP_007447169.1}; 86..100

MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPSSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKPHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_007447170   [XP_007447170] PREDICTED: yorkie homolog isoform X2
[Lipotes vexillifer].>tr:A0A340WJJ0_LIPVE [A0A340WJJ0] SubName: Full=yorkie
homolog isoform X2 {ECO:0000313|RefSeq:XP_007447170.1};   71..85
MDPGQQQPPPQPAPQGQGQPPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQT
VPMRLRKLPDSFFKPPEPKPHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQ
HLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSPPVQQNMMNSASGPLP
DGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRL
QQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_007447171   [XP_007447171] PREDICTED: yorkie homolog isoform X3
[Lipotes vexillifer].>tr:A0A340WEW9_LIPVE [A0A340WEW9] SubName: Full=yorkie
homolog isoform X3 {ECO:0000313|RefSeq:XP_007447171.1};   86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPSSGPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKPHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQ
ELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPD
DFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESV
LAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_007447424   [XP_007447424] PREDICTED: protein **FAM181**B [Lipotes
vexillifer].>tr:A0A340WJY8_LIPVE [A0A340WJY8] SubName: Full=protein **FAM181**B
{ECO:0000313|RefSeq:XP_007447424.1};   221..235
MAVQAALLSTHPFVPFGFGGSPDGLGSAFGALDKGCCFEDEETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAASAQTVPAQAHGK
AGPRREASQAAAAASLQSQSLAALFDSLSHVPGAADPAGVAEAAPAAGLVGAGAGGVGGDAAGPAGGPAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAAEFFELLGPDYGAGSEAGVLLAAEPLDVLLTGA
AVLRGPPELETGLFEPPPAMGGSLLYPEPWSAPGGSTTKKSPLAAPRGGLTLNEPLRPLYPAAADSPGGDDGPGL
LASFTPFFSDCTLPPPPPPPPPPPQVSYDYSAGYSRTAYASLWRPDGIWEGAPGEEGAHRD
PLRARNLPPSFFTEP

rs:XP_007447496   [XP_007447496] PREDICTED: protein **FAM181**A isoform X1
[Lipotes vexillifer].>tr:A0A340WFT7_LIPVE [A0A340WFT7] SubName:
Full=protein **FAM181**A isoform X1 {ECO:0000313|RefSeq:XP_007447496.1};
180..194
MKLLQMLIRGSPCCPQPEISPPGQLCALPWSRQPPAEPPSSWKAPCSGPLVMASDSDVKMLLNFVNLAS
SDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGSEDRPGRLPLDSGHSSSPGGGG
CCKEKALGNPYKEECLSKEQNLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTQSYPVGLEGGLGPREGPPYEGK
KHCKGLEPLGPETAPVPASPRAPTEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGALPQSPLPSLGLWR
KSSASPGELNHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL   PMRKRQLPASFWEEP

rs:XP_007447497   [XP_007447497] PREDICTED: protein **FAM181**A isoform X2
[Lipotes vexillifer].>tr:A0A340WIX9_LIPVE [A0A340WIX9] SubName:
Full=protein **FAM181**A isoform X2 {ECO:0000313|RefSeq:XP_007447497.1};
129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGSEDRPGRLPLDSGHSSSPGGGGCCKEKALGNPYKEECLSKEQNLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTQSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPASPRAPTEKEPLKMPGVSLVGRVNAWSCCPFQYH

GQPIYPGPPGALPQSPLPSLGLWRKSSASPGELNHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_007985859 [XP_007985859] PREDICTED: protein **FAM181**A isoform X1
[Chlorocebus sabaeus]. 257..271
MLGAGVVGGGGYHQGGRGLGLAFKWSSCLSSENKHLTGKLAAWCVGDGAGWECVPAPAMPPVAGSPWAS
CLTFLSLGCKKRAPDPSRLGEALLAPAASQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVKMLLNFVNL
ASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDLGPDSSPGG
GGGCKEKAPRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYE
GKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGL
WKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_007985860 [XP_007985860] PREDICTED: protein **FAM181**A isoform X2
[Chlorocebus sabaeus].>rs:XP_007985861 [XP_007985861] PREDICTED: protein
FAM181A isoform X2 [Chlorocebus sabaeus].>rs:XP_007985862 [XP_007985862]
PREDICTED: protein **FAM181**A isoform X2 [Chlorocebus sabaeus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKAPRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_017713486 [XP_017713486] PREDICTED: protein **FAM181**A [Rhinopithecus
bieti].>rs:XP_017713487 [XP_017713487] PREDICTED: protein **FAM181**A
[Rhinopithecus bieti].>rs:XP_010382821 [XP_010382821] PREDICTED: protein
FAM181A [Rhinopithecus roxellana]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_017730717 [XP_017730717] PREDICTED: protein **FAM181**B [Rhinopithecus
bieti].>tr:A0A2K6JYF4_RHIBE [A0A2K6JYF4] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSRBIP00000004049};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDLREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AVPRREAAQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVVAPVAGLGGAGTGGAGGDAVGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPHQVSYDYSAGYSRNAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_008490751 [XP_008490751] PREDICTED: protein **FAM181**A [Calypte
anna].>tr:A0A091HHE0_CALAN [A0A091HHE0] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KFO95708.1}; 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWH
RGAEDRGRGPQPEAPDPSPHGGAAAERGLQTAEVEESLTGEGVLQDQNLEASRPDQVPMRKRQLPASFWEEPRPA
QSLPARAFSTGPEGLPASRDPPPYEGKKSKRSLDAASPENPSESALHAGEKDTARVLTGRVGAWTCCPFPCPGPG
VYQPPGTLPPSPFPALGLWRKSTVAALPAEVPHFCKEADGTGQKLYRPVVLKPIPTKPTIPPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_008281832 [XP_008281832] PREDICTED: protein **FAM181**A [Stegastes
partitus]. 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYRC
AKPAGTVNQSVTVSEKANSDAQDVENVGSAVEQVPMRKRQLPASFWEEPKLTQTKREHSYLGLKRSPAATSEGGE
NEKRKRSYDEDAKAAMSASNRRSSADKETLKLDLTSHHCVSVCGCCPFQYHGHHQVLHSHIVVPHPPLGLWSKAA
GTETERPEHPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_008276992 [XP_008276992] PREDICTED: yorkie homolog isoform X1 [Stegastes partitus].>tr:A0A3B4ZTA6_9TELE [A0A3B4ZTA6] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSSPAP00000011011};
46..60
MDAHRGAPPAGQQVVHVRGDSQTELEALFSAVMNPSKAVRQPSSVPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVATTPIIPDDVPLPHGWEMAKTPTGQRYFLNHRDKTTTWH
DPRLSQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQNINPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPR
LAQKMNPGILGLAMQQRQEKERLRCKQGLPPQIGSQEAGGRSQMPGGMDHDRSAQTLVPPLDVRIRAPNHEPTLN
GAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGEPVEPPSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMD
METVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_008276993 [XP_008276993] PREDICTED: yorkie homolog isoform X2 [Stegastes partitus]. 46..60
MDAHRGAPPAGQQVVHVRGDSQTELEALFSAVMNPSKAVRQPSSVPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVATTPIIPDDVPLPHGWEMAKTPTGQRYFLNHRDKTTTWH
DPRLSQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQNINPETAQKMNPGILGLAMQQRQEKERLRCKQGLPPQIG
SQEAGGRSQMPGGMDHDRSAQTLVPPLDVRIRAPNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDT
GEPVEPPSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_008287715 [XP_008287715] PREDICTED: yorkie homolog [Stegastes partitus].>tr:A0A3B4ZWH1_9TELE [A0A3B4ZWH1] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSSPAP00000013238}; 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSAGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDAPLPAGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAAPPSSVPVPQQNLMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRITQSAPVKQGGPLPPSTHSGVMGGNNQLRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQ
DGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSMA
TQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_008288570 [XP_008288570] PREDICTED: protein **FAM181**B [Stegastes partitus].>tr:A0A3B5AW19_9TELE [A0A3B5AW19] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSSPAP00000017707};
155..169
MAVQAAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQGSPLTQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSEQDLYQGMPF
RVQPELGSPDPASYDAHHLVGGLLYSEPWTSCSGPSKKLGETLRTGPAQPPAYCHSEAASGPIEDNALCTLAFPN
FFTDCSIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_008696489 [XP_008696489] PREDICTED: protein **FAM181**A isoform X1 [Ursus maritimus].>rs:XP_026371172 [XP_026371172] protein **FAM181**A isoform X1 [Ursus arctos horribilis].>tr:A0A384CPS9_URSMA [A0A384CPS9] SubName: Full=protein **FAM181**A isoform X1 {ECO:0000313|RefSeq:XP_008696489.1};
187..201
MERGAGRTAGSGDVCTPTPNPGLLPHLCVVSSVPFPGAASDPQSPRSSWKAPCSGPLVMASDSDVKMLL
NFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLRRGADDRPGRLPLESGHD
SSPGGGGGCKEKALGNPYREECLSQEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPRE
GPPYEGKKRCKGLEPLDTEMAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYAGPPGALPQSSV
PGLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_008696497 [XP_008696497] PREDICTED: protein **FAM181**A isoform X2 [Ursus maritimus].>rs:XP_008696505 [XP_008696505] PREDICTED: protein **FAM181**A isoform X2 [Ursus maritimus].>rs:XP_008696507 [XP_008696507] PREDICTED: protein **FAM181**A isoform X2 [Ursus maritimus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLR
RGADDRPGRLPLESGHDSSPGGGGGCKEKALGNPYREECLSQEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYEGKKRCKGLEPLDTEMAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH

GQPVYAGPPGALPQSSVPGLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:NP_001102620 [NP_001102620] protein **FAM181**B [Rattus norvegicus].>tr:B0BN67_RAT [B0BN67] SubName: Full=Family with sequence similarity 181, member B {ECO:0000313|Ensembl:ENSRNOP00000014284}; SubName: Full=Similar to A830059I20Rik protein {ECO:0000313|EMBL:AAI58704.1}; SubName: Full=Similar to A830059I20Rik protein (Predicted) {ECO:0000313|EMBL:EDM18510.1};>gp:BC158703_1 [BC158703] similar to A830059I20Rik protein [Rattus norvegicus] 218..232
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESAVSAGALLSGSDGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPRPPSPSSTDTSAKRPPGAPGASTVATPAHCK
AAPRREATQAAAAASLQSRSLAALFDSLRHIPGGAETAGGAVAASVPGLGAASSAGDRAGTSASSVAPGTRKVPL
RARNLPPSFFTEPSRVGCCGGGGPSGQGVSLGDLEKGAEAVEFFELLAPDFSTGNDSGVLLAADPLDPFPAGATV
LRGPLELESVPFEQPAMVGNLLYPEPWNTPSCPQSKKPPLPGVRGNMTLNEPVRLLYPTALDSPGGEDAPALASF
TPFFPDCALPPPHQVSYDYSAGYSRAVYPSLWRPDGVWEGASGEEGAHPD PLRARNLPPSFFTEP

rs:XP_009465744 [XP_009465744] PREDICTED: protein **FAM181**A [Nipponia nippon].>tr:A0A091WCS4_NIPNI [A0A091WCS4] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFQ99425.1}; 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGAEDRGRGPQPEAPDPSPHNGAAAEKGLRTAEAEESLSGERVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
QSLLGRAFPALPEGLPAPRDPPPCEGKKRKRSSDAAGPESPPDSAPHPGEKDPAGVLSGRVGAWTCCPFPCPGPG
VYQPPGTLPPSPFPGLGLWRKSAATLPAEVPHFCKEADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_009870156 [XP_009870156] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**A-like [Apaloderma vittatum]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPSECGWR
RGPEDQGRGPQPEAPDPSPHGGATAEKVLLTAEVEESLAGERVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
QSLPARVFPASPEGLPAPRDPPPHEGKKSKRSLDSAGPESPPEPAPHTGEKDPAGVFSGRVGAWTCCPFSCPGPG
VYQPPGALPPSPFPGLGLWRKSGAKLPAEXCRTXXXXXXXYRPVVLKPIPTKPAIPPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_009893824 [XP_009893824] PREDICTED: protein **FAM181**A [Charadrius vociferus]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPGKPPESGWR
RVAEDRGRVPQPELPDPSPHGGAATEKVLRTTEAEESLAGERVLQEQNPEASRPDQVPMRKRQLPASFWEEPRPA
QSLPTRAFPPGLEGLPAPRDPPPYEGKKSKRSSDTTGPESPPDAAPHGREKDPTGVLSGRVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLRLWRKLPMHSVPLSFLQLRYIPVRPVLSSSVTPAQDRWLKATKTWVSQ
PMRKRQLPASFWEEP

rs:XP_006767680 [XP_006767680] PREDICTED: protein **FAM181**A [Myotis davidii]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEAPLR
RGPEDRPGRLPLNPGPDASPSSGGDCKEKALGNPYREECLSREQTLQGQNPGAARPGQVPMRKRQLPASFWEEPR
PTHSYPVALEGVLGPREGPPYECKQHCRGLELFGPDMALIPMSPRALAEKEPPKLPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPQGPVPSLGLWRKSPASPGELAHPAKDVDGPGQKVHRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_010002031 [XP_010002031] PREDICTED: protein **FAM181**A [Chaetura pelagica]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECVWR
RGAEDRGRGPQLEAPDPSPHGGAAAEKVLQTAEAEESLTAEQVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
PSLPARAFPAGPERLSAPRDSPPYEGKKSKRSLDAASPESSPESAPHNGEKDPPGVLSGQVGAWTCCPFPCPGPG
VYQPPGTLPPSPFPGLGLWRKSTAAVLPAEMPPFCKEADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_010143782 [XP_010143782] PREDICTED: protein **FAM181**A [Buceros rhinoceros silvestris]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHSSKPSECGWR
RGXEDRGRGPQPETPDPGPHGGAAAEKVLQTSEVEESLTGERVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPA
QSLPAGAFPTSPEGFPAPRDPPHYEGKKSKRSPGAASPESPPESVPHAREKDPARVLSGRVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLGLWRKSVATLPAEGPRFCKEAEGAGQKLFRPVVLKPIPTNPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_010159774 [XP_010159774] PREDICTED: protein **FAM181**A [Eurypyga helias].>tr:A0A093ILT3_EURHL [A0A093ILT3] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFV99728.1}; 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGAEDRGRGPQPEAPDSSPHGGAATEKVLQTAEAEESLTGEQVLQEQNPEVARPDQVPMRKRQLPASFWEEPRPA
QSLPARAFPAGPEGIPAPRDPPSYEGKKSKRSSDTAGPESPQEPAPHTGEKDPAGVLSGRVGSWTCCPFSCPGPG
VYQPPGTLPPSPFAGLGLWRKTAAALPAEVPHFCKEADSTGQKLYRPVVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_010074409 [XP_010074409] PREDICTED: protein **FAM181**A [Pterocles gutturalis]. 104..118
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGAEDRGHAEAEESLTGERVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPAQSLPARAFPAGPEGLLAPKDPPP
YEGKKSKWSSDTASPESPPESAPHAGEKDPAGGLLGGVGAWTCCPFPCPGPGVYQPPGTLPPSPFPGLGLWRKSA
ATLPAEVPHFCKEADGMGQNLYRPVVLKPIPTKPAVPPPIFNVFSYL PMRKRQLPASFWEEP

rs:XP_010202152 [XP_010202152] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**A-like [Colius striatus]. 124..138
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRXXXXXXXXXXXXPAEGGWRRGA
EERGRGPQPEAPDPGPHGRAAAEKVLQAGEAEETLARERVLQEQNPEASRPDQVPMRKRQLPASFWEEPRPVQSL
PARVFPEGLPSPRDPLLYEGKKSKRSPDIAGPESSPEPSSHAGEKDPAEVLSSRVGSWTCCPFPCPGPGVYQPPG
ALPPAPFPGLGLWTKSAALLPAEVPHFCKEADSVGQKLYRPVVLKPIPTKPTIPSPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_010210734 [XP_010210734] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**A [Tinamus guttatus]. 124..138
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPAECSVK
RGAEERGRXRPGAPHPSHHCRAEKALRAAEAEETFPGEQLLQAQNPEPAKPDQVPMRKRQLPASFWEEPRPAQSL
LARSFPDGLGGLPNSGEPLPYEEKKSRRSPEAAGPESPHEPMLHGGKKESAKAPGPPTAGRVAAWTCCPFQCPGQ
PLYQTPGALPPSPFPGLVLWRKSAALPGEVQHFCKEADSTGQKLYRPVVVKPIPTKPSVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_010295462 [XP_010295462] PREDICTED: protein **FAM181**A [Phaethon lepturus]. 24..38
MASDSEVKTLLNFVNMASRPDQVPMRKRQLPASFWEEPRPAQSLPTRAFPTGPEGLPAPRDPPPYEGKK
SKRSSDTAGPESPPESAPHTGDKDSTGVLSGQVGSWTCCPFPCPGPGVYQPPGALPPSPFPGLGLWRKSTAALPA
EVPHFCKEADSTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_010297499 [XP_010297499] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**A [Balearica regulorum gibbericeps]. 126..140
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPSETGWR
RGVGDRGRGTTPXXXXXXXXXPATEKVLRTAEVEEGLTGELVLQEQNPEAGRPDQVPMRKRQLPASFWEEPRPAP
SLPARAFPTGAEGLPSPRDPPPYEGKKSKRSSDTAGPESPPEPAPHAGEKDPAGVLSGRVGVWTCCPFPCPGPGV
YQPPGTLPPSPFPGLGLWRKSAATLPVEVPHFCKEADGMGQKLYRPVVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_010582179 [XP_010582179] PREDICTED: protein **FAM181**A [Haliaeetus leucocephalus]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECSWR
RGAEDRGRGPQAEAPDPSPHGGAAAEKVLQAAEAEDSLTGERVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
QSLPARAFAAGPEGLPAPRDPPPYEGKKSKRSPDGAGPESPPEPALHAGEKDPAGVLSGRVGAWTCCPFPCPGPG

VYQPPGTLPPSPFPGLGLWRKSAAVLPVEVPHFCKEADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_019940329 [XP_019940329] PREDICTED: protein **FAM181**A [Paralichthys olivaceus].>rs:XP_019940330 [XP_019940330] PREDICTED: protein **FAM181**A [Paralichthys olivaceus]. 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQRYSRVPRCHTHRPAEYAC
GRPAAGSSHQSVKGAEKASSDAQDVENAGSAVQVPMRKRQLPASFWEEPKLSPAKKERSLKRGSAGASEGGDNEK
RKRSCGEDTNKAALPASGRRSSADKEPLKLDLSSHHCVSVCGCCPFQYHGHQVLHSHIVVPHPPLGLWSKAAGTE
TPEHPYGQKLHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_019941647 [XP_019941647] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Paralichthys olivaceus]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATQQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAATQHPIAGTPIHAHSLSNPAPATQAQNINPETGPLPEGWEQAVTADGEVFYIDHINKTTAWVDPR
LAQKMNPGILSLALQQRQEKERLRCKQGLPPQTTPQEAGGRNQMTSGMDHDRNAQTLVPTLDVRIRAPNYEPTLN
GAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGENSSMSLQESMPVLPMSEGEELMPCIPEGLSSDLLMD
METVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_019941648 [XP_019941648] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Paralichthys olivaceus]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATQQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAATQHPIAGTPIHAHSLSNPAPATQAQNINPETAQKMNPGILSLALQQRQEKERLRCKQGLPPQTT
PQEAGGRNQMTSGMDHDRNAQTLVPTLDVRIRAPNYEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDT
GDSGENSSMSLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_019943703 [XP_019943703] PREDICTED: protein **FAM181**B [Paralichthys olivaceus]. 155..169
MAVQTAIMNPQFMNFCFSGSVVEYDVEKSLDGGLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNTAEAPVKRQGSPLAQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDFERGNPEAAEFFELLGPDYSNLVSDQDLYQNMPL
RVQPEMGGLDPATYDSHHLVGGLLYSEPWTSCSGPSKKAGESLRTGPAQPPLYCQSEAATTGPLEDNALCTLAFP
NFFTDCPIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_019943987 [XP_019943987] PREDICTED: transcriptional coactivator YAP1 [Paralichthys olivaceus]. 45..59
MDPSQHNPPAGHQIVHVRGDSQTDLETLFSAVMNPKGTIIPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGVTLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPHGWEMAKTTSGQRYF
LNHIDQSTTWQDPRKALLQMNQAAPANSLPVQQQNLMTPASGSLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DQRYALNQRISQSAPGKAGQLPPSIHSAVMGGNNQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQDG
STNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLPPSMATQ
PSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_010789373 [XP_010789373] PREDICTED: transcriptional coactivator YAP1 [Notothenia coriiceps]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPCVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGVVGGGSMSGMPPPGASPQHLRQSSYEIPDDVPLPPGWEMAKTGSGQRYF
LNHIDQTTTWQDPRKALLQMNQAAPPSSVPVQQQNIMNPASGPLPEAWEQAITSEGEIYYINHKNKSTSWLDPRL
DPRFGLNQQRITQSAPVKQGGPQPPQFMGGNNQMRLQQIEKERMRLKQQELLRQRPQELAIRNQLPTSMDQDGIT
NPVSSPMAQDARIMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLPPSMASQPS
RFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMETVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_010765329 [XP_010765329] PREDICTED: protein **FAM181**A [Notothenia coriiceps]. 104..118

MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEFGC
AKPVGAANQSVKVTEKASLDVQSAEKVRSATEQVPMRKRQLPASFWEEPKLTQTKGDDSHTGLKKNPAGPCAGSE
NENKKRSYDDDAKVTLSASSRRSTADKDTLKMDLSSHHCVSVCGCCPFQYHGHQVLHSHIVVPHPALGLWSKAAE
TERPEHPYGQKLHTHVVIKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_010782332 [XP_010782332] PREDICTED: protein **FAM181**B [Notothenia coriiceps]. 155..169
MAVQTAIMNPQFMSFCFPGSVMEYEVEKGLDGSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVADAAVKRQGSPLAQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSDQDLYQSMPV
RVLPEMGGLDPASYDAHHLVGGLLYSEPWTSCSGPSKKLEESLRTGPAQPPLYCPSETGSIEDNALCTLAFPNFF
TDCSIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_010791807 [XP_010791807] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Notothenia coriiceps]. 46..60
MDAHRGVPAAGQQIVHVRGDSQTELEALFNAVMNPSESVRQPPSLPMRMRKLPDSFFRQPDFRGHSRQA
SSDGGVYGSLTPPKHSRSQSSPASLPLNSLSTQAADVAVAAAAAAAALIPDDMPLPHGWEMAKTPTGQRYFLNHV
DKTTTWHDPRIAQLQSAAAQHPISGTPIHAHSLSNPAPTTLQQNINPETGPLPEGWEKAVTADGEVYYIDHINTT
TAWVDPRLAQKMIPGLHGLALQQRQEKERLRCKQGLPPQHTQEAGEGPDAPGWTMTGTH
PMRMRKLPDSFFRQP

rs:XP_010791808 [XP_010791808] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Notothenia coriiceps]. 46..60
MDAHRGVPAAGQQIVHVRGDSQTELEALFNAVMNPSESVRQPPSLPMRMRKLPDSFFRQPDFRGHSRQA
SSDGGVYGSLTPPKHSRSQSSPASLPLNSLSTQAADVAVAAAAAAAALIPDDMPLPHGWEMAKTPTGQRYFLNHV
DKTTTWHDPRIAQLQSAAAQHPISGTPIHAHSLSNPAPTTLQQNINPETAQKMIPGLHGLALQQRQEKERLRCKQ
GLPPQHTQEAGEGPDAPGWTMTGTH PMRMRKLPDSFFRQP

rs:XP_019363056 [XP_019363056] PREDICTED: uncharacterized protein LOC109290763 [Gavialis gangeticus]. 210..224
MAAGVIRNPAEFRLPTSFQHSFLHPAVHQDRDFQELSEEEEDEEEEEEMEEVELQGNPTAPIPGGERQE
VTATASLHDAEMTLQLLRFSELISSDIQRYFGRKAKEEDPDSCNIYEDCFSPQRSGRELYYADLMHLAQSGELDA
EDSHSAQVPLGQLDQQLWRSICNKDGGQKLGPLAELFEYGLRQYIKQTVSDSRRLRLEKKYAHITPMHRRKLPPS
FWKEPSPGPAGILNTNTPDFSDLLANWTVEPGQELPNASRELASELGRQAMEADQFNVL
PMHRRKLPPSFWKEP

rs:XP_019375546 [XP_019375546] PREDICTED: protein **FAM181**A [Gavialis gangeticus]. 126..140
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRSHPSKSMESNMK
RGVEDRSRSSHPDALDPNPCRAASEKALRGAEVEENLSGEQGLQEQSPESARPDQVPMRKRQLPASFWEEPRPAQ
SLLVGSFPAGLDGLPKSRDLPSYEGKKSKKSPDATGPESPPVPVQPSGEKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTPGALPQSPFPGLGLWRKNTAPQGEIQHFCKEADATGQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_019379708 [XP_019379708] PREDICTED: transcriptional coactivator YAP1 [Gavialis gangeticus]. 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPCTRVYSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGPASSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQPNLMNSASAMNARITQSAPVKQPPSLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKHQELLRQE
LALRSQLPTMEQDSGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010986244 [XP_010986244] PREDICTED: protein **FAM181**A [Camelus dromedarius]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPSRGAEPHLK
RVPEDRPGRLPRDSGHNSSPSGGGGYKEKALGNPYREECLPKEQTLQGQDPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGGLGPREGLPYEGKKHCKGLEPLGPETAPLPTEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYP

GPPGALPQSPVPGLGLWRKSSISPGELVHFCKDVESPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_010988476 [XP_010988476] PREDICTED: protein **FAM181**B, partial
[Camelus dromedarius]. 20..34
GGDAAGPAGGPLVPGARKVPLRARNLPPSFFTEPSRAGGGVCGPSGPGVSLGDLEKGAEAVEFFELLGP
DYGAGTETGVLLAAESLDVFPTGAAALRGPPELEPGLFEPPPAMVGSLLYPEPWSAPGCPPTKKPPLAAPRGGLT
LNEPLRPLYPAAADSPGGEDGPGLLATLAPFFSDCALPPPPLPQQVSYDYSAGYSRTAYSSLWRADGVWEGASGE
EGAHRD PLRARNLPPSFFTEP

rs:XP_010976098 [XP_010976098] PREDICTED: transcriptional coactivator
YAP1 [Camelus dromedarius]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_007094995 [XP_007094995] PREDICTED: protein **FAM181**A [Panthera
tigris altaica].>rs:XP_007094996 [XP_007094996] PREDICTED: protein **FAM181**A
[Panthera tigris altaica]. 129..143
MANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLDSGHDSRPGGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
ATHSYPLGLDGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_015439574 [XP_015439574] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Dufourea novaeangliae]. 46..60
MALNQDVDQLSKSNLVVRMDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAPGAGAGAGGNAPGTGTQGTGPASGQPTSGNTAGSGTNAAGAAAAAVAAAAAAGLTVAHPR
AHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTT
WEDPRKTAAAANVAAVAAAVDNGKTTSAATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAP
TSGAMLPQNWLQQPTGGGIQSNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQSTTDAAMDPFLSGI
NEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSEDF
SSDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_015439575 [XP_015439575] PREDICTED: transcriptional coactivator
yorkie isoform X2 [Dufourea novaeangliae]. 46..60
MALNQDVDQLSKSNLVVRMDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAPGAGAGAGGNAPGTGTQGTGPASGQPTSGNTAGSGTNAAGAAAAAVAAAAAAGLTVAHPR
AHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTT
WEDPRKTAAAANVAAVAAAVDNGKTTSAATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAP
TSGAMLPQNWLQQPTGGGIQSNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQSTTDAAMDPFLSGI
NEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSGEISSQMEAHPWRHQTFLL
PLRMRNLPDSFFNPP

rs:XP_011184542 [XP_011184542] PREDICTED: transcriptional coactivator
yorkie [Zeugodacus cucurbitae].>tr:A0A0A1WE41_ZEUCU [A0A0A1WE41] SubName:
Full=Protein yorkie {ECO:0000313|EMBL:JAC97171.1}; 61..75
MSLSKTVVSLNKGNAKEKERSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPE
SFFKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSIAAVPATITQPQVTANRLSISHSRAHSSPAS
LQQTYNIIGNVMETGACIQDGIGPVFTAGAVSFPPGVNAGSGVRMEQVDQSVTKDAPNTIQTFHMKQRSYDVVST
IQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKSKESVNLADNLGPLPE
GWEQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSL
QMDPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISESGSLNALSGIDCPDNLVSSLQLEDNICN
EMFSDVHSMLNATATKPDTLDWYKIN PFRMRQLPESFFKPP

rs:XP_015806780 [XP_015806780] PREDICTED: transcriptional coactivator
YAP1 [Nothobranchius furzeri].>tr:A0A1A7Z8P0_NOTFU [A0A1A7Z8P0] SubName:
Full=Yes-associated protein 1
{ECO:0000313|EMBL:SBP38863.1};>tr:A0A1A8D695_9TELE [A0A1A8D695] SubName:
Full=Yes-associated protein 1 {ECO:0000313|EMBL:SBQ28853.1}; 45..59
MDPSQHNPPAGHQIVHVRGDSETDLETLFNIVMNPSSANIPHSVPMRQRKLPDSFFNPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSAGSLSGLAPAGASPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQTSPPSSVPVPQQTLMNPTSGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
EPRYGLNQQRNTQSAPGKQGGPLPTNSHGGVNQMRLQQIEKERLRLKQHEVLRQRPQELALRNQLPTSMEQDGPT
NPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDQLPPSMATQPN
RFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEPLSSDILSDMESVLAATKIDKESFLTWL
PMRQRKLPDSFFNPP

rs:XP_015806792 [XP_015806792] PREDICTED: protein **FAM181**B [Nothobranchius
furzeri]. 155..169
MAVQTAIMNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGHVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAK
EVRGEKAKKPPLRHRNLPPSFFTEPANCSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPL
RAQPDLGGLDPVSYDAHHLVGGLLYSEPWTSCSGPPKKLGESLRTGLAQPPIYSQSEEASGSIDDSGLSSLAFSN
FFTDCSIPQVTYDLNCGYSKANYSSP PLRHRNLPPSFFTEP

rs:XP_015816184 [XP_015816184] PREDICTED: transcriptional coactivator
YAP1-like isoform X1 [Nothobranchius furzeri]. 47..61
MDAHRGGAPPAGQQVVHVRGDSKTELEALFSAVMDPGKASRQPQSLPMRMRKLPDSFFKPPEPRGHSRQ
ASSDGGVCGSLAPHHVRAHSSPASLPVNSLTAQADADVAATPIIPDDVPLPDGWELAKTLTGQRYFINHLEKTTT
WLDPRLSQLQSTAAQHPISCAPIHTHSFSNPAPTTQAQHIHPETGPLPEGWEQAVTADGEVYYIDHINKNTTWVD
PRLAQKMNPAILGLAMQQRQEKERLRCKQGLPPQITPQDAAGRNQIPRGMDHDRSAQMLVPSVDARIRALNQEPT
LNGAHSRNESTDSGLSVSSLPRTSDHLLSSVDHMDTGDSSEPSSVTMQETMPVLPITEGEELMPCIPDGLNSDLL
MDMETVLSGPHMDRDSLLTWL PMRMRKLPDSFFKPP

rs:XP_015816186 [XP_015816186] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Nothobranchius furzeri]. 47..61
MDAHRGGAPPAGQQVVHVRGDSKTELEALFSAVMDPGKASRQPQSLPMRMRKLPDSFFKPPEPRGHSRQ
ASSDGGVCGSLAPHHVRAHSSPASLPVNSLTAQADADVAATPIIPDDVPLPDGWELAKTLTGQRYFINHLEKTTT
WLDPRLSQLQSTAAQHPISCAPIHTHSFSNPAPTTQAQHIHPETAQKMNPAILGLAMQQRQEKERLRCKQGLPPQ
ITPQDAAGRNQIPRGMDHDRSAQMLVPSVDARIRALNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHLLSSVDHM
DTGDSSEPSSVTMQETMPVLPITEGEELMPCIPDGLNSDLLMDMETVLSGPHMDRDSLLTWL
PMRMRKLPDSFFKPP

rs:XP_015825575 [XP_015825575] PREDICTED: protein **FAM181**A [Nothobranchius
furzeri].>tr:A0A1A8A856_NOTFU [A0A1A8A856] SubName: Full=Family with
sequence similarity 181, member A
{ECO:0000313|EMBL:SBP51307.1};>tr:A0A1A8EA08_9TELE [A0A1A8EA08] SubName:
Full=Family with sequence similarity 181, member A
{ECO:0000313|EMBL:SBQ42396.1}; 98..112
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHAHKSADHRC
LKPPGTAAQETASHAQDVENVGIEVEQVPMRERQLPASFWEEPRQTKAKRDKTGLGLKKSAIGSSDGSKNEMRKA
ALDDGANASSSRRNSADKEVLKLDVTSHHFVSVCGCCPLQYHGHHVLHSHIVVPHPPLWSKAAAGTESEHPFGPR
IHTHVVVKPIPTKPTPQSPIFSVFGFI PMRERQLPASFWEEP

rs:XP_011558709 [XP_011558709] PREDICTED: LOW QUALITY PROTEIN:
transcriptional coactivator YAP1 [Plutella xylostella]. 44..58
MALNSDAEQKSTPFVRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSTSAGGTVPVSHSRAHSXQVSPSRAPSSPASLQQTYAAAGQQNQQPPLHHQHAKQRSYDVGPHL
QDDLGPLPPGWEQARTPEGQIYYLNHITKTTTWEDPRKSLAAAQVGAVQHQSAEPLGPLPDGWEQAATPEGEVYF
INHAARTTSWFDPRIPQHLQRTPSAGRERLKQRQQEIRLQQELMARQASSIVSSLATSAGAAADLPIDPFLSGLT
DHQRQESADSGLGMAVTQSYSMPHTPEDFLSSMDDRMDCTSESGANLDTNDISLADNDLLGEFTNDILLDDVQSL
INSTPSKPDNVLTWL PLRMRQLPKSFFNPP

rs:XP_003962706 [XP_003962706] PREDICTED: protein **FAM181**A [Takifugu rubripes]. 102..116
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHMHRSTDHGC
AKPAGAVYQKLAMKTDFDVPVAEKTTGASEQVPMRKRQLPASFWEEPKLTQTRRELLGLREDAGGDPEVSERETR
KRSRDADALASLSASGRRGSADKSSLKLDLTSGHCVSVCGCCPFQYHGHHILHGHIVFPHSPPWSKAAVTNAGRP
EHPYGPQIHTHVVVKPIPTKPAVQSSIFSVFGFI PMRKRQLPASFWEEP

rs:XP_003968635 [XP_003968635] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Takifugu rubripes].>tr:A0A3B5KIA1_TAKRU [A0A3B5KIA1] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSTRUP00000053107};44..58
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKSSVPPSVPMRMRKLPDSFFKPPEPKSHSRQAST
DAGSGGTLTPHHVRAHSSPASLQLGAVSGGSLPGLPPTSPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYFLNH
IEQTTTWQDPRKALLQMNQAAPANSVPVQQQNLMNPASGPLPDGWEQAFTSEGEIYYINHKNKTTSWLDPRLDAR
FAMNQQRITQSAPVKQGGPLPPNTHSQMRLQQMEKERLRLKQQELLRQRPQELALRNQLPTSMEQDGSTNPVSSP
MAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPTSMATQPSRFPDYL
DAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMESMLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_011606936 [XP_011606936] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Takifugu rubripes]. 44..58
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKSSVPPSVPMRMRKLPDSFFKPPEPKSHSRQAST
DAGSGGTLTPHHVRAHSSPASLQLGAVSGGSLPGLPPTSPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYFLNH
IEQTTTWQDPRKALLQMNQAAPANSVPVQQQNLMNPASAMNQQRITQSAPVKQGGPLPPNTHSQMRLQQMEKERL
RLKQQELLRQRPQELALRNQLPTSMEQDGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDPLPTSMATQPSRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDIL
NDMESMLAATKIDKESFLTWL PMRMRKLPDSFFKPP

rs:XP_003968705 [XP_003968705] PREDICTED: protein **FAM181**B [Takifugu rubripes]. 155..169
MAVQTAIMNPQFMNFAFPGSVMGYDMEKGLDEGLLCEADNEEDYRETTRDLLSFMDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQVSPLTQSSPLQSKTPPKREGIQASLQSKSLAALFSPVK
DVRGEKTKKPPLRHRNLPPSFFTEPVSCSKVSSTSGMTLRDLERANPETADFFDLLGPDYSSMVSEQDLYQGIPL
RVQPDLGGLDPACYDTHHLVGGLLYPEPWTSCSDTSKKAGSGPRSGPHQLPAYCPSDPCGPMEDHSLCTLAFPNL
FTDCSTPQVTYDLNGACNRPQYSSL PLRHRNLPPSFFTEP

rs:XP_011609930 [XP_011609930] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Takifugu rubripes].>tr:A0A3B5K7C1_TAKRU [A0A3B5K7C1] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSTRUP00000049270};46..60
MDAHHGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKASRQPPSLPMRMRKLPDSFFRQPDSRGHSRQA
SSDGGVCSSLTPHHIRAHSSPASLPVNSLSAQAPDVAAAPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRIAQLQSAAAQRPIAGTPVHTHSLSNPAQPATQPQNNMSPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVD
PRLAQKMNPNILGLSLQQRQEKERMRQQQGLPPQLPPQEAAGRNQVSGGLDHDRNTQMLVPPLDVRIRAPNHEPT
LNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGDASSMTLQESMPVLPMSEGEELIPCIPEGLGSDLL
MDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_011609931 [XP_011609931] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Takifugu rubripes].46..60
MDAHHGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKASRQPPSLPMRMRKLPDSFFRQPDSRGHSRQA
SSDGGVCSSLTPHHIRAHSSPASLPVNSLSAQAPDVAAAPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRIAQLQSAAAQRPIAGTPVHTHSLSNPAQPATQPQNNMSPETAQKMNPNILGLSLQQRQEKERMRQQQGLPPQ
LPPQEAAGRNQVSGGLDHDRNTQMLVPPLDVRIRAPNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHM
DTGDSGDASSMTLQESMPVLPMSEGEELIPCIPEGLGSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_016386960 [XP_016386960] PREDICTED: uncharacterized protein LOC107722971 [Sinocyclocheilus rhinocerous]. 154..168
MAASVIRTLSNLGLAKPFPPCFFPAEDEEETEEEYEEELREDSLEEEEDALASESQEEEPWSFDSYPNN

AEMTNQLLRFAELISSDVQRYFGRSQDPDACDIYAEKPCPKVGGRQRYYADFIKVASSGQGEEPESLGPLAELFQ
DAQRKGRGLPMSQRRLPVSFWTEPFAQQLDMLGDTSMQDNSRSMINTSESSININTSLSMFSNSSVCTMTSSSIS
GTLSSSSTPDFSDLLAHWAMDRENPNEFNCDYPLS PMSQRRLPVSFWTEP

rs:XP_016391649 [XP_016391649] PREDICTED: protein **FAM181**B-like
[Sinocyclocheilus rhinocerous]. 156..170
MAVQAAIMNSQFLNFCFPGSVMDYEVERGLEGGLLGEVDCEGDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISPGTTPVQEPCKRQGSPHNPTSNLSSKTPPKKDGIQANLQSKSLAALFNSA
KDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPDAAEFLELLGPDYSNMVSEQDLFHTAP
IRIQQEVTVGPEPYDSHHFVSGGFLYTEPWGTCSSTPKKSGDMRTVPVQPNLYTHTDLSGSVPVEQSSPCALTFS
NFFTDCSTPSVSYDLVNGYNRGSFSSL PLRHRNLPPSFFTEP

rs:XP_016391824 [XP_016391824] PREDICTED: protein **FAM181**B-like, partial
[Sinocyclocheilus rhinocerous]. 4..18
YATPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPDAAEFLELLGPDYSNMVSEQDLFHTAPIR
IQQEVTVGPEPYDSHHFVSGGFLYTEPWGTCSSTPKKSGDMRTVPVQPNLYTHTDLSGSVPVEQSSPCALTFSNF
FTDCSTPSVSYDLVNGYNRGSFSSL PLRHRNLPPSFFTEP

rs:XP_016408307 [XP_016408307] PREDICTED: protein **FAM181**B-like
[Sinocyclocheilus rhinocerous]. 157..171
MAVQAAIMNSQFLNFCFPGSVMDYEVEKGLEGGLLGEEVDCGGDFKETTRDLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGIISPGTTPVQEPCKRQGSPQTPTSNLSGKTPPKKDGMQASLQSKSLAALFNS
AKDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAAEFFELLGPDYSNMFSEQDLFHTA
PIRIQQEVTVGPEPYDSHHFVSGGFLYTEPWGTCSGTSKKSGDMRTVPVQPNLYTHTDLSGSVPVEQSSPCALTF
SNFFTDCSAPPVSYDLVNGYNRGSFSSL PLRHRNLPPSFFTEP

rs:XP_003725473 [XP_003725473] PREDICTED: uncharacterized protein
LOC100891483 [Strongylocentrotus purpuratus]. 243..257
MAMMNYQVPPSYPHSMQNYMDYSMHNPHIHNPLMHPVQNHHIHNPQIQNLPNIHFIQDEYYVDDSDDES
NFTSEDYEDDRMSDELFEREPNAVNQLLDFAETASMDIQKFFGKKRVLDEPELIADCNKKVRLSGRELYYADLLR
VAQHGDSADPCKEASEPNRIIRYGDDENSPDLTSNLSPKSMDSNGLGPLEELFNYAERSVCYNGHMLPMYGYSYQ
SGAWMPPTDNVNDTSLSGKPPVTPWSKRAMPKSFFTEPVSSSVPRIEVDQRFVALSLPLDTPCVGSVATSNQHEA
PDFSDLIATMESDEDHGLPRVTPVHG PWSKRAMPKSFFTEP

rs:XP_800421 [XP_800421] PREDICTED: uncharacterized protein LOC586927
[Strongylocentrotus purpuratus]. 139..153
MDKLVKPSASTSPPTANNGKRGPTCSLSGSSSSEGEGSDHEEIPPSPCSSTSSGPTYVRPPGFKHHGQE
IKVQEQRPKVNTSVRIKRKIKRQSMMKDVLPLSHVTSHPVTKVTMEEKTTGVQVLPPSGMKTKVRKEPIPMRLRA
LPQSFWQQPNTVNSASPGSMYSVLPPLCKMEQSNSDLADIRPVTPPSDGENVESREGDQPDVRLKERKDTLVDRD
SLVIKLEKDKERDLSREREVSPRDRDYSPREKDLSPRDRDTGREKESPRDKEKVRDGLKEGAGLESSKQLPPEAK
KKQPRPPPRIVRVSPANSELLAKLFEGFDGDGKKKIVRRGRPKREYNPQAAVLAVAAAQTAANTSNNNNTTTPTS
GNNASNPVTTLHHPYLTGDDPYMIDSVAEGLLPMLSLESSRQSSGPSSQLAIVTIRGDNNRMLSLPSLSVEQNHS
AILSELVKAL PMRLRALPQSFWQQP

rs:XP_011678315 [XP_011678315] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Strongylocentrotus purpuratus]. 45..59
MEPAGGRKQNAVVHVRGDSGAELDDLFRNVLNTPEAADKVPSQVPWRKRNMPASFFQEPRISHSRESSA
DSTNYSGNMSNASHEIASRSLGPQGMTIAHSRAHSSPASLQEMRNINPQDVIRNQHLRQQSYDISDTDNPNLPSG
WEMAVTPTGQKYFLDTPNSHSNQQTTWEDPRKPQPPSVPNQLSKPNTNTNNNQVQQIIMQGNGQPLPSMHDLGPL
PINWEQAVTPEGEVYFINHVERTTTWLDPRIAMRAPGTVQAAAAALQQSQNNSNPPPSHSVATASSTTSLSQQTP
QLPPPPPPPPISPPQPPSQQGGPMTQQQQLQQKLRLQRVLMERDCLQRQHMRILQQAQQNPKSLSSCPNLFPRSD
RFQNELALRRELRDSLPNNNNNDSITGGTDPFLSSSNTTNFHRREESGDSGCGLSNVSHPRTPEDLLNTLEDMDS
SEAPPTDRKPLDKQAPRPLPPLASMGDFLETLPSTNVDMASMDTMDPSDSGTAVTSMDSDDLVPSLPEALDSDIL
SDVGDVGDVNNFLTWL PWRKRNMPASFFQEP

rs:XP_789542 [XP_789542] PREDICTED: transcriptional coactivator YAP1
isoform X2 [Strongylocentrotus purpuratus]. 45..59
MEPAGGRKQNAVVHVRGDSGAELDDLFRNVLNTPEAADKVPSQVPWRKRNMPASFFQEPRISHSRESSA
DSTNYSGNMSNASHEIASRSLGPQGMTIAHSRAHSSPASLQEMRNINPQDVIRNQHLRQQSYDISDTDNPNLPSG

WEMAVTPTGQKYFLDHSNQQTTWEDPRKPQPPSVPNQLSKPNTNTNNNQVQQIIMQGNGQPLPSMHDLGPLPINW
EQAVTPEGEVYFINHVERTTTWLDPRIAMRAPGTVQAAAAALQQSQNNSNPPPSHSVATASSTTSLSQQTPQLPP
PPPPPPISPPQPPSQQGGPMTQQQQLQQKLRLQRVLMERDCLQRQHMRILQQAQQNPKSLSSCPNLFPRSDRFQN
ELALRRELRDSLPNNNNNDSITGGTDPFLSSSNTTNFHRREESGDSGCGLSNVSHPRTPEDLLNTLEDMDSSEAP
PTDRKPLDKQAPRPLPPLASMGDFLETLPSTNVDMASMDTMDPSDSGTAVTSMDSDDLVPSLPEALDSDILSDVG
DVGDVNNFLTWL PWRKRNMPASFFQEP

rs:XP_011939172 [XP_011939172] PREDICTED: protein **FAM181**A isoform X1
[Cercocebus atys]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAAPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_011939173 [XP_011939173] PREDICTED: protein **FAM181**A isoform X2
[Cercocebus atys]. 194..208
MPLEEKRSSGERNDAAYRKHRRPGEKKTPMACFVPQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASD
SDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRL
LLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLE
GGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLG
ALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAAPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_011887662 [XP_011887662] PREDICTED: protein **FAM181**A-like, partial
[Cercocebus atys]. 51..65
RVLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTH
SYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQP
IYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAAPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_011900067 [XP_011900067] PREDICTED: protein **FAM181**B [Cercocebus
atys].>tr:A0A2K5KKB9_CERAT [A0A2K5KKB9] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSCATP00000001130};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGVAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPVAGLGGAGTGGAGGDAAGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPHQVSYDYSAGYSRNAYSSLWRPDAVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_012136501 [XP_012136501] PREDICTED: transcriptional coactivator
YAP1 [Megachile rotundata]. 46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAVAAVGGGGAPGGNATGATPATGAXAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPH
ARHHHHPKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAANVAAVAAAVDNGKST
SAATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPQNWLQQQPAGGGIQSNQTL
QACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQSTTDAAMDPFLSGINEQHVRQESADSGLGLGSAYSLPHT
PEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSEDFSSDILDDVQSLINPNTTKPENVLTW
L PLRMRNLPDSFFNPP

rs:XP_018792030 [XP_018792030] PREDICTED: transcriptional coactivator
yorkie isoform X1 [Bactrocera latifrons].>tr:A0A0K8V6G4_BACLA [A0A0K8V6G4]
SubName: Full=Protein yorkie {ECO:0000313|EMBL:JAI34461.1}; 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACLQDGIGPVFTTGAVPFPPSVNAGAAVRMEQGEQPVPKDAPNIQTFHMKQRSYDVVSTIQ
LQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKGKESVNLADNLGPLPEGW

EQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQM
DPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISGNYSESGSLNALSGIDCPDNLVSSLQLEDNI
CNEMFSDVHSMLNASATKPDTLDWYKIN PFRMRQLPESFFKPP

rs:XP_018792031 [XP_018792031] PREDICTED: transcriptional coactivator yorkie isoform X2 [Bactrocera latifrons].>tr:A0A0K8WMQ1_BACLA [A0A0K8WMQ1] SubName: Full=Protein yorkie {ECO:0000313|EMBL:JAI52280.1}; 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACLQDGIGPVFTTGAVPFPPSVNAGAAVRMEQGEQPVPKDAPNIQTFHMKQRSYDVVSTIQ
LQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKGKESVNLADNLGPLPEGW
EQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQM
DPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISESGSLNALSGIDCPDNLVSSLQLEDNICNEM
FSDVHSMLNASATKPDTLDWYKIN PFRMRQLPESFFKPP

rs:XP_019497991 [XP_019497991] PREDICTED: protein **FAM181**A [Hipposideros armiger].>rs:XP_019497992 [XP_019497992] PREDICTED: protein **FAM181**A [Hipposideros armiger].>rs:XP_019497993 [XP_019497993] PREDICTED: protein **FAM181**A [Hipposideros armiger]. 128..142
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLR
RGPEDQSGRLSLDSGDSSPGGMGSCKEKALGNPYREECLSKEQTLQGQHPEAARPGQVPMRKRQLPASFWEEPRP
PHSYPVGLEGGLGPREGPPYEGKKHCKGVEPLGPEMAPVPMSPRAPVEKEPLKMPGISLVGRVNAWSCCPFQYHG
QPIYPGALPPSPVPSLALWRKSPVSSGELAHFCKDVDSLGQKVYRPVVLKPIPTKPTMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004262408 [XP_004262408] PREDICTED: protein **FAM181**A isoform X1 [Orcinus orca]. 180..194
MKLLQMLLRGSPCCPQPEISPPGQLRALPWSRQPPAEPPSSWKAPCSGPLVMASDSDVKMLLNFVNLAS
SDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGSEDRPGRLPLDSGHSSSPGGGG
CCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTQSYPVGLEGGLGPREGPPYEGK
KHCKGLEPRGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGALPQSPLPSLGLWR
KSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_004262409 [XP_004262409] PREDICTED: protein **FAM181**A isoform X2 [Orcinus orca]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGSEDRPGRLPLDSGHSSSPGGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTQSYPVGLEGGLGPREGPPYEGKKHCKGLEPRGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPQSPLPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004271880 [XP_004271880] PREDICTED: protein **FAM181**B [Orcinus orca].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGSAFGALDKGCCFEDEETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAASAQTVPVQAHGK
AAPRREASQAAAAASLQSQSLAALFDSLSHVPGAADPAGVAEAAPAAGLVGAGAGGVGGDAAGPAGGPAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAAEFFEMLGPDYGAGTEAGVLLAAEPLDVLLTGA
AVLRGPPELEPGLFEPPPAMGGSLLYPEPWSAPGGPTTKKSPLAAPRGGLTLNEPLRPLYPAAADSPGGDDGPGL
LASFTPFFSDCALPPPPPPPQVSYDYSAGYSRTAYASLWRPDGIWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_008270121 [XP_008270121] PREDICTED: protein **FAM181**A [Oryctolagus cuniculus]. 125..139
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPSRAAEPHLK
RGLEDRPGRLLLDSCPDSSPSCKEKALGSALPEECLSHEQALQGQDPEAARPGQVPMRKRQLPASFWEEPRPTHS
YPLGLEGGLGPREGAPYEGKKHCKGLEPLGPETASVPLSPRALADKELLKMPGIPLVGRVNAWSCCPFQYHGQPI
YPGPPGALPPSPVPGLGLWQKSPSRPGELSHFCKDVDGLGQKVCRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004394556 [XP_004394556] PREDICTED: protein **FAM181**A isoform X1 [Odobenus rosmarus divergens].>tr:A0A2U3VI75_ODORO [A0A2U3VI75] SubName: Full=protein **FAM181**A isoform X1 {ECO:0000313|RefSeq:XP_004394556.1};
180..194
MKLLQMLLRGRPAARGLRSARQVSSVPFPGAASHQQSPRSSWKAPGSGPLVMASDSDVKMLLNFVNLAS
SDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGKGAEPHLKRGPEDRPGRLPLDSGQDSSPSGGG
CYKEKALGNPYREECLSREQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGK
KHCKGLEPLDPETAPVPASPRALAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPIYAGHPGVLPQSPVPSLGLWR
KSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_012415778 [XP_012415778] PREDICTED: protein **FAM181**A isoform X2 [Odobenus rosmarus divergens].>tr:A0A2U3Z9Y3_ODORO [A0A2U3Z9Y3] SubName: Full=protein **FAM181**A isoform X2 {ECO:0000313|RefSeq:XP_012415778.1};
173..187
MTHLLEPNFLPRCGKVSSVPFPGAASHQQSPRSSWKAPGSGPLVMASDSDVKMLLNFVNLASSDIKAAL
DKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGKGAEPHLKRGPEDRPGRLPLDSGQDSSPSGGGCYKEKAL
GNPYREECLSREQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHCKGLE
PLDPETAPVPASPRALAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPIYAGHPGVLPQSPVPSLGLWRKSPASPG
ELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_004408705 [XP_004408705] PREDICTED: protein **FAM181**B [Odobenus rosmarus divergens].>tr:A0A2U3WIS2_ODORO [A0A2U3WIS2] SubName: Full=protein **FAM181**B {ECO:0000313|RefSeq:XP_004408705.1}; 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAPDAPAKRPLAAPGAQTVAVPLHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGDERAGGSVAAPVAGLGGAGAGGSGGDAAGPAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEQPPAMVGSLLYSESWSAPGCPPTKKPPLAGPRGGLTLNEPLRPLYPSAADSPGGEDAPGL
LASFAPFFSDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_012423426 [XP_012423426] PREDICTED: transcriptional coactivator YAP1 [Odobenus rosmarus divergens].>tr:A0A2U3ZXS7_ODORO [A0A2U3ZXS7] SubName: Full=transcriptional coactivator YAP1 {ECO:0000313|RefSeq:XP_012423426.1}; 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGS
LTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPT
SPPVQQSLMTSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRVSQSAPVKQPPPLAPQSPP
GGVLGSGGSSQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_002198083 [XP_002198083] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Taeniopygia guttata].>rs:XP_005516267 [XP_005516267] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Pseudopodoces humilis].>rs:XP_017671538 [XP_017671538] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Lepidothrix coronata]. 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTS
PSVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012425184 [XP_012425184] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Taeniopygia guttata].>rs:XP_014106279 [XP_014106279] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Pseudopodoces humilis].>rs:XP_017671540 [XP_017671540] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Lepidothrix coronata]. 13..27

MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTS
PSVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_002200202 [XP_002200202] PREDICTED: protein **FAM181**A [Taeniopygia guttata].>tr:H0ZQV8_TAEGU [H0ZQV8] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSTGUP00000012999};
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKAPECGWR
RGAEDRARGPQPEAPEPSPHGGAAADKVMQTAEAEESLTGERVLQEQKPEAARPDQVPMRKRQLPASFWEEPRPA
QSLTARAFAASPEGLQTPRDPPPYEGKKSKRSPDAAGPESPPDTAPHAGEKDPAGPLSGRVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLGLWRKSAAALPAEVPHFCKEADGQGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004754834 [XP_004754834] PREDICTED: protein **FAM181**A isoform X1 [Mustela putorius furo]. 162..176
MHGTVSSVPVPGAAGHQQSPRSSWTAPCRGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVD
HRKYLQKQLKRFSQKYSRLPRGLPGRGTEPHLKRGPEDRPGRLLLDPGHGSSPGVVGGCKEKALGNPYREECLSK
EQSLQRQNPEAARPGQVPMRKRQLPASFWEEPRPAHSYSLGLEGELGPREGSPYEGKKHCKGLEPWDPEMAPVPA
SPRAPAGKEPLKMSGVSLVGRVNAWGYCPFQYHGQPIYAGPPGALPQNPVPNLGLWRKSPASPGELAHFCKDVDG
PGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_012912896 [XP_012912896] PREDICTED: protein **FAM181**A isoform X2 [Mustela putorius furo].>rs:XP_004754836 [XP_004754836] PREDICTED: protein **FAM181**A isoform X2 [Mustela putorius furo].>rs:XP_004754838 [XP_004754838] PREDICTED: protein **FAM181**A isoform X2 [Mustela putorius furo]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGTEPHLK
RGPEDRPGRLLLDPGHGSSPGVVGGCKEKALGNPYREECLSKEQSLQRQNPEAARPGQVPMRKRQLPASFWEEPR
PAHSYSLGLEGELGPREGSPYEGKKHCKGLEPWDPEMAPVPASPRAPAGKEPLKMSGVSLVGRVNAWGYCPFQYH
GQPIYAGPPGALPQNPVPNLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004763556 [XP_004763556] PREDICTED: protein **FAM181**B, partial [Mustela putorius furo]. 217..231
AALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSFIDSA
SSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAVPGPPSPGAADTPAKRPLAAPGAQTVAVPPHGKAAPR
REASQAAAAASLQSRSLAALFDSLRHVPGGDERAGGSVAARVAGLGGAGAGGSGGDAAGSAGGTAVPGARKVPLR
ARNLPPSFFTEPSRAGGSGCGPSGPGVSLGDLEKGAGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGAAV
LRGPPELEPGLFEPPPAMVGSLLYSESWSAPGCPPTKKPPLAAPRGGLTLNEPLRPLYPTAADSPGGEDAPGLLA
SFAPFFSDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_004681652 [XP_004681652] PREDICTED: protein **FAM181**A [Condylura cristata]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDQPGRLPLHSGPDASPGGGGGFQEKALGNPYGEECLAKEQALQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGALGPREGPPCEGKRRCQRVEPAGPETAPVPLKMPGVSLAGRVNAWSCCPFQYHGQPVYPGPPGA
LPQSPVPSLGLWRKSPASPAELAPFCKDVDGLVQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004683765 [XP_004683765] PREDICTED: protein **FAM181**B [Condylura cristata]. 221..235
MAVQAALLSTHPFVPFGFGGSSDGLGGAFGALDKGCCFEDEETGTPASALLAGTEGGDVREATRDLLSF
MDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADAPAKRPLAAPGAQTVAVPAHGK
VAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPVGGTLAAPPAGLGAAGSGGGGGDAIGPLGGTAVPGARK
VPLRARNLPPSFFTEPSRAGSGACVPSGPGVSLGDLEKGAEAVEFFELLGPDYGATTEAGVLVAAEPLDVFPTGA

AVLRGSLELEPSLFEPPPAMVGSLLYPEPWSVPACPTTKKPPVAAPRGGLTLNEPLRPQYPAPADSPGGEDGPGL
LASFAPFFSDCALPPPLPPHQVSYDYSASYSRPAYSGLWRPDGVWEGAPGEEGAHPD   PLRARNLPPSFFTEP

rs:XP_012585407   [XP_012585407] PREDICTED: transcriptional coactivator
YAP1 [Condylura cristata].   13..27
MNPKTANVPQTLPMRLRNLPDSFFKPPEPKSHSRQASTDTGTAGALTPQHTRAHSSPASLTQGSVSPGT
LTPTGVVSGPAAAPTAQHLRQPSFEIPDEVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMFSQMNVTAPT
SPPVQQNMMNSPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGIMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGG
TQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLP
SQQNRFPDYLEALPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRNLPDSFFKPP

rs:XP_012674938   [XP_012674938] PREDICTED: protein **FAM181**A [Clupea
harengus]. 118..132
MANADSEVRTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSKRYSRLPRCRSYRTTELGM
KNISEDNPVVYSLEGIHQLNLRGKKESVASDLHQNSSNLHKNGDQNQVPMRKRQLPASFWKEPTSSQQSLTASLV
TVTKETDVPRGTIPLVPDGENIYRFNDNNINSLHTFSDSVESTPLKMDLTCRNVDLCGCYSLQYHGQILQRHLIA
PRSAFFSVGAPAAMAVDADRHNSPNRLEYHATHVVVKPIPTKPALSSSMFSMFGFI   PMRKRQLPASFWKEP

rs:XP_019660308   [XP_019660308] PREDICTED: protein **FAM181**A isoform X1
[Ailuropoda melanoleuca].   173..187
MAHLLELSSPPRCGKVSSVPFPGAASHPQSPRSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAAL
DKSAPCRRSVDHRKYLQKQLKRFSQKYPRLPRGLPGRGAETHLRRGADHRPGRLPLEAGHDSSPSGGGGCKEKAL
GNPYREECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHWKGLE
PLDPEMAPVPASPRALAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYAGPPGALPQSSVPGLGLWRKSPAPPG
ELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL   PMRKRQLPASFWEEP

rs:XP_019660309   [XP_019660309] PREDICTED: protein **FAM181**A isoform X2
[Ailuropoda melanoleuca].   129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYPRLPRGLPGRGAETHLR
RGADHRPGRLPLEAGHDSSPSGGGGCKEKALGNPYREECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYEGKKHWKGLEPLDPEMAPVPASPRALAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYAGPPGALPQSSVPGLGLWRKSPAPPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_019661666   [XP_019661666] PREDICTED: protein **FAM181**B [Ailuropoda
melanoleuca].   68..82
MQGGDVREATRDLLSFIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGVPL
RARNLPPSFFTEPSRAGGGGXGAAGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGAAVL
RGPPELEPGLFEPPPAMVGSLLYSESWSAPGXPSAKKPPLAAPRGGLTLNEPLRPLYPSAADSPGGEDGPGLLAS
FAPFFSDCALPPPPPPHQVSYEYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD   PLRARNLPPSFFTEP

rs:XP_012686357   [XP_012686357] PREDICTED: protein **FAM181**B [Clupea
harengus]. 160..174
MAVQAAIMNSQFLNFCFPGSVMEFGMEKDLEGGLLCDTDRDEGDFREATRDLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGIIAPSSPPQQSPSQATPQQQQQQQPGTFQGKMPPKRDGVQANLQSKSLAALF
NSAAKDNRGERAKKPPLRHRNLPPSFFTEPVNFPRVTSTSGMTLKDLERGNPEASEFFELLGPDYSNMLLEQDLF
QNGPGCLARVQQDVSAAGLEPVSYDSPHYVTGGFVYAEPWTTCVGPPKKVGEGMRTGPEGQASVYSPSDPSAPVA
LEDSSSCTLAFPPFFTDCSSSQVPYDGSLTGGYARGSFSSL PLRHRNLPPSFFTEP

rs:XP_012686408   [XP_012686408] PREDICTED: transcriptional coactivator
YAP1 [Clupea harengus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTILPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGTVSPGGLSGMAPAGTPPQHLRQSSYEFPDDMPLPPGWEMAKTASGQRYF
LNHLDQTTTWQDPRKTLLQMNPAPPSPLPVQQQQQQQQQQVMAPATGPLPEGWEQAITPEGEIYYINHKNKTTSW
LDPRLDARYAMNPQRLSQGTPVKQGGPLPTSPQGGTLGGNSQMRLQQLQMEKERLRLKHQELLRQRPQELALRNQ
LPVSMEQDGPGTQNPISSPGMAQDARTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEME

TNDSLGPASMVTQPNRFPDYLDAMPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKES
FLTWL PMRMRKLPDSFFKPP

rs:XP_004610324 [XP_004610324] PREDICTED: protein **FAM181**A [Sorex
araneus]. 113..127
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCSRLPRGLPGRGAEPPPR
RGPDDRPGKPPPEGSPGGGAEGGGGSGEETPGRDPDAAQPGQVPMRKRQLPASFWEEPRPTHGYPGGPAGPPYEG
KKPRQALEPLGPAAPRLQAHKELLRMPGVALAGRAGAWTCCPFQHHGQPIYPGPPGALPASPLPSLGLWRKSPPP
PGELAHFRKDVDGPGPKVHRPVVLKPIPTKPAVAPPLFNVFGYL PMRKRQLPASFWEEP

rs:XP_004584374 [XP_004584374] PREDICTED: protein **FAM181**A [Ochotona
princeps]. 130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAAEPHL
RRGSEDRPGRLLLDSCPDSSPSGGGSCKEKGLGNAVPRECLSQEQTLQGQDPEAARPGQVPMRKRQLPASFWEEP
RPTHSYPMGLEGGLGPRQGPPYEGKKTCKGLEPLGPETTLGPLSPRVLAEKELLKMPGVPLVGRVNAWSCCPFQY
HGQPIYPGPPGLLPLGPVPSLGLWQKSPACPGELSHFCKDVDGLGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_012782383 [XP_012782383] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Ochotona princeps]. 86..100
MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_004585064 [XP_004585064] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Ochotona princeps]. 86..100
MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012782384 [XP_012782384] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Ochotona princeps]. 86..100
MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_004585065 [XP_004585065] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Ochotona princeps]. 86..100
MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012782385   [XP_012782385] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Ochotona princeps].   86..100
      MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRP
QAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGL
SMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEA
LSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_004585066   [XP_004585066] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Ochotona princeps].   86..100
      MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMR
NINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSS
YSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSD
ILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_004585067   [XP_004585067] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Ochotona princeps].   86..100
      MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRP
QELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLN
SVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAAT
KLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_004585068   [XP_004585068] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Ochotona princeps].   86..100
      MDPAQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPTPQASQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGVLTPQHVRAHSSPASLQLGAVTPGTLT
PTGVVSGPAATPTAQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSP
PVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELA
LRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDE
MDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDK
ESFLTWL   PMRLRKLPDSFFKPP

rs:XP_004589899   [XP_004589899] PREDICTED: protein **FAM181**B [Ochotona princeps]. 219..233
      MAVQAALLSSHPFVPFGFGGSPDGLGGTFGVLDKGCCFEDDETGTPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPSAADTPAKRPPGAPTVAAPAHGKAAP
RREASQAAAAASLQSRSLAALFDSLRHVPGAAEPAGGAVASPVAAGLSGAGAAGNGEDAAGPVGGTVVPGSRKVP
LRARNLPLSFFTEPSRAGGGSGGCGPSTPGVSLGDLEKGAEAAEFFELLGPDYGAAGTEAGVLLAAEPLDVFPSA
GAVLRATPELEPGLFEPPPAMVGSLLYPETWSAPGCPQTKKPALAAPRGGLTLNEPLHPLYAAATDSPGAEDGSG
HLASFAPFFPDCALPPPAHPVSYDYSAGYSRSTYSSLWRPDGGWEGAPGEEGARRD   PLRARNLPLSFFTEP

rs:NP_001296578   [NP_001296578] transcriptional coactivator YAP1-like [Hydra vulgaris].>tr:A0A089Q509_HYDVU [A0A089Q509] SubName: Full=YAP {ECO:0000313|EMBL:AIR07404.1};>gp:KM065534_1 [KM065534] YAP [Hydra vulgaris]   43..57
      MDMNSTQRQGNFVLHVRQDSDTDLEQLFKNSVSTNKDIPRSKPFRDRKLPASFFRPPPSLETDQTAPIH
TRARSLPSNIGQIAQDQVILQQQLQQQHPQNNFLLTPSHQRTQSYGTLESNYLPSGCEMRTTASGQKYYINHQN
QSTSWQDPRKAQSMTVLPANPQNLLMDDLPEGWERAVTAEGEVYFINHQTKTTSWFDPRLNRPNNNLLLGGTNIQ
YYQQEKRHRQQQIQNQLLEREFLIHQRMNGQHTDSVLNNNSLINNLVREKYTAHMNSSVLGRGSSVDSGLDGMES
YLTFTSTDGLNDMDTADVDRNNQFDKNTSMEQGICFNNRLPEFFDSLQASNVDLDILEDGFELSSDLEAINTEAL
NDVDMILSPNNKPNAYMTWL   PFRDRKLPASFFRPP

rs:XP_008819911 [XP_008819911] PREDICTED: protein **FAM181**A [Nannospalax galili]. 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRATETHLQ
RGPEDRPGRLPLHPCPHSSPGGGGSCKEKALGTPFGEECLSKEQSLQGLSPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLGAREASLYESKKSCKGLESLGPETAPLPMSPRALADKEPLKMPGISLVGSLDAWGYCPFQYH
GQPIFSGLPGVLPQGPVPSLGLWRKNPASPGELAHFCKDVDGPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_018361461 [XP_018361461] PREDICTED: transcriptional coactivator YAP1 [Trachymyrmex cornetzi]. 46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVPATPNGGGGGGGGKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDP
RKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTAEGEIYFINHQTRTTSWFDPRIPSHLQRTPASGAMLPQN
WQLQQPTGIQSNQNLQACQKQKIRLQSLQLERERLKQRQQEIMRQVGIQQEMMLRQSTTDAVMDPFLSGINEHAR
QESADSGLGLGSAYSLPQASDDFLNIDENMDGTSDGGAPMDTPDLSTLSDNIDSTDDLLPSLQLNEEFSTDILDD
VQSLINPNTTKPENVLTWL PLRLRNLPDSFFNPP

rs:XP_018349476 [XP_018349476] PREDICTED: transcriptional coactivator YAP1 [Trachymyrmex septentrionalis]. 46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLG
PLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTAEGEIYFI
NHQTRTTSWFDPRIPSHLQRTPASGAMLPQNWQLQQPAGIQSNQNLQACQKQKIRLQSLQLERERLKQRQQEIMR
QVGIQQEMMLRQSTTDAVMDPFLSGINEQHARQESADSGLGLGSAYSLPQASDDFLNIDENMDSTSERHCALNDL
TKRLYRSHKYINGGTPMEPDLSTLSDNIDSTDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL
PLRLRNLPDSFFNPP

rs:XP_018545515 [XP_018545515] PREDICTED: protein **FAM181**A [Lates calcarifer]. 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRPAEYGC
GRPVGAVHQSVKVAEKANSDAQDVGNVGSAVEQVPMRKRQLPASFWEEPKLTQTRREHAHFGLKRSPPAGTSEGG
ENEKRKRSYGDDAKATLSASGRRSSADKEALKLDLTSHHCVSVCGCCPFQYHGHQVLHSHIVVPHPPLGLWSKAA
GTETERPEHPYGQKIHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_018546894 [XP_018546894] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Lates calcarifer]. 47..61
MDTHRGGAPPAGQQVVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDPRGHSRQ
ASSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTW
HDPRLSQLQSAAAQHPIPGAPVHSHSLSNPAPTTQPQNISPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDP
RLAQKMNPGILGLAMQQRQEKERLRCKQGLPQQITPQEAGGRNQMDHDRNAQTLVPSLDVRIRASNHEPTLNGAH
SRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGEPSSMTLQESMPVLPMSENEELMPCIPEGLSSDLLMDMET
VLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_018546895 [XP_018546895] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Lates calcarifer]. 47..61
MDTHRGGAPPAGQQVVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDPRGHSRQ
ASSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTW
HDPRLSQLQSAAAQHPIPGAPVHSHSLSNPAPTTQPQNISPETAQKMNPGILGLAMQQRQEKERLRCKQGLPQQI
TPQEAGGRNQMDHDRNAQTLVPSLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDS
GEPSSMTLQESMPVLPMSENEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_018520940 [XP_018520940] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**B [Lates calcarifer]. 246..260
MQVVGHKQRVKXPGVPLPLLFDVLTSLVQPPVRSPCXSSEPVTSTLECLQELHEQHQDQVFVRGKKTCS
EETFGSRIAADATGVAAGLNRVMAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNVGEAPVKRQGSPVAQPSPLQSKTLPKRDGVQ
ANLQSKSLAALFSPVKDIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAADFFELLGPD
YSNMVSDQDLYQSMPLRVQPEMGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGPAQPPVYCHSEAA
TGPIEDNALCTLAFPNFFTDCSIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_018521078   [XP_018521078] PREDICTED: transcriptional coactivator
YAP1 [Lates calcarifer].   45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKSTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGALTPHHVRAHSSPASLQLGAVSGGSLSGMGSAGASPQHLRQSSYEIPDDMPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAAPPSSVPVQQQNIMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
DQRYALNQQRISQSGPVKQGGQLPPSTHSGVMGGNNQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQ
DGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSMA
TQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_005090902   [XP_005090902] PREDICTED: transcriptional coactivator
YAP1-like isoform X1 [Aplysia californica].   41..55
MSQDRTGPIVHVRENSDTELEALFNIAMNPQLASETNKSVPLRMRNLPASFFRPPEPPKQNMQQQMGVN
ASKDGHSPADAPVFHGAVNSSVNIAHMRAHSSPASLQQNLSAAPPPPPTSHVRQHSYDLLDEQPLPAGWDMAKTP
QGQRYYLNHVLQITTWNDPRKTHTPGTTAPSGSSNNNNNNNNTSNLNSSPQTGSPAPSSQPAPNSTPVNVDKVPL
PPGWERAFTADCEVYFINHIDRTTSWFHPSIPVHLQRPGMKFQQQQQQQQQQQQQQQLSSGPISPQQEQLKHLKI
QQLQMEQELLKKRQDEIARQEMALRAQVNENMGTSGGDVTAISQSSEMTSVADPFFGQTTTSDHHRQESGDSGLG
GMGTSYSLPRTPDDFLGNMEDMDTGDGGPKLTGQADFSSMDLAGVNDVGDHLNMDSEDLVPSLQEEIASDLLKDV
ETVLGNKDNPLTWL   PLRMRNLPASFFRPP

rs:XP_005090903   [XP_005090903] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Aplysia californica].   41..55
MSQDRTGPIVHVRENSDTELEALFNIAMNPQLASETNKSVPLRMRNLPASFFRPPEPPKQNMQQQMGVN
ASKDGHSPADAPVFHGAVNSSVNIAHMRAHSSPASLQQNLSAAPPPPPTSHVRQHSYDLLDEQPLPAGWDMAKTP
QGQRYYLNHVLQITTWNDPRKTHTPGTTAPSGSSNNNNNNNNTSNLNSSPQTGSPAPSSQPAPNSTPVNVDKVPL
PPGWERAFTADCEVYFINHIDRTTSWFHPSIPVHLQRPGMKFQQQQQQQQQQQQQQQLSSGPISPQQEQLKHLKI
QQLQMEQELLKKRQDEIARQMALRAQVNENMGTSGGDVTAISQSSEMTSVADPFFGQTTTSDHHRQESGDSGLGG
MGTSYSLPRTPDDFLGNMEDMDTGDGGPKLTGQADFSSMDLAGVNDVGDHLNMDSEDLVPSLQEEIASDLLKDVE
TVLGNKDNPLTWL   PLRMRNLPASFFRPP

rs:XP_012944291   [XP_012944291] PREDICTED: uncharacterized protein
DDB_G0271670-like [Aplysia californica]. 359..373
MASTRPYTFQPQPPPLPRTTGGKRGPSGPINIASSSSEDEDSDQSITDFSPPVPSRLSVTDLASGPSTK
SNAVITVSSLSSPRNNFVTKKSTGLLPSPRSLSNASHVISGSFNHSSGSSSCSSGSNSLFGSNTISSGNGINVAN
HGAIGQSVTTTTTTPLINNANSSTSSSLPPAVPGPLTIQAHSTLNNKTSAFTTQNSLTSNATNSTASSSITCGNN
AGGSSSSSSDNGNATNSANTGSLVAATTSSSASSPSSRTCSVPEAASTSPRERSCSPASNFAYEHDHDYENVASP
CSSTASGPTYVRPPGFNHHAQEITVSSKNKLKKKKSSAAFISVRDGFKKREATPPKIKPKREPLPMKLRALPQSF
WQQPNVAHQVSPATLFPILPPLSQKESEEIMDVRPVTPPEDRDSSKKAPPPERKLTVANTDLLFKLFDGVTEEKK
STGTSKSRTHTRQRKTVPKSSTKGLFLGNDPYLVEDVTDKIFPTLTLEGSRHLSGGGNTSLQLITLKEGDRTVTL
PSLSMEQSYPQMLSELVMHI   PMKLRALPQSFWQQP

rs:XP_005149577   [XP_005149577] PREDICTED: protein **FAM181**A [Melopsittacus
undulatus]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSTECGWR
RGAEDLGRGPPPEAPDPSARGAAATERVLQTAGVEGSLTEERVLQEQNPEATRPDQVPMRKRQLPASFWEEPQPA
QSLLARAYPTSSEGLPAPRDPPPSEGKKSKRSPNTSGPESPPEPTPHAGDKDSAGILLGRVGAWTCCPFPCPGPG
VYQPPGTLSQSPFLGLGLWRKSAATLSAEVPHFCKEADGMEQKLYRPVVLKPIPTKPAVPPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_006278984   [XP_006278984] PREDICTED: protein **FAM181**A [Alligator
mississippiensis].>tr:A0A151P8Q3_ALLMI [A0A151P8Q3] SubName: Full=Protein
FAM181A {ECO:0000313|EMBL:KYO45477.1};   126..140
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRSHPSKSMESNMK
RGVEDRNRSSHPDALDPNPCRATSEKALRGAEVEENLSGEQGLQEQSPESARPDQVPMRKRQLPASFWEEPRPAQ
SLMVGSFPAGLDGLPKSRDLPSYEGKKSKKSPDATGPESPPVPVQPSGEKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTPGALPQSPFPGLGLWRKNTAPQGEIQHFCKETDATGQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_019337569 [XP_019337569] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Alligator mississippiensis]. 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGPASSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQPNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNPRITQSAPVKQPPSLAPQSPQ
GGVMGSGNSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDSGSQ
NPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSH
QNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_019337570 [XP_019337570] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Alligator mississippiensis].>tr:A0A151P7G7_ALLMI [A0A151P7G7] SubName: Full=Transcriptional coactivator YAP1 isoform D {ECO:0000313|EMBL:KYO44972.1}; 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGPASSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQPNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNPRITQSAPVKQPPSLAPQSPQ
GGVMGSGNSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDSGSQNPVSSPGMSQELRTMT
TNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNV
DLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_019337571 [XP_019337571] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Alligator mississippiensis]. 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGPASSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQPNIMNSASAMNPRITQSAPVKQPPSLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKHQELLRQV
RPQALRNINPSTANSPKHQELALRSQLPTMEQDSGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDS
GLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQ
EALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014456178 [XP_014456178] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Alligator mississippiensis].>tr:A0A151P7B6_ALLMI [A0A151P7B6] SubName: Full=Transcriptional coactivator YAP1 isoform C {ECO:0000313|EMBL:KYO44971.1}; 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGPASSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQPNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNPRITQSAPVKQPPSLAPQSPQ
GGVMGSGNSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDSGSQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014457652 [XP_014457652] PREDICTED: uncharacterized protein LOC106737997 [Alligator mississippiensis].>rs:XP_019345533 [XP_019345533] PREDICTED: uncharacterized protein LOC106737997 [Alligator mississippiensis].>rs:XP_014457655 [XP_014457655] PREDICTED: uncharacterized protein LOC106737997 [Alligator mississippiensis].
214..228
MAAGVIRNPAEFRLPTSFQHSFLHPAVHQDRDFQELSEEEEDEEEEEEEEEEMEEVESQGSPTAPIPGG
ERQEVTATASLHDAEMTLQLLRFSELISSDIQRYFGRKDKEEDPDSCNIYEDCFSPQRSGRELYYADLMHIAQSG
ELDDEDSHSAQVPLGQLDQQVWRSICNKDGGQKLGPLAELFEYGLRQYIKQTVSDSRRLRLEKKYAHITPMHRRK
LPPSFWKEPSPGPAGILNTNTPDFSDLLANWTVEPGQELPNASRELAGELGRQAMEADQFNVL
PMHRRKLPPSFWKEP

rs:XP_013032975 [XP_013032975] PREDICTED: protein **FAM181**A, partial [Anser cygnoides domesticus]. 115..129
FVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPGKPSECGPRRGAEDRARGCQS
EMPDPGPHSGAAAEKALRAAEAEESLAGERALPEQNPEAGRPDQVPMRKRQLPASFWEEPRPAQSLPSRGFPPGP
EGLSAPRDTPSFEGKKSKRSQDTAGPESPSEPALHTGEKDPAGVLSGRVGTWTCCPFPCPGPAVYQPPGTLPPSP
FPGLGLWRKSAATLPAEAQPFCKEAEGAGQKFYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_013134895 [XP_013134895] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Papilio polytes]. 44..58
MALNSDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQSAETMLAQATAPQTIAPATPTAAKSTSSSTASDPLGPLPDGWE
QAATPEGEVYFINHAARTTSWFDPRIPQHLQRTPVAGAGAAGGGWANASLQACQQKLRLQSLQMERERLKQRQQE
IMLQQELMGRQSSSIVSSLASGGAGAAGVPGAGGGAAADLDPFLSGLTEHQRQESADSGLGMAVNPSYSMPHTPE
DFLAGMDDRMDCTSEAGAIDPDISLGDNIDPTDDLVPSLQLSEFTNDILLDDVQSLINSTPSKTDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_013134896 [XP_013134896] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Papilio polytes]. 44..58
MALNSDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQSAETMLAQATAPQTIAPATPTAKSTSSSTASDPLGPLPDGWEQ
AATPEGEVYFINHAARTTSWFDPRIPQHLQRTPVAGAGAAGGGWANASLQACQQKLRLQSLQMERERLKQRQQEI
MLQQELMGRQSSSIVSSLASGGAGAAGVPGAGGGAAADLDPFLSGLTEHQRQESADSGLGMAVNPSYSMPHTPED
FLAGMDDRMDCTSEAGAIDPDISLGDNIDPTDDLVPSLQLSEFTNDILLDDVQSLINSTPSKTDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_013134897 [XP_013134897] PREDICTED: transcriptional coactivator yorkie isoform X3 [Papilio polytes]. 44..58
MALNSDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQSAETMLAQATAPQTIAPATPTAQHLQRTPVAGAGAAGGGWANA
SLQACQQKLRLQSLQMERERLKQRQQEIMLQQELMGRQSSSIVSSLASGGAGAAGVPGAGGGAAADLDPFLSGLT
EHQRQESADSGLGMAVNPSYSMPHTPEDFLAGMDDRMDCTSEAGAIDPDISLGDNIDPTDDLVPSLQLSEFTNDI
LLDDVQSLINSTPSKTDNVLTWL PLRMRQLPKSFFNPP

rs:XP_013176904 [XP_013176904] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Papilio xuthus]. 44..58
MALNTDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQSAETMLAQATAPQTIAPATPTAAKSTSSSAASDPLGPLPDGWE
QAATPEGEVYFINHAARTTSWFDPRIPQHLQRTPVAGAGAAGGGWANASLQACQQKLRLQSLQMERERLKQRQQE
IMLQQELMGRQSSSIVSSLASGGATAGVQGAGGGAAADLDPFLSGLTEHQRQESADSGLGMAVNPSYSMPHTPED
FLAGMDDRMDCSSEAGAIDPDISLGDNIDPTDDLVPSLQLSEFTNDILLDDVQSLINSTPNKTTDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_013176905 [XP_013176905] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Papilio xuthus]. 44..58
MALNTDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQSAETMLAQATAPQTIAPATPTAKSTSSSAASDPLGPLPDGWEQ
AATPEGEVYFINHAARTTSWFDPRIPQHLQRTPVAGAGAAGGGWANASLQACQQKLRLQSLQMERERLKQRQQEI
MLQQELMGRQSSSIVSSLASGGATAGVQGAGGGAAADLDPFLSGLTEHQRQESADSGLGMAVNPSYSMPHTPEDF
LAGMDDRMDCSSEAGAIDPDISLGDNIDPTDDLVPSLQLSEFTNDILLDDVQSLINSTPNKTTDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_013176906 [XP_013176906] PREDICTED: transcriptional coactivator yorkie isoform X3 [Papilio xuthus]. 44..58
MALNTDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQSAETMLAQATAPQTIAPATPTAQHLQRTPVAGAGAAGGGWANA
SLQACQQKLRLQSLQMERERLKQRQQEIMLQQELMGRQSSSIVSSLASGGATAGVQGAGGGAAADLDPFLSGLTE
HQRQESADSGLGMAVNPSYSMPHTPEDFLAGMDDRMDCSSEAGAIDPDISLGDNIDPTDDLVPSLQLSEFTNDIL
LDDVQSLINSTPNKTTDNVLTWL PLRMRQLPKSFFNPP

rs:XP_013194178 [XP_013194178] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Amyelois transitella]. 44..58

MALNTDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQAAPLHHQHSKQRSYDVVSHIPDDLGPLPPG
WEQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVASAVQQHQSSEALINQSPAQPAITPVATPAAKSTSSNTTT
ESIPLPEGWEQATTLEGETYFINHATRTTSWFDPRIPQHLQRTPAANAGVAGGGWANASLQASQQKLRLQSLQLE
RERLKQRQQEIRLQQELMSRQVTSLSNSIGTVTNTELSLDPFLSGLADHQRQESADSGLGMAVSQSYSMPHTPED
FLASMDDRMDCSSEAGANLDSTDMTLGDNLDTTEDLVPSLQLSEFTNDILLDDVQSLINSTPSKAGNVLTWL
PLRMRQLPKSFFNPP

rs:XP_013194179 [XP_013194179] PREDICTED: transcriptional coactivator yorkie-like isoform X2 [Amyelois transitella]. 44..58

MALNTDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQAAPLHHQHSKQRSYDVVSHIPDDLGPLPPG
WEQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVASAVQQHQSSEALINQSPAQPAITPVATPAQHLQRTPAAN
AGVAGGGWANASLQASQQKLRLQSLQLERERLKQRQQEIRLQQELMSRQVTSLSNSIGTVTNTELSLDPFLSGLA
DHQRQESADSGLGMAVSQSYSMPHTPEDFLASMDDRMDCSSEAGANLDSTDMTLGDNLDTTEDLVPSLQLSEFTN
DILLDDVQSLINSTPSKAGNVLTWL PLRMRQLPKSFFNPP

rs:XP_015019507 [XP_015019507] uncharacterized protein Dmoj_GI18856, isoform B [Drosophila mojavensis].>tr:A0A0Q9XKT2_DROMO [A0A0Q9XKT2] SubName: Full=Uncharacterized protein, isoform B {ECO:0000313|EMBL:KRG04903.1}; 61..75

MSLSNKSNISEKEIDDEDMLSPTKISTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEMQPSLTQQNQPSHSRLAIHHIRARSSPASLQQNYNVRTRNE
PSANNTNTNQGPAYPETSVDFVSASTANNIDLDVINTCMGPVPGPDAAALAATQTTIHKKQRSYDVVSPIQLQSQ
LGALPPGWEQAKTNDGQIYYLNHTSKTTQWEDPRIQFRQQQRALAERIKPNDVIQTTKPTSSSTIATHLGPLPD
GWEQAVTESGDIYFINHIDRTTSWNDPRIQSGLNVLDCPDNLVSSLQIGDNICSNIFNDTQAIINTPSSHKPDDL
EWYKIN PFRMRKLPNSFFNPP

rs:XP_002005853 [XP_002005853] uncharacterized protein Dmoj_GI18856, isoform A [Drosophila mojavensis].>tr:B4KLX8_DROMO [B4KLX8] SubName: Full=Uncharacterized protein, isoform A {ECO:0000313|EMBL:EDW09788.1}; 61..75

MSLSNKSNISEKEIDDEDMLSPTKISTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEMQPSLTQQNQPSHSRLAIHHIRARSSPASLQQNYNVRTRNE
PSANNTNTNQGPAYPETSVDFVSASTANNIDLDVINTCMGPVPGPDAAALAATQTTIHKKQRSYDVVSPIQLQSQ
LGALPPGWEQAKTNDGQIYYLNHTSKTTQWEDPRIQFRQQQRALAERIKPNESGLNVLDCPDNLVSSLQIGDNI
CSNIFNDTQAIINTPSSHKPDDLEWYKIN PFRMRKLPNSFFNPP

rs:XP_012594065 [XP_012594065] protein **FAM181**A [Microcebus murinus].>rs:XP_012594066 [XP_012594066] protein **FAM181**A [Microcebus murinus]. 129..143

MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLK
RGPEDRPGRLLLDPGPESGPGGGGGCKEKALGNPYGEECLSKEQVLQGQSPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGGLGPREGPLYEGKKNCKGLEPLGPEAALVPMSPRALAEKEPLKMPGVSLVGRGNAWSCCPLQYH
GQPIYPGLPGALPQSPIPGLGLWRKSPAFPGELAHFCKDVDGLGQVCRPVVLKPIPTKPAMAPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014904663 [XP_014904663] PREDICTED: transcriptional coactivator YAP1 [Poecilia latipinna].>rs:XP_007570007 [XP_007570007] PREDICTED: transcriptional coactivator YAP1 [Poecilia formosa].>tr:A0A3B3U6J2_9TELE [A0A3B3U6J2] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPLAP00000008955}; 45..59

MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPASLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LNHNDKSTTWQDPRKALLQTSQPAPPSSVPVQPQNLMNPANGPLPEHWEQAITSEGEIYYINHEKRTTSWLDPRL
EPRYALNQQRMTQSAPGKQSGQLPPSTHGGVMAGNNQLRLQQIEKDRLRLQQHRPQELALRNQLPTSMDQDGSTN
PISSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLPASMASQPSR

FPDYLDGIPGTDVDLGTLEGESMAVESEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRNLPDSFFKPP

rs:XP_014913692 [XP_014913692] PREDICTED: protein **FAM181**A [Poecilia
latipinna]. 102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQTLTSADYRC
ARGAERQRVTATDEASSDAQLAQSVGGVMDQVPMRKRQLPASFWEEPRLTKARRDKPCLDLRRSSSSGTSDGGEN
ERRRRSQEDAQKTANSSSGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQFQGHQVLHSQIVVPHPPFGLWSKAAEP
ERSEHPYGQKLHTHVVVKPIPTKATAQSPILSVFGFI PMRKRQLPASFWEEP

rs:XP_014831258 [XP_014831258] PREDICTED: protein **FAM181**A [Poecilia
mexicana]. 102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQTLTSADYRC
ARGAERQRVTATDEASSDAQHAQSVGGVMDQVPMRKRQLPASFWEEPRLTKARRDKPCLDLRRSSSSGTSDDGEN
ERRRSQEDAQKTANSSSGRRSSAEKEVLKLDLTSHRSVCFCSCCPFQFQGHQVLHSQIVVPHPPFGLWSKAAEPE
RSEHPYGQKLHTHVVVKPIPTKATAQSPILSVFGFI PMRKRQLPASFWEEP

rs:XP_005724066 [XP_005724066] PREDICTED: protein **FAM181**A [Pundamilia
nyererei].>rs:XP_026008629 [XP_026008629] protein **FAM181**A [Astatotilapia
calliptera].>rs:XP_005916781 [XP_005916781] PREDICTED: protein **FAM181**A
[Haplochromis burtoni]. 102..116
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYRC
AKPMGSVHQSVAEKASSGAQDVDQLGSSVEQVPMRKRQLPASFWEEPKLTPTKREHSYLGMKRSHAGTSEGTENE
KRKRSCDDDAKTAISACSRRSSADKETLKLDVTSHHCVSVCGCCPFQYHGHQILHNHIFVPHPPLGLWSKAAGTE
TERSEHPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_005735999 [XP_005735999] PREDICTED: transcriptional coactivator
YAP1 [Pundamilia nyererei].>tr:A0A3B4FS17_9CICH [A0A3B4FS17] SubName:
Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPNYP00000012413};
45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKVNTVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSGGSLSGMGSTGASPQHLRQSSYEIPDDLPLPDGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQPAPPSSVPVQPQPIMNPASGSLPDGWEQAITAEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRISQSAPVKQAGQLPPSISGVMGSNNQMRLQMEKERLRQKQQELLRQRPQELALRNQLPTSMDQDG
STNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMATQ
PSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_005736013 [XP_005736013] PREDICTED: protein **FAM181**B [Pundamilia
nyererei].>rs:XP_005926585 [XP_005926585] PREDICTED: protein **FAM181**B
[Haplochromis burtoni].>rs:XP_004560587 [XP_004560587] protein **FAM181**B
[Maylandia zebra]. 155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGETENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNAAEAPVKRQGSPLTQPSTLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKPKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEATEFFELLGPDYCNMVSDQDIYQGMPL
RVQPELGGPDPASYDTHHLVGGLLYSEPWTSCSGPSKKVGESMRTGPAQPPVYCQSEGATGPIEDNALCTLAFPN
FFADCPIPQVTYDLTGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_005751097 [XP_005751097] PREDICTED: transcriptional coactivator
YAP1-like isoform X1 [Pundamilia nyererei].>rs:XP_026037126 [XP_026037126]
transcriptional coactivator YAP1-like isoform X1 [Astatotilapia
calliptera].>rs:XP_026037127 [XP_026037127] transcriptional coactivator
YAP1-like isoform X1 [Astatotilapia calliptera]. 45..59
MDAHRGAPPAGQQIVHVRGDSQTELEALFTAVMNPNAAKQPSSLPMRMRKLPDSFFRQPDPRGHSRQAS
SDGGVCGSQAPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDMPLPRGWEMAKTPTGQRYFLNHLDKTTTWHD
PRLAQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPEKGPLPEGWEQAVTADGEMYYIDHINKNTTWVDPRL
AQKMNPSILGMAMQQSQEKDRLRCKQGIPQQIAPQDVGGRSQMPGGMDHDRSAQTLVPSLDVRIRASNHEPTLNG
AHSRNESTDSGLSVSSLPRTTDHMLSSVEHMDTGDSEPPSMALQDSMPVLPMSEGEELMPCIPEGLSSDLLMDME
TVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_005751098 [XP_005751098] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Pundamilia nyererei].>rs:XP_026037128 [XP_026037128] transcriptional coactivator YAP1-like isoform X2 [Astatotilapia calliptera].>rs:XP_006800089 [XP_006800089] PREDICTED: yorkie homolog [Neolamprologus brichardi]. 45..59
MDAHRGAPPAGQQIVHVRGDSQTELEALFTAVMNPNAAKQPSSLPMRMRKLPDSFFRQPDPRGHSRQAS
SDGGVCGSQAPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDMPLPRGWEMAKTPTGQRYFLNHLDKTTTWHD
PRLAQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPEKAQKMNPSILGMAMQQSQEKDRLRCKQGIPQQIAP
QDVGGRSQMPGGMDHDRSAQTLVPSLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTTDHMLSSVEHMDTG
DSEPPSMALQDSMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_006208286 [XP_006208286] PREDICTED: protein **FAM181**A [Vicugna pacos]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPSRGAEPHLK
RVPEDRPGRLPRDSGHNSSPSGGGGYKEKALGNPYREECLPKEQTLQGQDPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGGLGPREGLPYEGKKHCKGLEPLGPETAPLPTEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYP
GPPGALPQSPVSGLGLWRKSSASPGELVHFCKDVEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_013796471 [XP_013796471] PREDICTED: protein **FAM181**A [Apteryx australis mantelli]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSAECSVK
RGTEDRSRGSQSEVVDSSHHCRAAAEKVLRTAKVEENFSGEQVLQEQNPEPARPDQVPMRKRQLPASFWEEPRPA
QSLLARSFPAGLDGLPNSGDPVPYEGKKSRRSPEAAGPESPPEPVQHGSEDPAKAPGPPMSGRVAAWTCCPFQCP
GQPLYQTPGALPPSPFPGLGLWRKSAALPGEIQHFSKEADSTGQKLYRPMVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_013913644 [XP_013913644] PREDICTED: protein **FAM181**B [Thamnophis sirtalis]. 226..240
MAVQAAPPPPPHHPFVPFGFPTADFGALEKSCYGDGAALLLLEGGVGASGIGGVEGGVGGGVVGCPEAA
DFREATRELLSFIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCTGLLGGNAEPGAGSVPGSSPAPAAAAAA
PTNKQASASPAPSSGGGAAAAAPSCKPAKRESKSLAALFDSLRGAPTAVATAASPAGPSGCASGKEAGSAPPTAA
VACKKVPLRNRNLPRSFFTEPAPNRAPNPAGLEGGGGGGGAGPVPSVAEELFDLLAAPDYRALLQESSEPPPPPP
PVFPAELPLEPPLYEPLPSLAPLLYAETPLRPLPALYAAVAVSDPTAPFFADCPLPPPPSMPYDYGYSRGAPYPS
L PLRNRNLPRSFFTEP

rs:XP_013914507 [XP_013914507] PREDICTED: protein **FAM181**A [Thamnophis sirtalis]. 138..152
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHHHHLQPQLP
PARERRPPEGRVRGLSPESSLGRGHAASGASKGDKASKAPERLGGEEKQQQQQQQAGTSEAGARPDQVPMRKRQL
PASFWEEPRPAPGSPGVVSGVIFPMGVCSSPSSSSSSSKDLPPYEGKKNKIGLDGGSGGTGAVLESPPRRPEAEA
ALKGLRTWGCCPFQYHGPQASPGVYPPPLPAALPPLAPFSALGLWRKDAPSPTEGEPFCQPGQKVYRPVVWKPIP
TKPAAPPLIFSVFSYL PMRKRQLPASFWEEP

rs:XP_013929736 [XP_013929736] PREDICTED: transcriptional coactivator YAP1-like, partial [Thamnophis sirtalis].80..94
MDVGGQPQQAPSAAQPQPSQGQPTGQASPPAPQPGGGAVSGPPPAGHQVVHVRGDSETDLEALFNAVMN
PKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPALLGTVSPGALTPSGVVPGG
TPSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKTLLSQMNVTAPTSPPVQQNIMNSAT
PMRLRKLPDSFFKPP

rs:XP_013869014 [XP_013869014] PREDICTED: protein **FAM181**A [Austrofundulus limnaeus].>tr:A0A2I4BMP7_9TELE [A0A2I4BMP7] SubName: Full=protein **FAM181**A {ECO:0000313|RefSeq:XP_013869014.1}; 109..123
MRQAKDLANMANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCH
THRSTDYRCLKPAGAAHQSAQKGGSDARDAESVGGVEQVPMRKRQLPASFWEEPRLTKAKRDKSCSRRSPVGASD
GGEKRKTSGDDDAKASPSNRRSSADREVLKLDVSSQHSVSVCGCCPLQYHGHHVLHSHIVVPHPPLALWSKASGT
EEQPYVQRLHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_013858633 [XP_013858633] PREDICTED: transcriptional coactivator
YAP1-like isoform X1 [Austrofundulus limnaeus].>tr:A0A2I4AT48_9TELE
[A0A2I4AT48] SubName: Full=transcriptional coactivator YAP1-like isoform X1
{ECO:0000313|RefSeq:XP_013858633.1}; 48..62
MDAHRGGSAPPAGQQVVHVRGDSKSELEALFSAVMNPGKAARQPQSLPMRMRNLPDSFFKPPEPRGHSR
QASSDGGVCGSLAPHHVRAHSSPASLPVNSLSAQAAADVATSPILPDDVPLPDGWEMAKTPTGQRYFINHLQKTT
TWQDPRLSQLQSAAVHHQIPCAPVHAHSFSNPAPTTQPQTISSETGPLPEGWEQAVTADGEVYYIDHINKITTWV
DPRLAQKMNPGMLSLQQRQEKERLRGIKGIPPQIAPQEAAGRSQIPGGMDHDRSTQMLVPSVDVRIRALNQEPTL
NGAHSRNESTDSGLSVSSLPRSSDHMLSTVDHMDTGDSSEPPSVTMQEMPVLPITEGEELMPCIPDGLNSDLLMD
METVLSGPHMDRDSLLTWL PMRMRNLPDSFFKPP

rs:XP_013858634 [XP_013858634] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Austrofundulus limnaeus].>tr:A0A2I4AT23_9TELE
[A0A2I4AT23] SubName: Full=transcriptional coactivator YAP1-like isoform X2
{ECO:0000313|RefSeq:XP_013858634.1}; 48..62
MDAHRGGSAPPAGQQVVHVRGDSKSELEALFSAVMNPGKAARQPQSLPMRMRNLPDSFFKPPEPRGHSR
QASSDGGVCGSLAPHHVRAHSSPASLPVNSLSAQAAADVATSPILPDDVPLPDGWEMAKTPTGQRYFINHLQKTT
TWQDPRLSQLQSAAVHHQIPCAPVHAHSFSNPAPTTQPQTISSETAQKMNPGMLSLQQRQEKERLRGIKGIPPQI
APQEAAGRSQIPGGMDHDRSTQMLVPSVDVRIRALNQEPTLNGAHSRNESTDSGLSVSSLPRSSDHMLSTVDHMD
TGDSSEPPSVTMQEMPVLPITEGEELMPCIPDGLNSDLLMDMETVLSGPHMDRDSLLTWL
PMRMRNLPDSFFKPP

rs:XP_013858635 [XP_013858635] PREDICTED: transcriptional coactivator
YAP1-like isoform X3 [Austrofundulus limnaeus].>tr:A0A2I4AT08_9TELE
[A0A2I4AT08] SubName: Full=transcriptional coactivator YAP1-like isoform X3
{ECO:0000313|RefSeq:XP_013858635.1}; 48..62
MDAHRGGSAPPAGQQVVHVRGDSKSELEALFSAVMNPGKAARQPQSLPMRMRNLPDSFFKPPEPRGHSR
QASSDGGVCGSLAPHHVRAHSSPASLPVNSLSAQAAADVATSPILPDDVPLPDGWEMAKTPTGQRYFINHLQKTT
TWQDPRLSQLQSAAVHHQIPCAPVHAHSFSNPAPTTQPQTISSETGPLPEGWEQAVTADGEVYYIDHINKITTWV
DPRLAQKMNPGMLSLQQRQEKERLRGIKGIPPQIAPQEAAGRSQIPGGMDHDRSTQMLVPSVDVRIRALNQEPTL
NGAHSRNESTDSGLSVSSLPRSSDHMLSTVDHMDTVFPIM PMRMRNLPDSFFKPP

rs:XP_013868176 [XP_013868176] PREDICTED: protein **FAM181**B [Austrofundulus
limnaeus].>tr:A0A2I4BKA8_9TELE [A0A2I4BKA8] SubName: Full=protein **FAM181**B
{ECO:0000313|RefSeq:XP_013868176.1}; 155..169
MAVQTAIMNPQFMSFCFPDAVMEYDMEKSPDGGLLCEAENDGDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIIGPGNAAEAPAKRQGSPGSQPSPLQSKTLPKRDGLQANLQSKSLAALFNPGK
DVKGEKAKKPPLRHRNLPPSFFTEPAHCSKVSSTSGMTLKDLERGNPEAADFFELLGPDYSNMMSEQDLYQGAPL
RAQPDLGVMDPGSYDAHHLVGGLLYSEPWTGCSGPSKKLVTSPAPPAGYCQSEDASGPVDDNGLCTLAFSNFFTD
CSIPQVAYDLNCGYNKGNYSSL PLRHRNLPPSFFTEP

rs:XP_013868238 [XP_013868238] PREDICTED: transcriptional coactivator
YAP1 [Austrofundulus limnaeus].>tr:A0A2I4BKJ3_9TELE [A0A2I4BKJ3] SubName:
Full=transcriptional coactivator YAP1 {ECO:0000313|RefSeq:XP_013868238.1};
45..59
MDPSQHNPPAGHQIVHVRGDSETDLETLFNIVMNPNSPNIPHCVPMRQRKLPDSFFNPPEPKSHSRQAS
TDAGSGAVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGVSPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQAAPPPSVPVQQQNPMNPASGTLPDGWEQAITPDGEIYYINHKNKTTSWLDPRL
EPRYALNQQRITQSAPVKQGGQLPSSPHGGVMGGNNQLRLQQIEKERLRLKQHEALRQRPQELALRNQLPTSMDQ
DGGTNPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDQLPPSMA
TQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEPLSSDILSDMESVLAATKIDKESFLTWL
PMRQRKLPDSFFNPP

rs:XP_005516790 [XP_005516790] PREDICTED: protein **FAM181**B [Pseudopodoces
humilis]. 171..185
MAVPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAPPPPAACPPSACPARPPPRREPAQAAGSSLQSKSLAALFGSLQRGRGA
AGGAEAKAGGGGAGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPGPAARGPPAKEPEKGGGGAEATEFFELLCPE

YGALLPEHAAPTDAFGGRLPAELGLEHGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPAEPLRPLYPG
GAEPVPGGGGGEEPGGHLPAGVAPFFPECPLPPPQPPYDYGGGYHRGGYPGL PLRDRNLPPSFFTEP

rs:XP_014106265 [XP_014106265] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Pseudopodoces humilis]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAAAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALR
SQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMD
TGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKES
FLTWL PMRLRKLPDSFFKPP

rs:XP_005520227 [XP_005520227] PREDICTED: protein **FAM181**A [Pseudopodoces
humilis]. 128..142
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHHPSKPAECGW
RRGAEDRARGPLPEAPEPSSHGGATAEKVMQTAEAEESLTGDRVLQEQKPEAARPDQVPMRKRQLPASFWEEPRP
AQSLTARAFPASPEGLQAPRDPPPYEGKKSKRSPDAAGPESPPDTAPHAGEKDPAGPLSGRVGTWTCCPFPCPGP
GVFQPPGALPPSPFPGLGLWRKSAAPLPAEVPRFCKEADGPGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_005896258 [XP_005896258] PREDICTED: protein **FAM181**A [Bos mutus].
130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRSGRPLPLESGHGSSPGGGGGCKEKALGNLDREESLSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014354483 [XP_014354483] PREDICTED: uncharacterized protein
LOC102364766 [Latimeria chalumnae].>tr:M3XI84_LATCH [M3XI84] SubName:
Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSLACP00000022440};
120..134
MMAYFNDREVKTLLNFVNLASSDIKAALDKSAPCKRSVDHRKYLQKQLKRFSQKKLASKASPSPAKDPP
ANKHPSNMSSDSEVDSNSFSQPGIWTLPSRRYNGLLQPGEKMDSRKSESLPLRKRRLPASFWKEPGPLDKLAPPQ
LSDWESLLASEDARESQVPVPKSSTFLPSCGLPRELSAAQPNHHISCTASQECGCRCCVLSHSDCLVFPPLPQAL
IPLQFLPCVEVGALPFPTQREASFFQNEVETFAIWKPVVTKPAAVLQPYGPYGVN PLRKRRLPASFWKEP

rs:XP_006001898 [XP_006001898] PREDICTED: protein **FAM181**B [Latimeria
chalumnae].>tr:H2ZW23_LATCH [H2ZW23] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSLACP00000001594};
155..169
MAVQAAVMNPHFIHFCFPSPVMDYDMEKTYDGALLGEVDAGGEFREATRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGMISTGNVNQEVTKRQSSSPSNSNNFQCKPPAKRDGSHSNLQSKSLAALFDSVK
EIRGDKSKKVPLRNRNLPPSFFTEPANVSKVNSTSGMTLKDLERGNPEAADFFELLGPEYSNMISDQEVFQGASV
RIHQDLTTDHGLYEPHHLMGGFLYSDSWNPNNLTKKNTLGVCNMNTNENMRTIPVQTAMYTNAEPTVTPPMEESS
LSLPSFPHFFPDCSFPQVSYDYSTPYNRASYPVL PLRNRNLPPSFFTEP

rs:XP_014352180 [XP_014352180] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Latimeria chalumnae]. 45..59
MDPSQQHPPAGHQIVHVRGDSETDLEALFNAVMNPKSANVPHSVPMRMRKLPDSFFRQPEPKSHSRQAS
TDAGSAGALTPQHVRAHSSPASLQLGAVSPGTMTASGGVSGQGPQPQSQHLRQSSFEIPDDVPLPPGWEMAKTPS
GQRYFLNHIDQTTTWQDPRKALLPQMNVTAPTSPPVQQNIMSPSSGKQAGPLPDGWEQAMTQEGEIYYINHKNKT
TSWLDPRLDPRFGINQQRMSQSAPVKQAPPLAPPSPQSGVMGGSNQQQQMRLQQLQMEKERLRLKHQELLRQVRP
QELALRSQLPTMEQDGGSQNPVSPPGMSQDVRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLN
SVDEMDTGDTIGQSNLASQQNRFPDYLETIPGTNVDLGTLEEDGMNVEGEELMPSLQEALSTDILNDMESVLAAT
KIDKETFLTWL PMRMRKLPDSFFRQP

rs:XP_014352181 [XP_014352181] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Latimeria chalumnae]. 45..59
MDPSQQHPPAGHQIVHVRGDSETDLEALFNAVMNPKSANVPHSVPMRMRKLPDSFFRQPEPKSHSRQAS
TDAGSAGALTPQHVRAHSSPASLQLGAVSPGTMTASGGVSGQGPQPQSQHLRQSSFEIPDDVPLPPGWEMAKTPS
GQRYFLNHIDQTTTWQDPRKALLPQMNVTAPTSPPVQQNIMSPSSGPLPDGWEQAMTQEGEIYYINHKNKTTSWL
DPRLDPRFGINQQRMSQSAPVKQAPPLAPPSPQSGVMGGSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELA
LRSQLPTMEQDGGSQNPVSPPGMSQDVRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDE
MDTGDTIGQSNLASQQNRFPDYLETIPGTNVDLGTLEEDGMNVEGEELMPSLQEALSTDILNDMESVLAATKIDK
ETFLTWL PMRMRKLPDSFFRQP

rs:XP_014352182 [XP_014352182] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Latimeria chalumnae]. 45..59
MDPSQQHPPAGHQIVHVRGDSETDLEALFNAVMNPKSANVPHSVPMRMRKLPDSFFRQPEPKSHSRQAS
TDAGSAGALTPQHVRAHSSPASLQLGAVSPGTMTASGGVSGQGPQPQSQHLRQSSFEIPDDVPLPPGWEMAKTPS
GQRYFLNHIDQTTTWQDPRKALLPQMNVTAPTSPPVQQNIMSPSSGKQAGPLPDGWEQAMTQEGEIYYINHKNKT
TSWLDPRLDPRFGINQQRMSQSAPVKQAPPLAPPSPQSGVMGGSNQQQQMRLQQLQMEKERLRLKHQELLRQELA
LRSQLPTMEQDGGSQNPVSPPGMSQDVRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDE
MDTGDTIGQSNLASQQNRFPDYLETIPGTNVDLGTLEEDGMNVEGEELMPSLQEALSTDILNDMESVLAATKIDK
ETFLTWL PMRMRKLPDSFFRQP

rs:XP_006009477 [XP_006009477] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Latimeria chalumnae]. 45..59
MDPSQQHPPAGHQIVHVRGDSETDLEALFNAVMNPKSANVPHSVPMRMRKLPDSFFRQPEPKSHSRQAS
TDAGSAGALTPQHVRAHSSPASLQLGAVSPGTMTASGGVSGQGPQPQSQHLRQSSFEIPDDVPLPPGWEMAKTPS
GQRYFLNHIDQTTTWQDPRKALLPQMNVTAPTSPPVQQNIMSPSSGPLPDGWEQAMTQEGEIYYINHKNKTTSWL
DPRLDPRFGINQQRMSQSAPVKQAPPLAPPSPQSGVMGGSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQ
LPTMEQDGGSQNPVSPPGMSQDVRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTG
DTIGQSNLASQQNRFPDYLETIPGTNVDLGTLEEDGMNVEGEELMPSLQEALSTDILNDMESVLAATKIDKETFL
TWL PMRMRKLPDSFFRQP

rs:XP_014352183 [XP_014352183] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Latimeria chalumnae]. 45..59
MDPSQQHPPAGHQIVHVRGDSETDLEALFNAVMNPKSANVPHSVPMRMRKLPDSFFRQPEPKSHSRQAS
TDAGSAGALTPQHVRAHSSPASLQLGAVSPGTMTASGGVSGQGPQPQSQHLRQSSFEIPDDVPLPPGWEMAKTPS
GQRYFLNHIDQTTTWQDPRKALLPQMNVTAPTSPPVQQNIMSPSSGKQAGINQQRMSQSAPVKQAPPLAPPSPQS
GVMGGSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSPPGMSQDVRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTIGQSNLASQQNRFPDYLETIPGTNVDLG
TLEEDGMNVEGEELMPSLQEALSTDILNDMESVLAATKIDKETFLTWL PMRMRKLPDSFFRQP

rs:XP_014352184 [XP_014352184] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Latimeria chalumnae]. 45..59
MDPSQQHPPAGHQIVHVRGDSETDLEALFNAVMNPKSANVPHSVPMRMRKLPDSFFRQPEPKSHSRQAS
TDAGSAGALTPQHVRAHSSPASLQLGAVSPGTMTASGGVSGQGPQPQSQHLRQSSFEIPDDVPLPPGWEMAKTPS
GQRYFLNHIDQTTTWQDPRKALLPQMNVTAPTSPPVQQNIMSPSSGINQQRMSQSAPVKQAPPLAPPSPQSGVMG
GSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSPPGMSQDVRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTIGQSNLASQQNRFPDYLETIPGTNVDLGTLEE
DGMNVEGEELMPSLQEALSTDILNDMESVLAATKIDKETFLTWL PMRMRKLPDSFFRQP

rs:XP_006010249 [XP_006010249] PREDICTED: protein **FAM181**A [Latimeria chalumnae].>tr:H2ZZY0_LATCH [H2ZZY0] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSLACP00000002951};
128..142
MASDSEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSRLAETSLK
NTVEDKSRGFILDRSELNNFKTLHENVSRASELDCEGASKSDHILSDQGKEVGRQDHVPMRKRQLPASFWEEPRP
TKTLLTPSHLHVEQQSVPPVNESVSDVKSESRSRTCAESAQDTLGLPVQLCREKEPVKFQMTSISSRMSLCGCCS
FQYHGQHVFQTHIALPQSGFPDVDLWRKNGVSNIEVQNICKDSINGQNVHRPVVLKPIPTKPAVPPPIFNVFGFL
PMRKRQLPASFWEEP

rs:XP_014366949 [XP_014366949] PREDICTED: transcriptional coactivator YAP1 [Papilio machaon]. 44..58
MALNSDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQSLLRVSDIDYICQLPIYSIHVRLVLIDRYRLISAAKSTSSSAASDPLGPLPDGWEQAATPEGEVYFINHAART
TSWFDPRIPQHLQRTPVAGAGAAGGGWANASLQACQQKLRLQSLQMERERLKQRQQEIMLQQELMGRQSSSIVSS
LASGGGAGAAGVQGAGAGGGAAADLDPFLSGLTEHQRQESADSGLGMAVNPSYSMPHTPEDFLAGMDDRMDCTSE
AGAIDPDISLGDNIDPTDDLVPSLQLSEFTNDILLDDVQSLINSTPSKTDNVLTWL PLRMRQLPKSFFNPP

rs:XP_022077855 [XP_022077855] protein **FAM181**A [Acanthochromis polyacanthus]. 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYRC
AKPAGTVHQSVAVSEKASSDAQDVENVGSAVEQVPMRKRQLPASFWEEPKLTQTKREHSYLGLRKSPAGTSEGNE
NEKRKRSYDEDAKATMSASSRRNSVDKETLKLDLSSHQCVSVCGCCPFQYHGHQVLHSHIVVPHPPLGLWSKAAG
TETERLEHPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_022044655 [XP_022044655] LOW QUALITY PROTEIN: protein **FAM181**B [Acanthochromis polyacanthus]. 246..260
MQVVGHKQRVKXPALPLPLLFDVLTSLARPPERSPRXSSEPVTSTLECLQELHEQHQDQVFIRGKKTCS
EEILGSEITVDATGVAAGLNTVMAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQGSPLTQPSPLQSKTLPKRDGVQ
ANLQSKSLAALFSPVKDIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMSLKDLERGNPEAADFFELLGPD
YSNMVSDQDLYQGMPFRVQPELGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGPAQPPAYCHSEAA
SGPIEDNALCTLAFPNFFTDCSIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_022044766 [XP_022044766] transcriptional coactivator YAP1 [Acanthochromis polyacanthus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDAPLPAGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQPPPPSSVPVQQQNLMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRITQSAPVKQGGQLPPSHHSAVMGGNNQLRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQ
DGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPTSMA
TQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_014482249 [XP_014482249] PREDICTED: transcriptional coactivator YAP1 [Dinoponera quadriceps]. 45..59
MALNQDVDQLTKNLVVRIDQNSESDLQALFDSVLKPDSSRPLQVPLRMRKLPDSFFNPPSTGSKSPSIS
HSRENSADSAFGTAAAAVAATPSNPGAGGSAPNSSANGSGGGAGAAAAAAAAAAAGLTVAHPRAHSSPASLQQTY
ASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAAN
VAAVAAAVESGKSNGNTLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPQSWLQQPT
GGGIQSNQSMQACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQTTTEPMDPFLSGINEQHARQESADSGLGL
GSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLLPSLQLSEDFSSDILDDVQSLINPNT
TKPENVLTWL PLRMRKLPDSFFNPP

rs:XP_014598034 [XP_014598034] PREDICTED: transcriptional coactivator YAP1-like [Polistes canadensis]. 47..61
MALNQEIDQLSNSSNLVVRIDQNSESDLQALFDTVLKPDSKHPLQVPLRMRNLPDSFFNPPSTGSRSPS
ISHSRENSADSAFGSSGASGAVTGTTGGRNAESSGGGGGNVVTGGANVSVVGGGAGGGAGAGGSVGVTNGNGGGG
PAGGGSPGGGAGGVVAVAAAAAAAGTNVNGGNTGGGGAGATVNNGGPPPGPAGVPAGTAASASAVNGPAPAAAAA
AAAAAAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAQQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWE
QARTTEGQIYFLNHLTRTTTWEDPRKTVAAQNVAQVAAQVESGKAAAAGNTLGPLPDGWEQARTPEGEIYFINHQ
TRTTSWFDPRIPTHLQRAPSSGAMLPQNWLQQPTAGGIPNNQSLQVCQQKLRLQSLQMERERLKQRQQEIMRQQE
LMLRQTTTEAAMDPFLSGISEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLS
DNIDSTDDLVPSLQLSEDFSSDILEDVQCFISPNTIKPGNVLTWL PLRMRNLPDSFFNPP

rs:XP_014640698 [XP_014640698] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF

NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014640699 [XP_014640699] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014640700 [XP_014640700] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_004427460 [XP_004427460] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014640701 [XP_014640701] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014640702 [XP_014640702] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS

SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014640703 [XP_014640703] PREDICTED: transcriptional coactivator
YAP1 isoform X7 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_004427461 [XP_004427461] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014640704 [XP_014640704] PREDICTED: transcriptional coactivator
YAP1 isoform X9 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014640705 [XP_014640705] PREDICTED: transcriptional coactivator
YAP1 isoform X10 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014640706 [XP_014640706] PREDICTED: transcriptional coactivator
YAP1 isoform X11 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_004427462 [XP_004427462] PREDICTED: transcriptional coactivator
YAP1 isoform X12 [Ceratotherium simum simum]. 85..99
MDPGQQPPPQSAPQGQGQAPAQPPQGQGPPSGSGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTTPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL

RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_004434215 [XP_004434215] PREDICTED: protein **FAM181**B [Ceratotherium simum simum]. 17..31
MLALPAGSPLETLSKVPLRARNLPPSFFTEPSRAGGGGCGPSGPVVSLGDLEKGAEAVEFFELLGPDYG
TGTEAGVLLAAEPLDVFPTGAAALRGPPELEPGLFEPPSGMVGSLLYPEPWSAPGCPSTKKPPLAAPRGGLTLNE
HLRPLYPAAADSPGGEDGPGLLASFAPFFSDCALPAPPPPHQVSYDYSAGYGRTAYSSLWRPDGVWEGAPGEEGA
HRD PLRARNLPPSFFTEP

rs:XP_004434284 [XP_004434284] PREDICTED: protein **FAM181**A isoform X1 [Ceratotherium simum simum]. 228..242
MLCIWRGAPDWPEGPPSSGDSVSIQPTRGLHHRFQPDARSSPAAPGLAQVCGREPAGPRWWGPGPGART
LGPLCALLWSSQTLQNLLSSWKAPCSGPLAMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQL
KRFSQKYSRLPRGLPGRGAEPHLRRGPEDRPGRLPLDSGQDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNP
EAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGAPYEGKKPCKGLEPMGPELAPVPTSPRAPAEKE
PLKMPGVTLVGRVNAWNYCPLQYHGQPIYPGPPAALPQSSVPSLGLWRKSPASPGELAHFCKDVDSPGQKVYRPV
VLKPIPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_014645997 [XP_014645997] PREDICTED: protein **FAM181**A isoform X2 [Ceratotherium simum simum].>rs:XP_014645998 [XP_014645998] PREDICTED: protein **FAM181**A isoform X2 [Ceratotherium simum simum]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLR
RGPEDRPGRLPLDSGQDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGAPYEGKKPCKGLEPMGPELAPVPTSPRAPAEKEPLKMPGVTLVGRVNAWNYCPLQYH
GQPIYPGPPAALPQSSVPSLGLWRKSPASPGELAHFCKDVDSPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014669587 [XP_014669587] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Priapulus caudatus]. 38..52
MEPKKGTQVIHVRGDSDSELEALFKVALSPDPKNHSLPMRNRKLPESFWKPPETGSRSCNHSRESSTDS
THLMRAPPPGLVSSHSRAQSSPASMQQSQLSTPQTPPHHSQHIRQHSEIPDHIPLPPGWEVATMPKTGQRYFIKN
KEQQIRLRDGTGMQYRLGSPRNSVFPKRSHIEKSTTWTDPRLKYYSNMQTGTTLEPLPGGWEQATTEAGETYYIN
HINRTTSWFDPRLQPSMHAQRAGGPGGPGHLPPQLQQQPASQIPTSVGGNLPHLSPQARQQNLRLQSLQMERERL
RQRQQEIFRQVGSTQKPQSAVHEPPACHNQEMMLRNHLGGEERSTPVSTTVTGVVDPFLGSGGEYHARQESADSG
LELGTNYSLPRTPEDFLGNVDEMDTSDGNQSQNPQQHSRVPPDFLDSMQGTNVDLGGLESTTAGTNMESDDLVPS
LDINSDLLGDVEAVLNNNKIDNLLTWL PMRNRKLPESFWKPP

rs:XP_014669593 [XP_014669593] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Priapulus caudatus]. 38..52
MEPKKGTQVIHVRGDSDSELEALFKVALSPDPKNHSLPMRNRKLPESFWKPPETGSRSCNHSRESSTDS
THLMRAPPPGLVSSHSRAQSSPASMQQSQLSTPQTPPHHSQHIRQHSEIPDHIPLPPGWEVATMPKTGQRYFIKN
KEQQIRLRDGTGMQYRLGSPRNSVFPKRSHIEKSTTWTDPRLKYYSNMQTGTTLEPLPGGWEQATTEAGETYYIN
HINRTTSWFDPRLQPSMHAQRAGGPGGPGHLPPQLQQQPASQIPTSVGGNLPHLSPQARQQNLRLQSLQMERERL
RQRQQEIFRQEMMLRNHLGGEERSTPVSTTVTGVVDPFLGSGGEYHARQESADSGLELGTNYSLPRTPEDFLGNV
DEMDTSDGNQSQNPQQHSRVPPDFLDSMQGTNVDLGGLESTTAGTNMESDDLVPSLDINSDLLGDVEAVLNNNKI
DNLLTWL PMRNRKLPESFWKPP

rs:XP_014669600 [XP_014669600] PREDICTED: transcriptional coactivator YAP1-like isoform X3 [Priapulus caudatus]. 38..52
MEPKKGTQVIHVRGDSDSELEALFKVALSPDPKNHSLPMRNRKLPESFWKPPETGSRSCNHSRESSTDS
THLMRAPPPGLVSSHSRAQSSPASMQQSQLSTPQTPPHHSQHIRQHSEIPDHIPLPPGWEVATMPKTGQRYFINH
IEKSTTWTDPRLKYYSNMQTGTTLEPLPGGWEQATTEAGETYYINHINRTTSWFDPRLQPSMHAQRAGGPGGPGH
LPPQLQQQPASQIPTSVGGNLPHLSPQARQQNLRLQSLQMERERLRQRQQEIFRQVGSTQKPQSAVHEPPACHNQ
EMMLRNHLGGEERSTPVSTTVTGVVDPFLGSGGEYHARQESADSGLELGTNYSLPRTPEDFLGNVDEMDTSDGNQ
SQNPQQHSRVPPDFLDSMQGTNVDLGGLESTTAGTNMESDDLVPSLDINSDLLGDVEAVLNNNKIDNLLTWL
PMRNRKLPESFWKPP

rs:XP_014665935 [XP_014665935] PREDICTED: atrophin-1-like [Priapulus caudatus]. 128..142
MHVATSLSPVGDAGDPVSEETVALLQFIDEVSVSMKTVLDRPTKPRKKVNHRKYLQKQLRRCGAVVHAV
VATPTEKPPDKIPSASVGVSSAGGSSSSSRSKLLDALFDPKTVHEKCCATRRRVGAKMPLRSRNLPASFFVEPRC
ADDDVGQQPTNATHPMPTTTTVGGERANGVVRWWQSSPDASACDVVGAPLGYGLTGLADEEANRECAPYFYGDGL
APNHHVGYGAPGVGHYFGQVALAAQQSAYTELHHHHHHQQQQQQQQQQQQQEEEQQMSNKIGIACGGAEYRGVAP
PARVSHLDTSAAAAAAAVALTLHAVDRHAVYDQPQQSSPHSSCSSPRYQVTSAAPHLADVTAYHRPTPDAMSPPS
HLADVTSYHQPTAMSAHLYPSLSLDGLHHEFPANQSTMPSMDSTERLRHYDGLAAVQPLPAFPDVFPTTQRPEQH
RRLMQTTM PLRSRNLPASFFVEP

rs:XP_022361307 [XP_022361307] protein **FAM181**A [Enhydra lutris kenyoni].>tr:A0A2Y9JJY7_ENHLU [A0A2Y9JJY7] SubName: Full=protein **FAM181**A {ECO:0000313|RefSeq:XP_022361307.1}; 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGTEPHLK
RGPEDQPGRLLLDPGHDSSPGVVGGCKEKALGNPYREECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYSLGLEGELGPREGSPYEGKKHCKGLEPLDPEMAPVPASPRAPAGKEPLKMSGVSLVGRVNAWGCCPFQYH
GQPIYAGPPGALPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_022369806 [XP_022369806] protein **FAM181**B [Enhydra lutris kenyoni].>tr:A0A2Y9K8P3_ENHLU [A0A2Y9K8P3] SubName: Full=protein **FAM181**B {ECO:0000313|RefSeq:XP_022369806.1}; 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPGAADTPAKRPLAAPGAQTVAVPPHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGDERAGGSVAARVAGLGGASAGGSGGDAAGSAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGSGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEPPPAMVGSLLYSESWSAPGCPPTKKPPLAAPRGGLTLNEPLRPLYPTAADSPGGEDAPGL
LASFAPFFSDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_022694835 [XP_022694835] transcriptional coactivator YAP1-A-like isoform X1 [Varroa jacobsoni].>rs:XP_022643709 [XP_022643709] transcriptional coactivator YAP1-A-like isoform X1 [Varroa destructor].
43..57
MATEGFLEQQGPNHIVRIRQDQNLDELFKVAIEGGATKTGQLPMRMRNLPPSFFQQPAEGATALSGQIA
KPVVNHSRAHSSPASLEQTYRSAPQQPTHARQQSYDLVDEDPLPPGWQMMRTSIGQRYYLNHETHTTTWEDPRKK
LNGQVRATQRATAPPPPHTTNPSVINAETLGPLPAGWEQRTTSDGEVYFLNHNNRTTSWFDPRIPTHLQKAEYMA
RQNATQGAASSSGDVQTMEASQNHTVPGLHSPLGSNHNLKDAGSTDSINAVCAATSSLSLQQQIQQLQMQRIQQ
LELERERMKLRQQEILRQPAFGLSTNEPNNNTVVVNPNQLGVNSSLTDAFLGGPHSRQESADSGLGLGPNFSLPP
EEFLNSIDSTTGTSSLTSTNNNNTPNSIAGMDDSSLDAMGGGVGVGGGGAVGGPEQMDSDDLVPSLNEMPDLLPD
MEALLSDNKDSVLTWL PMRMRNLPPSFFQQP

rs:XP_014836471 [XP_014836471] PREDICTED: protein **FAM181**B [Poecilia mexicana].>rs:XP_007572434 [XP_007572434] PREDICTED: protein **FAM181**B [Poecilia formosa]. 246..260
MQVVGHKQRVKFPGFPSLLLFDVLTSSVLPPERSPSSSSVPVTSSLDCLWKLHEQHQEQVFIRRTKSCF
EETFSSGITVDATGVAAGLDRVMAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQGSPVSQQGPLQSKTLQKREGGQ
ANLQSKSLAALFSPVKEIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPD
YSNMVNEQDIYQGVPLRGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGPCKKPSEGLRTGPPQPPVYSQAEDTSV
PLDDNGLCTLTFPNFFPDCSISQVTYDLNGGYNKTNFSCL PMRHRNLPPSFFTEP

rs:XP_014848256 [XP_014848256] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Poecilia mexicana].>rs:XP_014848266 [XP_014848266] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Poecilia mexicana].>rs:XP_007556451 [XP_007556451] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Poecilia formosa]. 46..60
MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPVIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETGPLPKGWEQAVTAEGEVYYIDHIKQETTWDDPRLAPKV

NPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQESNLNGAHSR
NESTDSGLSVSSLSRTSDHMLSSVDHMDTGIGDSSEPPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVL
SGPHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_014848272 [XP_014848272] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Poecilia mexicana].>rs:XP_007556460 [XP_007556460] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Poecilia formosa].>tr:A0A096MBE9_POEFO [A0A096MBE9] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSPFOP00000028740}; 46..60

MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPVIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETGPLPKGWEQAVTAEGEVYYIDHIKQETTWDDPRLAPKV
NPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQESNLNGAHSR
NESTDSGLSVSSLSRTSDHMLSSVDHMDTGDSSEPPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSG
PHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_014848279 [XP_014848279] PREDICTED: transcriptional coactivator YAP1-like isoform X3 [Poecilia mexicana].>rs:XP_007556469 [XP_007556469] PREDICTED: transcriptional coactivator YAP1-like isoform X3 [Poecilia formosa]. 46..60

MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPVIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETAPKVNPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAG
GSNQMPGGMDHDRSAQMLVPSVDIRIRALNQESNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGIGDS
SEPPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_014885914 [XP_014885914] PREDICTED: protein **FAM181**B [Poecilia latipinna].>tr:A0A3B3UHT5_9TELE [A0A3B3UHT5] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSPLAP00000012177}; 246..260

MQVVGHKQRVKFPGFPLLLLFDVLTSSVLPPERSPSSSSVPVTSSLDCLWKLHEQHQEQVFIRRTKSCF
EETFSSGITVDATGVAAGLDRVMAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQGSPVSQQGPLQSKTLQKREGGQ
ANLQSKSLAALFSPVKEIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPD
YSNMVNEQDIYQGVPLRGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGPCKKPSEGLRTGPPQPPVYSQAEDTSV
PLDDNGLCTLTFPNFFPDCSISQVTYDLNGGYNKTNFSCL PMRHRNLPPSFFTEP

rs:XP_014844608 [XP_014844608] PREDICTED: transcriptional coactivator YAP1-like [Poecilia mexicana]. 45..59

MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPASLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LNHNDKSTTWQDPRKALLQTSQPAPPSSVPVPPQNLMNPANGPLPEHWEQAITSEGEIYYINHEKRTTSWLDPRL
EPRYALNQQRMTQSAPGKQSGQLPPSTLGGVMAGNNQLRLQQIEKDRLRLQQHRPQVSHQFGLGAFISEGGDGRG
TFPFCVL PMRMRNLPDSFFKPP

rs:XP_014900478 [XP_014900478] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Poecilia latipinna].>rs:XP_014900479 [XP_014900479] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Poecilia latipinna]. 46..60

MDAHRGAPPAGQQIVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPIIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETGPLPKGWEQAVTAEGEVYYIDHIKQETTWDDPRLAPKV
NPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQESNLNGAHSR
NESTDSGLSVSSLSRTSDHMLSSVDHMDTGIGDSSEPPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVL
SGPHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_014900480 [XP_014900480] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Poecilia latipinna].>tr:A0A3B3U0I4_9TELE [A0A3B3U0I4] SubName: Full=Uncharacterized protein

{ECO:0000313|Ensembl:ENSPLAP00000006159}; 46..60
MDAHRGAPPAGQQIVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPIIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETGPLPKGWEQAVTAEGEVYYIDHIKQETTWDDPRLAPKV
NPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQESNLNGAHSR
NESTDSGLSVSSLSRTSDHMLSSVDHMDTGDSSEPPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSG
PHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_014900481 [XP_014900481] PREDICTED: transcriptional coactivator YAP1-like isoform X3 [Poecilia latipinna]. 46..60
MDAHRGAPPAGQQIVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPIIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETAPKVNPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAG
GSNQMPGGMDHDRSAQMLVPSVDIRIRALNQESNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGIGDS
SEPPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_018414906 [XP_018414906] PREDICTED: protein **FAM181**A [Nanorana parkeri]. 112..126
MASDNEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHSGKSVELRKG
LVERINLAARSKGLSEKVMDENAVGGACLRENSAEGGRPDQVPMRKRQLPPSFWEEPRPSTSLLEMPCPSKLDIL
YKDRTSVTGTSLSSFENKKLKNTAAQETSGPSGPDKEAGKVPSLTPLAGRVNVCSCCPLQYHGQQMLYHHSHGTL
PPDPFAALALWSKSAAVPTVEIQHLCKDSGQRIYRHVVFKPIPTKPAMPASIFNVFGYI
PMRKRQLPPSFWEEP

rs:XP_018421209 [XP_018421209] PREDICTED: protein **FAM181**B [Nanorana parkeri]. 157..171
MAVQAAIMNHHFMPLYFPGSHVGFEKSYHEGVEFLGAVESAGDYKESSKDLLTFINSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGMIVNGNTSQGSPKGQLASPSSTSPQSYHCKPPPKRDTTQTNLQSKSLAALFDN
TKEVRGERCKKVPLRNRNLPPSFFTEPANCSSGLLPNSIATLKEMEKGSQETMEYFDLLDSDYNSLISEQEILQG
ASVRIHQDITAEHSMYEPHHLLNGILYSDPWNPCNLIKKSPVGTCGASPNENFKCLPMPGTVFTSHGDSSLPTGV
EDNCSTLTSFTPCYSECSLPQMFYDCSSGYNRIGYPVL PLRNRNLPPSFFTEP

rs:XP_023272958 [XP_023272958] protein **FAM181**A [Seriola lalandi dorsalis].>rs:XP_022606209 [XP_022606209] protein **FAM181**A [Seriola dumerili]. 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRPAEYGC
GRPVGTGHQSVKVAEKASSDAQDVENVGSAVEQVPMRKRQLPASFWEEPKLTQTKREHSHLALKRSPASTSEGGE
NEKRKRNYGNDAKATLSASSRRSSADKETLKLDLTSHHCVSVCGCCPFQYHGHQVLHSHIVVPHPPVGLWGKTAG
TESERPEHPYGQKIHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_023277281 [XP_023277281] transcriptional coactivator YAP1-like isoform X1 [Seriola lalandi dorsalis]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQATDVAAPQIIPDDVPLPHGWEMAKTPAGQRYFLNHLDKTTTWH
DPRLSQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQNINPETGPLPEGWEQAVTADGEVYYIDHINKTTAWVAPR
LAQKMNPGILGLALQQRQEKERLRCKGLPPQITPQEAGGRNQMTGGMDHDRNAPTLVPSLDVRIRSSNHEPTLNG
AHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGDNSSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDM
ETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_023277282 [XP_023277282] transcriptional coactivator YAP1-like isoform X2 [Seriola lalandi dorsalis].>rs:XP_022618503 [XP_022618503] transcriptional coactivator YAP1-like isoform X2 [Seriola dumerili].
46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQATDVAAPQIIPDDVPLPHGWEMAKTPAGQRYFLNHLDKTTTWH
DPRLSQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQNINPETAQKMNPGILGLALQQRQEKERLRCKGLPPQITP
QEAGGRNQMTGGMDHDRNAPTLVPSLDVRIRSSNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTG
DSGDNSSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_014214486 [XP_014214486] transcriptional coactivator yorkie isoform
X1 [Copidosoma floridanum]. 49..63
MALNQDVGDTGSANKRNLEVRIDQNSESDLQALFDSVLKPDKNRPLQVPLRMRNLPDSFFNPPSTGSKS
PSISHSRENSADSAFGAGVLGGVNPAAVASGIVSNGSGSNGTTSPGATGQIQSAGLTIAHPRAHSSPASLQQTYA
SAQQQSQHAPQPHSARHVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYYLNHITKTTTWEDPRKTAAAAS
VAAVAAAAVESSKANNSAAAVAAAAAAAANSALRPLPEGWEQARTPEGEIYFINHPARTTSWFDPRIPAHLQRAP
LSGAMLPQSWQLQQQQTATPGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQVSSQELVMRQSTTDAAM
DPFLSGINEQHARQESADSGLGLGTAYPLNGPHTPEDFLANIDDNMDGTTEGAPMDTPDLSIDTTDDLVTSLQLG
EDFSSDILEDVQSLINPNPTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_014214487 [XP_014214487] transcriptional coactivator yorkie isoform
X2 [Copidosoma floridanum]. 49..63
MALNQDVGDTGSANKRNLEVRIDQNSESDLQALFDSVLKPDKNRPLQVPLRMRNLPDSFFNPPSTGSKS
PSISHSRENSADSAFGAGVLGGVNPAAVASGIVSNGSGSNGTTSPGATGQIQSAGLTIAHPRAHSSPASLQQTYA
SAQQQSQHAPQPHSARHVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYYLNHITKTTTWEDPRKTAAAAS
VAAVAAAAVESSKANNSAAAVAAAAAAAANSALRPLPEGWEQARTPEGEIYFINHPARTTSWFDPRIPAHLQRAP
LSGAMLPQSWQLQQQQTATPGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQVSSQELVMRQSTTDAAM
DPFLSGINEQHARQESADSGLGLGTAYPLNGPHTPEDFLANIDDNMDGTTGAPMDTPDLSIDTTDDLVTSLQLGE
DFSSDILEDVQSLINPNPTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_014214488 [XP_014214488] transcriptional coactivator yorkie isoform
X3 [Copidosoma floridanum]. 49..63
MALNQDVGDTGSANKRNLEVRIDQNSESDLQALFDSVLKPDKNRPLQVPLRMRNLPDSFFNPPSTGSKS
PSISHSRENSADSAFGAGVLGGVNPAAVASGIVSNGSGSNGTTSPGATGQIQSAGLTIAHPRAHSSPASLQQTYA
SAQQQSQHAPQPHSARHVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYYLNHITKTTTWEDPRKTAAAAS
VAAVAAAAVESSKANNSAAAVAAAAAAAANSALRPLPEGWEQARTPEGEIYFINHPARTTSWFDPRIPAHLQRAP
LSGAMLPQSWQLQQQQTATPGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQQELVMRQSTTDAAMDPF
LSGINEQHARQESADSGLGLGTAYPLNGPHTPEDFLANIDDNMDGTTEGAPMDTPDLSIDTTDDLVTSLQLGEDF
SSDILEDVQSLINPNPTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_014214489 [XP_014214489] transcriptional coactivator yorkie isoform
X4 [Copidosoma floridanum]. 49..63
MALNQDVGDTGSANKRNLEVRIDQNSESDLQALFDSVLKPDKNRPLQVPLRMRNLPDSFFNPPSTGSKS
PSISHSRENSADSAFGAGVLGGVNPAAVASGIVSNGSGSNGTTSPGATGQIQSAGLTIAHPRAHSSPASLQQTYA
SAQQQSQHAPQPHSARHVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYYLNHITKTTTWEDPRKTAAAAS
VAAVAAAAVESSKANNSAAAVAAAAAAAANSALRPLPEGWEQARTPEGEIYFINHPARTTSWFDPRIPAHLQRAP
LSGAMLPQSWQLQQQQTATPGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQSTTDAAMDPFLSGINEQ
HARQESADSGLGLGTAYPLNGPHTPEDFLANIDDNMDGTTEGAPMDTPDLSIDTTDDLVTSLQLGEDFSSDILED
VQSLINPNPTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_003780911 [XP_003780911] protein **FAM181**B [Otolemur
garnettii].>tr:H0XWY9_OTOGA [H0XWY9] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSOGAP00000020632};
217..231
MAVQAALLSAHPFVPFGFGGPPDGLGGAFGALDKGCCFEDDETAAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAAPGPPSPGAADAPAKRPLAVPGAPTVTVPIHGK
AAPRREASQAAAAANLQSRSLAALFDSLRHIPGAAEPAGGEAAGLRGAGAGGAAGDGIGSAGAAAVPGARKVPLR
ARNLPPSFFTEPSRAGGGGCSLSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPTGAAVLR
GPPELEPGFFEPPPAVVGNVLYPEPWSVAGCPATKKPSLTTPRGCLTLNEPLRPVYPGVADSPGGEDGPGHLASF
VPFFPDCALPPPPPHQVSYDYSAGYSRSAYSSLWRPDGVWEGPPGEEGAPRD PLRARNLPPSFFTEP

rs:XP_023367100 [XP_023367100] transcriptional coactivator YAP1 isoform
X1 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF

PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012658817 [XP_012658817] transcriptional coactivator YAP1 isoform X2 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGG
SNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023367110 [XP_023367110] transcriptional coactivator YAP1 isoform X3 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_003780840 [XP_003780840] transcriptional coactivator YAP1 isoform X4 [Otolemur garnettii].>tr:H0WLN6_OTOGA [H0WLN6] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSOGAP00000002584}; 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGG
SNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQ
ELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEA
IPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023367125 [XP_023367125] transcriptional coactivator YAP1 isoform X5 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGD
GMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_003780841 [XP_003780841] transcriptional coactivator YAP1 isoform X6 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGG
SNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNS
GTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGM
NIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012658838 [XP_012658838] transcriptional coactivator YAP1 isoform X7 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV

MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMR
NINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSS
YSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSD
ILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_003780842 [XP_003780842] transcriptional coactivator YAP1 isoform
X8 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINP
STANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVP
RTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILND
MESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012658847 [XP_012658847] transcriptional coactivator YAP1 isoform
X9 [Otolemur garnettii]. 82..96
MDPGQQPPPQPAPPGQGQPPAQTPQGQGQPSGPGQPAPQAAPPAPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATSAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
SMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQ
LPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTG
DTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFL
TWL PMRLRKLPDSFFKPP

rs:XP_012658909 [XP_012658909] protein **FAM181**A [Otolemur
garnettii].>rs:XP_012658910 [XP_012658910] protein **FAM181**A [Otolemur
garnettii].>rs:XP_012658911 [XP_012658911] protein **FAM181**A [Otolemur
garnettii]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLK
RGPEDRPGRLLLDPGPESSPGGGGGYKEKALGNPYSEECLSKEQVLQGQSPEAARPGQVPMRKRQLPASFWEEPR
PTHSYSMGLEGGLGPREGPPYEGKKNCKGLESLGPEAAPVPMSPRALAEKEPLKMPGVSLVGRSSAWSCCPLQYH
GQPIYPGLSGTLPQSPIPSLGLWRKSPAFPGELAHFCKEVDGLGQVYRPVVLKPIPTKPAMAPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_002049990 [XP_002049990] uncharacterized protein Dvir_GJ20440,
isoform C [Drosophila virilis].>tr:B4LP14_DROVI [B4LP14] SubName:
Full=Uncharacterized protein, isoform C {ECO:0000313|EMBL:EDW61183.2};
61..75
MSLSNKSNISEKEIDDEDMLSPTKLSTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEIQPSLSQNQPSHSRLTIHHFRARSSPASLQQNYNVRSRNES
AANSNQGPAYPDNNVDFASSTANNIDLDVINTCMGQGPETPLSTQTIHKKQRSYDVVSPIQLQSQLGALPPGWEQ
AKTNDGQIYYLNHTTKTTQWEDPRIQFRQQQQRAMSDRKPADVIQTSKQASAPSISTHIGPLPDGWEQAVTESGD
IYFINHIDRTTSWNDPRIQSGLNVLDCPDNLVSSLQIGDNICSNIFNDTQTVINTPSSHKPDDLEWYKIN
PFRMRKLPNSFFNPP

rs:XP_018650022 [XP_018650022] hypothetical protein Smp_014840
[Schistosoma mansoni].>tr:G4VBX4_SCHMA [G4VBX4] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:CCD77398.1};>gp:HE601625_457
[HE601625] hypothetical protein [Schistosoma mansoni]38..52
MEGYDSRKPPSVRVTVLEDPNSSLQELFNPASQRQQVPLHQRNLPKSFFVPPGDVNDNSRLSKLNSVNC
NERNSTDFVVFHSKANSSPACLDAALRTSISANVPNHSHQKSLDVASKYKTDFSPDFAFSGSCGPGFFQGQRNSQ
QTALLYGPTMTFAISELPVGYDMAINESNQVYFLNHQTQETTWFDPRIPEKFQKWGMTPEELEQVHLRYAKQFLC
TTPSSNLNVCVQQMPYFAGTGIHYVDTYQIQSFSVWLT PLHQRNLPKSFFVPP

rs:XP_023695198 [XP_023695198] protein **FAM181**B [Paramormyrops
kingsleyae].>tr:A0A3B3QIA9_9TELE [A0A3B3QIA9] SubName: Full=Uncharacterized

protein {ECO:0000313|Ensembl:ENSPKIP00000005554}; 156..170
MAVQAPIVTSQFMNFCFLGSGMEYDAEKPFDGSLLGEVACEGDFRETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIIGSGGNLAQDQGKRQGSPTSHAGNIPGKPVARRDGIQANLQSKSLAALFEPT
KDIRGEKTRKPPLRQRNLPPSFFTEPAICPRVTSTSGMTLKDLERAGPEASEFFELLGPDYSDMLVEQDIPQGMP
MRVQQEALSGQDSYEPHHLSEGLLYAEPWGGCTGPSKKAAPCSLGENMRTIQAQPPLYCQLDSTVSLPVEENTLC
ALAFPNLFTDYSLPHATYDFASGYNRAAFPSL PLRQRNLPPSFFTEP

rs:XP_023656308 [XP_023656308] transcriptional coactivator YAP1-like [Paramormyrops kingsleyae].>rs:XP_023656309 [XP_023656309] transcriptional coactivator YAP1-like [Paramormyrops kingsleyae].>tr:A0A3B3T2R5_9TELE [A0A3B3T2R5] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSPKIP00000037402};45..59
MDPGQHNPPVGHQIVHVRGDSETDLEALFNAVMNPKNASVPPTLPMRMRKLPESFFQQPDPKSHSRQVS
TDAGTSGALTPQHIRAHSSPASLQLGSLSPAALAGTAPPASSSQHHRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHLDKTTTWQDPRKAMLPINQAAPLPVVSSATGPLPEGWEQAITPEGEIYYINHKNKSTSWLDPRLDSRIVLSS
QRVSQSTPEKLTSKSQSSGMSQVRIQQMQMKERLRHEHQELLRQAQTQEPSALRNQNHLAAGLEQDGSAPNAGSS
SGVSQDARTMTTNGSDPFLNSGTYHSRDESTDSGLSVSSYSVPRTPDDLLNSVEEMETGDSAAVTPTATQHSVFP
DYLDTIPGTSVDFGTLESESMAMESEELMPSLQEALNSDILSDMESVLAAAKCDKESFLTWL
PMRMRKLPESFFQQP

rs:XP_023658183 [XP_023658183] protein **FAM181**A [Paramormyrops kingsleyae].>rs:XP_023658184 [XP_023658184] protein **FAM181**A [Paramormyrops kingsleyae]. 128..142
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCSRMPSRCHAYRAGECG
VPKTLEDKSAVFAFEPANRNLQLSRLKDRSGSEVRSEDNSGLNAKPKAERDPHRQDQVPMRKRQLPASFWEEPSS
SRSKRDAFPVSWRKSPGDAGISGPSAPEEEKKKKSSDERKAHLILSSEQIAAEKEPLMLDITPGSVNVCGCCPFQ
YHGHHVFQGHIVLPHSSFSEVGLWGNTTVVHAETSDIQNGQKSQTHVVVKPIPTKPSVPSPIFSVFGFI
PMRKRQLPASFWEEP

rs:XP_023662914 [XP_023662914] transcriptional coactivator YAP1-like isoform X1 [Paramormyrops kingsleyae].>tr:A0A3B3SY94_9TELE [A0A3B3SY94] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPKIP00000035218};45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGSLTPQHVRAHSSPASLQLGTVSPSSLAGLAPPGASPQHLRQSSFEIPDDVPLPPGWEMAKTSSGQRYF
LNHIDQSTTWQDPRKAMMQMNQTSPNSPVSVQQNIMSSSSGTLPEGWEQAVTPEGEIYYINHKNKTTSWLDPRLD
SRYSLNQQRMSQSAPGKPPQAVPASPQGGGSQLRLQQLQMEKERLRLKQQELLRQRPQELTLRTQLPSSLEQEGG
TQSSISPSMAQDGRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDALGPASMAT
QPSRFPDYLDTIPGTNVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_023662915 [XP_023662915] transcriptional coactivator YAP1-like isoform X2 [Paramormyrops kingsleyae].>tr:A0A3B3SWU8_9TELE [A0A3B3SWU8] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPKIP00000035232};45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGSLTPQHVRAHSSPASLQLGTVSPSSLAGLAPPGASPQHLRQSSFEIPDDVPLPPGWEMAKTSSGQRYF
LNHIDQSTTWQDPRKAMMQMNQTSPNSPVSVQQNIMSSSSGLNQQRMSQSAPGKPPQAVPASPQGGGSQLRLQQL
QMEKERLRLKQQELLRQRPQELTLRTQLPSSLEQEGGTQSSISPSMAQDGRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDALGPASMATQPSRFPDYLDTIPGTNVDLGTLEGESMAVEGEELMPSL
QEALSSDILNDMESVLAATKIDKESFLTWL PMRMRKLPDSFFKPP

rs:XP_017199173 [XP_017199173] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Oryctolagus cuniculus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQ

NPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQ
QNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017199176 [XP_017199176] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Oryctolagus cuniculus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017199180 [XP_017199180] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Oryctolagus cuniculus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017199183 [XP_017199183] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Oryctolagus cuniculus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017199187 [XP_017199187] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Oryctolagus cuniculus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMT
TNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQNRFPDYLEAIPGTNV
DLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017199191 [XP_017199191] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Oryctolagus cuniculus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017199194 [XP_017199194] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Oryctolagus cuniculus]. 85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017199199 [XP_017199199] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Oryctolagus cuniculus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPQASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008261583 [XP_008261583] PREDICTED: LOW QUALITY PROTEIN: protein
FAM181B [Oryctolagus cuniculus]. 218..232
MAVQAALLSTHPFVAFGFGGSPDGLGGGFGALDKGCCFEDDETGXPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLRSRXXXXXXXXGAAPPGPPSPPAADTPAKRPPGAPTVAAPAHGKAAP
RREASQAAAAASLQSRSLAALFDSLRHVPGAAEPAGSAVASPAAGLSGAGAVGAGEDATGPVGGTVAPGARKVPL
RARNLPPSFFTEPSRAGGGGCGPSAPGVSLGDLEKGAEAAEFFELLGPDYGSAGTEAGVLLAAEPLDVFPGGGAV
LRATPELEPGLFEPPPAMVGSLLYSETWSAPGCPQSKKPALAAPRGGLTLNEPLRLLYPAAADSAGGEDGPGHLA
SFAPFFPDCALPPPPPSHQVSYDYSAGYGRSTYSSLWRPDGVWEGAPGEEGARRD PLRARNLPPSFFTEP

rs:XP_013416853 [XP_013416853] uncharacterized protein LOC106178273
[Lingula anatina].>tr:A0A1S3K2I7_LINUN [A0A1S3K2I7] SubName:
Full=uncharacterized protein LOC106178273
{ECO:0000313|RefSeq:XP_013416853.1}; 160..174
MEDYRSHYNISKSTNMSSVPKTTGGKLGPSTYAVVPNRPPSGGKRGPSGPLANSSDEEDAGDAVNISVS
STSTTTSSPSTPSPNASSDYENVASPGGSSTASGPIYVRPPGFAHHGQEILKTPASKPSWRKKRAILAMKEGLKK
REPTPPRPKSKKDPLPMRMRALPQSFFQQPNVPHNVSPGAAYPVLPPLMNRDSDVTEVRPVTPPEEKEKKNKAPK
PPERKITLGNPDLLFKLFEGYGDEKKKGGTSIIKRGRPKKVHSTQGKAFVTGEDPFIMDAVAEKLFPQLSLESSK
QQGYSGLGHSSQLHVVTLREGDKSVMLPALSREQNYSQMLSELVSHI PMRMRALPQSFFQQP

rs:XP_024110882 [XP_024110882] transcriptional coactivator YAP1 isoform
X1 [Pongo abelii].>rs:XP_016777348 [XP_016777348] transcriptional
coactivator YAP1 isoform X1 [Pan troglodytes].>rs:XP_005271435
[XP_005271435] transcriptional coactivator YAP1 isoform X1 [Homo sapiens].
85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_024110883 [XP_024110883] transcriptional coactivator YAP1 isoform
X2 [Pongo abelii].>rs:XP_016777349 [XP_016777349] transcriptional
coactivator YAP1 isoform X2 [Pan troglodytes].>rs:NP_001269030
[NP_001269030] transcriptional coactivator YAP1 isoform 9 [Homo sapiens].
85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP

VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_024110884 [XP_024110884] transcriptional coactivator YAP1 isoform X3 [Pongo abelii].>rs:XP_016777350 [XP_016777350] transcriptional coactivator YAP1 isoform X3 [Pan troglodytes].>rs:XP_005271437 [XP_005271437] transcriptional coactivator YAP1 isoform X2 [Homo sapiens].
85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_024110886 [XP_024110886] transcriptional coactivator YAP1 isoform X5 [Pongo abelii].>rs:XP_016777351 [XP_016777351] transcriptional coactivator YAP1 isoform X5 [Pan troglodytes].>rs:XP_005271438 [XP_005271438] transcriptional coactivator YAP1 isoform X3 [Homo sapiens].
85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024110887 [XP_024110887] transcriptional coactivator YAP1 isoform X6 [Pongo abelii].>rs:XP_016777352 [XP_016777352] transcriptional coactivator YAP1 isoform X6 [Pan troglodytes].>rs:NP_001269029 [NP_001269029] transcriptional coactivator YAP1 isoform 8 [Homo sapiens].
85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024110888 [XP_024110888] transcriptional coactivator YAP1 isoform X7 [Pongo abelii].>rs:XP_016777353 [XP_016777353] transcriptional coactivator YAP1 isoform X7 [Pan troglodytes].>rs:XP_005271440 [XP_005271440] transcriptional coactivator YAP1 isoform X4 [Homo sapiens].
85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024110889 [XP_024110889] transcriptional coactivator YAP1 isoform X8 [Pongo abelii].>rs:XP_016777354 [XP_016777354] transcriptional coactivator YAP1 isoform X8 [Pan troglodytes].>rs:NP_001181973 [NP_001181973] transcriptional coactivator YAP1 isoform 3 [Homo sapiens]. 85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024111254 [XP_024111254] protein **FAM181**B [Pongo abelii].>tr:A0A2J8V0L8_PONAB [A0A2J8V0L8] SubName: Full=**FAM181**B isoform 1 {ECO:0000313|EMBL:PNJ51058.1}; 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPAAGLGGAGTGGAGGDVAGPAGATAIPGARK
VPLRARNLPPSFFTEPSRAGGGGCVPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_024087613 [XP_024087613] protein **FAM181**A isoform X1 [Pongo abelii]. 178..192
MQPTQSTEGLGRKGQSTAKQVSSVPFLGAAGHQQSLPSSWKASCSGPLVMASDSDVKMLLNFVNLASSD
IKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDLGPDSSPGGGGGC
KEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKN
CKGLEPLGPETTPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGTLPQSPVPSLGLWRKS
PAFPGELTHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_003778403 [XP_003778403] protein **FAM181**A isoform X2 [Pongo abelii].>rs:XP_003778404 [XP_003778404] protein **FAM181**A isoform X2 [Pongo abelii].>rs:XP_003778405 [XP_003778405] protein **FAM181**A isoform X2 [Pongo abelii]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGTLPQSPVPSLGLWRKSPAFPGELTHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_013411604 [XP_013411604] uncharacterized protein LOC106174544 [Lingula anatina].>tr:A0A1S3JNQ1_LINUN [A0A1S3JNQ1] SubName: Full=uncharacterized protein LOC106174544 {ECO:0000313|RefSeq:XP_013411604.1}; 120..134
MATADRSGGGETGQQLLSFVDIASSNIKLALDKCGKSKRKVNHRKYLQKQLKKSNGSYDTETAVIHGGR
VSKPTRKETSYFGIQHKSLQALFDPRTLHKQCCADPQAKLVKGSCRSNRVPLKNRKLPPSFFTEPAKLLEQQSYT
AYYIENALQNYSYQSQLETVANGVYTCQQTTLDPPYFTHEDIHDIIGGQDGLARPSSCGSSQHSSSGSPQRETSS
TSSPPISPLLPISSRTDYRLQSWDQPYASSYNGTIFMDPNYNEPYGYQQELSGAFSNMGQVGNAMATLRSPHDGL
TSMENVYALPNFSQTFSSYVTGADVSSVDNPFVAPCMLNSYTCL PLKNRKLPPSFFTEP

rs:XP_023934073 [XP_023934073] transcriptional coactivator YAP1 [Bicyclus anynana]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGSAPVSHSRAHSSPASLQQTYAAGQPAQQPPLPHQHAKQRSYDVGTHLPDDLGPLPSGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQAMAGGVQHQSAEALLTQTVPSTPQIPTPTPAAKSTSTNTATDP
LGPLPEGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPTSGGAAGGGWANASIQACQQKLRLQSLQLERE
RLKQRQQEIRLQQSLMARQSSSIVSSLASSATTELPLDPFLSGLTDHQRQESADSGLGMAVTQSYSMPHTPEDFL

AGMDDRMDCTSEAGANLDTADITLGDTDDLVPSLQLGEFTNDILLDDVQSLINSTPNKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_015244037 [XP_015244037] PREDICTED: transcriptional coactivator YAP1 [Cyprinodon variegatus]. 45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKNSNAPASLPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDEMPLPAGWEMAKTPSGQRYF
LNHIDKTTTWQDPRKSLLQLNQPAPPSTVPVQPPNLLNPANGPLPEGWEQAMTPEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRITQSAPVKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQQHRPQELALRNQLPTSMDQDGSTN
PVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSIATQPNR
FPDYLDAIPGTDVDLGTLESESMAVESEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_015246868 [XP_015246868] PREDICTED: protein **FAM181**B [Cyprinodon variegatus]. 155..169
MAVQTAIMNPQFMSFCFPDSVMEYDMEKSLDCSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISPGNTSEAPVKRQSSPVNQQGPLQSKTLQKREGGQANLQSKSLAALFSPVK
EIRGEKAKKPPLRHRNLPPSFFTEPANCSRVSSTSGMMLKDLERGNPEAAEFFELLGPDYSNMVNEQDVYQAMPL
RVQQDLGGLDPASYDHLVSGLLYPDPWTNCSGPCKKPGEGLRTGPPQLPGYGQAEDPSGPIDDSGLCTLAFPSFF
PDCSIPQVTYDLNGGYNKTNYPCL PLRHRNLPPSFFTEP

rs:XP_015251719 [XP_015251719] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Cyprinodon variegatus].>rs:XP_015251720 [XP_015251720] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Cyprinodon variegatus]. 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFSAVMNPSKAARQPHSVPMRMRKLPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPVNSLSAQVDADAAATPLIPDDVPLPDGWEMAKTSTGQRYFINHVHKTTTW
QDPRLSQLQSAAAQHQIACTPIHAHSFSNPAPTTQPKNVIPETGPLPEGWEQAVTADGEMYYIDHINKTTTWDDP
RLAQKANPTMLSLAMQQRQEKLRQKQGILPQFAPQEAGSSNQMPGGMDHDRSAQMLVPSVDVRIRALNQEPNLNG
AHSRNESTDSGLSVSSLPRTSDHMLGSVDHMDTGDSSDPPSMSLQEPMPVLPINEELMPGIPDGLTSDILMDMDT
VLSGPHMDRDSLLTWL PMRMRKLPDSFFKPP

rs:XP_015251722 [XP_015251722] PREDICTED: transcriptional coactivator YAP1-like isoform X2 [Cyprinodon variegatus]. 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFSAVMNPSKAARQPHSVPMRMRKLPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPVNSLSAQVDADAAATPLIPDDVPLPDGWEMAKTSTGQRYFINHVHKTTTW
QDPRLSQLQSAAAQHQIACTPIHAHSFSNPAPTTQPKNVIPETAQKANPTMLSLAMQQRQEKLRQKQGILPQFAP
QEAGSSNQMPGGMDHDRSAQMLVPSVDVRIRALNQEPNLNGAHSRNESTDSGLSVSSLPRTSDHMLGSVDHMDTG
DSSDPPSMSLQEPMPVLPINEELMPGIPDGLTSDILMDMDTVLSGPHMDRDSLLTWL PMRMRKLPDSFFKPP

rs:XP_015252583 [XP_015252583] PREDICTED: protein **FAM181**A [Cyprinodon variegatus]. 102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRCQTLRSADYRC
TRGAGAERQMGKVIDKSSSDAQQSVGGVMEQVPMRKRQLPASFWEEPRLIKAKRDISCMDLRGSSTGSDGSEDEK
RKRSQDDAPKTPKTTISSSKRGSADKEVLKLDLTSHHSVCFCGCWPFQFHENQVLHSQLVVPHPPMGLWSKPAGP
ELERSEHPYGQKLHRHVVVKPIPTKPTAHSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_015279990 [XP_015279990] PREDICTED: transcriptional coactivator YAP1 [Gekko japonicus]. 85..99
MDPAGQPQPPSAASQQAASQQPPSGQPPQAAGAPPQPQQQPGAVSGAPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGTLTPQHVRAHSSPASLQLGTVSPGTLPP
TGVISGPSPSSQHLRQPSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQLNVTAPTSPPLQ
QNIINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMSQRISQSAPMKQPPPLAPQSPPGGVLG
SGSSNQQQQMRLQQLQVEKERLRLKHQELLRQALRNINPSTANSPKRQFQLLYGGGRIELHGQMLLHCANISQDL
VLCLELFKEYRFSGTNLLDKQVVHARGQIVAIDLEFHNFSAMYSS PMRLRKLPDSFFKPP

rs:XP_015263365 [XP_015263365] PREDICTED: protein **FAM181**B [Gekko japonicus]. 228..242
MAVQAATLHAHHPFAVPFCFPAAAGLADFGEAEKGYDDSGALLLAGGGGGGGSDPGDREATRDLLSFID

SASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGMIGAGGGGGGGAPATPGLQDAPTISANSGVHSNNSNHSQP
ANKRTSPTTGAPPASASPPAGGAAHCKAPAKREGGTLQSESLAALFDSLQQPSGFAPERPPGAAGPAGGREGGSG
PSAGGKKVPLRKRNLPPSFFTEPAAARSTAPPSPGLKDPAGPEELFDLLAASPEFGNLLPEQPPPPLFQTGGRLQ
TSDLGGETPLYESLPPLPHLMYPEPPLRPLPALYAGASDPAGAESSPTAHLPSFAPFFPDCPLPPPPAMPYDYPA
GYSRGGALF PLRKRNLPPSFFTEP

rs:XP_015281466 [XP_015281466] PREDICTED: protein **FAM181**A [Gekko
japonicus]. 140..154
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARLPRGHHHHHHLPPP
PPPPHARERRAAEERARGPSADAAETPVGQSSGGALLSHNGEPKACNKAAEPGDERQQSACEATSRPDQVPMRKR
QLPASFWEEPRPAPGPLGVSAGAFPTAAPPPASSSSKDLPLYEGKKSKKAPDGGQAAAPDSPSSGPDAEATVKVL
SAWSCCPFQCHGPQASPGLYPSALSAALPPAAPFPALGLWRKSAASSTEGEGFCKPSGGGAGQKVHRPVVWKPIP
TKPAAPPPIFSVFGYI PMRKRQLPASFWEEP

rs:XP_015519255 [XP_015519255] PREDICTED: transcriptional coactivator
yorkie [Neodiprion lecontei]. 45..59
MALNQDVDQLKSSLVVRIDQNSESDLQALFDSVLKPDAKRPLQVPLRMRNLPNSFFNPPSTGSKSPSIS
HSRENSADSAFGATGGGGGGGGGGGGGAAGGSTAPGSGCVSSGTTGAAGSCTTSAAGTPGSVVGSVAGVVVGASGA
GSNNGGLTVSHPRAHSSPASLQQTYASAQQSQQHIPQPHPRHHHHKQRSYDVISTVDDLGPLPPGWEQARTPEGQ
VYFLNHMTRTTTWEDPRKTAAAASVAAVAAAVESGTKNSSAATSSLGPLPDGWEQARTPEGEIYFINHQTRTTSW
FDPRIPTHLQRAPTSGAMLPQTWLQQPGAATIQSSQTIQACQRLHSLQLERERLKQRQQEIMRQQELMRQTTTEV
AMDPFLSGINEQHARQESADSGLGLGTAYSLPHTPEDFLANIDDNMDGRSEGAPMETPDLSTLSDNIDSTDDLVP
SLQLGEDFTSDILDDVQSLINPNTSKSENVLTWL PLRMRNLPNSFFNPP

rs:XP_006983846 [XP_006983846] PREDICTED: transcriptional coactivator
YAP1 [Peromyscus maniculatus bairdii]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSVVPGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPAPAS
PAVPQTLMNSASGPLPDGWEQAMTQDGDVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQG
GVLGGGNSNQQQQMQLQQLQMEKERLRLKQQELLRQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTQNAVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFP
DYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_006990968 [XP_006990968] PREDICTED: protein **FAM181**A [Peromyscus
maniculatus bairdii]. 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVTEPHLQ
RGPEERPGQLPLHPCPESSPGGGGGCKEKVLGTPFREECLSKEQSFGGLNPEAARPGQLPMRKRQLPASFWEEPR
PTLSYPMGLEVGLGPRETSLYENKKNCKGLESLGPETAPLPMSPRVLADMEPLKMPGVSLVGSLDAWSYCPFQYH
GQPIFPSLPGVLPQGPVPSLGLWRKSPASPVELAHFCKDVDSPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_006991949 [XP_006991949] PREDICTED: protein **FAM181**B [Peromyscus
maniculatus bairdii]. 218..232
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGAPAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPSAADAPAKRPPGAPGAPTVAAPAHCK
ATPRREATQAAAAASLQSRSLAALFDSLHQVPGGAEPAGGAVAVPVPGLGAASAAGDGAGTAGNSAASGTRKVPL
RARNLPPSFFTEPSRVGGCGCGPSGQGVSLGDLEKGAEAMEFFELLAPDFGAGTDSGALLAAEPLDAFPAGATVL
RGPLELESGPFEPPAMVGNLLYPEPWSAPTCPQTKKPPLVGVRCGVTLNEPVRFLYPTALDSPGGEDTPALTSFA
PFFPDCALPPPHQVSYDYSAGYSRAVYPSLWRPDGVWEGASGEDGAHPD PLRARNLPPSFFTEP

rs:XP_007664995 [XP_007664995] PREDICTED: protein **FAM181**B, partial
[Ornithorhynchus anatinus]. 142..156
FIDSASCNIKMALDKPGKSKRKVNHRKYLQKQIKRCTGMASTPGPSAPGPSSTPGSSTAASEVPPRRPP
AASPPAAASGTPAAQGRTPPPRREGGQAAAALQSRSLAALFDSLHPPRRGAPPAPAAAPRASAGSPGPAKKLPLR
HRNLPPSFFTEPTQARGLREPEKGGGEPAAEFFDLLGPDYGGAQLEPALFEGHPAVDVSYCGAASRGKM
PLRHRNLPPSFFTEP

rs:XP_007667539   [XP_007667539] PREDICTED: protein **FAM181**A
[Ornithorhynchus anatinus].>rs:XP_007667540 [XP_007667540] PREDICTED:
protein **FAM181**A [Ornithorhynchus anatinus].   125..139
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRNPRCHPGKTAEPHPK
KAAEEGRPRGAPADGVDHRRGCGEKASGKSETPEQSTQARALRDQSPGAARPDHVPMRKRQLPASFWEEPRPAQS
FPAGPDGLLAPGEVKKSKKDLEGAGPESASVAGAPRGEKESSKIPGAPLSSRANTWSCCPFQYHGQPVFQGPGAL
PQSPAPAPGLGPWRKSSAAPGDLMPFCKESSGATQKVYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_970492   [XP_970492] PREDICTED: transcriptional coactivator YAP1-A
isoform X1 [Tribolium castaneum].>tr:D6W803_TRICA [D6W803] SubName:
Full=Yorkie homolog-like Protein {ECO:0000313|EMBL:EFA11163.1}; 41..55
MALNQDEGKQVLRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFSSAASASGSSTAAAAAPAPLPSAHHRAHSSPASLQQTYAVGQAQATHHHIKQRSYDVASKVEDNTPLPTG
WEQARTPEGQLYYLNHITRTTTWEDPRKSLAAQAAAQQHQSAEQLLSSHQVSQAQAPNSTPPAKVSTDVDLGPLP
EGWEQAQTPEGEIYFINHQTRTTSWFDPRIPTHLQQRSPGTASVSGQSWPSGSLSQSSPAKQQQFRLQLLQFERD
RLKLRQQEIRMQQELMMRGSSNDLALDPFLNDHSRQESADSGLGLGTTYSMPHTPEDFFDCTEDLVPSLQLGEEF
PTDLGEEFPTVILDDDVQSLINPPTTKPDNVLIWL PWSMRKLPDSFFNPP

rs:XP_008200710   [XP_008200710] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Tribolium castaneum].   41..55
MALNQDEGKQVLRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFSSAASASGSSTAAAAAPAPLPSAHHRAHSSPASLQQTYAVGQAQATHHHIKQRSYDVASKVEDNTPLPTG
WEQARTPEGQLYYLNHITRTTTWEDPRKSLAAQAAAQQHQSAEQLLSSHQVSQAQAPNSTPPTHLQQRSPGTASV
SGQSWPSGSLSQSSPAKQQQFRLQLLQFERDRLKLRQQEIRMQQELMMRGSSNDLALDPFLNDHSRQESADSGLG
LGTTYSMPHTPEDFFDCTEDLVPSLQLGEEFPTDLGEEFPTVILDDDVQSLINPPTTKPDNVLIWL
PWSMRKLPDSFFNPP

rs:XP_025425738   [XP_025425738] transcriptional coactivator YAP1 [Sipha
flava].   73..87
MSGLQQQQQQQQQQQEQVTIKMEPSDPSSPATAVAAAINNNLVVRVDQDSETDLQALFDTVLKPDGKKP
LQLPLRMRQLPKSFFNPPSTGSKSSSISHSRENSGDSAFGTAPSIGQSCVAGGGPGPMHSRAHSSPASLQQTYGV
SAAKQQQQQHVKQRSYDVSSAIDELGPLPQGWEQARTPEGQIYFLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQ
LLSPGNDSGSSTNATSTPTNSPPHIHSTLQGTNKNVTLGPLPDGWEQAVTVDGETYFINHIARTTSWFDPRIPAH
LQRAPTSGAVLPSGSASWLLNGGSGLSQSLQVTQQKLRLHSLQMERERLKLRQQEIIRQQELMLHSGQTTNDLDP
FLSCSSSNVDHSRQESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDSQEMASLDVTD
DLVPSLQLGDEFSNDILDEVQSLIDPNNKPGSILTWL   PLRMRQLPKSFFNPP

rs:XP_015989479   [XP_015989479] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Rousettus aegyptiacus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_015989481   [XP_015989481] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Rousettus aegyptiacus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

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rs:XP_015989482   [XP_015989482] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Rousettus aegyptiacus]. 85..99
      MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_015989483   [XP_015989483] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Rousettus aegyptiacus]. 85..99
      MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_015989484   [XP_015989484] PREDICTED: transcriptional coactivator
YAP1 isoform X5 [Rousettus aegyptiacus]. 85..99
      MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL    PMRLRKLPDSFFKPP

rs:XP_015989485   [XP_015989485] PREDICTED: transcriptional coactivator
YAP1 isoform X6 [Rousettus aegyptiacus]. 85..99
      MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL     PMRLRKLPDSFFKPP

rs:XP_015989486   [XP_015989486] PREDICTED: transcriptional coactivator
YAP1 isoform X7 [Rousettus aegyptiacus]. 85..99
      MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL  PMRLRKLPDSFFKPP

rs:XP_015989487   [XP_015989487] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Rousettus aegyptiacus]. 85..99
      MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPP
VQQNMMNSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
```

LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_016000922 [XP_016000922] PREDICTED: protein **FAM181**A [Rousettus aegyptiacus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLHGRGAEPHLK
GGPEDRPGRPPLDSGPDAGPGGCGGCKEKALGNPYREVCLAKEQILQGQNPEVARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGGLGPRAGPPYEGKKHCKGLEPLGPEAARMPMSPRVPAEKEPLKMPGVSLVGRVNAWGCCPFQYH
GQPSYPGPPGALPPGPVPSLGLWRKSSVSPGELAHFCKDVDGLGQKVYRPVVLKPIPTKPALPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_016015776 [XP_016015776] PREDICTED: protein **FAM181**B [Rousettus aegyptiacus]. 221..235
MAVQAALLSTHPFVPFGFGGTPDGLGGAFGALDKGCCFEDDETGTPAAALLAGTEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSSLMGAAPPGPPSPGAVDTPAKRVLAAPSAQTAAVPAHGK
ATPRREASQAAAAASLQSRSLAALFDSLHHVPGGAELAGGSVVAPAAGLRGAGAAGAGGDAAGPAGGAALPGCRK
VPLRARNLPPSFFTEPSRAGGGSGCGPSGPGVSLGDLEKGAETVEFFELLGPDYGPGTETGVLLATEPLDVFPTG
AAVLRGPQELEPGLFEPPPATVGSLLYPEPWSALGCPPTKKPNLAAPRGGSTLNEPLRSLYPATADSPGGEDGTG
LLASFAPFFSDCALSPPPHQVSYDYSAGYGRTAFSGLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_011206098 [XP_011206098] PREDICTED: transcriptional coactivator yorkie [Bactrocera dorsalis].>tr:A0A034W9G2_BACDO [A0A034W9G2] SubName: Full=Protein yorkie {ECO:0000313|EMBL:JAC51349.1}; 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETNACIQDGIGPVFTTGAVPFPPSVNAGAAVRMEQGEQAVPKDAPNIQTFHMKQRSYDVVSTIQ
LQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKGKESVNLADNLGPLPEGW
EQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQM
DPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISESGSLNALSGIDCPDNLVSSLQLEDNICNEM
FSDVHSMLNASATKPDTLDWYKIN PFRMRQLPESFFKPP

rs:NP_001182697 [NP_001182697] transcriptional coactivator YAP1 [Xenopus tropicalis].>tr:E1CHM2_XENTR [E1CHM2] SubName: Full=Yes-associated protein 1 {ECO:0000313|EMBL:BAJ19431.1};>gp:AB551789_1 [AB551789] Yes-associated protein 1 [Xenopus tropicalis] 51..65
MEPGSQPSAPAQPPPAGHQIVHVRSDSETDLEALFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPEPKS
HSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPPGVVPGPAPAPNAQHLRQSSYEIPDDVPLPPGWE
MAKTPSGQRYFLNHMEQTTTWQDPRKAMLSQINLPAPTSPPVQQNIMTPTGPLPDGWEQALTPEGETYFINHKNK
TTSWLDPRLDPRFAMNQQRLSQSAPVKSPPALPPQSPQSGVLGSGGNQQQMRLQQLQMEKERLRLKHQELLRQVR
PQELALRSQIPPMEQDGGTQNPVCSTGISQEMRTMTMNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFL
NSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMESVLAA
TKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_009100036 [XP_009100036] PREDICTED: protein **FAM181**A [Serinus canaria]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGAEDRARGPLPEAPEPSPHGGAAADKVMHTAEAEESLTGERVLQEQKPEAARPDQVPMRKRQLPASFWEEPRPA
QSLAARAFAASPEGLQAPRDPPPYEGKKSKRSPDAAGPESPPDTAPLAGEKDPAGALSGRVGSWTCCPFPCPGPG
VYQPPGALPPSPFPGLGLWRKSVATLPAEVPPFCKEADGPGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_024831476 [XP_024831476] transcriptional coactivator YAP1 isoform X1 [Bos taurus].>rs:XP_027419731 [XP_027419731] transcriptional coactivator YAP1 isoform X2 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS

SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_024831477 [XP_024831477] transcriptional coactivator YAP1 isoform
X2 [Bos taurus].>rs:XP_027419733 [XP_027419733] transcriptional coactivator
YAP1 isoform X4 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_024831478 [XP_024831478] transcriptional coactivator YAP1 isoform
X3 [Bos taurus].>rs:XP_027419736 [XP_027419736] transcriptional coactivator
YAP1 isoform X6 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024831479 [XP_024831479] transcriptional coactivator YAP1 isoform
X4 [Bos taurus].>rs:XP_027419738 [XP_027419738] transcriptional coactivator
YAP1 isoform X8 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGD
GMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024831480 [XP_024831480] transcriptional coactivator YAP1 isoform
X5 [Bos taurus].>rs:XP_027419739 [XP_027419739] transcriptional coactivator
YAP1 isoform X9 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQA
MRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSM
SSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALS
SDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024831481 [XP_024831481] transcriptional coactivator YAP1 isoform
X6 [Bos taurus].>rs:XP_027419740 [XP_027419740] transcriptional coactivator
YAP1 isoform X10 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNI
NPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYS
VPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDIL
NDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024831482 [XP_024831482] transcriptional coactivator YAP1 isoform
X7 [Bos taurus].>rs:XP_027419741 [XP_027419741] transcriptional coactivator
YAP1 isoform X11 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQE
LALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024831483 [XP_024831483] transcriptional coactivator YAP1 isoform
X8 [Bos taurus].>rs:XP_027419742 [XP_027419742] transcriptional coactivator
YAP1 isoform X12 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALR
SQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMD
TGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKES
FLTWL PMRLRKLPDSFFKPP

rs:XP_010815609 [XP_010815609] protein **FAM181**A isoform X1 [Bos
taurus].>rs:XP_027377395 [XP_027377395] protein **FAM181**A isoform X1 [Bos
indicus x Bos taurus]. 240..254
MWERGRRLLGMLCIWRGAPDWPEGPPAPGTRRPPFSPLEGGTTASSRTTELAGRAKPGPGLQHGGNLCR
ATLAGARAPALSVGSVLFPGAASCLENPASSWKARCSGALVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRS
VDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRPLPLESGHGSSPGGGGGCKEKALGNLDREES
LSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTP
VPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQYHGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKD
AEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_010815610 [XP_010815610] protein **FAM181**A isoform X2 [Bos
taurus].>rs:XP_027377396 [XP_027377396] protein **FAM181**A isoform X2 [Bos
indicus x Bos taurus]. 230..244
MVPMVTICDGKECGNGAAACLGCFVSGEALLIGLRAPQLRGPVVLHSAHSRAAQLPPAGPRSSPAAPSL
AQVGSVLFPGAASCLENPASSWKARCSGALVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQ
LKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRPLPLESGHGSSPGGGGGCKEKALGNLDREESLSKERTLHGP
DPGAARPGQVPMRKRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTPVPTSPRAPAE
KEPLKMPGVSLVGRVSAWSCCPFQYHGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYR
PVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_024837885 [XP_024837885] protein **FAM181**A isoform X3 [Bos taurus].
130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRPLPLESGHGSSPGGGGGCKEKALGNLDREESLSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_020043968 [XP_020043968] protein **FAM181**A [Castor canadensis].
222..236
MRPLAPTPAQIISRYLTRIPLPRLCLERSGARVGILFASRFVGLGEGMGVWLFQRDSNSLWCPPGQLCI
LLGAAGPYQSSPSSWKALCSGPLVMAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQR
CSRLPRGLPGRVAEPDLKRGPEDQPGRLPLHATSDSSPGGGGGCKEKASGNPFREECLSKEPTLQGQSLEAAKPG
QVPMRKRQLPASFWEEPRPTHNYSMRLDGRLGPREGPPFESKKNCKGLESLGPEIAPVSMSPRVLADKESLKMPG
MSLVGRVDAWSCCPFQYHGQPIFPCPPGALPQNPVPSLGLWRKSPALPGELAHFCRDMDDPGQKVCRPVVLKPIP
TKPAVPSPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_016318830 [XP_016318830] PREDICTED: protein **FAM181**B-like
[Sinocyclocheilus anshuiensis]. 157..171
MAVQAAIMNSQFLNFCFPGSVMDYEVEKGLEGGLLGEEVDCGGDFKETTRDLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGIILPGTTPVQEPCKRQGSPQTPTSNLSGKTPPKKDGMQASLQSKSLAALFNS
AKDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAAEFFELLGPDYSNMVSEQDLFHTA
PIRIQQEVTVGPEPYDSHHFVSGGFLYTEPWGTCSGTSKKSGDMRTVPVQPNLYTHTDLSGSVPVEQSSPCALTF
SNFFTDCSAPPVSYDLVNGYNRDNFSSL PLRHRNLPPSFFTEP

rs:XP_016307523 [XP_016307523] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Sinocyclocheilus anshuiensis].45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAISPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVSPGTLSSMVPANPQPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPVPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQIRLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_016307525 [XP_016307525] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Sinocyclocheilus anshuiensis].45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAISPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVSPGTLSSMVPANPQPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQI
RLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGPSSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_016309011 [XP_016309011] PREDICTED: uncharacterized protein
LOC107663320 [Sinocyclocheilus anshuiensis]. 154..168
MAASVIRTLSNLGLAKPFPPCFFPAEDEEETEEEYEEELREDSLEEEEDAVASESQDEEPWSFDSSPNN
AEMTNQLLRFAELISSDVQRYFGRSQDPDACDIYAEKPCRKVGGRQRYYADFIKVASSGQGEEPESLGPLAELFQ
DAQRKGRGLPMSQRRLPVSFWTEPFAQQLDMLGDTSMQDNSLSMINTSESSINTNTSLSMFSKSSVCTMTSSSIS
GTLSSSSTPDFSDLLAHWAMDRENPNEFNCDYPLS PMSQRRLPVSFWTEP

rs:XP_016340120 [XP_016340120] PREDICTED: transcriptional coactivator
YAP1-like isoform X1 [Sinocyclocheilus anshuiensis]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVSPGTLSSMIPANAPPQHLRQSSYEIPDDVPLLPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQATPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQIRLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPSMGQDSRNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDSLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMVVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_016340121 [XP_016340121] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Sinocyclocheilus anshuiensis]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVSPGTLSSMIPANAPPQHLRQSSYEIPDDVPLLPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQATPASPVPVQQQNIMNPASAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQI
RLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQNPVSSPSMGQDSRNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDSLGPSSMATQPSRFPDYLDAIPGTDVDLGTLEGESMVVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_016340478 [XP_016340478] PREDICTED: protein **FAM181**A
[Sinocyclocheilus anshuiensis]. 107..121
MASSDSEVKTLLNFVNLASSDIKAALDRSAPCRRSVDHRKYLQKQLKRFSHRYAKMPRCHSHRNGDSAP
AKLSEDKAPPGPGSGREERLNAEDGARSGQGQGQAPTPMRKRQLPASFWKEPQSSSGSRERLERFLQSGHVRPPA
VNGERSTTGFDDLNANPLLSGSAACACSCCSLPYRFLLPHADAPLSSRAHVVIKPIPTKPSSSSSSSSSVFSVFG
FI PMRKRQLPASFWKEP

rs:NP_001182655 [NP_001182655] protein **FAM181**A [Mus musculus].>rs:XP_006515383 [XP_006515383] PREDICTED: protein **FAM181**A isoform X1 [Mus musculus].>rs:XP_006515384 [XP_006515384] PREDICTED: protein **FAM181**A isoform X1 [Mus musculus]. 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVAEPHLQ
RGPEERPGRPPLHPCPQSSPGGGGSCTEKALGTPFREECLSKDQGFRGLNPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPREASLYENKKNCKGLESLGPETAPLPMSPRVLADTEPLKMSGVSLVGSLDAWSYCPFQSH
GQPIFPGLPGVLPQGPVPSLGLWRRSLASPVDLAHFCKGVDTPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_016953626 [XP_016953626] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila biarmipes]. 90..104
MCACLIAKIFLCSFRLYTISAFYMLTTMSASSNSNANSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISIGNKAARVIQQPDDQSP
IAAIPTLQIQPSPQHSRLAIHHSRARSSPASLQQNFNVRARSDAAANNPNANPSSQQQPAGPTFPENSAQEFPSG
APASSGQIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQ
WEDPRIQYRQPQQILMAERIKQNDVLQTTKQTTTSTIANNMGPLPDGWEQAVTESGDIYFINHIDRTTSWNDPRM
QSGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_016953627 [XP_016953627] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila biarmipes]. 90..104
MCACLIAKIFLCSFRLYTISAFYMLTTMSASSNSNANSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISIGNKAARVIQQPDDQSP
IAAIPTLQIQPSPQHSRLAIHHSRARSSPASLQQNFNVRARSDAAANNPNANPSSQQQPAGPTFPENSAQEFPSG
APASSGQIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQ
WEDPRIQYRQPQQILMAERIKQNESGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN
PLRMRKLPNSFFTPP

rs:XP_017045308 [XP_017045308] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila ficusphila].>tr:A0A1W4UMV6_DROFC [A0A1W4UMV6] SubName: Full=transcriptional coactivator yorkie isoform X1 {ECO:0000313|RefSeq:XP_017045308.1}; 65..79
MLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQVPLRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNISGKAVQQTGGPDGQSPIAAIPQLQIQPSAQHSRLAIHHSRARS
SPASLQQNYNVRAARSDAANNPNANPSSQQPTAGPTFPENSAQEFPSGAPASSIDLDAMNTCMSQDMPMSMQTVH
KKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQFRQQQQILMAERIKQNDVLQTT
KQTTTSTIANNLGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQSGLSVLDCPDNLVSSLQIEDNLCSNLFN
DAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_017045309 [XP_017045309] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila ficusphila].>tr:A0A1W4V1D6_DROFC [A0A1W4V1D6] SubName: Full=transcriptional coactivator yorkie isoform X2 {ECO:0000313|RefSeq:XP_017045309.1}; 65..79
MLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQVPLRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNISGKAVQQTGGPDGQSPIAAIPQLQIQPSAQHSRLAIHHSRARS
SPASLQQNYNVRAARSDAANNPNANPSSQQPTAGPTFPENSAQEFPSGAPASSIDLDAMNTCMSQDMPMSMQTVH
KKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQFRQQQQILMAERIKQNESGLSV
LDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_017070335 [XP_017070335] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila eugracilis]. 90..104
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQVPLRMRNLPNSFFTPPAPSHSRANSADSTYDAGSQSNISISNKAVVQQTGGPGPDG
QSPIAAIPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAVNNPNANPSSQQPAGPTFPENSAQEFPS
GAPASSIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQW
EDPRIQYRQQQQILMAERIKQSDVLQTTKQTTTSTIANNMGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQ
SGLSVLDCPDNLVSSLQIEDNNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRNLPNSFFTPP

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rs:XP_017070336   [XP_017070336] PREDICTED: transcriptional coactivator
yorkie isoform X2 [Drosophila eugracilis].     90..104
      MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQVPLRMRNLPNSFFTPPAPSHSRANSADSTYDAGSQSNISISNKAVVQQTGGPGPDG
QSPIAAIPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAVNNPNANPSSQQPAGPTFPENSAQEFPS
GAPASSIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQW
EDPRIQYRQQQQILMAERIKQSESGLSVLDCPDNLVSSLQIEDNNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN
      PLRMRNLPNSFFTPP

rs:XP_017094176   [XP_017094176] PREDICTED: transcriptional coactivator
yorkie isoform X1 [Drosophila bipectinata].    65..79
      MLTTMSSSNTNSLIEKEIADEDMLPPIKSPNNLVLRVNQDTDDNLRLLFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNISSLNSISSLANAAQPVDGQPAISAIPQIQPSPQQRNLAIHHFR
ARSSPASLQQNYNVRQRSDPTKPSNQPPTAGPTFPENSAAEFPSGGAGAGAVAGAGAPASSIELDGMSMVEDMPM
STQTVHKKQRSYDVVSPIQLQLLRGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFQRQQQNIMAERITQN
EVLQTPKPTTTSAIANNLDPLPDGWEQALTENGDIYFINHIARTTSWNDPRMQPVPGLSVLDCPDNLVSSLQIED
NICSNMFNDAQTIVNPPSSHKPDDLEWYKIN     PFRMRKLPNSFFTPP

rs:XP_017094177   [XP_017094177] PREDICTED: transcriptional coactivator
yorkie isoform X2 [Drosophila bipectinata].    65..79
      MLTTMSSSNTNSLIEKEIADEDMLPPIKSPNNLVLRVNQDTDDNLRLLFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNISSLNSISSLANAAQPVDGQPAISAIPQIQPSPQQRNLAIHHFR
ARSSPASLQQNYNVRQRSDPTKPSNQPPTAGPTFPENSAAEFPSGGAGAGAVAGAGAPASSIELDGMSMVEDMPM
STQTVHKKQRSYDVVSPIQLQLLRGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFQRQQQNIMAERITQN
EVLQTPKPTTTSAIANNLDPLPDGWEQALTENGDIYFINHIARTTSWNDPRMQPVPGLSVLDCPDNLVSSPD
      PFRMRKLPNSFFTPP

rs:XP_017094178   [XP_017094178] PREDICTED: transcriptional coactivator
yorkie isoform X3 [Drosophila bipectinata].    65..79
      MLTTMSSSNTNSLIEKEIADEDMLPPIKSPNNLVLRVNQDTDDNLRLLFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNISSLNSISSLANAAQPVDGQPAISAIPQIQPSPQQRNLAIHHFR
ARSSPASLQQNYNVRQRSDPTKPSNQPPTAGPTFPENSAAEFPSGGAGAGAVAGAGAPASSIELDGMSMVEDMPM
STQTVHKKQRSYDVVSPIQLQLLRGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFQRQQQNIMAERITQN
EPVPGLSVLDCPDNLVSSLQIEDNICSNMFNDAQTIVNPPSSHKPDDLEWYKIN     PFRMRKLPNSFFTPP

rs:XP_017094179   [XP_017094179] PREDICTED: transcriptional coactivator
yorkie isoform X4 [Drosophila bipectinata].    65..79
      MLTTMSSSNTNSLIEKEIADEDMLPPIKSPNNLVLRVNQDTDDNLRLLFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNISSLNSISSLANAAQPVDGQPAISAIPQIQPSPQQRNLAIHHFR
ARSSPASLQQNYNVRQRSDPTKPSNQPPTAGPTFPENSAAEFPSGGAGAGAVAGAGAPASSIELDGMSMVEDMPM
STQTVHKKQRSYDVVSPIQLQLLRGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFQRQQQNIMAERITQN
EPVPGLSVLDCPDNLVSSPD    PFRMRKLPNSFFTPP

rs:XP_017094180   [XP_017094180] PREDICTED: transcriptional coactivator
yorkie isoform X5 [Drosophila bipectinata].    65..79
      MLTTMSSSNTNSLIEKEIADEDMLPPIKSPNNLVLRVNQDTDDNLRLLFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNISSLNSISSLANAAQPVDGQPAISAIPQIQPSPQQRNLAIHHFR
ARSSPASLQQNYNVRQRSDPTKPSNQPPTAGPTFPENSAAEFPSGGAGAGAVAGAGAPASSIELDGMSMVEDMPM
STQTVHKKQRSYDVVSPIQLQLLRGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFQRQQQNIMAERITQN
DENEYRIRNG  PFRMRKLPNSFFTPP

rs:XP_017005606   [XP_017005606] PREDICTED: transcriptional coactivator
yorkie isoform X1 [Drosophila takahashii].     90..104
      MCACLIAKIILCSFRLYTISAFYMLTTMSASSNSNANSLIEKEIDDEDMLSPIKPNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISIGSKAAQVVQQPDGQSP
IPQQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAVAAANNPNANPSSQQQPAGPTFPENSAQEFPS
GAPASSGQIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKST
QWEDPRIQYRQQQQILMAERIKQNDVLQTTKQTTTSTIANNMGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPR
MQSGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKINPLRMRKLPNSFFTPP
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rs:XP_017005607 [XP_017005607] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila takahashii]. 90..104
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNSNANSLIEKEIDDEDMLSPIKPNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISIGSKAAQVVQQPDGQSP
IPQQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAVAAANNPNANPSSQQQPAGPTFPENSAQEFPS
GAPASSGQIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKST
QWEDPRIQYRQQQQILMAERIKQNESGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKI
N PLRMRKLPNSFFTPP

rs:XP_017149868 [XP_017149868] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila miranda]. 65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSDANPGPSGQGPTYPENSAEFPNSAANNIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSDVLQTTKQTTTSTIANSLGPLPDGW
EQAVTESGDIYFINHIDRTTSWIDPRMQSGLPVLDCPDNLVSSLQIEDNICTNLFNDAQTIVNPPSSHKPDDLEW
YKIN PFRMRKLPNSFFTPP

rs:XP_017149869 [XP_017149869] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila miranda]. 65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSDANPGPSGQGPTYPENSAEFPNSAANNIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSESGLPVLDCPDNLVSSLQIEDNICT
NLFNDAQTIVNPPSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

rs:XP_017125498 [XP_017125498] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila elegans]. 88..102
MCACLIAKIILCSFHLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISNKSVVQVQQQQQQPGGPDG
QSPIAAIPQLQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAANNPNANPSSQQPTAGPTFPENSAQEFPSG
APASSIDLDAMNTCMSQDIPMAMQTAHKKQRSYDVVSPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWE
DPRIQYRQQQQILMAERIKQNDVLQTTKQTTTSTIANNMGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQS
GLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_017125499 [XP_017125499] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila elegans]. 88..102
MCACLIAKIILCSFHLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISNKSVVQVQQQQQQPGGPDG
QSPIAAIPQLQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAANNPNANPSSQQPTAGPTFPENSAQEFPSG
APASSIDLDAMNTCMSQDIPMAMQTAHKKQRSYDVVSPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWE
DPRIQYRQQQQILMAERIKQNESGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN
PLRMRKLPNSFFTPP

rs:XP_008424608 [XP_008424608] PREDICTED: protein **FAM181**B [Poecilia reticulata].>tr:A0A3P9PJ09_POERE [A0A3P9PJ09] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSPREP00000021871};
246..260
MQVVGHKQRVKFPGFPSLLLFDVLTSSVLPPERSPSSSSVPVTSSLDCLWKLHEQHQEQVFIHRTKSCF
EETFSSGITVDATGVAAGLDRVMAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQGSPVSQQGPLQSKTLQKREGGQ
ANLQSKSLAALFSPVKEIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPD
YSNMVNEQDIYQGVPLRGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGPCKKPSEGLRTGLPQPPVYSQAEDTSV
PLDDNGLCTLTFPNFFPDCSISQVTYDLNGGYNKTNFSCL PMRHRNLPPSFFTEP

rs:XP_008424630 [XP_008424630] PREDICTED: transcriptional coactivator YAP1 [Poecilia reticulata].>tr:A0A3P9PJP3_POERE [A0A3P9PJP3] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPREP00000022087};
45..59

MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPPSLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LNHNDKSTTWQDPRKALLQTSQPAPPSSVPVQPQNLMNPANGPLPEHWEQAITSEGEIYYINHEKRTTSWLDPRL
EPRYALNQQRMTQSAPGKQSGQLPPSTHGGVMAGNNQLRLQQIEKERLRLQQHRPQELALRNQLPTSMDQDGSTN
PVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLPASMASQPSR
FPDYLDGIPGTDVDLGTLEGESMVVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRNLPDSFFKPP

rs:XP_008425352 [XP_008425352] PREDICTED: transcriptional coactivator
YAP1-like isoform X1 [Poecilia reticulata].>rs:XP_017164245 [XP_017164245]
PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Poecilia
reticulata]. 46..60
MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCSSLAPHHVRAHSSPASLPINSVNAVATPIIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETGPLPKGWEQAVTAEGEVYYIDHIKQETTWDDPRLAPKV
NPAVLPLAIQQRLEKLRLKHAVLPQFAPQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRTLNQESNLNGAHSR
NESTDSGLSVSSLSRTSDHMLSSVDHMDIGDSSEPPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSG
PHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_008425353 [XP_008425353] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Poecilia reticulata]. 46..60
MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCSSLAPHHVRAHSSPASLPINSVNAVATPIIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETAPKVNPAVLPLAIQQRLEKLRLKHAVLPQFAPQVQEAG
GSNQMPGGMDHDRSAQMLVPSVDIRIRTLNQESNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDIGDSSE
PPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWLPMRMRKFPDSFFKPP

rs:XP_556728 [XP_556728] AGAP006045-PA [Anopheles gambiae str.
PEST].>tr:Q5TR76_ANOGA [Q5TR76] SubName: Full=AGAP006045-PA
{ECO:0000313|EMBL:EAL39988.3}; SubName: Full=Protein yorkie
{ECO:0000313|VectorBase:AGAP006045-PA}; 72..86
MAFNGGAAGSGNGSAAAAAAAAAVAAVAADENESTGANKKKNLIILVDKDSNDKLNELFDKALSNKVPL
QIPYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVAGVAATGPNGLPIHHSRAHSSPASLGK
IPVGMGGLGGGAVAAAAAAAAAAAAAGGNGAGGGGSGGGGGGGGGGTGGTGAAGAASKSAAAQAAAAAAAAQNDA
TSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYINHNTRTTTWEDPRITAMQ
ESLFQQQSSVETLARISSLRRKFTAGPNNVDLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLLQEQTVRLY
NLQLERERLRKRQQEIKSHMGDDPFLSGIADHARQESGDSGLSESSMTQSMPHTPEFLSSIDDSMDGLSMTDNTM
DTIAFGDNLETPDEFMLDDPLLLEKIDAVTNLSLMDPTSSKPDNTLYDII PYRMRKLPESFFMPP

rs:XP_020299484 [XP_020299484] transcriptional coactivator YAP1
[Pseudomyrmex gracilis]. 45..59
MALNQDVDQVPKSLVVTVDRNSESDLQALFDTVLKPDSKRPLQIPLRMRNLPNSFFNPPSTGSKSPSIS
HSRENSADSAFGTATPSTGGGGGAPSGGTGTGGGNAAGAAGGGGGAGGGGDANSGAGAVAAAAAVAVAGLTVSHP
RAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTT
TWEDPRKTAAAASVAAVAAAVESNKSTAQQVNSLGPLPDGWEQARTAEGETYFINHQTRTTSWFDPRIPTHLQRT
PASNTMLPQNWLQQQPTGSIQSNQSLQACQQKLRLQSLHMERERLKQRRQEIMRQQELMMQQSTTDAAMDPFLSG
INEHARQESADSGLGLGSAYSLSHTPDDFLAIDDNMDGTSEWHSVLIKKRLYRSHKYINGGAPMETPDLSTLSDN
IDSADDLLPSLQLSEDFNSDILDDMLRNSNSKTENVLTWL PLRMRNLPNSFFNPP

rs:XP_017675096 [XP_017675096] PREDICTED: LOW QUALITY PROTEIN: protein
FAM181B [Lepidothrix coronata]. 166..180
MAAPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAAPPPASCPPAACSTRPPPRREPAQAAGSSLQSKSLAALFGSLQRGRGA
AGGAEAKAGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPAPAARGPPAKEPEKGGGGAAEASEFFELLCPEYGAL
LPEHAAPPDAFGGRLPAELGLEHGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPPEPLRPLYAGGPEP
VPGGGGGSTEEPGGHLPAGFAPFFPECPLAPRSRPTTTALGTTARATPGCRAARFGVCRDGERSPEPARGADGRW
GSAEAVRGSAHPKPRPRPPQDPPLCTASRLLLPFGGRCK PLRDRNLPPSFFTEP

rs:XP_017685289 [XP_017685289] PREDICTED: protein **FAM181**A-like
[Lepidothrix coronata].>rs:XP_017669370 [XP_017669370] PREDICTED: protein
FAM181A [Lepidothrix coronata]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHPSKPPECGWR
RGAEDRGHGPQPEAPDPSPHGGAAAEKVMQTAEAEESLTGERVLQEQKPEAVRPDQVPMRKRQLPASFWEEPRPA
QSLTARAFPASPEGLPAPRDPPPYEGKKSKWSPDAASPESPPDPAPHAGEKDPAGVLSGRVGAWTCCPFPCPGTG
VYQPPGALPPSPFPGLGLWRKSAATLPAEVPHFCKEADGTGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_020373926 [XP_020373926] protein **FAM181**B [Rhincodon typus].
183..197
MAVQAAIMNPHFIHFCFPGSSVEYEVESAYSGALLGEMGSSGELKETTSALLNFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGMISGGGTSAGAGQEAGNKRQVSPASSSSSSGGSSSTGHFQCKPPPKKDGSQSS
LQSKSLAALFDSVRDLRRSAAGDRALVAAAAAGSSRKIPLRNRNLPPSFFTEPANVKITSTSGMSLKDLERGNPE
AAEFFELLGPDYSNMISGQEPFLGSALRIQQEGNCELASYDSYRSLGSLSGSFPHFPEPWLPCSAAKKSPTSGCN
LAVTEGARTLPVQTPLYPNNQAANSSPMEESPVXLASFPQFFPECSLPQVPYEYSPGYNCSRQNFPTL
PLRNRNLPPSFFTEP

rs:XP_020374035 [XP_020374035] protein **FAM181**A [Rhincodon typus].
108..122
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHPGRLLDSGS
KRAPDEQSRPCVLQLRASGAADCGEPPPPLPPARHGQVPMRKRQLPASFWEEPRPGKSLPPPRELLLRPPPPQQP
PPPPGERGVSPASVSPGPAAVAKQEPRCERGEPLRLQLASLARTVTLCACCPLQYHRLYQSHMALPHAASPDMGI
WRKAANLPAELHAYSKDSLNGQRIHKPIVFKPIPTKPTVPPPLYNAYGFL PMRKRQLPASFWEEP

rs:XP_020392912 [XP_020392912] transcriptional coactivator YAP1
[Rhincodon typus]. 61..75
MDPSQQQQQGTGTAPAAGPGAAVPRAGHQIVHVRGDSETDLEALFNAVMNPKNSNVPQSVPMRLRKLPD
SFFKQPEPKNHSRQASTDGPNAPPLQPQHVRAHSSPASLLSAAATASAPPASGSSGSSGSASPAAAVVSQGSGSS
PASAHLRQASYEIPDDVPLPPGWEMAKTPSGQRYYLNHIEQTTTWQDPRKPMSVLNSNTPASPASLQQNLMNTTS
SGPLPDGWEQGITPDGEIYYINHKNKTTSWLDPRLDPRYAVDQQRLTQSAPVKTPPSIGPHSPHSPQGGAMSGSN
TQQQMRLQQLQFEKERLRLKHQELLRQEMALRSQLPSMEQDGSPQTPVSSPAMSQDIRTMTTNSSDPFLNSGTYH
SREESTDSGLGMSSYSVPRTPDDFLNSVEEMDTVENLGPNNIGSQQNRFPDYLETIPGTNVDLGTLEEDSMNVEG
EELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_020387589 [XP_020387589] transcriptional coactivator YAP1-like
[Rhincodon typus]. 44..58
MDQNPIPPPGQTIVRVLGDSETDLEALFNAVMNPKPGAVPHQVPMRMRKLPESFFKQPDSGSHSRQSST
DSSSNLPQFQVQHIRSHSSPASLPVSANPNSQPYAHLRQQSFDNVDDVPLPPGWEMAKTPSGQRYFLK
PMRMRKLPESFFKQP

rs:XP_018398225 [XP_018398225] PREDICTED: LOW QUALITY PROTEIN:
transcriptional coactivator YAP1 [Cyphomyrmex costatus]. 47..61
MALNQDVVEQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGAAVPATPNGGSVPNGGTNGGSGAGGENGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQ
TYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAA
ASVAAVAAAVESSKSNALGPLPDGWEQARTAEGEIYFINHQTRTTSWFDPRIPSHLQRTPASGAMLPQNWQLQQP
TGIQNNQNLQACQKQKIRLQSLQLERERLKQRQQEIMRQVGIQQEMMLRQSTTDAVMDPFLSGINEQHARQESAD
SGLGLGTAYSMPQASDDFLNIDENMDGTSERHCALNDLTKRLYRSHKYINGGAPMDTPDLSTLSDNIDSTDDLLP
SLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_017449591 [XP_017449591] PREDICTED: protein **FAM181**A isoform X1
[Rattus norvegicus].>rs:XP_017449995 [XP_017449995] PREDICTED: protein
FAM181A-like isoform X1 [Rattus norvegicus]. 199..213
MQAARVLRGAGRSLTWWPQSLSPAECTKSLEHEGWYLLLPVKVCPGLSSELPAPSRTHTLHGKPCTVPV
VMAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVTEPHLQRGPEE
RPGRLPLHPCPQASTGGGGSCTEKALGTPFREECLSKEQSFRGLNPEATRPGQVPMRKRQLPASFWEEPRPTLSY
PMGLEVGLAPREASLYENKKNCKGLESLGPETAPLPMSPRVLTDTESLKMSGVSLVGSLDAWSYCPFQYHGQPIF

PGLPGVLPQGPVPSVGLWRKSPASPVELAHFCKDVDTPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_008762985 [XP_008762985] PREDICTED: protein **FAM181**A isoform X2 [Rattus norvegicus].>rs:XP_008763127 [XP_008763127] PREDICTED: protein **FAM181**A-like isoform X2 [Rattus norvegicus]. 167..181
MVGVSQLPGQVCPGLSSELPAPSRTHTLHGKPCTVPVVMAADSDVKMLLNFVNLASSDIKAALDKSAPC
RRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVTEPHLQRGPEERPGRLPLHPCPQASTGGGGSCTEKALGTPFRE
ECLSKEQSFRGLNPEATRPGQVPMRKRQLPASFWEEPRPTLSYPMGLEVGLAPREASLYENKKNCKGLESLGPET
APLPMSPRVLTDTESLKMSGVSLVGSLDAWSYCPFQYHGQPIFPGLPGVLPQGPVPSVGLWRKSPASPVELAHFC
KDVDTPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_006240571 [XP_006240571] PREDICTED: protein **FAM181**A isoform X3 [Rattus norvegicus].>rs:XP_006240577 [XP_006240577] PREDICTED: protein **FAM181**A-like isoform X3 [Rattus norvegicus].>rs:XP_006240578 [XP_006240578] PREDICTED: protein **FAM181**A-like isoform X3 [Rattus norvegicus]. 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVTEPHLQ
RGPEERPGRLPLHPCPQASTGGGGSCTEKALGTPFREECLSKEQSFRGLNPEATRPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPREASLYENKKNCKGLESLGPETAPLPMSPRVLTDTESLKMSGVSLVGSLDAWSYCPFQYH
GQPIFPGLPGVLPQGPVPSVGLWRKSPASPVELAHFCKDVDTPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_006242550 [XP_006242550] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Rattus norvegicus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQ
LQMEKERLRLKQQELFRQVRPQAIRNINPSTANAPKCQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLG
TLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006242551 [XP_006242551] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Rattus norvegicus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQVRPQAIRNINPSTANAPKCQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTL
EGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006242552 [XP_006242552] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Rattus norvegicus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQ
LQMEKERLRLKQQELFRQAIRNINPSTANAPKCQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEG
DAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006242553 [XP_006242553] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Rattus norvegicus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQAIRNINPSTANAPKCQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNSSDPFLN

SGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDA
MNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008764115 [XP_008764115] PREDICTED: transcriptional coactivator
YAP1 isoform X5 [Rattus norvegicus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQ
LQMEKERLRLKQQELFRQVRPQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNSSDPFLNSGTYHSRDES
TDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMP
SLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008764116 [XP_008764116] PREDICTED: transcriptional coactivator
YAP1 isoform X6 [Rattus norvegicus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQVRPQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSL
QEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006242554 [XP_006242554] PREDICTED: transcriptional coactivator
YAP1 isoform X7 [Rattus norvegicus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQ
LQMEKERLRLKQQELFRQELALRSQLPSLEQDGGTQNAVSSPGMTQELRTMTTNSSDPFLNSGTYHSRDESTDSG
LSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQE
ALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021062252 [XP_021062252] protein **FAM181**B [Mus pahari]. 218..232
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGASAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGSAPPRPASPSAADAPAKRPTGAPGAPTVATPAHCK
AAPRREATQAAAAASLQSRSLAALFDSLRHIPGGAETAGGAEAVSASSLGAASAAGDGAGIAVSSVAPGTRKVPL
RARNLPPSFFTEPSRVGCGGASGGPSGQGVSLGDLEKGAEAVEFFELLAPDFGSGNDSSVLMAADPLDPFPAGAT
VLRGPLELESGPFEQQAMVGNLLYPEPWNTPSCPQTKKPPLAGVRGGVTLNEPVRLLYPTALDSPGGEDAPALAS
FTPFFPDCALPPPHQVSYDYSAGYSRAVYPSLWRPDGLWEGASGEEGGHPD PLRARNLPPSFFTEP

rs:XP_021062508 [XP_021062508] transcriptional coactivator YAP1 isoform
X1 [Mus pahari]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQAIRNINPSTANAPKCQELALRSQLPALEQDGGTQNAVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLE
GDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021062509 [XP_021062509] transcriptional coactivator YAP1 isoform
X2 [Mus pahari]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQVRPQELALRSQLPALEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDE

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STDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELM
PSLQEALSSEILDVESVLAATKLDKESFLTWL    PMRLRKLPDSFFKPP

rs:XP_021062510   [XP_021062510] transcriptional coactivator YAP1 isoform
X3 [Mus pahari].  70..84
      MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQELALRSQLPALEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDS
GLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQ
EALSSEILDVESVLAATKLDKESFLTWL  PMRLRKLPDSFFKPP

rs:XP_021062511   [XP_021062511] transcriptional coactivator YAP1 isoform
X4 [Mus pahari].  70..84
      MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASAMNQR
ITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQMEKERLRLKQQELFRQVRPQAIRNINPSTANAPKC
QELALRSQLPALEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLN
SVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATK
LDKESFLTWL  PMRLRKLPDSFFKPP

rs:XP_021062512   [XP_021062512] transcriptional coactivator YAP1 isoform
X5 [Mus pahari].  70..84
      MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASAMNQR
ITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQMEKERLRLKQQELFRQAIRNINPSTANAPKCQELA
LRSQLPALEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDE
MDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKE
SFLTWL      PMRLRKLPDSFFKPP

rs:XP_021062513   [XP_021062513] transcriptional coactivator YAP1 isoform
X6 [Mus pahari].  70..84
      MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASAMNQR
ITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQMEKERLRLKQQELFRQVRPQELALRSQLPALEQDG
GTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTL
PSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_021062514   [XP_021062514] transcriptional coactivator YAP1 isoform
X7 [Mus pahari].  70..84
      MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASAMNQR
ITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQMEKERLRLKQQELFRQELALRSQLPALEQDGGTQN
AVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQ
SRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_021062515   [XP_021062515] transcriptional coactivator YAP1 isoform
X8 [Mus pahari].  70..84
      MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
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QLQMEKERLRLKQQELFRQVRPQAIRNINPSTANAPKCQELALRSQLPALEQDGGTQNAVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDL
GTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017460851 [XP_017460851] PREDICTED: transcriptional coactivator yorkie [Rhagoletis zephyria]. 76..90
MHNTERIITSGYFGNMSLSKTVGGLNKGNAKEKERSTGKESNNLVVRIDQDSDNNLQALFDSVLNPGES
KRPLQVPFRMRQLPESFFKPPATTSRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSIAAVPATITQPQVAAN
RLAISHSRAHSSPASLQQTYNVHIGNVMEAGACLQDGIGPVYTSNAVQFPPGVNAGSGVRMDQVDQSVTKDGSNA
IQTFHMKQRSYDVVSTIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQLKQQLFQEGLPHSVNLK
NKESVNLAENLGPLPEGWEQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQQIDKEQDYF
KQSSEQSSLTRQNGSLQMDPFLSGDNHARQESSDSGLSLSSNTFSATTDLMPNIDDSMDCISESGSLNALSGIDC
PDNLVSSLQLEDNICNEMFSDVHSMLNASATKPDTLDWYKIN PFRMRQLPESFFKPP

rs:XP_021058188 [XP_021058188] protein **FAM181**A [Mus pahari]. 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVAEPHLQ
RGPEERPGRPPLHPCPQSSPGGGGSCTEKALGTPFREECLSKEQGFRGLNPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPVGLEVGLAPRETSLYENKKNCKGLESLGPETAPLPMSPRVLADTEPLKMSGVSLVGSLDAWSYCPFQSH
GQPIFPGLPGVLPQGPVPSLGLWRSLASPVDLAHFCKGVDTPGPKVYRPIVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_021035100 [XP_021035100] protein **FAM181**A [Mus caroli]. 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVAEPHLQ
RGPEERPGRPPLHPCPQSSPGGGGSCTEKALGTPFREECLSKDQGFRGLNPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPREASLYENKKNCKGLESLGPETAPLPMSPRVLADTEPLKMSGVSLVGNLDAWSYCPFQSH
GQPIFPGLPGVLPQGPVPSLGLWRRSLASPVDLAHFCKGVDTPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_017532274 [XP_017532274] PREDICTED: protein **FAM181**A isoform X1 [Manis javanica]. 198..212
MLCIWRGAPDWPEGPPSSGDSSSIQPTRGLHNCFQPDTRSSRPRGPGPAASHQQKPPSSWKAQCSGPLV
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDQ
PGRLPLNSGHDSSPSVGGGCKEKSLGNPYREECLSKEQALQGQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYP
VGLEGVLGPREGPPYEGKKHCKGLEPLGPEMATAHTSPRVPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYP
GPPGALPQSLVPSLGLWRKSPASPGELAHFCKDVDGLGQKVYRPVVLKPIPTKPAMPPPIFNIFGYL
PMRKRQLPASFWEEP

rs:XP_017532275 [XP_017532275] PREDICTED: protein **FAM181**A isoform X2 [Manis javanica].>rs:XP_017532276 [XP_017532276] PREDICTED: protein **FAM181**A isoform X2 [Manis javanica].>rs:XP_017532277 [XP_017532277] PREDICTED: protein **FAM181**A isoform X2 [Manis javanica]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDQPGRLPLNSGHDSSPSVGGGCKEKSLGNPYREECLSKEQALQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGVLGPREGPPYEGKKHCKGLEPLGPEMATAHTSPRVPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPQSLVPSLGLWRKSPASPGELAHFCKDVDGLGQKVYRPVVLKPIPTKPAMPPPIFNIFGYL
PMRKRQLPASFWEEP

rs:XP_017664169 [XP_017664169] PREDICTED: sentrin-specific protease 3 [Lepidothrix coronata]. 169..183
MAGRQRQGVIQPLAELRLPSPFPHSLLLPTHPEPNFHNLSEEEEEEEEEEEEEVEAAEENVRPEPAISS
TAETTLRLLKFSELISCDIQRYFGRRGREEATGTQPVPKDCESPRSTGAQPEAPRGSPGAAHRLGPLAELFEYGV
HRCLSPRAAGSRTQRLERKYGHITPMHRRKLPPSFWKEPGPASLLHTGTPDFSDLLANWTVEPGPELPCAGRELP
LEPGRPGLEAEPFPGL PMHRRKLPPSFWKEP

rs:XP_017671536 [XP_017671536] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Lepidothrix coronata]. 86..100
MDPGQPQPQQPPQAAQPPAPQQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS

VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELAL
RSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_017671537 [XP_017671537] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Lepidothrix coronata]. 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTS
PSVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017671539 [XP_017671539] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Lepidothrix coronata].>tr:A0A218VAG6_9PASE [A0A218VAG6]
SubName: Full=Transcriptional coactivator YAP1
{ECO:0000313|EMBL:OWK62926.1}; 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTS
PSVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015481337 [XP_015481337] PREDICTED: LOW QUALITY PROTEIN: protein
FAM181B [Parus major]. 171..185
MAVPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAPPPPAACPPSACPARPPPRREPAQAAGSSLQSKSLAALFGSLQRGRGA
AGGAEAKAGGGGAGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPGPAARGPPAKEPEKGGGGAEATEFFELLCPE
YGALLPEHAAPTDAFGGRLPAELGLEHGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPAEPLRPLYPG
GPEPVPGGGGGEEPGGHLPAGFAPFFPECSLPPRSRPTTTAAGTTAGATPGCRAAGDRGPPGRRGGERSPRGGGR
TDGRTLGQRGGRTELRTPHCM PLRDRNLPPSFFTEP

rs:XP_015494803 [XP_015494803] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Parus major]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_015494813 [XP_015494813] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Parus major]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_015494821 [XP_015494821] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Parus major]. 85..99

MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015494831 [XP_015494831] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Parus major]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGD
GMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015494840 [XP_015494840] PREDICTED: transcriptional coactivator
YAP1 isoform X5 [Parus major]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQA
LRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSM
SSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALS
SDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015494849 [XP_015494849] PREDICTED: transcriptional coactivator
YAP1 isoform X6 [Parus major]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNI
NPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYS
VPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDIL
NDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015494859 [XP_015494859] PREDICTED: transcriptional coactivator
YAP1 isoform X7 [Parus major]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQE
LALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015494867 [XP_015494867] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Parus major]. 85..99
MDPGQPQTQQPPQAAQPPASQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEALF
NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSV
QQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALR
SQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMD
TGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKES
FLTWL PMRLRKLPDSFFKPP

rs:XP_015497850 [XP_015497850] PREDICTED: uncharacterized protein LOC107210955 [Parus major]. 169..183
MAAGVIQPLAELRLPSPFPHGLLLPTHPEPDFPDFSEEEEEEEEEEEEEEDVEAVEESVRPELASVSST
AETTLRLLKFSELISCDIQRYFGRRGREEASSHPVPEDCGSPQSAEAVAEAVAPRDSPGATHRLGPLAELFEYGV
HRCLPARVAGSRTQRLERKYGHITPMHRRKLPPSFWKEPGPGPASLLHTGTPDFSDLLANWTVEPGPELPGAGRE
LPGRPGLEAEPFAGL PMHRRKLPPSFWKEP

rs:XP_018862623 [XP_018862623] PREDICTED: protein **FAM181**A [Parus major]. 128..142
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHHPSKPPECGW
RRGAEDRARGPLPEAPEPSSHGGAAAEKVMQTAEAEESLTGDRVLQEQKPEAARPDQVPMRKRQLPASFWEEPRP
AQSLTARAFPASPEGLQAPRDPPPYEGKKSKRSPDAAGPESPPDTAPHVGEKDPAGPLSGRVGAWTCCPFPCPGP
GVFQPPGALPPSPFPGLGLWRKSAAPLPAEVPHFCKEADGPGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_017958673 [XP_017958673] PREDICTED: transcriptional coactivator yorkie [Drosophila navojoa]. 61..75
MSLSNKSNISEKEIDDEDMLSPTKISTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEIQPSLTQQNQPSHSRLAVHHFRARSSPASLQQNYNVRTRNE
PSVNNTNTNQGPAYPEASVDFASASTANNIDLDVINTCMGPVPGPDAAALAATQTTIHKKQRSYDVISPIQLQSQ
LGALPPGWEQAKTNDGQIYYLK PFRMRKLPNSFFNPP

rs:XP_012812060 [XP_012812060] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Xenopus tropicalis]. 51..65
MEPGSQPSAPAQPPPAGHQIVHVRSDSETDLEALFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPEPKS
HSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPPGVVPGPAPAPNAQHLRQSSYEIPDDVPLPPGWE
MAKTPSGQRYFLNHMEQTTTWQDPRKAMLSQINLPAPTSPPVQQNIMTPTGPLPDGWEQALTPEGETYFINHKNK
TTSWLDPRLDPRFAMNQQRLSQSAPVKSPPALPPQSPQSGVLGSGGNQQQMRLQQLQMEKERLRLKHQELLRQEL
ALRSQIPPMEQDGGTQNPVCSTGISQEMRTMTMNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVD
EMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMESVLAATKLD
KESFLTWL PMRMRKLPDSFFKQP

rs:XP_012812061 [XP_012812061] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Xenopus tropicalis]. 51..65
MEPGSQPSAPAQPPPAGHQIVHVRSDSETDLEALFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPEPKS
HSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPPGVVPGPAPAPNAQHLRQSSYEIPDDVPLPPGWE
MAKTPSGQRYFLNHMEQTTTWQDPRKAMLSQINLPAPTSPPVQQNIMTPTAMNQQRLSQSAPVKSPPALPPQSPQ
SGVLGSGGNQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQIPPMEQDGGTQNPVCSTGISQEMRTMTMN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDL
GTLEGEAMNVEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_012812062 [XP_012812062] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Xenopus tropicalis]. 51..65
MEPGSQPSAPAQPPPAGHQIVHVRSDSETDLEALFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPEPKS
HSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPPGVVPGPAPAPNAQHLRQSSYEIPDDVPLPPGWE
MAKTPSGQRYFLNHMEQTTTWQDPRKAMLSQINLPAPTSPPVQQNIMTPTAMNQQRLSQSAPVKSPPALPPQSPQ
SGVLGSGGNQQQMRLQQLQMEKERLRLKHQELLRQELALRSQIPPMEQDGGTQNPVCSTGISQEMRTMTMNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLE
GEAMNVEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_004912246 [XP_004912246] PREDICTED: protein **FAM181**B [Xenopus tropicalis]. 158..172
MAVQAPIMNHQFMSLYIPGSIADYEKNYQEGVDYLGSVESGDFKEATKDLLSFINTASSNIKLALDKPV
KSKRKVNHRKYLQKQIKRCTGLMGNGNTNQGSPKRSPTSPSNSSMSPSGFPCKPPTKRDSSQSNLQSKSLAALFD
NAKEIRGERCKKVPLRNRNLPPSFFTEPESPSSGLLSTAGAALKDLGKCNQETLEFFDLLGSDYNNMSEQEIIQG
ASVRVHQDVSAEQSLYEPHHLLNGLLYSDMWNPCNQVKKSPVGTANLSLNETLKSAPLHSAMYTNTQDPAMASPM
DDTCPGLTAYTPCFSSDCSLPQLFYDYNTQNYNRISYPVV PLRNRNLPPSFFTEP

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rs:XP_017915372   [XP_017915372] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Capra hircus].    84..98
      MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_017915373   [XP_017915373] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Capra hircus].    84..98
      MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_017915374   [XP_017915374] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Capra hircus].    84..98
      MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_017915375   [XP_017915375] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Capra hircus].    84..98
      MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_017915376   [XP_017915376] PREDICTED: transcriptional coactivator
YAP1 isoform X5 [Capra hircus].    84..98
      MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL    PMRLRKLPDSFFKPP

rs:XP_017915377   [XP_017915377] PREDICTED: transcriptional coactivator
YAP1 isoform X6 [Capra hircus].    84..98
      MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
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QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017915378 [XP_017915378] PREDICTED: transcriptional coactivator
YAP1 isoform X7 [Capra hircus]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017915379 [XP_017915379] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Capra hircus]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSASGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGD
GMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017921371 [XP_017921371] PREDICTED: protein **FAM181**A [Capra hircus].
130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRPLPLESGHGSSPGGGGGYKEKALGNPDREESLSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPIYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004917131 [XP_004917131] PREDICTED: protein **FAM181**A isoform X1
[Xenopus tropicalis]. 144..158
MGHAGWIILSNGIACIDFVWKSVFLNIMASDSEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQ
KQLKRFSQKYSRLPRCTPSKSVDLRKGLLDRQNTTSLNNGLSEKSMHALETEESIIKDTFTQENSSEAGRPDQVP
MRKRHLPASFWEEPRPSSSLLELHCPSRPDIFKESTDTLLPLYETKRGKNLAIHESHSSSSFYPSEDKESGKLPS
VASLTELVNACSCCPFQYHGQAMYQHYPGELSSNPFTALALWSKSTVPTLELQHLCKESGQRIYRHVVLKPIPTK
PAVHSSLFNVFGYI PMRKRHLPASFWEEP

rs:XP_004917132 [XP_004917132] PREDICTED: protein **FAM181**A isoform X2
[Xenopus tropicalis].>rs:XP_004917134 [XP_004917134] PREDICTED: protein
FAM181A isoform X2 [Xenopus tropicalis].>rs:XP_004917133 [XP_004917133]
PREDICTED: protein **FAM181**A isoform X2 [Xenopus tropicalis]. 117..131
MASDSEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCTPSKSVDLRKG
LLDRQNTTSLNNGLSEKSMHALETEESIIKDTFTQENSSEAGRPDQVPMRKRHLPASFWEEPRPSSSLLELHCPS
RPDIFKESTDTLLPLYETKRGKNLAIHESHSSSSFYPSEDKESGKLPSVASLTELVNACSCCPFQYHGQAMYQHY
PGELSSNPFTALALWSKSTVPTLELQHLCKESGQRIYRHVVLKPIPTKPAVHSSLFNVFGYI
PMRKRHLPASFWEEP

rs:XP_013831224 [XP_013831224] PREDICTED: protein **FAM181**B [Capra hircus].
212..226
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDEETGTPAGSLLAGAESGDAREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADMPAKRPLAGAQTVPVPAHGKAA
PRREASQAAAAASLQSRSLAALFDSLRHVPGGADPARAAEAAPAAGLVGGDTACSAGGPAVPGSRKVPLRARNLP
PSFFTEPSRAGGGGGGCGPSGPGVSLGDLEKGSEAAEFFELLGPDYGAGTEAGALLAAEPLDVFPAGAAVLRGPP
ELEPGLFESQPAMVGSLLYPEPWSAPGGPATKKPPLPAPGGGLTLNEPLRSVYPAAADSPGGDDGPGLLASFAPF
FSDCALPPAPPPPPQQVSYDYSAGYSRTAFPGLWRPDGAWEGAPGEEGAPRD PLRARNLPPSFFTEP

rs:XP_005157544 [XP_005157544] protein **FAM181**B [Danio rerio]. 156..170
MAVKAAIMNSQFLNFCFPGSVMDYEVENHLEGGLLSEEGCEGDFRETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISPGAAQVQEPCKRQSLPQTSTSNLSSKTTPKKDGIQANLQSKSLAALFNPA
KDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAAEFLELLGPDYSNMVSEQDLFNTTP
IRIQQEVTMGPEPFDSHHFVTGGFLYTEPWGTCSSTSKKSADMRTVPAQLNLYSHTDLSSSMPVEQSSPCALTFS
NFLTDCSTPPGSYDLANGYNRASFSSL PLRHRNLPPSFFTEP

rs:XP_005173719 [XP_005173719] transcriptional coactivator YAP1 isoform X1 [Danio rerio]. 45..59
MDPNQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRLRKLPDSFFTPPEPKSHSRQAS
TDAGTAGTVTPHHVRAHSSPASLQLGAVSPGALTSMGPANAPPQHLRQSSYEIPDDMPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASAMNQQRISQSAPVKQGSQLPSSPQSGVMSGNNPI
RLQQIHIEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGPGSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKENFLTWL PMRLRKLPDSFFTPP

rs:XP_005339213 [XP_005339213] protein **FAM181**A [Ictidomys tridecemlineatus].>tr:I3N9S7_ICTTR [I3N9S7] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSSTOP00000021124}; 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCSRLPRGLPGRAAEPHLK
RGPEDRPGRLPLHSGPGASPGGGGGCQEKALGNPWREERLPKEQSLQGQGPDAAKPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYESKKSCKGLESLGPETAPVPMSPRALADKEPLKMPGVSLVGRVDAWSCCPLQYH
GQPMYPGPPGALPHSQVPGLCLWRKSPASPGELALFCKEVEGAGQKVHRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_001664241 [XP_001664241] transcriptional coactivator yorkie isoform X1 [Aedes aegypti].>tr:A0A1S4G125_AEDAE [A0A1S4G125] SubName: Full=Uncharacterized protein {ECO:0000313|VectorBase:AAEL014022-PA}; 59..73
MAFNGSPSNNTSAASNTSDENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANQQQQ
QQSANNSSNVNSNKSQPGNVAGGGSGGDGPSAAVQQQQAQQQAQQQSLTRQAILHSRGRSYDVSNQHAHYGELPP
GWEQAKTQDGRIYYLNHNTRTTTWEDPRITAAMQQESLFQQQQQSSVETLFNTGSQTLLSPTISSPTPTNNVVFS
DSIEMSNDLPAPAPAPSNVSMLNSNSNVNLGPLPEGWEEGITAKGERYYINHATRTTTWRDPRLSNQDWAAQEQS
VRLYNLQLERERLRRRQQEIRSHIGEDPFLSGLTDHSRQESGDSGLSESSTSQSMPHTPDFLSSIDDSMDGLSMA
DNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVSNLNLIDPSSTKPDNTLYDII PLRMRKLPDSFFKPP

rs:XP_021696614 [XP_021696614] transcriptional coactivator yorkie isoform X2 [Aedes aegypti]. 59..73
MAFNGSPSNNTSAASNTSDENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANQQQQ
QQSANNSSNVNSNKSQPGNVAGGGSGGDGPSAAVQQQQAQQQAQQQSLTRQAILHSRGRSYDVSNQHAHYGELPP
GWEQAKTQDGRIYYLNHNTRTTTWEDPRITAAMQQESLFQQQQQSSVETLFNTGSQTLLSPTISSPTPTNNANQD
WAAQEQSVRLYNLQLERERLRRRQQEIRSHIGEDPFLSGLTDHSRQESGDSGLSESSTSQSMPHTPDFLSSIDDS
MDGLSMADNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVSNLNLIDPSSTKPDNTLYDII
PLRMRKLPDSFFKPP

rs:XP_019616212 [XP_019616212] PREDICTED: transcriptional coactivator YAP1-like isoform X1 [Branchiostoma belcheri]. 37..51
MDAQGRQVLSHGDPEGDLEKLFAAVMNKKEGQPVSVPMRMRNLPPSFFNPPPDRAKGGASAAAYPGPPP
TSQMSPHNLPIAHSRAHSSPASLQATQQASAQQFQHLRQQSYDPTAMDDLGPLPPGWEMAHTASGQRYYLNHNNQ
TTTWEDPRKSLSTSSLNQPQSPAGTPVRSPGSMSPLSPSPAHSQQGLNNINNIPLPEGWEQATTPEGEIYFINHR
TQTTTWLDPRLAMMQRQQSIPQHQQPPYQARSPTPQQQAQVNEQQRQQKLRLQRLQLERERLRMRQEQIMQQEMA
LRAGQMPEEQMNVAGMPPASQAAVSSASQNPTQTSSEMQAVTTTGMDPFLSSGTPYHSRDESADSGLGMSSNYSL
PRTPEDFLSNVDEMDTSENTGAEKMQTSRPNSTQPQPGGRGMPDILDTMQGTNVDLGFPETESSNVDSEELVPSL
QEALNSDILNDVENMLSPSKIDNFLTWL PMRMRNLPPSFFNPP

rs:XP_019616213   [XP_019616213] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Branchiostoma belcheri]. 37..51
      MDAQGRQVLSHGDPEGDLEKLFAAVMNKKEGQPVSVPMRMRNLPPSFFNPPPDRAKGGASAAAYPGPPP
TSQMSPHNLPIAHSRAHSSPASLQATQQASAQQFQHLRQQSYDPTAMDDLGPLPPGWEMAHTASGQRYYLNHNNQ
TTTWEDPRKSLSTSSLNQPQSPAGTPVRSPGSMSPLSPSPAHSQQGLNNINNIPLPEGWEQATTPEGEIYFINHR
TQTTTWLDPRLAMMQRQQSIPQHQQPPYQARSPTPQQQAQVNEQQRQQKLRLQRLQLERERLRMRQEQIMQQMAL
RAGQMPEEQMNVAGMPPASQAAVSSASQNPTQTSSEMQAVTTTGMDPFLSSGTPYHSRDESADSGLGMSSNYSLP
RTPEDFLSNVDEMDTSENTGAEKMQTSRPNSTQPQPGGRGMPDILDTMQGTNVDLGFPETESSNVDSEELVPSLQ
EALNSDILNDVENMLSPSKIDNFLTWL   PMRMRNLPPSFFNPP

rs:XP_019616214   [XP_019616214] PREDICTED: transcriptional coactivator
YAP1-like isoform X3 [Branchiostoma belcheri]. 37..51
      MDAQGRQVLSHGDPEGDLEKLFAAVMNKKEGQPVSVPMRMRNLPPSFFNPPPDRAKGGASAAAYPGPPP
TSQMSPHNLPIAHSRAHSSPASLQATQQASAQQFQHLRQQSYDPTAMDDLGPLPPGWEMAHTASGQSHNNQTTTW
EDPRKSLSTSSLNQPQSPAGTPVRSPGSMSPLSPSPAHSQQGLNNINNIPLPEGWEQATTPEGEIYFINHRTQTT
TWLDPRLAMMQRQQSIPQHQQPPYQARSPTPQQQAQVNEQQRQQKLRLQRLQLERERLRMRQEQIMQQEMALRAG
QMPEEQMNVAGMPPASQAAVSSASQNPTQTSSEMQAVTTTGMDPFLSSGTPYHSRDESADSGLGMSSNYSLPRTP
EDFLSNVDEMDTSENTGAEKMQTSRPNSTQPQPGGRGMPDILDTMQGTNVDLGFPETESSNVDSEELVPSLQEAL
NSDILNDVENMLSPSKIDNFLTWL   PMRMRNLPPSFFNPP

rs:XP_019621851   [XP_019621851] PREDICTED: protein **FAM181**B-like
[Branchiostoma belcheri].   165..179
      MRLDMSDSSPLLMELHPPPHPSQRLSPGATPGSNPSPSPSHSPACPSPRSSEVETDSLLSFMDTACNSI
KLALDRPSRSRRKVNHRKYLQKQIKRCTQKLSPGDGENDDKDDNASDKEAATANKPVSRRDSHIGVQSKSLAALF
DPNTLKRPVNPAPTRGRTRVPLRKRNLPPSFFTEPGNQSGHRGSLQTCAVAGSWPLDGYRHPAAGVSDSLDIFNP
DIADLITNWQDESGHISDPSMPAMPGNSTMGMAGSGDHAPIMLHMPSQPYGTNFNMNFPAQSQSNQGLLTTAPQS
WMPSTPSYPSTPSSNYTASREDYSRVGYQASSSAGLSSSLYAPQVHQMPNGLPDFPQAFGHGQAAIGQQWPNSLC
YTYL PLRKRNLPPSFFTEP

rs:XP_019637758   [XP_019637758] PREDICTED: uncharacterized protein
LOC109480050 [Branchiostoma belcheri].   134..148
      MAGKTGGKVGFPSGGKVGFSSGKRGAPAPVSSSDEEEIEKEVQEKEDYENIASPCSSTSSGPVYERQPG
FEKHGHEVVVPRRPKIKHKIKRKKMTNFMLGGDHDFYTASRGRRKDGTMVPTPPSKGKPKRDTVPMRLRALPQSF
WQQPNNMNNNSPGSLYPVLPPVVNKEVSDEYLGQVVSVPTEIRPVTPPEERTETDQQERTGRKEEETVVTKPEKT
VEKVAVKEDKEKTEKEKSEKEKTEKEKTEKEVKKEKIDLVEEGVTGATVTVTTTAPPRTRTVRTVTSTVPNTDLL
FSLFDGVDPETKRQTVKLKRGRPKRIHLEGMNAPRPRSQDNDPYMVDNIAERLFPVLSLENRKQNTNPANPNVTT
TLHYITLNGEDEKSSVSLPAVRVETNYSQMLSELVMHI   PMRLRALPQSFWQQP

rs:XP_019642504   [XP_019642504] PREDICTED: protein **FAM181**A-like
[Branchiostoma belcheri].   165..179
      MTQGEENAICGRAERTLQQARKCKMAQGSGGATADADVKTLLNFVNLASSDIKAALDKSAPCKRSVDHR
KYLQKQLKRFSQRRVLPRYVARPVKDTTSFLKRRPESTSSVNSESSGSGSESCSESGPILPENCNPIDLSMPDKD
QPVEKDQELGLQDPAAADSVPLRKRALPASFWQEPGVQKGQSSGSGGSPSAEESECSPGKQDAKPTGETTSVPPR
ITNHGLDRFPTAVPPAPLGYLPYHGYRPYLGYVPPPPCGFDPTQSLGHSAQGLAQAPGLCPRPKEAACSCCLGQN
TTVSAAYSRFPYGHHHPGYVSVPHSPLAAHAPYSPPWERTNPPSSSSSSPTTTKPKIWRPIPTKTVSTFPTRFHP
LHM   PLRKRALPASFWQEP

rs:XP_019804223   [XP_019804223] PREDICTED: protein **FAM181**B [Tursiops
truncatus].>tr:A0A2U4CFK5_TURTR [A0A2U4CFK5] SubName: Full=protein **FAM181**B
{ECO:0000313|RefSeq:XP_019804223.1};   221..235
      MAVQAALLSTHPFVPFGFGGSPDGLGSAFGALDKGCCFEDEETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAATSAQTVPVQAHGK
AAPRREASQAAAAASLQSQSLAALFDSLSHVPGAADPAGVAEAAPAAGLVGAGAGGVGGDAAGPAGVPAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAAEFFEMLGPDYGAGTEAGVLLAAEPLDVLLTGA
AVLRGPPELEPGLFEPPPAMGGSLLYPEPWSAPGGPTTKKSPLAAPRGGLTLNEPLRPLYPAAADSPGGDDGPGL
LASFTPFFSDCAVPPPPPPPPQVSYDYSAGYSRTAYASLWRPDGIWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_019810914   [XP_019810914] PREDICTED: protein **FAM181**B [Bos indicus].
      214..228

MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALXKGCCFEDEETGTPAGALLAGAESGDAREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXSLQSRSLAALFDSLRHVPGGADPAGVAEAVPAAGLVRGDAAGSAGGPAVPGARKVPLRARN
LPPSFFTEPSRAGGCVCGPSGPGVSLGDLEKGSEAAEFFELLGPDYGAGTEAGALLAAEPLDVFPAGAAVLRGPP
ELEPGLFDPQPAMVGSLLYPEPWSAPGGPATKKPPLPAPGGGLTLNEPLRSVYPAAADSPGGDDGPGLLASFTPF
FSDCALPPAPPPQQVSYDYSAGYSRTAFAGLWRPDGAWEGAPGEEGAPRD   PLRARNLPPSFFTEP

rs:XP_022116627   [XP_022116627] transcriptional coactivator YAP1-A isoform
X1 [Pieris rapae].   43..57
MALNSDEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSHS
RENSADSAFGSSSATGSAPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGSHLPDELGPLPAGWE
QARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVASGVQHQSAEALLTQTPSPQNLPTPTPAAKSTSTSATTDPLG
PLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPAANAGAAGGGWANASVQACQQKLRLQSLQLERER
LKQRQQEIRLQQELMARQSSSIVSSLTNSTATSTDLSLDPFLPGLNDHQRQESADSGLGMAVSQSYSMPHTPEGF
LGMDDRMDCTSEAGANLDTDMALGDTDDLLGDFTNDILLDDVQSLINSTPNKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_022116628   [XP_022116628] transcriptional coactivator yorkie isoform
X2 [Pieris rapae].   43..57
MALNSDEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSHS
RENSADSAFGSSSATGSAPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGSHLPDELGPLPAGWE
QARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVASGVQHQSAEALLTQTPSPQNLPTPTPAQHLQRTPAANAGAA
GGGWANASVQACQQKLRLQSLQLERERLKQRQQEIRLQQELMARQSSSIVSSLTNSTATSTDLSLDPFLPGLNDH
QRQESADSGLGMAVSQSYSMPHTPEGFLGMDDRMDCTSEAGANLDTDMALGDTDDLLGDFTNDILLDDVQSLINS
TPNKPDNVLTWL   PLRMRQLPKSFFNPP

rs:XP_022449645   [XP_022449645] protein **FAM181**B [Delphinapterus
leucas].>tr:A0A2Y9PVX0_DELLE [A0A2Y9PVX0] SubName: Full=protein **FAM181**B
{ECO:0000313|RefSeq:XP_022449645.1};   221..235
MAVQAALLSTHPFVPFGFGGSPDGLGSAFGALDKGCCFEDEETGTPAGALLVGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAASAQTVPVQAHGK
AAPRREASQAAAAASLQSQSLAALFDSLSHVPGAADPAGVAEAAPAAGLVGAGAGGVGGDAAGPAGGPAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAAEFFEMLGPDYGAGTEAGVLLAAEPLDVLLTGA
AVLRGPPELEPGLFEPPPAMGGSLLYPEPWSAPGGPTTKKSSLAAPRSGLTLNEPLRPLYPAAADSPGGDDGPGL
LASFSPFFSDCALPPPPPPPQVSYDYSAGYSRTAYASLWRPDGIWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_022417753   [XP_022417753] transcriptional coactivator YAP1 isoform
X1 [Delphinapterus leucas].>tr:A0A2Y9MKS8_DELLE [A0A2Y9MKS8] SubName:
Full=transcriptional coactivator YAP1 isoform X1
{ECO:0000313|RefSeq:XP_022417753.1};   86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQ
NPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQ
QNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_022417754   [XP_022417754] transcriptional coactivator YAP1 isoform
X2 [Delphinapterus leucas].>tr:A0A2Y9M6I5_DELLE [A0A2Y9M6I5] SubName:
Full=transcriptional coactivator YAP1 isoform X2
{ECO:0000313|RefSeq:XP_022417754.1};   86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN

RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_022417755 [XP_022417755] transcriptional coactivator YAP1 isoform
X3 [Delphinapterus leucas].>tr:A0A2Y9M7Q0_DELLE [A0A2Y9M7Q0] SubName:
Full=transcriptional coactivator YAP1 isoform X3
{ECO:0000313|RefSeq:XP_022417755.1}; 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_022417756 [XP_022417756] transcriptional coactivator YAP1 isoform
X4 [Delphinapterus leucas].>tr:A0A2Y9M9S8_DELLE [A0A2Y9M9S8] SubName:
Full=transcriptional coactivator YAP1 isoform X4
{ECO:0000313|RefSeq:XP_022417756.1}; 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_022417757 [XP_022417757] transcriptional coactivator YAP1 isoform
X5 [Delphinapterus leucas].>tr:A0A2Y9MFF0_DELLE [A0A2Y9MFF0] SubName:
Full=transcriptional coactivator YAP1 isoform X5
{ECO:0000313|RefSeq:XP_022417757.1}; 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMT
TNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNV
DLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_022417758 [XP_022417758] transcriptional coactivator YAP1 isoform
X6 [Delphinapterus leucas].>tr:A0A2Y9MKT3_DELLE [A0A2Y9MKT3] SubName:
Full=transcriptional coactivator YAP1 isoform X6
{ECO:0000313|RefSeq:XP_022417758.1}; 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_022417759 [XP_022417759] transcriptional coactivator YAP1 isoform
X7 [Delphinapterus leucas].>tr:A0A2Y9M6J0_DELLE [A0A2Y9M6J0] SubName:
Full=transcriptional coactivator YAP1 isoform X7
{ECO:0000313|RefSeq:XP_022417759.1}; 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT

PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_022417760 [XP_022417760] transcriptional coactivator YAP1 isoform
X8 [Delphinapterus leucas].>tr:A0A2Y9M7Q6_DELLE [A0A2Y9M7Q6] SubName:
Full=transcriptional coactivator YAP1 isoform X8
{ECO:0000313|RefSeq:XP_022417760.1}; 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQTAPPGSQAAPQAPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_022617223 [XP_022617223] transcriptional coactivator YAP1 [Seriola
dumerili].>rs:XP_023260693 [XP_023260693] transcriptional coactivator YAP1
[Seriola lalandi dorsalis].>tr:A0A3B4V6L6_SERDU [A0A3B4V6L6] SubName:
Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSSDUP00000026252};
45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKSTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGALTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAAPASSVPVQQQNLMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
DQRYALNQQRITQSAPVKQGGQLPPSHSAVMGANNQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQD
GSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSMAT
QPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_022618502 [XP_022618502] transcriptional coactivator YAP1-like
isoform X1 [Seriola dumerili].>tr:A0A3B4TH51_SERDU [A0A3B4TH51] SubName:
Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSSDUP00000005524};
46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQATDVAAPQIIPDDVPLPHGWEMAKTPAGQRYFLNHLDKTTTWH
DPRLSQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQNINPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVAPR
LAQKMNPGILGLALQQRQEKERLRCKGLPPQITPQEAGGRNQMTGGMDHDRNAPTLVPSLDVRIRSSNHEPTLNG
AHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGDNSSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDM
ETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_025321528 [XP_025321528] transcriptional coactivator YAP1 isoform
X1 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV
QQSMMTSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPPGVLG
GGGSSQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNISPSTANSPKCQELALRSQLPTLEQDGGTPNPVPS
PGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_025321529 [XP_025321529] transcriptional coactivator YAP1 isoform
X2 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV
QQSMMTSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPPGVLG

GGGSSQQQQMRLQQLQMEKERLRLKQQELLRQAMRNISPSTANSPKCQELALRSQLPTLEQDGGTPNPVPSPGMS
QELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLE
AIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_025321530   [XP_025321530] transcriptional coactivator YAP1 isoform
X3 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV
QQSMMTSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPPGVLG
GGGSSQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_025321531   [XP_025321531] transcriptional coactivator YAP1 isoform
X4 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV
QQSMMTSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPPGVLG
GGGSSQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLN
SGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDG
MNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025321533   [XP_025321533] transcriptional coactivator YAP1 isoform
X5 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV
QQSMMTSASAMNQRISQSAPVKQPPPLAPQSPPGVLGGGGSSQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAM
RNISPSTANSPKCQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMS
SYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSS
DILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025321534   [XP_025321534] transcriptional coactivator YAP1 isoform
X6 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV
QQSMMTSASAMNQRISQSAPVKQPPPLAPQSPPGVLGGGGSSQQQQMRLQQLQMEKERLRLKQQELLRQAMRNIS
PSTANSPKCQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSV
PRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILN
DMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025321535   [XP_025321535] transcriptional coactivator YAP1 isoform
X7 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV
QQSMMTSASAMNQRISQSAPVKQPPPLAPQSPPGVLGGGGSSQQQQMRLQQLQMEKERLRLKQQELLRQVRPQEL
ALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVD
EMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLD
KESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025321536   [XP_025321536] transcriptional coactivator YAP1 isoform
X8 [Canis lupus dingo]. 84..98
MDPGPPPPAAPPQAQGPPSAPPPPGQAPPSAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPV

QQSMMTSASAMNQRISQSAPVKQPPPLAPQSPPGVLGGGGSSQQQQMRLQQLQMEKERLRLKQQELLRQELALRS
QLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDT
GDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESF
LTWL PMRLRKLPDSFFKPP

rs:XP_025275284   [XP_025275284] protein **FAM181**B [Canis lupus dingo].
221..235
MAVQAALLSTHPFVPFGFGGSPDALGGAFGALDKGCCFEDDEPGPPAGALLAGAEGGDVREATRDLLSF
MDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADAPAKRPLGAAGAQAVAGPPPGK
AAPRREASQAAAANSLQSRSLAALFDSLRHVPAGDERPGASGAAPAAALGAAGAGGSGGDAAGPAGGTAGPGARK
VPLRARNLPPSFFTEPSRAGGGCGPSGPGVSLGDLEKGADAVEFLELLAPDYGAGAGAGAGAGAGAGAGVLLA
AEPLEVFPAGAAVLRGPPELEPGLFEPPAATVGALLYPEPWSAPGCPPAKRPPPAAPRGGLALTEPLRPAYPAAA
DCPGGEDAPGLLASFAPFFSDCALPPPPPPPPHQVSYEYGAGYGRSAYAGLWRPDAAWEGAPGEEGAPRD
PLRARNLPPSFFTEP

rs:XP_019839553   [XP_019839553] PREDICTED: protein **FAM181**A isoform X1 [Bos indicus].   252..266
MVPMVTICDGKECGNGAAACLGCFVSGEALPDWPEGPPAPGTRRPPFSPLEGGTTASSRTTELAGRAKP
GPGLQHGGNLCRATLAGARAPALSVGSVLFPGAASCLENPASSWKARCSGALVMASDSDVKMLLNFVNLASSDIK
AALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRXAEPHLKRGPEDRPGRPLPLESGHGSSPGGGGGCK
EKALGNLDREESLSKERTLHGPDPGATKPGQVPMRKRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHC
KGLEPLGPETTPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQYHGQPVYPSPPGALPQSPMPSLGLWRKSA
ASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_019839554   [XP_019839554] PREDICTED: protein **FAM181**A isoform X2 [Bos indicus].   130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRXAEPHLK
RGPEDRPGRPLPLESGHGSSPGGGGGCKEKALGNLDREESLSKERTLHGPDPGATKPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_019873447   [XP_019873447] PREDICTED: transcriptional coactivator YAP1-A isoform X1 [Aethina tumida]. 41..55
MALNQDEDKPVLRVDQDSETDLQALFDSVLKPNSKRPLQVPWSMRNMPDSFFNPPSTGSKSINHSRENS
VDSAFGSGAANSASVNSVPLQTAHHRAHSSPASLQQTYAVGQQQTPTHHHIKQRSYDVATKTEDDTPLPHGWEQA
RTPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAAQHQSAEHLLSSQTSHPSPTSTSAKLTTDVDLGPLPEGWEQAQ
TPEGEIYFINHQTRTTSWFDPRIPQHLQQRSPSNLVGSTWHSPLSQSPAKAQQARLHQLQLEREKLRQRQQEIRR
QELIRSSSPMDPYISNYTDHSRQESGDSGLGMGNFSLPHTPEDYLSNIDDNMDVASETHTMDTPDISTLSDNIDS
TDDLVPTLGLDEEFPILEEVQSLINTPTTRPDNVLIWL   PWSMRNMPDSFFNPP

rs:XP_019873448   [XP_019873448] PREDICTED: WW domain-containing transcription regulator protein 1 isoform X2 [Aethina tumida].   41..55
MALNQDEDKPVLRVDQDSETDLQALFDSVLKPNSKRPLQVPWSMRNMPDSFFNPPSTGSKSINHSRENS
VDSAFGSGAANSASVNSVPLQTAHHRAHSSPASLQQTYAVGQQQTPTHHHIKQRSYDVATKTEDDTPLPHGWEQA
RTPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAAQHQSAEHLLSSQTSHPSPTSTSQHLQQRSPSNLVGSTWHSPL
SQSPAKAQQARLHQLQLEREKLRQRQQEIRRQELIRSSSPMDPYISNYTDHSRQESGDSGLGMGNFSLPHTPEDY
LSNIDDNMDVASETHTMDTPDISTLSDNIDSTDDLVPTLGLDEEFPILEEVQSLINTPTTRPDNVLIWL
PWSMRNMPDSFFNPP

rs:XP_019525794   [XP_019525794] PREDICTED: transcriptional coactivator yorkie-like isoform X1 [Aedes albopictus].   59..73
MAFNGSPGNNSSATSNTSEENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANAAQQ
AANNSSNVNSNKTQQPGSVNGGGASSGGDGSSAAAAVQQQQQAQQQAAQQQSLTRQAILHSRGRSYDVSNQHAVY
GDLPPGWEQAKTQDGRIYYLNHNTRTTTWEDPRITAAMQQESLFQQQQQSSVETLFNTGSQTLLSPTISSPTPTN
NVVFSDSIEMSNDLPAPAPAAPSNVSMLNSSQNSNNNNNNQNANPNSNNNVGPLPDGWEEGITAKGERYYINHAT
RTTTWRDPRLSNQDWAAQEQSVRLYNLQLERERLRRRQQEIRSHIGEDPFLSGLTDHSRQESGDSGLSESSTSQS

MPHTPDFLSSIDDSMDGLSMADNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVSNLNLIDPSSTKPDNTLYDII
PLRMRKLPDSFFKPP

rs:XP_019525803 [XP_019525803] PREDICTED: transcriptional coactivator
yorkie-like isoform X2 [Aedes albopictus]. 59..73
MAFNGSPGNNSSATSNTSEENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANAAQQ
AANNSSNVNSNKTQQPGSVNGGGASSGGDGSSAAAAVQQQQQAQQQAAQQQSLTRQAILHSRGRSYDVSNQHAVY
GDLPPGWEQAKTQDGRIYYLNHNTRTTTWEDPRITAAMQQESLFQQQQQSSVETLFNTGSQTLLSPTISSPTPTN
NANQDWAAQEQSVRLYNLQLERERLRRRQQEIRSHIGEDPFLSGLTDHSRQESGDSGLSESSTSQSMPHTPDFLS
SIDDSMDGLSMADNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVSNLNLIDPSSTKPDNTLYDII
PLRMRKLPDSFFKPP

rs:XP_019548748 [XP_019548748] PREDICTED: transcriptional coactivator
yorkie-like isoform X1 [Aedes albopictus]. 59..73
MAFNGSPGNNSSATSNTSEENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANAAQQ
VANNSSNVNSNKTQQPGSVNGGGASSGGDGSSAAAAVQQQQQAQQQAAQQQSLTRQAILHSRGRSYDVSNQHAVY
GDLPPGWEQAKTQDGRIYYLNHNTRTTTWEDPRITAAMQQESLFQQQQQSSVETLFNTGSQTLLSPTISSPTPTN
NVVFSDSIEMSNDLPAPAPAAPSNVSMLNSSQNSNNNNNNNNQNANPNSNNNVGPLPDGWEEGITAKGERYYINH
ATRTTTWRDPRLSNQDWAAQEQSVRLYNLQLERERLRRRQQEIRSHIGEDPFLSGLTDHSRQESGDSGLSESSTS
QSMPHTPDFLSSIDDSMDGLSMADNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVSNLNLIDPSSTKPDNTLYD
II PLRMRKLPDSFFKPP

rs:XP_019548749 [XP_019548749] PREDICTED: transcriptional coactivator
yorkie-like isoform X2 [Aedes albopictus]. 59..73
MAFNGSPGNNSSATSNTSEENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANAAQQ
VANNSSNVNSNKTQQPGSVNGGGASSGGDGSSAAAAVQQQQQAQQQAAQQQSLTRQAILHSRGRSYDVSNQHAVY
GDLPPGWEQAKTQDGRIYYLNHNTRTTTWEDPRITAAMQQESLFQQQQQSSVETLFNTGSQTLLSPTISSPTPTN
NANQDWAAQEQSVRLYNLQLERERLRRRQQEIRSHIGEDPFLSGLTDHSRQESGDSGLSESSTSQSMPHTPDFLS
SIDDSMDGLSMADNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVSNLNLIDPSSTKPDNTLYDII
PLRMRKLPDSFFKPP

rs:XP_020023398 [XP_020023398] transcriptional coactivator YAP1 isoform
X1 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDSRFAMNQRISQSAPVKQPPPMAPQSPQGGV
MGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEPDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_020023399 [XP_020023399] transcriptional coactivator YAP1 isoform
X2 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDSRFGKAMNQRISQSAPVKQPPPMAPQSPQG
GVMGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEPDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_020023400 [XP_020023400] transcriptional coactivator YAP1 isoform
X3 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF

NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDSRFGKAMNQRISQSAPVKQPPPMAPQSPQG
GVMGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEPDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020023401 [XP_020023401] transcriptional coactivator YAP1 isoform X4 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDSRFAMNQRISQSAPVKQPPPMAPQSPQGGV
MGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEPDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020023402 [XP_020023402] transcriptional coactivator YAP1 isoform X5 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDSRFGKAMNQRISQSAPVKQPPPMAPQSPQG
GVMGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEPDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020023403 [XP_020023403] transcriptional coactivator YAP1 isoform X6 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDSRFAMNQRISQSAPVKQPPPMAPQSPQGGV
MGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEPDGGTQNPVSSPGMSQELRTMTTNSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGD
GMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020023404 [XP_020023404] transcriptional coactivator YAP1 isoform X7 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASAMNQRISQSAPVKQPPPMAPQSPQGGVMGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQAMRNI
NPSTANSPKCQELALRSQLPTLEPDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYS
VPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDIL
NDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020023405 [XP_020023405] transcriptional coactivator YAP1 isoform X8 [Castor canadensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASAMNQRISQSAPVKQPPPMAPQSPQGGVMGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQVRPQE
LALRSQLPTLEPDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020023406 [XP_020023406] transcriptional coactivator YAP1 isoform X9 [Castor canadensis]. 85..99

MDPGQQPPPQPAPQGPGQPPAQTPQAQGPPSGPGQPAPPAAQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VPQNMMNSASAMNQRISQSAPVKQPPPMAPQSPQGGVMGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQELALR
SQLPTLEPDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMD
TGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKES
FLTWL PMRLRKLPDSFFKPP

rs:XP_006133734 [XP_006133734] protein **FAM181**A [Pelodiscus
sinensis].>rs:XP_006133735 [XP_006133735] protein **FAM181**A [Pelodiscus
sinensis].>tr:K7EYK0_PELSI [K7EYK0] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSPSIP00000000860};
126..140
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCPTSKSIESSSK
RGTDDRNRSSNPDGLDPNHCRVSSEKALRLSEVEENFSGEQVLQEQSPESIRPDQVPMRKRQLPASFWEEPRPTQ
SLLVGSFPAGLDGLPNSRDLPPYKGKKSKKGPDTTEPGTPPLPAQPRGEKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTHGALPQSPFPGLGLWRKSTAPAGEIQHFCKEAGSMGQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_014381795 [XP_014381795] uncharacterized protein LOC106723032
[Alligator sinensis].>rs:XP_014381796 [XP_014381796] uncharacterized
protein LOC106723032 [Alligator sinensis].>tr:A0A1U8DX22_ALLSI [A0A1U8DX22]
SubName: Full=uncharacterized protein LOC106723032
{ECO:0000313|RefSeq:XP_014381795.1, ECO:0000313|RefSeq:XP_014381796.1};
214..228
MAAGVIRNPAEFRLPSSFQHSFLHPAVHQDRDFQELSEEEEDEEEEEEEEEEMEEVESQGSPTAPIPGG
ERQEVTATASLHDAEMTLQLLRFSELISSDIQRYFGRKDKEEDPDSCNIYEDCFSPQRSGRELYYADLMHIAQSG
ELDDEDSHSAQVPLGQLDQQVWRSICNKDGGQKLGPLAELFEYGLRQYIKQTVSDSRRLRLEKKYAHIIPMHRRK
LPPSFWKEPSPGPASILNTNTPDFSDLLANWTVEPGQELPNASRELAGELGRQAMEADQFNVL
PMHRRKLPPSFWKEP

rs:XP_012591562 [XP_012591562] protein **FAM181**B [Microcebus murinus].
221..235
MAVQAALLSTHPFVPFGFGGAPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAQGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAAPGPPSPSAADTPAKRPPVAPSAPTVAVPAQGK
AAPRREASQAAAAASLQSRSLAALFDSLRHLPGGAEPAGAAVAAPAAGLGGAGAGGSGGDGAGPSGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCSPSGPGVCLGDLEKGAEAVEFFELLGPDYSAGTEAAVLLAAEPLDVFPAGA
AVLRGPPELEPSFFEPPPAVVGNLLYPEPWSVPGCPATKKPPRGGLTLNEPLRPLYPAAADSPGGEDGPGHLASF
APFFPDCALPPPPPPHQVSYDYGAGYSRTAYSSLWRPDGVWEGPPGEEGAPRDPLRARNLPPSFFTEP

rs:XP_012625980 [XP_012625980] transcriptional coactivator YAP1 isoform
X1 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
AVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012625981 [XP_012625981] transcriptional coactivator YAP1 isoform
X2 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNAV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR

FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012625982 [XP_012625982] transcriptional coactivator YAP1 isoform
X3 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNAVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012625983 [XP_012625983] transcriptional coactivator YAP1 isoform
X4 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNAVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012625985 [XP_012625985] transcriptional coactivator YAP1 isoform
X5 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012625986 [XP_012625986] transcriptional coactivator YAP1 isoform
X6 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012625987 [XP_012625987] transcriptional coactivator YAP1 isoform
X7 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012625988 [XP_012625988] transcriptional coactivator YAP1 isoform
X8 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP

TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_012625989 [XP_012625989] transcriptional coactivator YAP1 isoform X9 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_012625990 [XP_012625990] transcriptional coactivator YAP1 isoform X10 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012625991 [XP_012625991] transcriptional coactivator YAP1 isoform X11 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012625992 [XP_012625992] transcriptional coactivator YAP1 isoform X12 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL   PMRLRKLPDSFFKPP

rs:XP_012625993 [XP_012625993] transcriptional coactivator YAP1 isoform X13 [Microcebus murinus]. 85..99
MDPGQQQPPQPAPQGQGQPPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
AVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTVLPKVYIRAR
PMRLRKLPDSFFKPP

rs:XP_022604687 [XP_022604687] protein **FAM181**B [Seriola dumerili].>rs:XP_023261647 [XP_023261647] protein **FAM181**B [Seriola lalandi dorsalis]. 155..169

MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQGSPLAQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSDQDLYHSMPL
RVQPEMGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKQGESLRTGPAQPPVYCHSEAATGPIEDNALCTLAFPN
FFTDCSIPQVTYDLSGGYNRANYSSL   PLRHRNLPPSFFTEP

rs:XP_012710185   [XP_012710185] protein **FAM181**A [Fundulus heteroclitus].>tr:A0A146SG82_FUNHE [A0A146SG82] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:JAQ79661.1};   104..118
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRCQTLRSADYRC
ARAAGAERQSAAVVDEAGSDAQHAQNVGGVTEQVPMRKRQLPASFWEEPRLTKTKRDKSCLDLRRSSSGTSEGTE
NEKRRRSQDDALKTAISSSSRRSSVDKDVLKLDLTSHHSVSFCGCWPFQFHGNQVLHSQIVVPHPPVSLWSKAAG
PEPERPEHPYGQKLHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_012710689   [XP_012710689] transcriptional coactivator YAP1-like isoform X1 [Fundulus heteroclitus]. 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPGKAARQPHSLPMRMRKLPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTPTGQRYFINHVHKTTTW
QDPRLSQLQSAAAQHQIACTPIHAHSFSNPAPTTQPKNIIPETGPLPEGWEQAVTADGEMYYIDHINKTTTWDDP
RLAQKVNPANLGLAMQQRQEKLRLKHSILPQFVPQESGGSNQMPGGMDHDRTAQMLVPSVDVRIRALKQEPNLNG
AHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSSEPPSMSLQESMPVLPMNDELMPGIPDGLTSDILMDMDT
VLSGSHMDRDSLLTWL PMRMRKLPDSFFKPP

rs:XP_012710690   [XP_012710690] transcriptional coactivator YAP1-like isoform X2 [Fundulus heteroclitus]. 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPGKAARQPHSLPMRMRKLPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTPTGQRYFINHVHKTTTW
QDPRLSQLQSAAAQHQIACTPIHAHSFSNPAPTTQPKNIIPETAQKVNPANLGLAMQQRQEKLRLKHSILPQFVP
QESGGSNQMPGGMDHDRTAQMLVPSVDVRIRALKQEPNLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTG
DSSEPPSMSLQESMPVLPMNDELMPGIPDGLTSDILMDMDTVLSGSHMDRDSLLTWL PMRMRKLPDSFFKPP

rs:XP_012730683   [XP_012730683] transcriptional coactivator YAP1 [Fundulus heteroclitus].>tr:A0A146P8N6_FUNHE [A0A146P8N6] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:JAQ39740.1};   45..59
MDPNQHNPPVGHQIIHVRGDSQTDLELLFNSVMNPKNSNVPASLPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSAGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDMPLPAGWEMAKTHSGQRYF
LNHIDKTTTWQDPRKSLLQMNQPAPPSSVPVPQQNLMNPASGALPEGWEQAITPEGEIYYINHKNKTTSWLDPRY
AQNQPRITQSAPVKQSGQLPPSTHGGVMGGNNQLRLPQIEKERLRLQQHRPQELAVRNQLPTSMDQDGSTNPVSS
PLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSIATQPNRFPDY
LDAIPGTDVDLGTLESESMVVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_012730671   [XP_012730671] LOW QUALITY PROTEIN: protein **FAM181**B [Fundulus heteroclitus].   262..276
MNSALHQRVFDLKLKHTWVAGHKQRVKSSGXPLLLLFDVLTSSALPPERSPSSSPEPVTPNLDCLWKLH
ERHQEQVFIRGRKSCSEETLSSRITVDATGVAAGLDRVMAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCE
AENDEDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQSSPVSQ
QGPLQSKNLQKREGGQANLQSKSLAALFSPEKEIRGEKAKKPPLRHRNLPPSFFTEPANCSRVSSTSGMTLKDLE
RGNPEAAEFFELLGPDYSNMVTEQDVYQGVSPRVQPDLGGLDSTSYDHLVSGLLYPEPWTNCLGPCKKPGDGLRT
GPPQPPVYGQAEDPSVSLDDSGLCTLAFPNFFPDCSIPQAAYDLNGGYSKTSYSCL   PLRHRNLPPSFFTEP

rs:NP_001116819   [NP_001116819] YAP65-like protein [Bombyx mori].>rs:XP_028040851 [XP_028040851] transcriptional coactivator YAP1 isoform X3 [Bombyx mandarina].>tr:B2CMB6_BOMMO [B2CMB6] SubName: Full=YAP65-like protein {ECO:0000313|EMBL:ACB41089.1};   44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAAKSTSNTTTDPLG
PLPEGWEQATTAEGEIYFINHAARTTSWFDPRIPQHLQRTPVGATGVAGGGWANASIQACQQKLRLQSLQLERDR

LKQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGLTDHQRQESADSGLGMAVPQSYSMPHTPE
DFLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:NP_001257838 [NP_001257838] protein **FAM181**A [Callithrix jacchus].>rs:XP_009004735 [XP_009004735] PREDICTED: protein **FAM181**A isoform X1 [Callithrix jacchus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGPEDRPGRLLLDLGPDSSPSGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLQGGLGPREGPPYEGKKNCKGLEPLGPETASVPMSPSALVEKESLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKDADGLGQKVCRPMVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_021448793 [XP_021448793] protein **FAM181**B isoform X1 [Oncorhynchus mykiss]. 195..209
MAVQTAIMNSPFVNFCFPGSVMMEYDMGQSLDGSPLEESEERGDYRETTRSLDGSPLEESEERGEYRET
TRNLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGFISPTGNPAAAPGANKRKVSGFPTQTQTQPQ
TQLQTQPSPFQQGKPVHKRDGLQANLQTKSLAALFNSVKEPVKGERAKKPPLRHRNLPPSFFTEPANTTTTSRVT
STPGMFLGDLERGAGNPDFFDLLGPDYSNMLSDQDVFQTRGLPSRVIDQDVFQTRGLPSRIIDQDMFQTRGLPSR
ILQHQQTQDITDQVSPYDPHHLVGGFLYTEPWTSSPSKKAGEGVRTGPGTQTPLYCQSGEGVRTGPGTQTPLYCQ
SGECVRTGPGTQTPLYCHSVSDSSATGSTEDSNSLCTLAFPNFFPDCSVSQVSYGLSSGGYNTKDFSSL
PLRHRNLPPSFFTEP

rs:XP_021448794 [XP_021448794] protein **FAM181**B isoform X2 [Oncorhynchus mykiss]. 195..209
MAVQTAIMNSPFVNFCFPGSVMMEYDMGQSLDGSPLEESEERGDYRETTRSLDGSPLEESEERGEYRET
TRNLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGFISPTGNPAAAPGANKRKVSGFPTQTQTQPQ
TQLQTQPSPFQQGKPVHKRDGLQANLQTKSLAALFNSVKEPVKGERAKKPPLRHRNLPPSFFTEPANTTTTSRVT
STPGMFLGDLERGAGNPDFFDLLGPDYSNMLSDQDVFQTRGLPSRVIDQDVFQTRGLPSRIIDQDMFQTRGLPSR
ILQHQQTQDITDQVSPYDPHHLVGGFLYTEPWTSSPSKKAGEGVRTGPGTQTPLYCQSGEGVRTGPGTQTPLYCH
SVSDSSATGSTEDSNSLCTLAFPNFFPDCSVSQVSYGLSSGGYNTKDFSSL PLRHRNLPPSFFTEP

rs:XP_021447504 [XP_021447504] transcriptional coactivator YAP1-like, partial [Oncorhynchus mykiss]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQTS
TDAGTAGAIAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSHLRQSSYEIPEDMPLPPGWEMAKTPSGQRYFLN
HLDQSTTWLDPRKALLQMNQAPPTSPVPVQQQNIMSPASGPLPDCWEQAVTSEGEVYYINH
PMRMRKLPDSFFKPP

rs:XP_021473000 [XP_021473000] transcriptional coactivator YAP1-like [Oncorhynchus mykiss]. 48..62
MDARQGQCAPPVGQQIVHVRGDSQTDLEALFNSVMNPKTSALPPSSLPMRMRKLPDSFFRQPDPRSHSR
QASSDGTIVGSLTPHHVRAHSSPASLPINALSAPATSAMATQPLPDDVPLPPGWEMTKTPSGQCYFLNHLDQTTT
WHDPRLSHLQTNAAAHLLSAPPPHTHTLAHPAPNTHTQSNTSSNTGPLPEGWEQAVTPEGEVYYINHITKTTSWL
DPHLVQSAVAQVKPSTLTSDPVGIAVVTKRRQQLQVEKDRLRRKQQDLARPIRLQDVAVRSGLEHDGKMRNNHVD
PALNGAHSRNQSTDSGLSVSSFTRTPDDLLNTVELMDTGDSGAGQPMAFLEAGPGVCMATDGEELMPSIQEALSS
DLLSDMDTVLWL PMRMRKLPDSFFRQP

rs:XP_022089413 [XP_022089413] uncharacterized protein LOC110978601 [Acanthaster planci].>rs:XP_022089414 [XP_022089414] uncharacterized protein LOC110978601 [Acanthaster planci]. 244..258
MMATEMAVGFGQGMSAASFGHNFPLHPHHPMGGYDYYAQPRNYQDHVMMGHRQQQDEEEEDIEDEDIDE
ESENESMYTSADMDSEIASEDLAEPEPNVAEQLLEFAEAVNRDIQKYFGRKKSAHEPESVGTLYEDRFASGKSGR
ELYYADLLRVAQNGDAAEPYTTGRSRRTDSSVSPRTSTSSASTENADVTNANYSCKKGLGPLKELFDFAIGGCVD
SVNNDRHGGQWQRQGSSQKCLQTLPWRKRALPSSFFMEPGARDQSRTGGAGNVGYGPHVTMITEHETPDFSDLVA
NFTSDYDSQITATTISH PWRKRALPSSFFMEP

rs:XP_022098030 [XP_022098030] transcriptional coactivator YAP1-A-like isoform X1 [Acanthaster planci]. 44..58

METQNQQAQPRQVLHVRSDSDAELEDLFKSVMNPRETSQSSSIPMRMRNLPSSFFKEPDRVHAHHSRES
SADSTNYGPSANGSNVSGSGQTLAAPGLTVAHSRAHSSPAALQEMHAVGAQSLQHQHLRQQSYDITDDNTPLPPG
WEMASTSTGQRYYLDDKGRFLLSTPKPDNNHNRHTTTWQDPRKTLSTSQLNKVNSVAPNPPPTLTAQINTMTPPP
PTGSQQPLPAMQDLGPLPPNWEQATTPEGEVYFINHLERTTTWLDPRIAMRAPGTVQAAAAALQNTQQTAQQPAQ
QTMAISPTPAQQASKVPGPDISLQQRQQQLRLQRLQMERECLQRRQQEILQQMAASGKNRSLPRNFWPQEGSAHM
KGGQGSVPKEMQLRRDLDPATVSNGSDGNAVSTTGLDPFLSSGNTSNFHSREESGDSGCGMSNYSHPRTPDDLLS
NVEDMEAIEGERKTPIPAPLTPRQHMDFLDSMPGTNIDMGPMEGNGDNSNQGNMDSDELVPSLHEALNTDILNDV
LSSPNRIENFLTWL PMRMRNLPSSFFKEP

rs:XP_022098031 [XP_022098031] transcriptional coactivator YAP1-A-like isoform X2 [Acanthaster planci]. 44..58
METQNQQAQPRQVLHVRSDSDAELEDLFKSVMNPRETSQSSSIPMRMRNLPSSFFKEPDRVHAHHSRES
SADSTNYGPSANGSNVSGSGQTLAAPGLTVAHSRAHSSPAALQEMHAVGAQSLQHQHLRQQSYDITDDNTPLPPG
WEMASTSTGQRYYLDHNRHTTTWQDPRKTLSTSQLNKVNSVAPNPPPTLTAQINTMTPPPPTGSQQPLPAMQDLG
PLPPNWEQATTPEGEVYFINHLERTTTWLDPRIAMRAPGTVQAAAAALQNTQQTAQQPAQQTMAISPTPAQQASK
VPGPDISLQQRQQQLRLQRLQMERECLQRRQQEILQQMAASGKNRSLPRNFWPQEGSAHMKGGQGSVPKEMQLRR
DLDPATVSNGSDGNAVSTTGLDPFLSSGNTSNFHSREESGDSGCGMSNYSHPRTPDDLLSNVEDMEAIEGERKTP
IPAPLTPRQHMDFLDSMPGTNIDMGPMEGNGDNSNQGNMDSDELVPSLHEALNTDILNDVLSSPNRIENFLTWL
PMRMRNLPSSFFKEP

rs:XP_022098032 [XP_022098032] transcriptional coactivator YAP1-A-like isoform X3 [Acanthaster planci]. 44..58
METQNQQAQPRQVLHVRSDSDAELEDLFKSVMNPRETSQSSSIPMRMRNLPSSFFKEPDRVHAHHSRES
SADSTNYGPSANGSNVSGSGQTLAAPGLTVAHSRAHSSPAALQEMHAVGAQSLQHQHLRQQSYDITDDNTPLPPG
WEMASTSTGQRYYLDDKGRFLLSTPKPDNNHNRHTTTWQDPRKTLSTSQLNKVNSVAPNPPPTLTAQINTMTPPP
PTGSQQPLPAMQDLGPLPPNWEQATTPEGEVYFINHLERTTTWLDPRIAMRAPGTVQAAAAALQNTQQTAQQPAQ
QTMAISPTPAQQASKVPGPDISLQQRQQQLRLQRLQMERECLQRRQQEILQQEMQLRRDLDPATVSNGSDGNAVS
TTGLDPFLSSGNTSNFHSREESGDSGCGMSNYSHPRTPDDLLSNVEDMEAIEGERKTPIPAPLTPRQHMDFLDSM
PGTNIDMGPMEGNGDNSNQGNMDSDELVPSLHEALNTDILNDVLSSPNRIENFLTWL PMRMRNLPSSFFKEP

rs:XP_005623810 [XP_005623810] protein **FAM181**A isoform X1 [Canis lupus familiaris].>rs:XP_025298440 [XP_025298440] protein **FAM181**A isoform X1 [Canis lupus dingo]. 173..187
MAHLLEQNSLQRCGKVSSVPFPGAASHQQSPPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAAL
DKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGAEDRPGRLPLGSGHDSSTGEGGGCKEKAL
GNPYREECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYESKKHCKGLE
PLDPETAPVPTSPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYAGPPGALPQSPVPGLGLWRKSPASPG
ELAHFCKHVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_005623811 [XP_005623811] protein **FAM181**A isoform X2 [Canis lupus familiaris].>rs:XP_022278047 [XP_022278047] protein **FAM181**A isoform X2 [Canis lupus familiaris].>rs:XP_025298441 [XP_025298441] protein **FAM181**A isoform X2 [Canis lupus dingo]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGAEDRPGRLPLGSGHDSSTGEGGGCKEKALGNPYREECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYESKKHCKGLEPLDPETAPVPTSPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYAGPPGALPQSPVPGLGLWRKSPASPGELAHFCKHVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_850835 [XP_850835] LOW QUALITY PROTEIN: protein **FAM181**B [Canis lupus familiaris]. 221..235
MAVQAALLSTHPFVPFGFGGSPDALGGAFGALDKGCCFEDDEPGPPAGALLAGAEGGDVREATRDLLSF
MDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADAPAKRPLGAAGAQAVAGPPPGK
AAPRREASQAAAANSLQSRSLAALFDSLRHVPAGDERPGASGAAPAAALGAAGAGGSGGDAAGPAGGTAGPGARK
VPLRARNLPPSFFTEPSRAGRGCGPSGPGVSLGDLEKGADALEILELAGSGTGAGAGAGVLLAAEPLEVFPAGAA
VLRGPPELEPGLFEPPAATVGALLYPEPWSAPGCPPAKRPPPAAPRGGLALTEPLRPAYPAAADCQGGEDAPGLL
ASFAPFFSDCALPPQPPRQPHQVSYEYGAGYGRSGYAGLWRPDAAWEGAPGEEGAPRD PLRARNLPPSFFTEP

rs:XP_023136250 [XP_023136250] transcriptional coactivator YAP1 [Amphiprion ocellaris].>tr:A0A3P8T0A1_AMPPE [A0A3P8T0A1] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSAPEP00000017206}; 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDAPLPAGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQPPPPSSVPVQQQNLMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRITQSAPVKQGGQLPPSHHSAVMGGNNQLRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQ
DGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPTSMA
TQPSRFPDYLDTIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_023141768 [XP_023141768] protein **FAM181**A [Amphiprion ocellaris]. 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYRC
AKPAGTVHQSVTVSEKASSDAQDVENVGSAVEQVPMRKRQLPASFWEEPKLTQTKREHSYLGLKKSPGTSEGNEN
EKRKRSYDEDAKATMSASSRRNSVDKETLKLDLSSHQCVSVCGCCPFQYHGHQVLHSHIVVPHPALGLWSKAAGT
ETERPEHPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_023144274 [XP_023144274] transcriptional coactivator YAP1-like isoform X1 [Amphiprion ocellaris].>rs:XP_023144276 [XP_023144276] transcriptional coactivator YAP1-like isoform X1 [Amphiprion ocellaris].>tr:A0A3P8UC39_AMPPE [A0A3P8UC39] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSAPEP00000033083}; 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFNAVMNPSSSARQPSSVPMRMRKLPDSFFRQPEPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVATTPIIPDDVPLPHGWEMAKTATGQRYFLNHRDKTTTWH
DPRLSQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPR
LAQKMNPGLLGLAMQQRQEKERLRCKQGLPPQITSQDAGGRSQMPGGMDHDRSTQTLVPPLDVRIRASNHEPTLN
GAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGESVEPPSMALQESMPVLPMSEGEELMPCIPEGLSSDLLMD
METVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_023144277 [XP_023144277] transcriptional coactivator YAP1-like isoform X2 [Amphiprion ocellaris]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFNAVMNPSSSARQPSSVPMRMRKLPDSFFRQPEPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVATTPIIPDDVPLPHGWEMAKTATGQRYFLNHRDKTTTWH
DPRLSQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPETAQKMNPGLLGLAMQQRQEKERLRCKQGLPPQIT
SQDAGGRSQMPGGMDHDRSTQTLVPPLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDT
GESVEPPSMALQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_023118553 [XP_023118553] LOW QUALITY PROTEIN: protein **FAM181**B [Amphiprion ocellaris]. 246..260
MQVVGHKQRVKXPALPLPLLFDVLTSLARPPERSPRXSSEPVTSTLECLQELHEQHQDQVFIRGKKTCS
EEIWGSEITVDATGVAAGLNRVMAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQGSPLTQPSPLQSKTLPKRDGVQ
ANLQSKSLAALFSPVKDIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMSLKDLERGNPEAADFFELLGPD
YSNMVSDQDLYQGMPFRVQPELGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKLGETLRTGPAQPPAYCHSEAA
SGPIEDNALCTLAFPNFFTDCSIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_024423123 [XP_024423123] protein **FAM181**A [Desmodus rotundus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGPEPHLK
RGPEDRPGRLPLNSGPDASPAGGGDCKEKALGNPYGVECLSKEQTLQGQNTEATRPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGVLGPREGLPYEGKKHCKGLELLGPEMALVPMSPRPPGEKEPPKMPGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQGPIPSLGLWRKSPTSPGELAHFCKDADGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_024428604 [XP_024428604] protein **FAM181**B [Desmodus rotundus]. 221..235
MAVQAALLSTHPFVPFGFGSSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGTEGGDVREATRDLLSF

IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAASPGPSSPGAADTPAKRALGAPSAQTVAVPVHGK
AAPRRDASQAATAASLQSRSLAALFDSLRHIPGAADSAGGSVAAPTVGLGGAGAGGAVGDAAGPAGVSALPGSRK
VPLRARNLPPSFFTEPRASGGGCGPSGPCLSLGDLEKGSENLEFFELLGPDYGAGPEAGVLLAAEPLDVFPTGAT
VLRGPPEMEPGLFEPPPAMVGSLLYPETWSAPACPPTKKQSLATPRGGSTLNEPLRRLYPVTVDSPGGEDGPGLL
ASFSPFFSDCALPPPPTPHQVSYEYSAGYGRTAYSSLWRSDGAWEGGPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_024430400 [XP_024430400] transcriptional coactivator YAP1 isoform
X1 [Desmodus rotundus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_024430401 [XP_024430401] transcriptional coactivator YAP1 isoform
X2 [Desmodus rotundus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRT
MTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGT
NVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024430403 [XP_024430403] transcriptional coactivator YAP1 isoform
X3 [Desmodus rotundus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024430404 [XP_024430404] transcriptional coactivator YAP1 isoform
X4 [Desmodus rotundus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020490507 [XP_020490507] transcriptional coactivator YAP1 isoform
X1 [Labrus bergylta]. 45..59
MDQGQHNPPAGHQIVHVRGDSETDLETLFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDGGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMPPAGASPQHLRQSSYEIPDDVPLPHGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNLMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRITQSAPGKQGGQLPPSHSAVMAGNQMRLQQIEKERLRLKQQELLRQRPQELALRTQLPMDQDGST
NPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLQPSMVTQPS
RFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_020490508 [XP_020490508] transcriptional coactivator YAP1 isoform
X2 [Labrus bergylta]. 45..59
MDQGQHNPPAGHQIVHVRGDSETDLETLFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDGGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMPPAGASPQHLRQSSYEIPDDVPLPHGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNLMNPASALNQQRITQSAPGKQGGQLPPSHSAVMAGNQMRL
QQIEKERLRLKQQELLRQRPQELALRTQLPMDQDGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSG

LSMSSYSVPRTPDDFLNSVDEMDTGDPLQPSMVTQPSRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEA
LSSDILNDMESVLAATKIDKESFLTWL PMRMRKLPDSFFKPP

rs:XP_020490554 [XP_020490554] protein **FAM181**B [Labrus bergylta].
155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEYYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQGSPLAQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DVRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSDQDLYQSMPL
RLQPEMGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKAGGSLRTGPAQPPVYCPSEAAGALEDNTLCTLAFPNF
FTDCSIPQVSYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_025062089 [XP_025062089] protein **FAM181**A [Alligator
sinensis].>tr:A0A3Q0GQL7_ALLSI [A0A3Q0GQL7] SubName: Full=protein **FAM181**A
{ECO:0000313|RefSeq:XP_025062089.1}; 126..140
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRSHPSKSMESNMK
RGVEDRNHSSHPDAVDPNPCRATSEKALRGAEVEENLSGEQGLQEQSPESARPDQVPMRKRQLPASFWEEPRPTQ
SLLVGSFPAGLDGLPKSRDLPSYEGKKSKKSPDATGPESPPVPVQPSGEKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTPGALPQSPFPGLGLWRKNTAPQGEIQHFCKETDATGQKLFRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_020818081 [XP_020818081] transcriptional coactivator yorkie isoform
X1 [Drosophila serrata]. 60..74
MSTSNTNNLIEKEIDDEDMLSPIKPNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMRKLPNS
FFTPPAPSHSRANSADSTYDAGSQSNISNISSIKAAQPVDGQPPISAISQIQQPSPQQSRLAIHHFRARSSPASL
QQNYNVRARSEANPGASQQPAGPTFPENSAAEFPSSGATAPSSIELDAMNSCMSQDMPMSTQTVHKKQRSYDVVS
PIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQFRQQQQSLMAERIKQNDVLQTTKQTTTSTIAN
NMGPGPLPDGWEQAVTESGDIYFINHIDRTTSWNDPRMQSGLSVLDCPDNLVSSLQIEDNICSNLFNDAQTIVNP
PSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

rs:XP_020818082 [XP_020818082] transcriptional coactivator yorkie isoform
X2 [Drosophila serrata]. 60..74
MSTSNTNNLIEKEIDDEDMLSPIKPNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMRKLPNS
FFTPPAPSHSRANSADSTYDAGSQSNISNISSIKAAQPVDGQPPISAISQIQQPSPQQSRLAIHHFRARSSPASL
QQNYNVRARSEANPGASQQPAGPTFPENSAAEFPSSGATAPSSIELDAMNSCMSQDMPMSTQTVHKKQRSYDVVS
PIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQFRQQQQSLMAERIKQNESGLSVLDCPDNLVSS
LQIEDNICSNLFNDAQTIVNPPSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

rs:XP_020849481 [XP_020849481] LOW QUALITY PROTEIN: protein **FAM181**B
[Phascolarctos cinereus]. 243..257
MAVQAAILSPHHFIPFCFPGSPGALGMDFGDLDKGCCYEEDEAGGTGVALLGEAVAAEGAGGGSGGGDL
REATRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGMMTSSSASSSGPAPSVSPSPGPAAAVPA
GAPEAPPKRLPAASPAAPGPQGKAPPKREGSQAAASLQSKSLAALFESLHQVRGNGGEKGGAGTLATVAGGGGGG
GGVGAEGGGPLVAAAGAGGGKKVPLRNRNLPPSFFTEPSRAGGCGPSGGGVTLRELEKGGEAVEFFELLSPDYCA
GGEVGGLLPSEPLDLFPAAVRAPQELEHILYDPHPTVVAGLLYSEPWSTPCPPAKKPAPASNRGGGGLTLSETLR
PLYPGTSDSAASSLGXPGGEDTAGHLTPFAQFFPDCALPTPPPPHQMPYDYGVGYSRVAYSGL
PLRNRNLPPSFFTEP

rs:XP_020851776 [XP_020851776] transcriptional coactivator YAP1 isoform
X1 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNVNPSTANSPKRQEIALRSQLPTMEQDG
GTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNI
PSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_020851777 [XP_020851777] transcriptional coactivator YAP1 isoform X2 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGT
QNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPS
QQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_020851778 [XP_020851778] transcriptional coactivator YAP1 isoform X3 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQN
PVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_020851779 [XP_020851779] transcriptional coactivator YAP1 isoform X4 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPV
SSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_020851780 [XP_020851780] transcriptional coactivator YAP1 isoform X5 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQEIALRSQLPTMEQDGGTQNPVSSPGMNQELR
TMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPG
TNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020851781 [XP_020851781] transcriptional coactivator YAP1 isoform X6 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTM
TTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTN
VDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020851782 [XP_020851782] transcriptional coactivator YAP1 isoform X7 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ

SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020851783 [XP_020851783] transcriptional coactivator YAP1 isoform X8 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020851784 [XP_020851784] transcriptional coactivator YAP1 isoform X9 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
VRPQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020851785 [XP_020851785] transcriptional coactivator YAP1 isoform X10 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
ALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020851786 [XP_020851786] transcriptional coactivator YAP1 isoform X11 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
VRPQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDD
FLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVL
AATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020851787 [XP_020851787] transcriptional coactivator YAP1 isoform X12 [Phascolarctos cinereus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
EIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_020855991 [XP_020855991] protein **FAM181**A [Phascolarctos cinereus].>rs:XP_020855992 [XP_020855992] protein **FAM181**A [Phascolarctos cinereus]. 118..132
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCYPNRSGESHSK
RGPEDGRCRTPSNGSTEKGPANPGMEENFPEEQTLQEQIPEASRPDQVPMRKRQLPASFWEEPRPAQSYSGGLDG

LSVHREVPAYEGKKSKKRPETLGSETAPLPASPRAEKESPKVPSASLMGRMSAWSCCPFQYHGQPLYQSPGGLPQ
SPVPGLGLWRKSPSSPGEMGHFCKEPGSPSQKVYRPVVLKPIPTKPGVPPPIFNVFSYI
PMRKRQLPASFWEEP

rs:XP_020862376 [XP_020862376] uncharacterized protein LOC110221959
[Phascolarctos cinereus]. 215..229
MAAGVIRNLCDFRLQAPFHQPFLPSTGHRDPDFPETSEEEEEEDGEEEEDGEKQVEDLELAGRSPGCQR
SDQELGKGSTRPSPSSTEMTLQLLRFSELISCDIQKYFGQKTKDDDPDACNIYEDSRPPGKSARELYYADLMQIV
QSGDQEDEDTDTVGLPRGFDCQARFISGRDRSQKLGPLVELFEYGLCQYARQRVSDSRRLRLEKKYGHITPMHKR
KLPQSFWKEPAPSSLCLLNTSTPDFSDLLANWTSDVVQELHSVGGRELGRHALEMDQLEEA
PMHKRKLPQSFWKEP

rs:XP_021024695 [XP_021024695] protein **FAM181**B [Mus caroli]. 215..229
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGSSAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPRPASPSAADAPAKRPPGAPTVATPAHCKAAP
RREATQAAAAASLQSRSLAALFDSLRHIPGGAEMAGGAEAVSVPSLGAASAAGDGAGTAVSSVALGTRKVPLRAR
NLPPSFFTEPSRVGCGGASGVPSGQGVSLGDLEKGAEAVEFFELLAPDFGSGNDSGVLMAADPLDPFPAGATVLR
GPLELESGPFEQPAMVGNLLYPEPWNTPSCPQTKKPPLAGVRGGVTLNEPVRLLYPTALDSLGGEDAPALASFTP
FFPDCALPQPHQVSYDYSAGYSRAVYPSLWRPDGVWEAASGEEGGHPD PLRARNLPPSFFTEP

rs:XP_021027507 [XP_021027507] transcriptional coactivator YAP1 isoform
X1 [Mus caroli]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLE
GDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021027508 [XP_021027508] transcriptional coactivator YAP1 isoform
X2 [Mus caroli]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAATPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDS
GLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQ
EALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_005068428 [XP_005068428] protein **FAM181**A [Mesocricetus
auratus].>tr:A0A1U7Q969_MESAU [A0A1U7Q969] SubName: Full=protein **FAM181**A
{ECO:0000313|RefSeq:XP_005068428.1}; 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVTEPHLQ
RAPEERPGQLPLHPCPESNPGGGGSYKEKALGTPFREECLSKEQSFQGLNPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPREASLYENKKNCKGLGSLGPETAPLPMSPRVLADMDPLKMSGVSLVGSLDAWSYCPFQYH
GQPVFPSLPGVLPQGPVPSLGLWRKSPASPVEMAHFCKDVDSSGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_005073995 [XP_005073995] protein **FAM181**B [Mesocricetus
auratus].>tr:A0A1U7QHD2_MESAU [A0A1U7QHD2] SubName: Full=protein **FAM181**B
{ECO:0000313|RefSeq:XP_005073995.1}; 221..235
MAVQAALLSSHPFIPFGFGGSTDGLVSAFGSLDKGCCFEDDESGAPAGALLSGSEGGDLREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPSAGDAPAKRPPGAPGAPTVAAPAHCK
ATPRREATQAAAAASLQSRSLAALFDSLHHVPGVAEPAGGAVAVPVPGLGAAGAASAAGDGASTAGSSAAPGTRK
VPLRARNLPPSFFTEPSRVGASGGCGCGPSSQGMSLGDLEKGAEAVEFFELLAPDFGAGNDTGVLLAAEPLDAFP
TGVLRGPLELESGPFEPPAMMGNLLYPEPWSTPSCPQPKKPPLAGVRSGVTLNEPVRLLYPTTLDSPGGEDTPAL
ASFTPFFPDCALPPPHQVSYDYSAGYSRAVYPSLWRSDGFWEGASGEDGAHPDPLRARNLPPSFFTEP

rs:XP_021501540 [XP_021501540] transcriptional coactivator YAP1 isoform
X1 [Meriones unguiculatus]. 76..90
MEPAQQQPQPPPPQPAPQGPAPPSASAPPAGAPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTA
NVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGSLTPSGVVSGPAA
TPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPAPAPASPAVPQTLMN
SASGPLPDGWEQAMTQEGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGS
SNQQQQIQLQQLQMEKERLRLKQQELLQQVRPQAIRNINPSTANAPKCQELALRRQLPTLEQDGGTQNAVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYL
EAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_021501541 [XP_021501541] transcriptional coactivator YAP1 isoform
X2 [Meriones unguiculatus]. 76..90
MEPAQQQPQPPPPQPAPQGPAPPSASAPPAGAPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTA
NVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGSLTPSGVVSGPAA
TPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPAPAPASPAVPQTLMN
SASGPLPDGWEQAMTQEGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSN
QQQQIQLQQLQMEKERLRLKQQELLQQVRPQAIRNINPSTANAPKCQELALRRQLPTLEQDGGTQNAVSSPGMSQ
ELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEA
IPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021501542 [XP_021501542] transcriptional coactivator YAP1 isoform
X3 [Meriones unguiculatus]. 76..90
MEPAQQQPQPPPPQPAPQGPAPPSASAPPAGAPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTA
NVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGSLTPSGVVSGPAA
TPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPAPAPASPAVPQTLMN
SASGPLPDGWEQAMTQEGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGS
SNQQQQIQLQQLQMEKERLRLKQQELLQQAIRNINPSTANAPKCQELALRRQLPTLEQDGGTQNAVSSPGMSQEL
RTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIP
GTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021501544 [XP_021501544] transcriptional coactivator YAP1 isoform
X4 [Meriones unguiculatus]. 76..90
MEPAQQQPQPPPPQPAPQGPAPPSASAPPAGAPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTA
NVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGSLTPSGVVSGPAA
TPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPAPAPASPAVPQTLMN
SASGPLPDGWEQAMTQEGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSN
QQQQIQLQQLQMEKERLRLKQQELLQQAIRNINPSTANAPKCQELALRRQLPTLEQDGGTQNAVSSPGMSQELRT
MTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGT
NVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWLPMRLRKLPDSFFKPP

rs:XP_021501545 [XP_021501545] transcriptional coactivator YAP1 isoform
X5 [Meriones unguiculatus]. 76..90
MEPAQQQPQPPPPQPAPQGPAPPSASAPPAGAPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTA
NVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGSLTPSGVVSGPAA
TPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPAPAPASPAVPQTLMN
SASGPLPDGWEQAMTQEGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGS
SNQQQQIQLQQLQMEKERLRLKQQELLQQELALRRQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGT
YHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDAMNI
EGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021501546 [XP_021501546] transcriptional coactivator YAP1 isoform
X6 [Meriones unguiculatus]. 76..90
MEPAQQQPQPPPPQPAPQGPAPPSASAPPAGAPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTA
NVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGSLTPSGVVSGPAA
TPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPAPAPASPAVPQTLMN
SASGPLPDGWEQAMTQEGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSN
QQQQIQLQQLQMEKERLRLKQQELLQQELALRRQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYH

SRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDAMNIEG
EELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021505112 [XP_021505112] protein **FAM181**A [Meriones unguiculatus].
129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVAEPHLQ
RGPEERPGQLPLHACPESSPGGGGNHAEKALGTPFGEECLSKEQSFRGLNPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPREASLYENKKNCKGLESLGPETAPLPMSPRVLADTEPLKMAGVSLVGSLDAWSYCPFQYH
GQPVFPSLPGVLPQGPVPGLGLWRKSPTSPVELAHFCKDVDSPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_021513741 [XP_021513741] protein **FAM181**B [Meriones unguiculatus].
218..232
MAVQAALLSSHPFIPFGFGGPADGLVSAFGSLDKGCCFEDEESGGSAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPPPPSPSAPDAPARRPPGPPGAPAVAAPAHCK
AAPRREATQAAAAASLQSRSLAALFDSLRHVPGGAETAGGAVAASVPGLGAASSAGDGAGTAGSLAGPGTKKVPL
RARNLPPSFFTEPSRVGGGGGCGPSGQGVSLGDLEKGAEAVEFFELLAPDFGAGNDAGVLLASDPLDTFPAGAAV
LRGPLELESGPFEPPAMGGNLLYPEPWNAPSCPQTKKPAPAGVRGGVTLNEPVRLLYPTALDSPGGEDAPALASF
TPFFPDCALPPPHQVSYDYSTGYSRAVYPSLWRPDGACWEGASGEEGAHPD PLRARNLPPSFFTEP

rs:XP_021194051 [XP_021194051] transcriptional coactivator YAP1 isoform
X1 [Helicoverpa armigera].>tr:A0A2W1BLM6_HELAM [A0A2W1BLM6] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:PZC75181.1}; 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGTHIPDDLGPLPPGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSTDALLTQAASPQNIPSTPAPAAKSTSSNTTTDP
LGPLPEGWEQAATAEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGGAVPDGGWANASLQACQQKLRLQSLQLER
ERLKQRQQEIRLQQELIMARQSSSIVSSLANSTGVASTDLPLDPFLSGLSDHQRQESADSGLGMAVPHSYSMPHT
PEGFLAGMDDRMDCTSEAGANIDSTDITLADNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_021194052 [XP_021194052] transcriptional coactivator YAP1 isoform
X2 [Helicoverpa armigera]. 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGTHIPDDLGPLPPGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSTDALLTQAASPQNIPSTPAPAKSTSSNTTTDPL
GPLPEGWEQAATAEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGGAVPDGGWANASLQACQQKLRLQSLQLERE
RLKQRQQEIRLQQELIMARQSSSIVSSLANSTGVASTDLPLDPFLSGLSDHQRQESADSGLGMAVPHSYSMPHTP
EGFLAGMDDRMDCTSEAGANIDSTDITLADNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_021194053 [XP_021194053] transcriptional coactivator YAP1 isoform
X3 [Helicoverpa armigera].>tr:A0A0S2I7P5_HELAM [A0A0S2I7P5] SubName:
Full=Yorkie {ECO:0000313|EMBL:ALO18798.1};>gp:KT153628_1 [KT153628] yorkie
[Helicoverpa armigera] 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGTHIPDDLGPLPPGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSTDALLTQAASPQNIPSTPAPAAKSTSSNTTTDP
LGPLPEGWEQAATAEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGGAVPDGGWANASLQACQQKLRLQSLQLER
ERLKQRQQEIRLQQELIMARQSSSIVSSLANSTGVASTDLPLDPFLSGLSDHQRQESADSGLGMAVPHSYSMPHT
PEGFLAGMDDRMDCTSEAGANIDSTDITLADNLDSTDDLLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_021194054 [XP_021194054] transcriptional coactivator YAP1 isoform
X4 [Helicoverpa armigera]. 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGTHIPDDLGPLPPGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSTDALLTQAASPQNIPSTPAPAQHLQRTPAAGGA
VPDGGWANASLQACQQKLRLQSLQLERERLKQRQQEIRLQQELIMARQSSSIVSSLANSTGVASTDLPLDPFLSG

LSDHQRQESADSGLGMAVPHSYSMPHTPEGFLAGMDDRMDCTSEAGANIDSTDITLADNLDSTDDLVPSLQLNEF
TNDILLDDVQSLINSTPSKPDNVLTWL   PLRMRQLPKSFFNPP

rs:XP_021194055   [XP_021194055] WW domain-containing transcription
regulator protein 1 isoform X5 [Helicoverpa armigera].   44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGTHIPDDLGPLPPGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSTDALLTQAASPQNIPSTPAPAQHLQRTPAAGGA
VPDGGWANASLQACQQKLRLQSLQLERERLKQRQQEIRLQQELIMARQSSSIVSSLANSTGVASTDLPLDPFLSG
LSDHQRQESADSGLGMAVPHSYSMPHTPEGFLAGMDDRMDCTSEAGANIDSTDITLADNLDSTDDLLNEFTNDIL
LDDVQSLINSTPSKPDNVLTWL PLRMRQLPKSFFNPP

rs:XP_022164255   [XP_022164255] transcriptional coactivator YAP1-A [Myzus
persicae]. 66..80
MSGLQQQQQEQHQQVSIKMEPTGPSSPTPAVNSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPLRM
RQLPKSFFTPPSSGSKSPSISHSRENSGDSAFGTNVGPSCSGPVPLHSRAHSSPASLQQTYAVGAAKQQQQHAKQ
RSYDVSSAIDELGPLPQGWEQARTPEGQIYYLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQLLSPGNDSGSSTN
ATSTPTNSPPHIHSTLQGANKNVTLGPLPDGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQRAPTSGAVLPS
GSASWLLNGASGLSQSLQVTQQKLRLHSLQLERERLKSRQQEIIRQQDLMLRSGQTNNDLDPFLSCSSSSVDHSR
QESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDPQEMSTLDVTDDLVPSLQLGDEFG
NDILDEVQLLIDPNNKPGSILTWL   PLRMRQLPKSFFTPP

rs:XP_021385006   [XP_021385006] transcriptional coactivator YAP1 isoform
X1 [Lonchura striata domestica].   86..100
MDPGQPQTQQPPQAAQPPAPQQQQPPPQPPGPVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_021385008   [XP_021385008] transcriptional coactivator YAP1 isoform
X2 [Lonchura striata domestica].   86..100
MDPGQPQTQQPPQAAQPPAPQQQQPPPQPPGPVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_021385009   [XP_021385009] transcriptional coactivator YAP1 isoform
X3 [Lonchura striata domestica].   86..100
MDPGQPQTQQPPQAAQPPAPQQQQPPPQPPGPVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_021396967   [XP_021396967] protein **FAM181**A [Lonchura striata
domestica]. 121..135
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKAPECGWR
RGAEDRARGPQPEAPEPSPHKVVQTAEAEESLTGERVLQEQKPEAARPDQVPMRKRQLPASFWEEPRPAQSLAAR
AFAASPEGLQAPRDPPPYEGKKSKRSPDAAGPESPPDSAPHAGEKEPAGPLSGRVGAWTCCPFPCPGPGVYQPPG

ALPPSPFPGLGLWRKSAATLPAEVPHFCKEADGQGQKLYRPMVLKPIPTKPAIPPPLFNVFGYL
PMRKRQLPASFWEEP

rs:XP_021400626 [XP_021400626] protein **FAM181**B [Lonchura striata domestica]. 142..156
MAVPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAAAGSSLQSRSLAALFGFLPRGRAAAGGAEPKAGGGEKAAGGPRKVPLR
DRNLPPSFFTEPALPGPAARGPPAKEPEKGGGSAEAAEFFELLCPEYGALLPEHAAATDAFGGRLPAELGLEPGL
YELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPAEPLRPIYPGGAEPVPGGGGSEEPGGHLPAGFAPFFPEC
PLPPPQPPYDYGGGYHRGGYPGL PLRDRNLPPSFFTEP

rs:XP_021437345 [XP_021437345] transcriptional coactivator YAP1 [Oncorhynchus mykiss]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPASVPMRMRKLPDSFFNPPEPKSHSRQAS
TDAVTAGALAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSNLRQSSYEIPDDMPLPPGWEVAQTPSGQRYFLN
HLDQSTTWLDPRKALLQMNQAPPTSPVPVQQQNIMSPASGLNQQRITQSAPGKQGSQLPSSPQSGGVMGGSNQIK
LQQLQMEKERLRLKHQELLRTRPQELALRNQLPTSMEQDGGTLNPVSSPGMGQDARIMTTNSNDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDSVPRTPDDFLNSLDSVPRTPDDFLNGVDEMDTGDSLPVSMGTQASRFP
DYLDVIPGTDVDLGTLENKSMAVEGEELMPSLQEALSSDILNDMESVLAATKMDKENFLTWL
PMRMRKLPDSFFNPP

rs:XP_021440594 [XP_021440594] protein **FAM181**A [Oncorhynchus mykiss].>tr:A0A060WPV5_ONCMY [A0A060WPV5] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:CDQ69413.1}; 158..172
MRILNRGHDFKDEEEYNLHGLVWWYGLKYLHCKMASADSDVKTLLNFVNLASSDIKAALDKSAPCRRSV
DHRKYLQKQLKRFSQKYARMPRCHTHRSTESSIAKDVVNKSSEYSLETIHPSTTRINEKGGSDAQDVENARMAQT
PTVDSDNSKQEQVPMRKRQLPASFWEEPRLAQTNTDYLQYGWKKSQCVIGINDVEKIKKAHEELTPSLLLCNRRG
SVEKEPLKLDVASHNVNVCGFCPFQYHGHHVFQSHIVVPQSAVGLWGKATVAETETPDITHRHKNYTHVVVKPIP
TKPTVPPSIFNVFGFI PMRKRQLPASFWEEP

rs:XP_004534732 [XP_004534732] transcriptional coactivator yorkie [Ceratitis capitata].>tr:W8BY76_CERCA [W8BY76] SubName: Full=Protein yorkie {ECO:0000313|EMBL:JAC04303.1}; 61..75
MSLSKTVGSLNKGNVKEKERSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPE
SFFKPPATTSRSPSVAHSRANSADSAYDTGSQPNVSQGNISTGSITAVPATITQPQVTANRLAISHSRAHSSPAS
LQQTYNVHIGNVMETGACIQDGIGAVYTAGGVTFPPGVNASSSVRMDQVDQSATKDAPNPIQTFHMKQRSYDVVS
TIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLTHNVTLKNKESVNLADNLGPLP
EGWEQAYTDSGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQNSLTRQNGN
LQMDPFLSGDNHARQESSDSGLSLSSNTFSTTTDLLPNIDDSMDCISESGSLNALSGIDCPDNLVSSLQLEDNIC
NEMFSDVHNMLNASATKPDTLDWYKIN PFRMRQLPESFFKPP

rs:XP_023171744 [XP_023171744] transcriptional coactivator yorkie isoform X1 [Drosophila hydei]. 61..75
MSLSNKSNISEKEIDDEDMLSPTKISTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEIQPSLTQNQPSHSRLTIHHFRARSSPASLQQNYNVRSRNES
SANNNQGPAYPENSVDFASSTANNIDLDVINTCMGPGPDTSLATQTTIHKKQRSYDVVSPIQLQSQLGALPPGWE
QAKTNDGQIYYLNHTSKTTQWEDPRIQFRQQQQRALTDRIKPNDVIQTTKPTSASTIATHIGPLPDGWEQAVTES
GDIYFINHIDRTTSWNDPRIQSGLNVLDCPDNLVSSLQIGDNICSNIFNDTQAIINTPSSHKPDDLEWYKIN
PFRMRKLPNSFFNPP

rs:XP_023171745 [XP_023171745] transcriptional coactivator yorkie isoform X2 [Drosophila hydei]. 61..75
MSLSNKSNISEKEIDDEDMLSPTKISTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEIQPSLTQNQPSHSRLTIHHFRARSSPASLQQNYNVRSRNES
SANNNQGPAYPENSVDFASSTANNIDLDVINTCMGPGPDTSLATQTTIHKKQRSYDVVSPIQLQSQLGALPPGWE
QAKTNDGQIYYLNHTSKTTQWEDPRIQFRQQQQRALTDRIKPNESGLNVLDCPDNLVSSLQIGDNICSNIFNDTQ
AIINTPSSHKPDDLEWYKIN PFRMRKLPNSFFNPP

rs:XP_014228517 [XP_014228517] transcriptional coactivator YAP1-A [Trichogramma pretiosum]. 53..67
MALNQESGGVGGVVKDEGSGKALVHVDRNSESDLQALFDTVLKPNSNQPLTVPLRMRKLPDSFFNPPST
GSKSPSISHSRENSADSAFGVVNAAAAVAAAAAAAAAQQNNGGGGGPGSTGPNSPANGPAQIPAGLVVAHPRAHS
SPASLQQTYASAQQQAQHAAPQPQSVRHVHHQKQRSYDVISTGVDDLGPLPHGWEQARTPEGQIYFLNHVTRTTT
WEDPRKTAAAANVAAVAAAAVESAGKAANQAAAAAAAAAAAAAVSNNALGPLPHGWEQARTPEGEIYFINHQERT
TSWFDPRIPSHLQRAPTSGAMLPQTWQIQQQQQQQVPSAASVQNNQTVQACQQKMRLHSLQMERERLKQRQQEIM
RQQERMLLQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDVTSEGTPMETPDGM
SLGDNIDNTDDLVPSLQLGEDFSSDILEDVQSLINPVGNTTKPENILTWL PLRMRKLPDSFFNPP

rs:XP_023348775 [XP_023348775] transcriptional coactivator YAP1-like [Eurytemora affinis]. 46..60
MAASVGPEKETNSKQVSIHIREDSDSELQALFDIPLKGGQRPLQVPMRMRNFPPSFWQPPVLGSKSPSV
HSRENSLDNSCGPFSPDPVASPQPPVGHHSRANSCPANLGQTLAVSLQHQNHALQNHHLRQQSYDVGGGGDDLGP
LPPGWEMAKAPNGQIYFMNHITKSTQWEDPRKAIQQQMLNQLNGTASPRSSAVSSPVPNGQGGVDLGPLPQGWEQ
SATPEGEMYFIHHLTKRTTWYDPRIPIHAQQVPLKQRQESTHAQAQKLQQEARLRRLENERRVLQQKRAELNQFI
TRQQQEKLEMMMRHTLSEGGTKLDPFLAQTNGDPHIRQESADSGLGMGSFPNLGTISEDMGRLIIIFGTISEDMG
RLNIIFGTISEDMGRLIIIFGTISEDMGRLIIIFGTISEDMGRLNIIFGTISEDMGRLIII
FGTISEDMGRLIIIFGTISEDMGMENMDTDLDTTLTDTNQQIQIQQQQGMDTEELIPTLPELGEELSRDFINTIF
NTNTPVENELTWL PMRMRNFPPSFWQPP

rs:XP_023321344 [XP_023321344] uncharacterized protein LOC111696052 [Eurytemora affinis]. 191..205
MNKEKRKPCKEMGEFDDGLLDLGDVSTDLEALGANDLEERGELNLDVEGESAPEYDYDSVSSPGGSTCS
GPTYIRHSGFGPDVNRPLSQLSAGSPPTYPGPPSPLTHSLSQPIILTKGLASRHKLPNQPYLDNYSNNQDSRKKK
KKGLLRPEFSEFGQDIRGQQISGSKLTGVKLGTLTSTRNKSRKEPLPMKLRALPQSFWQQPNLANPLPPGSVFST
LPPLPGQEGELENHAPPVSAVAGSGAEEFLRERMSTANTDLLFSLFNSVDSDLGSGRKIQMVRRGR
PMKLRALPQSFWQQP

rs:XP_023484091 [XP_023484091] protein **FAM181**A isoform X1 [Equus caballus]. 221..235
MAKNVGTGRCRLIGMLCIWRGAPDWPEGPPSSRDSVSIQPTRGLHNRLQPDARSSPAAPGRAQVRPVPF
SGAASPPQNPPSSWKAPCRGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKY
SRLPRGLPGRGAEPHLKRGPEDRPGRLPLGAGQDSSPGGGGGCTEKALGNPYREECLSKEQTLQGQNPEAARPGQ
VPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPVGPETAPVPASPRAPAEKEPLKMPGV
SLVGRVNAWSCCPFQYHGQPIYPGPPGALPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPT
KPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_005605469 [XP_005605469] protein **FAM181**A isoform X2 [Equus caballus].>rs:XP_008538988 [XP_008538988] PREDICTED: protein **FAM181**A isoform X1 [Equus przewalskii]. 159..173
MVRPVPFSGAASPPQNPPSSWKAPCRGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRK
YLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLGAGQDSSPGGGGGCTEKALGNPYREECLSKEQT
LQGQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPVGPETAPVPASPR
APAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGALPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQ
KVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_005605470 [XP_005605470] protein **FAM181**A isoform X3 [Equus caballus].>rs:XP_023484092 [XP_023484092] protein **FAM181**A isoform X3 [Equus caballus].>rs:XP_005605471 [XP_005605471] protein **FAM181**A isoform X3 [Equus caballus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLGAGQDSSPGGGGGCTEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPVGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023619829 [XP_023619829] protein **FAM181**A [Myotis lucifugus]. 129..143

MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPPLR
RGPEDRPGRLPLNPGPDASPSGGGDCKEKALGNPYREECLSREQTLQGQNPGAARPGQVPMRKRQLPASFWEEPR
PTHSYPVALEGVLGPREGPPYECKKHCRGLELFGPDMALIPMSPRALAEKEPPKLPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPPGPVPSLGLWRKSPASPGELAHLAKDVDGPGQKVHRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023603180 [XP_023603180] protein **FAM181**B [Myotis lucifugus].
163..177
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDEPGMPAGALLAGTEGGDAREATRDLLSF
IDSASSNIKLALDKPSKSKRKVNHRKYLQKQIKRCSGLMGAAPAGPPSPGAADTPAKRALGTPGAQTAARALGVR
EEMLPALRGTAAPGARKVPLRARNLPPSFFTEPSRASGGGCGPSGCSVNLCDLEKGPETLEFLELLGPDYGAGSE
AGVLLPAEPLDVFPTGATVLRGPPELEPGLFEPPPAMGGSLPYPEPWSAPACPATKKPSLAPPRGGSTLTEPLRL
LYPAAVNSPGGEDGPGPLASFGPFFSDCVLPQPPPPPQPRQVAYDVCAGYGRTAYSSLWRPDGLWEGDPGEEGAP
RD PLRARNLPPSFFTEP

rs:XP_003313276 [XP_003313276] protein **FAM181**B [Pan troglodytes].>tr:H2R532_PANTR [H2R532] SubName: Full=**FAM181**B isoform 1 {ECO:0000313|EMBL:PNI56970.1}; SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSPTRP00000047762};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGEVAAPAAGLGGAGTGGAGGDVAGPAGATAIPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGR
LASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_016777355 [XP_016777355] transcriptional coactivator YAP1 isoform X9 [Pan troglodytes].>rs:NP_001269028 [NP_001269028] transcriptional coactivator YAP1 isoform 7 [Homo sapiens].>tr:A0A2I3RHJ4_PANTR [A0A2I3RHJ4] SubName: Full=YAP1 isoform 3 {ECO:0000313|EMBL:PNI44637.1}; SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSPTRP00000064130};
85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_016777356 [XP_016777356] transcriptional coactivator YAP1 isoform X10 [Pan troglodytes].>rs:NP_001269026 [NP_001269026] transcriptional coactivator YAP1 isoform 6 [Homo sapiens].>gp:AB567720_1 [AB567720] yes-associated protein beta [Homo sapiens] 85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_016777357 [XP_016777357] transcriptional coactivator YAP1 isoform X11 [Pan troglodytes].>rs:NP_001269027 [NP_001269027] transcriptional coactivator YAP1 isoform 5 [Homo sapiens].>tr:A0A024R3E4_HUMAN [A0A024R3E4] SubName: Full=Yes-associated protein 1, 65kDa, isoform CRA_b {ECO:0000313|EMBL:EAW67014.1}; 85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF

NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_016777358   [XP_016777358] transcriptional coactivator YAP1 isoform
X12 [Pan troglodytes].>rs:NP_006097 [NP_006097] transcriptional coactivator
YAP1 isoform 2 [Homo sapiens].>tr:K7BI95_PANTR [K7BI95] SubName: Full=YAP1
isoform 4 {ECO:0000313|EMBL:PNI44638.1}; SubName: Full=Yes-associated
protein 1 {ECO:0000313|EMBL:JAA06372.1}; 85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL   PMRLRKLPDSFFKPP

rs:XP_014202427   [XP_014202427] LOW QUALITY PROTEIN: protein **FAM181**B [Pan
paniscus]. 99..113
MALLERGWAVLTSTSGVEEAQISDRSAQFSECEYHQDLQSRSLAALFDSLRHVPGGAEPXGGEVAAPAA
GLGGAGTGGAGGDVAGPAGATAIPGARKVPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFE
LLGPDYGAGTEAAVLLAAEPLDVFPAGASVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPR
GGLTLNEPLRPLYPAAADSPGGEDGPGHLASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEG
APGEEGAHRD PLRARNLPPSFFTEP

rs:XP_008952023   [XP_008952023] transcriptional coactivator YAP1 isoform
X1 [Pan paniscus].   13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGG
TQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLP
SQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014202459   [XP_014202459] transcriptional coactivator YAP1 isoform
X2 [Pan paniscus].   13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQ
NPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQ
QNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008952024   [XP_008952024] transcriptional coactivator YAP1 isoform
X3 [Pan paniscus].   13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008952025 [XP_008952025] transcriptional coactivator YAP1 isoform
X4 [Pan paniscus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRT
MTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGT
NVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWLPMRLRKLPDSFFKPP

rs:XP_014202461 [XP_014202461] transcriptional coactivator YAP1 isoform
X5 [Pan paniscus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMT
TNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNV
DLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008952026 [XP_008952026] transcriptional coactivator YAP1 isoform
X6 [Pan paniscus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014202462 [XP_014202462] transcriptional coactivator YAP1 isoform
X7 [Pan paniscus].>rs:XP_011839777 [XP_011839777] PREDICTED:
transcriptional coactivator YAP1 isoform X1 [Mandrillus leucophaeus].
13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014202463 [XP_014202463] transcriptional coactivator YAP1 isoform
X8 [Pan paniscus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQV
RPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDS
GLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQ
EALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014202464 [XP_014202464] transcriptional coactivator YAP1 isoform
X9 [Pan paniscus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQA
MRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSM
SSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALS
SDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014202465 [XP_014202465] transcriptional coactivator YAP1 isoform
X10 [Pan paniscus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT

LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQV
RPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDF
LNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLA
ATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014202466 [XP_014202466] transcriptional coactivator YAP1 isoform X11 [Pan paniscus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQE
LALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL PMRLRKLPDSFFKPP

rs:XP_003832850 [XP_003832850] protein **FAM181**A isoform X1 [Pan paniscus].>rs:XP_003832851 [XP_003832851] protein **FAM181**A isoform X1 [Pan paniscus].>rs:XP_008956482 [XP_008956482] protein **FAM181**A isoform X1 [Pan paniscus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTLVPMSPRALDEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_008956483 [XP_008956483] protein **FAM181**A isoform X2 [Pan paniscus].>rs:XP_009426629 [XP_009426629] protein **FAM181**A isoform X2 [Pan troglodytes].>tr:H2Q8U4_PANTR [H2Q8U4] SubName: Full=**FAM181**A isoform 2 {ECO:0000313|EMBL:PNI97566.1}; SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSPTRP00000011369};
191..205
MPLEERRSSGERNDAAHTNHRRPGEKRASTAKQVSSVPFLGAARHQQSLPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPRRLLLD
LGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPETTLVPMSPRALDEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWRKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_015143248 [XP_015143248] protein **FAM181**A [Gallus gallus].127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPTKPPECGPR
RGAEDRARSCQPEVPDPGPHSGAATEKVLQAAEAEESLTREQAVPEQNPETNRPDQVPMRKRQLPASFWEEPRPP
QSLPAGGFPPGPEGLPVPRDPPPFEGKKSKRSQDTIGPESHEPALNAGEKDPTGVLSGRVGAWTCCPFPCPGPAV
YQPPGTLPPSPFPGLGLWRKGTATLPAEAQPFCKDAEGTGQKLYRPVVLKPIPTKPTIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_022070041 [XP_022070041] transcriptional coactivator YAP1-like isoform X1 [Acanthochromis polyacanthus].46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSNSARQPSSVPMRMRKLPDSFFRQPEPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVATTPIIPDDVPLPHGWEMAKTATGQRYFLNHRDKTTTWH
DPRLSQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPR
LAQKMNPGLLGLAMQQRQEKERLRCKQGLPPQITSQEAGGRSQMSGGMDHDRSAQTLVPPLDVRIRASNHEPTLN
GAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGESVEPPSMALQESMPVLPMSEGEELMPCIPEGLSSDLLMD
METVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_022070042 [XP_022070042] transcriptional coactivator YAP1-like isoform X2 [Acanthochromis polyacanthus].46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSNSARQPSSVPMRMRKLPDSFFRQPEPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVATTPIIPDDVPLPHGWEMAKTATGQRYFLNHRDKTTTWH
DPRLSQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPETAQKMNPGLLGLAMQQRQEKERLRCKQGLPPQIT

SQEAGGRSQMSGGMDHDRSAQTLVPPLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDT
GESVEPPSMALQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_022084387 [XP_022084387] uncharacterized protein LOC110975858
[Acanthaster planci]. 167..181
MTLNACAYAGMPVYGNCNYSCSVPWTEGSQSSNNLVHFVDLASSNIKHALDRPVRSRRKVNHRKYLQKQ
IKRRSQQSQSGGLMGDQKVAQGIRDAAKSALSTEPGETPRAKYGTRSRETKAHLNVSQCKSLSAMFDLKALLHAE
TSGADEDGAKVKHQRPIGHEPVPLKRRNLPVSFFQEPDVSSLLLPHREILSSLSVDFDFPSVSTSEEEEDDDDIA
LRDTIDWLCSTADLDQILNPLLDEMRTAKAREERTATVSDTGHGEMGSGANGVLAGMQHGAFAHDFEKEPSHDDV
QQVQVIDPHGSNALEQWVGLDSAQPARNTGQLLYANTLHQHPNNVQQDNVTFTYNALEPNSTHYQSRIQKDSDTT
NQVDIDEYFTGNEGPRHEFVGGQLDSYGAAHHRAQPPQTHYNFTPAQQLCQGQSGCTSNPDMSYPAMIAEMRQHI
RQQDTHRSLTGGQSISTGGDRTLPTFPQAFMNEATPWSPSKDWS PLKRRNLPVSFFQEP

rs:XP_022085540 [XP_022085540] uncharacterized protein LOC110976517
[Acanthaster planci]. 133..147
MAKVPPPTPCSHATNKRGPSAPLSGSSSEGENSDLEDIPPSPCSSTSSGPIYVRPAGFNHHAQEIVQAV
PFRSCRSVKLKKKIKKNALTTDNLPCQQGTFSGFDQNNNTNNNNVRTAAPPSKAKQKPKKDPLPMKLRALPQSFW
QQPNSVNAVPPGSMYTVLPPVCKTDPPSIAEITDTRPITPPSDSDEKESLAVVKSEKPERAKSTEKPQPQDAAAL
REGALDAAAVEVVKSKPPKPPPRRTVRVSASSADLLAKLFDGIENDKKAPVAPTAKRGRPKRESSHPHHSKLLVN
KDDPYMIDAVSDSLLPLLSIESSRQSVGPASHLSVVSVKDGDKTLTLPALNVEQNYPAMLTELVKAL
PMKLRALPQSFWQQP

rs:XP_022431572 [XP_022431572] protein **FAM181**A isoform X1 [Delphinapterus
leucas].>tr:A0A2Y9NJK0_DELLE [A0A2Y9NJK0] SubName: Full=protein **FAM181**A
isoform X1 {ECO:0000313|RefSeq:XP_022431572.1};193..207
MLLRGSPCCPQPAISPPGRPRLECQTGVLPVLRENCQLRALPWSRQPPAEPPSSWKAPCSSPLVMASDS
DVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGSEDRPGRLP
LDSGHSSSPGGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTQSYPVGLEG
GLGPREGLPYEGKKHCKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGA
LPQSPLPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_022431573 [XP_022431573] protein **FAM181**A isoform X2 [Delphinapterus
leucas].>tr:A0A2Y9NQF7_DELLE [A0A2Y9NQF7] SubName: Full=protein **FAM181**A
isoform X2 {ECO:0000313|RefSeq:XP_022431573.1};174..188
MSVPRPRTLSRAEGCCGQLRALPWSRQPPAEPPSSWKAPCSSPLVMASDSDVKMLLNFVNLASSDIKAA
LDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGSEDRPGRLPLDSGHSSSPGGGGCCKEKA
LGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTQSYPVGLEGGLGPREGLPYEGKKHCKGL
EPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGALPQSPLPSLGLWRKSSASP
GELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_022431574 [XP_022431574] protein **FAM181**A isoform X3 [Delphinapterus
leucas].>rs:XP_022431575 [XP_022431575] protein **FAM181**A isoform X3
[Delphinapterus leucas].>tr:A0A2Y9N9T5_DELLE [A0A2Y9N9T5] SubName:
Full=protein **FAM181**A isoform X3 {ECO:0000313|RefSeq:XP_022431574.1,
ECO:0000313|RefSeq:XP_022431575.1}; 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGSEDRPGRLPLDSGHSSSPGGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTQSYPVGLEGGLGPREGLPYEGKKHCKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPQSPLPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_022901306 [XP_022901306] transcriptional coactivator YAP1-A isoform
X1 [Onthophagus taurus]. 42..56
MALNPDESGKQVVRVDQDSETDLQALFDTVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSREN
SVDSAFGSTTGTNSSATSTGATINPVQPVHHRAHSSPASLQQTYAVGQQQQQPAPAHHHIKQRSYDVATKTEDAT
PLPPGWEQARTPEGQVYYLNHITRTTTWEDPRKTLATQAAAQQHQSAEQLLTTHQVTSPTQTNSTGVNGSSDVEL
GPLPEGWEQAQTSEGEIYFINHQTRTTSWFDPRIPQHVQRSQVLGNQWVQGPVSPQSRCDKQSKLRLQLLQMERE

RLKQRQQEIRRQQELMMRGSSTELQMDPFLSSFTEHTRQESADSGLGMGTTLSMPQTPEDFLENIDDNMEVSSDS
HTMDTPDISLSENIDSTDDLVPSLHLGEEFPNIEDVQSLIRPENLIWL PWSMRKLPDSFFNPP

rs:XP_022901308 [XP_022901308] transcriptional coactivator YAP1-A isoform
X2 [Onthophagus taurus]. 42..56
MALNPDESGKQVVRVDQDSETDLQALFDTVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSREN
SVDSAFGSTTGTNSSATSTGATINPVQPVHHRAHSSPASLQQTYAVGQQQQQPAPAHHHIKQRSYDVATKTEDAT
PLPPGWEQARTPEGQVYYLNHITRTTTWEDPRKTLATQAAAQQHQSAEQLLTTHQVTSPTQTNSTGVNGSSDVEL
GPLPEGWEQAQTSEAQHVQRSQVLGNQWVQGPVSPQSRCDKQSKLRLQLLQMERERLKQRQQEIRRQQELMMRGS
STELQMDPFLSSFTEHTRQESADSGLGMGTTLSMPQTPEDFLENIDDNMEVSSDSHTMDTPDISLSENIDSTDDL
VPSLHLGEEFPNIEDVQSLIRPENLIWL PWSMRKLPDSFFNPP

rs:XP_022901309 [XP_022901309] transcriptional coactivator YAP1-A isoform
X3 [Onthophagus taurus]. 42..56
MALNPDESGKQVVRVDQDSETDLQALFDTVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSREN
SVDSAFGSTTGTNSSATSTGATINPVQPVHHRAHSSPASLQQTYAVGQQQQQPAPAHHHIKQRSYDVATKTEDAT
PLPPGWEQARTPEGQVYYLNHITRTTTWEDPRKTLATQAAAQQHQSAEQLLTTHQVTSPTQTNSTGVNGSSDVEL
GPLPEGWEQAQTSEGEIYFINHQTRTTSWFDPRIPQHVQRSQVLGNQWVQGPVSPQSRCDKQSKLRLQLLQMERE
RLKQRQQEIRRQQELMMRGSSTELQMDPFLSSFTEHTRQESADSGLGMYYFETHQQQ PWSMRKLPDSFFNPP

rs:XP_019689134 [XP_019689134] protein **FAM181**A isoform X1 [Felis
catus].>tr:M3WCW5_FELCA [M3WCW5] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSFCAP00000009492};
228..242
MLCIWRGAPDWPEGPPSAGDSSSIQPTRGLHDCFQPDARSSPATPGLAQVCRGEPARPRRRGARGRPAP
SVSSVPSPGAASHEQNPPASWKAPCSGLLVMANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQL
KRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDSGRDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNP
EAARPGQVPMRKRQLPASFWEEPRATHSYPLGLEGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKE
PLKMSGVSLVGRVNAWSCCPFQYHGQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPV
VLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_019689135 [XP_019689135] protein **FAM181**A isoform X2 [Felis catus].
207..221
MLCIWRGAPDWPEGPPSAGDSSSIQPTRGLHDCFQPDARSSPATPGLAQVSSVPSPGAASHEQNPPASW
KAPCSGLLVMANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEP
HLKRGPEDRPGRLPLDSGRDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWE
EPRATHSYPLGLEGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPF
QYHGQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGY
L PMRKRQLPASFWEEP

rs:XP_019689136 [XP_019689136] protein **FAM181**A isoform X3 [Felis
catus].>rs:XP_019689137 [XP_019689137] protein **FAM181**A isoform X3 [Felis
catus].>rs:XP_006933133 [XP_006933133] protein **FAM181**A isoform X3 [Felis
catus]. 129..143
MANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLDSGRDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
ATHSYPLGLEGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023094775 [XP_023094775] basic proline-rich protein-like [Felis
catus]. 386..400
MGLLTQIPSEESGVRSSGVESGVRSLPSGLPGPHQVMARLQYPRLGPRVDPTPGPLSLLPLDSPDPALG
PPPAPPPGPSRIRTWVRAPAPAPWIPRHAGPRAPRIPPTSAPAPPGFPRTRAPGVPPHPHLGAARPPRLPGGRAR
GRVTCGGPAGRAGRLQECGNSRAKVPARAGRGPGAGGRAEEGRAARRRGRRAARAGGSLNFSFGVGGEFLSQSGA
AAAGGERGEEGRKELREQSGQRGRGAPAAPPERSRRGRGARAGGAGSRPVPPRPRERPEGRRRRPPPPPPPRAEP
SAASSGRRRAWTPGRRPHSPRPPPAPRAPPPAQPPPGQGPPPAPGPAAPPGPQPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQVTGDGGAGGTGVPPPRVRRRGLPSLRGSRRGGGLGG
PPGGVQAFLEGAAGLARGRPGVGTQGAVRDSGGGTGGLGGAAGPGGASAGGRRDLFPPAPRDPGRSVRSGGDQPE

AGDTPPGECSHSDGLGPPLGVQGPEKLLELLAKPRVRPERGTAASFVRGRPRCAVPPPPSLAWVEVCSDAGYFLR
LESVTHSGR   PMRLRKLPDSFFKPP

rs:XP_012273110   [XP_012273110] transcriptional coactivator YAP1 [Orussus abietinus]. 46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGVAPPGVGGGSAAPGAATNGAAAAAAAAASAPGPPGAAAGPAQPPAAGPPTPAAAPGLTVAHP
RAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTT
TWEDPRKTAAAASVAAVAAAVESGKTSSGATSSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRA
PTSGAMLPQNWLQQPGGGGIQSSQTLQACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQSTTDAAMDPFLSG
INEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSEGGAPMETPDLSTLSDLVPSLQLGEEFSSDILD
DVQSLINPNTSKPENVLTWL   PLRMRNLPDSFFNPP

rs:XP_023295046   [XP_023295046] transcriptional coactivator yorkie isoform X1 [Lucilia cuprina].>tr:A0A0L0C8Y0_LUCCU [A0A0L0C8Y0] SubName: Full=Protein yorkie {ECO:0000313|EMBL:KNC28868.1};   65..79
MSLSKSSASDDASKCSVKTDDSTSAASKSSNNLVVHNYQNSDENLQILFDSVLNPSESKRPLQVPLRMR
KLPNSFFTPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQTSVATSLSDLQTAAAAAAAQASVQQQPATTINAQ
QPPPPPAAAGGTQADQPRLQICHSRAHSSPASLQQTYNIHGGNIGDDSTAASFLQQQQNAAGEVSNGGGGGGNSG
PGFPGTLLSYNAAAAAAAAAAAAGINSNNILALGGTGGGAPYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTND
GQIYYLNHTTKTTQWEDPRIQFKQQQALNAAANARLNNKTATAAGVLNGDLGPLPEGWEQALTETGEVYFINHID
RTTSWNDPRIPLLFQKEIKAKTEMSWVNATEIDKDTDIFKQKAGQKSLNKHNVSLHMDPFLSGDNHARQESSDSG
LSLSSNSFAVNPDFITHMDTSMDCISENGSIIDNLDTTLQLNDNICMLNDVLNSPLNKPDNLEWYKLN
PLRMRKLPNSFFTPP

rs:XP_023295048   [XP_023295048] transcriptional coactivator yorkie isoform X2 [Lucilia cuprina].   65..79
MSLSKSSASDDASKCSVKTDDSTSAASKSSNNLVVHNYQNSDENLQILFDSVLNPSESKRPLQVPLRMR
KLPNSFFTPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQTSVATSLSDLQTAAAAAAAQASVQQQPATTINAQ
QPPPPPAAAGGTQADQPRLQICHSRAHSSPASLQQTYNIHGGNIGDDSTAASFLQQQQNAAGEVSNGGGGGGNSG
PGFPGTLLSYNAAAAAAAAAAAAGINSNNILALGGTGGGAPYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTND
GQIYYLNHTTKTTQWEDPRIQFKQQQALNAAANARLNNKTATAAGVLNGDLGPLPEGWEQALTETGEVYFINHID
RTTSWNDPRIPLLFQKEIKAKTEMSWVNATEIDKDTDIFKQKAGQSLNKHNVSLHMDPFLSGDNHARQESSDSGL
SLSSNSFAVNPDFITHMDTSMDCISENGSIIDNLDTTLQLNDNICMLNDVLNSPLNKPDNLEWYKLN
PLRMRKLPNSFFTPP

rs:XP_012668939   [XP_012668939] transcriptional coactivator YAP1-like isoform X1 [Otolemur garnettii].   85..99
MDPEQQPPLQPAPQGQRQPPAQNTQEQAPPSGLEQPAPSASKEAPQAPFAGHQIVCVQGDSESDLEALF
NAVINPKTANVPQTVPMRLRKLPDSFFKPPEPKSCSPQASMDAGTAEDLTPQHVRAHSSPASLKLEAASPGTLTP
TGVVSDPATTSTAQHLLQSSLEIPDDVPLPAGWEIAETSAGQKYFLNHTDHTTSWQDPREAMLLQMNATASTSPP
AQQNMMNSASGPLPDGWEQAVTQDGEIYYINYKNMTAPWLDPSLDPRFGKAVNQRISQSAPDEQPPPLTPQSPQA
DVMGGSTSNQQQQMRLQLQMEEELLRLKQQELLWQEVALHGHLPTLEQDSGTQTPVSSPRMFQELRTMTANSFNL
LFNGGAHHSRDESTDSGLSVSSCGVPRTPEDILNSVDEMDTDDSVNQNTLLTLQNHLNDYLESIPGTSVDLGMAV
ALEGDEMYLEGEELMPNIQEAFNSDILNDMESVLAAAKLDKDSFLTWL   PMRLRKLPDSFFKPP

rs:XP_012668940   [XP_012668940] transcriptional coactivator YAP1-like isoform X2 [Otolemur garnettii].   85..99
MDPEQQPPLQPAPQGQRQPPAQNTQEQAPPSGLEQPAPSASKEAPQAPFAGHQIVCVQGDSESDLEALF
NAVINPKTANVPQTVPMRLRKLPDSFFKPPEPKSCSPQASMDAGTAEDLTPQHVRAHSSPASLKLEAASPGTLTP
TGVVSDPATTSTAQHLLQSSLEIPDDVPLPAGWEIAETSAGQKYFLNHTDHTTSWQDPREAMLLQMNATASTSPP
AQQNMMNSASAVNQRISQSAPDEQPPPLTPQSPQADVMGGSTSNQQQQMRLQLQMEEELLRLKQQELLWQAMWSL
SPSLANPPKCQEVALHGHLPTLEQDSGTQTPVSSPRMFQELRTMTANSFNLLFNGGAHHSRDESTDSGLSVSSCG
VPRTPEDILNSVDEMDTDDSVNQNTLLTLQNHLNDYLESIPGTSVDLGMAVALEGDEMYLEGEELMPNIQEAFNS
DILNDMESVLAAAKLDKDSFLTWL   PMRLRKLPDSFFKPP

rs:XP_012668941   [XP_012668941] transcriptional coactivator YAP1-like isoform X3 [Otolemur garnettii].   85..99
MDPEQQPPLQPAPQGQRQPPAQNTQEQAPPSGLEQPAPSASKEAPQAPFAGHQIVCVQGDSESDLEALF

NAVINPKTANVPQTVPMRLRKLPDSFFKPPEPKSCSPQASMDAGTAEDLTPQHVRAHSSPASLKLEAASPGTLTP
TGVVSDPATTSTAQHLLQSSLEIPDDVPLPAGWEIAETSAGQKYFLNHTDHTTSWQDPREAMLLQMNATASTSPP
AQQNMMNSASAVNQRISQSAPDEQPPPLTPQSPQADVMGGSTSNQQQQMRLQLQMEEELLRLKQQELLWQEVALH
GHLPTLEQDSGTQTPVSSPRMFQELRTMTANSFNLLFNGGAHHSRDESTDSGLSVSSCGVPRTPEDILNSVDEMD
TDDSVNQNTLLTLQNHLNDYLESIPGTSVDLGMAVALEGDEMYLEGEELMPNIQEAFNSDILNDMESVLAAAKLD
KDSFLTWL   PMRLRKLPDSFFKPP

rs:XP_010587122   [XP_010587122] protein **FAM181**A [Loxodonta africana].
130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLK
RGPEDRLSRLPLDSHDPSPSGVGGCKEKALGNPGREECLSRQQEQTLQGQNPEAAQPGQVPMRKRQLPASFWEEP
RPAHSFPLGLEGGLGAREGPPYEGKKTCQGLEPLGPETAPVPMSPRALAEKEPLKMPGVSLMGQVNAWSCCPFQY
HGQPIYPGPPGALPQGSVPNLGLWRTSPASTGELTPFCKDADGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023721985   [XP_023721985] transcriptional coactivator YAP1 isoform X1 [Cryptotermes secundus].   45..59
MALNPDSEQHKGNLVVRIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGGTTTTSASGASGLQVNHPRAHSSPASLQQTYASAQQQQHGHLKQRSYDITP
VDELGPLPPGWAQARTPEGQVYYLNHITRTTTWEDPRKTLAAQVTQSQQQQQQQQQQQQQQTSADLISNVAGSPH
SSTSPQPQGTKSVDASSLGPLPEGWDQATTQEGEVYFINHQTRTTSWFDPRIPTAMWSRTAIPSLVQRMRVLRLS
ANHTLHLQKSPAGSLLPQQSTSWIQPLSAQSQVCQQIRLQSLQMERERLKLRQQEIMRQGMMLRQPSTTDLPPGP
NSAGMDPFLSGLTDHSRQESADSGLGMCNSYSLPHTPEDFLANMDDNMDGVSEGGNPTDMAALDGPDISSLSDNI
DSTDDLVPSLQLSEEFSSDILDDVQSLINPNSRPDNVLTWL PLRMRKLPNSFFNPP

rs:XP_023721986   [XP_023721986] transcriptional coactivator yorkie isoform X2 [Cryptotermes secundus].   45..59
MALNPDSEQHKGNLVVRIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGGTTTTSASGASGLQVNHPRAHSSPASLQQTYASAQQQQHGHLKQRSYDITP
VDELGPLPPGWAQARTPEGQVYYLNHITRTTTWEDPRKTLAAQVTQSQQQQQQQQQQQQQQTSADLISNVAGSPH
SSTSPQPQGTKSVDASSLGPLPEGWDQATTQEGEVYFINHQTRTTSWFDPRIPTAMWSRTAIPSLVQRMRVLRLS
ANHTLHLQKSPAGSLLPQQSTSWIQPLSAQSQVCQQIRLQSLQMERERLKLRQQEIMRQGMMLRQPSTTDLPPGP
NSAGMDPFLSGLTDHSRQESADSGLGMCNSYSLPHTPEDFLANMDDNMDGVSEGGNPTDMAALDGPDISSLSDNI
DSTDDLVPSLQNCWKSLPHNHSLLRVMSLNTH   PLRMRKLPNSFFNPP

rs:XP_023721987   [XP_023721987] transcriptional coactivator YAP1 isoform X3 [Cryptotermes secundus].   45..59
MALNPDSEQHKGNLVVRIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGGTTTTSASGASGLQVNHPRAHSSPASLQQTYASAQQQQHGHLKQRSYDITP
VDELGPLPPGWAQARTPEGQVYYLNHITRTTTWEDPRKTLAAQVTQSQQQQQQQQQQQQQQTSADLISNVAGSPH
SSTSPQPQGTKSVDASSLGPLPEGWDQATTQEGEVYFINHQTRTTSWFDPRIPLHLQKSPAGSLLPQQSTSWIQP
LSAQSQVCQQIRLQSLQMERERLKLRQQEIMRQGMMLRQPSTTDLPPGPNSAGMDPFLSGLTDHSRQESADSGLG
MCNSYSLPHTPEDFLANMDDNMDGVSEGGNPTDMAALDGPDISSLSDNIDSTDDLVPSLQLSEEFSSDILDDVQS
LINPNSRPDNVLTWL   PLRMRKLPNSFFNPP

rs:XP_023721988   [XP_023721988] transcriptional coactivator yorkie isoform X4 [Cryptotermes secundus].   45..59
MALNPDSEQHKGNLVVRIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGGTTTTSASGASGLQVNHPRAHSSPASLQQTYASAQQQQHGHLKQRSYDITP
VDELGPLPPGWAQARTPEGQVYYLNHITRTTTWEDPRKTLAAQVTQSQQQQQQQQQQQQQQTSADLISNVAGSPH
SSTSPQPQGTKSVDASSLGPLPEGWDQATTQEGEVYFINHQTRTTSWFDPRIPTAMWSRTAIPSLVQRMRVLRLS
ANHTLHLQKSPAGSLLPQQSTSWIQPLSAQSQVCQQIRLQSLQMERERLKLRQQEIMRQGMMLRQPSTTDLPPGP
NSAGMDPFLSGLTDHSRQESADSGLGMCNSYSLPHTPEDFLANMDDNMDGVSEGGNPTDMAALDGPDISSLSDNI
DSTDDLVPSLQFPML   PLRMRKLPNSFFNPP

rs:XP_005287639   [XP_005287639] protein **FAM181**B [Chrysemys picta bellii].
195..209
MAVQAAILNPHHFIPFCFPASGGLADYVDLEKSYEDGGAALLAGGGVGGGEDPGDFKEATRDLLSFIDS
ASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIIASAPAAPAPAGGQELPKRPAPPAGAASPQPSCPPGPAGH

CKPPAKREASQAASSLQSKSLAALFDSLHQGRAGEKGPAGGSGGGGPRKVPLRNRNLPPSFFTEPAAPPPRAPPL
SASPKALERGGGSPEAAEFFELLGPDYGGLLPEQPPAQEGFPARLPPELGMEPALYEPHLPPLPPHLLGAMLYPE
PAWSPPAKKSPPAAASCSSLSLPETLRPLPAMGAPGAPLYPASSDPAPAGGEESPAQLAAAFAPYFPDCPLPPPP
AMPYEYSAGYNRVAYSGL PLRNRNLPPSFFTEP

rs:XP_005307536 [XP_005307536] protein **FAM181**A [Chrysemys picta bellii].>rs:XP_005307537 [XP_005307537] protein **FAM181**A [Chrysemys picta bellii]. 126..140
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSMESSSK
RGAEDRNRSSDPDGPDPNHCKASSEKALRLSEVEENFSGGQVLQEQSPESLRPDQVPMRKRQLPASFWEEPRPTQ
SLLVGSFPAGLDGLPNSRDLPPYEGKKSKKGPDTTEPGSPPLPAQPSGEKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTHGALPQSPFPGLGLWRKSTAPAGEIQHFCKEAGNMGQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_012246006 [XP_012246006] transcriptional coactivator YAP1 [Bombus impatiens]. 46..60
MALNQDVDQLSKSNLVVNIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAAVAGAGPAPGGNATGTSATGAAGAATGGSGNTAAGTGSNAAGAAXXXXXXXAAAGLTVA
HPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTR
TTTWEDPRKTAAAANVAAVAAAVDNGKSSTGATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQ
RAPTSGAMLPQNWLQQQQPTGGGIQSNQTLQACQQKLRLQSLQMERERLKQRQQEIIRQQELMLRQSTTDAAMDP
FLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQ
LSEDFSSDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_024616126 [XP_024616126] transcriptional coactivator YAP1 [Neophocaena asiaeorientalis asiaeorientalis].>tr:A0A341CMW9_9CETA [A0A341CMW9] SubName: Full=transcriptional coactivator YAP1 {ECO:0000313|RefSeq:XP_024616126.1}; 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTSPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011535599 [XP_011535599] protein **FAM181**A isoform X1 [Homo sapiens]. 169..183
MAAVGLESLGEVSSVPFLGAAGHQQSLPSSWKASCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSA
PCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPY
REECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGP
ETTLVSMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAH
LCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_006907601 [XP_006907601] transcriptional coactivator YAP1, partial [Pteropus alecto]. 53..67
PGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEP
KSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTPTGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAG
WEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINH
KNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELL
RQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSG
LSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQE
ALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006925613 [XP_006925613] protein **FAM181**A [Pteropus alecto].>rs:XP_006925612 [XP_006925612] protein **FAM181**A [Pteropus alecto].>rs:XP_011377919 [XP_011377919] protein **FAM181**A [Pteropus vampyrus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLDSGPDAGPGGGGGCKEKALGNPYREACLAKEQTLQGQNPEVARPGQVPMRKRQLPASFWEEPR

PTHSYPVGLEGGLGLRAGPPYEGKKHCKGLEPLGPEAARVPMSPRVPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPSYPGPPGALPQSPVPSLGLWRKSSVSPGELAHFCKDVDGLGQKVYRPVVLKPIPTKPALPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_024921608 [XP_024921608] transcriptional coactivator YAP1-like
[Cynoglossus semilaevis]. 74..88
MNLDSVDDVKKFGVSQLQTIIVPDLGDTMDAHRGAPPAGQQVVHVRGDSQTELEALFSAVMNPNKAVRQ
PASLPMRMRKLPDSFFRQPDPRGHSRQASSDGGVCGTLTPHHVRAHSSPASLPVNSLSTQTADVAATPIIPDDVP
LPHGWEMAKTSTGQRYFLNHHDKTTTWHDPRLSQLQSPAAQHPIAGPPLHAHSLSNPAQTTQQNINPETGPLPE
GWEQAVTADGEVYYIDHINKSTTWVDPRLAQNMNPGILGMVMQQRQEKERLRCKQGHPPQAAPQEVGGRNQMSGG
IDHDRNSQTLVPNLDVRIRSSNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGENSSITLQE
SMPVMPMSEGDELMPCIPEGLSSDLLMDMETVLSGSHMERDSLLTWL PMRMRKLPDSFFRQP

rs:XP_008307022 [XP_008307022] transcriptional coactivator YAP1
[Cynoglossus semilaevis].>tr:A0A3P8V333_CYNSE [A0A3P8V333] SubName:
Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSCSEP00000008524};
45..59
MDPSQHNPPAGHQIVHVRGDSETDLETLFNAVMNPKNTIIPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGTLTPHHVRAHSSPASLQLGAVSGGSMSGMPPAGASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPANTVPVQQQNLMNPASGALPEGWEQAMTPEGEIYFINHKNKSTSWLDPRL
DQRYALNQQRITQSAPVKQGGPLPPNTHSGVMGSNSQMRLQQIDKERLRLKQQELLRQRPQELALRNQLPNSMDQ
DGGTNPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLQSTMA
TQPSRFPDYLDAIPGTDVDLGTMESESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_008307029 [XP_008307029] LOW QUALITY PROTEIN: protein **FAM181**B
[Cynoglossus semilaevis]. 243..257
MQVVGHKQRVKSPGXPVPLLFDVLTSFVQPPVRSPCSXSQPVTFNRECLQEAVSGSECFPRAQTETCFE
ESLGSGITAGEAAELRSRVMAVQTAIMNPQFMNFCFPGSVMEYDVDKSLDGSLLGEAENDEDYKETTRDLLNFID
SASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGTGAEPPGKRQGSPLAQPSPLQNKTLPKRDGVQANL
QSKSLAALFSPAKEIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAVEFFELLGPDYSN
MVSDQDLYPNSSLRLQPEMGTLDPACYDSHHLVGGLLYSEPWTSCSGPSKNLRASPAQPPVYCQSEAAAAAAAAA
GNMDDNALCTLTFPNFFTDCSIPQVTYDLNGGYSRANYSSL PLRHRNLPPSFFTEP

rs:XP_015135770 [XP_015135770] LOW QUALITY PROTEIN: protein **FAM181**B
[Gallus gallus]. 304..318
MRPPLGSGLRTPRTAPHNPCPQNLPHLCSLPVQGPHRFRSRCVYVLRGIQPVRCPRCWGHVPAPPGHDP
PAPPLSPPEGSARPAPRCRREAGMPCPAPRWALLLSRPPLFPPTTAASAAPVPVQPCGARRRGAPPPAMAVPAAL
LSPHHLLSFCFPAGGLLGYADLEKGYEGGGGVGGGGGGGGCEAGDFKEATRDLLSFIDSASSNIKLALDKPVKSK
RKVNHRKYLQKQIKRCTGIIAPPPAAPPPSACPKPPPPPRREGSQAGSSLQSRSLAALFGSLQPGRGSAGSDGGG
AAGGGPRKVPLRDRNLPPSFFTEPGAKETEKGGGPEAAEFFELLGPEYGALLPEHAAPPQDAFPAGRRPPSWGWS
TGCTRAPLPAAPHPLLGGLLYPEPPWSPPGPCSPAKKAPPEALRPLYPEPAAGGDAFGPFFPECPLPPPQMPYDY
GGGFHRAAYTGL PLRDRNLPPSFFTEP

rs:XP_414952 [XP_414952] uncharacterized protein LOC416655 isoform X1
[Gallus gallus]. 202..216
MHGRAAAPRVSPGPGVSLCTDMAAGVIQPLAELRLPSPFPHGLLLPARPEPDFPDLSEEDDEEEEEEED
EEEAAEESAGCSGPEPAGPNAAETTLRLLRFSELISCDIQRYFGRRGREEAAGGHSVPEDCSSPHSSPRDASLGH
TARGGRAQPEAALGGHGAAQRLGPLAELFEYGVHRCLAPRVVSGKTQRLERKYGHITPMHRRKLPPSFWREPGPG
PGSLLHASTPDFSDLLAHWTVEPGPELPGSGRELPPVLGHAGLEAEPYSGL PMHRRKLPPSFWREP

rs:XP_015150107 [XP_015150107] uncharacterized protein LOC416655 isoform
X2 [Gallus gallus]. 181..195
MAAGVIQPLAELRLPSPFPHGLLLPARPEPDFPDLSEEDDEEEEEEEDEEEAAEESAGCSGPEPAGPNA
AETTLRLLRFSELISCDIQRYFGRRGREEAAGGHSVPEDCSSPHSSPRDASLGHTARGGRAQPEAALGGHGAAQR
LGPLAELFEYGVHRCLAPRVVSGKTQRLERKYGHITPMHRRKLPPSFWREPGPGPGSLLHASTPDFSDLLAHWTV
EPGPELPGSGRELPPVLGHAGLEAEPYSGL PMHRRKLPPSFWREP

rs:XP_006110881 [XP_006110881] transcriptional coactivator YAP1 isoform X9 [Pelodiscus sinensis]. 73..87
MDPGQPQQAQPPAQQQAPQPPGAQSGAGQPPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQVGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQSIMNSASGP
LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQM
RLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKRQELALRSQLPSMEQDGGSQNPVSSPGMSQELRTM
TTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNV
DLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006110882 [XP_006110882] transcriptional coactivator YAP1 isoform X10 [Pelodiscus sinensis]. 73..87
MDPGQPQQAQPPAQQQAPQPPGAQSGAGQPPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQVGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQSIMNSASGP
LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQM
RLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKRQELALRSQLPSMEQDGGSQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006110883 [XP_006110883] transcriptional coactivator YAP1 isoform X11 [Pelodiscus sinensis]. 73..87
MDPGQPQQAQPPAQQQAPQPPGAQSGAGQPPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQVGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQSIMNSASGP
LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQM
RLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPSMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHS
RDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEE
LMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006110884 [XP_006110884] transcriptional coactivator YAP1 isoform X12 [Pelodiscus sinensis].>tr:K7FW13_PELSI [K7FW13] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSPSIP00000012223}; 73..87
MDPGQPQQAQPPAQQQAPQPPGAQSGAGQPPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQVGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQSIMNSASGP
LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQM
RLQQLQMEKERLRLKHQELLRQELALRSQLPSMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDES
TDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPS
LQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006110888 [XP_006110888] transcriptional coactivator YAP1 isoform X13 [Pelodiscus sinensis]. 73..87
MDPGQPQQAQPPAQQQAPQPPGAQSGAGQPPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQVGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQSIMNSASAM
NQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPSMEQDGG
SQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPS
HQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_025122781 [XP_025122781] transcriptional coactivator YAP1 isoform X1 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN

RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_025122783 [XP_025122783] transcriptional coactivator YAP1 isoform X2 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_025122784 [XP_025122784] transcriptional coactivator YAP1 isoform X3 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_025122785 [XP_025122785] transcriptional coactivator YAP1 isoform X4 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_025122786 [XP_025122786] transcriptional coactivator YAP1 isoform X5 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_025122787 [XP_025122787] transcriptional coactivator YAP1 isoform X6 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_025122788 [XP_025122788] transcriptional coactivator YAP1 isoform X7 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN

AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025122789   [XP_025122789] transcriptional coactivator YAP1 isoform
X8 [Bubalus bubalis].   84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGD
GMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025122790   [XP_025122790] transcriptional coactivator YAP1 isoform
X9 [Bubalus bubalis].   84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQA
MRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSM
SSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALS
SDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025122791   [XP_025122791] transcriptional coactivator YAP1 isoform
X10 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNI
NPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYS
VPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDIL
NDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025122792   [XP_025122792] transcriptional coactivator YAP1 isoform
X11 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQE
LALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025122793   [XP_025122793] transcriptional coactivator YAP1 isoform
X12 [Bubalus bubalis]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVSTPTSPPV
QQNVMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALR
SQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMD
TGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKES
FLTWL PMRLRKLPDSFFKPP

rs:XP_025127517   [XP_025127517] protein **FAM181**A [Bubalus bubalis].
130..144

MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRSLPLESGHSSSPGGGGGCKEKALGNLDREESLSRERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGEPVYPSPPGALPQSPMPSLGLWRKSTASPGELAHFCKDMEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_006055691 [XP_006055691] protein **FAM181**B [Bubalus bubalis].
212..226
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDEETGTPAGALLAGAESGDAREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAGAQTVPVPAHGKAA
PRREASQAAAAASLQSRSLAALFDSLRHVPGGADPAGAAEAAPAAGLVGGDAAGSAGGPAVPGARKVPLRARNLP
PSFFTEPSRAGGGVCGPSGPGVSLGDLEKGSEAAEFFELLGPDYGAGTEAGALLAAEPLDVFPAGAAVLRGPPEL
EPGLFDPQPAMVGSLLYPEPWSAPGGPATKKPPLPAPGGGLTLNEPLRSVYPAAADSPGGDDGPGLLASFTPFFS
DCALPPAPPPPPQQVSYDYSAGYSRTAFAGLWRPDGAWEGAPGEEGAPRD PLRARNLPPSFFTEP

rs:XP_025726233 [XP_025726233] protein **FAM181**A [Callorhinus
ursinus].>rs:XP_027428711 [XP_027428711] protein **FAM181**A isoform X3
[Zalophus californianus].>rs:XP_027428712 [XP_027428712] protein **FAM181**A
isoform X3 [Zalophus californianus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDGPGRLPLDSGQDSSPSGGGCYKEKALGNPYGEECLSREQTLQRQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPLDPETAPVPASPRALAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPIYAGHPGVLPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_025749929 [XP_025749929] protein **FAM181**B [Callorhinus ursinus].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAPDAPAKRPLAGPGAQNVAVPLHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGDERAGGSVAAPVAGLGGAGAGGSGGDAAGPAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEQPPAMVGSLLYSESWSAPGCPPTKKPPLAAPRGGLTLNEPLRPLYPSAADSPGGEDAPGL
LASFAPFFSDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_008931850 [XP_008931850] protein **FAM181**A [Manacus vitellinus].
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHPSKPPECGWR
RGAEDRGRGPQLEAPDPSPHGGAATEKVMQTAEAEETLTGERVLQEQKPEAVRPDQVPMRKRQLPASFWEEPRPA
QNLTARAFPASPEGLPAPRDPPPYEGKKSKWSPDAAGPESPPDPAPHAGEKDPAGVLSGRVGAWTCCPFPCPGTG
VYQPPGALPPSPFPGLGLWRKSAATLPAEVPHFCKEADGTGQKLYRPMVLKPIPTKPTIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_005472252 [XP_005472252] transcriptional coactivator YAP1 isoform
X1 [Oreochromis niloticus]. 45..59
MDAHRGAPPAGQQIVHVRGDSQTELEALFTAVMNPNAAKQPSSLPMRMRKLPDSFFRQPDPRGHSRQAS
SDGGVCGSQAPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDMPLPRGWEMAKTPTGQRYFLNHLDKTTTWHD
PRLAQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPEKGPLPEGWEQAVTADGEMYYIDHINKTTTWVDPRL
AQKMNPSILGMAMQQSQEKDRLRCKQGIPQQIPPQDVGGRSQMPGGMDHDRSAQTLIPSLDVRIRASNHEPTLNG
AHSRNESTDSGLSVSSLPRTTDHMLSSVEHMDTGDSEPPSMALQDSMPVLPMSEGEELMPCIPEGLSSDLLMDME
TVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_005472253 [XP_005472253] transcriptional coactivator YAP1 isoform
X2 [Oreochromis niloticus]. 45..59
MDAHRGAPPAGQQIVHVRGDSQTELEALFTAVMNPNAAKQPSSLPMRMRKLPDSFFRQPDPRGHSRQAS
SDGGVCGSQAPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDMPLPRGWEMAKTPTGQRYFLNHLDKTTTWHD
PRLAQLQSAAAQHPISGPPVHAHSLSNPAPTTQPQNINPEKAQKMNPSILGMAMQQSQEKDRLRCKQGIPQQIPP
QDVGGRSQMPGGMDHDRSAQTLIPSLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTTDHMLSSVEHMDTG
DSEPPSMALQDSMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_003450207   [XP_003450207] transcriptional coactivator YAP1
[Oreochromis niloticus].>tr:I3JEC8_ORENI [I3JEC8] SubName: Full=Yes-
associated protein 1 {ECO:0000313|Ensembl:ENSONIP00000007219};   45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKVNTVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSGGSLSGMGSTGASPQHLRQSSYEIPDDMPLPDGWEMAKTASGQRYF
LNHIDQTTTWQDPRKAMLQMNQPPPPSSVPVQPQPIMNPASGPLPDGWEQAITAEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRISQSAPVKPPGQLPPSISGVMGSNNQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQD
GSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMAT
QPSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_005455123   [XP_005455123] protein **FAM181**B [Oreochromis
niloticus].>tr:I3L013_ORENI [I3L013] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSONIP00000026710};
155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGETENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNAAEAPVKRQGSPLTQPSTLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKPKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSDQDIYQGMPL
RVQPELGGPDPASYDTHHLVGGLLYSEPWTSCSGPSKKVGESLRTGPAQPPVYCQSEGATGPIEDNALCTLAFPN
FFADCPIPQVTYDLTGGYNRANYSSL   PLRHRNLPPSFFTEP

rs:XP_005477059   [XP_005477059] protein **FAM181**A [Oreochromis niloticus].
102..116
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYRC
AKPMGTVHQSVTEKASSGAQDVDHLGSSVEQVPMRKRQLPASFWEEPKLTPTKREHSYLGMKRSHAGTSEGTENE
KRKRSYDDDGAKAAISACSRRSSTDKETLKLDVTSHHCVSVCGCCPFQYHGHQILHNHIFVPHPPLGLWSKASGT
ETERSEHPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI   PMRKRQLPASFWEEP

rs:XP_018322696   [XP_018322696] transcriptional coactivator YAP1-A
[Agrilus planipennis].>tr:A0A1W4WFF7_AGRPL [A0A1W4WFF7] SubName:
Full=transcriptional coactivator YAP1-A
{ECO:0000313|RefSeq:XP_018322696.1};   42..56
MALNQDESSKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSREN
SVDSAFGSSSGGGSTTTAAVNTVPLQSAHHRAHSSPASLQQTYAVGQQQTAATHHHIKQRSYDVASKSDDTTPLP
PGWEQARTPEGQVYYLNHITRTTTWEDPRKSLAAQVASQQHQSAEQLLTSHQVSPTQSQTKTSTEVDLGPLPEGW
EQAQTPEGEIYFINHQTRTTSWFDPRIPQHLQRTPGIVQPQWHATSSLSPQSSPAKQQQLRLQLLQLERERLKQR
QQEIRRQQELMLRGSNTELPMDPFLSSLTDHSRQESADSGLGMGTSYSMPHTPEDFLANMDDNMEVGSETHNLDT
PDISSLSDNIDSTDLVPSLQLGEEFPSVILDDVQSLINPATTRSDNGLIWL PWSMRKLPDSFFNPP

rs:XP_025833269   [XP_025833269] transcriptional coactivator YAP1-A-like
[Agrilus planipennis]. 42..56
MALNQDESSKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSREN
SVDSAFGSSSGGGSTTTAAVNTVPLQSAHHRAHSSPASLQQTYAVGQQQTAATHHHIKQRSYDVASKSDDTTPLP
PGWEQARTPEGQVYYLK PWSMRKLPDSFFNPP

rs:XP_025862508   [XP_025862508] transcriptional coactivator YAP1 [Vulpes
vulpes].   119..133
MDMLLSSLQRQSGQQKLNIILKLGKWWGEVRWKRSQATGGPQCHSPGAGFKDMAVDRWDKCMAGVKEMG
VSKGKGSKGEEAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKAHSRQAST
DAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVSSGPAAAPSAQHLRQSSFEIPDDVPLPAGWEMAKTSSG
QRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPVQQSMMTSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLD
PRLDPRFAMNQRISQSAPVKQPPPLAPQSPPGVLGGGGSSQQQQMRLQQLQMEKERLRLKQQELLRQAMRNISPS
TANSPKCQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPR
TPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDM
ESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_025838343   [XP_025838343] protein **FAM181**A [Vulpes vulpes].129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGAEDRPGRLPLGSGHDSSTGEGGGCKEKALGNPYREECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPR

PTHSYPLGLEGGLGPREGPPYESKKHCKGLEPLDPEMAPVPTSPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYAGPPGALPQSPVPGLGLWRKSPASPGELAHFCKHVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_025963554 [XP_025963554] iroquois-class homeodomain protein IRX-3
[Dromaius novaehollandiae]. 218..232
MHGLSAALRVSRGPTCTAMAAGVIRHLAELWLPSPFPHALLLPTRPEPDFPDLSEEEEEDEEDEEEEEE
EEEEEEAADSTSRSGQELAGPSDAETTLQLLKFSELISCDIQRYFGRRGRDEDAEGWGTAEDCRSPRRSGRELYY
AELLRVAQSGEPQEEVARAPGGPRGWQPAGGPGGAPPLGPLAELFEYGLHRCLQPPAADGKTQRLERKYAHITPM
HKRKLPQSFWREPGPGPALHPSTPDFSDLLANWTAEPAPELPGAGRELPPEPGRPGLEAEHLGLL
PMHKRKLPQSFWREP

rs:NP_611879 [NP_611879] yorkie, isoform D [Drosophila
melanogaster].>gp:AE013599_5670 [AE013599] yorkie, isoform D [Drosophila
melanogaster] 65..79
MLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPLRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPIAAIPQLQIQPSPQHSRLAIHHSRAR
SSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAPASSAIDLDAMNTCMSQDIPMSMQ
TVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQILMAERIKQNESG
LSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:NP_001350857 [NP_001350857] yorkie, isoform H [Drosophila
melanogaster].>rs:XP_016029385 [XP_016029385] uncharacterized protein
Dsimw501_GD24973, isoform B [Drosophila simulans].>rs:XP_016029387
[XP_016029387] uncharacterized protein Dsimw501_GD24973, isoform D
[Drosophila simulans]. 88..102
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPIAA
IPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAP
ASSAIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWED
PRIQYRQQQQILMAERIKQNDVLQTTKQTTTSTIANNLGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQSG
LSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_026048079 [XP_026048079] transcriptional coactivator YAP1
[Astatotilapia calliptera].>rs:XP_004560573 [XP_004560573] transcriptional
coactivator YAP1 [Maylandia zebra].>tr:A0A3P9DD61_9CICH [A0A3P9DD61]
SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSMZEP00005032294}; 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKVNTVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSAGVLIPHHVRAHSSPASLQLGAVSGGSLSGMGSTGASPQHLRQSSYEIPDDMPLPDGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQPAPPSSVPVQPQPIMNPASGSLPDGWEQAITAEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRISQSAPVKQAGQLPPSISGVMGSNNQMRLQMEKERLRQKQQELLRQRPQELALRNQLPTSMDQDG
STNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMATQ
PSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_026048709 [XP_026048709] LOW QUALITY PROTEIN: protein **FAM181**B
[Astatotilapia calliptera]. 246..260
MQVVGHKQRVKXPAVPLPLLFDVLTSFVQPPERSPXLSSERVTSTLECLQELHEQHQDQVFIRGKRACC
EEILGSRITVDATGVAAGLNRVMAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGETENDEDYKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNAAEAPVKRQGSPLTQPSTLQSKTLPKRDGVQ
ANLQSKSLAALFSPVKDIRGEKPKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEATEFFELLGPD
YCNMVSDQDIYQGMPLRVQPELGGPDPASYDTHHLVGGLLYSEPWTSCSGPSKKVGESMRTGPAQPPVYCQSEGA
TGPIEDNALCTLAFPNFFADCPIPQVTYDLTGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_026119065 [XP_026119065] protein **FAM181**B-like [Carassius auratus].
156..170
MAVQAAIMNSQFLNFCFPGSVMDYEVEKGLEGGLLGEVDCEGDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISPGSIPVQEQCKRQGSPHNPTSNLSSKMPPKKDGMQANLQSKSLAALFNSA

KDVRAERAKKPPLRHRNLPPSFFMEPANSSRVTSTSGMSLKDLERGAPEAAEFLELLGPEYSNMVSEQDLFHTLP
NRIQQEVTVGPEPYDSHHFVSGGFLYTEPWSTCSSTPKKSGDLRTVPLQPNLYTHTDLSGSMPVEQSSPCALTFS
NFFTDCNATPVSYDVVNGYNRGSFSSL PLRHRNLPPSFFMEP

rs:XP_026138572 [XP_026138572] protein **FAM181**B [Carassius auratus].
156..170
MAVQAAIMNSQFLNFCFPGSVMDYEVEKGLEGGLLGEMDCGGDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISPGSTPVQEPCKRQGSPPTPTSNLSSKTPPKKDGMQASLQSKSLAALFNSA
KDERGEKAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAAEFLELLGPEYSNMVSEQDLLYTAP
IRIQQEVTAGPEPYDSHHFVSGGFLYTEPWGTCSGTSKKPGDMRTVPVQPNLYAHTDLSGSVPVEQSSPCALTFP
NFFTDCSTPPVSYDLVNGYNRGSFSSL PLRHRNLPPSFFTEP

rs:XP_026143466 [XP_026143466] transcriptional coactivator YAP1-like
isoform X1 [Carassius auratus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKSTIAPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVTPGSLSSMVPSNAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPAPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQIRLQQMQMENERMRIKQELLRQRPQELALRNQLPTSME
HDGGTQNPVSSPSMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDSLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_026143467 [XP_026143467] transcriptional coactivator YAP1-like
isoform X2 [Carassius auratus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKSTIAPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVTPGSLSSMVPSNAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPAPVQQQNIMNPASAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQI
RLQQMQMENERMRIKQELLRQRPQELALRNQLPTSMEHDGGTQNPVSSPSMGQDARNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDSLGPSSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_026085098 [XP_026085098] protein **FAM181**A [Carassius auratus].
105..119
MMSSDSEVKTLLNFVNLASSDIKAALDRSAPCRRSVDHRKYLQKQLKRFSHRYAKMPRCHPHRNGDSAL
AKLSEEKAPRGTGTGRDVSAGSEDEARSGQGQIPMPMRKRQLPASFWKEPQSSSGTRERLERFLKNNASATGHVR
TPAVNDEKRKMVFDDSKANPLLSGSAACACSCCSLPYRALHSRFLLPHADAPFRSRVEPAHSFSAGQQRSSAHVV
IKPIPTKPALSSSSSSSVFSVFGF PMRKRQLPASFWKEP

rs:XP_026086757 [XP_026086757] transcriptional coactivator YAP1 isoform
X1 [Carassius auratus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAISPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGNLSSMGPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNPQRISQSAPVKQGSQLPSSPQSGVLAGNNQIRLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLVP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMETVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_026086758 [XP_026086758] transcriptional coactivator YAP1 isoform
X2 [Carassius auratus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAISPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGNLSSMGPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASAMNPQRISQSAPVKQGSQLPSSPQSGVLAGNNQI
RLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLVPSSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMETVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_026288711 [XP_026288711] transcriptional coactivator YAP1 isoform
X1 [Frankliniella occidentalis]. 43..57

MSLNPDSGEKQQEVVLERDSETELQALFEIVLKPNAKRPLQKPMHMRKLPNSFFNPPSTGSKSPSVSHS
RENSADSAFANSLAGVVVPTVSSSGLPVSHPRHHSSPASLQQTYGAPPSAAQSPTQGPVSPGAQPIQHLKARSYD
MTQVDELGPLPPGWEKAHTLEGQIYFLNHTTQTTTWEDPRKSLAAQAQRQQQRSAELLTTPAALTLTHPHPAVSP
LPKAPSTPKPASPAPNELGPLPDGWEEAATPEGEIYYIDHKNHSTSWFDPRIPSHLQRPPGAGSTLATWQAITQS
QSLQSLQTDQRLQSLHLECEKLKQRQQEIMRQQELMRQHANDIATSGMDPFLGLADHSRQESNDSGLGLGPLPHT
PDFSYSMEDNMDGVSEGVGGSLDTPDLSSLDPSDDLVASLQLSDDFLEDVQALINPLNSSSKTDNVLTWL
PMHMRKLPNSFFNPP

rs:XP_026288712 [XP_026288712] transcriptional coactivator YAP1 isoform
X2 [Frankliniella occidentalis]. 43..57
MSLNPDSGEKQQEVVLERDSETELQALFEIVLKPNAKRPLQKPMHMRKLPNSFFNPPSTGSKSPSVSHS
RENSADSAFANSLAGVVVPTVSSSGLPVSHPRHHSSPASLQQTYGAPPSAAQSPTQGPVSPGAQPIQHLKARSYD
MTQVDELGPLPPGWEKAHTLEGQIYFLNHTTQTTTWEDPRKSLAAQAQRQQQRSAELLTTPAALTLTHPHPAVSP
LPKAPSTPKPASPAPNELGPLPDGWEEAATPEGEIYYIDHKNHSTSWFDPRIPSHLQRPPGAGSTLATWQAITQS
QSLQSLQTDQRLQSLHLECEKLKQRQQEIMRQQELMRQHANDIATSGMDPFLGLADHSRQESNDSGLGLGPLPHT
PDFSYSMEDNMDGVSEGVGGSLDTPDLSSLDPSDDLVASLQFQEDLLNEDTWSGF PMHMRKLPNSFFNPP

rs:XP_026298946 [XP_026298946] transcriptional coactivator YAP1 isoform
X1 [Apis mellifera]. 46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAAAAAAAVGGGGPTPGGNATGTPATGAAGAATGGSGNSAGSGSNAAGAAAAGLTVAHPRA
HSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTW
EDPRKTAAAANVAAVAAAVDNGKSSTGATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIRKFPILRIE
SFTLVSFILDNHFYPDRIINNNCAHVSATHLQRAPTSGAMLPQNWLQQQQPTGGGIQNNQTLQACQQKLRLQSLQ
MERERLKQRQQEIIRQQELMLRQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMD
GTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSEDFSSDILDDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_391844 [XP_391844] transcriptional coactivator YAP1 isoform X2
[Apis mellifera].>rs:XP_003697329 [XP_003697329] PREDICTED: transcriptional
coactivator YAP1 [Apis florea].>rs:XP_016914961 [XP_016914961] PREDICTED:
transcriptional coactivator YAP1 [Apis cerana].46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAAAAAAAVGGGGPTPGGNATGTPATGAAGAATGGSGNSAGSGSNAAGAAAAGLTVAHPRA
HSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTW
EDPRKTAAAANVAAVAAAVDNGKSSTGATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPT
SGAMLPQNWLQQQQPTGGGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIIRQQELMLRQSTTDAAMDPFLSG
INEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSED
FSSDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_023061095 [XP_023061095] protein **FAM181**A [Piliocolobus
tephrosceles]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDQPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPAPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023063876 [XP_023063876] transcriptional coactivator YAP1 isoform
X1 [Piliocolobus tephrosceles]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023063877 [XP_023063877] transcriptional coactivator YAP1 isoform X2 [Piliocolobus tephrosceles]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023063878 [XP_023063878] transcriptional coactivator YAP1 isoform X3 [Piliocolobus tephrosceles]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
AGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023064899 [XP_023064899] protein **FAM181**B [Piliocolobus tephrosceles]. 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVVAPVAGLGGSGTGGAGGDAAGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGSGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGT
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPHQVSYDYSAGYSRNAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_026487878 [XP_026487878] transcriptional coactivator YAP1 isoform X1 [Vanessa tameamea]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVAAGVQHQSAEALLTQTPAPQPIPPATPAAKSTSTNTTTDPL
GPLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGASAAGGGWANASIQACQQKLRLQSLQLERE
RLKQRQQEIRLQQELMARQSSSIVSSLASSTGTASTDLPLDPFLSGLTDHQRQESADSGLGMAVTQSSYSMPHTP
EDFLAGMDDRMDCTSEAGANLDTADITLGDTDDLVPSLQLGEFTNDILLDDVQSLINSTPSKPENVLTWL
PLRMRQLPKSFFNPP

rs:XP_026487879 [XP_026487879] transcriptional coactivator YAP1 isoform X2 [Vanessa tameamea]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVAAGVQHQSAEALLTQTPAPQPIPPATPAAKSTSTNTTTDPLG
PLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGASAAGGGWANASIQACQQKLRLQSLQLERER
LKQRQQEIRLQQELMARQSSSIVSSLASSTGTASTDLPLDPFLSGLTDHQRQESADSGLGMAVTQSSYSMPHTPE
DFLAGMDDRMDCTSEAGANLDTADITLGDTDDLVPSLQLGEFTNDILLDDVQSLINSTPSKPENVLTWL
PLRMRQLPKSFFNPP

rs:XP_026487880 [XP_026487880] transcriptional coactivator YAP1 isoform X3 [Vanessa tameamea]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVAAGVQHQSAEALLTQTPAPQPIPPATPAAKSTSTNTTTDPL
GPLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGASAAGGGWANASIQACQQKLRLQSLQLERE
RLKQRQQEIRLQELMARQSSSIVSSLASSTGTASTDLPLDPFLSGLTDHQRQESADSGLGMAVTQSSYSMPHTPE
DFLAGMDDRMDCTSEAGANLDTADITLGDTDDLVPSLQLGEFTNDILLDDVQSLINSTPSKPENVLTWL
PLRMRQLPKSFFNPP

rs:XP_026487882 [XP_026487882] transcriptional coactivator YAP1 isoform X4 [Vanessa tameamea]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVAAGVQHQSAEALLTQTPAPQPIPPATPAAKSTSTNTTTDPL
GPLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGASAAGGGWANASIQACQQKLRLQSLQLERE
RLKQRQQEIRLQQELMARQSSSIVSSLASSTGTASTDLPLDPFLSGLTDHQRQESADSGLGMAVTQSSYSMPHTP
EDFLAGMDDRMDCTSEAGANLDTADITLGDTDDLLGEFTNDILLDDVQSLINSTPSKPENVLTWL
PLRMRQLPKSFFNPP

rs:XP_026487883 [XP_026487883] transcriptional coactivator yorkie isoform X5 [Vanessa tameamea]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVAAGVQHQSAEALLTQTPAPQPIPPATPAQHLQRTPAAGASA
AGGGWANASIQACQQKLRLQSLQLERERLKQRQQEIRLQQELMARQSSSIVSSLASSTGTASTDLPLDPFLSGLT
DHQRQESADSGLGMAVTQSSYSMPHTPEDFLAGMDDRMDCTSEAGANLDTADITLGDTDDLVPSLQLGEFTNDIL
LDDVQSLINSTPSKPENVLTWL PLRMRQLPKSFFNPP

rs:XP_026487884 [XP_026487884] transcriptional coactivator yorkie isoform X6 [Vanessa tameamea]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVAAGVQHQSAEALLTQTPAPQPIPPATPAQHLQRTPAAGASA
AGGGWANASIQACQQKLRLQSLQLERERLKQRQQEIRLQELMARQSSSIVSSLASSTGTASTDLPLDPFLSGLTD
HQRQESADSGLGMAVTQSSYSMPHTPEDFLAGMDDRMDCTSEAGANLDTADITLGDTDDLVPSLQLGEFTNDILL
DDVQSLINSTPSKPENVLTWL PLRMRQLPKSFFNPP

rs:XP_026487885 [XP_026487885] transcriptional coactivator yorkie isoform X7 [Vanessa tameamea]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVAAGVQHQSAEALLTQTPAPQPIPPATPAQHLQRTPAAGASA
AGGGWANASIQACQQKLRLQSLQLERERLKQRQQEIRLQQELMARQSSSIVSSLASSTGTASTDLPLDPFLSGLT
DHQRQESADSGLGMAVTQSSYSMPHTPEDFLAGMDDRMDCTSEAGANLDTADITLGDTDDLLGEFTNDILLDDVQ
SLINSTPSKPENVLTWL PLRMRQLPKSFFNPP

rs:XP_026506573 [XP_026506573] uncharacterized protein LOC113406358 [Terrapene mexicana triunguis]. 205..219
MAAGVIRNLAEFRLPSSFQHSFLHPTPSQDMDFQDLSEEEEEEEDYDVEEDSPPCHSPGTEGQKVTAGC
SQSDAEMTLQLLKFSELISCDIQRYFGRKAKDEDPDSCNIYEDCFSPRRLGRELYYADLMRLAQSGELDDEDAQG
PAAPPGQLDQRVWRSICNKDGAQKLGPLAELFEYGLRRFLKRRAADGRKLRLEKKYAHIMPMHKRKLPQSFWKEP
SPGPLCILNTNPPDFSDLLANWTSEPGQELPSTGRELAGELARPAMETDQFSVL PMHKRKLPQSFWKEP

rs:XP_024052888 [XP_024052888] protein **FAM181**A [Terrapene mexicana triunguis]. 126..140
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSMESSSK
RGAEDRNRSSDPDGPDPNHCRASSEKALRLSEVEENFSGGQVLQEQSPESVRPDQVPMRKRQLPASFWEEPRPTQ
SLLVGSFPAGLDGLPNSRDLPPYEGKKSKKGPDTTEPGSPPLPAQPSGEKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTPGALPQSPFPGLGLWRKSTAPAGEIQHFCKEAGSMGQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_024072236 [XP_024072236] protein **FAM181**B [Terrapene mexicana triunguis]. 200..214
MAVQAAILNPHHFIPFCFPASGGLADYVDLEKSYEDGGAALLGGGGGGVGGGEDPGDFKEATRDLLSFI
DSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIIASAPAAPAPAGGQELPKRPAPPAGAASPQPSCPPGPA
GHCKPPAKREASQAASSLQSKSLAALFDSLHQGRAGEKGPAGGGGGSGGGGPRKVPLRNRNLPPSFFTEPAAPPP
RAPPLGASPKALERGGGSPEAAEFFELLGPDYGGLLPEQPPAQEAFPARLPPELGMEPALYEPHLPPLPPHLLGG

MLYPEPAWSPPAKKSPPAAAPCSSLSLPETLRPLPALGAPGAPLYPASSDPAPAGGEESPAHLAAAFAPYFPDCP
LPPPPAMPYEYSAGYNRVAYSGL PLRNRNLPPSFFTEP

rs:XP_024071425 [XP_024071425] transcriptional coactivator YAP1 isoform X3 [Terrapene mexicana triunguis]. 73..87
MDPGQPQQQAQPPAQQQAPPPGAPSGAGQTPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQNIMNSASGP
LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQM
RLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMAQDLRTMTTNSSDPFLNSGTYHS
RDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEE
LMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024071426 [XP_024071426] transcriptional coactivator YAP1 isoform X4 [Terrapene mexicana triunguis]. 73..87
MDPGQPQQQAQPPAQQQAPPPGAPSGAGQTPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQNIMNSASGP
LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQM
RLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMAQDLRTMTTNSSDPFLNSGTYHSRDES
TDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPS
LQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_024071429 [XP_024071429] transcriptional coactivator YAP1 isoform X5 [Terrapene mexicana triunguis]. 73..87
MDPGQPQQQAQPPAQQQAPPPGAPSGAGQTPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQNIMNSASAM
NQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTME
QDGGSQNPVSSPGMAQDLRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQS
NIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_024071430 [XP_024071430] transcriptional coactivator YAP1 isoform X6 [Terrapene mexicana triunguis]. 73..87
MDPGQPQQQAQPPAQQQAPPPGAPSGAGQTPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQNIMNSASAM
NQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGG
SQNPVSSPGMAQDLRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPS
HQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_005343545 [XP_005343545] protein **FAM181**A [Microtus ochrogaster]. 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRFPRGLPGRVMEPHLP
RGPEERPGQLPLHPCPESSPGGDGCCKEKALGTPFREECLSKEQSFGGLNAEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLTPREASLYENKKNCKGLESLGPETTPLPMSPRVLADTEPLKMSGVSLVGSLDAWSYCPFQYH
GQPIFPSLPGVLPQGPVPSLGLWRKSPASPVELTHFCKDVDNPGPKVHRPVVLKPIPTKPAMPPPLFNVFGYL
PMRKRQLPASFWEEP

rs:XP_005357663 [XP_005357663] protein **FAM181**B [Microtus ochrogaster]. 218..232
MAVQAALLSSHPFIPFGFGGSAEGLVSAFGSLDKGCCFEDDESGAPAGALLSASEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPSAPDAPAKRPPGAPGAPTVAAPAHCK
STPRREATQAAAAASLQSRSLAALFDSLHQVPGGAEPASGGVTVPVPGLGAANAAGDGAATTGSSAAPGTRKVPL
RARNLPPSFFTEPSRVSGSGGGTGGSGCGCGPSGQGVSLGDLEKGAEAVEFFELLAPDFCAGNESGVLLAAEPLD
AFPAGATVLRGPLELESGPFEPPAMVGNLLYPEPWSAPSCPQTKKPPLAGVRSGLTLNEPVRLLYPTALDSPGGE
DTTALASFPPFFPDCALPPPHQVSYDYSAGYSRAVYPNLWRPDGVWEGASGEDGAHPD PLRARNLPPSFFTEP

rs:XP_005346865   [XP_005346865] transcriptional coactivator YAP1, partial
[Microtus ochrogaster]. 48..62
PPGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSR
QASTDASTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTVVSGATTPAAQHLRQSSFEIPDDVPLPAGWEMAKTS
SGQRYFLNHIDQTTTWQDPRKAMLSQLNVPASASPAVPQTLMNAASGPLPDGWEQAMTQDGDVYYINHKNKTTSW
LDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGSVLGGGNSNQQQQMQLQQLQMEKERLRLKQQELLRQAIRNI
NPSTANAPKCQELALRSQLPTLEQDGGTQNAVSSGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSV
PRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILN
DMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_014119473   [XP_014119473] transcriptional coactivator YAP1 isoform
X1 [Zonotrichia albicollis]. 86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGPVTGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_005482648   [XP_005482648] transcriptional coactivator YAP1 isoform
X2 [Zonotrichia albicollis]. 86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGPVTGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014119474   [XP_014119474] transcriptional coactivator YAP1 isoform
X3 [Zonotrichia albicollis]. 86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGPVTGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_014119475   [XP_014119475] transcriptional coactivator YAP1 isoform
X4 [Zonotrichia albicollis]. 86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGPVTGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_026667993   [XP_026667993] protein vestigial-like, partial [Ceratina
calcarata]. 192..206
MSCSEVMYQYYPYIYQRPAPPPHPSHPHAAPHTHPHANPHAAHHSPARTAPFQSFSAATATHQYDRLNV
QRSLGAAGIEICPAGGSVPQGQPSSAGSVGSAPSPASPRPTPQPRPPLASTTAQPSRTLDDDRSTDAVGTGTAGE
DSDDGESRAQYLNPNCVVVTHYREDAASKVEEHFQRALAHDKKENISPMSMRNFPPSFWKHPGEVYEYPTDPWHS
HYSQYHHRVHDYQHPNMAAVTSYGGLLLGAARGLGPHAAHHAHPAASYKDWPSATPSQSLVDASTAPPYPHGPYA
PLS   PMSMRNFPPSFWKHP

rs:XP_017881065   [XP_017881065] protein vestigial-like, partial [Ceratina
calcarata]. 17..31
LANLKCKYWNTSENISPMSMRNFPPSFWKHPGEVYEYPTDPWHSHYSQYHHRVHDYQHPNMAAVTSYGG
LLLGAARGLGPHAAHHAHPAASYKDWPSATPSQSLVDASTAPPYPHGPYAPLSGFESQVQDSKDLYWF
PMSMRNFPPSFWKHP

rs:XP_017883902   [XP_017883902] transcriptional coactivator yorkie
[Ceratina calcarata].   46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTVAAVAAAAVAGPTPGGNGSGTPATGAAGAATGGSGNSAGSGSNAAGAAAAVVAAAAAAGLT
VAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHL
TRTTTWEDPRKTAAAANVAAVAAAVDNGKSTTGATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTH
LQRAPTSGAMLPQNWLQQQQPTGGGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQSTTDAAM
DPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPS
LQLSEDFSSDILDDVQSLINPNTTKAGNVLTWL   PLRMRNLPDSFFNPP

rs:XP_026705804   [XP_026705804] protein **FAM181**A [Athene cunicularia].
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPSECGWR
RVTEDRGRGPQPEAPDPSPHGGAASEKVLQAVEAEESLAGETVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPT
QSLPARAFPEGLPAPRDPPPYEGKKSRRSPDAAAPESPPEPAPHAGEKDPAGVLSGRVGAWTCCPFSCPGPGVYQ
PPGALPPSPFPGLGLWRKSVATLPAEMPHFCKEADVTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_026739446   [XP_026739446] transcriptional coactivator YAP1-like
isoform X1 [Trichoplusia ni]. 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGTHIPDDLGPLPHGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSSDALLTQATSPQTIPNTPAPAAKSTSSNTTTDP
LGPLPEGWEQAATAEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGGTGPEGVWANASLQACQQKLRLQSLQMER
ERLKQRQQEIRIQQELIMSRQASSIVSSLASSAGAGNTELPLDPFLSGLSEHQRQESADSGLGMAVPHSYSMPPT
PEGFLASMDDRMDCTSEAGANLDSTDMALADNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_026739447   [XP_026739447] transcriptional coactivator YAP1-like
isoform X2 [Trichoplusia ni]. 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGTHIPDDLGPLPHGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSSDALLTQATSPQTIPNTPAPAKSTSSNTTTDPL
GPLPEGWEQAATAEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGGTGPEGVWANASLQACQQKLRLQSLQMERE
RLKQRQQEIRIQQELIMSRQASSIVSSLASSAGAGNTELPLDPFLSGLSEHQRQESADSGLGMAVPHSYSMPPTP
EGFLASMDDRMDCTSEAGANLDSTDMALADNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_026739448   [XP_026739448] transcriptional coactivator YAP1-like
isoform X3 [Trichoplusia ni]. 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGTHIPDDLGPLPHGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSSDALLTQATSPQTIPNTPAPAAKSTSSNTTTDP
LGPLPEGWEQAATAEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGGTGPEGVWANASLQACQQKLRLQSLQMER
ERLKQRQQEIRIQQELIMSRQASSIVSSLASSAGAGNTELPLDPFLSGLSEHQRQESADSGLGMAVPHSYSMPPT
PEGFLASMDDRMDCTSEAGANLDSTDMALADNLDSTDDLLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_026739449   [XP_026739449] transcriptional coactivator YAP1-like
isoform X4 [Trichoplusia ni]. 44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGTHIPDDLGPLPHGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSSDALLTQATSPQTIPNTPAPAQHLQRTPAAGGT

GPEGVWANASLQACQQKLRLQSLQMERERLKQRQQEIRIQQELIMSRQASSIVSSLASSAGAGNTELPLDPFLSG
LSEHQRQESADSGLGMAVPHSYSMPPTPEGFLASMDDRMDCTSEAGANLDSTDMALADNLDSTDDLVPSLQLNEF
TNDILLDDVQSLINSTPSKPDNVLTWL   PLRMRQLPKSFFNPP

rs:XP_026739451   [XP_026739451] WW domain-containing transcription
regulator protein 1-like isoform X5 [Trichoplusia ni].   44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGTHIPDDLGPLPHGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSSDALLTQATSPQTIPNTPAPAQHLQRTPAAGGT
GPEGVWANASLQACQQKLRLQSLQMERERLKQRQQEIRIQQELIMSRQASSIVSSLASSAGAGNTELPLDPFLSG
LSEHQRQESADSGLGMAVPHSYSMPPTPEGFLASMDDRMDCTSEAGANLDSTDMALADNLDSTDDLLNEFTNDIL
LDDVQSLINSTPSKPDNVLTWL PLRMRQLPKSFFNPP

rs:XP_026759278   [XP_026759278] transcriptional coactivator YAP1-A isoform
X1 [Galleria mellonella].   44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVATHIPDELGPLPPGW
EQARTPEGQVYYLNHVTKTTTWDDPRKTLAAQTVTSGVQHQSAETLLSQTPTAQTIATAPAAKSTSSNTATDPLG
PLPEGWEQASTPEGETYFINHASRTTSWFDPRIPQHLQRTPAANAGAAGGGWANASIQASQQKLRLQSLQLERER
LKQRQQEIRLQQELMARQVTSSLSSSIGAVANTELSLDPFLSGLTDHQRQESADSGLGMGVAQSYSMPHTPEDFL
ASMDDRMDCGSEAGANMDSTDIPLGDNLDTTDLVPSLQLSELTNDMLLDDVQSLINPTSNKPGNALTWL
PLRMRQLPKSFFNPP

rs:XP_026759280   [XP_026759280] transcriptional coactivator YAP1-A isoform
X2 [Galleria mellonella].   44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVATHIPDELGPLPPGW
EQARTPEGQVYYLNHVTKTTTWDDPRKTLAAQTVTSGVQHQSAETLLSQTPTAQTIATAPAKSTSSNTATDPLGP
LPEGWEQASTPEGETYFINHASRTTSWFDPRIPQHLQRTPAANAGAAGGGWANASIQASQQKLRLQSLQLERERL
KQRQQEIRLQQELMARQVTSSLSSSIGAVANTELSLDPFLSGLTDHQRQESADSGLGMGVAQSYSMPHTPEDFLA
SMDDRMDCGSEAGANMDSTDIPLGDNLDTTDLVPSLQLSELTNDMLLDDVQSLINPTSNKPGNALTWL
PLRMRQLPKSFFNPP

rs:XP_026759281   [XP_026759281] transcriptional coactivator yorkie isoform
X3 [Galleria mellonella].   44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVATHIPDELGPLPPGW
EQARTPEGQVYYLNHVTKTTTWDDPRKTLAAQTVTSGVQHQSAETLLSQTPTAQTIATAPAQHLQRTPAANAGAA
GGGWANASIQASQQKLRLQSLQLERERLKQRQQEIRLQQELMARQVTSSLSSSIGAVANTELSLDPFLSGLTDHQ
RQESADSGLGMGVAQSYSMPHTPEDFLASMDDRMDCGSEAGANMDSTDIPLGDNLDTTDLVPSLQLSELTNDMLL
DDVQSLINPTSNKPGNALTWL   PLRMRQLPKSFFNPP

rs:XP_026769858   [XP_026769858] transcriptional coactivator YAP1
[Pangasianodon hypophthalmus].   45..59
MDPSQHNPPAGHQVVHVRGDSETDLEALFNAVMNPKSAAVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLSAVTSGTMSTLTPAGTSPQHLRQPSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHIDQSTTWQDPRKAMLQITQPNSASPVPVQQQNLLNPASGPLPEGWEQAITAEGEIYYINHKNKTTSWLDPRL
DPRYALNQQRITQSAPVKQGTQLPSSPQNPAVMGGNNQMRLQQLQLEKERLRLKHQELLRPRPQELALRNQLPTS
MEQDSGTQNPVSSPSMGQDGRSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSL
GPASLATQPSRFPNYLDEIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_026789822   [XP_026789822] protein **FAM181**A [Pangasianodon
hypophthalmus].   131..145
MRNGLKHKLWLKMASSDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCPRTP
RCHTHRISESAAAKLTEDKRVVFTHEREKNLLIEKQATHTRGEENVHGNPNSENRSAAGHIPMRKRQLPASFWEE
PRSSHISFEYAWKSHSSGTAGYGSSETDGEKRTTIEDELKANSWLRVRRGSSDLEPLKVDLTSSNVAVCAYCPLQ
CHGHRLLHSHLITPHSAFTEPGLRAKTPATELDMHKIRDGLKYRSTHVVVKPIPTKPVSSSIFSVFGFI
PMRKRQLPASFWEEP

rs:XP_026790522   [XP_026790522] protein **FAM181**B [Pangasianodon
hypophthalmus].   155..169
MAVQAAIMNSQFLNFCFPGSVMEYEVEKGLDGAFLGEVDCEGDFREATSDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIMGLGNGAPQESCKNHDSTPTPTSIIQNKTPKRDGAQANLQSKSLAALFNHAK
DLRGEKAKKPPLRHRNLPPSFFTEPANNARVTSTSGMSLKDLERGNPDAAEFFELLGPDYSNMVSEQELYHTMPN
RVQQQGTTGPEPISFDSHNFVTGGFLYAEPWATSGGVSKKTGDIKAVPGQSSLYGNTDSSCPVPMEQNSTCSLTF
PNFFTDCSVSQASYDLASGYSRGSFPSL PLRHRNLPPSFFTEP

rs:XP_026922312   [XP_026922312] protein **FAM181**A isoform X1 [Acinonyx
jubatus].   228..242
MLCIWRGAPDWPEGPPSAGDSSSIQPTRGLHDCFQPDARSSPATPGLAQVCRGEPARPRRRGARGRPAP
SVSSVPSPGAASHEQNPPASWKAPCSGLLVMANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQL
KRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDSGHDSSPVGGGGCEEKALGNPYREECLSKEQTLQGQNP
EAARPGQVPMRKRQLPASFWEEPRATHSYPLGLEGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKE
PLKMSGVSLVGRVNAWSCCPFQYHGQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPV
VLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_026922314   [XP_026922314] protein **FAM181**A isoform X2 [Acinonyx
jubatus].   207..221
MLCIWRGAPDWPEGPPSAGDSSSIQPTRGLHDCFQPDARSSPATPGLAQVSSVPSPGAASHEQNPPASW
KAPCSGLLVMANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEP
HLKRGPEDRPGRLPLDSGHDSSPVGGGGCEEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWE
EPRATHSYPLGLEGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPF
QYHGQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGY
L   PMRKRQLPASFWEEP

rs:XP_026922315   [XP_026922315] protein **FAM181**A isoform X3 [Acinonyx
jubatus].   190..204
MLLRGSPAAHSLRSARQAGPGLSARRGSCLSCVSSVPSPGAASHEQNPPASWKAPCSGLLVMANDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDS
GHDSSPVGGGGCEEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPRATHSYPLGLEGGPG
PREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYPGPPGALPQ
SPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_026922316   [XP_026922316] protein **FAM181**A isoform X4 [Acinonyx
jubatus].>rs:XP_026922317 [XP_026922317] protein **FAM181**A isoform X4
[Acinonyx jubatus].>rs:XP_026922318 [XP_026922318] protein **FAM181**A isoform
X4 [Acinonyx jubatus]. 129..143
MANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLDSGHDSSPVGGGGCEEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
ATHSYPLGLEGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_026895681   [XP_026895681] protein **FAM181**B [Acinonyx jubatus].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGELLAGNEGGDMREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAPSAQAVAVPPHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGDTERAGGSLAAPAAGIGGAGAGGSGGEAAGTAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEALEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEPPPAMVGSLLYSESWSAPGCPQTKKPPLAAPRGGLTLNEPLRPLYPSAADSPGAEDGPGL
LASFAPFFSDCALPAPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD   PLRARNLPPSFFTEP

rs:XP_026976636   [XP_026976636] protein **FAM181**A isoform X1 [Lagenorhynchus
obliquidens].   180..194
MKLLQMLLRGSPCCPQPEISPPGQLRALPWSRQPPAEPPSSWKAPCSGPLVMASDSDVKMLLNFVNLAS
SDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGSEDRPGRLPLDSGHSSSPGGGR
CCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTQSYPVGLEGGLGPREGPPYEGK

KHCKGLEPRGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWNCCPFQYHGQPIYPGPPGALPQSPLPSLGLWR
KSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_026976637 [XP_026976637] protein **FAM181**A isoform X2 [Lagenorhynchus obliquidens]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGSEDRPGRLPLDSGHSSSPGGGRCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTQSYPVGLEGGLGPREGPPYEGKKHCKGLEPRGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWNCCPFQYH
GQPIYPGPPGALPQSPLPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_026994878 [XP_026994878] transcriptional coactivator YAP1 isoform X1 [Tachysurus fulvidraco]. 45..59
MDPSQHNPPAGHQVVHVRGDSETDLEALFNAVMNPKSAVVPPSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVTSGTMSTLTPAGTSPQHLRQPSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHIDQSTTWQDPRKAMLQMNQTNSASPVPVQQQNLLNPASGPLPEGWEQAITAEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRITQSAPVKQGTQLPSSPQNPPVMGGNSQLRLQQLEKERLRLKHQELLRPRPQELALRNQLPTSME
QDSGTQNPVSSPGMGQDGRSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGP
ASLATQPSRFPNYLDEIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_026994964 [XP_026994964] transcriptional coactivator YAP1 isoform X2 [Tachysurus fulvidraco]. 45..59
MDPSQHNPPAGHQVVHVRGDSETDLEALFNAVMNPKSAVVPPSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVTSGTMSTLTPAGTSPQHLRQPSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHIDQSTTWQDPRKAMLQMNQTNSASPVPVQQQNLLNPASALNQQRITQSAPVKQGTQLPSSPQNPPVMGGNSQ
LRLQQLEKERLRLKHQELLRPRPQELALRNQLPTSMEQDSGTQNPVSSPGMGQDGRSMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGPASLATQPSRFPNYLDEIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027001732 [XP_027001732] protein **FAM181**B [Tachysurus fulvidraco]. 155..169
MAVQAAIMNSQFLNFCFPGSVMEYEVEKGLDGTFLGEVDCEGEFREATSDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIMGLGNGSPHDACKSHDSTPSPTSIIQNKTPKRDGAQANLQSKSLAALFNHAK
DLRGEKTKKPPLRHRNLPPSFFTEPANNARVTSTSGMSLKDLERGNPDATEFFELLGPDYSNMVSEQELYHTMPN
RVQQQGTTGPEPIPFDSHSFVTGGFLYAEPWTTSAGVSKKTGDIKIVPGQSSLYGNTDSSCPLPMEQNSTCSLTF
PNFFTDCSVSQVSYDLASGYSRGSFPSL PLRHRNLPPSFFTEP

rs:XP_027028511 [XP_027028511] protein **FAM181**A [Tachysurus fulvidraco]. 119..133
MASSDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCPRTPRCHTYRISESNA
AKLPEDKRVMFTHERAKNLLNEKQNTHTCGEENVGGNPYSENRSAPGHIPMRKRQLPASFWEEPRSSHISFEYAW
KTHTNGTVGYGSAETDGQKRTRIEDELKANSWLRVRRGSLDLEPLKVDLTSTNVAVCAYCPLQCHGHRLLHGHLI
TPHSAFTEPGLRAKTPTNELDTQKMKDGLKYRSPHVVVKPIPTKPVSSSIFSVFGFI PMRKRQLPASFWEEP

rs:XP_027046879 [XP_027046879] uncharacterized protein LOC113674593 [Pocillopora damicornis].>tr:A0A3M6TQW7_9CNID [A0A3M6TQW7] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:RMX43729.1}; 110..124
MDPQRKRLQHKDTLNWRTPPSISPPSPCGPSSPQSPPPLVVRGKSLSLNRVGAPALLPIRETPAKELSK
RGRKQRLLLSQAGNLALKRRETSPDFNKLEARLKPKRGPLPMRMRALPQSFWQEPKNIQNSSLSTEGTLSSLPPL
FHNANNTSYDVSKVRPVTPPEEKYLPRPPKEPKLVITSPQEQLLKLFETVEEDKTKKFVIRRGRPRRVQSDLTPC
QLPKLEEDPCMMTSLAEKLFPQLSLENNKQTPGANTSLSCVSVHDGDKSVTLPSLNVEQNYSQMLSEIVAHF
PMRMRALPQSFWQEP

rs:XP_027047666 [XP_027047666] transcriptional coactivator YAP1-A-like [Pocillopora damicornis].>tr:A0A3M6TNK5_9CNID [A0A3M6TNK5] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:RMX42939.1}; 46..60
MERKNNNCVVHVRQDSDNDLEALFHVISKNSVAKTHPEPASSQSLPMRLRKLPPSFFKQPPIDGSLSPD
QDVPKRLPISHSHSRSSPASLTVPTTLKGPPNHSLSPGVHHQRSTSFDNTALLEEPTPMPPGWEMRTTASGQRYF

MNHFEQLTTWQDPRKTQSTSNLNSVQPVGNLPDGWEQAITPEGDIYYINHIERTTSWIDPRLAMHCRNQENIRGS
TLPPDFNRQGHRTLQLHRLQREREQLLKRQQELLKQEIKLKRDILEEGGKPSLLGNLTREFSAQDPPVTNGGHIR
DESFDSGLGMGGGNYQFHDVDMNDSQPMFDANYNSKDTSFRADPRIPEILDSLPGTNVDLGVMEGTDNSTNMETE
DLGVGLEFNSEILNDMESVLISPTLTWL PMRLRKLPPSFFKQP

rs:XP_027059914   [XP_027059914] uncharacterized protein LOC113686491
[Pocillopora damicornis].>tr:A0A3M6UQ34_9CNID [A0A3M6UQ34] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:RMX55803.1};   148..162
MNSLVEESVATPTSLLNFVSNATSTLKFALDKPIKPKRKVNHRKYLQRQLNGRSSSATTSSFDGSWVSQ
GEMLFDHVLKSGQRGSPSAVVRAEKSTAISRENHSEKIQSLGERKRAQGKEEKSWRISRSQQINDCKSSEAPSSQ
PSQPLRKRKLPESFWTEPSPKASRKPLQATRQSNTNLATNELQRSELEILDWLRPELDDFIERWSEESECASNNS
SRPDSLSDSPSTLDPHSPYSDESENVGSMDEFFEQRVPFSFDSSTKNGEYTTNIPSIRNLSNTNLNFADNRTYSV
PQNYVQRQMSHSVSCYGGHYGFSANKWNANPVQPNYFETGYNILS   PLRKRKLPESFWTEP

rs:XP_027196464   [XP_027196464] transcriptional coactivator YAP1-like
[Dermatophagoides pteronyssinus].   67..81
MHLKPDETSSTTTNHTNNNNNNNNVNNNNGNVAIVRVDTAADEGLDELFKAVMSPNNGQSRLPQQVPMR
QRRLPPSFFRPPSAASSNNSLTSMGNHSRESSLDDGGYQSQGPSLNGENKIHNTPLIGYNQLANGLAIIHPRANS
SPAALPLNIGSSTTATNSSSNASLNHTQGTFGGSNDLAKSSNNSAATTTTHYRQMSYDLDQMRLPDGWEMSYTAT
GERYFLNHKEKTTTWEDPRKKIVEEMLRRSTPPPPVPPSVASQPSQSSSVAAATQQPIIQSITTAIPLQATTNPT
TTPITPSVVEQEHHLSYIDPLIVPLPDGWEQAQTSSGDIYFISHIDQTTTWFHPSIPRNLQMKRIQQQQNCSIQP
PPFQNLITTTTNIPTELVVALKNMNTSCQATPTPVSTLIPPTVNAITNQTTTSTQNQHLRDLELERERMKQRQEE
LLQSSLLNSVTASNIMLSSSSSSNDNAISTQSPFLSLQNECHSRQESIDSGLDIGNSSNFSMTSSSSSTAHTPDN
FLRMSTTTTGNNITAASASAISTSIAAQTNNNTATTISDDLPFENMQISSLDLDSESMDFMQGLDMDLLSNVEEL
LNSNKDNIMTWL   PMRQRRLPPSFFRPP

rs:XP_027202426   [XP_027202426] WW domain-containing transcription
regulator protein 1-like [Dermatophagoides pteronyssinus]. 49..63
MAQNNMSHESKMYVAPNPETHFEELFRVVQQQDVNNNNNNAIQPLNNVPMRQRNFPESFFRPPSCSSSA
SHSRESSLDATFNSNFVNKNNHSSAKPPTTPHRNNNNNHHNISSPPFVHQKAHSLPASLPNQKLTFTPITNLDNN
KSLVKTQPAAPPPPSPKQYRHQQQLKLANANLTNNNNFHFRQQSYDIDKIPLPDGWTMSFDSNGERYFIDHKRKL
TTWDDPRIKITQQNFTNLAQNPTNSIINHPNPVASYHQHQSSQPVQPSPALISHNSDSSFYGLSLDNHFTTLPDS
GLQFDSNMIAIPTEIASVTEKMKDQILTDDTNQQQQQQLFDPQLQYLTELRMEREKMRNRAEILKTNPMVRSDYL
PSLQTLPKSSNNKDSTTTTSMMMHGRQESQDSGLGGSTTSGTLNSINFPNEANLLTDFGSNGHVAVEQLDPNVVQ
CLMSDSVDCFAIADLDLDGLDFDQYIQHNPINNDIGQLFNHDETMTWNV   PMRQRNFPESFFRPP

rs:XP_027211634   [XP_027211634] transcriptional coactivator YAP1-like
[Penaeus vannamei].   49..63
MASSNKDDSLSMEQRGNQIVHVRADSDSELEALFEVVLKPSSQVPLQKPFKMRNLPASFFTPPAHRQSP
APTVTHSREGSADSTFGGGGVGGLRVSGAMSPNTAPQHFRHHSSPASLQQTFAVPQQQQVAHLNLNDDMGSLPPG
WEQARTAEGQIYYLNIYCRRTMNSFVVVGHRPTYSYRLSPQGDLAIIVEVN   PFKMRNLPASFFTPP

rs:XP_021129359   [XP_021129359] protein **FAM181**A [Anas platyrhynchos].
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPGKPTECGPR
RGAEDRARGCQPEVPDPGPHSGAAAEKVLQAAEAVESLAGERALPEQNPEAGRPDQVPMRKRQLPASFWEEPRPA
QSLPSRGFPPGPEGLSAPRDTPPFEGKKSKRSLDTAGPESPPEPALQAGEKDPAGVLSGRVGTWTCCPFPCPGPA
VYQPPGTLPPSPFPGLGLWRKSAATLPAEAQPFCKEAEGAGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:NP_001194003   [NP_001194003] protein **FAM181**A isoform 2 [Homo
sapiens].>rs:NP_001194002 [NP_001194002] protein **FAM181**A isoform 2 [Homo
sapiens].>rs:NP_001194000 [NP_001194000] protein **FAM181**A isoform 2 [Homo
sapiens].   129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTLVSMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027419730 [XP_027419730] transcriptional coactivator YAP1 isoform
X1 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027419732 [XP_027419732] transcriptional coactivator YAP1 isoform
X3 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027419734 [XP_027419734] transcriptional coactivator YAP1 isoform
X5 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027419737 [XP_027419737] transcriptional coactivator YAP1 isoform
X7 [Bos indicus x Bos taurus]. 84..98
MDPGPPPPQPAPQGQGPPPAQAPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027388184 [XP_027388184] protein **FAM181**B [Bos indicus x Bos
taurus]. 214..228
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDEETGTPAGALLAGAESGDAREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAGAQTVPVPVPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGADPAGVAEAAPAAGLVRGDAAGSAGGPAVPGARKVPLRARN
LPPSFFTEPSRAGGCVCGPSGPGVSLGDLEKGSEAAEFFELLGPDYGAGTEAGALLAAEPLDVFPAGAAVLRGPP
ELEPGLFDPQPAMVGSLLYPEPWSAPGGPATKKPPLPAPGGGLTLNEPLRSVYPAAADSPGGDDGPGLLASFTPF
FSDCALPPAPPPQQVSYDYSAGYSRTAFAGLWRPDGAWEGAPGEEGAPRD PLRARNLPPSFFTEP

rs:XP_027533148 [XP_027533148] transcriptional coactivator YAP1 isoform
X1 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNR

FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027533149 [XP_027533149] transcriptional coactivator YAP1 isoform X2 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027533150 [XP_027533150] transcriptional coactivator YAP1 isoform X3 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027533151 [XP_027533151] transcriptional coactivator YAP1 isoform X4 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027533152 [XP_027533152] transcriptional coactivator YAP1 isoform X5 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQ
ALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027533153 [XP_027533153] transcriptional coactivator YAP1 isoform X6 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRN
INPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027533154 [XP_027533154] transcriptional coactivator YAP1 isoform X7 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS

VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQMRLQQLQMEKERLRLKHQELLRQVRPQ
ELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027533155 [XP_027533155] transcriptional coactivator YAP1 isoform
X8 [Neopelma chrysocephalum]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPPQPPGAVSGASAGAVQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQMRLQQLQMEKERLRLKHQELLRQELAL
RSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_027533281 [XP_027533281] protein **FAM181**B [Neopelma chrysocephalum].
168..182
MAAPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAAPPPAACPPAACSTRPPPRREPAQAAGSSLQSKSLAALFGSLQRGQGA
AGGAEAKAGAGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPAPAARGPPAKEPEKGGGGAAEASEFFELLCPEYG
ALLPEHAAPPDAFGGRLPAELGLEHGLYELPLPAGPHALLGGLLYPEPPWSPAAPCSPPRKAPPEPLRPLYAGGP
EPVPGGGGSTEEPGGHLPAGFAPFFPECPLAPPQPPYDYGAGYHRAGYPGL PLRDRNLPPSFFTEP

rs:XP_027539541 [XP_027539541] sentrin-specific protease 3 isoform X1
[Neopelma chrysocephalum]. 171..185
MAGRQRQGVIQPLAELRLPSPFPHGLLLPAHPEPDFHNLSEEEEEEEEEEEEEEEVEAAEESVRPEPAI
SSTAETTLRLLKFSELISCDIQRYFGRRGREEAAGTQPVPKDCESPRSAGAQPEAPRGSPGAAHRLGPLAELFEY
GVHRCLSPRAAGGRTQRLERKYGHITPMHCRKLPPSFWKEPGPASLLHTGTPDFSDLLANWTVEPGPELPCAGRE
LPLEPGRPGLEAEPFTGL PMHCRKLPPSFWKEP

rs:XP_027539542 [XP_027539542] sentrin-specific protease 3 isoform X2
[Neopelma chrysocephalum]. 167..181
MAAGVIQPLAELRLPSPFPHGLLLPAHPEPDFHNLSEEEEEEEEEEEEEEEVEAAEESVRPEPAISSTA
ETTLRLLKFSELISCDIQRYFGRRGREEAAGTQPVPKDCESPRSAGAQPEAPRGSPGAAHRLGPLAELFEYGVHR
CLSPRAAGGRTQRLERKYGHITPMHCRKLPPSFWKEPGPASLLHTGTPDFSDLLANWTVEPGPELPCAGRELPLE
PGRPGLEAEPFTGL PMHCRKLPPSFWKEP

rs:XP_027493821 [XP_027493821] transcriptional coactivator YAP1 isoform
X1 [Corapipo altera].>rs:XP_027594860 [XP_027594860] transcriptional
coactivator YAP1 isoform X1 [Pipra filicauda]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027493893 [XP_027493893] transcriptional coactivator YAP1 isoform
X2 [Corapipo altera].>rs:XP_027594861 [XP_027594861] transcriptional
coactivator YAP1 isoform X2 [Pipra filicauda]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDY

LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027493970 [XP_027493970] transcriptional coactivator YAP1 isoform X3 [Corapipo altera].>rs:XP_027594863 [XP_027594863] transcriptional coactivator YAP1 isoform X3 [Pipra filicauda]. 86..100

MDPGQPQAQQPPQAAQPPAPQQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027494051 [XP_027494051] transcriptional coactivator YAP1 isoform X4 [Corapipo altera].>rs:XP_027594864 [XP_027594864] transcriptional coactivator YAP1 isoform X4 [Pipra filicauda]. 86..100

MDPGQPQAQQPPQAAQPPAPQQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027494136 [XP_027494136] transcriptional coactivator YAP1 isoform X5 [Corapipo altera].>rs:XP_027594865 [XP_027594865] transcriptional coactivator YAP1 isoform X5 [Pipra filicauda]. 86..100

MDPGQPQAQQPPQAAQPPAPQQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQ
ALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027494208 [XP_027494208] transcriptional coactivator YAP1 isoform X6 [Corapipo altera].>rs:XP_027594866 [XP_027594866] transcriptional coactivator YAP1 isoform X6 [Pipra filicauda]. 86..100

MDPGQPQAQQPPQAAQPPAPQQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRN
INPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027494287 [XP_027494287] transcriptional coactivator YAP1 isoform X7 [Corapipo altera].>rs:XP_027594867 [XP_027594867] transcriptional coactivator YAP1 isoform X7 [Pipra filicauda]. 86..100

MDPGQPQAQQPPQAAQPPAPQQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQ
ELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027494371 [XP_027494371] transcriptional coactivator YAP1 isoform X8 [Corapipo altera].>rs:XP_027594868 [XP_027594868] transcriptional coactivator YAP1 isoform X8 [Pipra filicauda]. 86..100
MDPGQPQAQQPPQAAQPPAPQQQQQPPQPPGAVSGASAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELAL
RSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_027511708 [XP_027511708] protein **FAM181**B [Corapipo altera].
169..183
MAAPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAAPPPASCPPAACSTRPPPRREPAQAAGSSLQSKSLAALFGSLQRGRGA
AGGAEAKAGGGGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPAPAARGPPAKEPEKGGGGAAEASEFFELLCPEY
GALLPEHAAPPDAFGGRLPAELGLEHGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPPEPLRPLYAGG
PDPVPGGGGGSTEEPGGHLAAGFAPFFPECPLAPPQPPYDYGAGYHRAGYPGLPLRDRNLPPSFFTEP

rs:XP_027494005 [XP_027494005] protein **FAM181**A [Corapipo altera].
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHPSKPPECGWR
RGAEDRGRGPQPEAPDPSPHGGAATEKVMQTAEAEESLTGERVLQEQKPEAVRPDQVPMRKRQLPASFWEEPRPA
QSLTARAFPASPEGLPAPRDPPPYEGKKSKWSPDAASPESPPDPAPHAGEKDPAGVLSSRVGAWTCCPFPCPGTG
VYQPPGALPPSPFPGLGLWRKSAATLPAEVPHFCKEADGTGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027510795 [XP_027510795] sentrin-specific protease 3 isoform X1 [Corapipo altera]. 171..185
MAGRQRQGVIQPLAELRLPSPFPHGLLLPTHPEPDFHNLSEEEEEEEEEEEEEEEEVEAAEENVRPEPAI
SSTAETTLRLLKFSELISCDIQRYFGRRGREEAASTQPVPKDCESPLSAGAQPEAPRGSPGAAHRLGPLAELFEY
GVHRCLSPRAAGGRTQRLERKYGHITPMHRRKLPPSFWKEPGPASLLHTSTPDFSDLLANWTVEPGPELPCAGRE
LPLELGRPGLEAEPFTGL PMHRRKLPPSFWKEP

rs:XP_027510796 [XP_027510796] sentrin-specific protease 3 isoform X2 [Corapipo altera]. 167..181
MAAGVIQPLAELRLPSPFPHGLLLPTHPEPDFHNLSEEEEEEEEEEEEEEEEVEAAEENVRPEPAISSTA
ETTLRLLKFSELISCDIQRYFGRRGREEAASTQPVPKDCESPLSAGAQPEAPRGSPGAAHRLGPLAELFEYGVHR
CLSPRAAGGRTQRLERKYGHITPMHRRKLPPSFWKEPGPASLLHTSTPDFSDLLANWTVEPGPELPCAGRELPLE
LGRPGLEAEPFTGL PMHRRKLPPSFWKEP

rs:XP_002037503 [XP_002037503] GM18275 [Drosophila sechellia].>tr:B4I2C6_DROSE [B4I2C6] SubName: Full=GM18275 {ECO:0000313|EMBL:EDW53921.1}; 61..75
MSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPLRMRKLPN
SFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPIAAIPQLQIQPSPQHSRLAIHHSRARSSPA
SLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAPASSAIDLDAMNTCMSQDIPMSMQTVHK
KQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQILMAERIKQNDVLQTTK
QTTTSTIANNLGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQSGLSVLDCPDNLVSSLQIEDNLCSNLFND
AQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_014443915 [XP_014443915] transcriptional coactivator YAP1 [Tupaia chinensis]. 85..99
MDPGQQPPPQPAPQGPGQPPAQPPQGQGPPSAPGQPAAPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVAGPTSTPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDY

LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_005241985 [XP_005241985] protein **FAM181**A [Falco peregrinus].
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECSWR
RGTEDRGRGPQPEAPDPSPPGGAATEKVPQTAEAEENLAGERVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
QSLPARAFPAGPEGVPAPRDPPPYEGKKSKRSPDAAGPESPPEPAPHAGEKDPAGVLSGRVGAWTCCPFPCPGLG
VYQPPSTLPPSPFPGLGLWRKSVAALPAEVPPFCKEAEGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027651996 [XP_027651996] uncharacterized protein LOC114014024
[Falco peregrinus]. 186..200
MHGWAAAPRVSPGPGVPLRADMAAGVIQPLAELRLPSPFPHGLLLPARPEPDFPDLSEEEEEEEEEEE
EVAEESMRPELAIPSAAETTLRLLKFSELISCDIQRYFGRQGRDEAISSRSMPEDCGSPRNVEAQQEATAPRGSP
GAMHRLGPLAELFEYGMHRCLPAQAAGGKTQRLEKKYGHITPMHRRKLPPSFWREPGPSPTSLLHAGTPDFSDLL
ANWTVEPGPELPDARQELPPEPGQPGLEAEPFAGL PMHRRKLPPSFWREP

rs:XP_027657652 [XP_027657652] uncharacterized protein LOC114015261
[Falco cherrug]. 146..160
MHGWAAAPRVSPGPGVPLSADMAAGVIQPLAELRLPSPFPHGLLLPARPEPDFPDLSEEEEEEEEEEE
VAEESMRPELAIPSAAETTLRLLKFSELISCDIQRYFGRQGRDEATSSRSMPEDSLPPRAAVGKTQRLEKKYGHI
TPMHRRKLPPSFWREPGPSPTSLLHAGTPDFSDLLANWTVEPGPELPDARQELPPEPGQPGLEAEPFAGL
PMHRRKLPPSFWREP

rs:XP_005438929 [XP_005438929] protein **FAM181**A [Falco cherrug].127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECSWR
RGAEDRGRGPQPEAPDPSPPGGAATEKVPQTAEAEENLAGERVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
QSLPARAFPAGPEGVPAPRDPPPYEGKKSKRSPDAAGPESPPEPAPHAGEKDPAGVLSGRVGAWTCCPFPCPGLG
VYQPPSTLPPSPFPGLGLWRKSVAALPAEVPPFCKEAEGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_006165466 [XP_006165466] protein **FAM181**A [Tupaia chinensis].
129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPSRVAEPHLK
RGPQDRPGRLPLDSGPDSSPGGGGGCKEKALGSPYGEECLSKEQTLRGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGGLGPREGPPYEGKKNCKGLEPLGPETAPMPVSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQCH
GQPLYPGPPGALPQSPVPSLGLWRKNPTSPGEPGEPAPFCKDVDSLGQKVHRPVVLKPSPTKPAVPPPIFNVFGY
L PMRKRQLPASFWEEP

rs:XP_027675589 [XP_027675589] transcriptional coactivator YAP1 [Chelonia
mydas]. 73..87
MDPGQPQQQAQPPAQQQAPPPGAPSGAGQPPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQNIMNSASGP
LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQM
RLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_007063510 [XP_007063510] protein **FAM181**A [Chelonia
mydas].>rs:XP_007063511 [XP_007063511] protein **FAM181**A [Chelonia
mydas].>tr:M7BWC5_CHEMY [M7BWC5] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:EMP32407.1}; 126..140
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSMESSSK
RGAEDRNRSSDPDGMDPNHCTVSSEKALRLSEVAENFSGEQVLQEQSPESVRPDQVPMRKRQLPASFWEEPRPTQ
SLLVGSFPAGLDGLPNSRDLPPYEGKKSKKGPDTTEPDSPPLPAQPSGEKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTHGALPQSPFPGLGLWRKSTAPTGEIQHFCKEVGSMGQKLYRPVVLKPIPTKPAGPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_027684642 [XP_027684642] uncharacterized protein LOC114021042 [Chelonia mydas].>tr:M7B1Z9_CHEMY [M7B1Z9] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EMP29460.1}; 208..222
MAAGVIRNLPEFRLPASFQHSFLHPTPPQDMDFQDLSDEEEVEEEDDYDVEEQDSPPCHSPGTEGQKVT
ADCSQSDAEMTLQLLKFSELISCDIQRYFGRKAKDEDPDSCNIYEDCFSPRRLGRELYYADLMRLAQSGELDDED
AQGPVAPPGQLDQRVWRSICNKDGVQKLGPLAELFEYGLHRFLKRRAADGRKLRLEKKDAHIMPMHKRKLPQSFW
KEPSPGPPCILNTNPPDFSDLLANWTSEPGQEQELPSTGRELARPAMETDQFSVL PMHKRKLPQSFWKEP

rs:XP_027738549 [XP_027738549] sentrin-specific protease 3 isoform X1 [Empidonax traillii]. 171..185
MAGQQRQGVIQPLAELRLPSPFPHGLLLPTHPEPDFHDLSEEEEEEEEEEEEEEEVEAAEESVRPEPAA
SSTAETTLRLLKFSELISCDIQRYFGRRGREEAASTQPVPKDCGSPQSAGAQPEAPRGSPGAAHRLGPLAELFEY
GVHRCLSPRAAGGRTQRLERKYGHITPMHRRKLPPSFWKEPGPAGLLHTGTPDFSDLLANWTVEPGPELPCAGRE
LPLEPGRPGLEAEPFTGL PMHRRKLPPSFWKEP

rs:XP_027738550 [XP_027738550] sentrin-specific protease 3 isoform X2 [Empidonax traillii]. 167..181
MAAGVIQPLAELRLPSPFPHGLLLPTHPEPDFHDLSEEEEEEEEEEEEEEEVEAAEESVRPEPAASSTA
ETTLRLLKFSELISCDIQRYFGRRGREEAASTQPVPKDCGSPQSAGAQPEAPRGSPGAAHRLGPLAELFEYGVHR
CLSPRAAGGRTQRLERKYGHITPMHRRKLPPSFWKEPGPAGLLHTGTPDFSDLLANWTVEPGPELPCAGRELPLE
PGRPGLEAEPFTGL PMHRRKLPPSFWKEP

rs:XP_027740276 [XP_027740276] protein **FAM181**B [Empidonax traillii].
170..184
MAAPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGGDAGDFREATRDLLSFIDSASSNIKLALDR
PVKSRRKVNHRKYLQKQIKRCTGIIAAAAPPPAACPPAACSARPPPRREPAQAAGSSLQSKSLAALFGSLQRGRG
AAGGAEARAGGGGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPAPAARGPPAKEPEKGGGGAAEASEFFELLCPE
YGALLPEHAAPPDAFGGRLPAELGLEHGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPPEPLRPLYPG
GPEPVPGGGGSTEEPGGHLPAGFAPFFPECPLAPPQPPYDYGAGYPRTGYPGLPLRDRNLPPSFFTEP

rs:XP_027786455 [XP_027786455] transcriptional coactivator YAP1 isoform X1 [Marmota flaviventris]. 85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027786456 [XP_027786456] transcriptional coactivator YAP1 isoform X2 [Marmota flaviventris]. 85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027786457 [XP_027786457] transcriptional coactivator YAP1 isoform X3 [Marmota flaviventris]. 85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS

SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027786458 [XP_027786458] transcriptional coactivator YAP1 isoform
X4 [Marmota flaviventris]. 70..84
MDPGQQPQPQPAPQGQGQPPPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPPVQQNLMNTPSGPLPD
GWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQ
QLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027786459 [XP_027786459] transcriptional coactivator YAP1 isoform
X5 [Marmota flaviventris]. 85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027786460 [XP_027786460] transcriptional coactivator YAP1 isoform
X6 [Marmota flaviventris]. 70..84
MDPGQQPQPQPAPQGQGQPPPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPPVQQNLMNTPSGPLPD
GWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQ
QLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDS
GLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQ
EALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027786461 [XP_027786461] transcriptional coactivator YAP1 isoform
X7 [Marmota flaviventris]. 85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027786462 [XP_027786462] transcriptional coactivator YAP1 isoform
X8 [Marmota flaviventris]. 85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027786463 [XP_027786463] transcriptional coactivator YAP1 isoform
X9 [Marmota flaviventris]. 85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ

ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027786464   [XP_027786464] transcriptional coactivator YAP1 isoform
X10 [Marmota flaviventris].   85..99
MDPGQQPQPQPAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL   PMRLRKLPDSFFKPP

rs:XP_027787266   [XP_027787266] protein **FAM181**A [Marmota
flaviventris].>rs:XP_027787267 [XP_027787267] protein **FAM181**A [Marmota
flaviventris].>rs:XP_015345156 [XP_015345156] PREDICTED: protein **FAM181**A
[Marmota marmota marmota].   129..143
MASDNDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCSRLPRGLPGRAAEPHLK
RGPEDRPGRLPLHSGPGASPGGGGGCKEKALGNPWREERLPKEQSPQGQTPEAAKPGQVPMRKRQLPASFWEEPR
PTHSCPLGLEGGLGPREGPPYESKKSCKGLESLGPETAPVPMSPRALADKEPLKMPGVSLVGRVDAWSCCPLQYH
GQPMYPGPPGALPHSQVPGLCLWRKSPASPGELAHFCKDVEGPGQKVHRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027798304   [XP_027798304] protein **FAM181**B [Marmota flaviventris].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGSTFGALDKGCCFEDEETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCNGLMGAAPPGPPSPSAADTPAKRPLAAPSASTAAAPVHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVSGGAEPVGGAVAVPVTGLGGASSGGAGGEASGLAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGSDYGAGTEAGVLLAAEPLDVFPT
GAAVLRGPLELEPGLFEPPPAMVGNLIYPEPWSAPSCAPTKKSPVAAARGGLTLNESLRPLYPAPSDSPGGEDGT
GHLASFAPFFPDCTLSPPPPPPHQVSYDYSAGYSSAAYSSLWRPDGVWEGAPGEEGAHRD
PLRARNLPPSFFTEP

rs:XP_027840529   [XP_027840529] transcriptional coactivator YAP1-like
[Aphis gossypii]. 67..81
MSGLQQQQQEQHQQVNIKMEPTGPGSPTPAPVNSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPLR
MRQLPKSFFNPPSTGSKSPSISHSRENSGDSAFGPAAAGQPCPVPMHSRAHSSPASLQQTYAVGVAKQQQQQQQ
HAKQRSYDVSSAIDELGPLPQGWEQARTPEGQIYYLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQLLSPGNDSG
SSTNATSTPTNSPPHIHSTLQGTNKNVTLGPLPDGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQRAPTSGA
VLPSGSASWLLNGASGLSQSLQVTQQKLRLHSLQLERERLKSRQQEIIRQQDLMLRPGQTNNDLDPFLSCSSSSV
DHSRQESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDSQEMATLDVTDDLVPSLQLG
DEFGNDILDEVSLLIDPNNKPGSILTWIILSQKSLKLNRFCFYSHLTRTTQWEDPRKSLAAQAANQHQRSAEQLL
SPGNDSGSSTNATSTPTNSPPHIHSTLQGTNKNVTLGPLPDGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQ
RAPTSGAVLPSGSASWLLNGASGLSQSLQVTQQKLRLHSLQLERERLKSRQQEIIRQQDLMLRPGQTNNDLDPFL
SCSSSSVDHSRQESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDSQEMATLDVTDDL
VPSLQLGDEFGNDILDEVSLLIDPNNKPGSILTWL PLRMRQLPKSFFNPP

rs:XP_027840585   [XP_027840585] transcriptional coactivator yorkie-like
[Aphis gossypii]. 66..80
MSGLQQQQEQHQQVNIKMEPTGPGSPTPAPVNSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPLRM
RQLPKSFFNPPSTGSKSPSISHSRENSGDSAFGPAAAGQPCPVPMHSRAHSSPASLQQTYAVGVAKQQQQQQHQH
AKQRSYDVSSAIDELGPLPQGWEQARTPEGQIYYLK   PLRMRQLPKSFFNPP

rs:XP_002433100   [XP_002433100] 65 kDa Yes-associated protein, putative
[Pediculus humanus corporis].>tr:E0W406_PEDHC [E0W406] SubName: Full=65 kDa
Yes-associated protein, putative {ECO:0000313|EMBL:EEB20362.1,
ECO:0000313|VectorBase:PHUM613740-PA};   111..125
MPSGNSNPSNNNNTSSSNNNSSGSNSNSGRESSNSNSSNNNNNANNSNNNNNSNNNNNNNSNSSSNNNS

NSSNKPSNSDNHVRIVQNSESDLQALFDSVLKPDSKRPLQVPWHMRNLPDSFFTPPSTGSKSPSVLSISHSRENS
ADAAFSTNTTPASLQVNHPRAHSSPASLQQTYASAQQKNPPQAPQGVHTHIKQRSYDMGATVVDELGPLPPGWEQ
ARTSQGQIYYLNHITRSTTWEDPRKTLAAQNLQAQHAELQNSRGNQQNSAAAAAAKATTLGISAAGLGPLPEGWE
QSSTPEGEIYFINHQTRTTSWFDPRIPLQLQRSPTGLIIPHGNSWIQSSAQQSSQNCQQELRVQLLQMERERLRQ
RQEEIRRQQELMTRTTELPPGSMDPFLSGLTDHGRQESTDSGLGMGNSYSLPQTPQDILDESMDGVSEGGHTDMT
SLDNTDISTDDLVPTLLGEDLTSDILDDVQSLINPTSTKPDNVLTWL PWHMRNLPDSFFTPP

rs:NP_033560 [NP_033560] transcriptional coactivator YAP1 isoform 2 [Mus musculus].>gp:BC039125_1 [BC039125] yes-associated protein 1 [Mus musculus]>gp:BC094313_1 [BC094313] yes-associated protein 1 [Mus musculus]
70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDS
GLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPSLQ
EALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_028014147 [XP_028014147] LOW QUALITY PROTEIN: protein **FAM181**B [Eptesicus fuscus]. 223..237
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDEPGMPAGALLAGTEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXKAAPRRDASQAAAASLQSQSLAALFDSLRHVPGGADSAGGSGAAPPAGLVGAGSGGAGGDALGPAGGTAVPGA
RKVPLRARNLPPSFFTEPSRTSGGGCGPSGCGVNLCDLEKGPETLEFFELLGPDYGAGSEAGVLLAAEPLEVFPA
GATVLRGPPELEPGLFEPPPAMGASLPYPEPWSAPACAPTKKPSLAAPRGGSTLTEPLRLLYPAAVSSPGGEDGP
GPLASFGPFFSDCVLPPPPPPPPPRQVSYDLCAGYGRAAYSGLWRPDGVWEGDPGEEGAPRD
PLRARNLPPSFFTEP

rs:XP_027992663 [XP_027992663] protein **FAM181**A isoform X1 [Eptesicus fuscus]. 224..238
MLCIWRGAPDWPEGPPSSGDLSSIQPTRGRHNRFQPDSRSSRAARAWPRSAAGASRATLAGRARTLGQL
CALPWSCQPRADHPLHGKPSEVAPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFS
QKYSRLPRGLPGRGAEPPLRRGPEDRPGRLPLNPGPDASPHSGGDCKEKALGNPYREECLSREQTLQGQNPGAAR
PGQVPMRKRQLPASFWEEPRPTHSYPVALEGVLGPREGPPYECKKHCRGLELFGPEMALIPMSPRALAEKEPPKL
PGVSLVGRVNAWSCCPFQYHGQPIYPGPPGALTQGPVPSLGLWRKSPASPGELAHLAKDADGPGQKVYRPVVLKP
IPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_008158157 [XP_008158157] protein **FAM181**A isoform X2 [Eptesicus fuscus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPPLR
RGPEDRPGRLPLNPGPDASPHSGGDCKEKALGNPYREECLSREQTLQGQNPGAARPGQVPMRKRQLPASFWEEPR
PTHSYPVALEGVLGPREGPPYECKKHCRGLELFGPEMALIPMSPRALAEKEPPKLPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALTQGPVPSLGLWRKSPASPGELAHLAKDADGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_012543242 [XP_012543242] transcriptional coactivator YAP1 isoform X1 [Monomorium pharaonis]. 46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTVGTPNGGSAPNGGASSGSGNGGGGGGGGGGGATGTGGGGGGGGAGAGSGANANGTANA
IAVAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPHGWE
QARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTPEGEIYFINHQTRTT
SWFDPRIHIIPSASHLQRTPANSGTMLPQAWQLQQPPGIQNNQSLQACQQKMRLQSLQMECERLKLRRQEIIRQA
FFSSLQQEMMRQSTTDASMDPMLRQSATDAPMDPFLSGIPGAEHARQESADSGLGLGSAYSLPQTSDDFLNIDEN
MDGTSERHCSLNDLTKRLYRSHKYINGTTMDTPDISLSENLDVPTDELLPSLQLNEEFSTDILEDVQSLINPNTT
KPENVLTWL PLRMRNLPDSFFNPP

rs:XP_012543243 [XP_012543243] transcriptional coactivator YAP1 isoform X2 [Monomorium pharaonis]. 46..60

MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTVGTPNGGSAPNGGASSGSGNGGGGGGGGGGGATGTGGGGGGGGAGAGSGANANGTANA
IAVAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPHGWE
QARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTPEGEIYFINHQTRTT
SWFDPRIPSHLQRTPANSGTMLPQAWQLQQPPGIQNNQSLQACQQKMRLQSLQMECERLKLRRQEIIRQAFFSSL
QQEMMRQSTTDASMDPMLRQSATDAPMDPFLSGIPGAEHARQESADSGLGLGSAYSLPQTSDDFLNIDENMDGTS
ERHCSLNDLTKRLYRSHKYINGTTMDTPDISLSENLDVPTDELLPSLQLNEEFSTDILEDVQSLINPNTTKPENV
LTWL PLRMRNLPDSFFNPP

rs:XP_012543245   [XP_012543245] transcriptional coactivator YAP1 isoform
X3 [Monomorium pharaonis].   46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTVGTPNGGSAPNGGASSGSGNGGGGGGGGGGGATGTGGGGGGGGAGAGSGANANGTANA
IAVAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPHGWE
QARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTPEGEIYFINHQTRTT
SWFDPRIHIIPSASHLQRTPANSGTMLPQAWQLQQPPGIQNNQSLQACQQKMRLQSLQMECERLKLRRQEIIRQQ
EMMRQSTTDASMDPMLRQSATDAPMDPFLSGIPGAEHARQESADSGLGLGSAYSLPQTSDDFLNIDENMDGTSER
HCSLNDLTKRLYRSHKYINGTTMDTPDISLSENLDVPTDELLPSLQLNEEFSTDILEDVQSLINPNTTKPENVLT
WL   PLRMRNLPDSFFNPP

rs:XP_028045498   [XP_028045498] transcriptional coactivator YAP1 isoform
X4 [Monomorium pharaonis].   46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTVGTPNGGSAPNGGASSGSGNGGGGGGGGGGGATGTGGGGGGGGAGAGSGANANGTANA
IAVAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPHGWE
QARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTPEGEIYFINHQTRTT
SWFDPRIPSHLQRTPANSGTMLPQAWQLQQPPGIQNNQSLQACQQKMRLQSLQMECERLKLRRQEIIRQQEMMRQ
STTDASMDPMLRQSATDAPMDPFLSGIPGAEHARQESADSGLGLGSAYSLPQTSDDFLNIDENMDGTSERHCSLN
DLTKRLYRSHKYINGTTMDTPDISLSENLDVPTDELLPSLQLNEEFSTDILEDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_012543246   [XP_012543246] transcriptional coactivator YAP1 isoform
X5 [Monomorium pharaonis].   46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTVGTPNGGSAPNGGASSGSGNGGGGGGGGGGGATGTGGGGGGGGAGAGSGANANGTANA
IAVAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPHGWE
QARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTPEGEIYFINHQTRTT
SWFDPRIHIIPSASHLQRTPANSGTMLPQAWQLQQPPGIQNNQSLQACQQKMRLQSLQMECERLKLRRQEIIRQA
FFSSLQQEMMRQSTTDASMDPMLRQSATDAPMDPFLSGIPGAEHARQESADSGLGLGSAYSLPQTSDDFLNIDEN
MDGTSDGTTMDTPDISLSENLDVPTDELLPSLQLNEEFSTDILEDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_012543247   [XP_012543247] transcriptional coactivator YAP1 isoform
X6 [Monomorium pharaonis].   46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTVGTPNGGSAPNGGASSGSGNGGGGGGGGGGGATGTGGGGGGGGAGAGSGANANGTANA
IAVAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPHGWE
QARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTPEGEIYFINHQTRTT
SWFDPRIHIIPSASHLQRTPANSGTMLPQAWQLQQPPGIQNNQSLQACQQKMRLQSLQMECERLKLRRQEIIRQQ
EMMRQSTTDASMDPMLRQSATDAPMDPFLSGIPGAEHARQESADSGLGLGSAYSLPQTSDDFLNIDENMDGTSDG
TTMDTPDISLSENLDVPTDELLPSLQLNEEFSTDILEDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_012543248   [XP_012543248] transcriptional coactivator YAP1 isoform
X7 [Monomorium pharaonis].   46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTVGTPNGGSAPNGGASSGSGNGGGGGGGGGGGATGTGGGGGGGGAGAGSGANANGTANA
IAVAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPHGWE
QARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTPEGEIYFINHQTRTT
SWFDPRIPSHLQRTPANSGTMLPQAWQLQQPPGIQNNQSLQACQQKMRLQSLQMECERLKLRRQEIIRQQEMMRQ

STTDASMDPMLRQSATDAPMDPFLSGIPGAEHARQESADSGLGLGSAYSLPQTSDDFLNIDENMDGTSDGTTMDT
PDISLSENLDVPTDELLPSLQLNEEFSTDILEDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_015707744 [XP_015707744] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Coturnix japonica]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGNVSGAPGGAAQQPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQAMRNPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_015707745 [XP_015707745] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Coturnix japonica]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGNVSGAPGGAAQQPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQE
LRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAI
PGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015707746 [XP_015707746] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Coturnix japonica]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGNVSGAPGGAAQQPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015707747 [XP_015707747] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Coturnix japonica]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGNVSGAPGGAAQQPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLN
SGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDG
MNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015707879 [XP_015707879] PREDICTED: LOW QUALITY PROTEIN: protein
FAM181B [Coturnix japonica]. 215..229
MPFRQEAGMPVSGPALVPPPLHPAAFSPTPASSSSRVPLQPCGARRRGAPPPAMAVPAALLSPHHLLSF
CFPAGGLLGYADLEKGYDGGGGGGGGGEAGDFKEATRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIK
RCTGIIAPPSAAPPTSACPKPPPPPRREGSQAGSSLQSRSLAALFGSLQPGRGSTGSDGGGAAGGGPRKVPLRDR
NLPPSFFTEPGAKETEKGGGPEAAEFFELLGPEYGALLPEHAAPPQDAFPAARPPAELGLEHGLYEAAPLPAAPH
PLLGGLLYPEPPWSPPGPCSPAKKAAADALRPLYPEPAAGGDAFGSFFPECPLPPRRCITSTAAASTGRPTPGCR
AGPAPGRGHLRVGXRKGEGAERGCGRDPRGGEESWARPHREGAGMAEHQKRPQLTLEGNRHRGRLRAPLSAXGDA
ALLRSN PLRDRNLPPSFFTEP

rs:XP_016154463 [XP_016154463] PREDICTED: protein **FAM181**A [Ficedula
albicollis].>tr:U3JII2_FICAL [U3JII2] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSFALP00000002586};
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKAPECGWR

RAAEERARGPQPEAPEPGPHGGAAAEKLLQTAEAEESLTGERLLQEQKPEAARPDQVPMRKRQLPASFWEEPRPA
QSLTGRAFPAGPEGLQAPRDAPPYEGKKSRRSPDAAGPESPPDPAAHGGEKEPAGALSGRVGAWTCCPFPCPGPG
VFQPPGALPPSPFPALGLWRKSAATLPAEVPHFGKEADGPGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_015670195 [XP_015670195] PREDICTED: transcriptional coactivator
YAP1 [Protobothrops mucrosquamatus]. 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPALLGTVSPGALT
PSGVVPGGTPSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKTLLSQMNVTAPTSPPLQ
QNIMNSATGPLPEGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPPGGVLG
GGNSSQQQQIRLQQLQMEKERLRLKHQELLRQELALRSQLPSMEQDGTQNRVSSPGMSQELRTMTTNSSDPFLNS
GTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTINQSTIPSHQNRFPDYLEAIPGTNVDLGTLEGDAM
NIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_015671185 [XP_015671185] PREDICTED: protein **FAM181**A [Protobothrops
mucrosquamatus]. 137..151
MASTDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHHHHLQPQLP
PARERRPPEGRARGLSPESSVGRGHAASGAAKGDKASQAPERLGGEEEQQQQQQPGASEAGARPDQVPMRKRQLP
ASFWEEPRPAPGSPGVYHGPQASPGLYPPPLPAALPPAAPFSALGLWRKDAPSPTEGEAFCQPGQKVYRPVVWKP
IPTKPAAAPPLIFSVFSYL PMRKRQLPASFWEEP

rs:XP_015682677 [XP_015682677] PREDICTED: protein **FAM181**B [Protobothrops
mucrosquamatus]. 265..279
MAVQAAPLPPPHHHPFVPFGFPPADFGALEKSYGGCEGGGGGVGGGGGALLLLEGVGGAHGGGVVGGVA
SCTDPGDFREATRELLSFIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCTGLIGGASANPEAAAAVASLAA
AAPGSVPGSANKAASTLTAPSSGGAAASSSSSCRPPAKRESHALQSKSLAALFDALRSPGLERKGSPTAVASAAA
AAAAAAATAAAAPAAGLGSDVGGKEAGSSPVAVAAAAAGGACKKVPLRNRNLPVSFFTEPAPPSRPPNPAGLEEA
VPSVAEELFDLLAAAPDYRGLLQEAAEPPAVFPGPALQVAAELPLEPPLYEPLPSMAPLLYAEPPLRPLPALYAA
VAASDPAAPFFADCPLPPPPAVPYDYGYNRGVPYPSL PLRNRNLPVSFFTEP

rs:XP_015761069 [XP_015761069] PREDICTED: uncharacterized protein
LOC107340231 [Acropora digitifera].147..161
MDESKMNLIQGDISSTASSLLNFVSTATSNLKFALQKPVKPKRRVNHRKYLQRQLKGRGVTLTGSCANS
CLIKEQEVNERNISLKSAGKLSALEKRAEDGKAMEENGVVRKRNERENKEKKCGNSIIKDPKEQMNNSLSNLPSA
QSPLRKRKLPESFWSEPTKQSVQSTRYSAINLTTNDFQRSELEILDWLRPELDEFIERWSEESDHVSNHSSRPSS
LCDSTSTVDPYSPYSEESDNTAAMDEFFEQRVPFSLELPLRVGNGNNGPGVRNFVLEHEIIKNCNIEQSYGQGQT
MNNPLNFINDHFGLSGPSWNTQYQAQENFIDGAYIV PLRKRKLPESFWSEP

rs:XP_015771341 [XP_015771341] PREDICTED: uncharacterized protein
LOC107349675 [Acropora digitifera].102..116
MDPLRKRVQNQDSLSWRSPPSPCGPSSPQSPPPLSIRGKSLSLNRVNPPLAPIREAKELSKRGRKQRLL
LSQAGNLTLKRRETSPDFSRLEARLKPKRGPLPMRMRALPQSFWQEPKDIQNSSMSTEGSLQTLPPLFHNANNTS
DDVSKLRPVTPPEEKHKPRPPKEPKLVISSPQEQLLKLFETVEEDKTKKFVIKRGRPRRAQSDLTALSLPKLEED
PCMMTSLAEKMFPQLSLEHKQSAGANTSLSCVSVHDGDKSVQLPSLNVEQNYSQMLSEIVAHF
PMRMRALPQSFWQEP

rs:XP_016092458 [XP_016092458] PREDICTED: transcriptional coactivator
YAP1 [Sinocyclocheilus grahami]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLSSMVPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISQSAPVKQGSQLPSSPQSGVLGGNNQIRLQQIQMEKERLRIKQELLRQRPQGGVSVQFTYVHSF
DLSKQLWPGVFLCSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDRLGPSSMATQPSRFPDYLDAIP
GTDVDLGTLEGESMVVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_016099741 [XP_016099741] PREDICTED: transcriptional coactivator
YAP1-like [Sinocyclocheilus grahami]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAISPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHIRAHSSPASLQLGAVSPGTLSSMVPANPQPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF

LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPVPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAPVIEVDELLTFGGTFSHQLQKHFYDYEPAANFPECSSEARLPVALQPTERSAGWKQPDQAAADPDGERET
EDQTRAPSPETPGARPEKPAADQHGAGWRHSKPCVLTRHGTRRP   PMRMRKLPDSFFKPP

rs:XP_016101694   [XP_016101694] PREDICTED: protein **FAM181**B-like
[Sinocyclocheilus grahami].   15..29
MSCQVVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPDAAEFLELLGPDYSTMVS
EQDLFHTAPIRIQQEVTVGPEPYDSHHFVSGGFLYTEPWGTCSSNPKKSGDMRTVPVQPNLYTHTDLSGSVPVEQ
SSPCALTFSNFFTDCSAPSVSYDLVNGYNRGSFSSL   PLRHRNLPPSFFTEP

rs:XP_016117131   [XP_016117131] PREDICTED: protein **FAM181**A
[Sinocyclocheilus grahami].   111..125
MASSDSEVKTLLNFVNLASSDIKAALDRSAPCRRSVDHRKYLQKQLKRFSHRYAKIPRCHSHRNGDSTP
AKRSEDKAPPGPGSGSGSGREERLNAEDGARSGQGQGQAPMPMRKRQLPASFWKEPQASSGSRERLERFLHTAHV
RPPAGNGERSTAGFEDLNANPLLSGGAACACSCCSLPYRFLLPHADAPLSSRAHVVIKPIPTKPSSSSSSSSSSS
SVFSVFGFI   PMRKRQLPASFWKEP

rs:XP_018900896   [XP_018900896] PREDICTED: transcriptional coactivator
YAP1-A-like [Bemisia tabaci]. 43..57
MALNQDDSKNNLMVRMDQNSETELQKLFDTVLKPDAKIPLQLPLRMRKLPPSFFNPPSTGSKSPSVSSI
SHSRENSADSAFGTTTITTSTSLQVNHPRAHSSPASLQQTYASAQQAEAQQKQQHQNLHLKQRSYDVTNQTVDDL
GPLPPGWEQAKTSEGQIYFLNHITRSTTWEDPRKALAAQVQSVQNQLAAQCNAAAAGGGGNQTSGSDQQLSSSTT
SVTSPGGVGKSPGPLSPATSPGSLGPLPEGWEQALTPEGEQYFINHQTRTTSWFDPRIPQHMQRTLSAGAILPSG
WPPTISSTTNSQASQQQLRLQSLQLEREKLKARQREIFRQQEFMLRPNSTADPFLSGLTDHSRQESADSGLGMGN
NYSLPHTPEDFLNTVDDNMDGVSEGGTLGPSDMSTLDSQEMSSLTDTIDLTEDLVPSLQLGEELSSDILDDVQSL
INPTSKADNVLTWL   PLRMRKLPPSFFNPP

rs:XP_018917904   [XP_018917904] PREDICTED: transcriptional coactivator
yorkie-like [Bemisia tabaci]. 43..57
MALNQDDSKNNLMVRMDQNSETELQKLFDTVLKPDAKIPLQLPLRMRKLPPSFFNPPSTGSKSPSVSSI
SHSRENSADSAFGTTTITTSTSLQVNHPRAHSSPASLQQTYASAQQAEAQQKQQHQNLHLKQRSYDVTNQTVDDL
GPLPPGWEQAKTSEGQIYFLK   PLRMRKLPPSFFNPP

rs:XP_010607503   [XP_010607503] PREDICTED: protein **FAM181**A [Fukomys
damarensis].   129..143
MASDTDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLK
RGPEDRPGRLLLHPGPDSGPGGGGGCKEKALGSPFGEECLSKEQILQGQGLGAAKPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGGLGPREGSPYESKKNCKGLESSVPEAAPGPMSPRVLANKEPLKMPGVSLVGCVDAWSCCPFQYH
GQPIYPSPPGALPPSPLPSLGLWRKSPALPAELAHFCKHVDSPGQKVYRPMVLKPIPTKPAVPPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_007556477   [XP_007556477] PREDICTED: transcriptional coactivator
YAP1-like isoform X4 [Poecilia formosa]. 46..60
MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPVIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETAPKVNPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAG
GSNQMPGGMDHDRSAQMLVPSVDIRIRALNQESNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGDSSE
PPSMGLQESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWLPMRMRKFPDSFFKPP

rs:XP_019289197   [XP_019289197] PREDICTED: transcriptional coactivator
YAP1 [Panthera pardus]. 154..168
MGLLTQIPLEESGVRSSGVESGVRSLPSGLPGPHQFLRAPAADPGRAGAQRKEGPRGGGADAPLGRAAL
STLVLASAASFCLSRAQPPPGEREGGRKEGTPGAERAAGEGSPRRPSRAQPAGARAGGAGXETDLEALFNAVMNP
KTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALAPQHVRAHSSPASLQLGAVSPGTLTPTGVVSG
PAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPVQQNMM
NSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAVNQRVGQSAPAKQPPPLAPQSPPGGVLGSG
GSNQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSSANSPKCQELALRSQLPTLDQEGGTQNPVPSPGMSQELR
TMTTTSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPG
TNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

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rs:XP_001370835   [XP_001370835] PREDICTED: protein FAM181A isoform X1
[Monodelphis domestica].>tr:F7BYB2_MONDO [F7BYB2] SubName: Full=Family with
sequence similarity 181 member A {ECO:0000313|Ensembl:ENSMODP00000032880};
      160..174
      MENWGVGENDWCTYCLPFVHLLSCRPGNSSSSWKSPGGVPREMASDSEVKMLLNFVNLASSDIKAALDK
SAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCYPNRSGESHSKRGPEDSHCRTPSNGSTEKGPGNRGMEENFPQVQ
ALQEQIPEASRPDQVPMRKRQLPASFWEEPRPAQSYSGGLDGLSGHREVPAYEGKKSKKRPETLGSETAPVPTSP
RAEKESPKVPSASLMGRMSAWSCCPFQYHGQPIYQSPGGLPQSPVPSLGLWRKSPASPGEMGHFCKEPGSPSQKV
YRPVVLKPIPTKPGVPPPIFNVFGYI    PMRKRQLPASFWEEP

rs:XP_007472634   [XP_007472634] PREDICTED: protein FAM181A isoform X2
[Monodelphis domestica].>rs:XP_007472635 [XP_007472635] PREDICTED: protein
FAM181A isoform X2 [Monodelphis domestica].>rs:XP_007472636 [XP_007472636]
PREDICTED: protein FAM181A isoform X2 [Monodelphis domestica].   118..132
      MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCYPNRSGESHSK
RGPEDSHCRTPSNGSTEKGPGNRGMEENFPQVQALQEQIPEASRPDQVPMRKRQLPASFWEEPRPAQSYSGGLDG
LSGHREVPAYEGKKSKKRPETLGSETAPVPTSPRAEKESPKVPSASLMGRMSAWSCCPFQYHGQPIYQSPGGLPQ
SPVPSLGLWRKSPASPGEMGHFCKEPGSPSQKVYRPVVLKPIPTKPGVPPPIFNVFGYI
      PMRKRQLPASFWEEP

rs:XP_007495026   [XP_007495026] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Monodelphis domestica]. 89..103
      MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQVRPQALRNVNPSTANSPKRQEIAIRSQIPTVEQDG
GIQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNI
PSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKQP

rs:XP_007495027   [XP_007495027] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Monodelphis domestica]. 89..103
      MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQVRPQALRNVNPSTANSPKRQEIAIRSQIPTVEQDGGI
QNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPS
QQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKQP

rs:XP_007495028   [XP_007495028] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Monodelphis domestica]. 89..103
      MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQALRNVNPSTANSPKRQEIAIRSQIPTVEQDGGIQN
PVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKQP

rs:XP_003341352   [XP_003341352] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Monodelphis domestica]. 89..103
      MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
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QGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQALRNVNPSTANSPKRQEIAIRSQIPTVEQDGGIQNPV
SSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKQP

rs:XP_007495029 [XP_007495029] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Monodelphis domestica]. 89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQVRPQEIAIRSQIPTVEQDGGIQNPVSSPGMNQELR
TMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPG
TNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_007495030 [XP_007495030] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Monodelphis domestica]. 89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQVRPQEIAIRSQIPTVEQDGGIQNPVSSPGMNQELRTM
TTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTN
VDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_007495031 [XP_007495031] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Monodelphis domestica]. 89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQEIAIRSQIPTVEQDGGIQNPVSSPGMNQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_003341353 [XP_003341353] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Monodelphis domestica]. 89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQEIAIRSQIPTVEQDGGIQNPVSSPGMNQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_016289376 [XP_016289376] PREDICTED: transcriptional coactivator YAP1 isoform X9 [Monodelphis domestica]. 89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQ
VRPQALRNVNPSTANSPKRQEIAIRSQIPTVEQDGGIQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_016289377 [XP_016289377] PREDICTED: transcriptional coactivator YAP1 isoform X10 [Monodelphis domestica].89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG

TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQ
ALRNVNPSTANSPKRQEIAIRSQIPTVEQDGGIQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKQP

rs:XP_016289378   [XP_016289378] PREDICTED: transcriptional coactivator
YAP1 isoform X11 [Monodelphis domestica].89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQ
VRPQEIAIRSQIPTVEQDGGIQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDD
FLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVL
AATKLDKESFLTWL   PMRLRKLPDSFFKQP

rs:XP_016289379   [XP_016289379] PREDICTED: transcriptional coactivator
YAP1 isoform X12 [Monodelphis domestica].89..103
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKQPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGAAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKALLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIRLQQLQLEKERLRLKHQELLRQ
EIAIRSQIPTVEQDGGIQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_001377183   [XP_001377183] PREDICTED: protein **FAM181**B [Monodelphis
domestica]. 245..259
MAVQAAILSPHHFIPFCFPGSPGALGMDFGDLDKGCCYEEDEAGGTGAALLGEAVAAEGADGGGGGGDF
REATRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGMMTSSPASASGPAPSASPSPGPAAAVSV
GALEAPTKRPPSASPAAPGTQSKAPPKREGSQAAASLQSKSLAALFDSLHQVRGGGGEKGGAGTLAAVTGGGGGG
GSGGAGVEGGVPAVAPPGAGGNKKVPLRNRNLPPSFFTEPSRAGSCGPSGGGVTLRELEKGGEAVEFFELLGPDY
CAGGEVGGLLPSEPLDLFPAAVRPPQELEHILYDPHPTLVAGLLYSEPWSTPCPPAKKPAPVSNRGGGGLTLNET
LRPLYSSTSDSAASSLSSPGGEDTAGHLTPFSQFFPDCALPTPPPPHQMPYDYGVGYSRVAYSGL
PLRNRNLPPSFFTEP

rs:XP_007499387   [XP_007499387] PREDICTED: uncharacterized protein
LOC100618561 [Monodelphis domestica].   214..228
MAAGVIRTLCDFRLQAPFHQPFVPTTSHQDPDFPETSEEEEEDGEEEEDGEKQIEDLELAGSSPGGQSS
DHELAKGPTRPSPSSTEMTLQLLRFSELISCDIQKYFGQKTKDEDPDACNIYEDSHPPGKSARELYYADLMQIVQ
SGDQEDEDTDTASLPRGLDCQVRFISSRDRALKLGPLVELFEYGLCQYARQRVSDSRRMRLEKKYGHITPMHKRK
LPQSFWKEPAPSSLCLLNTSTPDFSDLLANWTSDVAQELHSVGGRELGRHALEMDHLEEA
PMHKRKLPQSFWKEP

rs:XP_006786215   [XP_006786215] PREDICTED: protein **FAM181**A-like
[Neolamprologus brichardi].   102..116
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYRC
AKPMGSVHQSVAEKASSGAQDVDQLGGSVEQVPMRKRQLPASFWEEPKLTPTKREHSYLGMKRSHAGTSEGTENE
KRKRSYDDDAKAAISACSRRSSADKETLKVDVTSHHCVSVCGCCPFQYHGHQILHNHIFVPHPPLGLWSKAAGTE
TERSEHPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI   PMRKRQLPASFWEEP

rs:XP_006796689   [XP_006796689] PREDICTED: protein **FAM181**B-like
[Neolamprologus brichardi].   155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGETENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNAAEAPVKRQGSPLTQPSTLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKPKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEATEFFELLGPDYCNMVSDQDIYQGMPL
RVQPELGGPDPASYDTHHLVGGLLYSEPWTSCSGPSKKVGESLRTGPAQPPVYCQSEGATGPIEDNALCTLAFPN
FFADCPIPQVTYDLTGGYNRANYSSL   PLRHRNLPPSFFTEP

rs:XP_006796706   [XP_006796706] PREDICTED: yorkie homolog [Neolamprologus brichardi]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKVNTVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSGGSLSGMGSTGASPQHLRQSSYEIPDDLPLPDGWEMAKTASGQRYF
LNHLIKTNTWRTSTKSALLQMNQPAPPSSVPVQPQPIMNPASGPLPDGWEQAITAEGEIYYINHKNKTTSWLDPR
LEPRYALNQQRISQSAPVKQAGQLPPSISGVMGSNNQMRLQMEKERLRQKQQELLRQRPQELALRNQLPTSMDQD
GSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMAT
QPSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_006747631   [XP_006747631] PREDICTED: protein **FAM181**B [Leptonychotes weddellii].>tr:A0A2U3YV81_LEPWE [A0A2U3YV81] SubName: Full=protein **FAM181**B {ECO:0000313|RefSeq:XP_006747631.1};   221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADAPAKRHPAAPGAQTVAVPPHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGDERARGSVAAPVAGLGGAGAVGSGGDAAGPAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGVGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEPPPAMVGSLLYSESWSAPGCPPTKKPPLAAPRGGLTLNEPLRSLYPSAADSPGGEDAPGL
LASFAPFFSDCALPPPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD
PLRARNLPPSFFTEP

rs:XP_006747904   [XP_006747904] PREDICTED: protein **FAM181**A [Leptonychotes weddellii].>tr:A0A2U3YVZ0_LEPWE [A0A2U3YVZ0] SubName: Full=protein **FAM181**A {ECO:0000313|RefSeq:XP_006747904.1};   180..194
MKLLQMLLRGRPAARGLRSARQVSSVPFPGAASHQQSPRSSWKAPCSGPLVMASDSDVKMLLNFVNLAS
SDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDSGQDCSPGGGG
CYKEKALGNPYREECLSREQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGK
KHCKGLEPLDPEMAPVPASPRALAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPIYAGHPGALPQSPVPSLGLWR
KSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL   PMRKRQLPASFWEEP

rs:XP_006879161   [XP_006879161] PREDICTED: protein **FAM181**A [Elephantulus edwardii]. 130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLRRFSQKYSRLPRGLPGRGAEPHLR
RGPEDRPGRLPLDGHAPSPGLGGGCQEKALGNSDREECPSGEQEPTPQGQHPEGALPGQVPMRKRQLPASFWEEP
RPAHSFPMGLEGGLGPREGAPYEGKKTCQVLEPLGPEMVPMPLSPRALAEKELLKMSGVSLVGHINAWGCCPFQY
HGQPVYPGPPGVLPQCSVPSLGLWRTSPVSPGELPPFCKDVDSQKVHRPVVLKPIPTRPAVPPPLFNVFSYL
PMRKRQLPASFWEEP

rs:XP_006882960   [XP_006882960] PREDICTED: protein **FAM181**B [Elephantulus edwardii]. 221..235
MAVQAALLSPHPFVPFGFASASDGLGGAFGALDKGCCFEDDENRAPTGTLVAEAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRSPAAPSAPTVAVPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLHHVPASDEPAGGAVVTPAAGLSGTSAGSAGGDKVSPAGGAVTPGTRK
VPLRARNLPPSFFTEPSQAGGGGCGPAGPGVSLGDLEKGAEAAEFFELLEPDYGTGNEAGVLLAAEPLDVFPAGA
TALRGPPDLESGLFEPPPSMVGSLLYPESWSAPAPAAKKMPVAVARGGLTLNEPLRPLYPAAADSPGGEDGPGQL
ASFSPFFPDCALPLPPPPPHQAPYDYGAGYSRTPYTSLWRPDGVWEEVPGEEGAHQD PLRARNLPPSFFTEP

rs:XP_002734168   [XP_002734168] PREDICTED: yorkie homolog [Saccoglossus kowalevskii].   45..59
MTMDPKGHQIVHVRGDSDTDLEDLFRAVMNPTGIVKEPLPQHPVPLRMRKLPPSFFKEPDKPMASSPSG
SHSRESSTDSTNPGGPFGAQTLGLPVNHPRAHSSPASLQQMQAAAASQQQQQTVTPQHTRHTSYDVTTIEDLPLP
PGWEVARTPSGQRYFLNHMDQTTTWNDPRKNLTQAQLAQLQQAQQARALLQQQQPQQQQQPDLGPLPATWEQAS
TPEGELYFINHIDRTTSWLDPRLGLRATAGQTVGLSGTQLNRNQQIQQALQQQQLQAQQQGPLSRQQQHPQKERL
QQLQLEREKLRRRQLEIQQQEMLIRKEIVGEDGQPVSKSNQQSQDREMTSVSTTGVDPFLSGGTYHSRDESGDSG
LGMSSNYSLPRTPDDMLSNVDEMDTSDGKPDMNAATPIQTPMNDYLESMQGTNVDIGSLEDEEGDDLVPSLQEAL
SSDILTDVEAVLSPHKIENFLTWL   PLRMRKLPPSFFKEP

rs:XP_006887372   [XP_006887372] PREDICTED: yorkie homolog isoform X1 [Elephantulus edwardii].   85..99

MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRIGQSAPLKQPPPLAPQSPQGGI
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_006887373 [XP_006887373] PREDICTED: yorkie homolog isoform X2
[Elephantulus edwardii]. 85..99
MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRIGQSAPLKQPPPLAPQSPQGGI
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_006887374 [XP_006887374] PREDICTED: yorkie homolog isoform X3
[Elephantulus edwardii]. 85..99
MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRIGQSAPLKQPPPLAPQSPQGGI
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006887375 [XP_006887375] PREDICTED: yorkie homolog isoform X4
[Elephantulus edwardii]. 85..99
MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRIGQSAPLKQPPPLAPQSPQGGI
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006887376 [XP_006887376] PREDICTED: yorkie homolog isoform X5
[Elephantulus edwardii]. 70..84
MDPGQQPPPQPVPQGQGQPPPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPPTV
PMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSPTGVVSGPAATPTAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPPVQQNMMNSASGPLPD
GWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRIGQSAPLKQPPPLAPQSPQGGIMGGGNSNQQQQMRLQ
QLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006887377 [XP_006887377] PREDICTED: yorkie homolog isoform X6
[Elephantulus edwardii]. 85..99
MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAINQRIGQSAPLKQPPPLAPQSPQGGIMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006887378 [XP_006887378] PREDICTED: yorkie homolog isoform X7
[Elephantulus edwardii]. 85..99
MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAINQRIGQSAPLKQPPPLAPQSPQGGIMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006887379 [XP_006887379] PREDICTED: yorkie homolog isoform X8
[Elephantulus edwardii]. 85..99
MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAINQRIGQSAPLKQPPPLAPQSPQGGIMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006887380 [XP_006887380] PREDICTED: yorkie homolog isoform X9
[Elephantulus edwardii]. 85..99
MDPGQQPPPQPVPQGQGQPPAQPPQGQDQPSRPGQPAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGALSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPP
VQQNMMNSASAINQRIGQSAPLKQPPPLAPQSPQGGIMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_002737352 [XP_002737352] PREDICTED: E3 ubiquitin-protein ligase
BRE1A-like [Saccoglossus kowalevskii]. 113..127
MSGKRGPTLALSGSSDEDCSDHDEVANSTEDACPTSPCSSTNSGPTYVRTAGFKHHGHTFYKLHRTKQP
KHKKKKHMISTESLITTSFKKKRDPLAALGGPIHRTKPKKEPLPMKLRALPQSFWQQPNAVNTASPANMFKILPP
LYKQETGEDVTDVRPVTPPDETKEEKEEKLRETKEKEIKEAKDLKEAKEIKDAKEREIKDAKEREIKDAKEREMK
DTKEREIKDSKEKETKEKLRIRPPLCPRPPPRIFTASTAETDLLVTLFDGIENEKKKKIIKRGRPKRVQTVENKG
PLQGEDPYMIENITEGLLPMLSLENMKHSSVATHQLSMVSLREGDKSLTLPSLTVEQNYSHMLSELVNAL
PMKLRALPQSFWQQP

rs:XP_006833824 [XP_006833824] PREDICTED: yorkie homolog isoform X1
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGVGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRNLPDSFFKPP

rs:XP_006833825 [XP_006833825] PREDICTED: yorkie homolog isoform X2
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY

LEAIPGTNVDLGTLEGVGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRNLPDSFFKPP

rs:XP_006833826 [XP_006833826] PREDICTED: yorkie homolog isoform X3
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGVGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRNLPDSFFKPP

rs:XP_006833827 [XP_006833827] PREDICTED: yorkie homolog isoform X4
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
VGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRNLPDSFFKPP

rs:XP_006833828 [XP_006833828] PREDICTED: yorkie homolog isoform X5
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGVGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRNLPDSFFKPP

rs:XP_006833829 [XP_006833829] PREDICTED: yorkie homolog isoform X6
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGVGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRNLPDSFFKPP

rs:XP_006833830 [XP_006833830] PREDICTED: yorkie homolog isoform X7
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGVGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRNLPDSFFKPP

rs:XP_006833831 [XP_006833831] PREDICTED: yorkie homolog isoform X8
[Chrysochloris asiatica]. 85..99
MDPGQQPPPQSGPQGQGQPPAQPPQGQDAPARPGQPAPPGSQPAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRNLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQIRLQQLQMEKERLRLKQQELLRQELAL

RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGVGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRNLPDSFFKPP

rs:XP_006839692 [XP_006839692] PREDICTED: protein **FAM181**A [Chrysochloris asiatica]. 130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCSRLPRGLPGRAAEPHLK
RGSEDRPARLPLQCHQPSPGGVGGCQEKALGSPDRGEYLSGQQEQGLHGQSLEAARPGQVPMRKRQLPASFWEEP
RPAHSFPLGLEGGLGPREGPPYKCKKTCQGLESLGPETAPVCLSPRALVEETLRMPGVSLVGHVNAWSCCSLQYH
GQPMYPGPVGVLPQGSVPSLGLWRTSPVSPGELAPCCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFHVFGSL
PMRKRQLPASFWEEP

rs:XP_006865043 [XP_006865043] PREDICTED: protein **FAM181**B [Chrysochloris asiatica]. 221..235
MAVQAALLSPHPFVSFGFAGAPNGLGGAFGALDKGCCFEDDETRAPAGVLLAEAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPGAADTQAKRSPAAPSAPTVAVPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHIPAGDEPAGGAVAAPATGLSGSGAGNAGGEVVGPAGGAVVPGARK
VPLRARNLPPSFFTEPSRAGSGGCGTSGPGISLGDLEKGAEAVEFFEFLGPDYGAGTEAGVLLTPEPLDVFPTAT
AALRGPPELEPGLFEPSSAMVGSLLYSESWSTPGQPTKKMPLTGSRGALTLNEPLRPLYPAAADSQGGEDGPGHL
ASFAPFFPDCALPLTPAPHQVSYDYCASYNRTTYSNLWRSDGVWDEVPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_007900626 [XP_007900626] PREDICTED: WW domain-containing transcription regulator protein 1 isoform X1 [Callorhinchus milii].
46..60
MDGSTTPAPAPGHTIVRVLGDSETDLEALFKAVMNPQAGSLPQGVPMRLRKLPESFFRPPDSGSHSRQA
SGDSSPGPGPGGPPAGLPHFHIQHIRSHSSPASLPGPGPGPGGPGYSHHRQQSFDNIDDVPLPPGWEMAKTPSGQ
RYFLNHVDRITTWHDPRKTLSQMNLNTAGSPGQMQQRPMQLSHQNPGPVPEGWEQAVTPEGEIYFINHKTKSTSW
LDPRLDQLCMMTQQPLASGPTPALGSPGPRLPMLNLSTALSVQQKHQQKMRLQQIQMEKERIKHLQQELMRQEKA
LYNQIPNQIPIESDNIPTAQNAVSTPTMTQEMHAITNNGSDPFLNSGPYHSRQASADSGLGLGRTSEDFLGHVEE
MDTGDMGQSALTANQPSRFPDFLDSLPGTNVDLGTLEGEDLMPSLQEPFETDILPDVESSLNPKETFLTWL
PMRLRKLPESFFRPP

rs:XP_007900627 [XP_007900627] PREDICTED: WW domain-containing transcription regulator protein 1 isoform X2 [Callorhinchus milii].
46..60
MDGSTTPAPAPGHTIVRVLGDSETDLEALFKAVMNPQAGSLPQGVPMRLRKLPESFFRPPDSGSHSRQA
SGDSSPGPGPGGPPAGLPHFHIQHIRSHSSPASLPGPGPGPGGPGYSHHRQQSFDNIDDVPLPPGWEMAKTPSGQ
RYFLNHVDRITTWHDPRKTLSQMNLNTAGSPGQMQQRPMQLSHQNPVMTQQPLASGPTPALGSPGPRLPMLNLST
ALSVQQKHQQKMRLQQIQMEKERIKHLQQELMRQEKALYNQIPNQIPIESDNIPTAQNAVSTPTMTQEMHAITNN
GSDPFLNSGPYHSRQASADSGLGLGRTSEDFLGHVEEMDTGDMGQSALTANQPSRFPDFLDSLPGTNVDLGTLEG
EDLMPSLQEPFETDILPDVESSLNPKETFLTWL PMRLRKLPESFFRPP

rs:XP_007902057 [XP_007902057] PREDICTED: protein **FAM181**A [Callorhinchus milii]. 131..145
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSRFVESGL
KRVSEDKSRGSDTDHGDSNTPQPQPPCLKASCLLDQDPRGSLPGQPSAAEQGKQLSRQDQVPMRKRQLPASFWEE
PRPPKNLQRSLSAFQTAEKVYGLAEGPSGGGGHRSQAQDLPEAGKQVRAAQLQQDSSQREEPVKFHLTSLSRAMN
VCGCCPFQYHGQQVYHSHSHSHLALPHSSFQDLGLWRKALATPAHDLHTYSKDSLNGQKVHKPIVFKPIPTKPPP
LYNVYSFL PMRKRQLPASFWEEP

rs:XP_007942704 [XP_007942704] PREDICTED: protein **FAM181**A [Orycteropus afer afer]. 130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLK
RGPEDRPTRLLLDGHDPSPSGGGGCKEKVLGNPDREESLSREQAQTLRGQNPEAARPGQVPMRKRQLPASFWEEP
RPAHSFPMGLEGALGPREGPVYESKKTCQGLETLGPETAPVPMSPRALAEKEPLKMPGVSLVGRVNAWNCCPFQY
HGQPVYPGPPGALPQGSVPSLGLWRTSPTSPGELAPYCKDVDGLGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_007944206 [XP_007944206] PREDICTED: yorkie homolog isoform X1
[Orycteropus afer afer]. 85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_007944207 [XP_007944207] PREDICTED: yorkie homolog isoform X2
[Orycteropus afer afer]. 85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_007944208 [XP_007944208] PREDICTED: yorkie homolog isoform X3
[Orycteropus afer afer]. 74..88
MDPGQQPPPQPPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANV
PPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSPTGVVSGPAAAP
TAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQSMINSASG
PLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQ
MRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_007944209 [XP_007944209] PREDICTED: yorkie homolog isoform X4
[Orycteropus afer afer]. 85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_007944210 [XP_007944210] PREDICTED: yorkie homolog isoform X5
[Orycteropus afer afer]. 85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_007944211 [XP_007944211] PREDICTED: yorkie homolog isoform X6
[Orycteropus afer afer]. 85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS

MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_007944212   [XP_007944212] PREDICTED: yorkie homolog isoform X7
[Orycteropus afer afer].   85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_007944213   [XP_007944213] PREDICTED: yorkie homolog isoform X8
[Orycteropus afer afer].   85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_007944214   [XP_007944214] PREDICTED: yorkie homolog isoform X9
[Orycteropus afer afer].   85..99
MDPGQQPPPQPVPQGQGQPPTQPPQGQDPPSRTGQQAPPGSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHSRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQSMINSASAINQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL   PMRLRKLPDSFFKPP

rs:XP_007944428   [XP_007944428] PREDICTED: protein **FAM181**B [Orycteropus
afer afer]. 221..235
MAVQAALLSPHPFVSFGFAGAPDGLGVAFGALDKGCCFEDDETRAPAGALLAEAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGSADTPAKRQPVAPSAQTFAVPAHCK
AAPRREATQAAAAASLQSRSLAALFDSLHHVPAGDEPAGGAVVAPAAGVGGTSAGGAGGEAAGPVGGAVAPGTRK
VPLRARNLPPSFFTEPSRAGGGVCGPSGSGMSLGDLDKGADAMEFFELLGPDYCPSTEAGVLLAAEPLDGFPAGA
SALRGPPELEPGLFEPPPAMVGSLLYPEPWSAPGPPTKKMSLAAARGGLTLNEPLRPLYPAAEDSPGEDDRHGHL
ASFTPFFPDCALPQPPHQVSYDYSAGYSRPAYSSSLWRPDGVWEEVPGEERAHRD   PLRARNLPPSFFTEP

rs:XP_008018492   [XP_008018492] PREDICTED: protein **FAM181**B [Chlorocebus
sabaeus].>rs:XP_005579266 [XP_005579266] PREDICTED: protein **FAM181**B [Macaca
fascicularis].>rs:XP_011717516 [XP_011717516] protein **FAM181**B [Macaca
nemestrina].   221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPVAGLGGAGTGGAGGDAAGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPHQVSYDYSAGYSRNAYSSLWRPDAVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_008018830   [XP_008018830] PREDICTED: yorkie homolog isoform X1
[Chlorocebus sabaeus].>rs:XP_011927468 [XP_011927468] PREDICTED:
transcriptional coactivator YAP1 isoform X1 [Cercocebus
atys].>rs:XP_005579501 [XP_005579501] PREDICTED: transcriptional
coactivator YAP1 isoform X1 [Macaca fascicularis].   85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF

NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008018831 [XP_008018831] PREDICTED: yorkie homolog isoform X2 [Chlorocebus sabaeus].>rs:XP_011927470 [XP_011927470] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Cercocebus atys].>rs:XP_005579502 [XP_005579502] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Macaca fascicularis]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008018833 [XP_008018833] PREDICTED: yorkie homolog isoform X3 [Chlorocebus sabaeus].>rs:XP_011927471 [XP_011927471] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Cercocebus atys].>rs:XP_005579503 [XP_005579503] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Macaca fascicularis]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008018834 [XP_008018834] PREDICTED: yorkie homolog isoform X4 [Chlorocebus sabaeus].>rs:XP_011927472 [XP_011927472] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Cercocebus atys].>rs:XP_005579504 [XP_005579504] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Macaca fascicularis]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008018835 [XP_008018835] PREDICTED: yorkie homolog isoform X5 [Chlorocebus sabaeus].>rs:XP_011927473 [XP_011927473] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Cercocebus atys].>rs:XP_005579505 [XP_005579505] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Macaca fascicularis]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP

VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_008018836 [XP_008018836] PREDICTED: yorkie homolog isoform X6 [Chlorocebus sabaeus].>rs:XP_011927474 [XP_011927474] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Cercocebus atys].>rs:XP_005579506 [XP_005579506] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Macaca fascicularis].   85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_008018837 [XP_008018837] PREDICTED: yorkie homolog isoform X7 [Chlorocebus sabaeus].>rs:XP_011927476 [XP_011927476] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Cercocebus atys].>rs:XP_005579507 [XP_005579507] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Macaca fascicularis].   85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008018838 [XP_008018838] PREDICTED: yorkie homolog isoform X8 [Chlorocebus sabaeus].>rs:XP_011927477 [XP_011927477] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Cercocebus atys].>rs:XP_005579508 [XP_005579508] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Macaca fascicularis].   85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_008018839 [XP_008018839] PREDICTED: yorkie homolog isoform X9 [Chlorocebus sabaeus].>rs:XP_011927478 [XP_011927478] PREDICTED: transcriptional coactivator YAP1 isoform X9 [Cercocebus atys].>rs:XP_005579509 [XP_005579509] PREDICTED: transcriptional coactivator YAP1 isoform X9 [Macaca fascicularis].   85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_008018840 [XP_008018840] PREDICTED: yorkie homolog isoform X10 [Chlorocebus sabaeus].>rs:XP_011927479 [XP_011927479] PREDICTED:

transcriptional coactivator YAP1 isoform X10 [Cercocebus
atys].>rs:XP_005579510 [XP_005579510] PREDICTED: transcriptional
coactivator YAP1 isoform X10 [Macaca fascicularis]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008018841 [XP_008018841] PREDICTED: yorkie homolog isoform X11
[Chlorocebus sabaeus].>rs:XP_011927480 [XP_011927480] PREDICTED:
transcriptional coactivator YAP1 isoform X11 [Cercocebus
atys].>rs:XP_005579511 [XP_005579511] PREDICTED: transcriptional
coactivator YAP1 isoform X11 [Macaca fascicularis]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008018842 [XP_008018842] PREDICTED: yorkie homolog isoform X12
[Chlorocebus sabaeus].>rs:XP_011927482 [XP_011927482] PREDICTED:
transcriptional coactivator YAP1 isoform X12 [Cercocebus
atys].>rs:XP_005579512 [XP_005579512] PREDICTED: transcriptional
coactivator YAP1 isoform X12 [Macaca fascicularis]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_008566209 [XP_008566209] PREDICTED: yorkie homolog isoform X1
[Galeopterus variegatus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRT
MTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGT
NVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWLPMRLRKLPDSFFKPP

rs:XP_008566210 [XP_008566210] PREDICTED: yorkie homolog isoform X2
[Galeopterus variegatus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_008585279 [XP_008585279] PREDICTED: protein **FAM181**A [Galeopterus
variegatus].>rs:XP_008585280 [XP_008585280] PREDICTED: protein **FAM181**A
[Galeopterus variegatus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPSRAAEPHLK

RGPEDRPGRLPLDSGPDSSPGGGGGCKERALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSCPMGLEGGLGPREGTPYEGKKNCKGLETLGPETAPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGVLPQSPVPNLGAWRKSPVFPGDLAYFCKDVDSLGQKVYRPVVLKPIPTKPAMPPPVFNVFGYL
PMRKRQLPASFWEEP

rs:XP_013106141 [XP_013106141] PREDICTED: transcriptional coactivator yorkie [Stomoxys calcitrans].>tr:A0A1I8NXU6_STOCA [A0A1I8NXU6] SubName: Full=Uncharacterized protein {ECO:0000313|VectorBase:SCAU003030-PA};
65..79
MSLSKSSASDDANKCSVKTDESTSAASKSSINLVVRNYQNSDENLQALFDSVLNPSESNRPLQVPFRMR
KLPNSFFTPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQTSVASSLSDLQTPAAVQAQQQSTNAINTQPTAPS
TTAAQAEPPRLQICHSRAHSSPASLQQTYIHGNVADDAAPPFLQQQGDRGGSSTSTSAAPGFPNNLIGYNAAAAA
AGLNASNILGLSGAGASVPLQTYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKTTQWEDPR
TQFKQQQALNAVSNTRATAKVNGTDNILASSNLGPLPEGWEQALTETGEVYFINHIDRTTSWNDPRLNDPRFPLL
IQKELKPKTEMSWVNATDIDKDSDIFKQKSRQKSLNKPNISLHMDPFLSGDNHARQESSDSGLSLSSNSFAVNPD
FITHMDNSMDCISENGSIIDNLDTTLQLNDNIIMINDVLNSPSNKPDNLEWYKLN PFRMRKLPNSFFTPP

rs:XP_008941138 [XP_008941138] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**A [Merops nubicus]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKVPECGWR
RGAEFRGHGPQPEAPDPSPHGGATSEKVLQTAEVEESPTGERVLQEQNLEATRPDQLPMRKRQLPASFWEEPRPA
QSLLARAFSTGPEGLPAPRDPPPYEGKKTKRSLDAASPESPPEPASRAGEKDPAEVLSGRVGTWTCCPFPCPGPG
VYQPPGALPPSPFPELGLWRKGAATLPAEVPHFCKEASGTGQKLYRPVVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_009044945 [XP_009044945] hypothetical protein LOTGIDRAFT_136317 [Lottia gigantea].>tr:V4BET5_LOTGI [V4BET5] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ESP04342.1}; 43..57
MSQDRSERKGSQIVHVRENSDSDMDALFSYGLNPTPDSNKSIPLRMRNLPASFFQPPEPHQAGKEGSTD
STGYSSSNPTSTPNFSVNHTRVRSSPASLSQGQTLSTAPPPPCSQHVRQHSYDLAEEPLPPGWSIGVTHVGQRYF
LK PLRMRNLPASFFQPP

rs:XP_009047301 [XP_009047301] hypothetical protein LOTGIDRAFT_230552 [Lottia gigantea].>tr:V4AX52_LOTGI [V4AX52] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ESP02143.1}; 119..133
MDIQTAMSDFGQSDETVNLLNFVDMASSNIKMALDRPSKSKRRVNHRKYLQKQLKRCDSKKPGGKDDLS
KTVAKSSRKETHQIGLQIKSLQALFDPRTLHDQHRHDGQQRTTFNLPKAPMRARNLPASFFSEPSSGKNNVGLGS
FVQVDAMSTMDANSQMCTLPTDTLESILGHNDLNELLSGTWPETSRESVRTPGSDGSVDTCSSRSFSDSDSFCAT
SPNPLTRSPSWSPCLNSVSANSPFIQEDTPNPLLFPYNANLDNFQHEFDPVNYRNIIEPEQTQFGQSGLPTFPQA
FTRTNSGYHSTSINSWQQYPLEPPFTF PMRARNLPASFFSEP

rs:XP_009048055 [XP_009048055] hypothetical protein LOTGIDRAFT_157604 [Lottia gigantea].>tr:V4B1Y6_LOTGI [V4B1Y6] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ESP01421.1}; 201..215
MTTFQNLPRNPVYNGVPPSLLRKTFQPVVYDSDLRFDHQIMDKFVDDDDFSDHDSHYSEDLEDDFRFQL
LNCPSGTNMTKQLLNFADLVNNDIKKFFGPKKGSDDTCDIYADKWKTIKSGRERYYRDLLRIAEGDNDLSKNGKD
NSEYNQKIVDNRHTFSGRLDERLGLGPLKELFDRGLHGTNSERKTRTGRASKYESVPMHQRRFPDSFWRPPSNVT
KRYPLYIPNTHVQNSPKPPDFSDLLETWTMAADSEFNADFSSDVNSPVESFVHRRL PMHQRRFPDSFWRPP

rs:XP_009052896 [XP_009052896] hypothetical protein LOTGIDRAFT_159959 [Lottia gigantea].>tr:V3ZYD2_LOTGI [V3ZYD2] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ESO96543.1}; 40..54
METFPLIKAQNTVLNDREGFQRLELPSRSLNVVTNHPSLPLRQRPLPASFWQEPNRQVLPRPEEIFPMC
VDPLLQRSFMDQMLAYKLYMDSLQIPPISPLSSPYPFTEFLYGLKHRTSIPPNKVPPPFPDIRPPFIQPNGHLEL
PTTKDTSVSVVKPIATKSQSLSRPGHRYHPFLPPK PLRQRPLPASFWQEP

rs:XP_009058783 [XP_009058783] hypothetical protein LOTGIDRAFT_123177 [Lottia gigantea].>tr:V3ZGV6_LOTGI [V3ZGV6] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ESO90458.1}; 168..182

MEKIPSPRINLDLNTLKSGLPLDSKGNKFQNFSNRSPRSEALTVLTNLSSPTDSNISPASRSDSLSPAT
SSSYATEHDHDYENIASPCSSTASGPTYVRPPGFEHHAQEILSSSVKIKKKKTSALFAHRESLRKREPTPPKKFE
RHLFNLYKEELPMKTYFHFSEPLPMKLRALPQSFWQQPNQPHQVSPGNIFRVLPPLSIKDTGEDVTGKYFGQLCA
MREILSGL   PMKLRALPQSFWQQP

rs:XP_009557523   [XP_009557523] PREDICTED: protein **FAM181**A [Cuculus canorus].   95..109
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHASKPPECSWR
RGAEDRGRGPQPEAPDPSPHGPDQVPMRKRQLPASFWEEPRPAQTLPARAFPAGPDVLLAPRDSPSYEGKKSKRS
VEAAGPENPPEPALCAGDKDPAGVLSGRVGAWTCCPFPCPGPGVFQPPSTLPLSPFPGLGLWRKSAAVLPAEVPH
FCKEADGAGQKLYKPVVLKPIPTKPTVPPPIFNVFSYL   PMRKRQLPASFWEEP

rs:XP_009688058   [XP_009688058] PREDICTED: protein **FAM181**A [Struthio camelus australis].>tr:A0A093GX64_STRCA [A0A093GX64] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFV74858.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSAECSVK
RGVEDRSRGSQPEAADSSHHCRAAPEKVLRTAEVEETFSGEQVLQDQNPEAARPDQVPMRKRQLPASFWEEPRPA
QSLLAKSFPVSLNGLPNSGDPLPYEGKKSRRSPEVASPESPPEPVQRGGEKDPAKAPGPPVSSRVASWTCCPFPC
PGQPLYQSPGALPPSSFPGLGLWRKSTALPGEMQHFCKEADSTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_009694265   [XP_009694265] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**A [Cariama cristata].   124..138
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKTPECGXG
PGXXXXXXXXXAPQPPGGGPATEKVLQTAEEEDSLSGERVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPAQSL
PARAFPTIPEGLPAPRDPPPYEAKKSKQSLDAVGPESPPEPVPHAGEKDPAGVLSGRVGAWTCCPFPCPGPGVYQ
PPGPLPPSPFPGLGLWRKSAAALPAEVPRFCKEADGTGQKLYRPVVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_020738154   [XP_020738154] protein **FAM181**B [Odocoileus virginianus texanus].   113..127
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDEETGTPAGALLAGAESGDAREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLNARKVPLRARNLPPSFFTEPSRPGGGGGCGPSGPGVS
LGDLEKGSEAAEFFELLGPDYGAGTEAGALLAAEPLDVFPAGAAVLRGPPELEPGLFEPQPAMVGSLLYPEPWSA
PGGPATKKPPLPAPRGGLTLNEPLRSVYPAAADSPGGDDGPGLLASFAPFFSDCALPPAPPPPPQQVSYDYSAGY
SRSAFAGLWRPDGAWEGAPGEEGAPRD   PLRARNLPPSFFTEP

rs:XP_009905592   [XP_009905592] PREDICTED: protein **FAM181**A [Picoides pubescens].>tr:A0A093H135_DRYPU [A0A093H135] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFV73095.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKTPECGWR
RGAEDRGRGPQPETPDLSSHGGAAAEKMLQTAEVEDSLTGEHVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPA
QSLPTRAFPSGPEGHPAPRDPPSYEGKKSKQSADTAGPESSPEPAPHAGEKDPAGVLSGQVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLGLWRKSAATMPVEMPHFCKEADGMGQKLYRPVVLKPIPTKPTVAPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_009952313   [XP_009952313] PREDICTED: protein **FAM181**A [Leptosomus discolor].>tr:A0A091P7F2_LEPDC [A0A091P7F2] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFQ03311.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGAEDRGRGPQPEAPDPSSHGGAAAEKMLQTAEAEESLTEERVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPA
QSLLSRAFPARPEGLPNPRDPPPYEGKKSKWSPDAAGPESPHEPAPHAGEKDPAGVLSGRVGAWTCCPFPCPGPG
VYQPPGTLPPSPFPGLGLWRKSAAALPAEVPHFCKEADGTGQKLYRPMVLKPIPTKPAVPPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_010190511   [XP_010190511] PREDICTED: protein **FAM181**A [Mesitornis unicolor].>tr:A0A091SJV8_9GRUI [A0A091SJV8] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFQ40565.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPSECGWR

RGAEDRGRGPQPEAPDPSPHGGAAAEKVLRTAEAEESLAREQVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPT
QNLQARAFPPGPEGLPAPRDPPPYEGKKSKRSSDTASPEIPPESAPHIGEKDPAGVLSGRMGAWTCCPFPCTGPG
VYQPPGALPPSPFPGLGLWRKSAAVLPAEVPHFCKEVDGTGQKLYRPVVLKPIPTKPAVPPPIFNVFSYL
PMRKRQLPASFWEEP

rs:XP_010361180 [XP_010361180] PREDICTED: protein **FAM181**B [Rhinopithecus roxellana]. 221..235
MAGQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPCAPTVAAPAHCK
AVPRREAAQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVVAPVAGLGGAGTGGAGGDAVGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPHQVSYDYSAGYSRNAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_010377339 [XP_010377339] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Rhinopithecus roxellana].>rs:XP_025212438 [XP_025212438] transcriptional coactivator YAP1 isoform X1 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_010377340 [XP_010377340] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Rhinopithecus roxellana].>rs:XP_025212439 [XP_025212439] transcriptional coactivator YAP1 isoform X2 [Theropithecus gelada].>tr:A0A2K6PTL4_RHIRO [A0A2K6PTL4] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSRROP00000019863}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_010377341 [XP_010377341] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Rhinopithecus roxellana].>rs:XP_025212440 [XP_025212440] transcriptional coactivator YAP1 isoform X3 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_010377342 [XP_010377342] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Rhinopithecus roxellana].>rs:XP_025212441 [XP_025212441] transcriptional coactivator YAP1 isoform X4 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF

NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_010377343 [XP_010377343] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Rhinopithecus roxellana].>rs:XP_025212443 [XP_025212443] transcriptional coactivator YAP1 isoform X5 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010377344 [XP_010377344] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Rhinopithecus roxellana].>rs:XP_025212444 [XP_025212444] transcriptional coactivator YAP1 isoform X6 [Theropithecus gelada].>tr:A0A2K6PTJ7_RHIRO [A0A2K6PTJ7] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSRROP00000019865}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010377345 [XP_010377345] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Rhinopithecus roxellana].>rs:XP_025212445 [XP_025212445] transcriptional coactivator YAP1 isoform X7 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010377346 [XP_010377346] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Rhinopithecus roxellana].>rs:XP_025212446 [XP_025212446] transcriptional coactivator YAP1 isoform X8 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010377347 [XP_010377347] PREDICTED: transcriptional coactivator YAP1 isoform X9 [Rhinopithecus roxellana].>rs:XP_025212447 [XP_025212447]

transcriptional coactivator YAP1 isoform X9 [Theropithecus
gelada].>tr:A0A2K6PTL3_RHIRO [A0A2K6PTL3] SubName: Full=Yes associated
protein 1 {ECO:0000313|Ensembl:ENSRROP00000019866}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010377349 [XP_010377349] PREDICTED: transcriptional coactivator
YAP1 isoform X10 [Rhinopithecus roxellana].>rs:XP_025212448 [XP_025212448]
transcriptional coactivator YAP1 isoform X10 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010377350 [XP_010377350] PREDICTED: transcriptional coactivator
YAP1 isoform X11 [Rhinopithecus roxellana].>rs:XP_025212449 [XP_025212449]
transcriptional coactivator YAP1 isoform X11 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_010377351 [XP_010377351] PREDICTED: transcriptional coactivator
YAP1 isoform X12 [Rhinopithecus roxellana].>rs:XP_025212450 [XP_025212450]
transcriptional coactivator YAP1 isoform X12 [Theropithecus gelada].
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGQPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_010332927 [XP_010332927] PREDICTED: transcriptional coactivator
YAP1 [Saimiri boliviensis boliviensis].>rs:XP_021527402 [XP_021527402]
transcriptional coactivator YAP1 isoform X9 [Aotus nancymaae]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGG
TQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLP
SQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_010348846 [XP_010348846] PREDICTED: protein **FAM181**A isoform X1 [Saimiri boliviensis boliviensis].>tr:A0A2K6SBJ9_SAIBB [A0A2K6SBJ9] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSSBOP00000004749};225..239

MLCIWRGAPDWPEGPPSSGELSSIQPTQGLHNCFQPDGARPAVPGPVPGLQRGTCRVTLVGPRPAPLVS
SVSFLGAASHQQSPPSSWKALCGGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRF
SQKYSRLPRGLPGRAAEPYLKRGPEDRPGRLLLDLGPESSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAA
QAGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETASVPMSPSALAEKESLK
MPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAYLCKDADGLGQKVCRPMVLK
PIPTKPAVPPPVFNVFGYL PMRKRQLPASFWEEP

rs:XP_003939877 [XP_003939877] PREDICTED: protein **FAM181**A isoform X2 [Saimiri boliviensis boliviensis]. 129..143

MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGPEDRPGRLLLDLGPESSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAAQAGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETASVPMSPSALAEKESLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAYLCKDADGLGQKVCRPMVLKPIPTKPAVPPPVFNVFGYL

PMRKRQLPASFWEEP

rs:XP_010834522 [XP_010834522] PREDICTED: protein **FAM181**A [Bison bison bison]. 130..144

MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRPLPLESGHGSSPGGGGGCKEKALGNLDREESLSKEQTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL

PMRKRQLPASFWEEP

rs:XP_010967024 [XP_010967024] PREDICTED: protein **FAM181**A [Camelus bactrianus].>rs:XP_006184238 [XP_006184238] PREDICTED: protein **FAM181**A [Camelus ferus].>tr:S9X237_CAMFR [S9X237] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EPY81629.1}; 129..143

MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPSRGAEPHLK
RVPEDRPGRLPRDSGHNSSPSGGGGYKEKALGNPYREECLPKEQTLQGQDPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGGLGPREGLPYEGKKHCKGLEPLGPETAPLPTEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYP
GPPGALPQSPVPGLGLWRKSSISPGELVHFCKDVEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL

PMRKRQLPASFWEEP

rs:XP_010971617 [XP_010971617] PREDICTED: transcriptional coactivator YAP1 [Camelus bactrianus]. 13..27

MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL

PMRLRKLPDSFFKPP

rs:XP_010971746 [XP_010971746] PREDICTED: protein **FAM181**B, partial [Camelus bactrianus]. 66..80

GPRSLQSRSLAALFDSLRHVPGGAESAGATVAAPAAGLGRAGAGGAGGDAAGPAGGPLVPGARKVPLRA
RNLPPSFFTEPSRAGGGVCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTETGVLLAAESLDVFPTGAAALRG
PPELEPGLFEPPPAMVGSLLYPEPWSAPGCPPTKKPPLAAPRGGLTLNEPLRPLYPAAADSPGGEDGPGLLATLA
PFFSDCALPPPPLPQQVSYDYSAGYSRTAYSSLWRADGVWEGASGEEGAHRD PLRARNLPPSFFTEP

rs:XP_004342951 [XP_004342951] hypothetical protein CAOG_07866 [Capsaspora owczarzaki ATCC 30864].3..17

MPPLRDRNLPASFFRSPSSAAADRIDSSAMSEAGASHSRDSSLDSGISFVPHQPQLIMNGSTFPPVAFH
SRQSSAGSSEPTSQSHNLQQQLLLLQQQQQQQQLLYQQQQQQLSLPQQSGQMPGQSPGLLVPMYNQLQHSYQT
SQSSPFPPATPSSAHSSTFFSREPSISSFLEMSLHFEQQQQQPQQHSRPLSHSNSGNVLSAQANNPGLPASGNSS

NSLQRLSASSLDESPLPPGWEKGIKDGLPFFIDHNNKTTTWVDPRTDRATPGTQGLSERKRVPDVLSDPLLNPTL
NPLPAGWEMAMHSDGIPYFINHRKRTTTWIDPRTDVDMQEISPRNTPFSSFDSALPDPGYDQMTGNSSPLASFNL
TSPPPPVSPGITGMDSQSLAGLSQRELQARRMMLQKEQIRLKQMQLLQEELEIQRAQRNLAVLETTTRGGSAKLP
PPQLTVSECLTTTTATATADVTSRRSDQPSTRPCSS   PLRDRNLPASFFRSP

rs:XP_011305607   [XP_011305607] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Fopius arisanus].>tr:A0A0C9QIP1_9HYME [A0A0C9QIP1]
SubName: Full=Yap1_0 protein {ECO:0000313|EMBL:JAG73151.1};   46..60
MALNTDVDQLTKGNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTIISNGPGSNSNGGNTNGNGNQTSVPAGLTVAHPRAHSSPASLQQTYAAAQATQHAPQPHAR
HVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQVYFLNHLTRTTTWEDPRKTAAAANVTTIAAAENGKSPAGA
GANALGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPTNWIQPPGATGLQSNQTIQVC
QQKLRLQSLQMERERLKQRQAEIMRQQELMLRQSNTDASMDPFLSGMSEQHARQESADSGLGLGSAYSLPHTPED
FLSNIDDNMDATSDGGAPMETPDISTLSDNIDSTDDLVPSLQLGEEFTSDILDDVQSLINPSSTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_011305608   [XP_011305608] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Fopius arisanus].>tr:A0A0C9RQQ6_9HYME [A0A0C9RQQ6]
SubName: Full=Yap1_1 protein {ECO:0000313|EMBL:JAG80602.1};   46..60
MALNTDVDQLTKGNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTIISNGPGSNSNGGNTNGNGNQTSVPAGLTVAHPRAHSSPASLQQTYAAAQATQHAPQPHAR
HVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQVYFLNHLTRTTTWEDPRKTAAAANVTTIAAAENGKSPAGA
GANALGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPTNWIQPPGATGLQSNQTIQVC
QQKLRLQSLQMERERLKQRQAEIMRQQELMLRQSNTDASMDPFLSGMSEQHARQESADSGLGLGSAYSLPHTPED
FLSNIDDNMDATSDGGAPMETPDISTLSDNIDSTDDLVPSLQ   PLRMRNLPDSFFNPP

rs:XP_011501142   [XP_011501142] PREDICTED: transcriptional coactivator
yorkie isoform X1 [Ceratosolen solmsi marchali].   51..65
MALNQDVADVGATGGAKSNLVVRIDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGS
KSPSISHSRENSADSAFGAGVAGVANGSGVGGATSPGAAAAAAAAAAAAAAAAAPSAAPAGAAQVPQGLTVAHPR
AHSSPASLQQTYASAQQQNQHAPQPHSARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTT
TWEDPRKTAAAASVAAVAAAVESGKTSTAAAGSNALGPLPDGWEQARTPEGEIYFINHQARTTSWFDPRIPTHLQ
RAPTSGAMLPQNWQIQQQAGGGLQSSQTLQACQQKLRLQSLQMERERLKQRQQEIMRQVSSQELMLRQSTTDAAM
DPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSEGAPMETPDLSTLSDNIDSTDDLVPSL
QLGEDFSSDILEDVQSLINPVGNTTKPENILTWL PLRMRNLPDSFFNPP

rs:XP_011501143   [XP_011501143] PREDICTED: transcriptional coactivator
yorkie isoform X2 [Ceratosolen solmsi marchali].   51..65
MALNQDVADVGATGGAKSNLVVRIDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGS
KSPSISHSRENSADSAFGAGVAGVANGSGVGGATSPGAAAAAAAAAAAAAAAAAPSAAPAGAAQVPQGLTVAHPR
AHSSPASLQQTYASAQQQNQHAPQPHSARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTT
TWEDPRKTAAAASVAAVAAAVESGKTSTAAAGSNALGPLPDGWEQARTPEGEIYFINHQARTTSWFDPRIPTHLQ
RAPTSGAMLPQNWQIQQQAGGGLQSSQTLQACQQKLRLQSLQMERERLKQRQQEIMRQQELMLRQSTTDAAMDPF
LSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSEGAPMETPDLSTLSDNIDSTDDLVPSLQLG
EDFSSDILEDVQSLINPVGNTTKPENILTWL   PLRMRNLPDSFFNPP

rs:XP_011571321   [XP_011571321] PREDICTED: protein **FAM181**A [Aquila
chrysaetos canadensis]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECSWR
RGAEERGRGPQAEAPDPSPHGGAAAEKVLQAAEAEDSLTGERVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
QSLPARAFAAGPEGLPAPRDPPPYEGKKSRRSPDAAGPESPPEPALHAGEKDPAGVLSGRVGAWTCCPFPCPGPG
VYQPPGTLPPSPFPGLGLWRKSAAALPAEVPHFCKEADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_011585004   [XP_011585004] PREDICTED: sentrin-specific protease 3-
like [Aquila chrysaetos canadensis].   188..202
MHGRAAAPRVSPGPGVPLHADMAAGVIQPLAELRLPSPFPHGLLLPTRPEPDFPDLSEEEEEEEEEEEE
EEEAAEESMRPELAIPSAAETTLRLLKFSELISCDIQRYFGRRGREEAAGSRSAPEDCGSPRHAEAQPETAAPQG

GPGAVHRLGPLAELFEYGVHRCLPPRAAGSKTQRLERKYGHITPMHRRKLPPSFWREPGPSPASLLHAGTPDFSD
LLANWTAEPGPELPGAGRELPPEPGRPELEAEPFVGL PMHRRKLPPSFWREP

rs:XP_011686481 [XP_011686481] PREDICTED: transcriptional coactivator
yorkie [Wasmannia auropunctata]. 46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVTATPNGGGGGVPNGGTSSGGGGGGGSAGNAAGAAGAGGGSGGAGGGANGTVSAIAAAAV
AAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIY
FLNHLTRTTTWEDPRKTAAAASVAAVAAAVESNKSNSLGPLPDGWEQARTAEGETYFINHQTRTTSWFDPRIPSH
LQRTPASGAMLPQNWQLQQPTGIQSNQSLQACQKQKIRLQSLQMERERLKQRQQEIMRQQEMMLRQSNTDAVMDP
FLSGINEQHARQESADSGLGLGSAYPLPQAGTEDFLNIDENMDGTSDGGAPMDTPDISTLSDNIDTTDDLLPSLH
LNEDFTTDILDDVQSLINPNPTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_017345841 [XP_017345841] PREDICTED: protein **FAM181**B [Ictalurus
punctatus].>tr:A0A2D0STK5_ICTPU [A0A2D0STK5] SubName: Full=protein **FAM181**B
{ECO:0000313|RefSeq:XP_017345841.1}; 155..169
MAVQAATMNSQFLNFCFPGSVMEYEVEKGLDGAFLGEVDCEGDFREATSDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIMGLGNGTPQEAYKSHDSTSTPTSIIQNKTPKRDGAQANLQSKSLAALFNHAK
DLRGEKTKKPPLRHRNLPSSFFTEPANNARVTSTSGMSLKDLERGNPDATEFFELLGPDYSNMVSEQELFHTMPN
RVQQQGTVGLEPISFDSHNFVTGGFLYTEPWATSSGVSKKTGDIKTVPGQSSLYGNTDSSCPVPIEQNSTCSLTF
PNLFTDCSVSQVPYDLASGYSRGSFPSL PLRHRNLPSSFFTEP

rs:XP_011794294 [XP_011794294] PREDICTED: protein **FAM181**B [Colobus
angolensis palliatus]. 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPSAPTVAVPAHGK
AVPRREASQAAAASSLQSRSLAALFDSLRHVPGGAEPAGGAVVAPVAGLGGSATGGAGGDAAGPAGATAVTGARK
VPLRARNLPPSFFTEPSRAGGSGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPPHQVSYDYSAGYSRNAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_011847115 [XP_011847115] PREDICTED: protein **FAM181**A isoform X1
[Mandrillus leucophaeus]. 179..193
MMQPTESTEGPGRKRQGTAKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVKMLLNFVNLASS
DIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDLGPDSSPGGGGG
CKEKALRNPYREECLAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKK
NCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWKK
SPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_011847116 [XP_011847116] PREDICTED: protein **FAM181**A isoform X2
[Mandrillus leucophaeus].>rs:XP_011847117 [XP_011847117] PREDICTED: protein
FAM181A isoform X2 [Mandrillus leucophaeus].>rs:XP_011847119 [XP_011847119]
PREDICTED: protein **FAM181**A isoform X2 [Mandrillus leucophaeus]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_011847122 [XP_011847122] PREDICTED: protein **FAM181**A isoform X3
[Mandrillus leucophaeus]. 165..179
MACFVPQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRR
SVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREEC
LAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVP
VPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKD
VDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_011806945 [XP_011806945] PREDICTED: protein **FAM181**A isoform X1
[Colobus angolensis palliatus]. 177..191

MQPTESTEGPGRKRQGTAKQVSLPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVKMLLNFVNLASSDI
KAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRATEPYLKRGSEDRPGRLLLDLGPDSSPGGGGGCK
EKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNC
KGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWKKSP
AFPGELVHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_011806946 [XP_011806946] PREDICTED: protein **FAM181**A isoform X2 [Colobus angolensis palliatus].>rs:XP_011806947 [XP_011806947] PREDICTED: protein **FAM181**A isoform X2 [Colobus angolensis palliatus].>rs:XP_011806949 [XP_011806949] PREDICTED: protein **FAM181**A isoform X2 [Colobus angolensis palliatus]. 129..143

MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRATEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELVHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_011782007 [XP_011782007] PREDICTED: transcriptional coactivator YAP1, partial [Colobus angolensis palliatus]. 48..62

PAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSR
QASTDAGTAGAVTPQHVGVHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQSLQQSSFEIPDDVPLPADWEMAK
TSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTT
SWLDPRLDPRFAMNQRISQSDPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMR
NINPSTANSPKCQELALRSQLPTLEQDAGTPNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSS
YSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSD
ILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017546373 [XP_017546373] PREDICTED: protein **FAM181**A [Pygocentrus nattereri]. 117..131

MASSDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCSRMPRCHTHRVTDSAP
KVTEDKPATLTQESAASLSHANGKREPRTERLDLDPDPEDPQQTGQVPMRKRQLPASFWEEPRSSRGERPCFHHA
WKRNSHVGSHAYESDGEKSARIYDERKANLLPSARRCSPDLEPLRVALTCGCTPFQYRGSQALHTHAHTHLLLPQ
VPLTHVGLRAKVNGTDLDMQKMPDGLKNNTAHVVVKPIPTKPVSASIFSVFGFI PMRKRQLPASFWEEP

rs:XP_017552201 [XP_017552201] PREDICTED: protein **FAM181**B [Pygocentrus nattereri]. 156..170

MAVQAAIMNSQFLNFCFPGSVMEYEVEKGLDGSLLGEADCEDDFRETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIIASGNAATQEPCKGQDSPQAPTSTLQSKTPTKRDGSQANLQSKSLAALFNPA
KDLRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGNPDAAEFFELLGPDYSNMVSEQELFQSTP
IRVQQEGTGGPEPGSFDSHPFVTGGFLYAEPWDTSSNVAKKTGDMRTVPGQPHLYGNTDSSGPVQVEQSSPCALT
FPNFFTDCSVSQVSYDLASGYSRGSFPTL PLRHRNLPPSFFTEP

rs:XP_012228600 [XP_012228600] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Linepithema humile]. 46..60

MALNQDVDQLSKSNLVVRIDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAVTATPSNGGGSGAPNAGTNGAGGGGGGGGGGGGGGGNAAGAAGTGGGAGAGSGTNSAAGA
VAAAAAAAAAAAAVAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPH
GWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSTGNSLGPLPDGWEQARTAEGEIYFINH
QTRTTSWFDPRIPTHLQRTPASGAMLPQSWLQQSTGGGIQSNQSLQACQQKLRLQSLQLERERLKQRQQEIMRQQ
EMMMRQTTDAAMDPFLSGINEQHARQESADSGLGLSSAYSLPHTPEDFLANMDDNMDGTNDRHCVLNDLTKRLYR
SHKYINGSAPMETPDLSTLSDNIDSTDDLLPSLQLSEDFSSDILDDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_012228601 [XP_012228601] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Linepithema humile]. 46..60

MALNQDVDQLSKSNLVVRIDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAVTATPSNGGGSGAPNAGTNGAGGGGGGGGGGGGGGGNAAGAAGTGGGAGAGSGTNSAAGA
VAAAAAAAAAAAAVAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPH
GWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSTGNSLGPLPDGWEQARTAEGEIYFINH

QTRTTSWFDPRIPTHLQRTPASGAMLPQSWLQQSTGGGIQSNQSLQACQQKLRLQSLQLERERLKQRQQEIMRQQ
EMMMRQTTDAAMDPFLSGINEQHARQESADSGLGLSSAYSLPHTPEDFLANMDDNMDGTNDGSAPMETPDLSTLS
DNIDSTDDLLPSLQLSEDFSSDILDDVQSLINPNTTKPENVLTWL   PLRMRNLPDSFFNPP

rs:XP_009279071   [XP_009279071] PREDICTED: protein **FAM181**A [Aptenodytes forsteri].>tr:A0A087R539_APTFO [A0A087R539] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFM08593.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGTEDRGRGPQPEAPDPSPHSGAAAEKVLRTAEAEESLTGEWVLQEQNPEAVRPDQLPMRKRQLPASFWEEPRPA
QSLPARAFPAGPEGLPAPRDPPPYKGKKSKRSSDAAGPESPPESAPHTGEKDPAGVLSGRMGTWTCCPFPCPGPG
VYQPPGALPPSPFPGLGLWRKSAAALPAEVPHFCKEADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_003254700   [XP_003254700] PREDICTED: protein **FAM181**B [Nomascus leucogenys].   221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGDLDKGCCFEDDETGAPAGALLSGVEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AAPRREASQAAAAAFLXXXSLAALFDSLHHVPGGAEPAGGAVAAPAAGLGGAGTGGAGGDAAGPAGATAIPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD   PLRARNLPPSFFTEP

rs:XP_004093219   [XP_004093219] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**A [Nomascus leucogenys].   129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGXGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTPVPMSPRVLVEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKDAGGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_012497244   [XP_012497244] PREDICTED: protein **FAM181**B [Propithecus coquereli]. 221..235
MAVQAALLSTHPFVSFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAAPGPPSPSAADTPAKRPLVAPSAPAVAVPAPGK
PAPRREASQAAAAASLQSRSLAALFDSLRHLPGDAEPAGAAVAAPAAGLGGAGAGGAGGDGAGPSGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCSPSGPGVSLGDLEKGAEAAEFFELLGPDYSAGTEAAVLLAAEPLDAFPAGA
AVLRAPPELEPSFFEPPPAVVGNLLYPEPWSVPGCPATKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEEGPGP
LASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYASLWRPDGVWEGPPGEEGAHRD   PLRARNLPPSFFTEP

rs:XP_012510651   [XP_012510651] PREDICTED: protein **FAM181**A [Propithecus coquereli].>rs:XP_012510652 [XP_012510652] PREDICTED: protein **FAM181**A [Propithecus coquereli].   129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLK
RGSEDRPGRLLLDPGPESSPGGGGGCKEKAPGSPYGEECLSKEQVLQGQSPEATRPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGGLGPREGPPYEGKKHCKGLEPLGPEVALVPMSPRALAEKEPLEMPGVSLVGRGNAWSCCPLQYH
GQPIYPGLPGALPQSPVPSLGLWRKSPAFPGELAHLCKDVDGLGQVCRPVVLKPIPTKPAMAPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_012514677   [XP_012514677] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Propithecus coquereli]. 85..99
MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012514678 [XP_012514678] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Propithecus coquereli]. 85..99

MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL

PMRLRKLPDSFFKPP

rs:XP_012514679 [XP_012514679] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Propithecus coquereli]. 85..99

MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL

PMRLRKLPDSFFKPP

rs:XP_012514680 [XP_012514680] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Propithecus coquereli].>tr:A0A2K6FBS7_PROCO [A0A2K6FBS7] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSPCOP00000011436}; 85..99

MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL

PMRLRKLPDSFFKPP

rs:XP_012514681 [XP_012514681] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Propithecus coquereli]. 85..99

MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012514683 [XP_012514683] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Propithecus coquereli].>tr:A0A2K6FBT2_PROCO [A0A2K6FBT2] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSPCOP00000011440}; 85..99

MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012514684 [XP_012514684] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Propithecus coquereli]. 85..99

MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012514685   [XP_012514685] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Propithecus coquereli]. 85..99
MDPGQQQPPQPAPQGQGQQPAQTPQGQGPPSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_002169246   [XP_002169246] PREDICTED: uncharacterized protein
LOC100210921 [Hydra vulgaris].   190..204
MINEDVLATKDLENDKSDKDSGLIDDYIDFQLISEAFNVLPDEKTLSIDYDLELDLSDENFGSYNDFIV
DNHEASKTCKVDSNNNTNSNINTKKIGVEENFVISDTNKNTLLPGKYREFTKEQARQWRRKRILNTYNQNTIKKK
DHSVRVLPNNKLQPLFNVPSKPTVQEKLKDPLLAGEKIGANRGPVPMKHRALPQSFWKEPQAPQSSSLAGSHYSV
LPPLFASDESSNIQDMRPVTPPEETNRSPRHKKKVVESEKADTALLFSLFDHLENKIDEKLIVKRGRPKKQSTDQ
KQTTKQKPKSNNISKDNDPCIVDALADKLFPELSLHQAKEKINNLAAIIKIGKQTSTIVQFPAVNHNYPEIHQNY
SEMLNELIAHM PMKHRALPQSFWKEP

rs:XP_012560142   [XP_012560142] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Hydra vulgaris].   43..57
MDMNSTQRQGNFVLHVRQDSDTDLEQLFKNSVSTNKDIPRSKPFRDRKLPASFFRPPPSLETDQTAPIH
TRARSLPSNIGQIAQDQVILQQQQLQQQHPQNNFLLTPSHQRTQSYGTLESNYLPSGCEMRTTASGQNHQNQSTS
WQDPRKAQSMTVLPANPQNLLMDDLPEGWERAVTAEGEVYFINHQTKTTSWFDPRLNRPNNNLLLGGTNIQYYQQ
EKRHRQQQIQNQLLEREFLIHQRMNGQHTDSVLNNNSLINNLVREKYTAHMNSSVLGRGSSVDSGLDGMESYLTS
TSTDGLNDMDTADVDRNNQFDKNTSMEQGICFNNRLPEFFDSLQASNVDLDILEDGSELSSDLEAINTEALNDVD
MILSPNNKPNAYMTWL PFRDRKLPASFFRPP

rs:XP_004649371   [XP_004649371] PREDICTED: protein **FAM181**A [Jaculus
jaculus].   129..143
MAADSDVKTLLSFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQRCPRLPRGLPGRVAEPHLQ
RGPEDRPTRLPLHLGPDSSLDRAGGCKEQALGGPFREECLSMEHSLRGPSPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEVGFSSRETPPYESKKNCKGLESLGPDTAPVPMSPRALADKEPLRMPGVSLVGCLDAWSCCPFQYH
GQPIFPCPPGALPQGPMPNLGLWRTSPTLPGELAHFCKDVDSSGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_004658183   [XP_004658183] PREDICTED: protein **FAM181**B [Jaculus
jaculus].   117..131
MAVQAALLSSHPFVPFGFGGSADGLGGAFGAALEPGCCFEDDESGAAAGALLSGAEGGDVREATRDLLS
FIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSVSAVPGTKKVPLRARNLPPSFFTEPSRTAGGVGGCGPS
GPGVSLGDLEKGAEAGEFFELLAPDYGGGGDAGVLLSAEPLDVFPGAAAGLRGPLELEPGLFEPPPAVVENLLYP
EPWSAPSCPQTKKPPQAAARAGGLTLNEPLRPLYPAAAADSPGAEDAPAGPLASLAPFFPDCALPPPHPLSYDYG
GAGYGRGAFSGLWRPDGAWEGAPGDEAPHRD   PLRARNLPPSFFTEP

rs:XP_004661968   [XP_004661968] PREDICTED: transcriptional coactivator
YAP1 [Jaculus jaculus]. 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKPHSRQASTDAGTAEALIPQSIHVRAHSSPASLQLGAVSP
GTLTPTGVVSGPAGTPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVAA
PPSSAVQQNMMSPASGPLPDGWEQALTQDGEIYYINHKNKTTSWLDPRLDPCFAMNQRISQSAPVKQPPPLAPQS
PQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQS

RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012791995 [XP_012791995] hypothetical protein MS3_00346
[Schistosoma haematobium].>tr:A0A094ZHC0_SCHHA [A0A094ZHC0] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:KGB32229.1}; 38..52
MEGYDSRKPPSVRVTVLEDPNSSLQELFNPASQRQQVPLHQRNLPKSFFVPPGDVNDNSRLSKLNSVHS
NERNSADFVVFHSKANSSPACLDAALRTSVSANVPNHSHQKSLDVASKYKTEFSPDFAFSGSCSPGLFQGQRFDP
RIPEKFQKWGMTPEELEQVHLRYAKQFLCTIPSSNLNVCVQQVGEFIKILYDMSAR PLHQRNLPKSFFVPP

rs:XP_004698832 [XP_004698832] PREDICTED: protein **FAM181**A [Echinops
telfairi]. 131..145
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAADPHTK
RGLEDRPARLPVDGQVPCPAVGRGCQEKALGNPAAGGEVLPLQQEQTLQGQHAAAAQPGQVPMRKRQLPASFWKE
PRPVHSFPLGLEGGLGPGEGPPYEGKQTCQGLEPLAPGSPRTLVEERLKVPAVARGGRINTWSCCPFQYHGQPMY
PGPPGSLPQGAVPSFGLWRASLASPAELDGPGQKVYRPVVLKPIPTKPALAPPIFNVFGYL
PMRKRQLPASFWKEP

rs:XP_012870448 [XP_012870448] PREDICTED: protein **FAM181**A [Dipodomys
ordii].>tr:A0A1S3F1G0_DIPOR [A0A1S3F1G0] SubName: Full=protein **FAM181**A
{ECO:0000313|RefSeq:XP_012870448.1}; 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPRRLPLHLGPDCSPSGSGGYKEKALGHPFRQECLPTELALHGQSPEAAKPGQVPMRKRQLPASFWEEPR
PTHSYAVGLEGGLGSREGPPYENKKTCHGLEPLGLESTPVPMSPRVPADKNPLGMPGMSLGGRMDAWGCCPFQYH
GQPIFPGPPGTLPQSPVPSLGLWRKSPASPGELVHFCKDVDGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_012869428 [XP_012869428] PREDICTED: protein **FAM181**B [Dipodomys
ordii].>tr:A0A1S3EYD7_DIPOR [A0A1S3EYD7] SubName: Full=protein **FAM181**B
{ECO:0000313|RefSeq:XP_012869428.1}; 141..155
MAVQAALLSTHPFVPFGFGGPQDGLGSAFAGLDKGCCFEDEETGAPTGALLSGAEGGDLREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSAGGAGGDAAGPAGGTPAPGARKVPLRA
RNLPPSFFTEPSRAGGGSSGCSPSGSGVSLGDLEKGAEAVEFFELLGSDYGTGAEAGVLLAAEPLDVFPAGAAVL
RAPLELEPGLFEPPPALVGNLLYPDPWSTPSGPPTKKSSLTAARGGLTLNEPLRPLYPAAAAADVPGAEDGPGHL
ASFAPFFADCALPPAPPQVSYDYSAGYSRTAYASLWRQDGVWEGAPGEEGTHQD PLRARNLPPSFFTEP

rs:XP_013084689 [XP_013084689] PREDICTED: transcriptional coactivator
YAP1-like [Biomphalaria glabrata].>tr:A0A2C9JV78_BIOGL [A0A2C9JV78]
SubName: Full=Uncharacterized protein {ECO:0000313|VectorBase:BGLB008553-
PB}; 41..55
MSQDRTGPIVHVRENSDTELEALFNIAMNPSLSETHNKTVPLRMRNLPASFFRPPEPPKQMQQPLGVSK
DNTIDAPGYHGAVNSSSMNIAHTRAHSSPASLQQSLSAAPPPPPTSHVRQHSYDALDEQPLPAGWDMAKTPQGQR
YYLNHVLQITTWNDPRKTHSTNPATISSSNNNNNNTTTSNLNSLPQTGSPAPSTQPTLTAPINVDKVPLPPGWER
AYTAECEVYFINHIERTTSWFHPSIPVHLQRPGMKFQSQNATSGSNLLTSQQDQLKQLKLQQLQMEQEALKKRQD
EIARQEMALRAQVGESVLGTPGDITSLSQSSELTTDPFFGQTGTSDHHSRQESADSGLGGMGTSYSLPRTPDDFL
GNMEDMDTQDGGPKLSGQSDFGSMDMGGVSDVGDHLNMDSDDLVPSLQEEISSELLKDVEKVLGNKDHPLTWL
PLRMRNLPASFFRPP

rs:XP_018100216 [XP_018100216] PREDICTED: transcriptional coactivator
YAP1-A isoform X1 [Xenopus laevis]. 54..68
MEPGSQQQPSAPAQQPPPVGHQVVHVRTDSETDLEALFNAVMNPKNANLPQTLPMRMRKLPDSFFKQPQ
PEAKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLAAVSPGALSPQGVVTGLAPPSAPHLRQSSYEIPDDVPLP
PGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTGPLPDGWEQALTPEGEAYFIN
HKNKSTSWLDPRLDPRFAMNQQRLSQNAPVKAPPALPPPSPQTGVLGSGGNQQMRLQQLQMEKERLRLKHQELLR
QELALRSQIPPMEQDGGTQNPVCTTGISQELRTMTMNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLN
SVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMETVLAAT
KLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_018100217 [XP_018100217] PREDICTED: transcriptional coactivator
YAP1-A isoform X2 [Xenopus laevis]. 54..68
MEPGSQQQPSAPAQQPPPVGHQVVHVRTDSETDLEALFNAVMNPKNANLPQTLPMRMRKLPDSFFKQPQ
PEAKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLAAVSPGALSPQGVVTGLAPPSAPHLRQSSYEIPDDVPLP
PGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTAMNQQRLSQNAPVKAPPALPP
PSPQTGVLGSGGNQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQIPPMEQDGGTQNPVCTTGISQELRTM
TMNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTN
VDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMETVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_018100218 [XP_018100218] PREDICTED: transcriptional coactivator
YAP1-A isoform X3 [Xenopus laevis]. 54..68
MEPGSQQQPSAPAQQPPPVGHQVVHVRTDSETDLEALFNAVMNPKNANLPQTLPMRMRKLPDSFFKQPQ
PEAKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLAAVSPGALSPQGVVTGLAPPSAPHLRQSSYEIPDDVPLP
PGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTAMNQQRLSQNAPVKAPPALPP
PSPQTGVLGSGGNQQMRLQQLQMEKERLRLKHQELLRQELALRSQIPPMEQDGGTQNPVCTTGISQELRTMTMNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLG
TLEGEAMNVEGEELMPSLQEALSSDILNDMETVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_018103334 [XP_018103334] PREDICTED: protein **FAM181**B-like [Xenopus
laevis].>tr:A0A1L8HJT7_XENLA [A0A1L8HJT7] SubName: Full=Uncharacterized
protein {ECO:0000313|EMBL:OCT96352.1}; 158..172
MAVQAPIMNHQFMSLYIPASIADYEKSYQEGVDYLGAVESGDFKETTKDLLSFINTASSNIKMALDKPV
KSKRKVNHRKYLQKQIKRCTGLMGSGNLNQGSPKRSPTSPGNSSMSPSGFPCKPPTKRDSTQSNMQSKSLAALFD
SAKEIRGERCKKVPLRNRNLPPSFFTEPETPSLGLLSNSGVALRDLGKCNQETLEFFDFLNSDYNNTSDQEIIQG
ASVRVHQDVSAEQSLYEPHHLLSGFLYSDMWNPCNQVKKSPVGSCNLGFNETLKSAPLQGALYPNNQDPAMASPV
DDTCPNLTTYTPCFPSDCSLPQIFYDYNSQNCNRISYPVM PLRNRNLPPSFFTEP

rs:XP_018103464 [XP_018103464] PREDICTED: transcriptional coactivator
YAP1-B isoform X1 [Xenopus laevis].>tr:A0A1L8HAQ0_XENLA [A0A1L8HAQ0]
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:OCT93187.1};
54..68
MEPGSQQQPSAPGQQPPPVGHQIVHVRTDSETDLETLFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPE
PKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPQGVITGLAPPSAQHLRQSSYEIPDDVPLPPG
WEMAKTPSGQRYFLNHVDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTGPLPDGWEQALTPEGETYFINHK
NKTTSWLDPRLDPRFAMNQQRLSQSAPVKSPPALQPQSPPSGVLGSGGNQQMRLQQLQMEKERLRLKHQELLRQV
RPQELALRSQIPPMEQDSGPPNPVCSSGISQELRTMTMNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDF
LNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMETVLA
ATKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_018103465 [XP_018103465] PREDICTED: transcriptional coactivator
YAP1-B isoform X2 [Xenopus laevis]. 54..68
MEPGSQQQPSAPGQQPPPVGHQIVHVRTDSETDLETLFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPE
PKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPQGVITGLAPPSAQHLRQSSYEIPDDVPLPPG
WEMAKTPSGQRYFLNHVDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTGPLPDGWEQALTPEGETYFINHK
NKTTSWLDPRLDPRFAMNQQRLSQSAPVKSPPALQPQSPPSGVLGSGGNQQMRLQQLQMEKERLRLKHQELLRQE
LALRSQIPPMEQDSGPPNPVCSSGISQELRTMTMNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMETVLAATKL
DKESFLTWL PMRMRKLPDSFFKQP

rs:XP_018103466 [XP_018103466] PREDICTED: transcriptional coactivator
YAP1-B isoform X3 [Xenopus laevis]. 54..68
MEPGSQQQPSAPGQQPPPVGHQIVHVRTDSETDLETLFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPE
PKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPQGVITGLAPPSAQHLRQSSYEIPDDVPLPPG
WEMAKTPSGQRYFLNHVDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTAMNQQRLSQSAPVKSPPALQPQS
PPSGVLGSGGNQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQIPPMEQDSGPPNPVCSSGISQELRTMTM
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVD
LGTLEGEAMNVEGEELMPSLQEALSSDILNDMETVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_018103467   [XP_018103467] PREDICTED: transcriptional coactivator
YAP1-B isoform X4 [Xenopus laevis]. 54..68
MEPGSQQQPSAPGQQPPPVGHQIVHVRTDSETDLETLFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPE
PKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLGAVSPGALSPQGVITGLAPPSAQHLRQSSYEIPDDVPLPPG
WEMAKTPSGQRYFLNHVDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTAMNQQRLSQSAPVKSPPALQPQS
PPSGVLGSGGNQQMRLQQLQMEKERLRLKHQELLRQELALRSQIPPMEQDSGPPNPVCSSGISQELRTMTMNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTL
EGEAMNVEGEELMPSLQEALSSDILNDMETVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

rs:XP_018105870   [XP_018105870] PREDICTED: protein **FAM181**B-like [Xenopus
laevis].   158..172
MAVQSPIMNHQFLSLYIPGSIVDYEKRYQEGVDYLGAVESGDFKETTKDLLSFINTASSNIKLALDKPG
KSKRKVNHRKYLQKQIKRCTGLMGSGNINQGSPKRSPTSPGNSSMTPSGFPWKPPTKRDSTQSNLQSKSLAALFD
NVKEIRDERCKKVPLRNRNLPPSFFTEPESPCSGLLSNSGVALRDLGKCNQETLELFDFLGSDYNNMSEQEIIQG
ASVRLHQDVSVEQSLYEPHHLLNGLFYSDMWNPCNQVKKSSVGTGNLGLNETLKSAPLQGALYTNNQDPTMDSTM
DESCPSLTTYTPCFPSDCSLPQIFYDYNTQNCNRISYPVM PLRNRNLPPSFFTEP

rs:XP_018085938   [XP_018085938] PREDICTED: protein **FAM181**A-like [Xenopus
laevis].>rs:XP_018085939 [XP_018085939] PREDICTED: protein **FAM181**A-like
[Xenopus laevis].>tr:A0A1L8F9M8_XENLA [A0A1L8F9M8] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:OCT68267.1};   121..135
MLKVMASDSEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCTPSKSVD
LRKCLLDRQNTTTLNNGLSEKATHALETEENINKVTCTQENITEAGNPDQVPMRKRQLPASFWEEPRPSSSLLEL
HCPSRPDIIYKESTDASLTLYETKRGKNLMTHESNSSACFYPSEDKESGKLPSVASLTELVNACSCCPFQYHGQA
MYQHYPGELSPNPFTALTLWSKSTVPTLEIQHLCKESGQRIYRHVVLKPIPTKPAVHSSLFNVFGYI
PMRKRQLPASFWEEP

rs:XP_018087898   [XP_018087898] PREDICTED: protein **FAM181**A-like [Xenopus
laevis].>tr:A0A1L8F0D9_XENLA [A0A1L8F0D9] SubName: Full=Uncharacterized
protein {ECO:0000313|EMBL:OCT65057.1};   114..128
MASDSEVRTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCTPSKSVDLRKS
LLDRQNTTTLNNGLSDKATHTLENINKDTCAQENSTEAGSPDQVPMRKRQLPASFWEEPRPSSSLLELHCPSQPD
IIYKESTDTSLPLYETRRGKNVVIHGSHSSASFYPSEDKESGKLPSVASLTELVNACSCCPFQYHGQAMYQHYPG
ELSPNPFTGLTLWNKSTVPTLEIQHLCKESSQRIYRHVVLKPIPTKPAVHSSLFNVFGYI
PMRKRQLPASFWEEP

rs:XP_019305497   [XP_019305497] PREDICTED: protein **FAM181**B [Panthera
pardus].>rs:XP_025784993 [XP_025784993] protein **FAM181**B [Puma concolor].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGELLAGNEGGDMREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAPSAQAVAVPPHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGDTERAGGSLAAPAAGLGGAGAGGSGGEAAGTAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEALEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEPPPAMVGSLLYSESWSAPGCPQTKKPPLAAPRGGLTLNEPLRPLYPSAADSPGAEDGPGL
LASFAPFFSDCALPAPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD   PLRARNLPPSFFTEP

rs:XP_019317687   [XP_019317687] PREDICTED: protein **FAM181**A isoform X1
[Panthera pardus].   228..242
MLCIWRGAPDWPEGPPSAGDSSSIQPTRGLHDCFQPDARSSPATPGLAQVCRGEPARPRRRGARGRPAP
SVSSVPSPGAASHEQNPPASWKAPCSGLLVMANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQL
KRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDSGHDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNP
EAARPGQVPMRKRQLPASFWEEPRATHSYPLGLDGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKE
PLKMSGVSLVGRVNAWSCCPFQYHGQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPV
VLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_019317688   [XP_019317688] PREDICTED: protein **FAM181**A isoform X2
[Panthera pardus].   207..221
MLCIWRGAPDWPEGPPSAGDSSSIQPTRGLHDCFQPDARSSPATPGLAQVSSVPSPGAASHEQNPPASW
KAPCSGLLVMANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEP

HLKRGPEDRPGRLPLDSGHDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWE
EPRATHSYPLGLDGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPF
QYHGQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGY
L PMRKRQLPASFWEEP

rs:XP_019317689 [XP_019317689] PREDICTED: protein **FAM181**A isoform X3 [Panthera pardus].>rs:XP_019317690 [XP_019317690] PREDICTED: protein **FAM181**A isoform X3 [Panthera pardus].>rs:XP_019317691 [XP_019317691] PREDICTED: protein **FAM181**A isoform X3 [Panthera pardus]. 129..143
MANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLDSGHDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
ATHSYPLGLDGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_013366580 [XP_013366580] PREDICTED: transcriptional coactivator YAP1 [Chinchilla lanigera]. 75..89
MDPGPPPQPAPPAPGPGPAPAPAPGPPAPPAQAAPPPPPAGHQVVHVRGDSETDLEALFNAVMNPKTAN
VPQTVPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAAT
PAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPPVQQNLMNSAS
GPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAVNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQ
QMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_005390409 [XP_005390409] PREDICTED: protein **FAM181**A isoform X1 [Chinchilla lanigera]. 169..183
MPQAGLGPELPLCQPRTLLGVACPPKSAPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKS
APCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLRRGPEDHPGQLPLHPSVPCGPDPSPGGGGGCKEKA
LGSPFGEECLSKEQGPEAAKPGQVPMRKRQLPASFWEEPRPTHSYPMGLEGLPVIREGPPYESKKNCKGLESVVP
EAAPGPMSPRALVDKEPLKMPGVSLVGSVDAWSCCPFQYHGQPIYPGPPGALPASPIPGLGLWRKSPALPAELAH
FCEHVDGPGQKVYRPVVLKPIPTKPTVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_013372688 [XP_013372688] PREDICTED: protein **FAM181**A isoform X2 [Chinchilla lanigera].>rs:XP_005390410 [XP_005390410] PREDICTED: protein **FAM181**A isoform X2 [Chinchilla lanigera].>rs:XP_005390411 [XP_005390411] PREDICTED: protein **FAM181**A isoform X2 [Chinchilla lanigera]. 128..142
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLR
RGPEDHPGQLPLHPSVPCGPDPSPGGGGGCKEKALGSPFGEECLSKEQGPEAAKPGQVPMRKRQLPASFWEEPRP
THSYPMGLEGLPVIREGPPYESKKNCKGLESVVPEAAPGPMSPRALVDKEPLKMPGVSLVGSVDAWSCCPFQYHG
QPIYPGPPGALPASPIPGLGLWRKSPALPAELAHFCEHVDGPGQKVYRPVVLKPIPTKPTVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014043521 [XP_014043521] PREDICTED: protein **FAM181**A-like [Salmo salar].>rs:XP_014043558 [XP_014043558] PREDICTED: protein **FAM181**A-like [Salmo salar].>tr:A0A1S3QTX3_SALSA [A0A1S3QTX3] SubName: Full=protein **FAM181**A-like {ECO:0000313|RefSeq:XP_014043521.1, ECO:0000313|RefSeq:XP_014043558.1}; 125..139
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHTHRSAESGI
VKAMVDKSSAYSLETLHQSMTPINEKVCSGAQDEENIRMGQNPIADSANSKQDQVPMRKRQLPASFWEEPRLAQT
NTEPSLYGWNKSQGVTRINRVEKRIKNHQEPKPTLFQSNRLVSVEKEPLNVDLVSHNVSVCGCCPFQYHGHHVFQ
SHIVVPHSTVGLWGKAAVAEIETPDMAHGHNNQTHVVVKPIPTKPTVPSSIFSVFGVFGFI
PMRKRQLPASFWEEP

rs:XP_014066267 [XP_014066267] PREDICTED: protein **FAM181**A-like [Salmo salar].>tr:A0A1S3SPJ8_SALSA [A0A1S3SPJ8] SubName: Full=protein **FAM181**A-like {ECO:0000313|RefSeq:XP_014066267.1}; 125..139
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARMPRCHTHRSTESGI
AKDVVNKSSAYSLETIHPSTTRINEKGGSDAQDVENARMAQTPTVDSDNSKQEQVPMRKRQLPASFWEEPRLAQT

NTDYLQYGWKKSHGVTGTNEVEKIKKAHEEPTPTLFLSNRRGSVEKEPLKLDVASHNVNVCGFCPFQYHGHHVFQ
SHIVVPQSAVGLWGKATVAETATPDIAHRHKNYTHVVVKPIPTKPTVPPSIFNVFGFI PMRKRQLPASFWEEP

rs:XP_014071068 [XP_014071068] PREDICTED: transcriptional coactivator YAP1-like [Salmo salar].>tr:A0A1S3T396_SALSA [A0A1S3T396] SubName: Full=transcriptional coactivator YAP1-like {ECO:0000313|RefSeq:XP_014071068.1}; 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTVGPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGALAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSNLRQSSYEIPDDMPLPPGWEVAQTPSGQRYFLN
PVVFPPVSALSCSPLSQPCRVPPSLSPVVFPPLSALSCSPLSQPCRVPPSLSPVVFPPLSALSCLNQQRITQSAP
GKQGGQLPSRPQSEGVMVGSNQMRLQQLQMEKERLRLKHQELLRTRPQVSRNPYNLT PMRMRKLPDSFFKPP

rs:XP_014019163 [XP_014019163] PREDICTED: protein **FAM181**B isoform X1 [Salmo salar].>tr:A0A1S3NUS8_SALSA [A0A1S3NUS8] SubName: Full=protein **FAM181**B isoform X1 {ECO:0000313|RefSeq:XP_014019163.1}; 178..192
MAVQTAIMNSPFINFCFPGSVMMEYDMDQSLDGSPLEESEERGEYRETTRNLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGFISPTGNPVAAPGAGVNKRKGSGFPTQTQPQTQPQTQPQTQPGPFQQSKPVH
KRDGLQANLQTKSLAALFNSVKEPVRGERAKKPPLRHRNLPPSFFTEPDNTTTTTTSRVTSTSGMFLGDLERGGG
NPDFFDLLGPDYSNMLSDQDVFQNRGLPSRIIDQDMFQNRGLPSRILQHQQTQDITDQVSPYDPHHLVGGFLYTE
PWSTSSPNKKAGEGVRTGPGTQTPLYCQAGEGVRTGPGTQTPLYCQAGEGVRTGPGPQTPLYCQAGEGVRTGPGP
QTPLYCQAGEGVQTGPGTQTPLYCHSVSDSSVTGSTEDSNSLCTLTFPNFFPDCSVSQVSYGLSNGGYNTRDFSS
L PLRHRNLPPSFFTEP

rs:XP_014019164 [XP_014019164] PREDICTED: protein **FAM181**B isoform X2 [Salmo salar].>tr:A0A1S3NUU6_SALSA [A0A1S3NUU6] SubName: Full=protein **FAM181**B isoform X2 {ECO:0000313|RefSeq:XP_014019164.1}; 178..192
MAVQTAIMNSPFINFCFPGSVMMEYDMDQSLDGSPLEESEERGEYRETTRNLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGFISPTGNPVAAPGAGVNKRKGSGFPTQTQPQTQPQTQPQTQPGPFQQSKPVH
KRDGLQANLQTKSLAALFNSVKEPVRGERAKKPPLRHRNLPPSFFTEPDNTTTTTTSRVTSTSGMFLGDLERGGG
NPDFFDLLGPDYSNMLSDQDVFQNRGLPSRIIDQDMFQNRGLPSRILQHQQTQDITDQVSPYDPHHLVGGFLYTE
PWSTSSPNKKAGEGVRTGPGPQTPLYCQAGEGVRTGPGPQTPLYCQAGEGVQTGPGTQTPLYCHSVSDSSVTGST
EDSNSLCTLTFPNFFPDCSVSQVSYGLSNGGYNTRDFSSL PLRHRNLPPSFFTEP

rs:XP_014041893 [XP_014041893] PREDICTED: transcriptional coactivator YAP1-like, partial [Salmo salar].>tr:A0A1S3QPA9_SALSA [A0A1S3QPA9] SubName: Full=transcriptional coactivator YAP1-like {ECO:0000313|RefSeq:XP_014041893.1}; 45..59
MDPSQHNPPAGHQIIHVRGDSETDLETLFNAVMNPKNTIVPSSVPMRMRKLPDSFFKPPEPKSHSRQTS
TDAGTAGAVAPHHVRAHSSPASLQLGTVSPLLGMVPAGPPPSHLRQSSYEIPEDMPLPPGWEMAKTPSGQRYFLN
HLDQSTTWQDPRKALLQMNQAPPTSPVPVQQQNIMSPASGPLPDCWEQAITSEGEVYYINHKNKTTSWLDPRL
PMRMRKLPDSFFKPP

rs:XP_014090328 [XP_014090328] PREDICTED: transcriptional coactivator yorkie isoform X1 [Bactrocera oleae]. 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACIQDGIGPVFTTGAVPFPPGVNAGSAVRMEQGDQPVPKDAPNTIQTFHMKQRSYDVVSTI
QLQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKSKESVNLADNLGPLPEG
WEQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQ
MDPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISESGSLNALSGIDCPDNLVSSLQLEDNICNE
MFSDVHSMLNASATKPDTLDWYKIN PFRMRQLPESFFKPP

rs:XP_014090329 [XP_014090329] PREDICTED: transcriptional coactivator yorkie isoform X2 [Bactrocera oleae]. 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACIQDGIGPVFTTGAVPFPPGVNAGSAVRMEQGDQPVPKDAPNTIQTFHMKQRSYDVVSTI
QLQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNEGWEQAYTESGDVYFINHVNR
TTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQMDPFLSGDNHARQESSDSG

LSLSSNTFSTTADLMPNIDDSMDCISESGSLNALSGIDCPDNLVSSLQLEDNICNEMFSDVHSMLNASATKPDTL
DWYKIN PFRMRQLPESFFKPP

rs:XP_014090330 [XP_014090330] PREDICTED: transcriptional coactivator
yorkie isoform X3 [Bactrocera oleae]. 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACIQDGIGPVFTTGAVPFPPGVNAGSAVRMEQGDQPVPKDAPNTIQTFHMKQRSYDVVSTI
QLQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKSKESVNLADNLGPLPEG
WEQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQ
MDPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISA PFRMRQLPESFFKPP

rs:XP_005926600 [XP_005926600] PREDICTED: transcriptional coactivator
YAP1 [Haplochromis burtoni]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKVNTVPHSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSAGVLIPHHVRAHSSPASLQLGAVSGGSLSGMGSTGASPQHLRQSSYEIPDDMPLPDGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQPAPPSSVPVQPQPIMNPASGPLPDGWEQAITAEGEIYYINHKNKTTSWLDPRL
EPRYALNQQRISQSAPVKQAGQLPPSISGVMGSNNQMRLQMEKERLRQKQQELLRQRPQELALRNQLPTSMDQDG
STNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMATQ
PSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_008549061 [XP_008549061] PREDICTED: transcriptional coactivator
YAP1 [Microplitis demolitor].>rs:XP_008549062 [XP_008549062] PREDICTED:
transcriptional coactivator YAP1 [Microplitis demolitor]. 46..60
MALNQDVDQLSKGNLVVRIDQNSESDLQALFDSVLKPNSTRPLQVPLRMRNLPNSFFNPPSTGSKSPSI
SHSRENSADSAFGTIVTTNVASGPGASALGSGSEATGGGADAAGTGAAGAAPGLTVAHPRAHSSPASLQQTYASA
QQATQHTPQPHAPRHHHHQKQRSYDVISTVDDMGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAVSVA
AVAAAVESGKASSAAANSLGPLPEGWEQARTPEGEIYFINHQSRTTSWFDPRIPSHLQRAPTTNTMLPQNWLQQP
GAPGLQNNQNIQVCQQKLRLQSLQMERERLKQRQAEIMRQQELNLLRQSTTDAAMDPFLSGINEQHARQESADSG
LGLGSAYSLPHTPEDFLSNIDDNMDATSEGGAPMETPDLSTLSDNIDSTDDLVPSLQLGEEFTSDILDDVQSLIN
PSSTKPDNVLTWL PLRMRNLPNSFFNPP

rs:XP_005877902 [XP_005877902] PREDICTED: protein **FAM181**A [Myotis
brandtii].>tr:S7NEP9_MYOBR [S7NEP9] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:EPQ14920.1}; 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPPLR
RGPEDRPGRLPLNPGPDASPRSGGDCKEKALGNPYREECLSREQTLQGQNPGAARPGQVPMRKRQLPASFWEEPR
PTHSYPVALEGVLGPREGPPYECKKHCRGLELFGPDMALIPMSPRALAEKEPPKLPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPPGPVPSLGLWRKSPASPGELAHLAKDVDGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014695669 [XP_014695669] PREDICTED: protein **FAM181**B, partial [Equus
asinus]. 9..23
AVPGARKVPLRARNLPPSFFTEPSRADGGGGCGPSGPVVSLGDLEKGAEAVEFFELLAPDYGTGTEAGV
LLAAEPLDVFPTGAAALRGPPELEPGLFEPPPGMVGSLLYPEPWGAPGCPSTKKPQLAAPRGGLTLNEPLRPLYP
AAADSPGGEDAPGLLASFAPFFSDCALPPAPPPHQVSYDYSAGYGRTAYSSLWRADAAWEGAPGEEGAHRD
PLRARNLPPSFFTEP

rs:XP_014687590 [XP_014687590] PREDICTED: protein **FAM181**A isoform X1
[Equus asinus]. 159..173
MVRPVPFSGAASPPQNPPSSWKAPCRGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRK
YLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLGAGQDSSPGGGGSCTEKALGNPYREECLSKEQT
LQGQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPVGPETAPVPASPR
APAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGALPQSPVPSLGLWRKSPASPGELAHFCKDVGGPGQ
KVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_014687591 [XP_014687591] PREDICTED: protein **FAM181**A isoform X2
[Equus asinus].>rs:XP_014687592 [XP_014687592] PREDICTED: protein **FAM181**A

isoform X2 [Equus asinus].   129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLGAGQDSSPGGGGSCTEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPVGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPQSPVPSLGLWRKSPASPGELAHFCKDVGGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014739937   [XP_014739937] PREDICTED: protein **FAM181**A [Sturnus vulgaris]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPQCGWR
RAAEDRARGSQPEAPEPSPHGGAAAEKVVQTAEAEESLTGERVLQEQKPEAARPDQVPMRKRQLPASFWEEPRPA
QSLTARAFPASPEGLQAPRDPPPYEGKKSRRSPDAAGPESPPDTAPHAGEKDPAGALSGRVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLGLWRKSAAALPAEVPHFGKEADGPGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014742071   [XP_014742071] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Sturnus vulgaris].86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014742072   [XP_014742072] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Sturnus vulgaris].86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014742073   [XP_014742073] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Sturnus vulgaris].86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_014742074   [XP_014742074] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Sturnus vulgaris].86..100
MDPGQPQTQQPPQAAQPPASQQQQPPPQPPGAVSGAPAGAAQPPGAGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPS
VQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSIGQSNIPSHQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_014746410   [XP_014746410] PREDICTED: uncharacterized protein LOC106862112 [Sturnus vulgaris].   169..183

MAAGVIQPLAELRLPSPFPHGLLLPTHPEPDFPDLSEEEEEEEEEEEEEDVEAVEESVKPELASVSSTA
ETTLRLLKFSELISCDIQRYFGRRGREEIASSRPTPEDCGSPHSAEAVPEVVAPRDSLGATHRLGPLAELFEYGV
HRCLPARVAGSRTQRLERKYGHITPMHRRKLPPSFWKEPGPGPASLLHTGTPDFSDLLANWTVEPGPELPGTGRE
LLGRPGLEAEPFAGL   PMHRRKLPPSFWKEP

rs:XP_022836114   [XP_022836114] transcriptional coactivator yorkie-like
[Spodoptera litura].>tr:A0A2H1V2D1_SPOFR [A0A2H1V2D1] SubName:
Full=SFRICE_000106 {ECO:0000313|EMBL:SOQ34991.1};   44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGTHIPDDLGPLPPGW
EQARTPEGQIYYLK   PLRMRQLPKSFFNPP

rs:XP_014791770   [XP_014791770] PREDICTED: uncharacterized protein
LOC106884746 [Calidris pugnax].   187..201
MHGRAAAPRVNPGPGVPLRTDMAAGIIRPLAELRLPSPFPHSLLLPTRPEPDFPDLSEEEEEEEEEEEE
EEVAEESVRPELAIPSAAETTLRLLKFSELISCDIQRYFGRRGQEEATGSHGVPEDCGSPRRAEGQPEAVALRGG
PGATHRLGPLAELFEYGVHRCLPPRAAGGKTQRLERKYGHITPMHRRKLPPSFWREPGPGPVGLLHTGTPDFSDL
LANWTVEPGPELPGTGRELPPEPGHPGLEAEPFAGL   PMHRRKLPPSFWREP

rs:XP_014812970   [XP_014812970] PREDICTED: protein **FAM181**A [Calidris
pugnax].   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPGKAPESGWR
RVVEDRGRVPQPELPDPSPHGGAVTEKVLRTGEAEESLAREGVLQEQNPEASRPDQVPMRKRQLPASFWEEPRPA
PSLPARAFPAAIEGLPAPRDPPPYEGKKCKRSSDTASPESPPEPAPHAGDKDPVGVLSGRVGAWTCCPFPCPGPG
VYQAPGTLAPSPFPGLGLWRKSAAALPAEVPHFCKEADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014785644   [XP_014785644] PREDICTED: transcriptional coactivator
YAP1-like, partial [Octopus bimaculoides].   42..56
MSQQRTEQKGNQVVHVRGDSDSDLEALFKAAMNPSEVPHQLPLRMRNLPASFFTPPDPTQQKQHSREGS
TDSTGAGSGSVLNSPGLTIAHPRAHSSPASLAQTMSAAPPPSSQHVRQHSYDLTDEQPLPPGWEMAKTNQGHRYY
LKSRETDTDRQNRELQIPPKYEFKIAHSSSLHMQQQPVQGVRVQNPGQSPQSLKLSPGPQPQQQSPGGPPQVVNN
TNSNNQVNQGQRVMAPSIQQLQNLALEKEQLKKRAEEITRQELLLRAQMHPESEIPIPQTSEMTSVADPFLGHTT
NQADLHSRQESSDSGLGGMGTNYSLKSSEDFLSNVDEMDTQDG   PLRMRNLPASFFTPP

rs:XP_001960695   [XP_001960695] LOW QUALITY PROTEIN: uncharacterized
protein Dana_GF13481 [Drosophila ananassae].>tr:B3MDX2_DROAN [B3MDX2]
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EDV37517.2};
84..98
MLDKIILCSNFLYTISAFYMLTTMSSSNTNSLIEKEIADEDMLPPIKSPNNLVVRVNQDTDDNLRLLFD
SVLNPGDAKRPLQLPFRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISSLNSISSLANTAQPVDGQPAIST
IPQIQPSPQQRNLAIHHFRARSSPASLQQNYNVRQRSDPTNPTNQPPTAGPTFPENSAAEFPSGGAGAGAGGAGA
GAPASSIELDGMSMVQDMPMTTQTVHKKQRSYDVVSPIQLQLLRGALPPGWEQAKTNDGQIYYLNHTTKTTQWED
PRIQFRQQQNLMAERIKQNDVLQTTKQTTTSAIANNLGPLPDGWEQAVTETGDIYFINHIDRTTSWNDPRMQSGL
SVLDCPDNLVSSLQIEDNICSNMFNDAQTIVNPPSSHKPDDLEWYKIN   PFRMRKLPNSFFTPP

rs:XP_012008716   [XP_012008716] PREDICTED: protein **FAM181**B [Ovis aries
musimon].>rs:XP_011957662 [XP_011957662] protein **FAM181**B [Ovis aries].
212..226
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDEETGTPAGSLLAGAESGDAREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADMPAKRPLAGAQTVPVPAHGKAA
PRREASQAAAAASLQSRSLAALFDSLRHVPGGADPARAAEAAPAAGLVGGDTAGSAGGPAVPGSRKVPLRARNLP
PSFFTEPSRAGGGGGGCGPSGPGVSLGDLEKGSEAAEFFELLGPDYGAGTEAGALLAAEPLDVFPAGAAVLRGPP
ELEPGLFESQPAMVGSLLYPEPWSAPGGPGTKKPPLPAPGGGLTLNEPLRSVYPAAADSPGGDDGPGLLASFAPF
FSDCALPPAPPPPPQQVSYDYSAGYSRTAFAGLWRPDGAWEGAPGEEGAPRD PLRARNLPPSFFTEP

rs:XP_012014635   [XP_012014635] PREDICTED: protein **FAM181**A isoform X2
[Ovis aries musimon].   240..254
MWERGRRLLGMLCIWRGAPDWPEGPPAPGTRRPPFSPLEGGTTASSRTTELAGRTRPGPGLRRGGNLCR

AALAGSRAPAPLVGSVLFPGAASCLENPASSWKARGSGALVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRS
VDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRPLHLESGHGSSPSGGGGYKEKALGNPDREES
LSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAP
VPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQYHGQPIYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKD
AEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_012014637   [XP_012014637] PREDICTED: protein **FAM181**A isoform X1
[Ovis aries musimon].   130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRPLHLESGHGSSPSGGGGYKEKALGNPDREESLSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPIYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014999895   [XP_014999895] PREDICTED: protein **FAM181**A [Macaca
mulatta].>rs:XP_014999896 [XP_014999896] PREDICTED: protein **FAM181**A [Macaca
mulatta].>tr:A0A1D5R8Q2_MACMU [A0A1D5R8Q2] SubName: Full=Family with
sequence similarity 181 member A {ECO:0000313|Ensembl:ENSMMUP00000056692};
129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADSLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_014971028   [XP_014971028] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Macaca mulatta].   85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014971029   [XP_014971029] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Macaca mulatta].   85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014971030   [XP_014971030] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Macaca mulatta].   85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_002799819 [XP_002799819] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Macaca mulatta].>tr:F7FER5_MACMU [F7FER5] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSMMUP00000004529}; SubName: Full=Yorkie homolog isoform 1 {ECO:0000313|EMBL:AFJ71249.1};
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014971031 [XP_014971031] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Macaca mulatta]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014971032 [XP_014971032] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Macaca mulatta]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014971034 [XP_014971034] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Macaca mulatta].>tr:F7FEK3_MACMU [F7FEK3] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSMMUP00000004530};
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_002799820 [XP_002799820] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Macaca mulatta].>tr:I2CWB5_MACMU [I2CWB5] SubName: Full=Yorkie homolog isoform 3 {ECO:0000313|EMBL:AFJ71250.1}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014971035 [XP_014971035] PREDICTED: transcriptional coactivator YAP1 isoform X9 [Macaca mulatta].>tr:A0A1D5QLM0_MACMU [A0A1D5QLM0] SubName:

Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSMMUP00000048945};
85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_014971036   [XP_014971036] PREDICTED: transcriptional coactivator
YAP1 isoform X10 [Macaca mulatta]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_002799821   [XP_002799821] PREDICTED: transcriptional coactivator
YAP1 isoform X11 [Macaca mulatta]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014971037   [XP_014971037] PREDICTED: transcriptional coactivator
YAP1 isoform X12 [Macaca mulatta]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL   PMRLRKLPDSFFKPP

rs:XP_001360893   [XP_001360893] uncharacterized protein Dpse_GA17846,
isoform A [Drosophila pseudoobscura pseudoobscura].>tr:Q28ZZ4_DROPS
[Q28ZZ4] SubName: Full=Uncharacterized protein, isoform A
{ECO:0000313|EMBL:EAL25468.3};   65..79
MLTTMSTSNTNSIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSDANPGPSGQGPTYPENSAEFPNSAANNIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSESGLTGLDCPDNLVSSLQIEDNICT
NLFNDAQTIVNPPSSHKPDDLEWYKIN   PFRMRKLPNSFFTPP

rs:XP_015039803   [XP_015039803] uncharacterized protein Dpse_GA17846,
isoform B [Drosophila pseudoobscura pseudoobscura].>tr:A0A0R3NMI2_DROPS
[A0A0R3NMI2] SubName: Full=Uncharacterized protein, isoform B
{ECO:0000313|EMBL:KRT02241.1};   65..79
MLTTMSTSNTNSIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSDANPGPSGQGPTYPENSAEFPNSAANNIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSESGLTGLDCPDNLVSSLQVCN
PFRMRKLPNSFFTPP

rs:XP_015039804 [XP_015039804] uncharacterized protein Dpse_GA17846,
isoform C [Drosophila pseudoobscura pseudoobscura].>tr:A0A0R3NMX5_DROPS
[A0A0R3NMX5] SubName: Full=Uncharacterized protein, isoform C
{ECO:0000313|EMBL:KRT02242.1}; 65..79
MLTTMSTSNTNSIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSDANPGPSGQGPTYPENSAEFPNSAANNIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQRLMAERIKQSDVLQTTKQTTTSTIANSLGPLPDGW
EQAVTDSGDIYFINHIDRTTSWIDPRMQSGLTGLDCPDNLVSSLQIEDNICTNLFNDAQTIVNPPSSHKPDDLEW
YKIN PFRMRKLPNSFFTPP

rs:XP_015051649 [XP_015051649] uncharacterized protein Dyak_GE11487,
isoform B [Drosophila yakuba].>tr:A0A0R1DTX3_DROYA [A0A0R1DTX3] SubName:
Full=Uncharacterized protein, isoform B {ECO:0000313|EMBL:KRK00541.1};
88..102
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNSLIEKEIEDEDMLSLMKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPNAA
IPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAP
ASSAIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWED
PRIQYRQQQQILMAERIKQNESGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN
PLRMRKLPNSFFTPP

rs:XP_002092762 [XP_002092762] uncharacterized protein Dyak_GE11487,
isoform A [Drosophila yakuba].>tr:B4PAT4_DROYA [B4PAT4] SubName:
Full=Uncharacterized protein, isoform A {ECO:0000313|EMBL:EDW92474.1};
88..102
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNSLIEKEIEDEDMLSLMKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPNAA
IPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAP
ASSAIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWED
PRIQYRQQQQILMAERIKQNDVLQTTKQTTTSTIANNLGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQSG
LSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_015124110 [XP_015124110] PREDICTED: transcriptional coactivator
YAP1-A isoform X1 [Diachasma alloeum]. 46..60
MALNPDVDQLSKGNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTIISNSGPGNTTPSGNSNGNSTANQTSVPAGLTVAHPRAHSSPASLQQTYAAAQQATQHAPQ
PHARHVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQVYFLNHLTRTTTWEDPRKTAAAANVTTIAAAENGKS
PAGAGANALGPLPEGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPTNWIQPPGATGLQSNQT
IQVCQQKLRLQSLQMERERLKQRQAEIMRQQELMLRQSNTDASMDPFLSGMSEQHARQESADSGLGLGSAYSLPH
TPEDFLSNIDDNMDATSDGGAPMETPDISTLSDNIDSTDDLVPTLQFSEELSSDILDDVQSLINPSSTKPENVLT
WL PLRMRNLPDSFFNPP

rs:XP_015124111 [XP_015124111] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Diachasma alloeum].>rs:XP_015124112 [XP_015124112]
PREDICTED: transcriptional coactivator YAP1 isoform X3 [Diachasma alloeum].
46..60
MALNPDVDQLSKGNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTIISNSGPGNTTPSGNSNGNSTANQTSVPAGLTVAHPRAHSSPASLQQTYAAAQQATQHAPQ
PHARHVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQVYFLNHLTRTTTWEDPRKTAAAANVTTIAAAENGKS
PAGAGANALGPLPEGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPTNWIQPPGATGLQSNQT
IQVCQQKLRLQSLQMERERLKQRQAEIMRQQELMLRQSNTDASMDPFLSGMSEQHARQESADSGLGLGSAYSLPH
TPEDFLSNIDDNMDATSDGGAPMETPDISTLSDNIDSTDDLVPTLQ PLRMRNLPDSFFNPP

rs:XP_015124113 [XP_015124113] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Diachasma alloeum]. 46..60
MALNPDVDQLSKGNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTIISNSGPGNTTPSGNSNGNSTANQTSVPAGLTVAHPRAHSSPASLQQTYAAAQQATQHAPQ
PHARHVHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQVYFLNHLTRTTTWEDPRKTAAAANVTTIAAAENGKS

```
PAGAGANALGPLPEGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPTNWIQPPGATGLQSNQT
IQVCQQKLRLQSLQMERERLKQRQAEIMRQQELMLRQSNTDASMDPFLSGMSEQHARQESADSGLGLGSAYSLPH
TPEDFLSNIDDNMDATSV      PLRMRNLPDSFFNPP

rs:XP_015188814   [XP_015188814] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Polistes dominula].     47..61
      MALNQEIDQLSNNSNLVVRIDQNSESDLQALFDTVLKPDSKHPLQVPLRMRNLPDSFFNPPSTGSRSPS
ISHSRENSADSAFGAGGSGGASGAVTGTTGGRNAESSGGGGGNVVAGGANVSVVGGGAGGGAGAGGAGASVGVAN
GNGGGPAGGGSPGGGAGGVVAVAAAAVSANVNGGNTGGAGGTANGGPPNGGGAGGVSAGSAASANAVNGPAPAAA
AAAAAAAAAAAAAAGLTVAHPRAHSSPASLQQTYTSAQQAQQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHG
WEQARTTEGQIYFLNHLTRTTTWEDPRKTVAAQNVAQVAAQVESGKSAAAGNTLGPLPDGWEQARTPEGEIYFIN
HQTRTTSWFDPRIPTHLQRAPSSGAMLPQNWLQQPTAAGIPNNQSLQACQQKLRLQSLQMERERLKQRQQEIIRQ
QELMLRQTTTDAAMDPFLSGISEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSGKLLVHYENRWKV
DFAVFDAYFVDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSEDFSSDILEDVQCFISPNTIKPGNVLTWL
      PLRMRNLPDSFFNPP

rs:XP_015188817   [XP_015188817] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Polistes dominula].     47..61
      MALNQEIDQLSNNSNLVVRIDQNSESDLQALFDTVLKPDSKHPLQVPLRMRNLPDSFFNPPSTGSRSPS
ISHSRENSADSAFGAGGSGGASGAVTGTTGGRNAESSGGGGGNVVAGGANVSVVGGGAGGGAGAGGAGASVGVAN
GNGGGPAGGGSPGGGAGGVVAVAAAAVSANVNGGNTGGAGGTANGGPPNGGGAGGVSAGSAASANAVNGPAPAAA
AAAAAAAAAAAAAAGLTVAHPRAHSSPASLQQTYTSAQQAQQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHG
WEQARTTEGQIYFLNHLTRTTTWEDPRKTVAAQNVAQVAAQVESGKSAAAGNTLGPLPDGWEQARTPEGEIYFIN
HQTRTTSWFDPRIPTHLQRAPSSGAMLPQNWLQQPTAAGIPNNQSLQACQQKLRLQSLQMERERLKQRQQEIIRQ
QELMLRQTTTDAAMDPFLSGISEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLST
LSDNIDSTDDLVPSLQLSEDFSSDILEDVQCFISPNTIKPGNVLTWL PLRMRNLPDSFFNPP

rs:XP_015196863   [XP_015196863] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Lepisosteus oculatus].>rs:XP_006627849 [XP_006627849]
PREDICTED: transcriptional coactivator YAP1 isoform X1 [Lepisosteus
oculatus].>tr:W5MEM7_LEPOC [W5MEM7] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSLOCP00000006836};45..59
      MDPSQHNPPAGQPIVHVRGDSETDLEALFNAVMNPKSANVPPSVPMRLRKLPDSFFKQPEPKSHSRQAS
TDAGTAGTLAPQHVRAHSSPASLLNAVSPGSLAGVIPPGAPPQHLRQASYEIPDDVPLPPGWEMAKTPSGQRYFL
NHMDQTTTWQDPRKAMLSQMNAAAPASPMPVQQNIMNSTSGPLPEGWEQAITSDGEIYYINHKNKTTSWLDPRLD
PRYALNQQRITQSAPVKQASPLPSQSPQGGVLGGNNQMRLQQLQMEKERLRLKHQELLRQVRPQELALRNQLPTS
MEQDGGTQNAVSSPGMAQDVRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSL
GPSSMATQPSRFPDYLDTIPGTNVDLGTLEGDSMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
      PMRLRKLPDSFFKQP

rs:XP_015196864   [XP_015196864] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Lepisosteus oculatus].  45..59
      MDPSQHNPPAGQPIVHVRGDSETDLEALFNAVMNPKSANVPPSVPMRLRKLPDSFFKQPEPKSHSRQAS
TDAGTAGTLAPQHVRAHSSPASLLNAVSPGSLAGVIPPGAPPQHLRQASYEIPDDVPLPPGWEMAKTPSGQRYFL
NHMDQTTTWQDPRKAMLSQMNAAAPASPMPVQQNIMNSTSGPLPEGWEQAITSDGEIYYINHKNKTTSWLDPRLD
PRYALNQQRITQSAPVKQASPLPSQSPQGGVLGGNNQMRLQQLQMEKERLRLKHQELLRQELALRNQLPTSMEQD
GGTQNAVSSPGMAQDVRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLGPSS
MATQPSRFPDYLDTIPGTNVDLGTLEGDSMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
      PMRLRKLPDSFFKQP

rs:XP_006627850   [XP_006627850] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Lepisosteus oculatus].  45..59
      MDPSQHNPPAGQPIVHVRGDSETDLEALFNAVMNPKSANVPPSVPMRLRKLPDSFFKQPEPKSHSRQAS
TDAGTAGTLAPQHVRAHSSPASLLNAVSPGSLAGVIPPGAPPQHLRQASYEIPDDVPLPPGWEMAKTPSGQRYFL
NHMDQTTTWQDPRKAMLSQMNAAAPASPMPVQQNIMNSTSALNQQRITQSAPVKQASPLPSQSPQGGVLGGNNQM
RLQQLQMEKERLRLKHQELLRQVRPQELALRNQLPTSMEQDGGTQNAVSSPGMAQDVRTMTTNSSDPFLNSGTYH
SRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLGPSSMATQPSRFPDYLDTIPGTNVDLGTLEGDSMAVEG
EELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL     PMRLRKLPDSFFKQP
```

rs:XP_006627851 [XP_006627851] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Lepisosteus oculatus]. 45..59
MDPSQHNPPAGQPIVHVRGDSETDLEALFNAVMNPKSANVPPSVPMRLRKLPDSFFKQPEPKSHSRQAS
TDAGTAGTLAPQHVRAHSSPASLLNAVSPGSLAGVIPPGAPPQHLRQASYEIPDDVPLPPGWEMAKTPSGQRYFL
NHMDQTTTWQDPRKAMLSQMNAAAPASPMPVQQNIMNSTSALNQQRITQSAPVKQASPLPSQSPQGGVLGGNNQM
RLQQLQMEKERLRLKHQELLRQELALRNQLPTSMEQDGGTQNAVSSPGMAQDVRTMTTNSSDPFLNSGTYHSRDE
STDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLGPSSMATQPSRFPDYLDTIPGTNVDLGTLEGDSMAVEGEELM
PSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRLRKLPDSFFKQP

rs:XP_015197075 [XP_015197075] PREDICTED: protein **FAM181**B [Lepisosteus oculatus].>tr:W5NNT9_LEPOC [W5NNT9] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSLOCP00000022298}; 156..170
MAVQAAIMTPHFMHFCFPGSVMEYEMDKSFDGGVLGEMDCEGDFKETTRDLLSFIDSASSNIKLALDKP
VKSRRKVNHRKYLQKQIKRCTGMITPGSGGQEAVKRQGSPQSNPGTSFQCKPPPKREGIQSNLQSKSLAALFDSV
KDIRAEKGKKLPLRHRNLPRSFFTEPANSSKVTSTSGMTLKDLERGNPEAAEFFELLGPDYSNMIADHDAFQGVP
VRIQQEAALEPGSYDPQHLVGGFLYTEPWSTCSSPSKKTGICSLNVNENMRTIPVQPPVYCHSDSAVTSPQEENA
SGMPMFAHFFTDCSLPQYDYSSGYNRTNFSSL PLRHRNLPRSFFTEP

rs:XP_015206503 [XP_015206503] PREDICTED: protein **FAM181**A [Lepisosteus oculatus]. 127..141
MACTDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCQSYRTSESGI
GKALEDKSGTYPLETVNRNLSLAHLSEKIGSDLRCDDTVKPNPNSAHEKNYSRQDQVPMRKRQLPASFWEEPRSS
KSKHETFQAVWRKNQAVGGSGLSGSVEQIRKKCSEGPKTTSVHINRQSVAEKEPLTVEMTSLTGSASLCGCCPFQ
YHGQHVYQSHVVLPQSGFSDSSMWGKPSVAQTEGLDSCKDVAINGQKSHTHVVVKPIPTKPTVPSPIFSVFGFI
PMRKRQLPASFWEEP

rs:XP_005562134 [XP_005562134] PREDICTED: protein **FAM181**A [Macaca fascicularis].>rs:XP_005562136 [XP_005562136] PREDICTED: protein **FAM181**A [Macaca fascicularis]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKIPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_015358221 [XP_015358221] PREDICTED: LOW QUALITY PROTEIN: protein **FAM181**B [Marmota marmota marmota]. 211..225
MFSWTHPSSDSFSDFIFDNLSNIEATLVISSSFNLTPIILSSSIVLCFAYFLTFLHYNFIDSASSNIKL
ALDKPGKSKRKVNHRKYLQKQIKRCNGLMGAAPPGPPSPSAADTPAKRPLAAPSASTAAAPVHGKAAPRREASQA
AAAASLQSRSLAALFDSLRHVSGGRRASGGAVAVPVTGLGGASSGGAGGEASGLAGGTAVPGARKVPLRARNLPP
SFFTEPSRAGGGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGSDYGAGTEAGVLLAAEPLDVFPTGAAVLRGPLE
LEPGLFEPPPAMVGNLIYPEPWSAPSCAPTKKSPVAAARGGLTLNESLRPLYPAPSDSPGGEDGTGHLASFAPFF
PDCTLPPPPPPHQVSYDYSAGYSRAAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_015372505 [XP_015372505] PREDICTED: transcriptional coactivator YAP1-A [Diuraphis noxia]. 64..78
MSGLQQQEQHQQVSIKMEPTGPSSPTPSVNSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPLRMRQ
LPKSFFNPPSTGSKSPSISHSRENSGDSAFGTANVGPSCSGPVPLHSRAHSSPASLQQTYAVGAAKQQQQHAKQR
SYDVSSAIDELGPLPQGWEQARTPEGQIYYLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQLLSPGNDSGSSTNA
TSTPTNSPPHIHSTLQGANKNVTLGPLPDGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQRAPTSGAVLPSG
SASWLLNGASGLSQSLQVTQQKLRLHSLQLERERLKSRQQEIIRQQDLMLRSGQTNNDLDPFLSCSSSSVDHSRQ
ESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDSQEMSTLDVTDDLVPSLQLGDEFSS
DILDEVQLLIDPNNKPGSILTWL PLRMRQLPKSFFNPP

rs:XP_015720879 [XP_015720879] PREDICTED: protein **FAM181**A [Coturnix japonica]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHSTKPSECGPR
RGAEDRTRSCQPEVPDPGPHNGAAAEKVLQAAEVEESLAGEQAVPEQNPEANRPDQVPMRKRQLPASFWEEPRPP

QSLPVRGFPAAPEGLPVPREPPPPFEGKKSKRSEDTTGPESHEPALNAGEKDPTGVLSGRVGAWTCCPFPCPGPA
VYQPPGTLPPSPFPGLGLWRKGTATLPAEAQPFCKEAEGTGQKLYRPVVLKPIPTKPTIPSPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_015732722 [XP_015732722] PREDICTED: uncharacterized protein LOC107320912 [Coturnix japonica]. 201..215
MHGRAAAPRVSPGPGVSLCTNMAAGVIRPLAELRLPSPFPHGLLLPAHPEPDFPDLSEEDDEEEEEEDE
EEAAEESTACSGPEPVGPSTAETTLRLLRFSELISCDIQRYFGQRGREEAAGGHNVPEDCSSPHSSPHNASMGHT
ARGGRAQPEVALSGHGAAHRLGPLAELFEYGVHRCLAPRVASGKTQRLERKYGHITPMHRRKLPPSFWREPGPGP
GSLLHTGTPDFSDLLAHWTVEPGPELPGSGRELPPVPGHTGLETEPYSGL PMHRRKLPPSFWREP

rs:XP_015753743 [XP_015753743] PREDICTED: transcriptional coactivator YAP1-like [Acropora digitifera]. 46..60
MERTNNNCVVHVRQDSDTDLEALFHVVNPTTVPNSHPDTTPANSLPMRLRKLPPSFFKQPPIDGGLSPE
TDHPSGLQISHSRAHSSPASITVPSSLKGPPNHSLSSVVHQRSTSFDNTALLEEPAQMPPGWEIRSTPNGQHYFM
NHFDQITTWQDPRKTQSTSNLNSAQTSASLPDGWEQAITPEGDIYYINHIERTTSWVDPRIALQCRSQENVRSSS
IMPEMYRHRTIQLHRLQREREQLLKRQQELLKQEIKLKRDILEEGGTKSSLLGNLTREGLLPPHQDSTPVTNGGG
HIRDQSFDSGLGMGGGNYHDIDMNESQPMFDANYNSKDSSYRTDASRRLPEILDSLPATNVDLGVMEGNDSSSNM
DTDDLGVGLEFNSEMLNDVENFMSPGNKMSDNFLTWL PMRLRKLPPSFFKQP

rs:XP_016029386 [XP_016029386] uncharacterized protein Dsimw501_GD24973, isoform C [Drosophila simulans].>rs:XP_015011529 [XP_015011529] transcriptional coactivator yorkie isoform X2 [Drosophila erecta].>tr:B4QBI7_DROSI [B4QBI7] SubName: Full=GD24973 {ECO:0000313|EMBL:EDX08505.1}; 88..102
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPIAA
IPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAP
ASSAIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWED
PRIQYRQQQQILMAERIKQNESGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN
PLRMRKLPNSFFTPP

rs:XP_007529132 [XP_007529132] PREDICTED: protein **FAM181**A [Erinaceus europaeus].>tr:A0A1S3A4B3_ERIEU [A0A1S3A4B3] SubName: Full=protein **FAM181**A {ECO:0000313|RefSeq:XP_007529132.1}; 120..134
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARLPRGLPGRGTESLLR
RPSLHPGPEPTGGAGGYQEPALGRPYREECLSQELGPPGLNPEVAGPGQVPMRKRQLPASFWEEPRPTHSCPLGL
DGALGLREAPPYEGKQHCKGLGSLGPEVVPVPASPQPHAEKELLKMPGVSLLGCTNAWSCCPFQCRGHPVYPGLP
GALAPSPTPGLGFWRKSPATPGELAHFCKDADGLGPKVHRPVVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_016067971 [XP_016067971] PREDICTED: protein **FAM181**A [Miniopterus natalensis]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEQHLK
RGPEERPGRLPLNPGPDSSPSSGGDCKEKALGNPYREECLSQEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPMGLEGVLGPREAPPYEGKRYCKGLELLGPEMALIPMSPRVLAEKETPKMPGVSLVGRVNAWSCCPFQYH
GQPIYQGPPGALPQGPVPSLGLWRKSPVSPGELAHFCQDVDGPGQKIYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_007553200 [XP_007553200] PREDICTED: protein **FAM181**A [Poecilia formosa]. 102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQTLTSADYRC
ARGAERQRVTVTDEASSDAQLAQSVGGVMDQVPMRKRQLPASFWEEPRLTKARRDKPCLDLRRSSSSGTSDDGEN
ERRRSQEDAQKTANSSSGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQFQGHQVLHSQIVVPHPPFGLWSKAAEPE
RSEHPYGQKLHTHVVVKPIPTKATAQSPILSVFGFI PMRKRQLPASFWEEP

rs:XP_001948042 [XP_001948042] PREDICTED: transcriptional coactivator YAP1 [Acyrthosiphon pisum].>tr:J9JSR2_ACYPI [J9JSR2] SubName: Full=Uncharacterized protein {ECO:0000313|EnsemblMetazoa:ACYPI003364-PA};

66..80
MSGLQQQQQEQHQQVSIKMEPIGPSSPPSGVNSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPLRM
RQLPKSFFNPPSTGSKSPSISHSRENSGDSAFGTANVGPSCSGPVPLHSRAHSSPASLQQTYAVGAAMQQQKQQH
AKQRSYDISSTIDELGPLPQGWEQARTPEGQIYYLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQLLSPGNDSGS
STNATSTPTNSPPHIHSTLQGANKNVTLGPLPEGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQRAPTSGAV
LPSGSASWLANGVSGLSQSLQASQQKLRLQSLQLERERLKSRQQEIIRQQDLMQRSGQTNNDLDPFLSCSSSSVD
HSRQESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSMSVVDSQEMSTLDVTDDLVPSLQLGDE
FISMDEVQLLIDPNNKPGSILTWL   PLRMRQLPKSFFNPP

rs:XP_008108819   [XP_008108819] PREDICTED: protein **FAM181**A [Anolis
carolinensis].   144..158
MASSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARLPRCHHHHHPHH
MQQPSSLRERKAELEGKSRGLNTSESPEASEGRVAVVATTSASILAQSDKACKADHERQQQQGTSEALARPDQVP
MRKRQLPASFWEEPRPTQGPLSLFASSPLSSSKDLLPLYEGKKSLKGPDGFASLKNLVPLYEGKKSHKGPDRFIS
SKDLPPLYEGKKRQKGSDGGTSERPDAEALQVLSTWGCWPFQCHGPQTSPGLYVPPLPLAAALPSPAAPFPALGL
WRKNGGSSMEGEAFGKLGGMGQKVYHRPVVWKPIPTKPAAPPATLFSVFGYI PMRKRQLPASFWEEP

rs:XP_008106265   [XP_008106265] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Anolis carolinensis].   72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATGPLPDG
WEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMSQRISQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQL
QMEKERLRLKHQELLRQVRPQALRNINPSTANSPKRQELALRSQLPSMDQDGSQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVEEMDTGDTINQSNIPSHQNRFPDYLEAIPGTNVDLGTL
EGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_003219348   [XP_003219348] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Anolis carolinensis].>tr:G1KMR2_ANOCA [G1KMR2] SubName:
Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSACAP00000012509};
72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATGPLPDG
WEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMSQRISQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQL
QMEKERLRLKHQELLRQALRNINPSTANSPKRQELALRSQLPSMDQDGSQNPVSSPGMSQELRTMTTNSSDPFLN
SGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVEEMDTGDTINQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDA
MNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_016848161   [XP_016848161] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Anolis carolinensis].   72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATGPLPDG
WEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMSQRISQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQL
QMEKERLRLKHQELLRQVRPQELALRSQLPSMDQDGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVEEMDTGDTINQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_008106266   [XP_008106266] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Anolis carolinensis].   72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATGPLPDG
WEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMSQRISQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQL
QMEKERLRLKHQELLRQELALRSQLPSMDQDGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVEEMDTGDTINQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_008106267 [XP_008106267] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Anolis carolinensis]. 72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATAMSQRI
SQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKRQE
LALRSQLPSMDQDGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVE
EMDTGDTINQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLD
KESFLTWL PMRLRKLPDSFFKPP

rs:XP_008106268 [XP_008106268] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Anolis carolinensis]. 72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATAMSQRI
SQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKRQELALR
SQLPSMDQDGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVEEMDT
GDTINQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESF
LTWL PMRLRKLPDSFFKPP

rs:XP_016848162 [XP_016848162] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Anolis carolinensis]. 72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATAMSQRI
SQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPSMDQDGSQ
NPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVEEMDTGDTINQSNIPSH
QNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008106270 [XP_008106270] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Anolis carolinensis]. 72..86
MEASTTGQTPPQASAPESGGSGQPQQQAPPPPPPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPH
TLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHIRAHSSPASLQLGTVSPGALTPSSVVPGGAPSQHL
RQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKALLSQMNATAPTSPPVQQNIMNSATAMSQRI
SQSTPVKPPPLAPQSPPGGVLGGGNSSQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPSMDQDGSQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVEEMDTGDTINQSNIPSHQNRF
PDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008106371 [XP_008106371] PREDICTED: protein **FAM181**B [Anolis carolinensis].>rs:XP_008106372 [XP_008106372] PREDICTED: protein **FAM181**B [Anolis carolinensis]. 263..277
MAVQAAPLAPHGHPFLPFGFSALPAGSLGDFGDLEKGFEEGSTLLLDGGTADGDPGDFKELLSFIDSAS
SNIKLALDKPVKSKRKVNHRKYLQKQIKRCNGIIGGTSGTQESSPNPSSQPSFTNSMNSSHPHQQLNVHKRTSVS
LSPPSGGAIHSKPPQQPPNAHKRTTASLLPSSVTAAHCKPPFQQQKRTNPSLSPSSGGAVHCKPPQPSKRDASAA
TLVQSQSLAALFDSLQPSGVGLSSMQPEGGLGSSVPHVVGKKVPLRHRNLPPSFFTEPSHSLKEPGPEELFDLLE
YGGLLPEQQQQTSETSVFAPSRLQTSELGLEGPGLYESLPLPALLYSTETPLRPLPALYGPAAPSDSGSGELTAA
GPHLPSGAAFVPFFPDCPPLPAAYQYAPSGYSRNGAGALFQPLV PLRHRNLPPSFFTEP

rs:XP_016927695 [XP_016927695] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila suzukii]. 90..104
MCACLIAKIFLCSFRLYTISAFYMLTTMSASSNSNANSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISIGNKAAQVVQQPDGQSP
IAAIPTLQIQPSPQHSRLAIHHSRARSSPASLQQNFNVRARSDAAANNPNANPSSQQQPAGPTFPENSAQEFPSG
APASSGQIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQ
WEDPRIQYRQQQQILMAERIKQNDVLQTTKQTTTSTIANNMGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRM
QSGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_016927696 [XP_016927696] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila suzukii]. 90..104
MCACLIAKIFLCSFRLYTISAFYMLTTMSASSNSNANSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDN
LQALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISIGNKAAQVVQQPDGQSP
IAAIPTLQIQPSPQHSRLAIHHSRARSSPASLQQNFNVRARSDAAANNPNANPSSQQQPAGPTFPENSAQEFPSG
APASSGQIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQ
WEDPRIQYRQQQQILMAERIKQNESGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN
PLRMRKLPNSFFTPP

rs:XP_016971390 [XP_016971390] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila rhopaloa]. 88..102
MCACLIAKIILCSFHLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISNKSVVQVQQPGGPDGQSSI
AAIPQIQPSPQHSRLVIHHSRARSSPASLQQNYNVRARSDAANNPNANPSSQQPTAGPTFPENSAQEFPSGAPAS
SIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVVSPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRI
QYRQQQQILMAERIKQNDVLQTTKQTTTSTIANNMGPLPDGWEQAVTESGDLYFINHIDRTTSWNDPRMQSGLSV
LDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN PLRMRKLPNSFFTPP

rs:XP_016971391 [XP_016971391] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila rhopaloa]. 88..102
MCACLIAKIILCSFHLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSNISNKSVVQVQQPGGPDGQSSI
AAIPQIQPSPQHSRLVIHHSRARSSPASLQQNYNVRARSDAANNPNANPSSQQPTAGPTFPENSAQEFPSGAPAS
SIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVVSPIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRI
QYRQQQQILMAERIKQNESGLSVLDCPDNLVSSLQIEDNLCSNLFNDAQAIVNPPSSHKPDDLEWYKIN
PLRMRKLPNSFFTPP

rs:XP_017018760 [XP_017018760] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila kikkawai]. 60..74
MSTSNTNNLIEKEIDDEDMLSPIKPNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMRKLPNS
FFTPPAPSHSRANSADSTYDAGSQSNISNISSIKAAQPVDGQPPISAISQIQQPSPQQSRLAIHHFRARSSPASL
QQNYNVRARSEANPGASQQPAGPTFPENSAAEFTSSGATAPSSIELDAMNSCMSQDMPMSTQTVHKKQRSYDVVS
PIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQFRQQQQSLMAERIKQNDVLQTTKQTTTSTIAN
NMGPGPLPDGWEQAVTESGDIYFINHIDRTTSWNDPRMQSGLSVLDCPDNLVSSLQIEDNICSNLFNDAQTIVNP
PSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

rs:XP_017018761 [XP_017018761] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila kikkawai]. 60..74
MSTSNTNNLIEKEIDDEDMLSPIKPNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMRKLPNS
FFTPPAPSHSRANSADSTYDAGSQSNISNISSIKAAQPVDGQPPISAISQIQQPSPQQSRLAIHHFRARSSPASL
QQNYNVRARSEANPGASQQPAGPTFPENSAAEFTSSGATAPSSIELDAMNSCMSQDMPMSTQTVHKKQRSYDVVS
PIQLQRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQFRQQQQSLMAERIKQNESGLSVLDCPDNLVSS
LQIEDNICSNLFNDAQTIVNPPSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

rs:XP_008398305 [XP_008398305] PREDICTED: protein **FAM181**A [Poecilia reticulata]. 102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRAKSLTSADYRC
ARGAERQRATATDEASSDAQHAQSVGGVMDQVPMRKRQLPASFWEEPRLTKARRDKPCLDLRRSSSSGTSDGGEN
EKRRRSQDDAQKSANSSSGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQFQGHQVLHSQIVVPHPPFGLWSKAAEP
ERSEDPYGQKLHTHVVVKPIPTKATVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_006509915 [XP_006509915] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Mus musculus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQ
LQQLQMEKERLRLKQQELFRQVRPQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMT

TNSSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNV
DLGTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006509916 [XP_006509916] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Mus musculus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQVRPQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDL
GTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006509917 [XP_006509917] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Mus musculus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQ
LQQLQMEKERLRLKQQELFRQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGT
LEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006509918 [XP_006509918] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Mus musculus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQ
LQQLQMEKERLRLKQQELFRQVRPQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEE
LMPSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006509919 [XP_006509919] PREDICTED: transcriptional coactivator
YAP1 isoform X5 [Mus musculus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQVRPQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDE
STDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELM
PSLQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_006509920 [XP_006509920] PREDICTED: transcriptional coactivator
YAP1 isoform X6 [Mus musculus]. 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFGKAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQ
LQQLQMEKERLRLKQQELFRQELALRSQLPTLEQDGGTPNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDEST
DSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDYLEALPGTNVDLGTLEGDAMNIEGEELMPS
LQEALSSEILDVESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017321913 [XP_017321913] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Ictalurus punctatus].>tr:A0A2D0QU10_ICTPU [A0A2D0QU10]
SubName: Full=transcriptional coactivator YAP1 isoform X1
{ECO:0000313|RefSeq:XP_017321913.1}; 45..59
MDPSQHNPPAGHQVVHVRGDSETDLEALFNAVMNPKSAAVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLSAVTSGTMSTLAPAGAPPQHLRQPSYEIPDDVPLPPGWEMAKTPSGQRYF

LNHIDQSTTWQDPRKAMLQMNQTNSASPVPVQQQNLLNPATGPLPEGWEQAITAEGEIYYINHKNKTTSWLDPRL
DPRYALNQQRITQSAPVKQGTQLPSSPQNPAVMGGNNQMRLQQLQLEKERLRLKHQELLRPRPQELALRNQLPTS
MEQDSGTQNPVSSPGMGQDGRSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSL
GPVSLATQPSRFPNYLDEIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_017321914 [XP_017321914] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Ictalurus punctatus].>tr:A0A2D0QUC7_ICTPU [A0A2D0QUC7] SubName: Full=transcriptional coactivator YAP1 isoform X2 {ECO:0000313|RefSeq:XP_017321914.1}; 45..59
MDPSQHNPPAGHQVVHVRGDSETDLEALFNAVMNPKSAAVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLSAVTSGTMSTLAPAGAPPQHLRQPSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHIDQSTTWQDPRKAMLQMNQTNSASPVPVQQQNLLNPATALNQQRITQSAPVKQGTQLPSSPQNPAVMGGNNQ
MRLQQLQLEKERLRLKHQELLRPRPQELALRNQLPTSMEQDSGTQNPVSSPGMGQDGRSMTTNSSDPFLNSGTYH
SRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGPVSLATQPSRFPNYLDEIPGTDVDLGTLEGESMAVEG
EELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRMRKLPDSFFKPP

rs:XP_017332692 [XP_017332692] PREDICTED: protein **FAM181**A [Ictalurus punctatus].>rs:XP_017332693 [XP_017332693] PREDICTED: protein **FAM181**A [Ictalurus punctatus].>tr:A0A2D0RQA9_ICTPU [A0A2D0RQA9] SubName: Full=protein **FAM181**A {ECO:0000313|RefSeq:XP_017332692.1, ECO:0000313|RefSeq:XP_017332693.1}; 134..148
MWTRNGLKDKRWLKMASSDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCPR
TPRCHTHRISESSAAKLTEDKRVMFTHERAKNVLLNETQATHTRGEGNVDGNPNSENRSAPGHIPMRKRQLPASF
WEEPRSSHISFEYAWKSHSGGTVRYGSSEADGEKRTTIEDELKANSWLRVRRGSSDLEPLRVDLTSTNVAVCAYC
PLQCHGHRLLHSHLITPHSAFTGPGLRAKTPATELDMQKIKDELKYSSTHVVVKPIPTKPVSSSIFSVFGFI
PMRKRQLPASFWEEP

rs:XP_017388556 [XP_017388556] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017388557 [XP_017388557] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017388558 [XP_017388558] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Cebus capucinus imitator].>tr:A0A2K5S119_CEBCA [A0A2K5S119] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSCCAP00000034056}; 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS

PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017388559 [XP_017388559] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_017388560 [XP_017388560] PREDICTED: transcriptional coactivator
YAP1 isoform X5 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017388561 [XP_017388561] PREDICTED: transcriptional coactivator
YAP1 isoform X6 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017388562 [XP_017388562] PREDICTED: transcriptional coactivator
YAP1 isoform X7 [Cebus capucinus imitator].>tr:A0A2K5S0Y4_CEBCA
[A0A2K5S0Y4] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSCCAP00000034059}; 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017388563 [XP_017388563] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017388564 [XP_017388564] PREDICTED: transcriptional coactivator
YAP1 isoform X9 [Cebus capucinus imitator].>tr:A0A2K5S0W3_CEBCA

[A0A2K5S0W3] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSCCAP00000034039}; 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017388565 [XP_017388565] PREDICTED: transcriptional coactivator
YAP1 isoform X10 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017388566 [XP_017388566] PREDICTED: transcriptional coactivator
YAP1 isoform X11 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017388567 [XP_017388567] PREDICTED: transcriptional coactivator
YAP1 isoform X12 [Cebus capucinus imitator]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPASAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_017400427 [XP_017400427] PREDICTED: protein **FAM181**B [Cebus
capucinus imitator]. 218..232
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGASAGALLSGAEGGDLREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPGAPTVAAPAHGK
AAPRREASQATAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPAARLGAGGAGGDAAGHVGGAAVPGARKVPL
RARNLPPSFFTEPSLAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLEPDYGAGTAAAVLLAAEPLDVFPAGASVL
RGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPSGEDGPGHLAS
FAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_017402491 [XP_017402491] PREDICTED: protein **FAM181**A isoform X1
[Cebus capucinus imitator]. 225..239
MLCIWRGAPDWPEGPPSSGELSSIQPTQGLHNCFQPDGARPAVPGPVPGLQRGTCRATLVGPRPAPLVS
SVSFPGAASQQQSPPSSWKASCGGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRF
SQKYSRLPRGLPGRATEPYLKRGPDNQPGRLLLDLGPDSSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAA
RPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEAKKNCKGLEPLGPETASVSMSPSALAEKESLK
MPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPTFPGELAYLCKDADGLGQKVCRPMVLK
PIPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_017402492 [XP_017402492] PREDICTED: protein **FAM181**A isoform X2 [Cebus capucinus imitator]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRATEPYLK
RGPDNQPGRLLLDLGPDSSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAARPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEAKKNCKGLEPLGPETASVSMSPSALAEKESLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPTFPGELAYLCKDADGLGQKVCRPMVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_017402493 [XP_017402493] PREDICTED: protein **FAM181**A isoform X3 [Cebus capucinus imitator]. 374..388
MWRGRSSSAFAHRRAWLQVQTLLVNAMRSWESNSTSLTSFVRGKRTATLTERPREVFVWSSNTALVAVG
MCCVSTYNPFSSTFLSPSFLSSLFSSFLPPLFPQKVFGGKRVCVKNYGESFIRHQLTSHGVLPGGEAHYWLRKER
QLHKWAVQNGQAGLQVPWDLEEAGSRAEWLQKILMPLEERRSSRDRKDAAHIECRNLGGKGRAQRSKQLLGQVSS
VSFPGAASQQQSPPSSWKASCGGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFS
QKYSRLPRGLPGRATEPYLKRGPDNQPGRLLLDLGPDSSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAAR
PGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEAKKNCKGLEPLGPETASVSMSPSALAEKESLKM
PGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPTFPGELAYLCKDADGLGQKVCRPMVLKP
IPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_017563523 [XP_017563523] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Pygocentrus nattereri]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAAVPSSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGGLTAMTPTGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIEQTTTWQDPRKAMLQMNSAAPGSPVPVQQQNLLNPATGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFETDEARSKDTKTLQTTFPHPPPKSRARTSAGMLFHTSKGLRTLNQQRISQSAPVKQAAQLPSSPQNTGVMG
GNSQMRLLQMEKERQRLKHQELLRRPQELALRNQLPTSMEQDGGSQNPVSSPGMGQDARSMTTNSSDPFLNSGTY
HSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGPPSMATQPRGFPDYLDAIPGTDVDLGTLEGESMAVE
GEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017563524 [XP_017563524] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Pygocentrus nattereri]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAAVPSSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGGLTAMTPTGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIEQTTTWQDPRKAMLQMNSAAPGSPVPVQQQNLLNPATGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFDEARSKDTKTLQTTFPHPPPKSRARTSAGMLFHTSKGLRTLNQQRISQSAPVKQAAQLPSSPQNTGVMGGN
SQMRLLQMEKERQRLKHQELLRRPQELALRNQLPTSMEQDGGSQNPVSSPGMGQDARSMTTNSSDPFLNSGTYHS
RDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGPPSMATQPRGFPDYLDAIPGTDVDLGTLEGESMAVEGE
ELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017563525 [XP_017563525] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Pygocentrus nattereri].>tr:A0A3B4E9B4_PYGNA [A0A3B4E9B4] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPNAP00000031874};45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAAVPSSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGGLTAMTPTGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIEQTTTWQDPRKAMLQMNSAAPGSPVPVQQQNLLNPATGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFETDEARSKDTKTLQTTFPHPPPKSRARTSAGMLFHTSKALNQQRISQSAPVKQAAQLPSSPQNTGVMGGNS
QMRLLQMEKERQRLKHQELLRRPQELALRNQLPTSMEQDGGSQNPVSSPGMGQDARSMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGPPSMATQPRGFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_017563526 [XP_017563526] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Pygocentrus nattereri].>tr:A0A3B4E9E1_PYGNA [A0A3B4E9E1] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPNAP00000031871};45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAAVPSSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGGLTAMTPTGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIEQTTTWQDPRKAMLQMNSAAPGSPVPVQQQNLLNPATGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRISQSAPVKQAAQLPSSPQNTGVMGGNSQMRLLQMEKERQRLKHQELLRRPQELALRNQLPTSMEQ

DGGSQNPVSSPGMGQDARSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGPP
SMATQPRGFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_008627943 [XP_008627943] PREDICTED: protein **FAM181**A [Corvus
brachyrhynchos].>tr:A0A091F2P8_CORBR [A0A091F2P8] SubName: Full=Protein
FAM181A {ECO:0000313|EMBL:KFO56115.1}; 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGAEDRARGPQPEAPDSGPHGGAAAEKVMQTAEAEENLTGERVLQEQKPEAARPDQVPMRKRQLPASFWEEPRPA
QSLTGRAFPASPEGFQAPRDPPPYEGKKSKRSPDAAGQESPPDPAPHAGEKDPAGALSGRVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLGLWRKSAAALPAEVPHFCKEADGPGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_017596717 [XP_017596717] PREDICTED: uncharacterized protein
LOC108448429 [Corvus brachyrhynchos]. 171..185
MAAGVIQPLAELRLPSPFPHGLLLPTHPEPDFPDVSEEEEEEEEEEDEEEEEVEAVEESVRPELAGVSS
TAETTLRLLKFSELISCDIQRYFGRRGREEAPSSRPVPEDCGSPQSTEAVPEAVVPRRSPGATHMLGPLAELFEY
GVHRCLPARVAGSKTQRLERKYGHITPMHHRKLPPSFWKEPGPGPASLLHAGTPDFSDLLANWTVEPGPELPGTG
RELPGRLGLEAEPFAGL PMHHRKLPPSFWKEP

rs:XP_017789666 [XP_017789666] PREDICTED: transcriptional coactivator
YAP1 [Habropoda laboriosa]. 46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAXXXXXXXXAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLG
PLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAANVAAVAAAVDNGKSSTGATNSLGPLPDGWEQARTPEG
EIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPQNWLQQQQPTGGGIQSNQTLQACQQKLRLQSLQMERERLKQ
RQQEIMRQQELMLRQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAP
METPDLSTLSDNIDSTDDLVPSLQLSEDFSSDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:NP_001180963 [NP_001180963] protein **FAM181**B [Macaca
mulatta].>tr:F7A8C3_MACMU [F7A8C3] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSMMUP00000036810};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSATDTPAKRPLAAPSAPTVAAPAHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPVAGLGGAGTGGAGGDAAGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPHQVSYDYSAGYSRNAYSSLWRPDAVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_017835831 [XP_017835831] PREDICTED: transcriptional coactivator
yorkie isoform X1 [Drosophila busckii]. 62..76
MSLSNKSGNINDKEIDDEDMLSPTKLSTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLP
NSFFNPPAPLHSRANSADSTYDGSQTNINKTAQVSPSEIQSSISQNQPSQSRLQIHHFRARSSPASLQQNYTVRS
RNEPSANTSQAPGPAYPDNGVDFNSSGVAASNIDVDAMNTCMAQGQEAAVAAAALSTQTSIHKKQRSYDVVSPIQ
LQIQLGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFRQQQQRVIAERIKPNDILQTTKQTNAPTIGSQM
GPLPEGWEQAVTESGDIYFINHIDRTTSWNDPRTQSGLSGLDCPDNIVSTLQIGDNICNNIFNDAQNIITPSSQK
PADLEWYKIN PFRMRKLPNSFFNPP

rs:XP_017835832 [XP_017835832] PREDICTED: transcriptional coactivator
yorkie isoform X2 [Drosophila busckii].>tr:A0A0M4EIM3_DROBS [A0A0M4EIM3]
SubName: Full=Yki {ECO:0000313|EMBL:ALC42660.1};>gp:CP012524_2239
[CP012524] yki [Drosophila busckii] 62..76
MSLSNKSGNINDKEIDDEDMLSPTKLSTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLP
NSFFNPPAPLHSRANSADSTYDGSQTNINKTAQVSPSEIQSSISQNQPSQSRLQIHHFRARSSPASLQQNYTVRS
RNEPSANTSQAPGPAYPDNGVDFNSSGVAASNIDVDAMNTCMAQGQEAAVAAAALSTQTSIHKKQRSYDVVSPIQ
LQIQLGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFRQQQQRVIAERIKPNESGLSGLDCPDNIVSTLQ
IGDNICNNIFNDAQNIITPSSQKPADLEWYKIN PFRMRKLPNSFFNPP

rs:XP_017835834 [XP_017835834] PREDICTED: transcriptional coactivator yorkie isoform X3 [Drosophila busckii]. 62..76
MSLSNKSGNINDKEIDDEDMLSPTKLSTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLP
NSFFNPPAPLHSRANSADSTYDGSQTNINKTAQVSPSEIQSSISQNQPSQSRLQIHHFRARSSPASLQQNYTVRS
RNEPSANTSQAPGPAYPDNGVDFNSSGVAASNIDVDAMNTCMAQGQEAAVAAAALSTQTSIHKKQRSYDVVSPIQ
LQIQLGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFRQQQQRVIAERIKPNVLTDTYKKMKA
PFRMRKLPNSFFNPP

rs:XP_017835835 [XP_017835835] PREDICTED: transcriptional coactivator yorkie isoform X4 [Drosophila busckii]. 62..76
MSLSNKSGNINDKEIDDEDMLSPTKLSTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLP
NSFFNPPAPLHSRANSADSTYDGSQTNINKTAQVSPSEIQSSISQNQPSQSRLQIHHFRARSSPASLQQNYTVRS
RNEPSANTSQAPGPAYPDNGVDFNSSGVAASNIDVDAMNTCMAQGQEAAVAAAALSTQTSIHKKQRSYDVVSPIQ
LQIQLGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFRQQQQRVIAERIKPNVLPILS
PFRMRKLPNSFFNPP

rs:XP_017866532 [XP_017866532] PREDICTED: transcriptional coactivator yorkie isoform X1 [Drosophila arizonae]. 61..75
MSLSNKSNISEKEIDDEDMLSPTKISTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEMQPSLTQQNQPSHSRLAIHHIRARSSPASLQQNYNVRTRNE
PSANNANTNQGPAYPETSVDFVSASTANNIDLDVINTCMGPVPGPDAAALAATQTTIHKKQRSYDVVSPIQLQSQ
LGALPPGWEQAKTNDGQIYYLNHTSKTTQWEDPRIQFRQQQRALAERIKPNDVIQTTKPTSSSTIATHLGPLPD
GWEQAVTESGDIYFINHIDRTTSWNDPRIQSGLNVLDCPDNLVSSLQIGDNICSNIFNDTQAIINTPSSHKPDDL
EWYKIN PFRMRKLPNSFFNPP

rs:XP_017866533 [XP_017866533] PREDICTED: transcriptional coactivator yorkie isoform X2 [Drosophila arizonae]. 61..75
MSLSNKSNISEKEIDDEDMLSPTKISTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQLPFRMRKLPN
SFFNPPAPLHSRANSADSTYDGSQTNINKTAQPEMQPSLTQQNQPSHSRLAIHHIRARSSPASLQQNYNVRTRNE
PSANNANTNQGPAYPETSVDFVSASTANNIDLDVINTCMGPVPGPDAAALAATQTTIHKKQRSYDVVSPIQLQSQ
LGALPPGWEQAKTNDGQIYYLNHTSKTTQWEDPRIQFRQQQRALAERIKPNESGLNVLDCPDNLVSSLQIGDNI
CSNIFNDTQAIINTPSSHKPDDLEWYKIN PFRMRKLPNSFFNPP

rs:XP_009005426 [XP_009005426] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Callithrix jacchus]. 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_009005427 [XP_009005427] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Callithrix jacchus].>tr:F6W3S6_CALJA [F6W3S6] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSCJAP00000001114}; SubName: Full=Yorkie homolog isoform 1 {ECO:0000313|EMBL:JAB10536.1};
84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_009005428 [XP_009005428] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Callithrix jacchus].>tr:U3DLA3_CALJA [U3DLA3] SubName: Full=Yorkie homolog isoform 1 {ECO:0000313|EMBL:JAB10535.1}; 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_002754685 [XP_002754685] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Callithrix jacchus].>tr:F6W3W8_CALJA [F6W3W8] SubName: Full=Yorkie homolog isoform 1 {ECO:0000313|EMBL:JAB10538.1}; 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_009005429 [XP_009005429] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Callithrix jacchus]. 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_009005430 [XP_009005430] PREDICTED: transcriptional coactivator YAP1 isoform X6 [Callithrix jacchus].>tr:F6W445_CALJA [F6W445] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSCJAP00000001100}; SubName: Full=Yorkie homolog isoform 3 {ECO:0000313|EMBL:JAB10537.1}; 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_009005431 [XP_009005431] PREDICTED: transcriptional coactivator YAP1 isoform X7 [Callithrix jacchus].>tr:U3FID6_CALJA [U3FID6] SubName: Full=Yorkie homolog isoform 3 {ECO:0000313|EMBL:JAB38540.1}; 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_002754686 [XP_002754686] PREDICTED: transcriptional coactivator YAP1 isoform X8 [Callithrix jacchus].>tr:U3EDT0_CALJA [U3EDT0] SubName: Full=Yorkie homolog isoform 3 {ECO:0000313|EMBL:JAB23746.1}; 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGD
GMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_009005432 [XP_009005432] PREDICTED: transcriptional coactivator YAP1 isoform X9 [Callithrix jacchus].>tr:F6WZY5_CALJA [F6WZY5] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSCJAP00000046343}; 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQA
MRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSM
SSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALS
SDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_003734188 [XP_003734188] PREDICTED: transcriptional coactivator YAP1 isoform X10 [Callithrix jacchus]. 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNI
NPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYS
VPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDIL
NDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_009005433 [XP_009005433] PREDICTED: transcriptional coactivator YAP1 isoform X11 [Callithrix jacchus]. 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQE
LALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSV
DEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL PMRLRKLPDSFFKPP

rs:XP_009005434 [XP_009005434] PREDICTED: transcriptional coactivator YAP1 isoform X12 [Callithrix jacchus].>tr:U3DIQ5_CALJA [U3DIQ5] SubName: Full=Yorkie homolog isoform 2 {ECO:0000313|EMBL:JAB38538.1}; 84..98
MDPGQQPPPQAAPQGQGQPPAQPQGQGPSSAPGQPAPAATQAASQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALR
SQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMD
TGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKES
FLTWL PMRLRKLPDSFFKPP

rs:XP_002754796 [XP_002754796] PREDICTED: protein **FAM181**B [Callithrix jacchus].>tr:F6V7Z5_CALJA [F6V7Z5] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSCJAP00000042161}; SubName: Full=Protein **FAM181**B {ECO:0000313|EMBL:JAB05080.1}; 218..232
MAVQAALLSTHPFVPFGFGGSADGLGGAFGALDKGCCFEDDETGMPAGALLSGAEGGDVREATRDLLSF

IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAAPGPPSPSAADTPAKRPLAAPGAPTVAAPAHSK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVVTPAAGLGAGGAGGDAAGLAGGAAVPGAKKVPL
RARNLPPSFFTEPSRAGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPTGASVLR
GPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKPPLTVPRGGLTLNEPLRPLYPAAADSPGGEDGPGHLASF
APFFPDCALPPPPPPHQVPYDYSAGYSRTAYSSLWRPDGVWEGEPGEEGAHRDPLRARNLPPSFFTEP

rs:XP_018020788   [XP_018020788] PREDICTED: transcriptional coactivator
YAP1-like isoform X1 [Hyalella azteca].   50..64
METSEHEDKVVGEPQKGSHVVHVRADSDSELQALFDCVLKPSKQMPLQKPFKMRNLPASFFKPPTHRQS
PAPTVTHSRESSADSTYGGGGGGGPIRVGGAMSPAAAPLPPAPQHFRHHSSPASLQQTFAVAQQTNIGGHAKQHS
YDALAEDMSPLPPGWEQARTPQGQIYYLNCHSSGYRRHITQTTTWDDPRKKVQANPSQTNANQQQPAPQQQQQQQ
QQPQPAPTTVQSNPVAVQQTQNNVVQLTTPSLPAQNPAQPNPAQHLGALNTNGTALTNPLLNTDLLGPLPEGWEQ
AITADGEIYYINHQEKATSWFDPRIPRRYQTAQLQKTPLAHQHSPIASPNSQLQQLVGGMMGPRSPSTQHLPRLP
LDNNRLKNRPNSPDARKKLRHLRRHEDVIWVNQAPSTLVSTSINNAINNNNVLNTTNSTTLLQLQQQLTHNQLQQ
QQMSNQQAQQQQQQQLQQQQEQLQQQMLRAAVGGGDPFLLSTLPPADLHARQESADSGLGLGGNGGAHNGSTPGS
AHSYTPHQTPTTPEDFLAAMEDVEITPSENRRGVVNSPAPPMMEANDLESMDSEDLVPSINIPCELSSDFLSEVI
GSNRMDNTWL PFKMRNLPASFFKPP

rs:XP_018020789   [XP_018020789] PREDICTED: transcriptional coactivator
YAP1-like isoform X2 [Hyalella azteca].   50..64
METSEHEDKVVGEPQKGSHVVHVRADSDSELQALFDCVLKPSKQMPLQKPFKMRNLPASFFKPPTHRQS
PAPTVTHSRESSADSTYGGGGGGGPIRVGGAMSPAAAPLPPAPQHFRHHSSPASLQQTFAVAQQTNIGGHAKQHS
YDALAEDMSPLPPGWEQARTPQGQIYYLNHITQTTTWDDPRKKVQANPSQTNANQQQPAPQQQQQQQQQPQPAPT
TVQSNPVAVQQTQNNVVQLTTPSLPAQNPAQPNPAQHLGALNTNGTALTNPLLNTDLLGPLPEGWEQAITADGEI
YYINHQEKATSWFDPRIPRRYQTAQLQKTPLAHQHSPIASPNSQLQQLVGGMMGPRSPSTQHLPRLPLDNNRLKN
RPNSPDARKKLRHLRRHEDVIWVNQAPSTLVSTSINNAINNNNVLNTTNSTTLLQLQQQLTHNQLQQQQMSNQQA
QQQQQQQLQQQQEQLQQQMLRAAVGGGDPFLLSTLPPADLHARQESADSGLGLGGNGGAHNGSTPGSAHSYTPHQ
TPTTPEDFLAAMEDVEITPSENRRARVAGVVNSPAPPMMEANDLESMDSEDLVPSINIPCELSSDFLSEVIGSNR
MDNTWL   PFKMRNLPASFFKPP

rs:XP_018020790   [XP_018020790] PREDICTED: transcriptional coactivator
YAP1-like isoform X3 [Hyalella azteca].   50..64
METSEHEDKVVGEPQKGSHVVHVRADSDSELQALFDCVLKPSKQMPLQKPFKMRNLPASFFKPPTHRQS
PAPTVTHSRESSADSTYGGGGGGGPIRVGGAMSPAAAPLPPAPQHFRHHSSPASLQQTFAVAQQTNIGGHAKQHS
YDALAEDMSPLPPGWEQARTPQGQIYYLNCHSSGYRRHITQTTTWDDPRKKVQANPSQTNANQQQPAPQQQQQQQ
QQPQPAPTTVQSNPVAVQQTQNNVVQLTTPSLPAQNPAQPNPAQHLGALNTNGTALTNPLLNTDLLGPLPEGWEQ
AITADGEIYYINHQEKATSWFDPRIPRRYQTAQLQKTPLAHQHSPIASPNSQLQQLVGGMMGPRSPSTQHLPRLP
LDNNRLKNRPNSPDARKKVNQAPSTLVSTSINNAINNNNVLNTTNSTTLLQLQQQLTHNQLQQQQMSNQQAQQQQ
QQQLQQQQEQLQQQMLRAAVGGGDPFLLSTLPPADLHARQESADSGLGLGGNGGAHNGSTPGSAHSYTPHQTPTT
PEDFLAAMEDVEITPSENRRARVAGVVNSPAPPMMEANDLESMDSEDLVPSINIPCELSSDFLSEVIGSNRMDNT
WL   PFKMRNLPASFFKPP

rs:XP_018020791   [XP_018020791] PREDICTED: transcriptional coactivator
YAP1-like isoform X4 [Hyalella azteca].   50..64
METSEHEDKVVGEPQKGSHVVHVRADSDSELQALFDCVLKPSKQMPLQKPFKMRNLPASFFKPPTHRQS
PAPTVTHSRESSADSTYGGGGGGGPIRVGGAMSPAAAPLPPAPQHFRHHSSPASLQQTFAVAQQTNIGGHAKQHS
YDALAEDMSPLPPGWEQARTPQGQIYYLNCHSSGYRRHITQTTTWDDPRKKVQANPSQTNANQQQPAPQQQQQQQ
QQPQPAPTTVQSNPVAVQQTQNNVVQLTTPSLPAQNPAQPNPAQHLGALNTNGTALTNPLLNTDLLGPLPEGWEQ
AITADGEIYYINHQEKATSWFDPRIPRRYQTAQLQKTPLAHQHSPIASPNSQLQQLVGGMMGPRSPSTQHLPRLP
LDNNRLKNRPNSPDARKKLRHLRRHEDVIWESADSGLGLGGNGGAHNGSTPGSAHSYTPHQTPTTPEDFLAAMED
VEITPSENRRARVAGVVNSPAPPMMEANDLESMDSEDLVPSINIPCELSSDFLSEVIGSNRMDNTWL
PFKMRNLPASFFKPP

rs:XP_018020792   [XP_018020792] PREDICTED: transcriptional coactivator
YAP1-like isoform X5 [Hyalella azteca].   50..64
METSEHEDKVVGEPQKGSHVVHVRADSDSELQALFDCVLKPSKQMPLQKPFKMRNLPASFFKPPTHRQS
PAPTVTHSRESSADSTYGGGGGGGPIRVGGAMSPAAAPLPPAPQHFRHHSSPASLQQTFAVAQQTNIGGHAKQHS
YDALAEDMSPLPPGWEQARTPQGQIYYLNCHSSGYRRHITQTTTWDDPRKKVQANPSQTNANQQQPAPQQQQQQQ
QQPQPAPTTVQSNPVAVQQTQNNVVQLTTPSLPAQNPAQPNPAQHLGALNTNGTALTNPLLNTDLLGPLPEGWEQ

AITADGEIYYINHQEKATSWFDPRIPRRYQTAQLQKTPLAHQHSPIASPNSQLQQLVGGMMGPRSPSTQHLPRLP
LDNNRLKNRPNSPDARKKESADSGLGLGGNGGAHNGSTPGSAHSYTPHQTPTTPEDFLAAMEDVEITPSENRRAR
VAGVVNSPAPPMMEANDLESMDSEDLVPSINIPCELSSDFLSEVIGSNRMDNTWL   PFKMRNLPASFFKPP

rs:XP_018008841   [XP_018008841] PREDICTED: uncharacterized protein
LOC108666470 [Hyalella azteca].   154..168
MSSAKRKPRTPSPLEDEGLFTGPNQEDSYTGQNTEDSFTGKNKEDSFAGRKLSVSEFDSPALLDYDAVA
SPSASSTSSEPSYVRQPGFEHHAHEVPVGRSSHTQQSDLKTQKNLLPKRIKKKKCRPDEGCDMIAIDVGPSVPST
RPKIKKEPLPMKLRDLPPSFWVQPNRASCLPPSGTLLPPLLLGKDYHDVTDVRPVTPPEVGEQRVCRGDGSKYSV
SSPSPTLSSHSLLNLHHSPSSSSIISSTINTSPSSSSLSALASQTSSSSSQPKSSIFTGSLHSPPPDAVMSPNIQ
PCTSPTSLYSASQSPTMKHHPSYSSQSSCPALFGDLSQSPHSSSPILLSSTKSYQERRGETIIKVGNTDLLFSLF
DKVEQGDRRKLQLLKRTRVRKGSNPPPVRHHRDDDPCLVGAVTEGLLPLLDSTPHSSGASTPLGTRHTQQVVEMV
NLKGSNRTWSLPSLNVEPNYSQMLSELVMKL   PMKLRDLPPSFWVQP

rs:XP_018054102   [XP_018054102] PREDICTED: LOW QUALITY PROTEIN:
transcriptional coactivator YAP1-like [Atta colombica].   46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVPATPNGGGSGVPNGGTNGSGGSGGGGGXXXXSXAAAGLTVSHPRAHSSPASLQQTYASA
QQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAA
VAAAVESSKSNALGPLPDGWEQARTAEGEIYFINHQTRTTSWFDPRIPSHLQRTPASGAMLPQNWQLQQPTGIQS
NQNLQACQKQKIRLQSLQLERERLKQRQQEIMRQVGIQQEMMLRQSTTDAVMDPFLSGINEHARQESADSGLGLG
SAYSLPQASDDFLNIDENMDGTSERHCALNDLTKRLYRSHKYINGGAPMDTPDLSTLSDNIDSTDDLLPSLQAYY
RCTGNLGM   PLRLRNLPDSFFNPP

rs:XP_018299804   [XP_018299804] PREDICTED: LOW QUALITY PROTEIN:
transcriptional coactivator YAP1 [Trachymyrmex zeteki].   46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDNKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVPATPNGGSSVPNGGTNGGGGGGGGGNAAGAAGTGAVAAAAGLTVSHPRAHSSPASLQQ
TYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAA
ASVAAVAAAVESSKSNALGPLPDGWEQARTAEGEIYFINHQTRTTSWFDPRIPSHLQRTPASGAMLPQNWQLQQP
TGIQSNQNLQACQKQKIRLQSLQLERERLKQRQQEIMRQVGIQQEMMLRQSTTDAVMDPFLSGINEQHARQESAD
SGLGLGSAYSLPQASDDFLNIDENMDSTSDGGAPMDTPDLSTLSDNIDSTDDLLPSLQLNEEFSTDILDDVQSLI
NPNTTKPENVLTWL   PLRLRNLPDSFFNPP

rs:XP_018494750   [XP_018494750] PREDICTED: LOW QUALITY PROTEIN:
transcriptional coactivator YAP1-A [Galendromus occidentalis].   42..56
MATEGFVEQQGPNHVVRYRQDSNLDELFKVAMEGKSTLFGLPMRMRNLPPSFFQQPVEGPGGIIPRPQI
NHSRAHSSPASLEQTYRSAPQQPTHTRQQSYDLVDEEPLPEGWEMARTNTGQRYFLNHVTHTTTWEDPRKKLNGQ
LSANHHSTAPPPPHTTNPSVINAKTLGPLPDGWEQSTSPEGEVYFINHVDRTTSWFDPRIPINLQKAPTSXADLI
PDSGSTDSINAVCAATSTLSLAQQQLQRLQQLQLERERMKQRQLEILRQPAFGLTTEQNNNTINPNQLAVNNNNS
NNLGHTDPFLGGPHSRQESADSGLGLGPSFSLPEEFPTPFDNSANIGMEDASMDAMPVGAIVPANNCVAPEQMDS
DDLMPSLNEMPDMPDLLPDMEALLTDNKDSVLTWL PMRMRNLPPSFFQQP

rs:XP_018496354   [XP_018496354] PREDICTED: transcription cofactor
vestigial-like protein 2 [Galendromus occidentalis]. 154..168
MTRVAAPNPPPTSGGYFIAGPSSPQDFVPPSAFVEQKPENLHFEKFSSPPALKENYSSPSPPHGLISPG
TSSPTIAPIDLPSTSTAVCSPSPEVLESKDDVGEATYVSPKCVVIKYYKTDVASVLDDHFQKALAQAGFGGPSRR
SDDDTMDSKPLSQRNLPQSFFCPPNPQSVAASSGSYPPSPSSTSSYPQAGPSQASPQIRASPSQMNGPSPSHLAS
HSGHPSPSYLPLPSTSSNQSLTDFYPPPPTPSSNDYESWSHYVHGYRAAHLSPQDLQTYAVAANRHQFAQHQVSK
EPFPESPKSPKSPNDPPASPELTYLTAEEPPQVVRMKMYNSLLNLGNQQQRASCSAAVLGVNEKVMDTWGQSVAR
YHEQIQMNINMSGHPVAIQEPYPSNYAHPMSAAMTGLEATADTKDMYWF   PLSQRNLPQSFFCPP

rs:XP_004051940   [XP_004051940] PREDICTED: protein **FAM181**B [Gorilla
gorilla gorilla].>tr:G3QJ85_GORGO [G3QJ85] SubName: Full=Family with
sequence similarity 181 member B {ECO:0000313|Ensembl:ENSGGOP00000002470};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGEVAAPAAGLGGAGTGGAGGDVAGPAGATAIPGARK

VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVELFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_018895535 [XP_018895535] PREDICTED: protein **FAM181**A isoform X1
[Gorilla gorilla gorilla]. 165..179
MACFVPQVSSVSFLGAASHQQSLSSSWKASCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRR
SVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPYLKRGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPYREEC
LAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTL
VPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKD
VDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_004055657 [XP_004055657] PREDICTED: protein **FAM181**A isoform X2
[Gorilla gorilla gorilla].>rs:XP_004055658 [XP_004055658] PREDICTED:
protein **FAM181**A isoform X2 [Gorilla gorilla gorilla].>rs:XP_018895536
[XP_018895536] PREDICTED: protein **FAM181**A isoform X2 [Gorilla gorilla
gorilla]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPYLK
RGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTLVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_018924866 [XP_018924866] PREDICTED: LOW QUALITY PROTEIN: protein
FAM181B-like [Cyprinus carpio]. 156..170
MAVQAAIMNSQFLNFCXPGSVMDYEVEKGLEGGFLGEVDCEGDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISPGTTPVQEPCKRQGLPHNPTSNLSSKTPPKKDGIQANLQSKSLAALFNSA
KDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAAEFLELLGPDYSNMVSEQDLFHTAP
NRIQQEVTVGPEPYDSHHFVSGGFLYTEPWGTCSSSPKKSADLRTVPLQPNIYTHTDLSGSMPMEQSSPCALTFS
NFFTDCSAPPVSYDLVNGYNRGSFSSL PLRHRNLPPSFFTEP

rs:XP_018924872 [XP_018924872] PREDICTED: LOW QUALITY PROTEIN: protein
FAM181B-like [Cyprinus carpio]. 156..170
MAVQTAIMNSQFLNFCFPGSVMDYGVEKGLEGGLLGEVDCGGDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVTPRKYLQKQIKRCTGIISPGTTPVQEPCKRQGSPQTPTSNLPAKMPPKKDGMQASLQSKSLAALFNSA
KDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAVDFLELLGPEYSNMVSEQDLFYTAP
IRIQQDVTVGPEPYDSHHFVSGGFLYTEPWGTCGGTSKKSGDMRTVPVQPNLYTHTDLSGSVPVEQSSPCALTFS
NFFTDCSAPPVSYDLVNGYNRGSFSSL PLRHRNLPPSFFTEP

rs:XP_018944764 [XP_018944764] PREDICTED: transcriptional coactivator
YAP1-like [Cyprinus carpio]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLSSMVPSNAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISQSAPVKQGSQLPSSPQSAVLGGNNQIRLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSME
HDGGTQNPVSSPSMGQDARNMTTNSSDPFLSSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDSLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_018969752 [XP_018969752] PREDICTED: protein **FAM181**A [Cyprinus
carpio]. 111..125
MMSSDSEVKTLLNFVNLASSDIKAALDRSAPCRRSVDHRKYLQKQLKRFSHRYAKMPRCHPHRNGDSAL
AKLSEEKAPHGTGTGRDVSAGSEEEARSGQGQGQGHGQIPMPMRKRQLPASFWKEPQSSSGSRERLERFLKNNAS
ATGRVRSPAVNGEKSKVVFDDSKANPLLSGSAACACACCTLPYRALHSRFLLPHADAPFRSRAEPAHSFGDGQQR
SGAHVVIKPIPTKPALSSSSAFSVFGF PMRKRQLPASFWKEP

rs:XP_018978767 [XP_018978767] PREDICTED: transcriptional coactivator
YAP1 isoform X1 [Cyprinus carpio]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLEALFNAVMNPKNAITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS

TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLSSMGPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYAMNQQRISQGAPVKQGSQLPSSPQSGVLGGNNQIRLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMETVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_018978768 [XP_018978768] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Cyprinus carpio]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLEALFNAVMNPKNAITPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLSSMGPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASAMNQQRISQGAPVKQGSQLPSSPQSGVLGGNNQI
RLQQIQMEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGPSSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEE
LMPSLQEALSSDILNDMETVLAATKIDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_012991334 [XP_012991334] PREDICTED: transcriptional coactivator YAP1 [Esox lucius].>tr:A0A3P9ANY5_ESOLU [A0A3P9ANY5] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSELUP00000042445}; 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFTPPEPKSHSRQAS
TDAGTAGALPPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSHLRQSSYEIPEDMPLPPGWEMAKTPSGQRYFLN
HLDQSTTWQDPRKALLQMNQAPPTSPVPVQPQNILNPASGPLPDGWEQAITSDGEIYYINHKNKTTSWLDPRLDT
RYGLNQQRITQSAPGKQGGQLPSSPQSGGVMAGNNQLRLQQVQMEKERLRLKHQELLRARPQELALRNQLPTNME
QDVGTPNPVSSPGMVQDARTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLPA
SMGTQPSRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFTPP

rs:XP_012987194 [XP_012987194] PREDICTED: transcriptional coactivator YAP1 [Esox lucius]. 48..62
MDARQGQGAPPVGQQIVHVRGDSQTDLEALFNAVINPKTATLPPSSLPMRMRKLPDSFFRQPDPRSHSR
QASSDGNMVGSLAPHHVRAHSSPASLPINTLVTPATNSMATQPLPDDMPLPPGWEMAKTTSGQPYFLNHLEQTTT
WHDPRLSHLQTTAAPHPLSAPPPHTHTLAHPGPNTHTHTQSNASPNTGPLPEGWEQAVTPEGEVYYINHTTKTTS
WLDPRLVQSTVSQVKPTTLTSDPVGVVTQRRQQLQAEKDRLRRKQQDLVRPIRAQDVSVRSGLEHDGKTRNHVDP
ALNGAHSRNESTDSGLSVSSFTRTPDDLLNTVELMDTGDSGAAQPMAFLEAGPGVCMAMDGEELMPSIQEALSSE
LLSDMDTVLWL PMRMRKLPDSFFRQP

rs:XP_010877164 [XP_010877164] PREDICTED: protein **FAM181**A [Esox lucius]. 124..138
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHAHKASESGV
AKALVDKCSSYPLETIHPSMTRINEKGCSDGQDENLKTGQNPTLDNDKTKQDQVPMRKRQLPASFWEEPRLPQNN
KDTSQHVWKRSNGVTVINEAEKRKKTNEEPKSTFFLSNRRGSVEKEPFKLEVASHNVSVCGCCPFQYHGHHVFQS
HIVVPHSTMGFWGKATMSQTETPDMAQGHKHLAHVVVKPIPTKPTVQPSIFSVFGFI PMRKRQLPASFWEEP

rs:XP_019406804 [XP_019406804] PREDICTED: protein **FAM181**A [Crocodylus porosus]. 126..140
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRSHPSKSMESNMK
RGVEDRNRSSHPDALDPNPCRAASEKALRGAEVEENLSGEKGLQEQSPESARPDQVPMRKRQLPASFWEEPRPTQ
SLLVGSFSAGLDGLPKSRDLPSYEGKKSKKSPDAIGPESPPVPVQPSREKEPIKVPGTSLSGRMNAWSCCPFQYH
GQPVYQTPGALPQSPFPGLGLWRKNTAPQGEIQHFCKEADATGQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_019485877 [XP_019485877] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ

NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_019485878   [XP_019485878] PREDICTED: transcriptional coactivator
YAP1 isoform X2 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_019485879   [XP_019485879] PREDICTED: transcriptional coactivator
YAP1 isoform X3 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_019485881   [XP_019485881] PREDICTED: transcriptional coactivator
YAP1 isoform X4 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_019485882   [XP_019485882] PREDICTED: transcriptional coactivator
YAP1 isoform X5 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_019485883   [XP_019485883] PREDICTED: transcriptional coactivator
YAP1 isoform X6 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_019485884   [XP_019485884] PREDICTED: transcriptional coactivator
YAP1 isoform X7 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF

NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_019485885 [XP_019485885] PREDICTED: transcriptional coactivator
YAP1 isoform X8 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_019485886 [XP_019485886] PREDICTED: transcriptional coactivator
YAP1 isoform X9 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_019485887 [XP_019485887] PREDICTED: transcriptional coactivator
YAP1 isoform X10 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_019485888 [XP_019485888] PREDICTED: transcriptional coactivator
YAP1 isoform X11 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_019485889 [XP_019485889] PREDICTED: transcriptional coactivator
YAP1 isoform X12 [Hipposideros armiger]. 85..99
MDPGQQPPPQPAPQGQGQPSAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_019471397 [XP_019471397] PREDICTED: protein **FAM181**A [Meleagris
gallopavo].>rs:XP_003206749 [XP_003206749] PREDICTED: protein **FAM181**A

[Meleagris gallopavo].>tr:G3UU06_MELGA [G3UU06] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSMGAP00000019245}; 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPAKPLECGPR
RGAEDRARSCQPEMPDPGPLSGAATEKVLQAAETEESLVGEQAVPEQNPEVNRPDQVPMRKRQLPASFWEEPRPP
QSLPARGFHPGPEGLPVPRDPPPFEGKKSKRNQDSIGPESHEPALNAGEKDATGVLSGQVGAWTCCPFPCPGPAV
YQPPGTLHPSPFPGLGLWRKGTATLPAEAQPFCKEAEGTGQKLYRPVVLKPIPTKPTIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_019725814 [XP_019725814] PREDICTED: protein **FAM181**A [Hippocampus comes]. 105..119
MANADSEVRTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPLRSAQCAK
PIADLHFPQGPEKGGGSVGCVQTSADKVGGSVEQVPMRKRQLPASFWEEPKMRKTEHSHSGLRKNHSALSETREH
RKGGQDEDAKVKEVLRLERNSHHGLSVCACCPFQFQQQHQQQILHGHVVVPHPALGLWCKAEPERLEQPRGQKIH
THVVVKPIPTKPSIPSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_019742859 [XP_019742859] PREDICTED: protein **FAM181**B [Hippocampus comes]. 136..150
MAAIMNPQFMSFCFPGSAMDGGLLGEPEKEEDYKETTRELLSFMDSASSNIKLALDKPVKSKRKVNHRK
YLQKQIKRCTGIVNVTDAAGKGHGSSAPAGKTVPKRDGVQASLQNRSLAALFSPAKEIRGEKARKPPLRHRNLPP
SFFTEPANCSKVNPVAGMSLRELERANPEAADFFDLLGPDYVGVAAEQELYQSVPGPDAATATSCDGHHFVGGLP
YPESWTSCSPPLARKLPTPAQPPLYCHQEAATPVGAEDNALCSLAFSNFFTDCSVPQVNYDLTCDYNRTHYSSL
PLRHRNLPPSFFTEP

rs:XP_019742896 [XP_019742896] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Hippocampus comes].>rs:XP_019742897 [XP_019742897] PREDICTED: transcriptional coactivator YAP1 isoform X1 [Hippocampus comes]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTGGALTPHHVRAHSSPASLQMGTVSGGSLSGMPAAAASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNLMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRISQSAPVKQGGQLPSGTLSGVNQLRLQKMEKERLRLKQELLRQRPQELALRNQLPTSMEQDGGGT
NPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPSSMGTQPS
RFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSEILNDMESVLAATKIDKESFLTWLRGGGGARRGH
LLHPSPPPPPPACF PMRMRKLPDSFFKPP

rs:XP_019742898 [XP_019742898] PREDICTED: transcriptional coactivator YAP1 isoform X2 [Hippocampus comes]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTGGALTPHHVRAHSSPASLQMGTVSGGSLSGMPAAAASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNLMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRISQSAPVKQGGQLPSGTLSGVNQLRLQKMEKERLRLKQELLRQRPQELALRNQLPTSMEQDGGGT
NPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPSSMGTQPS
RFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSEILNDMESVLAATKIDKESFLTWLGGGGARRGHL
LHPSPPPPPPACF PMRMRKLPDSFFKPP

rs:XP_019742899 [XP_019742899] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Hippocampus comes].>rs:XP_019742900 [XP_019742900] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Hippocampus comes].>rs:XP_019742901 [XP_019742901] PREDICTED: transcriptional coactivator YAP1 isoform X3 [Hippocampus comes]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTGGALTPHHVRAHSSPASLQMGTVSGGSLSGMPAAAASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNLMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRISQSAPVKQGGQLPSGTLSGVNQLRLQKMEKERLRLKQELLRQRPQELALRNQLPTSMEQDGGGT
NPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPSSMGTQPS
RFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSEILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_019742903 [XP_019742903] PREDICTED: transcriptional coactivator YAP1 isoform X4 [Hippocampus comes]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTGGALTPHHVRAHSSPASLQMGTVSGGSLSGMPAAAASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNLMNPASALNQQRISQSAPVKQGGQLPSGTLSGVNQLRLQK
MEKERLRLKQELLRQRPQELALRNQLPTSMEQDGGGTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSG
LSMSSYSVPRTPDDFLNSVDEMDTGDPLPSSMGTQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEA
LSSEILNDMESVLAATKIDKESFLTWLRGGGGARRGHLLHPSPPPPPPACF PMRMRKLPDSFFKPP

rs:XP_019742904 [XP_019742904] PREDICTED: transcriptional coactivator YAP1 isoform X5 [Hippocampus comes]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTGGALTPHHVRAHSSPASLQMGTVSGGSLSGMPAAAASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAPPPSSVPVQQQNLMNPASALNQQRISQSAPVKQGGQLPSGTLSGVNQLRLQK
MEKERLRLKQELLRQRPQELALRNQLPTSMEQDGGGTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSG
LSMSSYSVPRTPDDFLNSVDEMDTGDPLPSSMGTQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEA
LSSEILNDMESVLAATKIDKESFLTWL PMRMRKLPDSFFKPP

rs:XP_019715103 [XP_019715103] PREDICTED: transcriptional coactivator YAP1-like [Hippocampus comes]. 49..63
MDAHRGGGSAPPAGQQVVHVRGDSQSELEALFSAVMNPAKAPQQPASLPMRMRKLPDSFFKPPDPRSHS
RQASSDGGACASLTPHHVRAHSSPASLPVNMPDAAAAVAAAAASPPVIPDDVPLPHGWEMAKTPTGQRYFLNHLD
KTTTWHDPRLTQLQSAAPPQPSPSPVHAHSLSNPATATTPPNCNPDAGGLPEGWERAATAEGDVYYIDHVNKSTT
WLHPRLGLLSLVTQQRKEKERLRCKQQMQMNTQVITNFAENLFFFFFFFLNSQGAITDAERCVVINAQARVVSSL
PRSSDLALASADHMDTGECGESSTLQDSMPAMSESEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFKPP

rs:XP_019760455 [XP_019760455] PREDICTED: transcriptional coactivator YAP1-A isoform X1 [Dendroctonus ponderosae]. 41..55
MARNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFTPPSTGSKSINHSRENS
VDSAFDVSGPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQPPAHHHIKQRSYDVASKSEDNTPLPPGWEQARTPE
GQVYYLDHTTRTTTWEDPRKTLAATQQHQSQEHLVSHPHTSPTSTNAKVNNDVELGALPEGWEQAQTPEGEIYFI
NHQTRTTSWFDPRIPQHLQQRSPGSTLVQPPWHASISSSPQKAQQIRLQQLQLERERLKQRQQEIRRQQEIMMRP
SSTDLPVMDPFLSGLTDHSRQESGDSGLGMGTSYSMPHTPEDYLSNMEDNIDVGSDSHPLTPDMSISDNIDSTDL
VPTLSLDEFPILDDVQSLINPATTKPDNSLIWL PWSMRKLPDSFFTPP

rs:XP_019760457 [XP_019760457] PREDICTED: WW domain-containing transcription regulator protein 1 isoform X2 [Dendroctonus ponderosae].
41..55
MARNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFTPPSTGSKSINHSRENS
VDSAFDVSGPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQPPAHHHIKQRSYDVASKSEDNTPLPPGWEQARTPE
GQVYYLDHTTRTTTWEDPRKTLAATQQHQSQEHLVSHPHTSPTSTTQHLQQRSPGSTLVQPPWHASISSSPQKAQ
QIRLQQLQLERERLKQRQQEIRRQQEIMMRPSSTDLPVMDPFLSGLTDHSRQESGDSGLGMGTSYSMPHTPEDYL
SNMEDNIDVGSDSHPLTPDMSISDNIDSTDLVPTLSLDEFPILDDVQSLINPATTKPDNSLIWL
PWSMRKLPDSFFTPP

rs:XP_005177963 [XP_005177963] PREDICTED: transcriptional coactivator yorkie [Musca domestica].>tr:A0A1I8MML4_MUSDO [A0A1I8MML4] SubName: Full=Uncharacterized protein {ECO:0000313|VectorBase:MDOA006533-PA};
65..79
MSLSKSSASDDANKCSVKTEDSTSAASKSSINLVVRNYQNSDENLRALFDSVLNPSESNRPLQVPFRMR
KLPNSFFTPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQTSVASSLSDLQTTAATAVQVQQQSTSTINSQSAA
STSAAPQGEPRLQICHSRAHSSPASLQQSYNIHGGGNVAEETPFLQQQSDVARAANNASNAPGFPSNLLGYNAAT
AAVAAAAGLNNNSIIGISGAGAPGPLQSYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTHDGQIYYLNHTTKTT
QWEDPRTQFKQQQTLNSASNARAIGKTAAGENILASSNLGPLPEGWEQAMTETGEVYFINHIDRTTSWNDPRLSD
PRFPILIQKEIKPKTEMSWVNATEIDKDSDMFKQKAGQKSVNKHNISLHMDPFLSGDNHARQESSDSGLSLSSNS
FAVNNDFITHMDNSMDCISENGSIIDNLDTTLQLNDNIIMMNDMLNSPSNKPDNLEWYKLN
PFRMRKLPNSFFTPP

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rs:XP_010863506   [XP_010863506] PREDICTED: protein FAM181B [Esox lucius].
      173..187
      MAVQTAVMNSPFINFCFPGAVLMEYDMDKSLDGSLLGEMGSEEGGDFRETTRDLLSFIDSASSNIKLAL
DKPVKSKRKVNHRKYLQKQIKRCTGIISPLGNPAPAAPGPGLGPNKRQGSGSPTQAQPHTSPFQPGKPILKRDGL
QANLQSKSLAALFKPVKDPVKGERAKKPPLRHRNLPLSFFTEPANSPTTATNTPGVTSTSGMFLEDLERGGGNPE
AADFFELLGPDYSQMLGDQDLFQPQSRAGRVFQHLNPDINGPDQALPPSYDPQQLVGGFLYAEPWSTTSCTGPSK
KGGENTRNSLGPQTMLYSHSDPPMTGSGEDNTLCALAFSNYFPDCSVPQVSYDLSGGGYTRTVFSSLQQ
      PLRHRNLPLSFFTEP

rs:XP_011424676   [XP_011424676] PREDICTED: uncharacterized protein
LOC105326371 isoform X1 [Crassostrea gigas].   123..137
      MFQVQQSRELDMKRHNESTSSLLNFVDIASSNIKMALDRPTKSKRKVNHRKYLQKQLKSCGTVQQEDHS
RRQLSGTQSIKLMRKDGAQSGVQMKSLQDLFDPRTLHEKCCADPCSKSRGSKVPLRKRNLPPSFFLEPSRPEQRD
SLVESLTSALPDDFLHSFHRAPELDTLSSDTLDSILGNHDFQELLNVGQWNDSSRDSSESDPCSSNSDYSTFNNT
VYFSEIRSPDEFPQEAWLSPQICSNTSQTMFTDNASSQVCHQPFEQLLLPEPKSNPGMSPRDTSSKLPTFPQAFL
NRDCLSSSQQWGEVPFYSCYTYL PLRKRNLPPSFFLEP

rs:XP_011424677   [XP_011424677] PREDICTED: uncharacterized protein
LOC105326371 isoform X2 [Crassostrea gigas].>tr:K1QP49_CRAGI [K1QP49]
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EKC30580.1};
      112..126
      MKRHNESTSSLLNFVDIASSNIKMALDRPTKSKRKVNHRKYLQKQLKSCGTVQQEDHSRRQLSGTQSIK
LMRKDGAQSGVQMKSLQDLFDPRTLHEKCCADPCSKSRGSKVPLRKRNLPPSFFLEPSRPEQRDSLVESLTSALP
DDFLHSFHRAPELDTLSSDTLDSILGNHDFQELLNVGQWNDSSRDSSESDPCSSNSDYSTFNNTVYFSEIRSPDE
FPQEAWLSPQICSNTSQTMFTDNASSQVCHQPFEQLLLPEPKSNPGMSPRDTSSKLPTFPQAFLNRDCLSSSQQW
GEVPFYSCYTYL      PLRKRNLPPSFFLEP

rs:XP_019924740   [XP_019924740] PREDICTED: transcriptional coactivator
YAP1-A isoform X1 [Crassostrea gigas].   43..57
      MSQDMQERKGTQVVHVRENSGNELEALFQYAANPNSELGGQIPFRQRKLPESFFHEPKSSRPGHMKQGS
NDSTGFPGQMNPGMGAHMRAHSSPATLQQSLSAVPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYL
NTSEKNLYKIDKGKEMLLPMDNEGHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPHGWEQASTPE
GDIYFINHIERTTSWYDPRIPEQLQQLRLSTSQPQSVQQQVQRQMNARMGQPPPVQPPVNRMGAKSPASVQFSKI
QMEKELLRKRQEDLQHQEMLLRAQMQQQQIHDNPPTSQGIVISQSMEMTTVADPFLGQSNVSANHIKQESSDSGV
GGMGTGTPYGLSRTPEDFLSNVSEMEQDGGGHRHSEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDM
ESVLNVNKLDNILAGDNSLTWL  PFRQRKLPESFFHEP

rs:XP_019924741   [XP_019924741] PREDICTED: transcriptional coactivator
YAP1-A isoform X2 [Crassostrea gigas].   43..57
      MSQDMQERKGTQVVHVRENSGNELEALFQYAANPNSELGGQIPFRQRKLPESFFHEPKSSRPGHMKQGS
NDSTGFPGQMNPGMGAHMRAHSSPATLQQSLSAVPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYL
NTSEKNLYNHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPHGWEQASTPEGDIYFINHIERTTSW
YDPRIPEQLQQLRLSTSQPQSVQQQVQRQMNARMGQPPPVQPPVNRMGAKSPASVQFSKIQMEKELLRKRQEDLQ
HQEMLLRAQMQQQQIHDNPPTSQGIVISQSMEMTTVADPFLGQSNVSANHIKQESSDSGVGGMGTGTPYGLSRTP
EDFLSNVSEMEQDGGGHRHSEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMESVLNVNKLDNILAG
DNSLTWL     PFRQRKLPESFFHEP

rs:XP_019924742   [XP_019924742] PREDICTED: transcriptional coactivator
YAP1-A isoform X3 [Crassostrea gigas].   43..57
      MSQDMQERKGTQVVHVRENSGNELEALFQYAANPNSELGGQIPFRQRKLPESFFHEPKSSRPGHMKQGS
NDSTGFPGQMNPGMGAHMRAHSSPATLQQSLSAVPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYL
NHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPHGWEQASTPEGDIYFINHIERTTSWYDPRIPEQ
LQQLRLSTSQPQSVQQQVQRQMNARMGQPPPVQPPVNRMGAKSPASVQFSKIQMEKELLRKRQEDLQHQEMLLRA
QMQQQQIHDNPPTSQGIVISQSMEMTTVADPFLGQSNVSANHIKQESSDSGVGGMGTGTPYGLSRTPEDFLSNVS
EMEQDGGGHRHSEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMESVLNVNKLDNILAGDNSLTWL
      PFRQRKLPESFFHEP

rs:XP_011434467   [XP_011434467] PREDICTED: uncharacterized protein
LOC105333263 [Crassostrea gigas].   262..276
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MASLSAAQVPLLDVNFGLGSTQKSYGGKKAPHGFHSYTEEDEPLHLTSNIPTKSYGGKRAPTSSLITVN
LDEDSKLTCVKKSTLSNIIVLNEDEESSRYKSYGLKKIISSNNGLVSQENEEATSQGGKRSNIPLTDIKEEGQLD
SEKLTLPQHGSKRGASGPLVTSSDEEESLPPSPRSSVNSSSSVQHAYEHDHDYENVASPSGSSTASGPVYIRPPG
FRHHAQEIKKVKKKKTTEFDFKSALKKRAPTPPKVRPKRESVPMRLRALPQSFWKQPNVPNPVSPAPLFPSLPPL
GSKDSSEDITDMRPITPPDEKERHKKQPKQSERKVYITGDTDLLLKHLFDRAVEDKKNPQIKRGRPRKIAVPRET
GTKALISGDDPYLVDAVTQKLFPQLSLESRQGQIGSTTLQLVTLRDGDKSVTLPSLSIEQNYSQMLSDLAMNI
PMRLRALPQSFWKQP

rs:XP_020324580 [XP_020324580] transcriptional coactivator YAP1
[Oncorhynchus kisutch]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQTS
TDAGTAGAIAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSHLRQSSYEIPEDMPLPPGWEMAKTPSGQRYFLN
HLDQSTTWLDPRKALLQMNQAPPTSPVPVQQQNIMSPASGPLPDCWEQAVTSEGEVYYINHKNKTTSWLDPRLDP
RLDPRLDPRYGLNQQRITQSGPSKQGGQLPSSPESRGVMGGSNQMRLQQLQMEKERLRLKHQELLRTRPQELALR
TQLPVSMEQDGGTPNPVSSPGMGQDARTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDALPVSMGTQPSRFPDYLDTIPGTDVDLGTLESDNMAMEGEELMPSLQEALSSDILNDMESVLAATKIDKES
FLTWL PMRMRKLPDSFFKPP

rs:XP_020331022 [XP_020331022] transcriptional coactivator YAP1-like,
partial [Oncorhynchus kisutch]. 45..59
MDPSQHNPPAGHXIVHVRGDSETDLEALFNAVMNPKNTIVPASVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAVTAGALAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSNLRQSSYEIPDDMPLPPGWEVAQTPSGQRYFLN
HLDQSTTWLDPRKALLQMNQAPPTSPVPVQQQNIMSPAS PMRMRKLPDSFFKPP

rs:XP_020331055 [XP_020331055] protein **FAM181**B [Oncorhynchus kisutch].
195..209
MAVQTAIMNSPFVNFCFPVMMEYDMGQSLDGSPLEESEERGEYRETTRSLDGSPLEESEERGEYRETTR
NLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGFISPTGNPAAAPGANKRKVSGFPTQTQTQIQPQ
TQLQTQPSPFQQGKPVHKRDGLQANLQTKSLAALFNSVKEPVKGERAKKPPLRHRNLPPSFFTEPANTTTTSRVT
STSGMFLGDLERGVGNPDFFDLLGPDYSNMLSDQDVFQTRGLPSRIIDQDMFQTRGLPSRILQHQQTQDITDQVS
PYDPHHLVGGFLYTEPWSTSSPSKKAGEGVRTGPGTQTPLYCQSGEGVRTGPGTQTPLYCQSGEGVRTLNG
PLRHRNLPPSFFTEP

rs:XP_020333735 [XP_020333735] transcriptional coactivator YAP1-like
[Oncorhynchus kisutch]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQTS
TDAGTAGAIAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSHLRQSSYEIPEDMPLPPGWEMAKTPSGQRYFLK
PHRPAARAVSSLLGMVLLALPHRTSDSRLMRSRGHALPRAEMAKTPSDKILPNVSVPQCERPPV
PMRMRKLPDSFFKPP

rs:XP_020356794 [XP_020356794] protein **FAM181**A [Oncorhynchus kisutch].
125..139
MASTDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARMPRCHTHRSTESSI
AKDVVNTSSEYSLETIHPSTTRINEKGGSDARDVENARMAQTPTVDSDNSKQEQVPMRKRQLPASFWEEPRLAQT
NTDYLQYGWKKSQGVIGINDVEKIKKAHEELTPSLLISNRRGSVEKEPLKLDVASHNVNVCGFCPFQYHGHHVFQ
SHIVVPQSAVGLWGKATVAETETPDITHRHKNYTHVVVKPIPTKPTVPPSIFNVFGFI PMRKRQLPASFWEEP

rs:XP_020320732 [XP_020320732] transcriptional coactivator YAP1-like
isoform X1 [Oncorhynchus kisutch]. 48..62
MDARQGQCAPPVGQQIVHVRGDSQTDLEALFNSVMNPKTSALPPSSLPMRMRKLPDSFFRQPDPRSHSR
QASSDGTIVGSLTPHHVRAHSSPASLPINALSAQHQCMATQPLPDDVPLPPGWEMTKTPSGQCYFLNHLDQTTTW
HDPRLSHLQTNAAAHLLSAPPPHTHTLAHPAPNTHTQSNTGSNTGPLPEGWEQAVTPEGEVYYINHITKTTSWLD
PHLVQSAVAQVKPSTLTSDPVGIATVVTKRRQQLQVEKDRLRRKQQDLARPIRVQCNPCQDVAVRSGLEHDGKMR
NNHVDPALNGAHSRNQSTDSGLSVSSFTRTPDDLLNTVELMDTGDSGAGQPMAFLEAGPGVCMATDGEELMPSIQ
EALSSDLLSDMDTVLWL PMRMRKLPDSFFRQP

rs:XP_020320734 [XP_020320734] transcriptional coactivator YAP1-like
isoform X2 [Oncorhynchus kisutch]. 48..62
MDARQGQCAPPVGQQIVHVRGDSQTDLEALFNSVMNPKTSALPPSSLPMRMRKLPDSFFRQPDPRSHSR

QASSDGTIVGSLTPHHVRAHSSPASLPINALSAQHQCMATQPLPDDVPLPPGWEMTKTPSGQCYFLNHLDQTTTW
HDPRLSHLQTNAAAHLLSAPPPHTHTLAHPAPNTHTQSNTGSNTGPLPEGWEQAVTPEGEVYYINHITKTTSWLD
PHLVQSAVAQVKPSTLTSDPVGIATVVTKRRQQLQVEKDRLRRKQQDLARPIRVQDVAVRSGLEHDGKMRNNHVD
PALNGAHSRNQSTDSGLSVSSFTRTPDDLLNTVELMDTGDSGAGQPMAFLEAGPGVCMATDGEELMPSIQEALSS
DLLSDMDTVLWL PMRMRKLPDSFFRQP

rs:XP_020500920 [XP_020500920] protein **FAM181**A [Labrus bergylta].
105..119
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAGYGC
VKPVGTAHQTVKVAEKASSSDAQGVESSGSAVEQVPMRKRQLPASFWEEPKLTQNEREHPLFKLKKNPTGTTEGS
ENEKNKRSYDDGKAALSEEKETLKLGLSSHHCVSVCGCCPFQYHGHQVLHSHIVVPHPPLGLWSKAAGTVTERPE
HPYGQKIHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_020508661 [XP_020508661] transcriptional coactivator YAP1-like
isoform X1 [Labrus bergylta]. 50..64
MDAHRGGGGGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKSARQPSSLPMRMRKLPDSFFRQPDSRGH
SRQASSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAVTPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKT
TTWHDPRLSQLQSAAAQHPISGAPIHAHSLSNPAPTSQPPNINQDTGPLPEGWEQAVSADGEVFYIDHINKSTAW
VDPRLAQKMNPALLGLALQQRQEKERLRCKQQGLPPQITAQEAGGRNQMPGGMDHDRNAQTLVPSLDLRIRASNH
EPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGETSMTLQESMPVLPMSDGEELMPCIPEGLSSD
LLMDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_020508662 [XP_020508662] transcriptional coactivator YAP1-like
isoform X2 [Labrus bergylta]. 50..64
MDAHRGGGGGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKSARQPSSLPMRMRKLPDSFFRQPDSRGH
SRQASSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAVTPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKT
TTWHDPRLSQLQSAAAQHPISGAPIHAHSLSNPAPTSQPPNINQDTAQKMNPALLGLALQQRQEKERLRCKQQGL
PPQITAQEAGGRNQMPGGMDHDRNAQTLVPSLDLRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSV
DHMDTGDSGETSMTLQESMPVLPMSDGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_020446464 [XP_020446464] protein **FAM181**A [Monopterus albus].
102..116
MADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYGCTK
PMGTVQHSVKVAEKAHSDAQDVENMGSAVEQLPMRKRQLPASFWEEPKLTQTERENSYLGFKKSPGGTSEGGENE
KRKRSYDEDTKVTLSAPSRRIFADKETLKLDLTSHHCVSVCSCCPFQYHGHQVLHSHIVVPHPPLGLWSKAAGTE
TGRPEHSFGQKIHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_020454162 [XP_020454162] transcriptional coactivator YAP1-like
isoform X1 [Monopterus albus].>rs:XP_020454163 [XP_020454163]
transcriptional coactivator YAP1-like isoform X1 [Monopterus albus].
46..60
MDAHRGAPPAGQQVVHVRGDSQTELEALFNAVMNPGKAGKQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCSSLTPHHVRAHSSPASLPVNSLSTQAADVAVTPNIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAPAQLPISGAPVHAHSLSNPAPATQPQNINPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPR
LAQKMNPSILGLVMQQRQEKERLRCKQGLPHQITAQDAGGRNQMLGGMDHDRNAQTLLPTLDVRIRASNHEPTLN
GAHSRNESTDSGLSVSSLPRSSDHMLSSVDHMDTGDSGETSSMSLQESMPVLPMSEGEELMPCIPESLGSDLLMD
METVLSGSHMDRDTLLTWL PMRMRKLPDSFFRQP

rs:XP_020454164 [XP_020454164] transcriptional coactivator YAP1-like
isoform X2 [Monopterus albus]. 46..60
MDAHRGAPPAGQQVVHVRGDSQTELEALFNAVMNPGKAGKQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCSSLTPHHVRAHSSPASLPVNSLSTQAADVAVTPNIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAPAQLPISGAPVHAHSLSNPAPATQPQNINPETAQKMNPSILGLVMQQRQEKERLRCKQGLPHQIT
AQDAGGRNQMLGGMDHDRNAQTLLPTLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRSSDHMLSSVDHMDT
GDSGETSSMSLQESMPVLPMSEGEELMPCIPESLGSDLLMDMETVLSGSHMDRDTLLTWL
PMRMRKLPDSFFRQP

rs:XP_020470406 [XP_020470406] transcriptional coactivator YAP1
[Monopterus albus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKPHSRQAS
TDAGSGGALTPHHVRAHSSPASLQMGTVSGGSLSGMTSAGASPQHLRQSSYEIPDDMPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAAPASSVPVQQQNLMNPASGPLPDGWEQAVTSEGEIYYINHKNKTTSWLDPRL
DTHYALNQQRISQSAPVKQGGQLPSSTHSGVMGSNNQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPSSMDQ
DGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSMA
TQPSRFPDYLDAIPGTDVDLGTLESDSMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_020470443 [XP_020470443] protein **FAM181**B [Monopterus albus].
155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDVSLLGEAENDEDYKETTKDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVEEVPVKRQGSPLAQSSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAIEFFELLGPDYSNMVSDQDPYQSMPL
RGQPDMGGPDPTSYDAHHLVGGLLYSEPWTNCSGASKKLGDSLRTGPAQPPLYCHSEAATGPLEDNTLCTLAFPN
FFTDCSIPQVTYDLSGSYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_020608389 [XP_020608389] transcriptional coactivator YAP1-like
[Orbicella faveolata].>rs:XP_020608390 [XP_020608390] transcriptional
coactivator YAP1-like [Orbicella faveolata]. 47..61
MERKNSNCVVHVRQDSDNDLEALFHVVNKNAVAKTHPDPTSSANSLPMRLRKLPPSFFKQPPLDGTLSP
DQDTPTGLISHSRAHSSPASLTVPTSLKGPHSLSPVVHQRSTSFDNTALLEEPAQMPPGWEMRTTPNGQRYFMNH
FDQVTTWQDPRKTQSTSNLNSIQPAGNLPDGWEQAITPEGDIYYINHIERTTSWVDPRIAMHCRNQENMRGPQLP
PEMNRHRTMQLQRLQREREHLLKRQQELLKQEIRLKRDILEEGGTKSSLLGNLTREVSLLSAQDPPVTSGGHIRD
ESFDSGLGMGGGNYQFHDVDMNDSQPMFDANYNSKDSSFRTEPGRRLPEILDSLPGTNVDLGVLEGTDNSSNMET
DDLGVGLEFNSEFNDAVESVLISPTKIADNFLTWL PMRLRKLPPSFFKQP

rs:XP_020610110 [XP_020610110] uncharacterized protein LOC110048674
[Orbicella faveolata]. 147..161
MKNSAEENTTTISLLNFVSNATNTLKFALDKPVKPKRKVNHRKYLQRQLKGKASSTTCTMSYESSWMSH
GEVLDHVLKPEQQQNSSGERSSTKNSKENRAEKLQALEINTPAFNHEQGKGKTRDIKRKQRISDARFPEEIFSTP
SQPLRKRNLPESFWSEPSSAKVSRQSVQATRHPTASFTNNDLQRSELEMLDWLRPELDDFIERWSEESDCASNNS
SRPASLSDGSSSVDPYSPYSDESENNLASMDEFFEQRVPFSFDNSAKAEDFSAPSVRSYATSHTVNDIACNMQQN
YSQRQATHASTCYGGNYGFSASKWSAANQTRASYFENGYNILS PLRKRNLPESFWSEP

rs:XP_020616320 [XP_020616320] uncharacterized protein LOC110054284
[Orbicella faveolata]. 106..120
MDPLRKRTQQKDTLNWRSPPSPCGPSSPQSPPPLVVRGKSLSLNRVAAPALLSPIRETGAKELSKRGRK
QRLLLSQAGNLTLKRRETSPDFNKLEARLKPKRGPLPMRMRALPQSFWQEPKDIQNSSMSTEGTLSSLPPLFHNA
NNTSYDVSKVRPVTPPEEKYLPRPPKEPKLVITSPQEQLLKLFETVEEDKTKKFVIRRGRPRRVQSDLTHCQLPK
LEEDPCMMDSLAEKMFPQLSLENSNKQTTGANTSLSCVSIHEGDKSVTLPSLNVEQNYSQMLSEIVAHF
PMRMRALPQSFWQEP

rs:XP_020657878 [XP_020657878] protein **FAM181**A [Pogona
vitticeps].>rs:XP_020657879 [XP_020657879] protein **FAM181**A [Pogona
vitticeps]. 137..151
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHHHHMQPQPP
PPPVKERKAAEARTRGLAAADGAEVSAGRSGSASATPRGDKAAEPVGEAHPRQPQSAAEATPRPDQVPMRKRQLP
ASFWEEPRTATGPLSVNGVLFPTNASPPPPPPPPLKDSPLYERKKSKKGADSDGTGSAAESPQNEPDRGAVKVLS
AWSCCPFQYHRPQASPGAYPPPLAAALPPAAPYSTLGLWRKNVACPTEGEAFCKPDGSGAGQKVHRPVVWKPIPT
KPAAPPPIFSVFGYI PMRKRQLPASFWEEP

rs:XP_020668160 [XP_020668160] histone-lysine N-methyltransferase SETD1B
[Pogona vitticeps]. 224..238
MAAGVIQSLSKFRLAPGFQHLFLSSTTSQEMALHDSSEEEEMEEEEEEEAEEEEVEGGGGGRGEEMEATD
DDPEGHGPRGKQETPTVAADLSGAEMTAQLLRFAERVSEDIQRYFGRKSQDDDSEACNIYEDRGSPQLSGRLLYY
TDLVQISQSRAPEEDNEDDEDLPPASTPTWRSLGSKAEEDERLGPLAELFEYALCRYAKPQALHDPEKLRMERKY
GHLSPMHGRKLPQSFWKEPAFSPIGVLGSNPPDFSDLLANWTSETSQEELHAS PMHGRKLPQSFWKEP

rs:XP_003398315   [XP_003398315] transcriptional coactivator YAP1 [Bombus terrestris].   46..60
MALNQDVDQLSKSNLVVNIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAAVAGAGPAPGGNATGTSGTGAAGAATGGSGNTAAGTGSNAAGAAAAAVAAAAAAGLTVA
HPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTR
TTTWEDPRKTAAAANVAAVAAAVDNGKSSTGATNSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQ
RAPTSGAMLPQNWLQQQQPTGGGIQSNQTLQACQQKLRLQSLQMERERLKQRQQEIIRQQELMLRQSTTDAAMDP
FLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQ
LSEDFSSDILDDVQSLINPNTTKPENVLTWL   PLRMRNLPDSFFNPP

rs:XP_020731593   [XP_020731593] protein **FAM181**A [Odocoileus virginianus texanus].>rs:XP_020731594 [XP_020731594] protein **FAM181**A [Odocoileus virginianus texanus].   130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLR
RGPEDRPGRPLPLESGHGSSPGGGGGCKEKALGNPDREESLSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPASPRALAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_020775228   [XP_020775228] protein **FAM181**A [Boleophthalmus pectinirostris]. 129..143
MSANGPAKLKRTRGEREIRGMVETYVLWTEFIKLNMADSEVKTLLNFVNLASSDIKAALDKSAPCRRSV
DHRKYLQKQLKRFSQKYSRVPKCHAHRPAEHGKPGGSAHESVKGRAQDAENVGNAVEQVPMRKRQLPASFWEEPK
LSQDRKENSISGFKKSDWADKRTRACEDVAKASASSSTRRDKDALLLDLTSHHCVSVCGCCPLQYHGQQVLHSHI
VVPHPPLGLWSKAARTDAEMSEHPYGHKIHTHVVVKPIPTKPTIQSPIFSVFGFI   PMRKRQLPASFWEEP

rs:XP_020778634   [XP_020778634] transcriptional coactivator YAP1-like isoform X1 [Boleophthalmus pectinirostris].   46..60
MDGHYGAPPAGQQVVHVRGDSQTELEALFNAVMNPSKAQRQPTSVPMKDRKLPKSFFTQPEPRGHSRQA
SSDGGVSNTLPPRHVRAHSSPAILPPQADVTTAPIIPDDIPLPHGWEMAKTPTGQRYFLNHVDKTTTWHDPRLAQ
HQTAAPQHPLSAAVPPSHSHSLSNPAPSVQPQNINPETGPLPEGWEQAVTGDGEVYYIDHINKITTWVDPRLAKM
NPGLLSLAIQQRQENERLRCKQQVTTQDAAVRNRMPGGMDHDRNTQTLVPPLDVRIRASNHEPTLNGAHSRNEST
DSGLSVSSLPRTTEHMLSPVDHMDTGDSGESSSLTLQESMPPVLPMSEGDELMGLSSDLLMDMETVLSGSHMDRD
SLLTWL   PMKDRKLPKSFFTQP

rs:XP_020778635   [XP_020778635] transcriptional coactivator YAP1-like isoform X2 [Boleophthalmus pectinirostris].   46..60
MDGHYGAPPAGQQVVHVRGDSQTELEALFNAVMNPSKAQRQPTSVPMKDRKLPKSFFTQPEPRGHSRQA
SSDGGVSNTLPPRHVRAHSSPAILPPQADVTTAPIIPDDIPLPHGWEMAKTPTGQRYFLNHVDKTTTWHDPRLAQ
HQTAAPQHPLSAAVPPSHSHSLSNPAPSVQPQNINPETGPLPEGWEQAVTGDGEVYYIDHINKITTWVDPRLGTK
MNPGLLSLAIQQRQENERLRCKQQVTTQDAAVRNRMPGGMDHDRNTQTLVPPLDVRIRASNHEPTLNGAHSRNES
TDSGLSVSSLPRTTEHMLSPVDHMDTGDSGESSSLTLQESMPPVLPMSEGDELMGLSSDLLMDMETVLSGSHMDR
DSLLTWL   PMKDRKLPKSFFTQP

rs:XP_020778636   [XP_020778636] transcriptional coactivator YAP1-like isoform X3 [Boleophthalmus pectinirostris].   46..60
MDGHYGAPPAGQQVVHVRGDSQTELEALFNAVMNPSKAQRQPTSVPMKDRKLPKSFFTQPEPRGHSRQA
SSDGGVSNTLPPRHVRAHSSPAILPPQADVTTAPIIPDDIPLPHGWEMAKTPTGQRYFLNHVDKTTTWHDPRLAQ
HQTAAPQHPLSAAVPPSHSHSLSNPAPSVQPQNINPETAKMNPGLLSLAIQQRQENERLRCKQQVTTQDAAVRNR
MPGGMDHDRNTQTLVPPLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTTEHMLSPVDHMDTGDSGESSSL
TLQESMPPVLPMSEGDELMGLSSDLLMDMETVLSGSHMDRDSLLTWL PMKDRKLPKSFFTQP

rs:XP_020784177   [XP_020784177] transcriptional coactivator YAP1 [Boleophthalmus pectinirostris].   46..60
MEQGQHNPPAGQKVVVHVRGDSETDLEALFNAVMNPKSTIMPPSVPMRLRKLPDSFFKPPEPKSHSRQA
STDAGSGATQAPHHVRAHSSPANLQLGAGSTGSLSGIGSAGASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRY
FLNHIEQTTTWQDPRKALLQLNQPAPTSTVPVQQQNLMNPATGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPR
LDPRFGLNQQRISQSAPVKPTGQLPPHSAVMGGNNQMRLQQLEKERLRLKQQELLRQRPQELALRNQLPMDQDGG
SNPVSSPMAQDTRTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEPQQTSMVSQP

SRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDIFNDMESVLTGKIDKENFLTWL
PMRLRKLPDSFFKPP

rs:XP_020784429 [XP_020784429] protein **FAM181**B [Boleophthalmus pectinirostris]. 154..168
MNPQFLNFCFPGSVMEYDVEKSLDDGSILGEAETEEDYKETTRDLLSFIDSASSNIKLALDKPVKSKRK
VNHRKYLQKQIKRCTGIISPSNAAEPPPPVKRHGSPPMAQTSSALHTKNLPKRDGVHANLQSKSLAALFSPVQDV
RGGDKAKKPPLRHRNLPPSFFTEPANCSRVSPTAGTMLKELERGNTEPVDFFELLGPDYSSMVSEQDLYQTLPVR
GHPEMGGLENASYDSQHLVGGLLYSTEPKLTNTQAPGFCHSDATSGPTEDGSLCTLAFPNFFTDCSIPQVTYDIS
GAFSRPNYSSL PLRHRNLPPSFFTEP

rs:XP_020897246 [XP_020897246] uncharacterized protein LOC110236100 [Exaiptasia pallida]. 108..122
MEKSRQNQFQNSNHLEWRDPKSPCSPSSPASPQSPPSLEVRGKGLSLSRWKPVIKENAPRELSKKGRKQ
RLLLSQNGGLSKLKRRETSPDFHLHHNEHRAKPKRDPLPMRMRALPQSFFHEPHEIXTSSLNSSSTLPGLPPLFH
NANNTGDDVSNLRPVTPPEEKLKPRPPKERKVSYAATTSEDLLFKLFETVEEDKTKKFVIKRGRPRRVQSDLTPN
MLPKLEEDPSMVENLANRLFPQLSIEKKLKPHQQPSTSLSCVSVQDGEKSVTLPSLSVDQNYSQMLLEIVAHF
PMRMRALPQSFFHEP

rs:XP_020902626 [XP_020902626] transcriptional coactivator YAP1-like [Exaiptasia pallida].>rs:XP_020903682 [XP_020903682] transcriptional coactivator YAP1-like [Exaiptasia pallida]. 47..61
MTMERNSNQNCYLNVRTDSENDLEALFNVVQSASTTIANEPSSNSLPMKLRKLPPSFFKQPKGLDSNKL
SPEDNTGLKISHSRAHSSPASLPIPTSSAGMYSIQPPSHTRTQSYDGTAFEESQLPPGWEMRTSPSGQPYFMDHI
QQITTWVDPRKTQSTNNLTSSNPLPDGWEQAITPEGEIYYINHLTRTTSWVDPRIAMAPCRTNPQQHPPQQGRRP
PQQHKAMLERVQLEQEQLKKRQQELQKQEILLKHGLLENGGSKSMLGNLVREAGLAQLAPQPDTTTPNGHIRDES
FDSGLGMNTGYSNTYNSDIDLNTGSDSQMFDANYNSKDTSSRNSSRLPDFFDNLPGTNVDFGTIEGESTPSAMDT
DDLGVGLDLPTDMLNDVESVLTPNLSKMTDPNFLTWL PMKLRKLPPSFFKQP

rs:XP_003356830 [XP_003356830] LOW QUALITY PROTEIN: protein **FAM181**A [Sus scrofa]. 226..240
MLCIWRGAPDWPEGPPSSGDSSSIQPTRGLHNCLQPDHGARRPRGAWPRSAAGNLPGHLGRAPGPAPSV
SSVAFPGAASRLQNSPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKR
FSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDTGHNSSPSGGGGCKEKASGNPYREESLPKEQTLHGQDPEA
ARPGQVPMRKRQLPASFWEEPQPTHSYPVGLEGGXGPREGPPYDGKKHCKGLEPLGPETSPRAPAEKEPLKMPGV
SLGGRVSAWSCCPFQYHGQPIYPGPPGALPQGPVPSLGLWRKSSASPSELAHFCKDAEGPGQKVYRPVVLKPIPT
KPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_003129763 [XP_003129763] protein **FAM181**B [Sus scrofa].>tr:F1STW2_PIG [F1STW2] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSSSCP00000015818};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDEETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPCPPSPGATDTPAKRPLAAAGAQTVAVATHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAESAGAAVAATAGGLGGAGAGGSGGDAAGTAGCPVVPGARK
VPLRARNLPPSFFTEPSRAVSGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYCQGTEAGVLLAAEPLDVFPTGA
AVVRGSPELEPGLFEPPPAMVGSLLYPEPWSAPGCPAPKKPPLAAPRGGLTLNEPLRPLYPAAPDSPGGEDGPGL
LASFAPFFSDCALPPPPPQQVSYEYSAGYSRSAYSSLWRPDGVWEGAPGEEEAPRD PLRARNLPPSFFTEP

rs:XP_020918365 [XP_020918365] LOW QUALITY PROTEIN: transcriptional coactivator YAP1 [Sus scrofa]. 86..100
MDPGQQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAATQXPPAGHQIVHVRGDSETDLEAL
FNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAISPGTLT
PTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMGGGSSNQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_021003463 [XP_021003463] transcriptional coactivator YAP1-like [Parasteatoda tepidariorum]. 48..62
MSQQRDVIEQKQGHNKILRIRGDSETNLDDLFNAVMHPKGNQAHQSKPMRSRNLPKSFFQQPERGSKSA
SHSRESSTDNTFSSPPPQQVPQSNNNNNNRSAASPGISNSNNAVSPPPAHPNGLVINHPRAHSSPASLQQTYNAA
QHQHLRQQSYDITDIIPMPAGWEMARTENGQRYFLNHLTKTTTWEDPRKNLSTGSLSSSSGVTSLSPSTSPASSL
INLQLVNNLAQGPLPDGWEQATTPDNEIYYINHRTQTTSWYDPRLPPQLQNTPVVPILGYGAHSQSVLGLSSQQS
QASAASVTTSLTAASNQTLQQQQQQLRLQRLQMERERLRLRQQEILRNSNLGNSSPTLNEYLMRKTLQEEGVANS
SSSNRHTDASQSNSTNLDPFISADADFHSRQESGDSGLGLSSNYSLPNTPEDYLMGMDEGTEDVLLDIAELNLEP
IPGGALDMVPENMDSDDLEPSLHEELNPDILSDVEALLNKESVMKWL PMRSRNLPKSFFQQP

rs:XP_015911304 [XP_015911304] transcriptional coactivator YAP1-like [Parasteatoda tepidariorum]. 47..61
MSQQQDVIEQKGTNQVVHIRSDSETKLDELFNAVIHPKDYPVPGTLPMRLRNLPPSFFQQPEKGSKSPS
HSRESSADNTNYPTGPNPSQKQQTIPTQLPSGLQINHPRAHSSPASLQQGYSKSGPVSHQHLRQRSYGDLLDDNT
PLPPGWEMAKTSAGQTYFLNHLTQTTTWVDPRKKLTSGNMAASVNMQNLGALPKGWEQATTLEGEVYFINHIDRT
TSWLDPRIPAHLQNPPTVTAPTQMSVSAALQSQTSSQIPGANNVNLLRQLPTQTIKLPSSIAAAAMSLQQQQQQ
QQLQQQNLRVQSLEMEREQLRLRQQEIMRQQEILLRQSLGEKLTLAASPTGSTDLPPVSTNLDLFLDGGTDFHSR
QESADSGLGLGPNYSLPHTPEDFLSNLDDVEDRQSNDLGLDLQTNLDLGDDNMDTDDLVPSLQEELNADILSDVE
ALLAANTKDNVLTWL PMRLRNLPPSFFQQP

rs:XP_021100619 [XP_021100619] protein **FAM181**A isoform X1 [Heterocephalus glaber]. 167..181
MAAAGPESFRGGQPCTLLRAASPLQKAPSSWKAPCSGPLVMASDTDVKMLLNFVNLASSDIKAALDKSA
PCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLRRGPQDRPGRLALHPGPDSSPGGGGGCKEKALGSPF
GEECLSKEQNLQGPGAAKPGQVPMRKRQLPASFWEEPRPTHSYAMGLEGGLGPRERSPYESKKNCKGLESMVPEA
APGPMSPRALADKEPLKMPGVSLVGCVDAWSCCPFQYHRQPIYPGPPGALPPSPMPSLGLWRKSPALPPEQAHFC
KRVDGPGQKVYRPVVLKPIPTKPAMPPPIFNIFGYL PMRKRQLPASFWEEP

rs:XP_021100626 [XP_021100626] protein **FAM181**A isoform X2 [Heterocephalus glaber]. 158..172
MCGQPCTLLRAASPLQKAPSSWKAPCSGPLVMASDTDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHR
KYLQKQLKRFSQKYSRLPRGLPGRAAEPHLRRGPQDRPGRLALHPGPDSSPGGGGGCKEKALGSPFGEECLSKEQ
NLQGPGAAKPGQVPMRKRQLPASFWEEPRPTHSYAMGLEGGLGPRERSPYESKKNCKGLESMVPEAAPGPMSPRA
LADKEPLKMPGVSLVGCVDAWSCCPFQYHRQPIYPGPPGALPPSPMPSLGLWRKSPALPPEQAHFCKRVDGPGQK
VYRPVVLKPIPTKPAMPPPIFNIFGYL PMRKRQLPASFWEEP

rs:XP_004837100 [XP_004837100] protein **FAM181**A isoform X3 [Heterocephalus glaber].>rs:XP_004837105 [XP_004837105] protein **FAM181**A isoform X3 [Heterocephalus glaber].>rs:XP_004837102 [XP_004837102] protein **FAM181**A isoform X3 [Heterocephalus glaber]. 127..141
MASDTDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLR
RGPQDRPGRLALHPGPDSSPGGGGGCKEKALGSPFGEECLSKEQNLQGPGAAKPGQVPMRKRQLPASFWEEPRPT
HSYAMGLEGGLGPRERSPYESKKNCKGLESMVPEAAPGPMSPRALADKEPLKMPGVSLVGCVDAWSCCPFQYHRQ
PIYPGPPGALPPSPMPSLGLWRKSPALPPEQAHFCKRVDGPGQKVYRPVVLKPIPTKPAMPPPIFNIFGYL
PMRKRQLPASFWEEP

rs:XP_021121636 [XP_021121636] LOW QUALITY PROTEIN: transcriptional coactivator YAP1-like, partial [Heterocephalus glaber]. 41..55
PPPAPAGHQIVHVQGDSETDLEALFNAVMNPKTASVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAG
TAGALTPQHVGAHSSPASLQLGAISPGTLTPTGVVSGPAATPAAQHLHQASFEIPDDVPLPPGWEMTKTSSGQRY
FLNHIDQTTTWQDPRKAMLSQMNVTDPTNPPVQQNLMNSAPGPLPDGWEQAITQDGEIYYINHKNKTTSWLDPRL
DXRFAMSQRISQSAPVKQPPPLPSQSPQEGVVGGSNSNQQQQMRLQQLXMEKERLRLKQQELLQQAMQNINPSTA
NSPKCQELALRSQLPTLEQDGGTQNPLFSLGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTP
DDFLNSVDEMDTGDTINRSTLPSQQNHFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMES
VLDATKLDKKSFLTWL PMRLRKLPDSFFKPP

rs:XP_004868338 [XP_004868338] protein **FAM181**B [Heterocephalus glaber].
214..228
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDENGAPAGALLPGAEGGDVREATRDLLSF

IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGGGPPSPGAADGPAKRPPALPCAPAVPTPAHGKAVP
RREASQAAAAASLQSRSLAALFDSLRYVPGGAEPAGGAEAVRAQGHGGASAGGAGGDAAGPAVSGSRKVPLRARN
LPPSFFTEPSRAGGGGGGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAESEAGVLLAAEPLDAFPTGAAVLRGPL
ELEPGLFEPPPPVIVGNLLYPEPWSAQSCPPAKKPPLEAAPAGLTLNEALRPLYPAAADSPGVEDGPGPVAPFAP
FFPDCALPQPHHQVSYDYSTGYSRTPYSSLWRPDGVWDGAPGEEGLPRD PLRARNLPPSFFTEP

rs:XP_004870870 [XP_004870870] transcriptional coactivator YAP1
[Heterocephalus glaber]. 85..99
MDPGQQPPPQPAPQGPGQPPAQPAPGQGPPSAPGQPAPPVSQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAISPGTLTP
TGVVSGPAPTPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTNPP
VQQNLMNSASGPLPDGWEQAITQDGEIYYINHKNKTTSWLDPRLDPRFAMSQRISQSAPVKQPPPLASQSPQGGV
VGGSNSSQQHQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEDVQTPPAPRSPRRSQGGGARAVLCAAGWRDAGRAAAHANFSPCEPEYSSVT
DPLAKIASADLTSEASSKHRKPTPEELAPRCG PMRLRKLPDSFFKPP

rs:XP_005506187 [XP_005506187] protein **FAM181**A [Columba
livia].>tr:A0A2I0MNP1_COLLI [A0A2I0MNP1] SubName: Full=Family with sequence
similarity 181, member A {ECO:0000313|EMBL:PKK31296.1}; 107..121
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKAPDPSPH
GGAATDKVLRTAELEESLTGERVLQEQNPEASRPDQVPMRKRQLPASFWEEPRPAQSLAARAFPSNPEGLPVSRD
PPPYEGKKSKRSSDTASPESPPESALHTGEKDPASVTSGRVGPWTCCPFPCPRPGVYQPPGSLPPSPFLGLGLWR
KSAATLPVEVPHFCKEADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_012549101 [XP_012549101] YAP65-like protein isoform X1 [Bombyx
mori].>rs:XP_028040849 [XP_028040849] transcriptional coactivator YAP1
isoform X1 [Bombyx mandarina]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAAKSTSNTTTDPLG
PLPEGWEQATTAEGEIYFINHAARTTSWFDPRIPQHLQRTPVGATGVAGGGWANASIQACQQKLRLQSLQLERDR
LKQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGLTDHQRQESADSGLGMAVPQSYSMPHTPE
DFLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_012549102 [XP_012549102] YAP65-like protein isoform X2 [Bombyx
mori].>rs:XP_028040850 [XP_028040850] transcriptional coactivator YAP1
isoform X2 [Bombyx mandarina]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAKSTSNTTTDPLGP
LPEGWEQATTAEGEIYFINHAARTTSWFDPRIPQHLQRTPVGATGVAGGGWANASIQACQQKLRLQSLQLERDRL
KQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGLTDHQRQESADSGLGMAVPQSYSMPHTPED
FLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_012549103 [XP_012549103] YAP65-like protein isoform X3 [Bombyx
mori]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAKSTSNTTTDPLGP
LPEGWEQATTAEGEIYFINHAARTTSWFDPRIPQHLQRTPVGATGVAGGGWANASIQACQQKLRLQSLQLERDRL
KQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGLTDHQRQESADSGLGMAVPQSYSMPHTPED
FLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_012549104 [XP_012549104] YAP65-like protein isoform X4 [Bombyx
mori].>rs:XP_028040852 [XP_028040852] WW domain-containing transcription

regulator protein 1 isoform X4 [Bombyx mandarina]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAQHLQRTPVGATGV
AGGGWANASIQACQQKLRLQSLQLERDRLKQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGL
TDHQRQESADSGLGMAVPQSYSMPHTPEDFLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLVPSLQLNEFT
NDILLDDVQSLINSTPSKPDNVLTWL PLRMRQLPKSFFNPP

rs:XP_012549105 [XP_012549105] YAP65-like protein isoform X5 [Bombyx mori].>rs:XP_028040853 [XP_028040853] transcriptional coactivator yorkie isoform X5 [Bombyx mandarina]. 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAQHLQRTPVGATGV
AGGGWANASIQACQQKLRLQSLQLERDRLKQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGL
TDHQRQESADSGLGMAVPQSYSMPHTPEDFLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLLNEFTNDILL
DDVQSLINSTPSKPDNVLTWL PLRMRQLPKSFFNPP

rs:XP_021236669 [XP_021236669] transcriptional coactivator YAP1 isoform X1 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQAMRNPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_021236679 [XP_021236679] transcriptional coactivator YAP1 isoform X2 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQE
LRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAI
PGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021236685 [XP_021236685] transcriptional coactivator YAP1 isoform X3 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021236690 [XP_021236690] transcriptional coactivator YAP1 isoform X4 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMG
GSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLN
SGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDG
MNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021236700 [XP_021236700] transcriptional coactivator YAP1 isoform
X5 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQAM
RNPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021236709 [XP_021236709] transcriptional coactivator YAP1 isoform
X6 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNPS
TANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPR
TPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDM
ESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021236717 [XP_021236717] transcriptional coactivator YAP1 isoform
X7 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQEL
ALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVD
EMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLD
KESFLTWL PMRLRKLPDSFFKPP

rs:XP_021236724 [XP_021236724] transcriptional coactivator YAP1 isoform
X8 [Numida meleagris]. 84..98
MDPGQPQPQQPPQAAQPPAPQQAAPQPPGAVSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQ
QNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRS
QLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDT
GDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESF
LTWL PMRLRKLPDSFFKPP

rs:XP_021266772 [XP_021266772] uncharacterized protein LOC110405637
[Numida meleagris]. 201..215
MHGRAAAPRVSPGPGVSLRTDMAAGVIRPLAELQLPSPFPHGLLLPTRPEPDFPDLPEEDEEEEEEDE
EDAAEESTGCSGPESAGPNAAESTLRLLRFSELISCDIQRYFGRRGREEATGGHSVPEDCSSPHSSPRNASPGHG
ARGGQAQPEAALGGHGAAHRLGPLAELFEYGVHRCLAPRAASGKTQRLERKYGHITPMHRRKLPPSFWREPGPGP
ASLLHAGTPDFSDLLAHWTVEPGPELPGSGRELPPAPGHAELEAEPYSGL PMHRRKLPPSFWREP

rs:XP_021259375 [XP_021259375] protein **FAM181**A [Numida
meleagris].>rs:XP_021259376 [XP_021259376] protein **FAM181**A [Numida
meleagris]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPTKPPECGPR
RGAEDRARSCQPEVPDPGPHSAAATEKVLQAAEAEESLAGEQVVPEQNPEASRPDQVPMRKRQLPASFWEEPRPA
QSIPARGFPTGPEGLPVPRDPPPFEGKKSKRSQDTAGPESHDPALHAGEEEPTGVLSGRVGAWTCCPFPCPGPAV
YQPPGTLPPTPFPGLGLWRKGTATLPAEAQPFCKEAEGTGQKLYRPVVLKPIPTKPTIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_021346267 [XP_021346267] uncharacterized protein LOC110445799
[Mizuhopecten yessoensis].>tr:A0A210QYT0_MIZYE [A0A210QYT0] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:OWF53909.1}; 140..154

MTSVMSLPFLPEVGEPRNAVSSRPHDSETSNLLSFVDMASSNIKLALDKPSRSKRKVNHRKYLQKQLKR
CGNSSTSHSEGRQVDIQGALCNGGQTKCSRKETTQIGLQIKSLQALFDPKTLHEKCCTDQTTKPTSTTKVPLRKR
NLPPSFFIEPASSLEGIDPDQVLQATENTHTDLQLCSDVTNHEFPADTLDSILGQTELQELLAGPWTDSIRDNFS
MPRCDHSLDNCSPRSFSDSSDGMSSSASVSPGIPGQSSDWIANFLSQQTGNFQNSSMFADGYTSAQNPLIPIGDS
RIGDVTDSQSLEDRLFIEQTFPGQTFSGSNGTPCDTTPLPTFPQAFCSSASLQENFQNVYPWSDAQIQPCYTYL
PLRKRNLPPSFFIEP

rs:XP_021356127 [XP_021356127] transcriptional coactivator YAP1-like
isoform X1 [Mizuhopecten yessoensis]. 43..57
MSQDQTERKGTQVVHVREDSGSELDALFNAVMNPKSGQSGQIPLRMRNLPASFWKPPDQPQRPVQHMKQ
GSNDSTGGYPGHPSGVGPSQGNLQIAHMRAHSSPASLQQTLSTVPQGPPQAPAHHARQHSCDALLDNEPLPPGWE
IAKMPDGQRYYLKQNPPPDIFNKASSPNSNHLTQSTTWQDPRKAVSTTALNSQQSPPSSQQSPNVSMQNLNLDSL
PQGWEQASTPEGDIYYINHHERTTSWYDPRIPERMRQQARINSVGPGPGQRQMGQQLAPPPQHPQQNGGTQRSQQ
ANLQFSKLQMEKERLRKRQEEIARQEMLLRAQMQAQQQLQQQQQQQQQDAIPVSQSINISQANEMTSVTDPFLGQ
TNSSDHSRQESTDSGVEGGMGTGTNYSMPRTPEDFLSNVDEMDTQEGGHRQGDFNNMDIGGNIGESGEPSNMDSE
DLVPSLQEDISNELLNDMENVLNSNKLEDNLLTWL PLRMRNLPASFWKPP

rs:XP_021356128 [XP_021356128] transcriptional coactivator YAP1-like
isoform X2 [Mizuhopecten yessoensis]. 43..57
MSQDQTERKGTQVVHVREDSGSELDALFNAVMNPKSGQSGQIPLRMRNLPASFWKPPDQPQRPVQHMKQ
GSNDSTGGYPGHPSGVGPSQGNLQIAHMRAHSSPASLQQTLSTVPQGPPQAPAHHARQHSCDALLDNEPLPPGWE
IAKMPDGQRYYLKQNPPPDIFNKASSPNSNHLTQSTTWQDPRKAVSTTALNSQQSPPSSQQSPNVSMQNLNLDSL
PQGWEQASTPEGDIYYINHHERTTSWYDPRIPERMRQQARINSVGPGPGQRQMGQQLAPPPQHPQQNGGTQRSQQ
ANLQFSKLQMEKERLRKRQEEIARQEMLLRAQMQAQQQLQQQQQQQQQDAIPVSQSINISQANEMTSVTDPFLGQ
TNSSDHSRQESTDSGVGGMGTGTNYSMPRTPEDFLSNVDEMDTQEGGHRQGDFNNMDIGGNIGESGEPSNMDSED
LVPSLQEDISNELLNDMENVLNSNKLEDNLLTWL PLRMRNLPASFWKPP

rs:XP_021356129 [XP_021356129] transcriptional coactivator YAP1-like
isoform X3 [Mizuhopecten yessoensis]. 43..57
MSQDQTERKGTQVVHVREDSGSELDALFNAVMNPKSGQSGQIPLRMRNLPASFWKPPDQPQRPVQHMKQ
GSNDSTGGYPGHPSGVGPSQGNLQIAHMRAHSSPASLQQTLSTVPQGPPQAPAHHARQHSCDALLDNEPLPPGWE
IAKMPDGQRYYLKQNPPPDIFNKASSPNSNHLTQSTTWQDPRKAVSTTALNSQQSPPSSQQSPNVSMQNLNLDSL
PQGWEQASTPEGDIYYINHHERTTSWYDPRIPERMRQQARINSVGPGPGQRQMGQQLAPPPQHPQQNGGTQRSQQ
ANLQFSKLQMEKERLRKRQEEIARQMLLRAQMQAQQQLQQQQQQQQQDAIPVSQSINISQANEMTSVTDPFLGQT
NSSDHSRQESTDSGVEGGMGTGTNYSMPRTPEDFLSNVDEMDTQEGGHRQGDFNNMDIGGNIGESGEPSNMDSED
LVPSLQEDISNELLNDMENVLNSNKLEDNLLTWL PLRMRNLPASFWKPP

rs:XP_021356130 [XP_021356130] transcriptional coactivator YAP1-like
isoform X4 [Mizuhopecten yessoensis]. 43..57
MSQDQTERKGTQVVHVREDSGSELDALFNAVMNPKSGQSGQIPLRMRNLPASFWKPPDQPQRPVQHMKQ
GSNDSTGGYPGHPSGVGPSQGNLQIAHMRAHSSPASLQQTLSTVPQGPPQAPAHHARQHSCDALLDNEPLPPGWE
IAKMPDGQRYYLNHLTQSTTWQDPRKAVSTTALNSQQSPPSSQQSPNVSMQNLNLDSLPQGWEQASTPEGDIYYI
NHHERTTSWYDPRIPERMRQQARINSVGPGPGQRQMGQQLAPPPQHPQQNGGTQRSQQANLQFSKLQMEKERLRK
RQEEIARQEMLLRAQMQAQQQLQQQQQQQQQDAIPVSQSINISQANEMTSVTDPFLGQTNSSDHSRQESTDSGVE
GGMGTGTNYSMPRTPEDFLSNVDEMDTQEGGHRQGDFNNMDIGGNIGESGEPSNMDSEDLVPSLQEDISNELLND
MENVLNSNKLEDNLLTWL PLRMRNLPASFWKPP

rs:XP_021356131 [XP_021356131] transcriptional coactivator YAP1-like
isoform X5 [Mizuhopecten yessoensis]. 43..57
MSQDQTERKGTQVVHVREDSGSELDALFNAVMNPKSGQSGQIPLRMRNLPASFWKPPDQPQRPVQHMKQ
GSNDSTGGYPGHPSGVGPSQGNLQIAHMRAHSSPASLQQTLSTVPQGPPQAPAHHARQHSCDALLDNEPLPPGWE
IAKMPDGQRYYLKQNPPPDIFNKASSPNSNHLTQSTTWQDPRKAVSTTALNSQQSPPSSQQSPNVSMQNLNLDSL
PQGWEQASTPEGDIYYINHHERTTSWYDPRIPERMRQQARINSVGPGPGQRQMGQQLAPPPQHPQQNGGTQRSQQ
ANLQFSKLQMEKERLRKRQEEIARQEMLLRAQMQAQQQLQQQQQQQQQDAIPVSQSINISQANEMTSVTDPFLGQ
TNSSDHSRQESTDSGVEGGMGTGTNYSMPRTPEDFLSNVDEMDTQEGGHRQGDFNNC PLRMRNLPASFWKPP

rs:XP_021356132 [XP_021356132] transcriptional coactivator YAP1-like
isoform X6 [Mizuhopecten yessoensis]. 43..57
MSQDQTERKGTQVVHVREDSGSELDALFNAVMNPKSGQSGQIPLRMRNLPASFWKPPDQPQRPVQHMKQ

GSNDSTGGYPGHPSGVGPSQGNLQIAHMRAHSSPASLQQTLSTVPQGPPQAPAHHARQHSCDALLDNEPLPPGWE
IAKMPDGQRYYLNHLTQSTTWQDPRKAVSTTALNSQQSPPSSQQSPNVSMQNLNLDSLPQGWEQASTPEGDIYYI
NHHERTTSWYDPRIPERMRQQARINSVGPGPGQRQMGQQLAPPPQHPQQNGGTQRSQQANLQFSKLQMEKERLRK
RQEEIARQEMLLRAQMQAQQQLQQQQQQQQDAIPVSQSINISQANEMTSVTDPFLGQTNSSDHSRQESTDSGVG
GMGTGTNYSMPRTPEDFLSNVDEMDTQEGGHRQGDFNNMDIGGNIGESGEPSNMDSEDLVPSLQEDISNELLNDM
ENVLNSNKLEDNLLTWL PLRMRNLPASFWKPP

rs:XP_021368712 [XP_021368712] uncharacterized protein LOC110460234
[Mizuhopecten yessoensis].>tr:A0A210Q2Y9_MIZYE [A0A210Q2Y9] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:OWF43082.1}; 186..200
MSTTLIELPPTTPKQHGGKKGAPGLITLSENQVIPVANIPLTPRAPQLNGAAKRGASGPIVTTSDEESD
GCSSPRSNISHNLSYQPKHQSSSQNQHHQPQPPQSQSQQRAYEAYEHDHDYENVASPSGSSTASGPVYVRPPGFR
HHAQEIKKTKKKKTALLEFRSSGLKKRAPTPPKVRPKRESVPMRLRALPQSFWKQPNVPNQVSPANVFPSLPPLY
YKESMEEITDVRPITPPEEREARQKKTLQRPPERKLIIGDTDLLLKNLFAGVNQADEKKVQHIKRGRPRKVTVPK
ATSTKTLISGDDPYLMETMTEKFFPQLTLESRQAHLAGNTSLQLVTIRNGDKSVMLPSLSINQDYSQMLSELAMN
I PMRLRALPQSFWKQP

rs:XP_021535334 [XP_021535334] protein **FAM181**A [Neomonachus
schauinslandi].>tr:A0A2Y9GC40_NEOSC [A0A2Y9GC40] SubName: Full=protein
FAM181A {ECO:0000313|RefSeq:XP_021535334.1}; 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLDSGQDCSPGGGGCYKEKALGNPYREECLSREQTLQRQNPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPLDPEMAPVPASPRALAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPIYAGHPGALPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_021542175 [XP_021542175] protein **FAM181**B [Neomonachus
schauinslandi].>tr:A0A2Y9GWF6_NEOSC [A0A2Y9GWF6] SubName: Full=protein
FAM181B {ECO:0000313|RefSeq:XP_021542175.1}; 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADAPAKRPLAAPGAQTVAVPPHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGDERARGSVAAPVAGLGGAGAGGSGGDAAGPAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGVGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEPPPAMVGSLLYSESWSAPGCPPTKKPPLAAPRGGLTLNEPLRSLYPSAADSPGGEDAPGL
LASFAPFFSDCALPPPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD
PLRARNLPPSFFTEP

rs:XP_021527383 [XP_021527383] transcriptional coactivator YAP1 isoform
X1 [Aotus nancymaae].>tr:A0A2K5DRN6_AOTNA [A0A2K5DRN6] SubName:
Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSANAP00000023613};
85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_021527384 [XP_021527384] transcriptional coactivator YAP1 isoform
X2 [Aotus nancymaae]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY

LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_021527385 [XP_021527385] transcriptional coactivator YAP1 isoform
X3 [Aotus nancymaae].>tr:A0A2K5DRL9_AOTNA [A0A2K5DRL9] SubName:
Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSANAP00000023615};
85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021527389 [XP_021527389] transcriptional coactivator YAP1 isoform
X4 [Aotus nancymaae]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021527395 [XP_021527395] transcriptional coactivator YAP1 isoform
X5 [Aotus nancymaae].>tr:A0A2K5DRP0_AOTNA [A0A2K5DRP0] SubName:
Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSANAP00000023618};
85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021527398 [XP_021527398] transcriptional coactivator YAP1 isoform
X6 [Aotus nancymaae]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021527399 [XP_021527399] transcriptional coactivator YAP1 isoform
X7 [Aotus nancymaae]. 85..99
MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_021527400 [XP_021527400] transcriptional coactivator YAP1 isoform
X8 [Aotus nancymaae]. 85..99

MDPGQQPPPQAAPQGQGQPPAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_021527473 [XP_021527473] LOW QUALITY PROTEIN: protein **FAM181**B
[Aotus nancymaae]. 218..232
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPGAPTVAAPAHGK
AAPRREASQAAAAASLQXRSLAALFDSLRHVSGGAEPAGGAVLAPAAGLGAGGAGGDTAGPAGGAAVPGARKVPL
RARNLPPSFFTEPSRGGGSGCGASGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGASVL
RGPPELEPGLFEPPPSVVGNLLYPEPWSVPGCPPTKKPPLTAPARLDLERALAPLYPAASDSPGGEDGPGHLASF
APFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSXWRPDGVWEGAPGEEGAHRTDFEAPFPPLETAMESAAPPGVA
PKSKERWENARGDEAGF PLRARNLPPSFFTEP

rs:XP_012308592 [XP_012308592] protein **FAM181**A [Aotus nancymaae].
129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAESYLK
RGPENRPGRLLLDLGPDSSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAARPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETASGPMSPSALAEKESLKMPEVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKDADGLGQKVCRPMVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_012309692 [XP_012309692] protein **FAM181**B, partial [Aotus
nancymaae]. 6..20
GARKVPLRARNLPPSFFTEPSRAGGSGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAA
EPLDVFPAGASVLRGPPELEPGLFEPPPSVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAASD
SPGGEDGPGHLASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD
PLRARNLPPSFFTEP

rs:XP_009210433 [XP_009210433] protein **FAM181**A isoform X1 [Papio anubis].
268..282
MDIPAPRYRVLPRPPFPTGISAPPDLEGPPSLIPGDPGREGGGGGRGERERERERETETERQKERRRES
ERERATQRSRTAGKAARPSLPRPIVCPHWSMAAVGLESLGEVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDS
DVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAPEPYLKRGSEDRPGRLL
LDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEG
GLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGA
LPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_003902250 [XP_003902250] protein **FAM181**A isoform X2 [Papio
anubis].>rs:XP_003902249 [XP_003902249] protein **FAM181**A isoform X2 [Papio
anubis]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAPEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_003910531 [XP_003910531] protein **FAM181**B [Papio
anubis].>tr:A0A096NY93_PAPAN [A0A096NY93] SubName: Full=Family with
sequence similarity 181 member B {ECO:0000313|Ensembl:ENSPANP00000018054};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPVAGLGGAGTGGAGGDAAGPAGATAVPGARK

VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPPHQVCYDYSAGYSRNAYSSLWRPDAVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_021913908 [XP_021913908] uncharacterized protein LOC110827008 isoform X1 [Zootermopsis nevadensis]. 235..249
MSGKRKPSPESSLTLISPNALLLSSPFCTYPFYGDDDRNSSKNNGGTSFLKLNQQKIRELTKSTKIVQR
PQKQKAVLSTRSKTFDSIPPSLEVNNNPFPPSSSPFDYDSVHSPGGVSNASSEGPTYVRTPGFEHHAQEFEIQRK
RQQCSKSHAPFASRVDEQLSCNDQDAACGQEHVRSSSKASQNGSVSNATSKKKKSVVFGTSDGKHETEAVKKTDP
SQQTTSKHKPKKEPLPMKLRALPQSFWQQPNNTNSLSPGAVYPVLPPLSSFGAAKDDVESVAAGVRSTSPPEDGL
HPLREVSVANTDLLFSLFRGIEEEQPRVTVVRRGRPKKPPSTVLTRVLRDDDPCLVSAVTESILPLIPDRTGSGS
HASRLAQGQQVLAMVSLKDGDKSLSLPSLNVEHNYSQILSELVIKL PMKLRALPQSFWQQP

rs:XP_021937265 [XP_021937265] transcriptional coactivator YAP1 isoform X1 [Zootermopsis nevadensis]. 45..59
MALNPDSEQHKGNLVVTIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGGTTTTSAAGANGLQVNHPRAHSSPASLQQTYASAQQQQHGHLKQRSYDITT
VDELGPLPPGWEQARTREGQVYYLNHITRTTTWEDPRKTLAAQVAQSQQQTSADLISNVAGSPHSSSSPQPQGTK
SVDGSSLGPLPEGWEQATTQEGEVYFINHQTRTTSWFDPRIPTAMWSRTAIPSLVQRMRVLRLSANHTMHLQKSP
AGTILPQHSASWIQPLSTQSQLCQQKIRLQSLQMERERLKLRQQEIMRQQGIMLRQASTTDLPPGANSAGMDPFL
SGLTDHSRQESADSGLGMCNSYSLPHTPEDFLANMDDNMDGVSEGGNPADMATLDGPDISSLSDNIDSTDDLVPS
LQLSEEFSSDILDDVQSLINPNSRPDNVLTWL PLRMRKLPNSFFNPP

rs:XP_021937266 [XP_021937266] transcriptional coactivator YAP1 isoform X2 [Zootermopsis nevadensis]. 45..59
MALNPDSEQHKGNLVVTIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGGTTTTSAAGANGLQVNHPRAHSSPASLQQTYASAQQQQHGHLKQRSYDITT
VDELGPLPPGWEQARTREGQVYYLNHITRTTTWEDPRKTLAAQVAQSQQQTSADLISNVAGSPHSSSSPQPQGTK
SVDGSSLGPLPEGWEQATTQEGEVYFINHQTRTTSWFDPRIPMHLQKSPAGTILPQHSASWIQPLSTQSQLCQQK
IRLQSLQMERERLKLRQQEIMRQQGIMLRQASTTDLPPGANSAGMDPFLSGLTDHSRQESADSGLGMCNSYSLPH
TPEDFLANMDDNMDGVSEGGNPADMATLDGPDISSLSDNIDSTDDLVPSLQLSEEFSSDILDDVQSLINPNSRPD
NVLTWL PLRMRKLPNSFFNPP

rs:XP_021947208 [XP_021947208] transcriptional coactivator YAP1-like isoform X1 [Folsomia candida].>rs:XP_021947209 [XP_021947209] transcriptional coactivator YAP1-like isoform X1 [Folsomia candida].
51..65
MATGGSGGGLPNGQSHKNQVIHIRGDSDSELQALFDSVLAPNANRRPKQVPLRLRNLPDSFFNPPSIGS
KSPSCSVSHSRENSVDSTLNPVRRSPLSTAGASHSRAHSSPATLEQTYSVAAALPGLSLSQSGSANNLSDDPLPP
GWEQACTPEGQIYFINHITRSTTWEDPRKAQTQQILAAIGNGTGSLSSQANHSGNVIQAVGSAVGPLPEGWEQAI
TPEGEIYFIDHMNRTTSWFDPRIPMHLQRPQVLQHQINAAALAQASALAAASAAAISASSNVNTAVTSAAGTASL
LNNNTSIQLSRQQEVRLQQLQLERERLKLRQQEIMQQMEKEQARLRQQNRLQQMEDGEIDPFLGGSMVNPSTPSS
DFHSRQESADSGLGMGNSYSLPNTPEDFLSNMDDNMDTISESIDAPDIGTLGNDNVESTDDLVPSLDISELNSEL
SNELLDEMQTIMNSSRSDNTMTWL PLRLRNLPDSFFNPP

rs:XP_021947210 [XP_021947210] transcriptional coactivator YAP1-like isoform X2 [Folsomia candida]. 51..65
MATGGSGGGLPNGQSHKNQVIHIRGDSDSELQALFDSVLAPNANRRPKQVPLRLRNLPDSFFNPPSIGS
KSPSCSVSHSRENSVDSTLNPVRSPLSTAGASHSRAHSSPATLEQTYSVAAALPGLSLSQSGSANNLSDDPLPPG
WEQACTPEGQIYFINHITRSTTWEDPRKAQTQQILAAIGNGTGSLSSQANHSGNVIQAVGSAVGPLPEGWEQAIT
PEGEIYFIDHMNRTTSWFDPRIPMHLQRPQVLQHQINAAALAQASALAAASAAAISASSNVNTAVTSAAGTASLL
NNNTSIQLSRQQEVRLQQLQLERERLKLRQQEIMQQMEKEQARLRQQNRLQQMEDGEIDPFLGGSMVNPSTPSSD
FHSRQESADSGLGMGNSYSLPNTPEDFLSNMDDNMDTISESIDAPDIGTLGNDNVESTDDLVPSLDISELNSELS
NELLDEMQTIMNSSRSDNTMTWL PLRLRNLPDSFFNPP

rs:XP_022200458 [XP_022200458] transcriptional coactivator yorkie-like [Nilaparvata lugens]. 42..56
MALNQDVERNQVVRIDQDSDTELQALFDTVLKPDSKRPLQVPFRMRKLPTSFFNPPTTGSKSPSVSSIS

HSRENSADSAFGTTTNTGLQVNHPRAHSSPASLQQTYASAQQQPPPQVQQHLKQRSYDITGGTIDELGPLPPGWE
QARTPEGQVYFLK PFRMRKLPTSFFNPP

rs:XP_022223909 [XP_022223909] transcriptional coactivator yorkie isoform
X1 [Drosophila obscura]. 65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQTNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSEANPGTSSQGPSYPENSAEFPNSAANNIELDGMNTCMGAQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQRLMAERIKQSDVLQTTKQTTTSTIANSLGPLPDGW
EQAVTESGDIYFINHIDRTTSWIDPRMQSGLTGLDCPDNLVSSLQIEDNICTNLFNDAQTIVNPPSSHKPDDLEW
YKIN PFRMRKLPNSFFTPP

rs:XP_022223910 [XP_022223910] transcriptional coactivator yorkie isoform
X2 [Drosophila obscura]. 65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQTNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSEANPGTSSQGPSYPENSAEFPNSAANNIELDGMNTCMGAQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQRLMAERIKQSESGLTGLDCPDNLVSSLQIEDNICT
NLFNDAQTIVNPPSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

rs:XP_013791735 [XP_013791735] transcriptional coactivator YAP1-like
isoform X1 [Limulus polyphemus]. 46..60
MSHSRDVIEQKGPNQTVCYDSETNLDDLFKAAMLPKDSQVQLSGPPMRLRNLPRSFFQPPEGGSKSASH
SRESSFEGTFSPPPPSSTGPNSMSKSPEQHTSGLTVSHRHTHSSPASLQQTYKQNTSQHQHLRQQSADSTDSVSL
PPGWEMAKTPSGQRYFINHETKTTTWKDPRKNLSVGTLTTSRSANPLVSTSSSGANLLPINLGPLPEGWEQAYTP
EGEVYFINHNDCTTSWFDPRLTLQLGRLPLMQSPHHGQQPPPLSSPQQQGQQQPQVQASSTGTQSLAQNIAAASI
SAAVTTMTGAVNSQLNLQQQQQQKLRLHRLQLERERLRLRQQEILRQPASLGNSMLNEMMLRRTLGEENPVVSK
SPTGNTMDMTPVCTTGMDPFLGSSNQHARQGSEDSGLGLGTNCSVPHTPENFLGSLEDVMDGGDIGQQRGSDVTM
EVLHSTNLSLGIDSMDSDDLVPSIQEEITEELLSDMESLLTSNKDNILTWL PMRLRNLPRSFFQPP

rs:XP_022236543 [XP_022236543] transcriptional coactivator YAP1-like
isoform X2 [Limulus polyphemus]. 46..60
MSHSRDVIEQKGPNQTVCYDSETNLDDLFKAAMLPKDSQVQLSGPPMRLRNLPRSFFQPPEGGSKSASH
SRESSFEGTFSPPPPSSTGPNSMSKSPEQHTSGLTVSHRHTHSSPASLQQTYKQNTSQHQHLRQQSADSTDSVSL
PPGWEMAKTPSGQRYFINHETKTTTWKDPRKNLSVGTLTTSRSANPLVSTSSSGANLLPINLGPLPEGWEQAYTP
EGEVYFINHNDCTTSWFDPRLTLQLGRLPLMQSPHHGQQPPPLSSPQQQGQQQPQVQASSTGTQSLAQNIAAASI
SAAVTTMTGAVNSQLNLQQQQQQKLRLHRLQLERERLRLRQQEILRQEMMLRRTLGEENPVVSKSPTGNTMDMT
PVCTTGMDPFLGSSNQHARQGSEDSGLGLGTNCSVPHTPENFLGSLEDVMDGGDIGQQRGSDVTMEVLHSTNLSL
GIDSMDSDDLVPSIQEEITEELLSDMESLLTSNKDNILTWL PMRLRNLPRSFFQPP

rs:XP_022236545 [XP_022236545] transcriptional coactivator YAP1-like
isoform X3 [Limulus polyphemus]. 46..60
MSHSRDVIEQKGPNQTVCYDSETNLDDLFKAAMLPKDSQVQLSGPPMRLRNLPRSFFQPPEGGSKSASH
SRESSFEGTFSPPPPSSTGPNSMSKSPEQHTSGLTVSHRHTHSSPASLQQTYKQNTSQHQHLRQQSADSTDSVSL
PPGWEMAKTPSGQRYFINHETKTTTWKDPRKNLSVGTLTTSRSANPLVSTSSSGANLLPINLGPLPEGWEQAYTP
EALQLGRLPLMQSPHHGQQPPPLSSPQQQGQQQPQVQASSTGTQSLAQNIAAASISAAVTTMTGAVNSQLNLQQQ
QQQQKLRLHRLQLERERLRLRQQEILRQPASLGNSMLNEMMLRRTLGEENPVVSKSPTGNTMDMTPVCTTGMDPF
LGSSNQHARQGSEDSGLGLGTNCSVPHTPENFLGSLEDVMDGGDIGQQRGSDVTMEVLHSTNLSLGIDSMDSDDL
VPSIQEEITEELLSDMESLLTSNKDNILTWL PMRLRNLPRSFFQPP

rs:XP_022247787 [XP_022247787] transcriptional coactivator YAP1-like
isoform X1 [Limulus polyphemus]. 48..62
MSQLRDVVEQKGPNQTVCYDSETNLILDDLFKAAMLPRDSQVQLGGPPMRLRNLPRSFFQPPEGGSKSA
SHSRESSFEGTFSPPSSVGPSSTAPSPRQQASGLTVSHRHTHSSPATLQQSYNQNTPQNQHLRQQSADSTDSVPL
PPGWEMAKTSSGQRYFINHETKSTTWTDPRKNLSVGSLTMPRNTNTLMSTSAPNLPPINLGPLPEGWEQAFTPES
EVYFINHNDRTTSWFDPRLTLNLGRLPLMHHPHHGQQPPSMPSLQEQQSQVQANSSGTQSLAQNISAAASISAAV
TTLTGAVNNQLSLQQQQQQQKLRLQRLQMERERLRLRQQEILRQPTSLGNSMLNEMMLRRNLVEENPMIPKSPT
VTTMDMTPICTTGIDPLLGSSNQHARQGSEDSGLGLGTSYSVPHTPENFLGSLEDTMDGGGSDINIEGLQSTNLN
LGSENMDSDDLVPSIQEELTEEILSDMESLLTSNKDNILTWL PMRLRNLPRSFFQPP

rs:XP_022247788 [XP_022247788] transcriptional coactivator YAP1-like
isoform X2 [Limulus polyphemus].>rs:XP_022247789 [XP_022247789]
transcriptional coactivator YAP1-like isoform X2 [Limulus polyphemus].
48..62
MSQLRDVVEQKGPNQTVCYDSETNLILDDLFKAAMLPRDSQVQLGGPPMRLRNLPRSFFQPPEGGSKSA
SHSRESSFEGTFSPPSSVGPSSTAPSPRQQASGLTVSHRHTHSSPATLQQSYNQNTPQNQHLRQQSADSTDSVPL
PPGWEMAKTSSGQRYFINHETKSTTWTDPRKNLSVGSLTMPRNTNTLMSTSAPNLPPINLGPLPEGWEQAFTPES
EVYFINHNDRTTSWFDPRLTLNLGRLPLMHHPHHGQQPPSMPSLQEQQSQVQANSSGTQSLAQNISAAASISAAV
TTLTGAVNNQLSLQQQQQQQKLRLQRLQMERERLRLRQQEILRQPTSLGNSMLNEMMLRRNLVEENPMIPKSPT
VTTMDMTPICTTGIDPLLGSSNQHARQGSEDSGLGLGTSYSVPHTPENFLGSLEDTMDGGGSDINIEGLQSTNLN
LGSENMDSDDLVPSIQCTVYTLDTDDASSILTRRNSILLE PMRLRNLPRSFFQPP

rs:XP_022247790 [XP_022247790] transcriptional coactivator YAP1-like
isoform X3 [Limulus polyphemus]. 48..62
MSQLRDVVEQKGPNQTVCYDSETNLILDDLFKAAMLPRDSQVQLGGPPMRLRNLPRSFFQPPEGGSKSA
SHSRESSFEGTFSPPSSVGPSSTAPSPRQQASGLTVSHRHTHSSPATLQQSYNQNTPQNQHLRQQSADSTDSVPL
PPGWEMAKTSSGQRYFINHETKSTTWTDPRKNLSVGSLTMPRNTNTLMSTSAPNLPPINLGPLPEGWEQAFTPES
EVYFINHNDRTTSWFDPRLTLNLGRLPLMHHPHHGQQPPSMPSLQEQQSQVQANSSGTQSLAQNISAAASISAAV
TTLTGAVNNQLSLQQQQQQQKLRLQRLQMERERLRLRQQEILRQEMMLRRNLVEENPMIPKSPTVTTMDMTPIC
TTGIDPLLGSSNQHARQGSEDSGLGLGTSYSVPHTPENFLGSLEDTMDGGGSDINIEGLQSTNLNLGSENMDSDD
LVPSIQEELTEEILSDMESLLTSNKDNILTWL PMRLRNLPRSFFQPP

rs:XP_013780310 [XP_013780310] transcriptional coactivator YAP1-like
[Limulus polyphemus]. 50..64
MSQVRDVIEQNGPNQIVRIRRDSETNLDDLFKAVLQPKDSQVQLSRRTVPMRLRNLPPSFFQQPETKSA
SHSRESSSDTTFSPCVSPVPGASPSPQGAQHSSNNILQVHHPRANSSPATLEQTYNQNTGQQHQHFRQHSYDNII
DDVPLPSGWEMARTPSGQRYFLK PMRLRNLPPSFFQQP

rs:XP_022248441 [XP_022248441] transcriptional coactivator YAP1-like
isoform X1 [Limulus polyphemus].>rs:XP_022248442 [XP_022248442]
transcriptional coactivator YAP1-like isoform X1 [Limulus polyphemus].
46..60
MSQSRDVFEQKGPNQTVCYDSETNLDDLFKAAMLPKDSQVQLSGPPMRLRNLPRSFFQPPDGGSKSASH
SRESSFEGTFSPPPPCSVGSNSATTSPQQQHIIVSGLTVSHRHTHSSPASLQQSYNQTTSQHQHPRQQSADSIDS
IPLPPGWEMAKTQSGERYFINHETKTTTWKDPRKNLSVGALTTPRSSNLLVSTSTSGSNIPPINLGPLPEGWEQA
CTPEGEVYFINHNDCTTSWLDPRLTLQLGRLPLMQSPHHGLQQPTMPSSQQLGQQQPQVQANSTGTQSCVQNNAA
SASISAAVTTVAGSVNSQLNLQQQQQQQKQRLHRLQLERERLRLRQQEILRQPASLGNSMLNEMMLRRTLGEENS
VIPKSPPGNTVDMIPVCTSGIDPFLGSSNQHARQGSEDSGLGLGTNYSVPHTPENFLGSLEDVMDGGDIGQQAGG
DISMEVLQNTNLNLGSDTMDSDDLVPSIQEEITEELLSDMESLLTSNKDNVLTWL PMRLRNLPRSFFQPP

rs:XP_022248443 [XP_022248443] transcriptional coactivator YAP1-like
isoform X2 [Limulus polyphemus]. 46..60
MSQSRDVFEQKGPNQTVCYDSETNLDDLFKAAMLPKDSQVQLSGPPMRLRNLPRSFFQPPDGGSKSASH
SRESSFEGTFSPPPPCSVGSNSATTSPQQQHIIVSGLTVSHRHTHSSPASLQQSYNQTTSQHQHPRQQSADSIDS
IPLPPGWEMAKTQSGERYFINHETKTTTWKDPRKNLSVGALTTPRSSNLLVSTSTSGSNIPPINLGPLPEGWEQA
CTPEGEVYFINHNDCTTSWLDPRLTLQLGRLPLMQSPHHGLQQPTMPSSQQLGQQQPQVQANSTGTQSCVQNNAA
SASISAAVTTVAGSVNSQLNLQQQQQQQKQRLHRLQLERERLRLRQQEILRQEMMLRRTLGEENSVIPKSPPGNT
VDMIPVCTSGIDPFLGSSNQHARQGSEDSGLGLGTNYSVPHTPENFLGSLEDVMDGGDIGQQAGGDISMEVLQNT
NLNLGSDTMDSDDLVPSIQEEITEELLSDMESLLTSNKDNVLTWL PMRLRNLPRSFFQPP

rs:XP_022248444 [XP_022248444] transcriptional coactivator YAP1-like
isoform X3 [Limulus polyphemus]. 46..60
MSQSRDVFEQKGPNQTVCYDSETNLDDLFKAAMLPKDSQVQLSGPPMRLRNLPRSFFQPPDGGSKSASH
SRESSFEGTFSPPPPCSVGSNSATTSPQQQHIIVSGLTVSHRHTHSSPASLQQSYNQTTSQHQHPRQQSADSIDS
IPLPPGWEMAKTQSGERYFINHETKTTTWKDPRKNLSVGALTTPRSSNLLVSTSTSGSNIPPINLGPLPEGWEQA
CTPEGEVYFINHNDCTTSWLDPRLTLQLGRLPLMQSPHHGLQQPTMPSSQQLGQQQPQVQANSTGTQSCVQNNAA
SASISAAVTTVAGSVNSQLNLQQQQQQQKQRLHRLQLERERLRLRQQEILRQPASLGNSMLNEMMLRRTLGEENS
VIPKSPPGNTVDMIPVCTSGIDPFLGSSNQHARQGSEDSGLGLGTNYSVPHTPENFLGSLEDVMDGGDIGQQAGG
DISMEVLQNTNLNLGSDTMDSDDLVPSIQKSQKNCSLIWSLF PMRLRNLPRSFFQPP

rs:XP_013791100 [XP_013791100] transcriptional coactivator YAP1-like isoform X1 [Limulus polyphemus].>rs:XP_022258909 [XP_022258909] transcriptional coactivator YAP1-like isoform X1 [Limulus polyphemus].
50..64
MSQARDVIEQKGPNQIVRIRRDSETNLDDLFKAVLQPKDSQVQLSRRTVPMRLRNLPPSFFQQPETKSA
SHSRDSSCDATFSPTCVSPVSGAPPSPQLQVQAQHSISTNINNALQVHHPRANSSPASLEQTYNQNSGQQHQHLR
QHSYDNMIDDVPLPSGWEMARTSSGQRYFLNHEAIHTQLT PMRLRNLPPSFFQQP

rs:XP_022258910 [XP_022258910] transcriptional coactivator YAP1-like isoform X2 [Limulus polyphemus]. 50..64
MSQARDVIEQKGPNQIVRIRRDSETNLDDLFKAVLQPKDSQVQLSRRTVPMRLRNLPPSFFQQPETKSA
SHSRDSSCDATFSPTCVSPVSGAPPSPQLQVQAQHSISTNINNALQVHHPRANSSPASLEQTYNQNSGQQHQHLR
QHSYDNMIDDVPLPSGWEMARTSSGQRYFLK PMRLRNLPPSFFQQP

rs:XP_022322033 [XP_022322033] uncharacterized protein LOC111123761 [Crassostrea virginica]. 115..129
MKQESESTSSLLNFVDVASSNIKMALDRPPKSKRKVNHRKYLQKQLKSCGNVQQQQQENSRRSLTGAH
QIRLVRRENPQSGVQMKSLQDLFDPRTLHEKCCADPSSKNRGSKIPLRKRNLPPSFFLEPSRLEQRDNLLESLTS
ALPDDFFHSLHRSPDLDTLSSDTLDSILGNNDFSEFPNTGQWNDSSSTDSFESDPCGSPNSDYSGLNNTVYFTEY
PNSNPEFTPDYWSGTPACSRIQQPTFTENSFPQVCHPSFEPLRSTEQSFHGVTSYRESSFSKLPTFPQAFLSRNC
VNSNQSAEHWGNSCYTYL PLRKRNLPPSFFLEP

rs:XP_022343587 [XP_022343587] uncharacterized protein LOC111136777 [Crassostrea virginica]. 264..278
MASISAAQVPLLDVNFGLGATQKSYGGKKAPHAFHSYSEEEETLHLSSNLAAKSYGGKRAPSSSLIAVN
LDEDSKLACVKKSTLSNIIVLNDDEESPCYKSYGLKKIIPTNALVNHDGEDMSQTTSQAGKRSNVSLTDIKEEGQ
KDYEKVTLPQQGSKRGAPGPLVTSSDEDESLPPSPRSSVNSSSSVQHAYEHDHDYENVASPSGSSTASGPVYIRP
PGFRHHAQEIKKVKKKKITEFDFKSALKKRAPTPPKVKPKRESVPMRLRALPQSFWKQPNVPNPVSPAPLFPSLP
PLGSKDSSEDITDMRPITPPDDKERHKKQTRQPERKVYVTGDTDLLLKHLFDRAVEDKKNSHIKRGRPRKIAVPR
ETSTKALISGDDPYLVDAVTQKLFPQLSLESRMGQIGSTSLQLVTLRDGDKSVTLPSLSIEQNYSQMLTDLAMNI
PMRLRALPQSFWKQP

rs:XP_022286669 [XP_022286669] transcriptional coactivator YAP1-like isoform X1 [Crassostrea virginica]. 43..57
MSQDMQERKGTQVVHVRENSGNELDALFQYAANPNSELGGQIPFRQRKLPPSFFNEPKPSGHVKQGSND
STGFPGQMNPAMGAHMRAHSSPANLQQTLSAAPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYLNS
SEKSLYKVDKGKEMLLPMDNEGHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPPGWEQASTPEGD
IYFINHMERTTSWYDPRIPEQLQQLRLTSSQPGAQQVPPRQMNPRQMGQPPPQPPVNRAMGAKSPASLQFSKIQM
EKELLRKRQEDLQRQEMMLRAQMQQQQIHDNPPSSQGIVISQSMEMPIVADPFLGQSNVTANHIKQESSDSGVGG
MGTGTPYGLSRTPEDFLSNVSEMEQDGGGHRHGEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMES
VLNVNKLDNILAGDNSLTWL PFRQRKLPPSFFNEP

rs:XP_022286670 [XP_022286670] transcriptional coactivator YAP1-like isoform X2 [Crassostrea virginica]. 43..57
MSQDMQERKGTQVVHVRENSGNELDALFQYAANPNSELGGQIPFRQRKLPPSFFNEPKPSGHVKQGSND
STGFPGQMNPAMGAHMRAHSSPANLQQTLSAAPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYLNS
SEKSLYKVDKGKEMLLPMDNEGHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPPGWEQASTPEGD
IYFINHMERTTSWYDPRIPEQLQQLRLTSSQPGAQQVPPRQMNPRQMGQPPPQPPVNRAMGAKSPASLQFSKIQM
EKELLRKRQEDLQRQEMMLRAQMQQQQIHDNPPSSQGIVISQSMEMPIVADPFLGQSNVTANHIKQESSDSGVGM
GTGTPYGLSRTPEDFLSNVSEMEQDGGGHRHGEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMESV
LNVNKLDNILAGDNSLTWL PFRQRKLPPSFFNEP

rs:XP_022286671 [XP_022286671] transcriptional coactivator YAP1-like isoform X3 [Crassostrea virginica]. 43..57
MSQDMQERKGTQVVHVRENSGNELDALFQYAANPNSELGGQIPFRQRKLPPSFFNEPKPSGHVKQGSND
STGFPGQMNPAMGAHMRAHSSPANLQQTLSAAPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYLKV
DKGKEMLLPMDNEGHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPPGWEQASTPEGDIYFINHME
RTTSWYDPRIPEQLQQLRLTSSQPGAQQVPPRQMNPRQMGQPPPQPPVNRAMGAKSPASLQFSKIQMEKELLRKR
QEDLQRQEMMLRAQMQQQQIHDNPPSSQGIVISQSMEMPIVADPFLGQSNVTANHIKQESSDSGVGGMGTGTPYG

LSRTPEDFLSNVSEMEQDGGGHRHGEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMESVLNVNKLD
NILAGDNSLTWL PFRQRKLPPSFFNEP

rs:XP_022286672 [XP_022286672] transcriptional coactivator YAP1-like
isoform X4 [Crassostrea virginica]. 43..57
MSQDMQERKGTQVVHVRENSGNELDALFQYAANPNSELGGQIPFRQRKLPPSFFNEPKPSGHVKQGSND
STGFPGQMNPAMGAHMRAHSSPANLQQTLSAAPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYLNS
SEKSLYNHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPPGWEQASTPEGDIYFINHMERTTSWYD
PRIPEQLQQLRLTSSQPGAQQVPPRQMNPRQMGQPPPQPPVNRAMGAKSPASLQFSKIQMEKELLRKRQEDLQRQ
EMMLRAQMQQQQIHDNPPSSQGIVISQSMEMPIVADPFLGQSNVTANHIKQESSDSGVGGMGTGTPYGLSRTPED
FLSNVSEMEQDGGGHRHGEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMESVLNVNKLDNILAGDN
SLTWL PFRQRKLPPSFFNEP

rs:XP_022286673 [XP_022286673] transcriptional coactivator YAP1-like
isoform X5 [Crassostrea virginica]. 43..57
MSQDMQERKGTQVVHVRENSGNELDALFQYAANPNSELGGQIPFRQRKLPPSFFNEPKPSGHVKQGSND
STGFPGQMNPAMGAHMRAHSSPANLQQTLSAAPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYLNH
LTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPPGWEQASTPEGDIYFINHMERTTSWYDPRIPEQLQ
QLRLTSSQPGAQQVPPRQMNPRQMGQPPPQPPVNRAMGAKSPASLQFSKIQMEKELLRKRQEDLQRQEMMLRAQM
QQQQIHDNPPSSQGIVISQSMEMPIVADPFLGQSNVTANHIKQESSDSGVGGMGTGTPYGLSRTPEDFLSNVSEM
EQDGGGHRHGEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMESVLNVNKLDNILAGDNSLTWL
PFRQRKLPPSFFNEP

rs:XP_022286674 [XP_022286674] transcriptional coactivator YAP1-A-like
isoform X6 [Crassostrea virginica]. 43..57
MSQDMQERKGTQVVHVRENSGNELDALFQYAANPNSELGGQIPFRQRKLPPSFFNEPKPSGHVKQGSND
STGFPGQMNPAMGAHMRAHSSPANLQQTLSAAPQPPSHARQRSCDALLDPIESEPLPPGWEMAKTQDGQRYYLNS
SEKSLYKVDKGKEMLLPMDNEGHLTQITTWQDPRKGSSNALNSRTPPNSQSPNVSLQNLGPLPPGWEQASTPEGD
IYFINHMERTTSWYDPRIPEQLQQLRLTSSQPGAQQVPPRQMNPRQMGQPPPQPPVNRAMGAKSPASLQFSKIQM
EKELLRKRQEDLQRQEMMLRAQMQQQQIHDNPPSSQGIVISQSMEMPIVADPFLGQSNVTANHIKQESSDSGVGG
HRHGEFNNMDIGNIGGNEENSNMDSEDLVPSLQEDISNELLNDMESVLNVNKLDNILAGDNSLTWL
PFRQRKLPPSFFNEP

rs:XP_007236793 [XP_007236793] protein **FAM181**B [Astyanax mexicanus].
156..170
MAVQAAIMNSQFLNFCFPGSVMEYEVEKGLDGGLLGEADCERDFRETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISSGTAATQEPCKRQDSPQTPTSTLQSKTPPKRDGAQANLQSKSLAALFNPA
KDLRGERAKKPPLRHRNLPPSFFTEPANCSRVTSTSGMSLKDLERGNPDAAEFFELLGPDYSNMVTEQELFHTTT
PVRVQQEGTGGPEPGAFDHFVTGGFLYAEPWGTTGSGASKKTGDMRTVPGQPPLYGSTDSSGPAPAEQSSPCSSL
TFPNFFTDCPVSQVSYDLASGYTRGSFPSL PLRHRNLPPSFFTEP

rs:XP_022520645 [XP_022520645] LOW QUALITY PROTEIN: transcriptional
coactivator YAP1-like [Astyanax mexicanus]. 45..59
MDPGQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAAVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLTGLPQPGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQSTTWQDPXKAMLQMNQPPPGSPVPVQQQNLLNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRISQSAPVKPGPPLPSSPPNAGVIGGSCQMRLQQLQMEKERLRLKHQELLRRPQELALRNQLPTSM
EQDGGTQNPVSSPGMGQDARSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLV
PASMATQPRGFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_007257521 [XP_007257521] protein **FAM181**A [Astyanax mexicanus].
118..132
MASSDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHAHRAPDSAP
KPIEDKPTPLTHESPAFLPHLTEKREPRAERLDPNPDREEDPSRAGQLPMRKRQLPASFWEEPRAPHGAHPCFHH
AWKRRAHAGTRTQRESGGDERAADLLPPARRGSPDLEPLRVALTCGCAPFQYRGSQALHTHAHTHLLLPQASLAH
VGLRTKIGGTELDMQKVPDALKNSTTHVVVKPIPTKPVSTSIFSVFGFI PMRKRQLPASFWEEP

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rs:XP_022779114   [XP_022779114] transcriptional coactivator YAP1-A-like
[Stylophora pistillata].>tr:A0A2B4SPA1_STYPI [A0A2B4SPA1] SubName:
Full=Yorkie-like {ECO:0000313|EMBL:PFX32504.1};46..60
      MERKNNNCVVHVRQDSDNDLEALFHVVSKNSVAKTHPEPASSQSLPMRLRKLPPSFFKQPPIDGGLSPD
HDVPKRLPISHSHSRSSPASLTVPTTLKGPPNHSLSPGVHHQRSTSFDNTALLEEPTPMPPGWEMRTTASGQRYF
MNHFEQLTTWQDPRKTQSTSNLNSVQPVGNLPDGWEQAITPEGDIYYINHIERTTSWIDPRLAMHCRNQESMRGS
TLPPDFNRHGHRTLQLHRLQREREQLLKRQQELLKQEIKLKRDILEEGGKPSLLGNLTREFSAPDPPVTNGGHIR
DESFDSGLGMGGGNYQFHDVDMNDSQPMFDANYNSKDTSFRADPRIPEILDSLPGTNVDLGVMEGTDNSTNMETE
DLGVGLEFNSEILNDMESVLISPTLTWL  PMRLRKLPPSFFKQP

rs:XP_022780118   [XP_022780118] uncharacterized protein LOC111321491
[Stylophora pistillata].>tr:A0A2B4SSR6_STYPI [A0A2B4SSR6] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:PFX31950.1};      110..124
      MDPQRKRLQHKDTLNWRTPPSISPPSPCGPSSPQSPPPLVVRGKSLSLNRVGAPALLPIRETPAKELSK
RGRKQRLLLSQAGNLALKRRETSPDFNKLEARLKPKRGPLPMRMRALPQSFWQEPKNIQNSSMSTEGTLSSLPPL
FHNANNTSYDVSKVRPVTPPEEKCLPRPPKEPKLVITSPQEQLLKLFETVEEDKTKKFVIRRGRPRRVQSDLTPC
QLPKLEEDPCMMTSLAEKLFPQLSLENNKQTPGANTSLSCVSVHDGDKSVTLPSLNVEQNYSQMLSEIVAHF
      PMRMRALPQSFWQEP

rs:XP_022793172   [XP_022793172] uncharacterized protein LOC111332152
[Stylophora pistillata].     156..170
      MNSLGEESVATPTSLLNFVSNATSALKFALDKPIKPKRKVNHRKYLQRQLSGRSSSAATSSFDGSWISQ
GEILFDHVLKSGQRGSASAVARAEKSSTAIPWKNRSEETQALGTDNVLDVFQKKRAQGKEKNWKITRSQQINDTK
TSQALFSQPSQPLKKRKLPESFWTEPSPKASRKPLQATRNSKTNLATNELQRSELEILDWLRPELDDFIERWSEE
SECASNNSSRPDSLSDSPSTIDPHSPYSDESENVGLMDEFFEQRVPFSFDSSTKNGECTSNIPSTRNYANANINF
VNNRTYNVPQDYVQRPLNHSVSCYGGQYGFSANEWSANPVQPNYFETGYNVLS PLKKRKLPESFWTEP

rs:XP_018565735   [XP_018565735] transcriptional coactivator YAP1-A isoform
X1 [Anoplophora glabripennis].     41..55
      MALNQDEAKQEVRVNQDSETDLQALFDTVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATAAAPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQAPVHHIKQRSYDVASKTEDNTPLPPGWEQAR
TPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAQQHQSAEQLLTAHQISHPQSPNPNTAKVNSDVDLGPLPEGWEQA
QTPEGEIYFINHQTRTTSWFDPRIPTHLQQRPAGANLVGSTWHSQALSSSPSKAQQIRLQQLRMERERLKQRQQE
IMRQQDIMMRSSSDLPVMDPFLSSLTDHSRQESGDSGLGMGTTYSMPHTPEDFLANMDDNMDVGSESHTMDTPDI
STLSDNIDSTDDLVPTLQLGEEFPILDDVQSLINPPTTKPDNVLIWL PWSMRKLPDSFFNPP

rs:XP_018565736   [XP_018565736] WW domain-containing transcription
regulator protein 1 isoform X2 [Anoplophora glabripennis]. 41..55
      MALNQDEAKQEVRVNQDSETDLQALFDTVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATAAAPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQAPVHHIKQRSYDVASKTEDNTPLPPGWEQAR
TPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAQQHQSAEQLLTAHQISHPQSPNPNTTHLQQRPAGANLVGSTWHS
QALSSSPSKAQQIRLQQLRMERERLKQRQQEIMRQQDIMMRSSSDLPVMDPFLSSLTDHSRQESGDSGLGMGTTY
SMPHTPEDFLANMDDNMDVGSESHTMDTPDISTLSDNIDSTDDLVPTLQLGEEFPILDDVQSLINPPTTKPDNVL
IWL   PWSMRKLPDSFFNPP

rs:XP_023500466   [XP_023500466] transcriptional coactivator YAP1 isoform
X1 [Equus caballus].   85..99
      MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_023500467   [XP_023500467] transcriptional coactivator YAP1 isoform
X2 [Equus caballus].   85..99
      MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
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NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023500468 [XP_023500468] transcriptional coactivator YAP1 isoform
X3 [Equus caballus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023500469 [XP_023500469] transcriptional coactivator YAP1 isoform
X4 [Equus caballus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023500470 [XP_023500470] transcriptional coactivator YAP1 isoform
X5 [Equus caballus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023500471 [XP_023500471] transcriptional coactivator YAP1 isoform
X6 [Equus caballus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023500472 [XP_023500472] transcriptional coactivator YAP1 isoform
X7 [Equus caballus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023500473 [XP_023500473] transcriptional coactivator YAP1 isoform X8 [Equus caballus]. 85..99

MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023500474 [XP_023500474] transcriptional coactivator YAP1 isoform X9 [Equus caballus]. 85..99

MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGSSNQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023500475 [XP_023500475] transcriptional coactivator YAP1 isoform X10 [Equus caballus]. 85..99

MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGSSNQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023500476 [XP_023500476] transcriptional coactivator YAP1 isoform X11 [Equus caballus]. 85..99

MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGSSNQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_023500477 [XP_023500477] transcriptional coactivator YAP1 isoform X12 [Equus caballus]. 85..99

MDPGQQPPPQPAPQGQGQPPAQAPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTLPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGSGSSNQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_023501415 [XP_023501415] protein **FAM181**B [Equus caballus]. 221..235

MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDESGTPGGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAPGAQTVAGPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGSVAAPAAGLGGAGAGGAGGDAAGPAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGGGCGPSGPVVSLGDLEKGAEAVEFFELLAPDYGTGTEAGVLLAAEPLDVFPT
GAAALRGPPELEPGLFEPPPGMVGSLLYPEPWGAPGCPSTKKPQLAAPRGGLTLNEPLRPLYPAAADSPGGEDAP
GLLASFAPFFSDCALPPAPPPHQVSYDYSAGYGRTAYSSLWRADADWEGAPGEEGAHRD
PLRARNLPPSFFTEP

rs:XP_012370487 [XP_012370487] protein **FAM181**B [Octodon degus].112..126
MAVQAALLRAHPFAPFGFGGAPDGLGGAFGAADGGCCFEEDERAASAAEATRELLSFIDSASSNIKLAL
DKPGKSRRKVNHRKYLQKQIKRCGGLAGAAPPPPAPDGAAKVPLRARKLPASFFTEPARAGPSGPSLGELEPGAA
ELLELLGPDYGADPEAGVLLAAEPLDVFPAAGLRASLELEPGLFEPPAVVGSLLYPEPWGAPGCPPAGKPPLAAA
RGGLSPSESLRPLYPATAADSAGEDGPGPAAAFAPFFPDCAPPPPPPPPHQASYDFSASYSRSPYPGLWRPDGAW
DGAPGEPGVHPD PLRARKLPASFFTEP

rs:XP_007104739 [XP_007104739] protein **FAM181**A isoform X1 [Physeter catodon].>tr:A0A2Y9ELA9_PHYCD [A0A2Y9ELA9] SubName: Full=protein **FAM181**A isoform X1 {ECO:0000313|RefSeq:XP_007104739.2};193..207
MLLRGSPCCPQPEISPPGRPRLECQTGVLPVLRENCQLGALPWSRQPPAEPPSSWKAPCSGPLAMASDS
DVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRRAEPHLKSGSEDRPGRLP
LDSGHRPSPSGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTHSYPVGLEG
GLGPREGPPYEGKKHCKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPVYPGPPGA
LPQSPHPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023986714 [XP_023986714] protein **FAM181**A isoform X2 [Physeter catodon].>tr:A0A2Y9TF16_PHYCD [A0A2Y9TF16] SubName: Full=protein **FAM181**A isoform X2 {ECO:0000313|RefSeq:XP_023986714.1};129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRRAEPHLK
SGSEDRPGRLPLDSGHRPSPSGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQSPHPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023993306 [XP_023993306] protein **FAM181**A [Salvelinus alpinus].
125..139
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARMPRCHTHRSTESSI
AKDVVNKSSAYSLETIHPSTTRINEKGGSDAQDVENARMAQTPTVDSDNSKQEQVPMRKRQLPASFWEEPRLAQT
NTDYLQYGWKKSQGVTGINEVEKIKKAHEEPTPTLFLSNRRGSVEKEPLKLDVASHNVNVCGFCPFQYHGHHVFQ
SHIVVPQSAVGLWGKATVAETETPDIAHRYKNYTHVVVKPIPTKPTVPPSIFNVFGFI PMRKRQLPASFWEEP

rs:XP_023993347 [XP_023993347] transcriptional coactivator YAP1-like [Salvelinus alpinus]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLETLFNAVMNPKNTSVPPSVPMRMRKLPDSFFKPPEPKSHSRQTS
TDAGTAGAIAPTTWRAHSSPASLQLGAVVSPVGHGPAAPPHPPPTVVL PMRMRKLPDSFFKPP

rs:XP_024000598 [XP_024000598] protein **FAM181**B [Salvelinus alpinus].
174..188
MAVQTAIMNSPFINFCFPGSVMMEYDMDQSLDGSLLEESEERGEYKETTRNLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGFISPTGNPAAAPGAGANKRKGSGFPTQTQPQTQPQTQPSPFQQGKPVHKRDG
LQANLQTKSLAALFNSVKEPVRGERAKKPPLRHRNLPPSFFTEPANTTTTSRVTSTSGTFLGDLERGGGNPDFFD
LLGPDYSNMLSDQDVFQTRGLPSRIIDQDLFQTRGLPSRILQHQQTQDITDQVSPYDPHHLVGGFLYTEPWSTSS
PSKKAGEGVRTGPGPQTPLYCQAGEGVRTGPGTQTPLYCQAGEGVRAGPGTQTPLYCQAGEGVRTGPGTQTPMSA
RQERAYGGPRNTDTPVLPSRRGRTGRTGTQTPCTVTLCLTPL PLRHRNLPPSFFTEP

rs:XP_014241727 [XP_014241727] transcriptional coactivator YAP1-A-like isoform X1 [Cimex lectularius]. 45..59
MSGNPEVDQFKSNLVVRIDQDSDSELQALFDSVLKPDSKRPLQVPLRMRNLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTKTTTVSLQVNHPRAHSSPASLQQTYASAQQQTPQHLKQRSYDMTALDELGPLPPGWEQA
RTSEGQIYFLNHITQTTTWEDPRKTAAAQQQRSQEMLNTVPTSPHPPTSPQPHQSKNGGVSSPAGSATLGPLPDG
WEQASTAEGEVYFINHQTKTTSWFDPRIPVHLQRAPTAAGTLPGWLQPLTQSQNLQAATQQKLRLQSLQMERERL
KLRQQEIMRQQELMLRDAPATTGLDPFLSGLADHSRQESADSGLGLGNSYSLPHTPDDFLSSMDDNMDGVSEGGT
GAEIASLDSHEITSLSDNIDSTDDLVPSLQLGEEFTSDILDDVQALINPNSKPGNSLTWL
PLRMRNLPNSFFNPP

rs:XP_014241728 [XP_014241728] transcriptional coactivator yorkie-like isoform X2 [Cimex lectularius]. 45..59

MSGNPEVDQFKSNLVVRIDQDSDSELQALFDSVLKPDSKRPLQVPLRMRNLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTKTTTVSLQVNHPRAHSSPASLQQTYASAQQQTPQHLKQRSYDMTALDELGPLPPGWEQA
RTSEGQIYFLNHITQTTTWEDPRKTAAAQQQRSQEMLNTVPTSPHPPTSPQPHQTVHLQRAPTAAGTLPGWLQPL
TQSQNLQAATQQKLRLQSLQMERERLKLRQQEIMRQQELMLRDAPATTGLDPFLSGLADHSRQESADSGLGLGNS
YSLPHTPDDFLSSMDDNMDGVSEGGTGAEIASLDSHEITSLSDNIDSTDDLVPSLQLGEEFTSDILDDVQALINP
NSKPGNSLTWL PLRMRNLPNSFFNPP

rs:XP_023018395 [XP_023018395] transcriptional coactivator YAP1-A-like
[Leptinotarsa decemlineata]. 41..55
MALNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATSAAPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQSAVHHIKQRSYDVASKTEDNTPLPPGWEQAR
TPEGQVYYLK PWSMRKLPDSFFNPP

rs:XP_023027462 [XP_023027462] transcriptional coactivator YAP1-A-like
[Leptinotarsa decemlineata]. 41..55
MALNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATSAAPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQSAVHHIKQRSYDVASKTEDNTPLPPGWEQAR
TPEGQVYYLNHTTRTTTWEDPRKSLAAQAAQQHQSAELLIPHPQSPNPNTAKVNTDVDLGPLPEGWEQAQTPEGE
IYFINHQTRTTSWFDPRIPTHLQQRSPGGNLVGPAWHSAASTSATAQKIRLQQLQMERERLKQRQQEIRRQEILM
RSSSDIPVMDPFLSSLTDHSRQESGDSGLGMGTSYSMPHTPEDFLVDNMDDNMEVGRESHTMDTPDLTSLSDNID
STDDLVPTLQLGEEFPILEDVQSLINPPTTRPDNVLIWL PWSMRKLPDSFFNPP

rs:XP_023028438 [XP_023028438] transcriptional coactivator YAP1-A-like
[Leptinotarsa decemlineata]. 42..56
MMALNQDKDKQVIRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPESFFTPPSTGSKSINHSREN
SADSAFGGGSAGTALVKSVPQQVAHHRAHSSPASLQQTHAVGPRQDVGHHVKQRSYDVAVRTEDNTPLPPGWEQA
CTPEGQIYYLNHITRTTTWEDPRKLLVTQTAAQQHHNTELSMPHQQSPDTIKVNPDLGPLPEGWEQAQTPEGEIY
FMNHRTRTTSWFDPRIPAHLQQLSPGRNIVRPDWPSAVSTSITAQKIRLQQLQMERERLKQRQQEIMHQEILMRS
SNDIPVLDPFLSGLTDHSRQESGDSGLGMGTTCSMPHTPEDFLGDNMEVGGESHAVETPDMSSLRENIDSTDDLV
PTLQLGEEFPILEDVQSLISPLTTRPDNILTWL PWSMRKLPESFFTPP

rs:XP_002063466 [XP_002063466] transcriptional coactivator yorkie isoform
X1 [Drosophila willistoni].>tr:B4MQR3_DROWI [B4MQR3] SubName: Full=GK21386
{ECO:0000313|EMBL:EDW74452.1}; 68..82
MLTTMSISNTSNINEKEIDDEDMLSPSPTKLSNNHVVRVNQDIIDDNLQELFDTVLNPQDAKRPLQLPF
RMRKLPNSFFNPPAPSHSRANSADSTFDGGSQTNININKTAQPQPVEAIQQSGISALSAAISQNQNPIQPSQSRL
AVYHARARSSPASLQQNYNVRSRSDANANANASTQGPAYPDNNVDFGNSAANNIELDGNVMTGIGIGQGQVQEMP
ISTQTVHKKQRSYDVVSPIQLQSQLGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQLRQQQHRAMAERIKQ
NDVLQTPKQTATTIGPLPDGWEQAVTESGDIYFINHIDRTTSWNDPRMQSGLSVLDCPDNLVSSLQIDDNMCSNL
FTDAQITPSSNKPDDLEWYKIN PFRMRKLPNSFFNPP

rs:XP_015034195 [XP_015034195] transcriptional coactivator yorkie isoform
X2 [Drosophila willistoni]. 68..82
MLTTMSISNTSNINEKEIDDEDMLSPSPTKLSNNHVVRVNQDIIDDNLQELFDTVLNPQDAKRPLQLPF
RMRKLPNSFFNPPAPSHSRANSADSTFDGGSQTNININKTAQPQPVEAIQQSGISALSAAISQNQNPIQPSQSRL
AVYHARARSSPASLQQNYNVRSRSDANANANASTQGPAYPDNNVDFGNSAANNIELDGNVMTGIGIGQGQVQEMP
ISTQTVHKKQRSYDVVSPIQLQSQLGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQLRQQQHRAMAERIKQ
NESGLSVLDCPDNLVSSLQIDDNMCSNLFTDAQITPSSNKPDDLEWYKIN PFRMRKLPNSFFNPP

rs:XP_015782860 [XP_015782860] transcription factor SPT20 homolog
[Tetranychus urticae].>tr:T1JSN4_TETUR [T1JSN4] SubName:
Full=Uncharacterized protein {ECO:0000313|EnsemblMetazoa:tetur01g11150.1};
41..55
MAGNHKSNHIVRLNEDANHNLDELFRAAIGPKDGRVPLSKPMRQRDLPASFFTPPEKGSKSASHSRESS
LDATSLDSTPTLCNPTPRPGITINHFRAHSSPATLQATFAVAPQPRGYDFDKLPEGWQMAFEAKTGKPYYINHIS
RTTTWEDPRLTAFRLRNEALQLEMQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQTQQQQQPQPQPQQQ
QPPPPLPQPQPSSQQQTQLQPQPQPQPQPQQPQQQPQQPQPQPQPQPQPQPQQIPQQLPQTLPQLQVQLQQQQSQ
PQPQQQQQSQPQTQPLPLPIPQLQAQLQQQIQQELALRRVKELTDEREKLRQRAAEIQNQQKNFTTNIDPFLSGS

DAIILDHSRQESADSGLGLSHNLDLPYTPNDLQNADDLGLDSLSITNMDLETDAMDLMCLPEELNTDIVLSDLEA
FLTNANITTSKDVWI   PMRQRDLPASFFTPP

rs:XP_023197954   [XP_023197954] transcriptional coactivator YAP1-like isoform X1 [Xiphophorus maculatus].>rs:XP_027887757 [XP_027887757] transcriptional coactivator YAP1-like isoform X1 [Xiphophorus couchianus].>rs:XP_027887758 [XP_027887758] transcriptional coactivator YAP1-like isoform X1 [Xiphophorus couchianus]. 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKATRQPPSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTSTGQRYFINHVHRTTTW
QDPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIVPETGPLPEGWEQAVTTDGEMYYIDHINQATTWDDP
RLAPKVNPAILSLAMQQRLEKLRLKQGIPPQFAPQLNETKHTRIQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIR
IRALNQEPNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGDSSEPPSMGLQESMPVLPINEDLMPGIPD
SLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_014326808   [XP_014326808] transcriptional coactivator YAP1-like isoform X2 [Xiphophorus maculatus].>rs:XP_027887759 [XP_027887759] transcriptional coactivator YAP1-like isoform X2 [Xiphophorus couchianus].>tr:M4A8R8_XIPMA [M4A8R8] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSXMAP00000010862};46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKATRQPPSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTSTGQRYFINHVHRTTTW
QDPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIVPETGPLPEGWEQAVTTDGEMYYIDHINQATTWDDP
RLAPKVNPAILSLAMQQRLEKLRLKQGIPPQFAPQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNL
NGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGDSSEPPSMGLQESMPVLPINEDLMPGIPDSLTSDMLMEM
DTVLSGPHMDRDSLLTWL   PMRMRKFPDSFFKPP

rs:XP_023197955   [XP_023197955] transcriptional coactivator YAP1-like isoform X3 [Xiphophorus maculatus].>rs:XP_027887760 [XP_027887760] transcriptional coactivator YAP1-like isoform X3 [Xiphophorus couchianus].
46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKATRQPPSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTSTGQRYFINHVHRTTTW
QDPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIVPETGPLPEGWEQAVTTDGEMYYIDHINQATTWDDP
RLAPKVNPAILSLAMQQRLEKLRLKQGIPPQFAPQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNLNG
AHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGDSSEPPSMGLQESMPVLPINEDLMPGIPDSLTSDMLMEMDT
VLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_023197956   [XP_023197956] transcriptional coactivator YAP1-like isoform X4 [Xiphophorus maculatus].>rs:XP_027887761 [XP_027887761] transcriptional coactivator YAP1-like isoform X4 [Xiphophorus couchianus].
46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKATRQPPSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTSTGQRYFINHVHRTTTW
QDPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIVPETAPKVNPAILSLAMQQRLEKLRLKQGIPPQFAP
QLNETKHTRIQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNLNGAHSRNESTDSGLSVSSLSRTSD
HMLSSVDHMDTGDSSEPPSMGLQESMPVLPINEDLMPGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL
PMRMRKFPDSFFKPP

rs:XP_005796947   [XP_005796947] protein **FAM181**B [Xiphophorus maculatus].
246..260
MQVVGHKQRVKFPGFPSLLLFDVLTSSVLPPERSPSSSSVAVTSSLDCLWKLHEQHQEQVFIRRTKSCF
EETFSSGITVDATGVAAGLDRVMAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQGSPVSQQGPVQSKTLQKREGGQ
ANLQSKSLAALFSPVKEIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPD
YSNMVNEQDIYQGVPLRGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGQCKKPSEGLRSGPPQPPVYSQAEDTSV
PLDDNGLCTLTFPNFFPDCSISQVTYDLNGGYNKTHFSCL PMRHRNLPPSFFTEP

rs:XP_023207215 [XP_023207215] transcriptional coactivator YAP1 isoform
X1 [Xiphophorus maculatus].>tr:A0A3B5QAT5_XIPMA [A0A3B5QAT5] SubName:
Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSXMAP00000027369};
45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQASYEIPDDVPLPAGWEMAKTNSGQRYF
LKLQNSEKEQDISSHNEKTTTWQDPRKSLLQMNQPAPVPPSSVPVQPQNLMNPASGSLPEGWEQAVTQEGEIYYI
NHTNKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQQHRPQELALR
NQLPTSMDQDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDT
GDPLPASIASQPSRFPDYLDAIPGTDVDLGTLEGENMAVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFL
TWL PMRMRKLPDSFFKPP

rs:XP_005796894 [XP_005796894] transcriptional coactivator YAP1 isoform
X2 [Xiphophorus maculatus].>tr:M3ZZC2_XIPMA [M3ZZC2] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSXMAP00000007566}; 45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQASYEIPDDVPLPAGWEMAKTNSGQRYF
LNHNEKTTTWQDPRKSLLQMNQPAPVPPSSVPVQPQNLMNPASGSLPEGWEQAVTQEGEIYYINHTNKTTSWLDP
RLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQQHRPQELALRNQLPTSMDQDGS
TNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPASIASQP
SRFPDYLDAIPGTDVDLGTLEGENMAVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_005801202 [XP_005801202] protein **FAM181**A [Xiphophorus maculatus].
102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQSLTSADNRC
ARGAERQRATATDQASSDAQHAQSVGGLMDQVPMRKRQLPASFWEEPRLTKARRDKPFLDLRRSSSSGTSDGGEN
EKRRRSQEDAQKTANSSSGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQFHGHQVLHSQIVVPHPPFGLWSKAAEP
QRSEHPYGQKLHTHVVVKPIPTKATAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_023227613 [XP_023227613] uncharacterized protein LOC111628119
[Centruroides sculpturatus]. 135..149
MSGKRKPFVPSSPKSVDSEVEEDFSSGSSSARGKDGSKLVDYDDVGSPSGSSTASGPVYVRTPGFENHG
HSVRVKPPQSRRGSYESQKDGKEAIQTQGQSSCKKKKNSIISIHDMSCLQEKGQTHKSKQRKEPLPMKLRALPQS
FWQQPNNASNVSPAIVVPMLPPLFKHDTADDVTKVRPVTPPEEREKGSATSTRSEGSRIIRVSNTDLLHKLFDGI
NEKDKQMAPVVRRGRPKKIPSTLNQRTLRGEDPCLVSTATEGILPLLNLDREGNKNSTQTLTLVSIRDGDKSVTL
PALNVEQNYSQMLSELVVRL PMKLRALPQSFWQQP

rs:XP_023241799 [XP_023241799] transcription cofactor vestigial-like
protein 2 isoform X1 [Centruroides sculpturatus]. 104..118
MTCIDIMYQPYAQYFPYQRPTIQPSLADTKKYGDPMTTDYSESNQSKDRKYCGDTHFLSANCMVVTYYK
GDISSVVDEHFTRALSQTGSYAPDPGKGYCKDGPPMSQRNFPPSFWNQPATQALGSAGHPPDLSYTDPYHAGTLH
TSLHQGDPWHYTLSAPPTSAYRPELTYPSANRFSPQYGSFLLQPSVRTTRLNPVAGSCTALDKSTDTWGAARYTD
TLTHNLGHMETNYGAAYSPMGTMSDATSGNYMFELYKMHAPRSCR PMSQRNFPPSFWNQP

rs:XP_023241800 [XP_023241800] transcription cofactor vestigial-like
protein 2 isoform X2 [Centruroides sculpturatus]. 104..118
MPTPDWHFSLGAGVTLYLCNARSNSWRKVDKYGDPMTTDYSESNQSKDRKYCGDTHFLSANCMVVTYYK
GDISSVVDEHFTRALSQTGSYAPDPGKGYCKDGPPMSQRNFPPSFWNQPATQALGSAGHPPDLSYTDPYHAGTLH
TSLHQGDPWHYTLSAPPTSAYRPELTYPSANRFSPQYGSFLLQPSVRTTRLNPVAGSCTALDKSTDTWGAARYTD
TLTHNLGHMETNYGAAYSPMGTMSDATSGNYMFELYKMHAPRSCR PMSQRNFPPSFWNQP

rs:XP_023241801 [XP_023241801] transcription cofactor vestigial-like
protein 2 isoform X3 [Centruroides sculpturatus]. 104..118
MTCIDIMYQPYAQYFPYQRPTIQPSLADTKKYGDPMTTDYSESNQSKDRKYCGDTHFLSANCMVVTYYK
GDISSVVDEHFTRALSQTGSYAPDPGKGYCKDGPPMSQRNFPPSFWNQPATQALGSAGHPPDLSYTDPYHAGTLH
TSLHQGDPWHYTLSAPPTSAYRPELTYPSANRFSPQYGSFLLQPSVRTTRLNPVAGSCTALDKSTDTWGAARYTD
TLTHNLGHMETNYGAAYSPMGTMSGLESQVADASKDLYWF PMSQRNFPPSFWNQP

rs:XP_023241802   [XP_023241802] transcription cofactor vestigial-like protein 2 isoform X4 [Centruroides sculpturatus].>rs:XP_023241803 [XP_023241803] transcription cofactor vestigial-like protein 2 isoform X4 [Centruroides sculpturatus]. 69..83
MTTDYSESNQSKDRKYCGDTHFLSANCMVVTYYKGDISSVVDEHFTRALSQTGSYAPDPGKGYCKDGPP
MSQRNFPPSFWNQPATQALGSAGHPPDLSYTDPYHAGTLHTSLHQGDPWHYTLSAPPTSAYRPELTYPSANRFSP
QYGSFLLQPSVRTTRLNPVAGSCTALDKSTDTWGAARYTDTLTHNLGHMETNYGAAYSPMGTMSDATSGNYMFEL
YKMHAPRSCR PMSQRNFPPSFWNQP

rs:XP_023210095   [XP_023210095] transcriptional coactivator YAP1-like [Centruroides sculpturatus]. 46..60
MSQQRDVIEQKGNQIVRINSDSKTDLDDLFKAVMQPKDSQVPQSVPMRMRNLPPSFFKQPDRGSKSASH
SRESSTDATYSGPPPPTQQQQRGLTINHPRANSSPATLQQTYTANRQTTSPTQHLRQQSFEISDDVPLPSGWEMA
KTPSGQRYFLNHITQTTTWEDPRKNLNAATLHPSVSHTSVVSPTASTLSSHSPTSAGPPITLHNLGPLPEGWDQA
TTPEGEVYFINHIDRTTSWLDPRIPAHLQRPVLLSRSGHSQLPSHPSVQGQTQVQPSSTPSITSQLTVQSNIAGG
GISPTITTTSGTTNNQTNLQFQQKMRLHKLQVERERLRVRQQEILRQEMILRRNIGEEMIIPTSPPGSNTELPPA
NTTTTGMDPFLGGNDFHARQESGDSGLGLGPNYSLPHTPEDFLMEDNEDTGNNDTVQQNNDLGFDSLQSSNLDLG
TENMDSDDLVPSLQEELNADILSDVEALLDSPNKDSVLTWL PMRMRNLPPSFFKQP

rs:XP_023212895   [XP_023212895] uncharacterized protein LOC111615695 [Centruroides sculpturatus]. 27..41
MEKENKSEKISSSVEDSKEDEAVASVPLRQRRFPASFWQEPSRLPEKWLYVSQVPNQNPGSSAFVSQTN
VSVMSRPSSSGMVNCPCSACKTPFYYPLRWTVPYYCQTIVSHPYSFYPNVSPQCCHPCKICDSPRFESRKSFRYY
PV   PLRQRRFPASFWQEP

rs:XP_003756204   [XP_003756204] protein **FAM181**A [Sarcophilus harrisii].>tr:G3VUJ0_SARHA [G3VUJ0] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSSHAP00000006845};
118..132
MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCYPNRSGESHPK
RGPEDGRCRTPSNGSTEKGPGNPEMEENFPEEQALQEQIPEASRPDQVPMRKRQLPASFWEEPRPAQSYSGGLDG
LPVHREVPAYEGKKSKKRLETLGSETAPVPASPRAEKESPKVPSASLMGRMSAWSCCPFQYHGQPIYQSPGGLPQ
SPVPSLGLWRKSPSSPGEIGHFCKEPGSPSQKVYRPVVLKPIPTKPGVPPPIFNVFSYI
PMRKRQLPASFWEEP

rs:XP_003764324   [XP_003764324] LOW QUALITY PROTEIN: transcriptional coactivator YAP1 [Sarcophilus harrisii]. 88..102
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGQPAPPGAPGSQAAPPPPAGHQIVHVRGDSETDLE
ALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LSPSGVVSAPGAAPSGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GSVMGGGSSNQQQQMRLQQLQVEKERLRLKHQELLRQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPVS
SPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_023353609   [XP_023353609] uncharacterized protein LOC100922283 [Sarcophilus harrisii]. 214..228
MAAGVIRNLCDFRLQAAFHQPFLPTSGHRDPDFPETSEEEEEDGEEEEEGEKLGDNLELAGSNPGCQRS
DQNLITGPTRSSPSSAEMTLQLLRFSELISCDIQKYFGQKTKDDDPDACNIYEDCRPPGKSARELYYADLMQIVQ
SGDQEDEDTDVVGLPKGLDCPARFISSRDRSQKLGPLVELFEYGLCQYARQRVSDSRRLRLEKKYGHITPMHKRK
LPQSFWKEPAPSSLCLLNTSTPDFSDLLANWTSDVAQELHGVGGRELDRQALEMDQLEEV
PMHKRKLPQSFWKEP

rs:XP_005008579   [XP_005008579] LOW QUALITY PROTEIN: protein **FAM181**A [Cavia porcellus].   133..147
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGXPGRAAEPHLR
RGPEDHPEQLPLHPSIPCGPDSSPGGIGGCKEKALGSPFGEEYLSKEQTLQGQGPGAANLGQVPMRKRQLPASFW
EEPRPTHSYPMGLEGGPDPREGLLYECKKNCKGLESVVPEAAPGPLSPRALADKEPLKMPGVSLVGRVDAWNYCP

FQYHGQPIYPGPPGALPASPIPGLGLWSKSPALPTELAHFCKHVDGPGQKVYRPVVLKPIPTKPAVPPPLFNVFG
YL PMRKRQLPASFWEEP

rs:XP_011367726 [XP_011367726] transcriptional coactivator YAP1 isoform X1 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_011367727 [XP_011367727] transcriptional coactivator YAP1 isoform X2 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_011367728 [XP_011367728] transcriptional coactivator YAP1 isoform X3 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_011367730 [XP_011367730] transcriptional coactivator YAP1 isoform X4 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_011367731 [XP_011367731] transcriptional coactivator YAP1 isoform X5 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011367732 [XP_011367732] transcriptional coactivator YAP1 isoform X6 [Pteropus vampyrus]. 85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011367733 [XP_011367733] transcriptional coactivator YAP1 isoform
X7 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011367734 [XP_011367734] transcriptional coactivator YAP1 isoform
X8 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011367735 [XP_011367735] transcriptional coactivator YAP1 isoform
X9 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011367736 [XP_011367736] transcriptional coactivator YAP1 isoform
X10 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY
SVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011367737 [XP_011367737] transcriptional coactivator YAP1 isoform
X11 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_011367738 [XP_011367738] transcriptional coactivator YAP1 isoform
X12 [Pteropus vampyrus]. 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQGPPSGPGQPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTP
TGVVSGPAPTPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL PMRLRKLPDSFFKPP

rs:XP_011371422 [XP_011371422] protein **FAM181**B [Pteropus vampyrus].
221..235
MAVQAALLSTHPFVPFGFGGTPEGLGGAFGALDKGCCFEDDETGTPAAALLAGTEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSSLMGAAPPGPPSPGAVDTPAKRVLAAPSAQTVAVPAHGK
ATPRREASQAAAAASLQSRSLAALFDSLHHVPGGAEPAGGSVAAPAAGLGGAGAGGAGGDAAGPAGGTALPGCRK
VPLRARNLPPSFFTEPSRAGGGSGCGPSGPGVSLGDLEKGADTVEFFELLGPDYCAGTETGVLLAAEPLDVFPTG
AAVLRGPQELEPSLFEPPPAMVGSLLYPEPWSAPGCPPTKKLNLAVPRGASTLNEPLRSLYPAAADSPGGEDGTG
LLASFAPFFSDCALSPPPHQVSYDYSAGYGRTAFSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_023575457 [XP_023575457] protein **FAM181**A [Octodon
degus].>rs:XP_004635202 [XP_004635202] protein **FAM181**A [Octodon degus].
179..193
MERLPMARLDSREFPDPGSAVHPPRSCPPPQRPPSSWKAPCRGPLVMASDSDVKMLLNFVNLASSDIKA
ALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLRRGPEDLPGRLPLHPSVPCGPDSSLGGGGG
CKEKALGSSFGEECLSNEQSLQGQGLGAAKPGQVPMRKRQLPASFWEEPRPTHSYPMGLEGGPGPREGPPYENKK
NCQGLESMVPEAAPGPMSPRALADKEPLKMPGVSLVGRVDAWSCCPFQYHGQPIYPGPPGALPASPIPGLGLWRK
SPALPAELAHFCKHVDGPGQKVHRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_004376749 [XP_004376749] protein **FAM181**A [Trichechus manatus
latirostris].>tr:A0A2Y9DLE0_TRIMA [A0A2Y9DLE0] SubName: Full=protein
FAM181A {ECO:0000313|RefSeq:XP_004376749.1}; 130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGHPGRAAEPHLK
RGPEDRPSRLSFDGQDPSPGGGGGCKEKALGNLGREEFLSGEQEQTLQGQNPEAAQPGQVPMRKRQLPASFWEEP
RPAHSFPMGLEGGLGPREGPPYEGKKTCQGLEPLGPEMAPVPLSPRALVEKEPLKMPGVSLMGRVNAWSCCPFQY
HGQPIYPGPPGALLQGSMPSLGLWRTSPASPGELAPFCKDVDSLGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_023595577 [XP_023595577] protein **FAM181**B [Trichechus manatus
latirostris].>tr:A0A2Y9RM86_TRIMA [A0A2Y9RM86] SubName: Full=protein
FAM181B {ECO:0000313|RefSeq:XP_023595577.1}; 213..227
MAVQAALLSPHPFVPFGFAGAPDGLGGAFGALDKGCCFEDDETGAPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXASLQSRSLAALFDSLRHVPAGDEPARGAVTAPAVGSCGTGAGGTGGDAAGPTGGAVAPGARKIPLRARNL
PPSFFTEPSRAGSGGSGPSGPGLSLGDLEKGAEAVEFFELLGPDYGAGTEAGVLLAAEPLDVFPAGAAALRGSLE
LEPGLFEPPPAMVGSLLYPEPWSAPGPQIKKTPLAAARGGLTLNEPLRPLYAAAADSPGGEDGPGHLTSFAPFFP
DCALPPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEEVPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_012413684 [XP_012413684] transcriptional coactivator YAP1 isoform
X1 [Trichechus manatus latirostris].>tr:A0A2Y9G046_TRIMA [A0A2Y9G046]
SubName: Full=transcriptional coactivator YAP1 isoform X1
{ECO:0000313|RefSeq:XP_012413684.1}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPPGGV
MGGSNSNQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_004385920 [XP_004385920] transcriptional coactivator YAP1 isoform
X2 [Trichechus manatus latirostris].>tr:A0A2Y9E3U4_TRIMA [A0A2Y9E3U4]
SubName: Full=transcriptional coactivator YAP1 isoform X2
{ECO:0000313|RefSeq:XP_004385920.1}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPPGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_012413685 [XP_012413685] transcriptional coactivator YAP1 isoform
X3 [Trichechus manatus latirostris].>tr:A0A2Y9G3L9_TRIMA [A0A2Y9G3L9]
SubName: Full=transcriptional coactivator YAP1 isoform X3
{ECO:0000313|RefSeq:XP_012413685.1}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPPGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_004385921 [XP_004385921] transcriptional coactivator YAP1 isoform
X4 [Trichechus manatus latirostris].>tr:A0A2Y9E2Q4_TRIMA [A0A2Y9E2Q4]
SubName: Full=transcriptional coactivator YAP1 isoform X4
{ECO:0000313|RefSeq:XP_004385921.1}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAINQRISQSAPVKQPPPLAPQSPPGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012413686 [XP_012413686] transcriptional coactivator YAP1 isoform
X5 [Trichechus manatus latirostris].>tr:A0A2Y9G2A5_TRIMA [A0A2Y9G2A5]
SubName: Full=transcriptional coactivator YAP1 isoform X5
{ECO:0000313|RefSeq:XP_012413686.1}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPPGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012413687 [XP_012413687] transcriptional coactivator YAP1 isoform
X6 [Trichechus manatus latirostris].>tr:A0A2Y9FZY2_TRIMA [A0A2Y9FZY2]
SubName: Full=transcriptional coactivator YAP1 isoform X6
{ECO:0000313|RefSeq:XP_012413687.1}; 85..99
MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPPGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRN
INPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSY

SVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDI
LNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_012413688   [XP_012413688] transcriptional coactivator YAP1 isoform X7 [Trichechus manatus latirostris].>tr:A0A2Y9G017_TRIMA [A0A2Y9G017] SubName: Full=transcriptional coactivator YAP1 isoform X7 {ECO:0000313|RefSeq:XP_012413688.1};   85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPPGGVMGGSNSNQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
ELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_004385922   [XP_004385922] transcriptional coactivator YAP1 isoform X8 [Trichechus manatus latirostris].>tr:A0A2Y9E4A1_TRIMA [A0A2Y9E4A1] SubName: Full=transcriptional coactivator YAP1 isoform X8 {ECO:0000313|RefSeq:XP_004385922.1};   85..99

MDPGQQPPPQPAPQGQGQPPAQPPQGQDPPSGPGQPAPRGSQGAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPPTVPMRLRKLPDSFFKPPEPKSHNRQVSTDAGTAGALAPQHVRAHSSPASLQLGAVSPGTLSP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMINSASAINQRISQSAPVKQPPPLAPQSPPGGVMGGSNSNQQQMRLQQLQMEKERLRLKQQELLRQELAL
RSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEM
DTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKE
SFLTWL   PMRLRKLPDSFFKPP

rs:XP_023817148   [XP_023817148] transcriptional coactivator YAP1 isoform X1 [Oryzias latipes].>tr:A0A3P9L2P7_ORYLA [A0A3P9L2P7] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSORLP00020014857};>tr:A0A0M3HEQ8_ORYLA [A0A0M3HEQ8] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|Ensembl:ENSORLP00000003377}; 45..59

MDPSQHNPPVGHQIVHVRGDSETDLEALFNAVMNPKGAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHIDQTTTWQDPRKALLQLNQATPPSTVPVQQQNLLSPASGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
ETRYALNQQRITQSAPVKQGGPLPPNPHGGVMGGNNQMRLQQMEKERIRLKQQELLRQSQRPQELALRNQLPTSM
DQDGSSNPVSSPMAQDARTMTANSNDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPS
MATQPSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_023817149   [XP_023817149] transcriptional coactivator YAP1 isoform X2 [Oryzias latipes].   45..59

MDPSQHNPPVGHQIVHVRGDSETDLEALFNAVMNPKGAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHIDQTTTWQDPRKALLQLNQATPPSTVPVQQQNLLSPASALNQQRITQSAPVKQGGPLPPNPHGGVMGGNNQM
RLQQMEKERIRLKQQELLRQSQRPQELALRNQLPTSMDQDGSSNPVSSPMAQDARTMTANSNDPFLNSGTYHSRD
ESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMATQPSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELM
PSLQEALSSDILNDMESVLAATKIDKESFLTWL   PMRMRKLPDSFFKPP

rs:XP_023817726   [XP_023817726] protein **FAM181**B [Oryzias latipes].
155..169

MAVQTAIMNPQFMSFCFPGSVMEFDVEKSLDGSLLCEAEQDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNGAETPVKRQSSPVSQQSSLQNKVLPKRDGVQANLQSKSLAALFSPVK
ELRGERAKKPPLRHRNLPPSFFTEPANCSKVSPTSEVTLKDLERGSPDFFELLGPDYSSMVSDQDLYPSVPLRMQ
SELGGLDPASYDAHVVAHHLYTADPWTSCSGPSKKLGENPRAGPVQPPAYFQSEEASGGMDDNALCTLAFPNFFP
DCSLPQVTYDLNSGYNRSSYSSL PLRHRNLPPSFFTEP

rs:XP_023818352 [XP_023818352] transcriptional coactivator YAP1 isoform X1 [Oryzias latipes].>tr:A0A3P9M061_ORYLA [A0A3P9M061] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSORLP00020026432};>tr:H2LLU5_ORYLA [H2LLU5] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSORLP00000007010};
42..56
MDAHRSGRQVVHVRGDSQKELEALFSRVMNPSEASRQPSSVPMRMRKLPDSFFKPPEPRGHSRQASSDG
GVCGSLTPHHSRTVSAPAALPVNSLSTQAADVAATSIIPDDVPLPPGWEMAKTPAGQRYFLNHLDKTTTWLDPRL
SQLQSAQHPIANAPVHSHSFSNPAPTTQAQSVNPESGPLPEGWEQAVTPEGEMYYIDHINKTTTWVDPRLAQKMS
PGVLSLAMQRQEKLRCKQGAPPQVTQQEGAGRNQMSAGLDHDRSGQVLVPSVDARIRAPNHETAMNGAHSRNEST
DSGLSVSSLPRTNDHMLSPVDHMDTGDPSEPPSMALQEPMLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMD
RDNLLTWL PMRMRKLPDSFFKPP

rs:XP_023818353 [XP_023818353] transcriptional coactivator YAP1 isoform X2 [Oryzias latipes]. 42..56
MDAHRSGRQVVHVRGDSQKELEALFSRVMNPSEASRQPSSVPMRMRKLPDSFFKPPEPRGHSRQASSDG
GVCGSLTPHHSRTVSAPAALPVNSLSTQAADVAATSIIPDDVPLPPGWEMAKTPAGQRYFLNHLDKTTTWLDPRL
SQLQSAQHPIANAPVHSHSFSNPAPTTQAQSVNPESAQKMSPGVLSLAMQRQEKLRCKQGAPPQVTQQEGAGRNQ
MSAGLDHDRSGQVLVPSVDARIRAPNHETAMNGAHSRNESTDSGLSVSSLPRTNDHMLSPVDHMDTGDPSEPPSM
ALQEPMLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDNLLTWL PMRMRKLPDSFFKPP

rs:XP_004085278 [XP_004085278] protein **FAM181**A [Oryzias latipes].
103..117
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRAPRCHTHRSVDYKC
AKPVGTVHQSATVSEKASSDVQDESAGSTVEQVPMRKRQLPASFWEEPKLTNAENALMRLKGSPAGMCEGSAKEK
QKTVHVDPKVPAPGRRSCTDKETLKMDLISPVSLSVCSCCPFQYHGQHVVHSHIVVPHPPLGLWSKAANDLGRPD
HLYEQKIHTHVVVKPIPTKPAAQTPIFSVFGLI PMRKRQLPASFWEEP

rs:XP_024261059 [XP_024261059] transcriptional coactivator YAP1-like, partial [Oncorhynchus tshawytscha]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQTS
TDAGTAGAIAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSHLRQSSYEIPEDMPLPPGWEMAKTPSGQRYFLN
HLDQSTTWLDPRKALLQMNQAPPTSPVPVQQQNIMSPASGPLPDCWEQAVTSEGEVYYINHITKTTSWLDPHLVQ
SAVAQVKPSTLTSDPVGIATVVTKRRQQLQVEKDRLRRKQQDLARPIRVQDVAVRSGLEHDGKMRNNHVDPALNG
AHSRNQSTDSGLSVSSFTRTPDDLLNTVE PMRMRKLPDSFFKPP

rs:XP_024263547 [XP_024263547] protein **FAM181**B [Oncorhynchus tshawytscha]. 176..190
MAVQTAIMNSPFVNFCFPGSVMMEYDMGQSLDGSPLEESEERGEYRETTRNLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGFISPTGNPAAAPGANKRKGSGFPTQTQTQIQPQTQLQTQPSPFQQGKPVHKR
DGLQANLQTKSLAALFNSVKEPVKGERAKKPPLRHRNLPPSFFTEPANTTTTSRVTSTSGMFLGDLERGGGNPDF
FDLLGPDYSNMLSDQDVFQTRGLPSRIIDQDMFQTRGLPSRILQHQQTQDITDQVSPYDPHHLVGGFLYTEPWST
SSPSKKAGEGVRTGPATQTPLYCQSGEGVRTGPGTQTPLYCQSGEGVRTGPGTQTPLYCHSVSDSSATGSTEDSN
SLCTLAFPNFFPDCSVSQVSYGLSCGGYNTKGFSSL PLRHRNLPPSFFTEP

rs:XP_024265549 [XP_024265549] transcriptional coactivator YAP1 [Oncorhynchus tshawytscha]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQTS
TDAGTAGAIAPHHVRAHSSPASLQLGAVSPLLGMVPAGAPPSHLRQSSYEIPEDMPLPPGWEMAKTPSGQRYFLN
HLDQSTTWLDPRKALLQMNQAPPTSPVPVQQQNIMSPASGPLPDGWEQAGTSEGEIYYINHKNKTTSWLDPRLEP
CYSLNQQRITQSAPGKQGSQLPSSPQSGGVMGGSNQIKLQQLQMEKERLRLKHQELLRTRPQELALRNQLPTSME
QDGGTLNPVSSPGMGQDARIMTTNSNDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDSVPRTPDDFL
NGVDEMDTGDSLPVSMGTQPSRFPDYLDVIPGTDVDLGMLENKSMAMEGEELMPSLQEALSSDILNDMESVLAAT
KMDKENFLTWL PMRMRKLPDSFFKPP

rs:XP_002108065 [XP_002108065] predicted protein [Trichoplax adhaerens].>tr:B3RLX5_TRIAD [B3RLX5] SubName: Full=Predicted protein {ECO:0000313|EMBL:EDV28863.1}; 35..49
MDQKPQPVVHERHDSKEELERLFNVLNSQNNPTVPMRDRRLPYSFFQGPTRPYDSNNTTATLSTDNNFG

VGDSIVHPRIKSSPASFPYHNNNSDMTNSNNSAFQHRNQPLHPKHHSSSAAFRNENAHSNKSFPADVNYKNLINP
NVAMRQLPMARFDDKCSIINCQTFSLKLLNYGIVCTWRPVQQNGLHIRGGSGSGLHPNNGPMQAKLPDGWEKAFT
PEGQVYFVNHITRTTSWNDPRRSMMQAQSPNPVIQSPLKTTYDLPNDKAMQELQMMQLERKHLEQKREEMLRKES
EIKRQIETYQRQQIPVGRTEQLLHRPGLATTAAPNGIPNHNPGLIKREPSSPSPMQIDYPTPQHNSLPTDIQANL
SQGQMLNYRGGNISINNQLANGGFNNQIMSENNEPDIEELIQSLSTSAQDLDIEATLIDRDAIAKIESDLVNTEP
DWY PMRDRRLPYSFFQGP

rs:XP_017268811 [XP_017268811] protein **FAM181**A [Kryptolebias marmoratus].
109..123
MKQAKDLTNMASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCH
AHRTADYRCLKPTGAAHQSAEKAGSDAQDVENAGSVEQVPMRKRQLPASFWEEPRLSKTKRDKSCLKRSPAGTSD
GGEKRKTIADDDAKASPSNRRSSADKEVLKLDVTSHHSVSVCGCCPLQYHGHHVLHSHIVVPHPPLGLWSKAAGT
EEHPYGQRLHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_025079917 [XP_025079917] uncharacterized protein LOC112555666
[Pomacea canaliculata]. 231..245
MVLVSNVVCFEAPVIDLQILDNGIYISLPVSATASSTPRTTGGKRGPSGPLIVSSSSEDEESDTNECLH
PALQQQSNVRTDLLPRNGHILPPACLRSTVGIDRLTSQLPSPRKDSNTACGTEISTSETEVETVLSSNPTAEAHT
PSLNFAHEHDHDYDNVTSPSSSTSSGPIYVRPPGFKTHAQQVECIRSKLARKKSRPPAVITVKDELKHREETPLR
RKHEEVKYRSTPMKLRALPQSFWQQPNLAQQVSPATMYPLLPPLCNKDTEEDIAEVRPVTPPNESGAETKRLAPE
RKISVANTDLLFKLFENISDEKKTATVHLKRGRPRRMPIKSCTKGLLFGNDPYLVDAIADTLFPQLSIESSRFGG
NTSLQLVTLGTGDKTVTLPSLTLEQNYPQMLSELVTHI PMKLRALPQSFWQQP

rs:XP_025088359 [XP_025088359] LOW QUALITY PROTEIN: mastermind-like
domain-containing protein 1 [Pomacea canaliculata]. 156..170
MIAQPSVVLPGLALDRSQHRSQQASAPHQQQQNDDTINLLQFIDMASSNIKLALDRPXKSKRKVNHRK
YLQKQLKRCGSQSGKRSGDSPRGEGSSGGGGGEPAAGCSNLRCARKMTSQVGLQIKSLQALFDPKTESXQXLLHT
PVGKSTLSPKAPLRCRNLPPSFFVEPGLRASDVPDRIGVMLSSDTGDVVGGSVREVRDPTQLQKTPHHTSPYLDT
GRCSVPFSALPTDTLESILGQADLSELLSGRWQQGRDSNHTPCDGSVGTSSPRSFSDSSDAYCTSSPRPSSTQSR
SPSWSPCLPAGSLGSSFGTYMTPSLEEGVTGRHLDPGGGYFLQQQQHHQQHHSMQPHHHQQPERLSHVAQLQPER
HPADQPLLHQPQQTLQTLPSQPVQHQQRHQQKQQQQEHYKLSSQDANIPADLIFRGDFVTPTTAYFHELPQQPHQ
HLQQQHQGFAETHELLTFPQIFPSGESGQGYNNGDFGSWQSLQPDSFFPYMS PLRCRNLPPSFFVEP

rs:XP_025079638 [XP_025079638] transcriptional coactivator YAP1-A-like
isoform X1 [Pomacea canaliculata]. 37..51
MSQERTSSHVVHVRENSASDLEALFDPHAAEAKKSIPLRDRNLPASFFQQPGLNQMGHGKNGPEVPGYN
EVGPISHIRAHSSPASLQQTLSAAPQPPPPSQHLRQHSCDMLDEPLPPGWGMARTPQGQRYFLNHVLQTTTWQDP
RKSHPSSNMGSTQQPGSPVSGTQSPPNTMDITKMPLPLGWERAYTPEGEIYFINHIERTTSWFHPSIPAAQQRPG
MRLHPQQQQQQAALAPSPQQPQQASPLMRSPISGASSPPVPPGQHGPLTAEQQRQLKLKQLQMEKELLKKRQEEL
ARQEMMIQLGAGGETTDTTADLTTVTDPFLGQTGSTDHHSRQESADSGLGGMGTGYNLPRTPEDFLSNMEEMDIP
DGGHKSQAQGDFINMDIGSVGDVSDSHNMDSDDLVPSLQEVIGTDLLRDVENVLSCNKADHLLTWL
PLRDRNLPASFFQQP

rs:XP_025079639 [XP_025079639] transcriptional coactivator YAP1-A-like
isoform X2 [Pomacea canaliculata]. 37..51
MSQERTSSHVVHVRENSASDLEALFDPHAAEAKKSIPLRDRNLPASFFQQPGLNQMGHGKNGPEVPGYN
EVGPISHIRAHSSPASLQQTLSAAPQPPPPSQHLRQHSCDMLDEPLPPGWGMARTPQGQRYFLNHVLQTTTWQDP
RKSHPSSNMGSTQQPGSPVSGTQSPPNTMDITKMPLPLGWERAYTPEGEIYFINHIERTTSWFHPSIPAQQRPGM
RLHPQQQQQQAALAPSPQQPQQASPLMRSPISGASSPPVPPGQHGPLTAEQQRQLKLKQLQMEKELLKKRQEELA
RQEMMIQLGAGGETTDTTADLTTVTDPFLGQTGSTDHHSRQESADSGLGGMGTGYNLPRTPEDFLSNMEEMDIPD
GGHKSQAQGDFINMDIGSVGDVSDSHNMDSDDLVPSLQEVIGTDLLRDVENVLSCNKADHLLTWL
PLRDRNLPASFFQQP

rs:XP_025079640 [XP_025079640] transcriptional coactivator YAP1-A-like
isoform X3 [Pomacea canaliculata]. 37..51
MSQERTSSHVVHVRENSASDLEALFDPHAAEAKKSIPLRDRNLPASFFQQPGLNQMGHGKNGPEVPGYN
EVGPISHIRAHSSPASLQQTLSAAPQPPPPSQHLRQHSCDMLDEPLPPGWGMARTPQGQSHVLQTTTWQDPRKSH
PSSNMGSTQQPGSPVSGTQSPPNTMDITKMPLPLGWERAYTPEGEIYFINHIERTTSWFHPSIPAAQQRPGMRLH
PQQQQQQAALAPSPQQPQQASPLMRSPISGASSPPVPPGQHGPLTAEQQRQLKLKQLQMEKELLKKRQEELARQE

MMIQLGAGGETTDTTADLTTVTDPFLGQTGSTDHHSRQESADSGLGGMGTGYNLPRTPEDFLSNMEEMDIPDGGH
KSQAQGDFINMDIGSVGDVSDSHNMDSDDLVPSLQEVIGTDLLRDVENVLSCNKADHLLTWL
PLRDRNLPASFFQQP

rs:XP_025195803 [XP_025195803] transcriptional coactivator YAP1
[Melanaphis sacchari].>tr:A0A2H8TPG0_9HEMI [A0A2H8TPG0] SubName:
Full=Yorkie {ECO:0000313|EMBL:MBW16063.1}; 68..82
MSGLQQQQQQQEQHQQVSIKMEPTGPNSPPPAANSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPY
RMRQLPKSFFNPPSTGSKSPSISHSRENSGDSTFGIATASAQSCTGGGPVPLHSRAHSSPASLQQTYAVSAAKQQ
QQQQQHSKQRSYDVSSAIDELGPLPQGWEQARTPEGQIYYLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQLLSP
GNDSGSSTNATSTPTNSPPHIHSTLQGTNKNVTLGPLPDGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQRA
PTSGAVLPSGSASWLLNGASGLSQSLQVTQQKLRLHSLQLEREHLKSRQQEIIRQQDLMLRTGQTNNDLDPFLSC
SSNSVDHSRQESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDSQEMATLDVTEDLVP
SLQLGDDFGNDILDEVQLLIDPNNKPGSILTWL PYRMRQLPKSFFNPP

rs:XP_024123677 [XP_024123677] protein **FAM181**A [Oryzias
melastigma].>rs:XP_024123746 [XP_024123746] protein **FAM181**A [Oryzias
melastigma]. 103..117
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRAPRCHTHRSVDYKC
AKPVGTVHQSATVTDKASSDAQEESVGSAVEQVPMRKRQLPASFWEEPKLTNSENALVRLKGSPAGMREGSAKEK
QKTVHVDPKVPAPASSRRSWTDKETLKLDLISPVSVSVCSCCPFQYHGHHVLHSHIVVPHPPLGLWSKAASDLGR
PDHPYEQKIHTHVVVKPIPTKPAAQTPIFSVFGLI PMRKRQLPASFWEEP

rs:XP_024122107 [XP_024122107] transcriptional coactivator YAP1-like
isoform X1 [Oryzias melastigma].>tr:A0A3B3DUB5_ORYME [A0A3B3DUB5] SubName:
Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSOMEP00000033024};
42..56
MDAHRSGRQVVHVRGDSQKELEALFSRVMNPSEASRQPSSVPMRMRKLPDSFFKPPEPRGHSRQASSDG
GVCGSLTPHHSRTVSAPAALPVNSLATQAADVAATSIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWLDPRL
SQLQSAQQHPISTAPVHSHSFSNPAPTTPAQSINPEPGPLPEGWEQAVTPEGEMYYIDHINKTTTWVDPRLAQKM
SPGVLSLAMQRQEKLRCKQGAPPQVTQQEAAGRNQMSAGMDHDRSGQVLVPSVDARIRAPNHETALNGAHSRNES
TDSGLSVSSLPRTNDHMLSPVDHMDIGDSSDPPSMALQEPMLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHM
DRDNLLTWL PMRMRKLPDSFFKPP

rs:XP_024122108 [XP_024122108] transcriptional coactivator YAP1-like
isoform X2 [Oryzias melastigma]. 42..56
MDAHRSGRQVVHVRGDSQKELEALFSRVMNPSEASRQPSSVPMRMRKLPDSFFKPPEPRGHSRQASSDG
GVCGSLTPHHSRTVSAPAALPVNSLATQAADVAATSIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWLDPRL
SQLQSAQQHPISTAPVHSHSFSNPAPTTPAQSINPEPAQKMSPGVLSLAMQRQEKLRCKQGAPPQVTQQEAAGRN
QMSAGMDHDRSGQVLVPSVDARIRAPNHETALNGAHSRNESTDSGLSVSSLPRTNDHMLSPVDHMDIGDSSDPPS
MALQEPMLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDNLLTWL PMRMRKLPDSFFKPP

rs:XP_024132222 [XP_024132222] protein **FAM181**B [Oryzias
melastigma].>tr:A0A3B3B6C4_ORYME [A0A3B3B6C4] SubName: Full=Family with
sequence similarity 181 member B {ECO:0000313|Ensembl:ENSOMEP00000000712};
155..169
MAVQTAIMNPQFMSFCFPGSVMEFDMEKSLDGSLLCEAEQDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIIAPANGAETPVKRQSSPVTQQSSLQNKVLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSPASEVTLKDLERGSPDFFELLGPDYSGMVSDQELYQSVPLRMQ
PELGGLDPASYDAHHLVAHHLYADPWTSCSGPSKKLGENLRAGPAQPPAYFQSEEASGGMDDNALCTLAFPNFFT
DCSIPQVTYDLNSGYSRSSYSSL PLRHRNLPPSFFTEP

rs:XP_024133526 [XP_024133526] transcriptional coactivator YAP1 isoform
X1 [Oryzias melastigma].>tr:A0A3B3CY65_ORYME [A0A3B3CY65] SubName:
Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSOMEP00000022104};
45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKGAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTTSGQRYF
LNHIDQTTTWQDPRKALLQLNQATPPSTVPVQQQNLISPASGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL

ETRYALNQQRITQSAPVKQGGPLPPNPHGGVMGGNSQMRLQQLEKERMRLKQQELLRQRPQELALRNQLPTSMDQ
DGSSNPVSSPMAQDARTMTANSTDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMG
TQPSRFPDYLDTIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMETVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_024133527 [XP_024133527] transcriptional coactivator YAP1 isoform X2 [Oryzias melastigma]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKGAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTTSGQRYF
LNHIDQTTTWQDPRKALLQLNQATPPSTVPVQQQNLISPASALNQQRITQSAPVKQGGPLPPNPHGGVMGGNSQM
RLQQLEKERMRLKQQELLRQRPQELALRNQLPTSMDQDGSSNPVSSPMAQDARTMTANSTDPFLNSGTYHSRDES
TDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLAPSMGTQPSRFPDYLDTIPGTDVDLGTLESESMAVEGEELMPS
LQEALSSDILNDMETVLAATKIDKESFLTWL PMRMRKLPDSFFKPP

rs:XP_024285962 [XP_024285962] protein **FAM181**A [Oncorhynchus tshawytscha]. 125..139
MASTDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARMPRCHTHRSTESSI
AKDVVNTSSEYSLETTHPSTTRVNEKGVSDARDVENARMAQTPTVDSDNSKQEQVPMRKRQLPASFWEEPRLAQT
NTDYLQYGWKKSQGVIGINDVEKIKKAHEELTPSLLLSNRRGSVEKEPLKLDVASHNVNVCGFCPFQYHGHHVFQ
SHIVVPQSAVGLWGKATVAETETPDITHRHKNYTHVVVKPIPTKPTVPPSIFNVFGFI PMRKRQLPASFWEEP

rs:XP_024215400 [XP_024215400] transcriptional coactivator YAP1-like isoform X1 [Halyomorpha halys]. 45..59
MSSKQPEVEQFKNLVVRIDQDSDTDLQALFDSVLKPDSKRPLQVPFRMRNLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGATNTTVSGLQVSHPRAHSSPASLQQTYASAGQQPTAGHHLKQRSYDMDELGPLPPGWEQA
RTSEGQIYFLNHITQTTTWEDPRKTVQAQQAQRAELLASSPHPSTSPQPHATGKSSGTSNTTSGLGPLPDGWEQA
ATAEGEIYFINHQAKTTSWFDPRIPVHLQRTPSAGNVLPAWLQPAVAQSQSLQATQQKLRLQSLQMERERLKLRQ
QEIMRQQELMLRDAPSSGLVDPFLSSLTDHSRQESADSGLGLGNSYSLPHTPDDFLNIDDNMDGVSEGGTGDIPS
LDSHEITSLSDNIDSTDDLVPTLQLGEEFTSDILDDVQSLINPTSKAGNLTWLPFRMRNLPNSFFNPP

rs:XP_024215401 [XP_024215401] transcriptional coactivator yorkie-like isoform X2 [Halyomorpha halys]. 45..59
MSSKQPEVEQFKNLVVRIDQDSDTDLQALFDSVLKPDSKRPLQVPFRMRNLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGATNTTVSGLQVSHPRAHSSPASLQQTYASAGQQPTAGHHLKQRSYDMDELGPLPPGWEQA
RTSEGQIYFLNHITQTTTWEDPRKTVQAQQAQRAELLASSPHPSTSPQPHATAVHLQRTPSAGNVLPAWLQPAVA
QSQSLQATQQKLRLQSLQMERERLKLRQQEIMRQQELMLRDAPSSGLVDPFLSSLTDHSRQESADSGLGLGNSYS
LPHTPDDFLNIDDNMDGVSEGGTGDIPSLDSHEITSLSDNIDSTDDLVPTLQLGEEFTSDILDDVQSLINPTSKA
GNLTWL PFRMRNLPNSFFNPP

rs:XP_024615864 [XP_024615864] protein **FAM181**A isoform X1 [Neophocaena asiaeorientalis asiaeorientalis].>tr:A0A341CMJ6_9CETA [A0A341CMJ6] SubName: Full=protein **FAM181**A isoform X1 {ECO:0000313|RefSeq:XP_024615864.1};
193..207
MLLRGSPCCPQPAISLPGRPRLECQTGVLPVLRENCQLRALPWSRQPPAEPPSSWKAPCSGPLVMASDS
DVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGSEDRPGRLP
LDSGHSSSPGGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTQSYPVGLEG
GLGPREGPPYEGKKHCKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGA
LPQSPLPSLGLWRKSSAAPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_024615872 [XP_024615872] protein **FAM181**A isoform X2 [Neophocaena asiaeorientalis asiaeorientalis].>tr:A0A341CPW3_9CETA [A0A341CPW3] SubName: Full=protein **FAM181**A isoform X2 {ECO:0000313|RefSeq:XP_024615872.1};
129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGSEDRPGRLPLDSGHSSSPGGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTQSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPPGALPQSPLPSLGLWRKSSAAPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_011715448 [XP_011715448] protein **FAM181**A [Macaca
nemestrina].>rs:XP_011715449 [XP_011715449] protein **FAM181**A [Macaca
nemestrina].>rs:XP_011715450 [XP_011715450] protein **FAM181**A [Macaca
nemestrina]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_017271841 [XP_017271841] LOW QUALITY PROTEIN: protein **FAM181**B
[Kryptolebias marmoratus]. 244..258
MQVVGHKQRVKSRGXPLLLLFDVLTSSVLPPXKISFLSSNPSLPLWNVYGKLHKSHRVFICRTKPCSEG
TSASGITVDATGVASGLNRVMAVQTAIMNPQFMSFCFPDAVMEYDMEKSLDGGLLCEAENDEDFKETTRDLLSFI
DSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIIAPANAAEAPVKRQGSPVTQPSPLQSKTLPKRDGVQAN
LQSKSLAALFNPGKDIRGEKAKKPPLRHRNLPPSFFTEPAHCSKVSSTSGMTLKDLERGNPEAADFFELLGPDYS
NMVSDQDLYQGMPLRVQPDLGGMDPTSYDSHHLVGGLLYSEPWTSCSGPSKKLGESLHAGPAQPPVYCQSEDASG
PVDDSGLCTLAFSNFFTDCSIPQVTYDLNCGYNKANYSSL PLRHRNLPPSFFTEP

rs:XP_017271941 [XP_017271941] transcriptional coactivator YAP1
[Kryptolebias marmoratus]. 45..59
MDPSQHNPPAGHQIIHVRGDSETDLETLFNIVMNPNSPNIPHCVPMRMRKLPDSFFNPPEPKSHSRQAS
TDAGSGAVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQAPPPSSVPVQQQNLMNPATGPLPDGWEQAITPDGEIYYINHKNKTTSWLDPRL
EPRYALNQQRITQSAPVKQGGQLPPSTHSGVLGGNNQMRLQQIEKERLRLKQHEALRQRPQELALRNQLPTSMEQ
DGGSNPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDQLPPSMA
TQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEPLSSDILSDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFNPP

rs:XP_017273649 [XP_017273649] transcriptional coactivator YAP1-like
isoform X1 [Kryptolebias marmoratus].>rs:XP_017273650 [XP_017273650]
transcriptional coactivator YAP1-like isoform X1 [Kryptolebias
marmoratus].>rs:XP_024862090 [XP_024862090] transcriptional coactivator
YAP1-like isoform X1 [Kryptolebias marmoratus].50..64
MDAHRGGGGGAPPAGQQVVHVRGDSKTELEALFSAVMNPGKAARQPQSLPMRMRKLPDSFFKPPDPRGH
SRQASSDGGVCGALAPHHVRAHSSPASLPVNSLTAQADADAAAAPILPDDMPLPDGWEMAKTPTGQRYFINHLQK
TTTWQDPRLSQLQSAAAQHQISCAPVHAHSFSNPAPTTQPQTISPEPGPLPEGWEQAVTADGEVYYIDHINKTTT
WVDPRLAQKMNPGILGLQQRQEKERLRLKQGIPPQIAPQEAAGRSQMPGGMDHDRSVQMLVPSVDIRIRALNQEP
TLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSSEPPSVTMQESMPVLPISEGEELMPSIPDGLNSDL
LMDMETVLSGPHMDRDSLLTWL PMRMRKLPDSFFKPP

rs:XP_017273652 [XP_017273652] transcriptional coactivator YAP1-like
isoform X2 [Kryptolebias marmoratus]. 50..64
MDAHRGGGGGAPPAGQQVVHVRGDSKTELEALFSAVMNPGKAARQPQSLPMRMRKLPDSFFKPPDPRGH
SRQASSDGGVCGALAPHHVRAHSSPASLPVNSLTAQADADAAAAPILPDDMPLPDGWEMAKTPTGQRYFINHLQK
TTTWQDPRLSQLQSAAAQHQISCAPVHAHSFSNPAPTTQPQTISPEPAQKMNPGILGLQQRQEKERLRLKQGIPP
QIAPQEAAGRSQMPGGMDHDRSVQMLVPSVDIRIRALNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDH
MDTGDSSEPPSVTMQESMPVLPISEGEELMPSIPDGLNSDLLMDMETVLSGPHMDRDSLLTWL
PMRMRKLPDSFFKPP

rs:XP_011648280 [XP_011648280] transcriptional coactivator YAP1
[Pogonomyrmex barbatus]. 47..61
MAINPEVVDQLTKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTATPNGGGGAGGGASNGGASGSGSGGGGGGGGNAAGAAGTGGAAAGLTVSHPRAHSS
PASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHITRTTTWEDP
RKTAAAASVAAVAAAAVESNKPNSLGPLPDGWEQARTAEGEVYFINHQSRTTSWFDPRIPAHLQRTPASGAMLPQ
NWLQQPTGGLQNNQNAVCQQKLRLYSLHQERERLKQRQAEIMRQQEMMRLSITDAAIDPFVSGINEQHARQESTD
SGVGLVSAYSLPHASEDYVIDENMDGTSDGGAPMETPDLSTLSDNIDSPDDLLPSLQLNEEFSTDILDDVQSLIN
PNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_025213170 [XP_025213170] protein **FAM181**B [Theropithecus gelada].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPVAGLGGAGTGGAGGDAAGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPPHQVSYDYSAGYSRNAYSSLWRPDAVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_025248178 [XP_025248178] protein **FAM181**A isoform X1 [Theropithecus gelada]. 179..193
MMQPTESTEGPGRKRQGTAKQVSLVAFLGAAGHQQSPPSSWKASCSGPLVMASDSDVKMLLNFVNLASS
DIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDLGPDSSPGGGGG
CKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKK
NCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWKK
SPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_025248184 [XP_025248184] protein **FAM181**A isoform X3 [Theropithecus gelada]. 165..179
MACFVPQVSLVAFLGAAGHQQSPPSSWKASCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRR
SVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREEC
LAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPEIVP
VPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWKKSPAFPGELAHLCKD
ADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

rs:XP_015595189 [XP_015595189] transcriptional coactivator YAP1 [Cephus cinctus]. 47..61
MALNQDGVEQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGTAAVVAVGGSAAGTAAPGGSAGATGTAGGASGAAAVAGAAGAAGLTVAHPRAHSSPASLQQ
TYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAA
ANVAAVAAAVESGKTSTGATSSLGPLPDGWEQARTQEGEIYFINHQTRTTSWFDPRIPSHLQRAPTSGAMLPQNW
LQQPGGGGIQSNQTLQACQQKLRLQSLQMERERLKQRQQEIIRQQELMLRQSNTDAAMDPFLPGINEQHARQESA
DSGLGLGSAYSLPHTPEDFLANIDDNMDGTSEGGAPMETPDLSTLSDNIDSTDDLVPSLQLGEEFSSDILDDVQS
LINPNPSKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_008306240 [XP_008306240] protein **FAM181**A [Cynoglossus semilaevis].
104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQRYSRVPRCHTHRPAEYGC
SRLAGAAHQSEKLAATASSGAQDAGNVGSAVEQVPMRKRQLPASFWEEPKLTPSKSGRSHLLGLKRVPVGAFEGS
ENEKRKRGCGEDAKVAMSAASRRNSADKETLKLDLTSHHCVSVCACCPFLNHGHQVLHSHIVVPHPPLGLWSKAA
GTEAERPEHPFTQKVHTHVVVKPIPTKPTLQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_025028171 [XP_025028171] protein **FAM181**A [Python bivittatus].
135..149
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHHHLQPQLPP
ARERRAPEGRARGLSVADGPESSVGRGHAAPGTAKGDKASRAPERLGDEEQQQETPEAGARPDQVPMRKRQLPAS
FWEEPRPAPGSPGVVSGVIFPVGVSSSPSSSSSPSSSSKDLPPYEGKKNKTGLDSGGTGTVLESPPRRPEAEAAK
GLRAWSCCPFQCHGLQASPGVYPPPRRKDAPSPTEGEAFCQAGQKVYRPVVWKPIPTKPAAPPLIFSVFGYL
PMRKRQLPASFWEEP

rs:XP_025155622 [XP_025155622] transcriptional coactivator YAP1 [Harpegnathos saltator]. 46..60
MALNQDVDQLTKSNLVVRIDQNSESDLQALFDSVLKPDSTRPLQVPLRMRKLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAAATPSNAAGGGAGSNASNGGANGSGAGAGGAGGGAGGGNAAADAAGAGAGGGAGGGAAGG
GGAAGGGAGGANSAAGAAAAAAAAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRS
YDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAANVAAVAAAVESGKSNGNTLGPLPDGW
EQARTPEGEIYFINHQTRTTSWFDPRIPSHLQRAPTSGAMLPQSWLQQPTGGGIQSSQSLQACQQKLRLQSLQME
RERLKQRQQEIMRQQELMLRQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGT

SDGGAPMETPDLSTLSDNIDSTDDLLPSLQLTEDFSSDILDDVQSLINPNTTKPENVLTWL
PLRMRKLPDSFFNPP

rs:XP_025264222 [XP_025264222] transcriptional coactivator YAP1 isoform X1 [Camponotus floridanus].>rs:XP_025264223 [XP_025264223] transcriptional coactivator YAP1 isoform X1 [Camponotus floridanus]. 46..60
MALNQDVDQLSKSNLVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAATPSGGSGGGGGGGGGGGGGGAPNVSANGSGNGTGSTAGAGGAAGGGGGAGGGGGANSAA
GAVAAAAAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISSQVDDLGPL
PHGWEQARTAEGQIYFLKGNDLQLFTIPSNPSNERHNLLLLSHLTRTTTWEDPRKTAAAANVAAVAAAVENSKSN
PNSLGPLPDGWEQARTTEGEIYFINHQTRTTSWFDPRIQDIIVALATHLQRTPASGAMLPQNSWLQPAGVIQSNQ
NLQVCQQKLRLQSLQMERERLKQRQQEIMRSQQELMLRQSTTDAAMDPFLSGINEHARQESADSGLGLGSAYSLP
HTPEDFLANIDDNMDGTSERHCALIDLTKRLYRSHKYLNGGAPMETPDLSTLSDNIDSTDDLLPSLHMSEDFSSD
ILDDVQSLINPNTTKADNVLTWL PLRMRNLPDSFFNPP

rs:XP_025264224 [XP_025264224] transcriptional coactivator YAP1 isoform X2 [Camponotus floridanus]. 46..60
MALNQDVDQLSKSNLVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAATPSGGSGGGGGGGGGGGGGGAPNVSANGSGNGTGSTAGAGGAAGGGGGAGGGGGANSAA
GAVAAAAAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISSQVDDLGPL
PHGWEQARTAEGQIYFLKGNDLQLFTIPSNPSNERHNLLLLSHLTRTTTWEDPRKTAAAANVAAVAAAVENSKSN
PNSLGPLPDGWEQARTTEGEIYFINHQTRTTSWFDPRIPTHLQRTPASGAMLPQNSWLQPAGVIQSNQNLQVCQQ
KLRLQSLQMERERLKQRQQEIMRSQQELMLRQSTTDAAMDPFLSGINEHARQESADSGLGLGSAYSLPHTPEDFL
ANIDDNMDGTSERHCALIDLTKRLYRSHKYLNGGAPMETPDLSTLSDNIDSTDDLLPSLHMSEDFSSDILDDVQS
LINPNTTKADNVLTWL PLRMRNLPDSFFNPP

rs:XP_025264225 [XP_025264225] transcriptional coactivator YAP1 isoform X3 [Camponotus floridanus]. 46..60
MALNQDVDQLSKSNLVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAATPSGGSGGGGGGGGGGGGGGAPNVSANGSGNGTGSTAGAGGAAGGGGGAGGGGGANSAA
GAVAAAAAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISSQVDDLGPL
PHGWEQARTAEGQIYFLKGNDLQLFTIPSNPSNERHNLLLLSHLTRTTTWEDPRKTAAAANVAAVAAAVENSKSN
PNSLGPLPDGWEQARTTEGEIYFINHQTRTTSWFDPRIQDIIVALATHLQRTPASGAMLPQNSWLQPAGVIQSNQ
NLQVCQQKLRLQSLQMERERLKQRQQEIMRSQQELMLRQSTTDAAMDPFLSGINEHARQESADSGLGLGSAYSLP
HTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLLPSLHMSEDFSSDILDDVQSLINPNTTKADNVL
TWL PLRMRNLPDSFFNPP

rs:XP_025264226 [XP_025264226] transcriptional coactivator YAP1 isoform X4 [Camponotus floridanus]. 46..60
MALNQDVDQLSKSNLVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAATPSGGSGGGGGGGGGGGGGGAPNVSANGSGNGTGSTAGAGGAAGGGGGAGGGGGANSAA
GAVAAAAAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISSQVDDLGPL
PHGWEQARTAEGQIYFLNHLTRTTTWEDPRKTAAAANVAAVAAAVENSKSNPNSLGPLPDGWEQARTTEGEIYFI
NHQTRTTSWFDPRIQDIIVALATHLQRTPASGAMLPQNSWLQPAGVIQSNQNLQVCQQKLRLQSLQMERERLKQR
QQEIMRSQQELMLRQSTTDAAMDPFLSGINEHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSERHCAL
IDLTKRLYRSHKYLNGGAPMETPDLSTLSDNIDSTDDLLPSLHMSEDFSSDILDDVQSLINPNTTKADNVLTWL
PLRMRNLPDSFFNPP

rs:XP_025264227 [XP_025264227] transcriptional coactivator YAP1 isoform X5 [Camponotus floridanus]. 46..60
MALNQDVDQLSKSNLVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAATPSGGSGGGGGGGGGGGGGGAPNVSANGSGNGTGSTAGAGGAAGGGGGAGGGGGANSAA
GAVAAAAAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISSQVDDLGPL
PHGWEQARTAEGQIYFLNHLTRTTTWEDPRKTAAAANVAAVAAAVENSKSNPNSLGPLPDGWEQARTTEGEIYFI
NHQTRTTSWFDPRIPTHLQRTPASGAMLPQNSWLQPAGVIQSNQNLQVCQQKLRLQSLQMERERLKQRQQEIMRS
QQELMLRQSTTDAAMDPFLSGINEHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSERHCALIDLTKRL
YRSHKYLNGGAPMETPDLSTLSDNIDSTDDLLPSLHMSEDFSSDILDDVQSLINPNTTKADNVLTWL
PLRMRNLPDSFFNPP

rs:XP_025264228 [XP_025264228] transcriptional coactivator YAP1 isoform X6 [Camponotus floridanus]. 46..60

MALNQDVDQLSKSNLVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAATPSGGSGGGGGGGGGGGGGAPNVSANGSGNGTGSTAGAGGAAGGGGGAGGGGGANSAA
GAVAAAAAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISSQVDDLGPL
PHGWEQARTAEGQIYFLNHLTRTTTWEDPRKTAAAANVAAVAAAVENSKSNPNSLGPLPDGWEQARTTEGEIYFI
NHQTRTTSWFDPRIPTHLQRTPASGAMLPQNSWLQPAGVIQSNQNLQVCQQKLRLQSLQMERERLKQRQQEIMRS
QQELMLRQSTTDAAMDPFLSGINEHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLST
LSDNIDSTDDLLPSLHMSEDFSSDILDDVQSLINPNTTKADNVLTWL PLRMRNLPDSFFNPP

rs:XP_012266693 [XP_012266693] transcriptional coactivator YAP1 isoform X1 [Athalia rosae]. 45..59

MALNQDVDQLKSSLVVRIDQNSESDLQALFDSVLKPDAKRPLQVPLRMRNLPDSFFNPPSTGSKSPSIS
HSRENSADSAFGATGGGSGASSGCVSSGTTGTGAGAGGGTSCTTNSAGTPGSGAGVGGTAGSTVAANNGLTVSHP
RAHSSPASLQQTYASAQQAQQHTPQPHPRHHHHKQRSYDVISTVDDLGPLPPGWEQARTPEGQVYFLNHMTRTTT
WEDPRKTAAAASVAAVAAAVESGTKNSSAATSSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRA
PTSGAMLPQTWLQQPGAGGIQSSQTIQACQRLHSLQLERERLKQRQQEIMRQQELMRQTTTEVAMDPFLSGINEQ
HARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGRSEGAPMETPDLSTLSDNIDSTDDLVPSLQLGEEFTSDI
LDDVQSLINPNTSKSENVLTWL PLRMRNLPDSFFNPP

rs:XP_020711642 [XP_020711642] transcriptional coactivator YAP1 isoform X2 [Athalia rosae]. 45..59

MALNQDVDQLKSSLVVRIDQNSESDLQALFDSVLKPDAKRPLQVPLRMRNLPDSFFNPPSTGSKSPSIS
HSRENSADSAFGATGGGSGASSGCVSSGTTGTGAGAGGGTSCTTNSAGTPGSGAGVGGTAGSTVAANNGLTVSHP
RAHSSPASLQQTYASAQQAQQHTPQPHPRHHHHKQRSYDVISTVDDLGPLPPGWEQARTPEGQVYFLNHMTRTTT
WEDPRKTAAAASVAAVAAAVESGTKNSSAATSSLGPLPDGWEQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRA
PTSGAMLPQTWLQQPGAGGIQSSQTIQACQRLHSLQLERERLKQRQQEIMRQELMRQTTTEVAMDPFLSGINEQH
ARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGRSEGAPMETPDLSTLSDNIDSTDDLVPSLQLGEEFTSDIL
DDVQSLINPNTSKSENVLTWL PLRMRNLPDSFFNPP

rs:XP_025775740 [XP_025775740] protein **FAM181**A [Puma concolor].129..143

MANDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRLPLDSGHDSSPVGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPR
ATHSYPLGLEGGPGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYH
GQPVYPGPPGALPQSPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_025902748 [XP_025902748] protein **FAM181**A [Nothoprocta perdicaria].
125..139

MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPVECSGK
KGTEERGRGAQPEAADSSPQCRAERALRAAEAEETFPGEQLLQEQNPEPARPDQVPMRKRQLPASFWEEPRPAQS
LLGRSFPAGLDGLPNSGEPLPYEGKKSRRSPEAAGPESAHEPVLHGGEKDRAKAAGPPAAARVPAWTCCPFQCAG
QPLYQSPAALPPSLFPGLALWRKSAALPGEVQHFCKEADNAGQKLYRPVVVKPIPTKPPVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_025890735 [XP_025890735] transcriptional coactivator YAP1 isoform X1 [Nothoprocta perdicaria]. 87..101

MDPGQPQPQQPPPPAAQPAAPQPPPQQQPPPGAVSGAAAGAAQPPGAGPPPAGHQIVHVRGDSETDLEA
LFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTL
SPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGG
VMSGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_025890736 [XP_025890736] transcriptional coactivator YAP1 isoform X2 [Nothoprocta perdicaria]. 87..101

MDPGQPQPQQPPPPAAQPAAPQPPPQQQPPPGAVSGAAAGAAQPPGAGPPPAGHQIVHVRGDSETDLEA

LFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTL
SPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSP
PVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMSGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELA
LRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDE
MDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDK
ESFLTWL PMRLRKLPDSFFKPP

rs:XP_025890737 [XP_025890737] transcriptional coactivator YAP1 isoform X3 [Nothoprocta perdicaria]. 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LSPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTS
PPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQG
GVMSGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_025935500 [XP_025935500] protein **FAM181**A [Apteryx rowi]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSAECSVK
RGTEDRSRGSQSEVVDSSHHCRAAAEKVLRTAEVEENFSGEQVLQEQNPEPARPDQVPMRKRQLPASFWEEPRPA
QSLLARSFPAGLDGLPNSRDPVPYEGKKSRRSPEAAGPESPPEPVQHGSEDPAKAPGPPMSGRVAAWTCCPFQCP
GQPLYQTPGALPPSXFPGLGLWRKSAALPGEIQHFSKEADSTGQKLYRPMVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_025968286 [XP_025968286] protein **FAM181**A [Dromaius novaehollandiae]. 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKSAECSMK
RGAEERSHVPQPEAPDSSHHCRAAAEKALGTAEVEETFSGEQVLQEQNPEPARPDQVPMRKRQLPASFWEEPRPA
QSLLARSFPAGLDGLPNSGDPLPYEGKKSRRSPEAASPESPPEPVQRGGEKDPAKAPGPPVSGRVAAWTCCPFQC
PGQPLYQTPGTLPPSPFPGLGLWRKSTALPGEVQHFCKEADSTXQKLYRPVVLKPIPTKPAVPPPIFNVFGYI
PMRKRQLPASFWEEP

rs:XP_011165255 [XP_011165255] transcriptional coactivator YAP1-A isoform X1 [Solenopsis invicta].>rs:XP_025986169 [XP_025986169] transcriptional coactivator YAP1-A isoform X1 [Solenopsis invicta].>rs:XP_025986170 [XP_025986170] transcriptional coactivator YAP1-A isoform X1 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIHIIYSASHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLK
QRRQEIIRQVSMQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSER
HCSLNDLTKRLYRSHKYINGAPMETPDLSLSDNIDATDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTW
L PLRMRNLPDSFFNPP

rs:XP_011165256 [XP_011165256] transcriptional coactivator YAP1-A isoform X2 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIHIIYSASHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLK
QRRQEIIRQQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSERHCS
LNDLTKRLYRSHKYINGAPMETPDLSLSDNIDATDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_011165257 [XP_011165257] transcriptional coactivator YAP1-A isoform X3 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS

ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIPSHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLKQRRQE
IIRQVSMQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSERHCSLN
DLTKRLYRSHKYINGAPMETPDLSLSDNIDATDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_025986171 [XP_025986171] transcriptional coactivator YAP1-A isoform X4 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIPSHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLKQRRQE
IIRQQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSERHCSLNDLT
KRLYRSHKYINGAPMETPDLSLSDNIDATDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

rs:XP_011165258 [XP_011165258] transcriptional coactivator YAP1-A isoform X5 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIHIIYSASHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLK
QRRQEIIRQVSMQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSDG
APMETPDLSLSDNIDATDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_011165259 [XP_011165259] transcriptional coactivator YAP1-A isoform X6 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIHIIYSASHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLK
QRRQEIIRQVSMQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSER
HCSLNDLTKRLYRSHKYINGAPMETPDLSLSDNIDATDDLLPSLQVWWYNGNVN PLRMRNLPDSFFNPP

rs:XP_025986172 [XP_025986172] transcriptional coactivator YAP1 isoform X7 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIHIIYSASHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLK
QRRQEIIRQQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSDGAPM
ETPDLSLSDNIDATDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWLPLRMRNLPDSFFNPP

rs:XP_011165262 [XP_011165262] transcriptional coactivator YAP1 isoform X8 [Solenopsis invicta]. 47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGTPSGGASGSGGGGGGGGGGGGGGGGGGNAAGVTGTGSGNAG
AGGGANGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQHARHHHHQKQRSYDVIAPTV
DDLGPLPTGWEQARTQEGQIYFLNHVTRTTTWEDPRKTAAAANVAAVAAAVESNKNNALGPLPDGWEQARTQEGE
VYFINHQTRTTSWFDPRIPSHLQRTPAAGVMLPQNWQLQQPTGIQSNQSLQACQQKIRLQSLQMECERLKQRRQE
IIRQQEMMLQQSRTDAAMDPFLPSGISEHARTESADSGLGLGSAYPLPQTSDDFLNIDENMDGTSDGAPMETPDL
SLSDNIDATDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

rs:XP_026154346 [XP_026154346] protein **FAM181**A [Mastacembelus armatus].
103..117
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHAHRSAEYGC
AKPMGPVHQSVKVAEKARSDVQDVENMSAVEQVPMRKRQLPASFWEEPKLSQTKRENSHLGFKKSPAATSEGGES
ERRKRSYDEDAKVPLSASSRRSYTNKETLKLDLTSHHCVSVCGCCPFQYHGHQVLHSHIVVPHPPLGLWSKAAGT
DTGRPEQPYGQKIHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_026153482 [XP_026153482] protein **FAM181**B [Mastacembelus armatus].
155..169
MAVQTAIMNPQFMNFCFPGSVIEYDVEKSLDVSLLGEAENDEDYKETTKDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVEETPAKRQASPLAQPSPLQSKTLPKRDGVQASLQSKSLAALFSPVK
DIRGEKTKKPPLRHRNLPPSFFTEPANCSKVSSTSGMMLKDLERGNPDAAEFFELLGPDYSNMVSDQDLYQTMPL
RVQPEMGAPDPTSYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGPAQPPLYCHSETASGPLEDNALCTLAFPN
FFTDCSIPQVTYDLCSGYNKANYSSL PLRHRNLPPSFFTEP

rs:XP_026154302 [XP_026154302] transcriptional coactivator YAP1
[Mastacembelus armatus]. 45..59
MDPNQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKSAIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGALTPHHVRAHSSPASLQLGAVSGGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTTSGQRYFLNHI
DQTTTWQDPRKALLQMNQAAPANSVPVQQQNLMNPASGPLPEGWEQAITSEGEIYYINHKNKTTSWLDPRLDPRF
AMNQQRISQSAPVKQGGQLPSSTHSVVMGSNNQMRLQQIDKERLRLKQQQELLRQRPQELALRNQLPTSMDQDGS
TNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSISSYSVPRTPDDFLNSVDEMDTGDPLPPSMTTQP
SRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_026184175 [XP_026184175] transcriptional coactivator YAP1-like
isoform X1 [Mastacembelus armatus].>rs:XP_026184176 [XP_026184176]
transcriptional coactivator YAP1-like isoform X1 [Mastacembelus armatus].
46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFNAVMNPGKAGRQPPSVPMRLRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATTIVPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLTQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQSINPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPR
LAQKMNPGVLGLVMQQRQEKERLRCKQGLPPQIIPQEAGGRNQMPGGMDHDRNAQTLVPSLDVRIRASNHEPTLN
GAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGEASMALQESMPVLPMSEGEELMPCIPEGLSSDLLMDM
ETVLSGSHMDRDSLLTWL PMRLRKLPDSFFRQP

rs:XP_026184177 [XP_026184177] transcriptional coactivator YAP1-like
isoform X2 [Mastacembelus armatus]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFNAVMNPGKAGRQPPSVPMRLRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATTIVPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLTQLQSAAAQHPISGTPVHAHSLSNPAPTTQPQSINPETAQKMNPGVLGLVMQQRQEKERLRCKQGLPPQII
PQEAGGRNQMPGGMDHDRNAQTLVPSLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDT
GDSGEASMALQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRLRKLPDSFFRQP

rs:XP_026222413 [XP_026222413] protein **FAM181**B [Anabas testudineus].
155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLQVSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVEEAPVKRQGSPPAQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMISEQDHYQSMPL
RVQPEVGSLDPASYDSHHLVGGLLYSEPWTSCSGPSKKLGESLRTGPAQPSLYCHSTEAAAGPVEDNTLCTLAFS
NFFTDCSIPQVTYDLSGSCNRANYSSL PLRHRNLPPSFFTEP

rs:XP_026225556 [XP_026225556] transcriptional coactivator YAP1 isoform
X1 [Anabas testudineus]. 45..59
MDPNQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGSGGALTPHHVRAHSSPASLQLGAVSGGSLSGMGSAGASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIEQTTTWQDPRKALLQMNQPTPTSSVPVQQQNIMNPATGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRYALNPQRITQSAPVKQGGPLPPSTHSGIMGTNNQLRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQ

DGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLQPSMG
TQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSEILNDMESVLAATKIDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_026225560 [XP_026225560] transcriptional coactivator YAP1 isoform X2 [Anabas testudineus]. 45..59
MDPNQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGSGGALTPHHVRAHSSPASLQLGAVSGGSLSGMGSAGASPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIEQTTTWQDPRKALLQMNQPTPTSSVPVQQQNIMNPATDGWEQAITSEGEIYYINHKNKTTSWLDPRLDPRY
ALNPQRITQSAPVKQGGPLPPSTHSGIMGTNNQLRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQDGST
NPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLQPSMGTQPS
RFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSEILNDMESVLAATKIDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_026209476 [XP_026209476] protein **FAM181**A [Anabas testudineus].
110..124
MKVLANMANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHR
STEYGCTKPGTTAHQRLKGAEKVSSGAQDVENAGCAVEQVPMRKRQLPASFWEEPKLTQTKREHSHFGFKKSPAG
TSEGDGIEKRRRSYDEDAKVTLSASGRRSSAEKETLKLDLTSHHCVSVCGCCPFQYHGHQLLHSHIVAPHPPLGL
WSKASVTETERPEHPYGQKIHAHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_026227257 [XP_026227257] transcriptional coactivator YAP1-like isoform X1 [Anabas testudineus].>rs:XP_026227258 [XP_026227258] transcriptional coactivator YAP1-like isoform X1 [Anabas testudineus].
46..60
MDAHRGAPPAGQQVVHVRGDSQTELEALFNAVMNPSKEARHPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTPATDVAAAPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAAAHPIPGTPVHAHSLSNPAPTTQPQNIIPETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPHL
AQKMNPGLLGLVMQQRQEKLRCEGLSAQITPQEAAGRNQMPGGMDHDRNAQTLVPPLDVRIRASNHEPTLNGAHS
RNESTDSGLSISSLPRTSDHMLSSVDHMDTGDSGDTTSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETV
LSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_026227259 [XP_026227259] transcriptional coactivator YAP1-like isoform X2 [Anabas testudineus]. 46..60
MDAHRGAPPAGQQVVHVRGDSQTELEALFNAVMNPSKEARHPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTPATDVAAAPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAAAHPIPGTPVHAHSLSNPAPTTQPQNIIPETAQKMNPGLLGLVMQQRQEKLRCEGLSAQITPQEA
AGRNQMPGGMDHDRNAQTLVPPLDVRIRASNHEPTLNGAHSRNESTDSGLSISSLPRTSDHMLSSVDHMDTGDSG
DTTSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_026243106 [XP_026243106] protein **FAM181**B [Urocitellus parryii].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGSTFGALDKGCCFEDEETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCNGLMGASPPGPPSPSAADTPAKRPLAAPSASTAAAPVHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVSGGAEPVGGAVAVPVTGLGGTSSGGAGGEASGPAGGSAVPGARK
VPLRARNLPPSFFTEPSRAGGGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGSDYGAGTEAGVLLAAEPLDVFPT
GAAALRGPLELEPGLFEPPPAMVGNLIYPEPWSAPSCAPTKKSPMAAARGGLTLNESLRPLYPAPSDSPGGEDGT
GHLASFAPFFPDCTLPPPPPHQVSYDYNAGYSRSAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_026248236 [XP_026248236] transcriptional coactivator YAP1 isoform X1 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQN
PVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_026248237 [XP_026248237] transcriptional coactivator YAP1 isoform X2 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_026248238 [XP_026248238] transcriptional coactivator YAP1 isoform X3 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_026248239 [XP_026248239] transcriptional coactivator YAP1 isoform X4 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_026248240 [XP_026248240] transcriptional coactivator YAP1 isoform X5 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG
GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_026248241 [XP_026248241] transcriptional coactivator YAP1 isoform X6 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_026248242 [XP_026248242] transcriptional coactivator YAP1 isoform X7 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQG

GVMGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_026248243 [XP_026248243] transcriptional coactivator YAP1 isoform
X8 [Urocitellus parryii]. 85..99
MDPGQQPQPQQAPQGQGQPPAQPPQGQGPTSGPGQPAPPASQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVPAPTSPP
VQQNLMNTPSGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGSGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPF
LNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEG
DGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_026250062 [XP_026250062] protein **FAM181**A [Urocitellus
parryii].>rs:XP_026250063 [XP_026250063] protein **FAM181**A [Urocitellus
parryii]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCSRLPRGLPGRAAEPHLK
RGPEDRPGRLPLHSGPGASPGGGGGCQEKALGNPLREERLPKEQSLQGQSPDAAKPGQVPMRKRQLPASFWEEPR
PTHSYPLGLEGGLGPREGPPYESKKSCKGLESLGPETAPVPMSPRALADKEPLKMPGVSLVGRVDAWSCCPLQYH
GQPMYPGPPGALSHSQVPGLCLWRKSPASPGELALFCKEVEGPGQKVHRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_026282008 [XP_026282008] uncharacterized protein LOC113208941
[Frankliniella occidentalis]. 97..111
MDHRDDDSGLGAVQDADDADLLLGAVRDHHDYAKRRRSGSDRENNVVSELDELSLPVPKKSKAVAGSKG
LGKGRQLRDPEGGTYISARSRARKSPLPMKLRALPASFWEQPNLNKGPSPGTIFSALPPLGPLCKEDGADGPRDA
LRGANPARGPGLGGGELGMQAGNGLVTHSPADTDLLFSLFRSVEPKTNLHRRTRGRPRRPPPAPGPGGGAQRDDD
PCLLGSLTSTLTTSLSLACGHIADGRDRGVSALRGGAAAITVGADNNNFAQILSDLVVKL
PMKLRALPASFWEQP

rs:XP_026320225 [XP_026320225] transcriptional coactivator YAP1-A isoform
X1 [Hyposmocoma kahamanoa]. 44..58
MALNTDGEQKSNLVLRVDQDSETVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGSHIPDELGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKSLAAQAVTNSVQHQSAETLLSQNTAQTINSPTTAAAKSTSSNTTTDPL
GSLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPVGSTGAAGGDWASASLQACQQKLRLQSLQLERE
RLKHRQQEIRLQQELMARQASSIVSSLSGSTTVASTELPLDPFLSGLTDHQRQESADSGLGMAVTQSYSMPHTPE
DFLAGMDDRMDCSSETGANLDSTDIALGDNIDSTDDLVSSLQLSEFPNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_026320226 [XP_026320226] transcriptional coactivator YAP1 isoform
X2 [Hyposmocoma kahamanoa]. 44..58
MALNTDGEQKSNLVLRVDQDSETVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGSHIPDELGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKSLAAQAVTNSVQHQSAETLLSQNTAQTINSPTTAAAKSTSSNTTTDPLG
SLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPVGSTGAAGGDWASASLQACQQKLRLQSLQLERER
LKHRQQEIRLQQELMARQASSIVSSLSGSTTVASTELPLDPFLSGLTDHQRQESADSGLGMAVTQSYSMPHTPED
FLAGMDDRMDCSSETGANLDSTDIALGDNIDSTDDLVSSLQLSEFPNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_026320227 [XP_026320227] transcriptional coactivator YAP1-A isoform
X3 [Hyposmocoma kahamanoa]. 44..58
MALNTDGEQKSNLVLRVDQDSETVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGSHIPDELGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKSLAAQAVTNSVQHQSAETLLSQNTAQTINSPTTAAAKSTSSNTTTDPL
GSLPDGWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPVGSTGAAGGDWASASLQACQQKLRLQSLQLERE
RLKHRQQEIRLQQELMARQASSIVSSLSGSTTVASTELPLDPFLSGLTDHQRQESADSGLGMAVTQSYSMPHTPE

DFLAGMDDRMDCSSETGANLDSTDIALGDNIDSTDDLLSEFPNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

rs:XP_026320229 [XP_026320229] transcriptional coactivator YAP1 isoform X4 [Hyposmocoma kahamanoa]. 44..58
MALNTDGEQKSNLVLRVDQDSETVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGSHIPDELGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKSLAAQAVTNSVQHQSAETLLSQNTAQTINSPTTAAQHLQRTPVGSTGA
AGGDWASASLQACQQKLRLQSLQLERERLKHRQQEIRLQQELMARQASSIVSSLSGSTTVASTELPLDPFLSGLT
DHQRQESADSGLGMAVTQSYSMPHTPEDFLAGMDDRMDCSSETGANLDSTDIALGDNIDSTDDLVSSLQLSEFPN
DILLDDVQSLINSTPSKPDNVLTWL PLRMRQLPKSFFNPP

rs:XP_026320230 [XP_026320230] transcriptional coactivator yorkie isoform X5 [Hyposmocoma kahamanoa]. 44..58
MALNTDGEQKSNLVLRVDQDSETVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQPPLHHQHTKQRSYDVGSHIPDELGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKSLAAQAVTNSVQHQSAETLLSQNTAQTINSPTTAAQHLQRTPVGSTGA
AGGDWASASLQACQQKLRLQSLQLERERLKHRQQEIRLQQELMARQASSIVSSLSGSTTVASTELPLDPFLSGLT
DHQRQESADSGLGMAVTQSYSMPHTPEDFLAGMDDRMDCSSETGANLDSTDIALGDNIDSTDDLLSEFPNDILLD
DVQSLINSTPSKPDNVLTWL PLRMRQLPKSFFNPP

rs:XP_026373987 [XP_026373987] protein **FAM181**B [Ursus arctos horribilis]. 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAHGAQTVAVPPHGK
AAPRREASQAAAAASLQSRSLAALFDSLSHVPGGDERAGGSAAAPVVGLGGAGAGGSGGDAAGPVGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEPPPAMVGSLLYSESWSSPGCPPTKKPPLAAPRGGLTLNEPLRPLYPSAADSPGGEDGPGL
LASFAPFFSDCALPPPPPPHQVSYEYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_026476618 [XP_026476618] transcriptional coactivator YAP1-like [Ctenocephalides felis]. 46..60
MALNQDLEQQKPHHIVTMDQNSDSDLQALFDSVLKPDSTKKPLQVPFRMRNLPNSFFNPPSTGSKSPSI
SHSRENSADSAFGSAAGGGSAGAGGQVTVPGLQVSHSRAHSSPASLQQTYNGSVLGAQTQAQQQHHHMKQRSYDV
VSAAQLQEELGPLPPGWEQARTLEGQIYYLNHVTRTTTWDDPRKTLAAQAAAQHQSADTLLSAPAQAQQAQTAVS
KATSPTNDALGPLPEGWEQAATAEGEIYFINHQARTTSWFDPRIPTHLQRSPGTCVPGHTAAMQQSWLAGNGGGT
AANAVSGTGPVGATVGGQSSVVHQASQQKLRLQQLQQERERLKQRQHEIRMQELMRQQTSTELQMDPFLSGVTDH
SRQESADSGLGLGNPYSMPHTPEDFLANIDDNMDCASESGAAMDATDISALSDNIDSTEDLVPSLQLGEDFSSDI
LEDVQSLINPVAKPDNELTWL PFRMRNLPNSFFNPP

rs:XP_026465940 [XP_026465940] transcriptional coactivator yorkie-like, partial [Ctenocephalides felis]. 46..60
MALNQDLEQQKPHHIVTMDQNSDSDLQALFDSVLKPDSTKKPLQVPFRMRNLPNSFFNPPSTGSKSPSI
SHSRENSADSAFGSAAGGGSAGAGGQVTVPGLQVSHSRAHSSPASLQQTYNGSVLGAQTQAQQQHHHMKQRSYDV
VSAAQLQEELGPLPPGWEQARTLEGQIYYL PFRMRNLPNSFFNPP

rs:XP_026475527 [XP_026475527] transcriptional coactivator yorkie-like [Ctenocephalides felis]. 46..60
MALNQDLEQQKPHHIVTMDQNSDSDLQALFDSVLKPDSTKKPLQVPFRMRNLPNSFFNPPSTGSKSPSI
SHSRENSADSAFGSAAGGGSAGAGGQVTVPGLQVSHSRAHSSPASLQQTYNGSVLGPQTQAQQQHHHMKQRSYDV
VSAAQLQEELGPLPPGWEQARTLEGQIYYLK PFRMRNLPNSFFNPP

rs:XP_026531432 [XP_026531432] transcriptional coactivator YAP1 [Notechis scutatus]. 84..98
MDVAGQPQQAPSGAAAAPQPSSAQPQPTGQPSPPAPQPGGGAVSGPPPAGHQVVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPALLGTVSPVALTPSVV
VPGGTPSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKTLLSQMNVPAPTSPPVQQNIM
NSATGPLPEGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKSSWHLKFFPPPVHPPFPQSFLNWQELALRSQ
LPSMEQDGTQNRVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGD

TINQSSIPSHQNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLT
WL PMRLRKLPDSFFKPP

rs:XP_026535010 [XP_026535010] protein **FAM181**A [Notechis scutatus].
142..156
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHHHHHHHHHL
QPQLPPARERRPPEGRARGLSPESSLGRGHGAPGPAKGDKASKAPERLGGEQQQQQQQQAGTSEAGARPDQVPMR
KRQLPASFWEEPRPAPGSPGVVSGVIFPVGVCSSPSSSSSPSSSSKDLPPYEGKKNIIGLDGGGTGTVPESPQRR
PEAEDALKGLRTWGCCPFQYHGPQASPGVYPPPLPAALPPAAPFSALGSWRKDAPSPTEGEAFCQPGQKVYRPVV
WKPIPTKPAAPPLIFSVFSYL PMRKRQLPASFWEEP

rs:XP_026536299 [XP_026536299] protein **FAM181**B [Notechis scutatus].
239..253
MAVQAAPLPPPHHPFGPFGFPAADFGALVEKSCYGGDGALLLLEGGVGGATDGSCGALDGCNEAADFRE
ATRELLSFIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCTGLLGGNAEAASGTGPGSVPGPAAAAPASKQA
PASTAPSSGGGAAAPSSSSSSCKLPPPAKRESKSLAALFDSWRASPFQPGGAPTTLVATPDSAPAGPGHGASGLQ
DRATAAAVVPPAPLACKKVPLRNRNLPRSFFTEPAPNRAPNPAGLEGGAAAPSVAEELFELLTAPDYRALLKEAA
EPPPPPPPVFPGSALQAAAELPLEPPLYEPLPSLAPLLYAETPLRPLPALYAAVAAVSDPAAPFFADCPPLPPPP
AMPYDYGYSRGAPYSSL PLRNRNLPRSFFTEP

rs:XP_026561201 [XP_026561201] protein **FAM181**A [Pseudonaja textilis].
145..159
MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHHHHHHHHHH
LQPQLPPARERRPPEGRARGLSPERSLGRGHGASGPAKGDKASKAPERLGGEQQQQQQQQQQAGTSEAGARPDQV
PMRKRQLPASFWEEPRPAPGSPGVVSGVIFPVGVCSSPSSSSSPSSSSKDLPPYEGKKNIIGLDGGGTGTVPESP
QRRPEAEAALKGLRTWGCCPFQYHGPQASPGVYPPPLPAALPPAAPFSALGSWRKDAPSPTEGEAFCQPGQKVYR
PVVWKPIPTKPSAPPLIFSVFSYL PMRKRQLPASFWEEP

rs:XP_026562550 [XP_026562550] protein **FAM181**B [Pseudonaja textilis].
223..237
MAVQAAPLPPPHHPFGPFGFPAADFGALVEKSCYGDGGGTLLLLEGGVGGATDGSCGALDGCNNEAADF
REATRELLSFIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCTGLLGGNAEAAPGTGPGSVPGPAVVAAAVP
ASKQLPPPAKRESKSLAALFDSWRSSPFQPGGAPTTLVATPDSAPVGPGHGASGLQDRAASASASAVVPPAPLAC
KKVPLRNRNLPRSFFTEPAAPNRAPNPAGLEGGAAAAPSVAEELFELLTAPDYRALLKEAAEPPPPVFPGSALQA
AAELPLEPPLYEPLPSLAPLLYAETPLRPLPALYAAVAAVSDPSAPFFADCPPLPPPPAMPYDYGYSRGAPYSSL
PLRNRNLPRSFFTEP

rs:XP_026562669 [XP_026562669] transcriptional coactivator YAP1 isoform
X1 [Pseudonaja textilis]. 84..98
MDVAGQPQQAPSGAAAAPQPSSAQPQPTGQPSPPAPQPGGGAVSGPPPAGHQVVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPALLGTVSPVALTPSGV
VPGGTPSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKTLLSQMNVPAPTSPPVQQNIM
NSATGPLPEGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLASQSPPGGVLGGGTS
NQQQQIRLQQLQMEKERLRQKHQELLRQVRPQALRNINPSTANAPKRQELALRSQLPSMEQDGTQNRVSSPGMSQ
ELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSIPSHQNRFPDYLEA
IPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_026562670 [XP_026562670] transcriptional coactivator YAP1 isoform
X2 [Pseudonaja textilis]. 84..98
MDVAGQPQQAPSGAAAAPQPSSAQPQPTGQPSPPAPQPGGGAVSGPPPAGHQVVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPALLGTVSPVALTPSGV
VPGGTPSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKTLLSQMNVPAPTSPPVQQNIM
NSATGPLPEGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLASQSPPGGVLGGGTS
NQQQQIRLQQLQMEKERLRQKHQELLRQALRNINPSTANAPKRQELALRSQLPSMEQDGTQNRVSSPGMSQELRT
MTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSIPSHQNRFPDYLEAIPGT
NVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWLPMRLRKLPDSFFKPP

rs:XP_026562671 [XP_026562671] transcriptional coactivator YAP1 isoform
X3 [Pseudonaja textilis]. 84..98

MDVAGQPQQAPSGAAAAPQPSSAQPQPTGQPSPPAPQPGGGAVSGPPPAGHQVVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPALLGTVSPVALTPSGV
VPGGTPSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKTLLSQMNVPAPTSPPVQQNIM
NSATAMNQRISQSAPVKQPPPLASQSPPGGVLGGGTSNQQQQIRLQQLQMEKERLRQKHQELLRQVRPQALRNIN
PSTANAPKRQELALRSQLPSMEQDGTQNRVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVP
RTPDDFLNSVDEMDTGDTINQSSIPSHQNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILND
MESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_026562672 [XP_026562672] transcriptional coactivator YAP1 isoform
X4 [Pseudonaja textilis]. 84..98
MDVAGQPQQAPSGAAAAPQPSSAQPQPTGQPSPPAPQPGGGAVSGPPPAGHQVVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPALLGTVSPVALTPSGV
VPGGTPSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKTLLSQMNVPAPTSPPVQQNIM
NSATAMNQRISQSAPVKQPPPLASQSPPGGVLGGGTSNQQQQIRLQQLQMEKERLRQKHQELLRQALRNINPSTA
NAPKRQELALRSQLPSMEQDGTQNRVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPD
DFLNSVDEMDTGDTINQSSIPSHQNRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSDILNDMESV
LAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_018670705 [XP_018670705] uncharacterized protein LOC100178849
[Ciona intestinalis].>tr:A0A1W5BEC6_CIOIN [A0A1W5BEC6] SubName:
Full=uncharacterized protein LOC100178849
{ECO:0000313|RefSeq:XP_018670705.1}; 527..541
MINNEARARSRLLTTPKLHRRVSQSQSSTKGKAEYKCPPISTKDATNLLTDGFTENSQTNLSPRRPSIV
PARKVSPTDGNCSPLSPANGVSAACTAMANACSHDHDYISVEQPRIRRQPPITPSQISPASTVLQPRCVNSDRTN
VSSLTAREDDSCYCPDIKSNRPIQQPVPPPKLLQPTIPNHAKPPREARCTLRRRYFRQNDTGPSDKATATTEELS
KNKLVFVSTSKTAEPRTHSRKLKQLSEERRPNDLAQSEVGPTACLSKMEESVAPQVVNNSDFNIKTDKLTVAWLS
LVNSVGKGDANEKNLPDVPGEDIQAHPDLNHENQHSSAPLACASPNPPKVQQIGGDTDSCIGCPTKCNQHETDSA
YSSLASSLCSPPPTSANVPLLSGEFRPSSSSRPASGSRPPSGGKRVAPCSLSSSSSSSCATSSDDDSDMSASSPR
SDICRRDQMINPMIDDSHTHKPVVDKPHNSRSSATRKGHKVVTTKNGKKFLRQKASSKQIMAGHLVLPTPPHKKP
SSKKDSVPMRLRALPTSFWQEPNRVNPSPYSVLPPVQPLFRQGYADNVADIRPVTPPAELENEVCSVDEVRGDSP
DKSTIINGGDPDLLFRLFDSVEPQNRSVAIKNKRGRPKKTSREMPPPRLKLDNNPCIIQSITEKLFPKLTIDRGC
ISMHAADKSFNLEEDFGSYVSDDKDYSAIGLYALSGQQGRVLDDEQETSDEHMHVMSPAAMTRVTSLSLPQLSVN
QDYSQMLSEVAAVL PMRLRALPTSFWQEP

rs:XP_009859006 [XP_009859006] transcriptional coactivator YAP1 isoform
X1 [Ciona intestinalis].>tr:A0A1W3JPW8_CIOIN [A0A1W3JPW8] SubName:
Full=transcriptional coactivator YAP1 isoform X1
{ECO:0000313|RefSeq:XP_009859006.1}; 50..64
MDMEENNEPTTQTTFTHHNQIIHVRQDSASELEALFNTVMNPNFKSKSLPMKARNLPKSFFTQPDKPRQ
QAAYHHGHSQSVGGLVAPNSVQINHSRSSSSDSNASHASAIHATNTNNNNGSSVGSTTMAPGSPMNGNINHKSNY
PMSPAQRRVAHGAFVNSQGHGSLQLPQVSHSRSKSSPASLQLMDIGSLSVKASDIPHDMPLPHGWSAAKTADGQQ
YYMNHNDRSTTWEDPRIGILKQQRQNQVVMQNQSIATNIHQQVAPSHSPAHNIQSDVSQIPLPSGWEQAATPQGE
IYFINHQTKSTSWVDPRFQGITPTNNNNPPNNSQLQQQLMKVNQMDISSVSQSRPTTTMPAQQQSMLKHLVQEKE
HLMRRQLMKQKQLSNPGMENFMGGGNPSFHQRDASLDSGVGMGSNYSLPRTPDGFLNNVEEMETGDVSRRVHGNP
QPATQQHTHTNNQRFPDFLDTLPASSVDFTSSPVPTSGGQRVCTTSASLDGSELVPSLQDSLPQDFDVESMLNHV
KTENMDNGMIWL PMKARNLPKSFFTQP

rs:XP_002130260 [XP_002130260] transcriptional coactivator YAP1 isoform
X2 [Ciona intestinalis].>tr:A0A1W2WKP2_CIOIN [A0A1W2WKP2] SubName:
Full=transcriptional coactivator YAP1 isoform X2
{ECO:0000313|RefSeq:XP_002130260.1}; 50..64
MDMEENNEPTTQTTFTHHNQIIHVRQDSASELEALFNTVMNPNFKSKSLPMKARNLPKSFFTQPDKPRQ
QAAYHHGHSQSVGGLVAPNSVQINHSRSSSSDSNASHASAIHATNTNNNNGSSVGSTTMAPGSPMNGNINHKSNY
PMSPAQRRVAHGAFVNSQGHGSLQLPQVSHSRSKSSPASLQLMDIGSLSVKASDIPHDMPLPHGWSAAKTADGQQ
YYMNHNDRSTTWEDPRIGILKQQRQNQVVMQNQSIATNIHQQVAPSHSPAHNIQSDVSQIPLPSGWEQAATPQGE
IYFINHQTKSTSWVDPRFQGITPTNNNNPPNNSQLQQQLMKVNQMDISSVSQSRPTTTMPAQQQSMLKHLVQEKE
HLMRRQLMKQLSNPGMENFMGGGNPSFHQRDASLDSGVGMGSNYSLPRTPDGFLNNVEEMETGDVSRRVHGNPQP

ATQQHTHTNNQRFPDFLDTLPASSVDFTSSPVPTSGGQRVCTTSASLDGSELVPSLQDSLPQDFDVESMLNHVKT
ENMDNGMIWL PMKARNLPKSFFTQP

rs:XP_026841171   [XP_026841171] transcriptional coactivator yorkie isoform
X1 [Drosophila persimilis].   65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSDANPGPSGQGPTYPENSAEFPNSAANTIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSDVLQTTKQTTTSTIANSLGPLPDGW
EQAVTDSGDIYFINHIDRTTSWIDPRMQSGLTGLDCPDNLVSSLQIEDNICTNLFNDAQTIVNPPSSHKPDDLEW
YKIN PFRMRKLPNSFFTPP

rs:XP_002016582   [XP_002016582] transcriptional coactivator yorkie isoform
X2 [Drosophila persimilis].   65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNY
NVRSRSDANPGPSGQGPTYPENSAEFPNSAANTIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLG
ALPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSESGLTGLDCPDNLVSSLQIEDNICT
NLFNDAQTIVNPPSSHKPDDLEWYKIN   PFRMRKLPNSFFTPP

rs:XP_019889908   [XP_019889908] transcriptional coactivator yorkie isoform
X1 [Ooceraea biroi].>tr:A0A3L8DQS6_OOCBI [A0A3L8DQS6] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:RLU22800.1};   46..60
MALNQDVEQLSKSNLVVRIDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPESFFNPPSAGSKSPSI
SHSRENSADSAFGAAVVATPNGGTERAGGGAGGGAPTGGAAGGGNAAGGGNAAGAAGTGGGAAGGAAAGGGTGGG
GANNPAGAVAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGP
LPHGWEQARTAEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNSLGPLPDGWEQARTAEGELYFIN
HQTRTTSWFDPRIPAAHLQQRSPASNAMLPQNWLQQPPSAIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIMR
QQELMLRQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDMS
TLNDPTDDLLPSLQLSDADFGSDILDDVQSLINPNTTKPENVLTWL PLRMRNLPESFFNPP

rs:XP_011351605   [XP_011351605] transcriptional coactivator yorkie isoform
X2 [Ooceraea biroi].   46..60
MALNQDVEQLSKSNLVVRIDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPESFFNPPSAGSKSPSI
SHSRENSADSAFGAAVVATPNGGTERAGGGAGGGAPTGGAAGGGNAAGGGNAAGAAGTGGGAAGGAAAGGGTGGG
GANNPAGAVAVAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGP
LPHGWEQARTAEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNSLGPLPDGWEQARTAEGELYFIN
HQTRTTSWFDPRIPAHLQQRSPASNAMLPQNWLQQPPSAIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIMRQ
QELMLRQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDMST
LNDPTDDLLPSLQLSDADFGSDILDDVQSLINPNTTKPENVLTWL   PLRMRNLPESFFNPP

rs:XP_026867400   [XP_026867400] protein **FAM181**A [Electrophorus
electricus].   121..135
MASSDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHAHRITDASA
PKITEDKPIILTHERAKNMSHLNEKQELNMRAGEDLDLNLNTEKQNLSGQVPMRKRQLPASFWEEPRSSQGSREY
FEYAWKRSSNGIVRYESAESGGEKRIKVHDEQKANLLLSNRRGTSDTEPLKVDLTSTHVHLCGCCPFQYHGNHIF
QSHLIAPHTNIPDVGLRSKIYGNEFEDGLTNNTKHVVVKPIPTKPVSSSIFSVFGFI   PMRKRQLPASFWEEP

rs:XP_026868543   [XP_026868543] transcriptional coactivator YAP1 isoform
X1 [Electrophorus electricus].   45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAVVPPSLPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTITPQHVRAHSSPASLQLGAVSPGTLAGMTPAGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQSTTWQDPRKAMLQINQATPGSPAPVQQQNLLNPASGPLPDGWEQAITAEGEIYYINHKNKTTSWLDPRL
DPRYALNQQRISQSAPVKPGAPLPPSPQNAPILGGNSQMRLQQLQMDKERLRLKHQELLRQRPQELALRNQLATS
MEQDGGSQNPVSSPSMPQDARSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSL
GPASMATQPNRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_026868544 [XP_026868544] transcriptional coactivator YAP1 isoform
X2 [Electrophorus electricus]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAVVPPSLPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTITPQHVRAHSSPASLQLGAVSPGTLAGMTPAGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQSTTWQDPRKAMLQINQATPGSPAPVQQQNLLNPASALNQQRISQSAPVKPGAPLPPSPQNAPILGGNSQ
MRLQQLQMDKERLRLKHQELLRQRPQELALRNQLATSMEQDGGSQNPVSSPSMPQDARSMTTNSSDPFLNSGTYH
SRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLGPASMATQPNRFPDYLDAIPGTDVDLGTLEGESMAVEG
EELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRMRKLPDSFFKPP

rs:XP_026851499 [XP_026851499] protein **FAM181**B [Electrophorus
electricus]. 156..170
MAVQTAIMNSQFLGFCFPGSVMEFGAEKVLEGRLLGEVDGEGDVRQTSRDLLSFINSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGITAPVSMSAQESCKRPDSSQAPASVLQSKMPPKRDGLQESLQSKSLAALFNAA
QEVRGERPRKPPLRHRNLPRSFFTEPASSSSVTSTSGMSLKDLERGNPDAAEFFELLGPDYSNMVSEQEVFHTPS
PRIQQGSGGPEPGVLDSHHFVTGGFLYAEPWGTNSVQAYKKTEGTRTGAAQPALYGSTQPPGPAGAPCSLSLYSF
SDYSGSQVSYDQTGGYGRTSFPPL PLRHRNLPRSFFTEP

rs:XP_026939436 [XP_026939436] protein **FAM181**B [Lagenorhynchus
obliquidens]. 221..235
MAVQAALLSTHPFVPFGFGGSPDGLGSAFGALDKGCCFEDEETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAASAQTVPVQAHGK
AAPRREASQAAAAASLQSQSLAALFDSLSHVPGAADPAGVAEAAPAAGLVGAGAGGVGGDAAGPAGGPAVPGARK
VPLRARNLPPSFFTEPSRAGGGGGCGPSGPGVSLGDLEKGAEAAEFFEMLGPDYGAGTEAGVLLAAEPLDVLLTG
AAVLRGPPELEPGLFEPPPAMGGSLLYPEPWSAPGGPTTKKSPLAAPRGGLTLNEPLRPLYPAAADSPGGDDGPG
LLASFTPFFSDCALPPPPPPPQVSYDYSAGYSRTAYASLWRPDGIWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_010748515 [XP_010748515] transcriptional coactivator YAP1 isoform
X1 [Larimichthys crocea]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDSRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAASQHPISGAPVHAHSLSNPASTTQPQNINPDAGPLPEGWEQAVTADGEVYYIDHINKTTAWFDPR
LAQKMNPGILGLALQQRQEKERLRCKQQGLPPQITPQEAGGRNQMPGGMDHDRNTQTLVPSLDVRIRAPNHEPTL
NGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDTGETSSMTLQESMPVLPMSEGEELMPSIPEGLSSDLLM
DMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

rs:XP_010748523 [XP_010748523] transcriptional coactivator YAP1 isoform
X2 [Larimichthys crocea]. 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDSRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRLSQLQSAASQHPISGAPVHAHSLSNPASTTQPQNINPDAAQKMNPGILGLALQQRQEKERLRCKQQGLPPQI
TPQEAGGRNQMPGGMDHDRNTQTLVPSLDVRIRAPNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMD
TGDTGETSSMTLQESMPVLPMSEGEELMPSIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

rs:XP_010732225 [XP_010732225] protein **FAM181**A [Larimichthys
crocea].>tr:A0A0F8AUS3_LARCR [A0A0F8AUS3] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KKF12131.1}; 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYGC
TKPMGTIHQSVKVAEKSSPDAQSVENVGCAVEQVPMRKRQLPASFWEEPKLTQTKREHTHLGVKRNHAGTSEGSE
NEKRKKSYDDDAKANLSASSRRNTADKDSLKLDLTSHHCVSVCACCPFQYHGHQVLHSHIVVPHPPLGLWSKAAG
SEIERPEHPYGQKIHTHVVVKPIPTKPTVQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_010738019 [XP_010738019] transcriptional coactivator YAP1
[Larimichthys crocea]. 45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGALTPHHVRAHSSPASLQLGAVSGGSLSGMPPAGASPQHLRQSSYEIPDDMPLPPGWEMAKTASGQRYF
LNHIDQTTTWQDPRKALLQMNQAAPASSVPVQQQNLMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFALNQQRITQSAPVKQGGPLPPSIHSAVVGGNNQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPTSMDQ
DGSTNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLQPSMA

TQPSRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMESVLAATRIDKESFLTWL
PMRMRKLPDSFFKPP

rs:XP_019128567 [XP_019128567] protein **FAM181**B [Larimichthys crocea].
155..169
MAVQAAIMNPQFMNFCFPGSVMEYDMEKSLDGSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNIAEAPVKRQGSPLAQPSPLQSKILPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSDQDLYQSMPL
RVQQEMGGPDPASYDSHHLVGGLLYSEPWTSCSGASKKLGGSLRSGPVQPPVYCPSSEATGPIEDHALCTLAFPN
FFTDCSIPQVTYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

rs:XP_007645663 [XP_007645663] protein **FAM181**A [Cricetulus
griseus].>rs:XP_027275367 [XP_027275367] protein **FAM181**A [Cricetulus
griseus].>tr:G3HU80_CRIGR [G3HU80] SubName: Full=**FAM181**A
{ECO:0000313|EMBL:RLQ65388.1}; SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:EGW13383.1}; 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVTEPHLQ
RGPEERPGQLPLHPCPESNPGGGGGYKEKALGTPFREECLSKEQSFQGLNPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPREASLYENKKNCKGLESLGPETAPAPLPMSPRVLADMEPLKMSGVSLVGSLDAWSYCPFQ
YHGQPIFPSLPGVLPQGPVPSLGLWRKSPASPVELAHFCKDVDSSGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027263749 [XP_027263749] protein **FAM181**B [Cricetulus griseus].
218..232
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGAPAGALLSGSEGGDLREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPSAADAPAKRPPGAPGAPTVAAPAHCK
ATPRREATQAAAAASLQSRSLAALFDSLHHVPGVAEPAGGAVAVPVPGLGAASAAGDGASTAGSSATPGAKKVPL
RARNLPPSFFTEPSRVGGSGSGGCGCGPSSQGVSLGDLEKGAEAVEFFELLAPDFGAGNDSGVLLAAEPLDAFPT
GATVLRGPLELESGPFEPPAMVGNPLYSEPWSAPSCPQTKKPPLAGVRSGVTLNEPVRLLYPTALDSPGGEDTPA
LASFAPFFPDCALPPPHQVSYDYSAGYSRAVYPSLWRPDGFWEGASGEDRAHTV PLRARNLPPSFFTEP

rs:XP_027270966 [XP_027270966] transcriptional coactivator YAP1 isoform
X5 [Cricetulus griseus]. 72..86
MEPAQQPPPQPAPQGPVPPSAPAPPSGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQ
TVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTVVSGPAATPAAQ
HLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPTPASTAVPQTLMNSASGPLP
DGWEQAMTQDGDVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGNSSQQQQMQL
QQLQMEKERLRLKQQELLRQVRPQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVD
LGTLEGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027270967 [XP_027270967] transcriptional coactivator YAP1 isoform
X6 [Cricetulus griseus]. 72..86
MEPAQQPPPQPAPQGPVPPSAPAPPSGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQ
TVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTVVSGPAATPAAQ
HLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPTPASTAVPQTLMNSASGPLP
DGWEQAMTQDGDVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGNSSQQQQMQL
QQLQMEKERLRLKQQELLRQAIRNINPSTANAPKCQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTL
EGDAMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027270968 [XP_027270968] transcriptional coactivator YAP1 isoform
X7 [Cricetulus griseus]. 72..86
MEPAQQPPPQPAPQGPVPPSAPAPPSGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQ
TVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTVVSGPAATPAAQ
HLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPTPASTAVPQTLMNSASGPLP
DGWEQAMTQDGDVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGNSSQQQQMQL
QQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRD

ESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDAMNIEGEEL
MPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027270969 [XP_027270969] transcriptional coactivator YAP1 isoform
X8 [Cricetulus griseus]. 72..86
MEPAQQPPPQPAPQGPVPPSAPAPPSGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQ
TVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTVVSGPAATPAAQ
HLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQLNVPTPASTAVPQTLMNSASGPLP
DGWEQAMTQDGDVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGNSSQQQQMQL
QQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNAVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQSRFPDYLEAIPGTNVDLGTLEGDAMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_001987073 [XP_001987073] GH20170 [Drosophila
grimshawi].>tr:B4J6D9_DROGR [B4J6D9] SubName: Full=GH20170
{ECO:0000313|EMBL:EDW01940.1}; 63..77
MSLNNKSNLSEKEIDDEDMLSPSPTKLSTNLVVRVNQDSDDNLQALFDSVLNPGDAKLPLQIPFRMRKL
PNSFFNPPAPLHSRANSADSTYDGSQTNINKTGVQSELQQQQQQPSLAQQSQPSHRSLAIHHFRARSSPASLQPN
YNVRTRNAESSASNNPSNQGQSGPAYPDNNVEFNSSPANNVEDVLNTCMGQGQDAPSLSTQTIHKKQRSYDVVSP
IQLQSQLGALPPGWEQAKTNDGQIYYLNHTTKTTQWEDPRIQFRQQQQQRAIVDRIKPNESGLSVLDCPDNLVSS
LQIGDNICNNIFNDAQTIINPPSSHKPDDLEWYKIN PFRMRKLPNSFFNPP

rs:XP_027322827 [XP_027322827] protein **FAM181**B [Anas platyrhynchos].
193..207
MAVPAALLSPHHHLLSFCFPAGGLLGYADLEKGYEGGGGGGGGGGGGGGGEAGDFKEATRDLLSFIDSA
SSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIIAAAAPPPSSSSSSSSSSSPAAAACPAKQPPPPRREASTAA
SSLQSKSLAALFGSLQPGRGSASGCGAAGGGGGGSSGGSAAAGGPRKVPLRARNLPPSFFTEPALPPRGPPPASK
ETEKGGGAEAAEFFELLGPDYGALLPEHAAPQDAFPAARLPAELGLEHGLYEAPLPSLPAAHHPLLGGLLYPEPP
WSPAGPCSPPKKSPPEALRPLYSGGAESGSETFGSFFPECPLAPPQVPYDYSTGYHRATYSGL
PLRARNLPPSFFTEP

rs:XP_027323768 [XP_027323768] transcriptional coactivator YAP1 isoform
X1 [Anas platyrhynchos]. 94..108
MDPGQPPAQQPQQQQPPAAAQPPASQQAPPQPPGAVVVAAAGGTPGGGAQPPGGGPPPAGHQIVHVRGD
SETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLG
AVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMN
VTAPTSPPVQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLA
PQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNINPSTANSPKHQELALRSQLPTMEQ
DGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQS
NIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027323779 [XP_027323779] transcriptional coactivator YAP1 isoform
X2 [Anas platyrhynchos]. 94..108
MDPGQPPAQQPQQQQPPAAAQPPASQQAPPQPPGAVVVAAAGGTPGGGAQPPGGGPPPAGHQIVHVRGD
SETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLG
AVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMN
VTAPTSPPVQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLA
PQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGS
QNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPS
HQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027323790 [XP_027323790] transcriptional coactivator YAP1 isoform
X3 [Anas platyrhynchos]. 94..108
MDPGQPPAQQPQQQQPPAAAQPPASQQAPPQPPGAVVVAAAGGTPGGGAQPPGGGPPPAGHQIVHVRGD
SETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLG
AVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMN
VTAPTSPPVQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLA

PQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQE
LRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAI
PGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_027323792   [XP_027323792] transcriptional coactivator YAP1 isoform
X4 [Anas platyrhynchos].   94..108
MDPGQPPAQQPQQQQPPAAAQPPASQQAPPQPPGAVVVAAAGGTPGGGAQPPGGGPPPAGHQIVHVRGD
SETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLG
AVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMN
VTAPTSPPVQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLA
PQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTM
TTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTN
VDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027323799   [XP_027323799] transcriptional coactivator YAP1 isoform
X5 [Anas platyrhynchos].   94..108
MDPGQPPAQQPQQQQPPAAAQPPASQQAPPQPPGAVVVAAAGGTPGGGAQPPGGGPPPAGHQIVHVRGD
SETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLG
AVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMN
VTAPTSPPVQQNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQE
LLRQALRNINPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_027323806   [XP_027323806] transcriptional coactivator YAP1 isoform
X6 [Anas platyrhynchos].   94..108
MDPGQPPAQQPQQQQPPAAAQPPASQQAPPQPPGAVVVAAAGGTPGGGAQPPGGGPPPAGHQIVHVRGD
SETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLG
AVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMN
VTAPTSPPVQQNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQE
LLRQVRPQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPR
TPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDM
ESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_027323815   [XP_027323815] transcriptional coactivator YAP1 isoform
X7 [Anas platyrhynchos].   94..108
MDPGQPPAQQPQQQQPPAAAQPPASQQAPPQPPGAVVVAAAGGTPGGGAQPPGGGPPPAGHQIVHVRGD
SETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLG
AVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMN
VTAPTSPPVQQNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQE
LLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDD
FLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVL
AATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_027324833   [XP_027324833] LOW QUALITY PROTEIN: splicing factor,
arginine/serine-rich 19 [Anas platyrhynchos].   268..282
MDSRDNPAATHPRAQGDVFSCPLSHRWGVQPRCPTTTPHSTPLLPPWGQTLLWGTGTGTPRGAATLTPL
SLPRRVSPGPGLPLRPDMAAGVIRPLAGLRLPSPFPHGLLLPARPEPDFPDLSEEEEEDDEEEEEEEDEEEAAED
STSCRGLELAGPNAAEATLRLLRFSELISGDIQRYFGRRGQEEPAGGRGTPEDCSSPRCTAREPGTASLPQPEAV
MARGGLWGXTQRLGPLAELFEYGVHRCLPPRAAGGKTQRLERKYGHITPMHRRKLPPSFWKEPGPGPAGLLHTGX
PDFSDLLANWTVEPGPELPGAGRELLPEAGRLGLDAEPFVGL   PMHRRKLPPSFWKEP

rs:XP_027428708   [XP_027428708] protein **FAM181**A isoform X1 [Zalophus
californianus].   232..246
MGVCYCLSSKGMMLPASMARRAAACDQTQSAQEAEPDARISLATPGLAQVCSGEPARPRRRRRRRGARG
RPAPSVSSVPFPGAASHQQSPRSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYL
QKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDGPGRLPLDSGQDSSPSGGGCYKEKALGNPYGEECLSREQTLQ
RQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPLDPETAPVPASPRAL

AEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPIYAGHPGVLPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQKV
YRPVVLKPIPTKPAVPPPIFNVFGYL   PMRKRQLPASFWEEP

rs:XP_027428709   [XP_027428709] protein **FAM181**A isoform X2 [Zalophus californianus].   211..225
MKEPLCPALMELTQPDARISLATPGLAQVCSGEPARPRRRRRRRGARGRPAPSVSSVPFPGAASHQQSP
RSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGR
GAEPHLKRGPEDGPGRLPLDSGQDSSPSGGGCYKEKALGNPYGEECLSREQTLQRQNPEAARPGQVPMRKRQLPA
SFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHCKGLEPLDPETAPVPASPRALAEKEPLKMSGVSLVGRVNAWS
CCPFQYHGQPIYAGHPGVLPQSPVPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFN
VFGYL PMRKRQLPASFWEEP

rs:XP_027434080   [XP_027434080] transcriptional coactivator YAP1 isoform X1 [Zalophus californianus]. 89..103
MDPGPPPQPPQPPPAAAQGQGPPAAPPPSGQGPAPAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
SLTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAP
TSPPVQQSLMTSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRVSQSAPVKQPPPLAPQSP
PGGVLGSGGSSQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGT
PNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPS
QQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027434081   [XP_027434081] transcriptional coactivator YAP1 isoform X2 [Zalophus californianus]. 89..103
MDPGPPPQPPQPPPAAAQGQGPPAAPPPSGQGPAPAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
SLTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAP
TSPPVQQSLMTSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRVSQSAPVKQPPPLAPQSP
PGGVLGSGGSSQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTPNPV
PSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027434082   [XP_027434082] transcriptional coactivator YAP1 isoform X3 [Zalophus californianus]. 89..103
MDPGPPPQPPQPPPAAAQGQGPPAAPPPSGQGPAPAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
SLTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAP
TSPPVQQSLMTSASGPLPDGWEQAVTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRVSQSAPVKQPPPLAPQSP
PGGVLGSGGSSQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSG
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_027434083   [XP_027434083] transcriptional coactivator YAP1 isoform X4 [Zalophus californianus]. 89..103
MDPGPPPQPPQPPPAAAQGQGPPAAPPPSGQGPAPAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
SLTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAP
TSPPVQQSLMTSASAMNQRVSQSAPVKQPPPLAPQSPPGGVLGSGGSSQQQQMRLQQLQMEKERLRLKQQELLRQ
VRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_027434084   [XP_027434084] transcriptional coactivator YAP1 isoform X5 [Zalophus californianus]. 89..103
MDPGPPPQPPQPPPAAAQGQGPPAAPPPSGQGPAPAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
SLTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAP

TSPPVQQSLMTSASAMNQRVSQSAPVKQPPPLAPQSPPGGVLGSGGSSQQQMRLQQLQMEKERLRLKQQELLRQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

rs:XP_027434085   [XP_027434085] transcriptional coactivator YAP1 isoform
X6 [Zalophus californianus]. 89..103
MDPGPPPQPPQPPPAAAQGQGPPAAPPPSGQGPAPAPGPPAPPGSQAAPQAPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
SLTPTGVVSGPAAAPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAP
TSPPVQQSLMTSASAMNQRVSQSAPVKQPPPLAPQSPPGGVLGSGGSSQQQMRLQQLQMEKERLRLKQQELLRQ
ELALRSQLPTLEQDGGTPNPVPSPGMSQELRTMTTSGSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027436606   [XP_027436606] protein **FAM181**B [Zalophus californianus].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAPDAPAKRSLAGPGAQNVAVPLHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGDERAGGSVAAPVAGLGGAGAGGSGGDAAGPAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEQPPAMVGSLLYSESWSAPGCPPTKKPPLAAPRGGLTLNEPLRPLYPSAADSPGGEDAPGL
LASFAPFFSDCALPTPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_027529683   [XP_027529683] protein **FAM181**A [Neopelma chrysocephalum].
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHPSKPPECGWR
RGAEDRGRGPQPEAPDPSPHGGAAAEKVMQTAEAEESLTGERVLQEQKPEAVRPDQVPMRKRQLPASFWEEPRPA
QSLTARTFPASPEGLPAPRDPPPYEGKKSKWSPDAASPESPPDPAPHAGEKDPAGVLSGRVGAWTCCPFPCPGTG
VYQPPGALPPSPFPGLGLWRKSAATLPAEVPHFCKEVDGTGQKLCRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_001627495   [XP_001627495] predicted protein [Nematostella
vectensis].>tr:A7SLN5_NEMVE [A7SLN5] SubName: Full=Predicted protein
{ECO:0000313|EMBL:EDO35395.1};   44..58
MERKNSNVVVHVRSDSGKELDALFHVIQSASAAVEQQPSSSSLPMKLRKLPPSFFKQPTILDPSKLAPD
DSSGLTISHSRANSSPASLSVPTSSAGPPNYSLHPAHSRTQSYGGSAYEESNQLPPGWEMRTSPTGQPYFMNHYE
QITTWQDPRKSQSTSNLNNSNSLPDGWEQAITPEGEVYFINHITRTTSWIDPRNIAIAHRRTSSQQSTFSGAAQQ
QDHRQKAMLERLQLEKEKLKKRQQQLLEQEILLKHGMLEEGGSKSLLGNLAREAALAQMPSQENTTSVHMRDESF
DSGLGMSSTGGYGYNTDVDLNGGGGSDSQMFDANYNSKELTSRSEGRTGSGRLPEFFDNIPGTNVDFGTIEGENT
PTNMETDDLGVGLDLNTDILNDVESVLTPNMSKIPDPNFLTWL   PMKLRKLPPSFFKQP

rs:XP_001636222   [XP_001636222] predicted protein [Nematostella
vectensis].>tr:A7RWP5_NEMVE [A7RWP5] SubName: Full=Predicted protein
{ECO:0000313|EMBL:EDO44159.1};   86..100
MASGSANSPQFFVGANGNMIREAVQSGCCRPQSQSADGYCLFTFFEENPRVAVERHFEEALKHFFSTER
AMEANQTKNVTDTRLLPMKQRNLPASFWCPPETDAIQLNKVHHGHTTFTGMVPYTVNQVMTTGRPRTTTRPVQRQ
DLPDSDPAPLLVSCRRLPVTSTDVIGTIAHAQSKQQARYMTIVHGPRPGDGFNPRYNSLLVQPNVFVELPRVHGE
PRSKSG   PMKQRNLPASFWCPP

rs:XP_027585196   [XP_027585196] protein **FAM181**A [Pipra filicauda].
127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHPSKPPECGWR
RGAEDRGRGPQPEAPDPSPHGGAAAEKVMQTAEAEESLTGERVLQEQKPEAVRPDQVPMRKRQLPASFWEEPRPA
QSLTARAFPASPEGLPAPRDLPPYEGKKSKWSPDAASPESPPDPAPHAGEKDPAGVLSGRVGAWTCCPFPCPGTG
VYQPPGALPPSPFPGLGLWRKSAATLPVEVPHFCKEADGTGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027606701 [XP_027606701] sentrin-specific protease 3 isoform X1 [Pipra filicauda]. 171..185

MAGRQRQGVIQPLAELRLPSPFPHSLLLPTHPEPDFHNLSEEEEEEEEEEEEEEEVEAAEENMRPEPAI
SSTAETTLRLLKFSELISCDIQRYFGRRGREEAAGTQPVPKDCESPRSAGAQPEAPRGSPGAVHRLGPLAELFEY
GVHRCLSPRAAGGRTQRLERKYGHITPMHRRKLPPSFWKEPGPTSLLHTGTPDFSDLLANWTVEPGPELPCAGRE
LPLEPGRPGLEAEPFPGL PMHRRKLPPSFWKEP

rs:XP_027606702 [XP_027606702] sentrin-specific protease 3 isoform X2 [Pipra filicauda]. 167..181

MAAGVIQPLAELRLPSPFPHSLLLPTHPEPDFHNLSEEEEEEEEEEEEEEEVEAAEENMRPEPAISSTA
ETTLRLLKFSELISCDIQRYFGRRGREEAAGTQPVPKDCESPRSAGAQPEAPRGSPGAVHRLGPLAELFEYGVHR
CLSPRAAGGRTQRLERKYGHITPMHRRKLPPSFWKEPGPTSLLHTGTPDFSDLLANWTVEPGPELPCAGRELPLE
PGRPGLEAEPFPGL PMHRRKLPPSFWKEP

rs:XP_027568317 [XP_027568317] protein **FAM181**B [Pipra filicauda]. 166..180

MAAPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAAPPPASCPPAACSTRPPPRREPAQAAGSSLQSKSLAALFGSLQRGRGA
AGGAEAKAGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPAPAARGPPAKEPEKGGGGAAEASEFFELLCPEYGAL
LPEHAAPPDAFGGRLPAELGLEHGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPPEPLRPLYAGGPEP
VPGGGGGSTEEPGGHLPAGFAPFFPECPLAPPQPPYDYGAGYHRAGYPGL PLRDRNLPPSFFTEP

rs:XP_027746068 [XP_027746068] protein **FAM181**A [Empidonax traillii]. 127..141

MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHPSKPSECGWR
RGAEDRGRGPQPEAPDSNPHGGAAAEKVMQTIEAEESLTGERVLQEQKPDAIRPDQVPMRKRQLPASFWEEPRPA
QSLTTRAFPASPEGLPAPRDPPPYEGKKSKRSPDAADPENPPDPAPHAGEKDPAGVLSGRMGAWTCCPFPCPGTG
VYQPPGALPPSPFPGLGLWRKSAATLPAEVPHFCKEADGTGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027763749 [XP_027763749] transcriptional coactivator YAP1-like [Empidonax traillii]. 86..100

MDPGQPQAQQPSQAAQPPAPQQQQPPQPPGAVSGAAAGAAQPPGGGPPPAGHQIVHVRGDSETDLEAL
FNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLT
PSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLKFCFLLKTNKNLIFQDERLLDSYPFAFLL
LCAEDGKELWVS PMRLRKLPDSFFKPP

rs:XP_027718445 [XP_027718445] uncharacterized protein LOC114043588 [Vombatus ursinus].>rs:XP_027718446 [XP_027718446] uncharacterized protein LOC114043588 [Vombatus ursinus].>rs:XP_027718447 [XP_027718447] uncharacterized protein LOC114043588 [Vombatus ursinus]. 215..229

MAAGVIRNLCDFRLQTPFHQPFLPSTGPRDPDFPETSEDEEEEDGEQEEDGEKQMEDLELAGCSPGFQR
SDQELGKGSTRPSPSSTEMTLQLLRFSELISCDIQKYFGQKTKDDDPDACNIYEDSRPPGKSARELYYADLMQIV
QSGDQEDEDPDIVGLPRGFDCQTRFISSRDRSQKLGPLVELFEYGLCQYARQRVSDSRRLRLEKKYGHITPMHKR
KLPQSFWKEPAPSSLCLLNTSTPDFSDLLANWTSDVAQELHSVGGRELGRHALEMDHLEEA
PMHKRKLPQSFWKEP

rs:XP_027725682 [XP_027725682] protein **FAM181**A [Vombatus ursinus]. 118..132

MASDSEVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCYPSRSGESHSK
RGPEDGRCRTPSNGSTEKGPGNPGMEENFPEEQTLQEQIPEACRPDQVPMRKRQLPASFWEEPRPAQSYSGGLDG
LSVHREVPAYEGKKSKKRPETLGSETAPVPASPRAEKESPKVPSASLMGRMSAWSCCPFQYHGQPIYQSPGGLPQ
SPVPGLGLWRKSPSSPGEMGHFCKEPGSPSQKVYRPVVLKPIPTKPGVPPPIFNVFSYI
PMRKRQLPASFWEEP

rs:XP_027704080 [XP_027704080] protein **FAM181**B [Vombatus ursinus]. 243..257

MAVQAAILSPHHFIPFCFPGSPGALGMDFGDLDKGCCYEEDETGGTGVALLGEAVAAEAAGGGGGGGDF
REATRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGMMTSSSASASGPAPSVSPSPGSAAAVPA

```
GAPEVPPKRLPAASPTTPGPQGKAPPKREGSQAAASLQSKSLAALFESLHQVRGNGGEKGGAGTLATVAGGGGGG
GGVGAEGGGSVVAAAGAGGGKKVPLRNRNLPPSFFTEPSRAGGCGPSGGGVTLRELEKGGEAVEFFELLSPDYCT
GGEVGGLLPSEPLDLFPAAVRAPQELEHIVYDPHPTVVAGLLYSEPWSTQCPPAKKPVPASNRGGGGLTLNETLR
ALYPGTSDSAASSLGSPGGEDTAGHLTPFSQFFPDCALPTPPPPHQMPYDYGVGYSRVAYSGL
      PLRNRNLPPSFFTEP

rs:XP_027705314   [XP_027705314] transcriptional coactivator YAP1 isoform
X1 [Vombatus ursinus].  89..103
      MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNVNPSTANSPKRQEIALRSQLPTMEQDG
GTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNI
PSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_027705316   [XP_027705316] transcriptional coactivator YAP1 isoform
X2 [Vombatus ursinus].  89..103
      MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGT
QNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPS
QQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_027705317   [XP_027705317] transcriptional coactivator YAP1 isoform
X3 [Vombatus ursinus].  89..103
      MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQN
PVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQ
NRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_027705318   [XP_027705318] transcriptional coactivator YAP1 isoform
X4 [Vombatus ursinus].  89..103
      MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPV
SSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

rs:XP_027705319   [XP_027705319] transcriptional coactivator YAP1 isoform
X5 [Vombatus ursinus].  89..103
      MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQEIALRSQLPTMEQDGGTQNPVSSPGMNQELR
TMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPG
TNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL     PMRLRKLPDSFFKPP
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rs:XP_027705320 [XP_027705320] transcriptional coactivator YAP1 isoform X6 [Vombatus ursinus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQVRPQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTM
TTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTN
VDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027705321 [XP_027705321] transcriptional coactivator YAP1 isoform X7 [Vombatus ursinus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQ
SPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTT
NSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVD
LGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027705322 [XP_027705322] transcriptional coactivator YAP1 isoform X8 [Vombatus ursinus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027705323 [XP_027705323] transcriptional coactivator YAP1 isoform X9 [Vombatus ursinus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
VRPQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTD
SGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSL
QEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027705324 [XP_027705324] transcriptional coactivator YAP1 isoform X10 [Vombatus ursinus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
ALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027705325 [XP_027705325] transcriptional coactivator YAP1 isoform X11 [Vombatus ursinus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
VRPQEIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDD
FLNSVDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVL
AATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_027705327 [XP_027705327] transcriptional coactivator YAP1 isoform X12 [Vombatus ursinus]. 89..103
MDPGQQPPQAPSQGQGQAPSQPPQGQGQGPPTGPGQQAPPGAPGSQAAPPPPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLSPSGVVSGPGTAPTGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQ
EIALRSQLPTMEQDGGTQNPVSSPGMNQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDSISQSNIPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATK
LDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_002399565 [XP_002399565] conserved hypothetical protein [Ixodes scapularis].>tr:B7PRF1_IXOSC [B7PRF1] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EEC09173.1, ECO:0000313|VectorBase:ISCW007670-PA};
45..59
MTRGDLIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNLPASFFQQPERSKSASHSR
ESSNDATFSPSSEATAAVVAAAAAVPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQQSYDLADEGSLPPGWEMAK
TSTGQRYFLK PMRLRNLPASFFQQP

rs:XP_014956207 [XP_014956207] transcriptional coactivator YAP1 isoform X1 [Ovis aries]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014956208 [XP_014956208] transcriptional coactivator YAP1 isoform X2 [Ovis aries]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSP
GMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPD
YLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014956209 [XP_014956209] transcriptional coactivator YAP1 isoform X3 [Ovis aries]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_014956210 [XP_014956210] transcriptional coactivator YAP1 isoform X4 [Ovis aries]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN

SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014956211 [XP_014956211] transcriptional coactivator YAP1 isoform X5 [Ovis aries]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVL
GGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014956212 [XP_014956212] transcriptional coactivator YAP1 isoform X6 [Ovis aries]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLE
GDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

rs:XP_014956206 [XP_014956206] transcriptional coactivator YAP1 isoform X7 [Ovis aries]. 84..98
MDPGPPPPQPAPQGQGPPPAQGPQGQGPPSAPGQPAPPGPPAAPQAPPAGHQIVHVRGDSETDLEALFN
AVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPT
GVVSGPAAAPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPV
QQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFGKAMNQRISQSAPVKQPPPLAPQSPQGG
VLGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNP
VSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQN
RFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

rs:XP_027813325 [XP_027813325] protein **FAM181**A [Ovis aries]. 130..144
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGPEDRPGRPLHLESGHGSSPSGGGGYKEKALGNPDREESLSKERTLHGPDPGAARPGQVPMRKRQLPASFWEEP
RPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTPVPTSPRAPAEKEPLKMPGVSLVGRVSAWSCCPFQY
HGQPIYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_027887762 [XP_027887762] transcriptional coactivator YAP1-like isoform X5 [Xiphophorus couchianus]. 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKATRQPPSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTSTGQRYFINHVHRTTTW
QDPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIVPETAPKVNPAILSLAMQQRLEKLRLKQGIPPQFAP
QVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMD
TGDSSEPPSMGLQESMPVLPINEDLMPGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL
PMRMRKFPDSFFKPP

rs:XP_027887763 [XP_027887763] transcriptional coactivator YAP1-like isoform X6 [Xiphophorus couchianus]. 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKATRQPPSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTSTGQRYFINHVHRTTTW
QDPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIVPETAPKVNPAILSLAMQQRLEKLRLKQGIPPQFAP
QEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTG
DSSEPPSMGLQESMPVLPINEDLMPGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

rs:XP_027900342 [XP_027900342] protein **FAM181**B [Xiphophorus couchianus].
246..260
MQVVGHKQRVKFPGFPSLLLFDVLTSSVLPPERSPSSSSVAVTSSLDCLWKLHEQHQEQVLIRRTKSCF
EETFSSGITVDATGVAAGLDRVMAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLS
FIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPLKRQGSPVNQQGPVQSKTLQKREGGQ
ANLQSKSLAALFSPVKEIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPD
YSNMVNEQDIYQGVPLRGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGQCKKPSEGLRSGPPQPPVYSQAEDTSV
PLDDNGLCTLTFPNFFPDCSISQVTYDLNGGYNKTHFSCL PMRHRNLPPSFFTEP

rs:XP_027901385 [XP_027901385] transcriptional coactivator YAP1 isoform
X1 [Xiphophorus couchianus]. 45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQASYEIPDEVPLPAGWEMAKTNSGQRYF
LKLQNSEKEQDISSHNEKTTTWQDPRKSLLQMNQPAPVPPSSVPVQPQNLMNPASGSLPEGWEQAVTQEGEIYYI
NHTNKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQQHRPQELALR
NQLPTSMDQDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDT
GDPLPASIASQPSRFPDYLDAIPGTDVDLGTLEGENMAVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFL
TWL PMRMRKLPDSFFKPP

rs:XP_027901386 [XP_027901386] transcriptional coactivator YAP1 isoform
X2 [Xiphophorus couchianus]. 45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQASYEIPDEVPLPAGWEMAKTNSGQRYF
LNHNEKTTTWQDPRKSLLQMNQPAPVPPSSVPVQPQNLMNPASGSLPEGWEQAVTQEGEIYYINHTNKTTSWLDP
RLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQQHRPQELALRNQLPTSMDQDGS
TNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPASIASQP
SRFPDYLDAIPGTDVDLGTLEGENMAVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

rs:XP_027855919 [XP_027855919] protein **FAM181**A [Xiphophorus couchianus].
102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQSLTSADNRC
ARGAERQRATATDQASSDAQHAQSVGGLMDQVPMRKRQLPASFWEEPRLTKARRDKSFLDLRRSSSSGTSDGGEN
EKRRRSQEDAQKTANSSSGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQFHGHQVLHSQIVVPHPPFGLWSKAAEP
QRSEHQYGQKLHTHVVVKPIPTKATAQSPIFSVFGFI PMRKRQLPASFWEEP

rs:XP_027982546 [XP_027982546] protein **FAM181**B [Eumetopias jubatus].
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGALLAGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAPDAPAKRSLAGPGAQNVAVPLHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGDERAGGSVAAPVAGIGGAGAGGSGGDAAGPAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEQPPAMVGSLLYSESWSAPGCPPTKKPPLAAPRGGLTLNEPLRPLYPSAADSPGGEDAPGL
LASFAPFFSDCALPTPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

rs:XP_007184309 [XP_007184309] protein **FAM181**A [Balaenoptera
acutorostrata scammoni]. 129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLK
RGSEDQPGRLPLDSGHSSSPSGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPR
PTHSYPVGLEGGLGPREGPPYEGKKHRKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPVYPGPAGALPQSPLPSLGLWRKSSASPSELAHFCKDVEGPGQKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

rs:XP_026812708 [XP_026812708] transcriptional coactivator YAP1
[Rhopalosiphum maidis]. 66..80
MSGLQQQQQEQHQQVSIKMEPTGPSSPTPAVNSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPLRM
RQLPKSFFNPPSTGSKSPSISHSRENSGDSAFGTAAAGQSCTGGPVPMHSRAHSSPASLQQTYAVGAAKQQQQQQ
QHAKQRSYDVSSAIDELGPLPQGWEQARTPEGQIYYLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQLLSPGNDS
GSSTNATSTPTNSPPHIHSTLQGTNKNVTLGPLPDGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQRAPTSG

AVLPSGSASWLLNGASGLSQSLQVTQQKLRLHSLQLERERLKSRQQEIIRQQDLMSRSGHTNNDLDPFLSCSSSS
VDHSRQESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDSQEMATLDVTDDLVPSLQL
GDEFGNDILDEVQLLIDPNNKPGSILTWL PLRMRQLPKSFFNPP

rs:NP_001029174 [NP_001029174] transcriptional coactivator YAP1 [Rattus norvegicus].>gp:DQ186898_1 [DQ186898] neuron-specific YAPdeltaC insert61 isoform [Rattus norvegicus] 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQAIRNINPSTANAPKCQTVRAGISSPQPVALTGAGWRDSECSVFSRDDSGIEDNDNQ
PMRLRKLPDSFFKPP

rs:NP_067402 [NP_067402] protein **FAM181**B [Mus musculus]. 215..229
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGATAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPRPASPSAADAPAKRPPGAPTVATPAHCKAAP
RREATQAAAAASLQSRSLAALFDSLRHIPGGAETAGGAEAVSVPGLGAASAVGDGAGTAVSSVAPGTRKVPLRAR
NLPPSFFTEPSRVGCGGASGVPSGQGVSLGDLEKGAEAVEFFELLAPDFGSGNDSGVLMAADPLDPFPAGATVLR
GPLELESGPFEQPAMVGNLLYPEPWNTPSCPQTKKPPVAGVRGGVTLNEPVRLLYPTALDSPGGEDAPALSSFTP
FFPDCALPPPHQVSYDYSAGYSRAVYPSLWRPDGVWEGASGEEGGHPD PLRARNLPPSFFTEP

rs:XP_002604434 [XP_002604434] hypothetical protein BRAFLDRAFT_122292 [Branchiostoma floridae].>tr:C3YGX4_BRAFL [C3YGX4] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EEN60445.1}; 222..236
MKEDGSFSRKGHSFIHSFTDFCNGGAAMVAFIFGSRLHLRGPSGPKMTQGEENAICGRAERTHQQGRKC
KMAQGSGGGPADADVKTLLNFVNLASSDIKAALDKSAPCKRSVDHRKYLQKQLKRFSQRRVLPRYVATRPVKDIT
ATTTPPAASLLKRRPESTSSVNSESSSGSGSESCGSEAGPILAESCHPIDLSMPDRELPGEKEQEAGLQDPAGAD
SVPLRKRALPASFWQEPGVQKGQSSSSRGSPSCSAEESSAGSPGKQDCQPAGETTAXPPRDITSHGLDRFPTAGA
ARTARVTAVPRVPPVPRVRPPSSLRVRPRSAAGSAAGTLRSPWPGAGARTVRPPPTKGVVLVLPGAEHFRLGGVQ
SVPVRTPPPRVRARTPQSAGGGTRAILPSMGPDKPSPLLVLTNHNNKTQNMETDSHKNCLNLPHEIPPTAHVGPG
IFRHYFVPRLLLRGLNFLPKDYIGYSRNGRFSVALL PLRKRALPASFWQEP

rs:XP_002598271 [XP_002598271] hypothetical protein BRAFLDRAFT_69626 [Branchiostoma floridae].>tr:C3YZL2_BRAFL [C3YZL2] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EEN54283.1}; 165..179
MRLDMTDSNPMLMELHPPPHPSQRLSPGGTPGSNPSPSPSHSPSCPSPRPSEVETDSLLSFMDTACNSI
KLALDRPSRSRRKVNHRKYLQKQIKRCTQKLSPGDGESDDKDDNASDKEAATANKPTSRRDSHIGAQSKSLAALF
DPNTLKRPVNPAPTRGRTRVPLRKRNLPPSFFTEPGNQSGPRGAFQTCTVAGSWPLDGYRHPGVSDSLDIFNPDI
ADLITNWQDESGHISDPSMSAHAMPGNTAMAAPGDHASIMLHMPSQPYGTNFNMNYPQTQSNQGLLTTAPQSWMS
GSPSYPSAPASNYPASRDDFSRVGYPSSSSAGLSGSLYAPQVHQMPSGLPDFPQAFGHGQAAIGQQWPNSLCYTY
L PLRKRNLPPSFFTEP

rs:XP_002590553 [XP_002590553] hypothetical protein BRAFLDRAFT_86233 [Branchiostoma floridae].>tr:C3ZLU1_BRAFL [C3ZLU1] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EEN46564.1}; 135..149
MAGKTGGKVGFPSGGKVGFSSGKRGASAPVSSSDEEEIEKEVQEPKEDYENIASPCSSTSSGPVYERQP
GFEKHGHEVVVPRRPKIKHKIKRKKMANFMLGGDHDFYTASRGRRKDGTMVPTPPSKGKPKRDTVPMRLRALPQS
FWQQPNNMNNNSPGSLYPVLPPVVNKEVSDEDLGQVVSVPTEIRPVTPPEERTETDVQEKERTVRKDEEIIPTKP
EKSVEKVTIKDDKEKTEKEVKKEKIDLVEEVVSGATVTVTTTAPPRTRTVRTVTSTVPNTDLLFSLFDGVDPETK
RQTVKLKRGRPKRIHLEGMNAPRPRSQDNDPYMVDNIAERLFPVLSLENRKQNTNPANPNVTTTLHYITLNGEDE
KSSVSLPAVRVETNYSQMLSELVMHI PMRLRALPQSFWQQP

rs:XP_001841862 [XP_001841862] conserved hypothetical protein [Culex quinquefasciatus].>tr:B0VZH8_CULQU [B0VZH8] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EDS31715.1, ECO:0000313|VectorBase:CPIJ000289-PA}; 65..79
MAFNSNSSSASNNNNNTASNTSASEENDGASKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQIPYRMR
KLPDSFFKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVNPVTGPNGLPIHHSRAHSSPASLGKIPAGLISSL

TGGGGSGSGVAQATGNSSKAQQQADSSSLGASSVAQQQQQQAQQGLPKQAIQHLHARGRSYDVSNLHANFGELPP
GWEQAKTQDGRIYYIK PYRMRKLPDSFFKPP

tr:G3V5K4_HUMAN   [G3V5K4] SubName: Full=Protein **FAM181**A
{ECO:0000313|Ensembl:ENSP00000452393}; Flags: Fragment;   129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTLVSMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALP   PMRKRQLPASFWEEP

tr:A0A183VN97_TRIRE   [A0A183VN97] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:VDP97832.1, ECO:0000313|WBParaSite:TRE_0000195501-mRNA-1};   38..52
MEGYDSRKPPSVRVTVLEDPNSSLQELFNPVSQRQQVPLHQRKLPKSFFVPPGDANETSRFSKLNSLHC
NERNSSDFVVFHSKANSSPACLDAALRTPVSVNAPNHAHQKSLDVASKYISEFSPDFSFSDSCSPGFIQRQTPLL
CRPTVAFAISDLPVGYDMAINESNQVYFLNHQTQETTWIPEKFQNWGMTPEELEQVHIRYAKQFLCTNPSANLNV
NIQQVGDFSYDFQFCRFNKEVAVEFIMIFSSLA   PLHQRKLPKSFFVPP

tr:A0A182GV27_AEDAL   [A0A182GV27] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KXJ73217.1, ECO:0000313|VectorBase:AALF016259-PA};
59..73
MAFNGSPGNNSSATSNTSEENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANAAQQ
AANNSSNVNSNKTQQPGSVNGGGASSGGDGSSAAAAVQQQQAQQQAAQQQSLTRQAILHSRGRSYDVSNQHAVY
GDLPPGWEQAKTQDGRIYYLNRRRNREPVLCQPVTASLAAMYACMRSISRTAVQLPSPVASTVHQTKPNQAESLI
SNLTGLKFYTKPFLPAGALIRSPNPSSD PLRMRKLPDSFFKPP

tr:A0A182H4T7_AEDAL   [A0A182H4T7] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KXJ71032.1, ECO:0000313|VectorBase:AALF021713-PA};
59..73
MAFNGSPGNNSSATSNTSEDNDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANAAQQ
AANNSSNVNSNKTQQPGSVNGGGASSGGDGSSAAAAVQQQQAQQQAAQQQSLTRQAILHSRGRSYDVSNQHAVY
GDLPPGWEQAKTQDGRIYYLK   PLRMRKLPDSFFKPP

tr:A0A0A9VUR8_LYGHE   [A0A0A9VUR8] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAF99448.1};   48..62
MSGNPDGRGVQQGSNLVVRIDHDSETELQALFDSVLKPEAKQRPQSKPFRMRNLPNSFFNPPSTGSKSP
SVSSISHSRENSADSAFGTTTTTMGGLTVNHPRAHSSPASLQQTYASASVVASSPQHLKQRSYDISSLDDLGPLP
LGWEQARTSEGQIYFLNHMTQTTTWEDPRKTAAAQQQAAQQRSQELLNTVATSPHPSTSPQPHQGKNGGVSPGST
AGLGPLPDGWEQAQTLEGEVYFINHRTKTTSWFDPRIPVHLQRAPAAGNVLPSWLQQSLSPSANIAASQQQKLRL
QSLQQERERLKVRQAEIMRQQELMLRDAPATTGLDPFLSGLADHSRQESADSGLGLGNNYSLPHTPDDFLSTMDD
NMDGVSEAGAEMGSLDSHELTISDNIDSTDDLVPSLQLGEEFSSDILDDVQALINPNSKPGNSLTWL
PFRMRNLPNSFFNPP

tr:A0A146LGQ5_LYGHE   [A0A146LGQ5] SubName: Full=Yorkie
{ECO:0000313|EMBL:JAQ06137.1};   48..62
MSGNPDGRGVQQGSNLVVRIDHDSETELQALFDSVLKPEAKQRPQSKPFRMRNLPNSFFNPPSTGSKSP
SVSSISHSRENSADSAFGTTTTTMGGLTVNHPRAHSSPASLQQTYASASVVASSPQHLKQRSYDISSLDDLGPLP
LGWEQARTSEGQIYFLNHMTQTTTWEDPRKTAAAQQQAAQQRSQELLNTVATSPHPSTSPQPHQGTHHEFAFVEV
NRVKLECKNGGVSPGSTAGLGPLPDGWEQAQTLEGEVYFINHRTKTTSWFDPRIPVHLQRAPAAGNVLPSWLQQS
LSPSANIAASQQQKLRLQSLQQERERLKVRQAEIMRQQELMLRDAPATTGLDPFLSGLADHSRQESADSGLGLGN
NYSLPHTPDDFLSTMDDNMDGVSEAGAEMGSLDSHELTISDNIDSTDDLVPSLQLGEEFSSDILDDVQALINPNS
KPGNSLTWL   PFRMRNLPNSFFNPP

tr:A0A0A9WFH8_LYGHE   [A0A0A9WFH8] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAG07202.1};   48..62
MSGNPDGRGVQQGSNLVVRIDHDSETELQALFDSVLKPEAKQRPQSKPFRMRNLPNSFFNPPSTGSKSP
SVSSISHSRENSADSAFGTTTTTMGGLTVNHPRAHSSPASLQQTYASASVVASSPQHLKQRSYDISSLDDLGPLP

LGWEQARTSEGQIYFLNHMTQTTTWEDPRKTAAAQQQAAQQRSQELLNTVATSPHPSTSPQPHQAVHLQRAPAAG
NVLPSWLQQSLSPSANIAASQQQKLRLQSLQQERERLKVRQAEIMRQQELMLRDAPATTGLDPFLSGLADHSRQE
SADSGLGLGNNYSLPHTPDDFLSTMDDNMDGVSEAGAEMGSLDSHELTISDNIDSTDDLVPSLQLGEEFSSDILD
DVQALINPNSKPGNSLTWL   PFRMRNLPNSFFNPP

tr:A0A0K8T574_LYGHE   [A0A0K8T574] SubName: Full=Yorkie
{ECO:0000313|EMBL:JAQ05452.1};   48..62
MSGNPDGRGVQQGSNLVVRIDHDSETELQALFDSVLKPEAKQRPQSKPFRMRNLPNSFFNPPSTGSKSP
SVSSISHSRENSADSAFGTTTTTMGGLTVNHPRAHSSPASLQQTYASASVVASSPQHLKQRSYDISSLDDLGPLP
LGWEQARTSEGQIYFLNHMTQTTTWEDPRKTAAAQQQAAQQRSQELLNTVATSPHPSTSPQPHQAVHLQRAPAAG
NVLPSWLQQSLSPSANIAASQQQKLRLQSLQQERERLKVRQAEIMRQELMLRDAPATTGLDPFLSGLADHSRQES
ADSGLGLGNNYSLPHTPDDFLSTMDDNMDGVSEAGAEMGSLDSHELTISDNIDSTDDLVPSLQLGEEFSSDILDD
VQALINPNSKPGNSLTWL   PFRMRNLPNSFFNPP

tr:A0A183KYQ6_9TREM   [A0A183KYQ6] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:VDP71499.1, ECO:0000313|WBParaSite:SCUD_0002020601-mRNA-1};   38..52
MEGYDSRKPPSVRVTVLEDPNSSLQELFNPASQRQQVPLHQRNLPKSFFVPPGDVNDNSRLSKLNSVHS
NERNSADFVVFHSKANSSPACLDAALRTSVSANVPNHSHQKSLDVASKYKTEFSPDFAFSGSCSPGFFQGQRNSQ
QTALLYGPTMTFAISELPVGYDMAINESNQVYFLNHQTQETTWFDPRIPEKFQKWGMTPEELEQVHLRYAKQFLC
TIPSSNLNVCVQQVGEFIKILYDMSAR   PLHQRNLPKSFFVPP

tr:A0A132A5J4_SARSC   [A0A132A5J4] SubName: Full=Yorkie-like protein
{ECO:0000313|EMBL:KPM06232.1, ECO:0000313|VectorBase:SSCA010042-PA};
52..66
MHLKSESESNNTDHHNNGNAIVRVESAAGLDELFKAIMSPNDGQSRLPHQVPMRQRRLPPSFFRPPSAS
SSNNSLASASHSRESSLDGGYQSGQTPVNTPNNGQAKQNNVTVLNYSGANNGMIIHPRANSSPAALQPANESVNN
LSSSGGQSFNSNEVLAKPSNESATINSAPLTTHFRQMSYDLNQIRLPDGWEMSFTASGERYFLNHKEKTTTWEDP
RKKIVEEMLHHNNSSSKQLPSINSLHPQNVGSLSSASNMQPQQQQQQSSAIQTSVQNGLSQQQNSSGSITSTPLP
ASNSTHVVHEHLSYIDPTLVPLPNGWEQAQTNTGDIYFISHIDQTTTWFHPSIPRNLQMKRIQQQTCSIQPPPFQ
TNGAKNASTINNNAMNIPPELVVALKNMNTSCQQQQTSASITASSIMPPVASMVTNPLEMSMQKTPQNQHLRDLE
LERERMKQRQEELLQSSLLNSSASNNLLSVSNDQATSSPFMLQNECHSRQDSIDSGLDLGNSSGFSSTPLLTIDS
NMFRLTNNPTSSTTTTPAQTNFLPTVISNQTVSSNTANTNNAPLSDEMMAFENMQISGLDLDSESMDFMQGLDID
LLSNVEELLNSNKDNIMTWL   PMRQRRLPPSFFRPP

tr:A0A084W439_ANOSI   [A0A084W439] SubName: Full=AGAP006045-PA-like protein {ECO:0000313|EMBL:KFB44983.1};   68..82
MAYNASGAGGSGAGAAAAAVAGNGTEENEPTGASKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQIPY
RMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVTTGPNGLPIHHSRAHSSPASLGKIPVGM
GGLGGGVVAAAVAAAAAAAAASGNGGNGGAGGGGGGGGSGGGAGVVNGQKAAAVAAAQNGQQNDASSLGAAVLQQ
AALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIK   PYRMRKLPESFFMPP

tr:Q16HH7_AEDAE   [Q16HH7] SubName: Full=AAEL014018-PA
{ECO:0000313|EMBL:EAT33707.1};   59..73
MAFNGSPSNNTSAASNTSDENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANQQQQ
QQSANNSSNVNSNKSQPGNVAGGGSGGDGPSAAVQQQQAQQQAQQQSLTRQAILHSRGRSYDVSNQHAHYGELPP
GWEQAKTQDGRIYYLNHNTRTTTWEDPRITAAMQQESLFQQQQQSSVETLFNTGSQTLLSPTISSPTPTNNVDNV
NNHFA PLRMRKLPDSFFKPP

tr:Q1DGN2_AEDAE   [Q1DGN2] SubName: Full=AAEL015564-PA
{ECO:0000313|EMBL:EAT32311.1};   59..73
MAFNGSPSNNTSAASNTSDENDGARKKENLILLVAKDSNDKLNELFDKTLSNRLPLQIPLRMRKLPDSF
FKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASINAANQQQQ
QQSANNSSNVNSNKSQPGNVAGGGSSGDGPSASVQQQQAQQQAQQQSLTRQAILHSRGRSYDVSNQHAHYGELPP
GWEQAKTQDGRIYYLK PLRMRKLPDSFFKPP

tr:A0A1Y9IVQ1_9DIPT   [A0A1Y9IVQ1] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:AMIN015771-PA, ECO:0000313|VectorBase:AMIN015771-

PB, ECO:0000313|VectorBase:AMIN015771-PC};   70..84

      MAFNGGAAGGNGSAAGAVAAGAANNASDENEPTGANKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQI
PYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVATGPNGLPIHHSRAHSSPASLGKIPV
GLGGLGGGAVAAAAAAAAAAAAAAGGGNGTGGGGGGGGGNGGGGGAGNNGGASGSKTAVAVAQAAAAAAAAQNDA
SSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYINHNTRTTTWEDPRITAMQ
ESLFQQQSSVETLFNTGSQTLLSPTISSPTPTNNVVFPDTIQMTNDNLAPSNAAPPASMLTGSSNVDLGPLPDGW
EEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLRKRQQEIKSHMGDDPFLSGIADHT
RQESGDSGLSESSMTQSMPHTPEFLSSIDDSMDGLSMTDNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVTNLT
LMDPTSSKAENTLYDII PYRMRKLPESFFMPP

tr:A0A336K5U7_CULSO   [A0A336K5U7] SubName: Full=CSON013516 protein
{ECO:0000313|EMBL:SSW98968.1};   801..815

      MKLMVDGLEVYFPYEFIYPEQYAYMVELKKAIDAKGHCLLEMPSGTGKTTTLLSLIVAYMLNHPGVVRK
LIYCSRTVPEIEKVMAELKILMDYYEKSTGQRPDLLGVVLTSRKNLCIHPEVSKEREGKLVDAKCYGLTASYVRE
RHNMDDSTSVCQYYEWWNNEGKETMMPPGIYSIDDLKKVGQTRTWCPYFMTRQAIVSAQIVVYSYHYLLDPKIAE
VVSKELTKESVIVFDEAHNIDNVCIDSMSVKINKRIIERSTTALGQLEKIVAEVKEDDQNRLTEEYQRLVQGLRE
ANVARETDMVLANPVLPNDVLKEVVPGNIRNAEHFLGFLRRFIEYIKIRLRVRHVVQESPASFLKDVQQKVCIER
KPLKFCAERLASLMRTLEITELHEYSSLTVITHFATLVSTYTQGFTIICEPFDDKTPSVSNPILYFSCLDSSIAM
RAVFQRFQTVVITSGTLSPMEMYPKILDFNPAVMASFTMTLARPCLLPMVVSRGNDQVAMSSKFETREDTAVIRN
YGQLLVETAKAVPDGVVCFFTSYLYLESVVASWYDQGIVDTLLKYKLLFIETQDSAETSYALMNYVKACECGRGA
ILLAVSRGKVSEGVDFDHHLGRAVLMFGIPYVYTQSRVLKARLDFLRDMFQIRENDFLTFDALRHAAQCVGRAIR
GKTDYGIMIFADKRYARQDKRSKLPKWIQDHLTDNLINLSTEEAIQIAKRWLRQMAQPFCRDDQLGTALLTLDQL
QNMEKEKLDSQVQVVAEETESGNKKKNLIIVVEKDSQDKLDELFNKALSNKVPLTVPLRMRNLPDSFFNPPSSGS
KSPSVSVSHSRENSADSAFGSGTTILGGVTSINGLPIHHSRAQSSPASLGIGINLPMGLNAGGNTTSNATSKLAT
GNNLNNNNNNSNNNPTTNTLGTPTTQKGFPNLHSRGRSYDVTNFQFGPLPEGWEQAKTEDGRIYYINHNNRTTQW
EDPRTMPTTSPPLFNSNSSVETLFNSNTTSPTNQTSTPANHEWAAHEQSLRLYNLQMERERLRRRQQEIKSHIGE
TDPFLPGNLDTHTRQESGDSGLSLPSSSTSQSTSHTPDFLSNIDDSMDGLSDNTMDTMPFNDNIDNSDEFMLNDP
LLLERFDADAVDNLISPANNKTTGSNVFGI   PLRMRNLPDSFFNPP

tr:R7UUL4_CAPTE   [R7UUL4] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:ELU07602.1, ECO:0000313|EnsemblMetazoa:CapteP224020};
      101..115

      MADESANNLLNFVDNASSGIKLALDRPTGSKRKVNHRKYLQKNLKVSPEKKNSGDKVKAKKKKKDCNPI
GLQAKSLQELFDLRTLHEKCCTDPMQKTPRIPLRKRKLPPSFFSEPGTDVTKYQSCRYGSGVQRLTGSWQLPGSL
SGYSDCRLSNNQAVDPDISRMYYHGYQNYCASDSNKRQLNALDYSGYSQDAAYGYNPVSMTTDPPQGHNMLCSVP
LTAMADFAFS PLRKRKLPPSFFSEP

tr:R7UVZ3_CAPTE   [R7UVZ3] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:ELU10793.1, ECO:0000313|EnsemblMetazoa:CapteP200232};
      115..129

      MSAGGQGKRGASGPIASASDEEEQDPQSPVSTNTEPPAISPTLLDHDYENVSSPGNSSTASGPTYARQP
GFTIHAHEITVSKVKKKKSAIISVKEGVRRREPTPPKSKPKRDPLPMRMRALPQSFWQQPNIPHNVSPANAYPVL
PPLYTREGEAVPDERPVTPPGDEDPAKELVPTPPAPPPPQPPPPPPSTTSSHKPHATHVRIGERKITIANTDLLF
KLFEGVEKAKSSPFPQLKRSRPRKFVPCSSKTFLSGEDPYLMECVTDKMFPHLSLEQSGGRAGSRNNYIVNLGMF
CVLLVRVRVRTCTHARTHSYIPLTSQGQGQEWAKSSLPPVENKTLKYG   PMRMRALPQSFWQQP

tr:R7U458_CAPTE   [R7U458] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:ELT98461.1, ECO:0000313|EnsemblMetazoa:CapteP205574};
      212..226

      MLTVSRRSSKDREIRQNLADETMTSKESIHDDVTGCEGASVCDRNHGNNNSVCAKDYERKRGNDEMEFD
EEDEDDIVCLVKMSSPKMSETSSKLLQFMDIVNGDIQKYFGTHGGSEDSHRGMYDNQWEKGQSGKELYYAQLMRV
AQGIDTDGDGGTSKGSGVMNKKVGLGPLKELFEYGLKDYWVDPLSARKLKKLKKFRSSSGSVEDCCAPLKKRSLP
QSFWSEPKGGIAKAPDFSDLLESWTGDEDKCLTE PLKKRSLPQSFWSEP

tr:A0A183MK24_9TREM   [A0A183MK24] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:VDP20854.1, ECO:0000313|WBParaSite:SMRZ_0001640001-mRNA-1};   38..52

      MEGYDSRKPPSVRVTVLEDPNSSLQELFNPASQRQQVPLHQRNLPKSFFVPPGDVNDNSRLSKLNSVHS
NERNSADFVVFHSKANSSPACLDAALRTSVSANVPNHSHQKSLDVASKYKTEFSPDFAFSGSCSPGLFQGQRNSQ

QTALLYGPTMTFAISELPVGYDMAINESNQVYFLNHQTQETTWFDPRIPEKFQKWGMTPEELEQVHLRYAKQFLC
TIPSSNLNVCVQQVGEFIKILYDMSAR   PLHQRNLPKSFFVPP

tr:W5JNH1_ANODA   [W5JNH1] SubName: Full=Yorkie
{ECO:0000313|EMBL:ETN64868.1};   82..96
MAFNGSTPGVSGNGNAAAAAAAAVAAAVAVGASAAGASEENDPTASATKKKNLIILVDKDSNDKLNELF
DKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVVTTGPNGLPIHHS
RAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAAGGGAGAGAGGGASVGGGGGGGAAGTGTAAAAAAASDA
SSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAKTQDGRIYYINHNTRTTTWEDPRITAMQ
ESLFQQQSSVETLFNTGSQTLLSPTISSPTPTPNNVVFPDAIQMTNEIVPPSNAAPPAAMLTGSNADLGPLPEGW
EEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLRKRQQEIKSHMGDDPFLSGIADHT
RQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGDNLETPDEFMLDDPLLLEKIDAVTNLN
LIDPTSSKPENTLYDII PYRMRNLPESFFLPP

tr:A0A0P5H4F2_9CRUS   [A0A0P5H4F2] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAK18483.1}; SubName: Full=Transcriptional
coactivator YAP1 {ECO:0000313|EMBL:KZS19500.1};46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANEL
SSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDFHARQESADSGLGMGGSYSLPHTPE
DFLASMDDTMDTTLDCN PFRLRNLPDSFFKPP

tr:A0A0P4WV48_9CRUS   [A0A0P4WV48] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAI72949.1};   46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANEL
SSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDFHARQESADSGLGMGGSYSLPHTPE
DFLASMDDTMDTTLDCPASVGTVDMNDMNDMNGGLETGDLPAHMDTTDDLVPTLDLGEELSTDILNDVLLNSNKV
DNVLTWL   PFRLRNLPDSFFKPP

tr:A0A0P5Z9I2_9CRUS   [A0A0P5Z9I2] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAM56754.1};   46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGEDSSSL
NSNASMHPCLYKDLVSIHKMVCVGTSQPTLTPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENN
SGSQQQTEFAMRRNPLHSQSNSNSSAANELSSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPS
SLATDFHARQESADSGLGMGGSYSLPHTPEDFLASMDDTMDTTLDCPASVGTVDMNDMNDMNGGLETGDLPAHMD
TTDDLVPTLDLGEELSTDILNDVLLNSNKVDNVLTWL   PFRLRNLPDSFFKPP

tr:A0A183NWY3_9TREM   [A0A183NWY3] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:VDP34829.1, ECO:0000313|WBParaSite:SMTD_0000661801-mRNA-1};   38..52
MEGYDSRKPPSVRVTVLEDPNSSLQELFNPASQRQQVPLHQRNLPKSFFVPPGDVNDSSRLSKLNSVHS
NERNSADFVVFHSKANSSPACLDAALRTSVSANVPNHSHQKSLDVASKYKTEFSPDFAFSGSCSPGLFQGQRFDP
RIPEKFQKWGMTPEELEQVHLRYAKQFLCTIPSSNLNVCVQQVGEFTKILYDMSAR   PLHQRNLPKSFFVPP

tr:N6UDN5_DENPD   [N6UDN5] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:ENN76772.1, ECO:0000313|EnsemblMetazoa:ENN76772}; Flags:
Fragment;   70..84
MKAGKGNCSTLGTVSSKGSRKELWDSSVIMARNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQV

PWSMRKLPDSFFTPPSTGSKSINHSRENSVDSAFDVSGPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQPPAHHH
IKQRSYDVASKSEDNTPLPPGWEQARTPEGQVYYLE PWSMRKLPDSFFTPP

tr:A0A1B0BZ43_9MUSC [A0A1B0BZ43] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:GPPI031037-PA, ECO:0000313|VectorBase:GPPI044830-PA}; 63..77
MSLSKSSANDENKCSVKTDDSSTTAKTSNNLVVRINQDSDENLQALFDSVLNPHESKRPLQVPFRMRKL
PNSFFNPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQASVATSLSDLQSTTAVVQQPTTTAITQQQPPPPPPE
TQRLQICHSRAHSSPASLQQSYNLHGGNISDDATTSFIQQQQQQGDSSTGAVAGTGFTNNMVGFTAAAAAGLNAN
SIIGLVNQANAGATGAGGPLQTYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKTTQWEDPR
IQFKQQQALNAAANARLNNKTGGNAASLLNGDLGPLPEGWEQALTETGDVYFINHIDRTTSWNDPRIPILFQKAV
KAKNEMSWVNAVEVDKDNDIFKQKTIQKPLNKHNVSLHMDPFLSGDNHARQESSDSGLSLSSNSFAVNTDFITHM
DSSMDCISENGSIIDNLDTTLQLNDNICMLNDVLNSPSTKPDNLEWYKLN PFRMRKLPNSFFNPP

tr:A0A0K8WIZ1_BACLA [A0A0K8WIZ1] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:JAI50805.1}; 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACLQDGIGPVFTTGAVPFPPSVNAGAAVRMEQGEQPVPKDAPNIQTFHMKQRSYDVVSTIQ
LQNELGPLPPGWEQAKTNDGQIYYLK PFRMRQLPESFFKPP

tr:A0A151XC60_9HYME [A0A151XC60] SubName: Full=Yorkie like protein
{ECO:0000313|EMBL:KYQ57976.1}; 46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDNKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVPATPNGGSSVVAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQK
QRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDG
WEQARTAEGEIYFINHQTRTTSWFDPRIPSHLQRTPASGAMLPQNWQLQQPTGIQSNQNLQACQKQKIRLQSLQL
ERERLKQRQQEIMRQQQEMMLRQSTTDAVMDPFLSGINEQHARQESADSGLGLGSAYSLPQASDDFLNIDENMDS
TSDGGAPMDTPDLSTLSDNIDSTDDLLPSLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL
PLRLRNLPDSFFNPP

tr:A0A1A9WP76_9MUSC [A0A1A9WP76] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:GBRI026830-PA}; 63..77
MSLSKSSANDENKCSVKTDDSSTTAKTSNNLVVRINQDSDENLQALFDSVLNPSESKRPLQVPFRMRKL
PNSFFNPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQASVATSLSDLQSTTAVVQQPTATTITQQQPPPPPPE
TQRLQICHSRAHSSPASLQQSYNLHGGNISDDATTTFIQQQQQPQGDGTAATVTGTGFTNNMVGFTAAAAAAGLN
ANSIIGLVNQANAAGATGAGGPLQTYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKTTQWE
DPRIQFKQQQALNAAANARLNNKTAGNAASLLNGDLGPLPEGWEQALTETGDVYFINHIDRTTSWNDPRIPLLFQ
KAVKAKNEMSWVNAVEMDKDNDIFKQKTVQKPLNKHNVSLHMDPFLSGDNHARQESSDSGLSLSSNSFAVNNDFI
THMDNSMDCISENGSIIDNLDTTLQLNDNICMLNDVLNSPSTKPDNLEWYKLN PFRMRKLPNSFFNPP

tr:A0A2M4BIW5_9DIPT [A0A2M4BIW5] SubName: Full=Putative transcriptional
coactivator yorkie {ECO:0000313|EMBL:MBW52972.1}; 85..99
MAFNGSPAGVSGNGGNAASAAAAAAVAAAVAVGGGASGAGASEENDPASATKKKNLIILVDKDSNDKLN
ELFDKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVTTGPNGLPIH
HSRAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAGGAGGAGAGGGGGGGASAGGAGGGAATGTGAAGVKQ
QQSAAQQQQQQNAAAAAAAAAAASSDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAK
TQDGRIYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTNNVVFPDAIQMTNEIV
PPSNAAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERE
RLRKRQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGD
NLETPDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII PYRMRNLPESFFLPP

tr:A0A2M4BJ16_9DIPT [A0A2M4BJ16] SubName: Full=Putative transcriptional
coactivator yorkie {ECO:0000313|EMBL:MBW52973.1}; 85..99
MAFNGSPAGVSGNGGNAASAAAAAAVAAAVAVGGGASGAGASEENDPASATKKKNLIILVDKDSNDKLN
ELFDKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVTTGPNGLPIH
HSRAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAGGAGAAGAGGGGGGGASAGGAGGGAATGTGAAGVKQ
QQSAAQQQQQQNAAAAAAAAAAASSDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAK
TQDGRIYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTNNVVFPDAIQMTNEIV

PPSNAAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERE
RLRKRQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGD
NLETPDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII PYRMRNLPESFFLPP

tr:A0A2M4BIZ0_9DIPT [A0A2M4BIZ0] SubName: Full=Putative transcriptional coactivator yorkie {ECO:0000313|EMBL:MBW53017.1}; 85..99
MAFNGSPAGVSGNGGNAASAAAAAAVAAAVAVGGGASGAGASEENDPASATKKKNLIILVDKDSNDKLN
ELFDKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVTTGPNGLPIH
HSRAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAGGAGGAGAGGGGGGGASAGGATTGTGAAGVKQQQSA
AQQQQQQNAAAAAAAAAAASSDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAKTQDG
RIYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTNNVVFPDAIQMTNEIVPPSN
AAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLRK
RQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGDNLET
PDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII PYRMRNLPESFFLPP

tr:A0A2M4BJ40_9DIPT [A0A2M4BJ40] SubName: Full=Putative transcriptional coactivator yorkie {ECO:0000313|EMBL:MBW52971.1}; 85..99
MAFNGSPAGVSGNGGNAASAAAAAAVAAAVAVGGGASGAGASEENDPASATKKKNLIILVDKDSNDKLN
ELFDKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVTTGPNGLPIH
HSRAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAGGAGGGGAGGGGGGGASAGGAGGGAATGTGAAGVKQ
QQSAAQQQQQQNAAAAAAAAAAASSDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAK
TQDGRIYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTNNVVFPDAIQMTNEIV
PPSNAAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERE
RLRKRQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGD
NLETPDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII PYRMRNLPESFFLPP

tr:A0A2M4BJQ2_9DIPT [A0A2M4BJQ2] SubName: Full=Putative transcriptional coactivator yorkie {ECO:0000313|EMBL:MBW53018.1}; 85..99
MAFNGSPAGVSGNGGNAASAAAAAAVAAAVAVGGGASGAGASEENDPASATKKKNLIILVDKDSNDKLN
ELFDKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVTTGPNGLPIH
HSRAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAGGAGGGGAGGGGGGGASAGGATTGTGAAGVKQQQSA
AQQQQQQNAAAAAAAAAAASSDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAKTQDG
RIYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTNNVVFPDAIQMTNEIVPPSN
AAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLRK
RQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGDNLET
PDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII PYRMRNLPESFFLPP

tr:A0A069DTH5_9HEMI [A0A069DTH5] SubName: Full=Putative ww domain-containing transcription regulator protein 1 {ECO:0000313|EMBL:JAC87066.1};>tr:A0A224XQR7_9HEMI [A0A224XQR7] SubName: Full=Putative ww domain-containing transcription regulator protein 1 {ECO:0000313|EMBL:JAW10790.1}; 44..58
MAGNPDVEFKSSLVVRIDQDSDSELQALFDSVLKPGSKRPLQVPLRMRKLPDSFFNPPSTGSKSPSVSS
ISHSRENSADSAFGNATTTVSGLQVNHPRAHSSPASLQQTYASAQQTQPQHLKQRSYDITALDELGPLPPGWEQA
RTSEGQVYFLNHITQTTTWEDPRKANAVAQQRASDLLNAAASSPGHSTSPQPHQAVHLQRAPSTTGALPSWLQPV
VTQSQTLQATQQKLRLQSLQMERERLKIRQQEIMRQQELMLRDAPATTGLDPFLPGVTDHSRQESADSGLGLGNS
YSLPQTPDDFLTSMDMDASVSDGGTASEMAGLDSHEITSLSDNIDSTDDLVPSLQLGEEFTSDILDDVQALINPT
SKGGNSLTWL PLRMRKLPDSFFNPP

tr:A0A212F1Y3_DANPL [A0A212F1Y3] SubName: Full=YAP65 protein {ECO:0000313|EMBL:OWR47724.1}; 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTAPVSHSRAHSSPASLQQTYAAGQQNQQPPLPHQHAKQRSYDVASHIPDELGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKTLAAQTVSAGVQHQNEILTPPQTIAATPTAAKSTSTNTTTDPLGPLPD
GWEQATTPEGEIYFINHAARTTSWFDPRIPQHLQRTPTSGGAAGGGWANAACQQKLRLQSLQLERERLKQRQQEI
RLQQELMARQSSSIVSSLATTEVSLDPFLSGISEHTRQESADSGLGMVQYSVPHTPEDFLASMDDRMDVASEPGA
PMDADITLGDTDLLGDFTNDILDDVQSLINSTPNKPDNVLTWL PLRMRQLPKSFFNPP

tr:A0A0D2WY30_CAPO3 [A0A0D2WY30] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KJE97763.1}; 48..62
MDTTGRGSTVDPLYAPVLPHNRSQSESNQYHISQPSLDSLHSTLSMPPLRDRNLPASFFRSPSSAAADR
IDSSAMSEAGASHSRDSSLDSGISFVPHQPQLIMNGSTFPPVAFHSRQSSAGSSEPTSQSHNLQQQLLLLQQQQ
QQQQQLLYQQQQQQLSLPQQSGQMPGQSPGLLVPMYNQLQHSYQTSQSSPFPPATPSSAHSSTFFSREPSISSFL
EMSLHFEQQQQQPQQHSRPLSHSNSGNVLSAQANNPGLPASGNSSNSLQRLSASSLDESPLPPGWEKGIKDGLPF
FIDHNNKTTTWVDPRTDRATPGTQGLSERKRVPDVLSDPLLNPTLNPLPAGWEMAMHSDGIPYFINHRKRTTTWI
DPRTDVDMQEYFRNQTYSAATSVRRRDSGRSAHALSFGNGASPSPAPGLENGPPSELRVHASTMTRISPRNTPFS
SFDSALPDPGYDQMTGNSSPLASFNLTSPPPPVSPGITGMDSQSLAGLSQRELQARRMMLQKEQIRLKQMQLLQE
ELEIQRAQRNLAVLETTTRGGSAKLPPPQLTVSECLTTTTATATADVTSRRSVSDTSMPEPVVVATKANRSSSTA
GSTLYSPMQQLVLRLA PLRDRNLPASFFRSP

tr:A0A0K8TQ71_TABBR [A0A0K8TQ71] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAI16537.1}; 59..73
MALNNSMNANNNNNNTIDSDAVKQGNLVVRIDQDSDDNLQALFDSVLKPGDSKRPLQVPLHMRKLPKSF
FNPPSNGSKSPSVSHSRANSTDSAFSTGSQGAPPTAPPATNRGIQISHSRAHSSPASLQQTYAGSGMNAQNNNNS
TGSGSGTGGNATGNNGNATQGGQTNTVQPVHMKQRSYDVVSAIQLQDELGDLPPGWEQARTVEGQIYYLNHITRT
TQWEDPRKQLAQQAALAQHQSAESLLRSPIQQTADYLQRASSLTSRQETSNTNTNNWVNIRNLEKEREYLKQRQQ
EIQHQDLLTRQNQQTMGLQMDPFLSGITDHTRQESGDSGLSLSSNNFSVTPDFLSNIDDSMDCISESGNLDSLGG
LEGADDLVPSLQLGDNICTEMLNDVQSLINPVTTKPDNLNWFKI PLHMRKLPKSFFNPP

tr:E9HCY1_DAPPU [E9HCY1] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:EFX70433.1}; 46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLTLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTAPVAGSNAAAVLAASQQALTQAL
GPLPDGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGTQSAAALQQQQITQQPAASGTSQQTL
TPAQAAQQQLRLQRLQQEQDRLRQRQQEIIAMMERETRQESADSGLGMGGSYSLPHTPEDFLASMDDTMDTLGPA
SVGTVDMNDMNDMNGGLEAGDLPAHMDTTDDLVPTLDLGEELSTDILNDVLLNSNKVDNVLTWL
PFRLRNLPDSFFKPP

tr:A0A0K8TQV3_TABBR [A0A0K8TQV3] SubName: Full=Putative ww domain-containing protein {ECO:0000313|EMBL:JAI16536.1}; 59..73
MALNNSMNANNNNNNTIDSDAVKQGNLVVRIDQDSDDNLQALFDSVLKPGDSKRPLQVPLHMRKLPKSF
FNPPSNGSKSPSVSHSRANSTDSAFSTGSQGAPPTAPPATNRGIQISHSRAHSSPASLQQTYAGSGMNAQNNNNS
TGSGSGTGGNATGNNGNATQGGQTNTVQPVHMKQRSYDVVSAIQLQDELGDLPPGWEQARTVEGQIYYLNHITRT
TQWEDPRKQLAQQAALAQHQSAESLLRSPIQQTATITVKDPAVTDPLGPLPEGWEQAVTSSGEIYFINHINRTTS
WVDPRISDYLQRASSLTSRQETSNTNTNNWVNIRNLEKEREYLKQRQQEIQHQDLLTRQNQQTMGLQMDPFLSGI
TDHTRQESGDSGLSLSSNNFSVTPDFLSNIDDSMDCISESGNLDSLGGLEGADDLVPSLQLGDNICTEMLNDVQS
LINPVTTKPDNLNWFKI PLHMRKLPKSFFNPP

tr:A0A1B6JRF0_9HEMI [A0A1B6JRF0] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAT01791.1}; 45..59
MALNPDVEQLKGNLVVRIDQDSDSELQALFDSVLKPDSRRPLQVPFRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGNNTTTTTTTTGLQVNHPRAHSSPASLQQTYASAHQQQQQHIKQRSCDMTALEQDLGPLPA
GWEQARTLEGQVYFLNHITRTTTWEDPRKTIAAQVANQQQRSAELLNTPHPATSPQPQGKGSSPATSPAPLGPLP
EGWEQAATPEGEIYFINHQTRTTSWFDPRIPTHLQRPPTSGALLPAALSSWLPQVQSSASQQKLRLQSLQLERER
LKLRQQEIMRQQELMMRQSTTDSGMDPFLSGLTDHARQESADSGLGMSNNYSLPHTPEDFLSTMDDNMDGVSEGG
TPGPADIALDSHEMTSLTDNIDSTDDLVPSLQLGEEFSSDILDDVQALINPKVDNGLTWL
PFRMRKLPNSFFNPP

tr:A0A026X1A6_OOCBI [A0A026X1A6] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:EZA61144.1}; 46..60
MALNQDVEQLSKSNLVVRIDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPESFFNPPSAGSKSPSI
SHSRENSADSAFGAAVVATPNGGTERAGGGAGGGAPTGGAAGGGNAAGGGNAAGAAGTGGLTVAHPRAHSSPASL
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PLRMRNLPESFFNPP

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tr:A0A1B6J527_9HEMI     [A0A1B6J527] SubName: Full=Uncharacterized protein
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SISHSRENSADSAFGNNTTTTTTTTGLQVNHPRAHSSPASLQQTYASAHQQQQQHIKQRSCDMTALEQDLGPLPA
GWEQARTLEGQVYFLNHITRTTTWEDPRKTIAAQVANQQQRSAELLNTPHPATSPQPQGKGSSPATSPAPLGPLP
EGWEQAATPEGEIYFINHQTRTTSWFDPRIPTHLQRPPTSGALLPAALSSWLPQVQSSASQQKLRLQSLQLERER
LKLRQQEIMRQQELMMRQSTTDSGMDPFLSGLTDHARQESADSGLGMSNNYSLPHTPEDFLSTMDDNMDGVSEGG
TPGPADIALDSHEMTSLTDNIDSTDDLVPSLQLAADDPIFPANIFGGSIL   PFRMRKLPNSFFNPP

tr:A0A182FD52_ANOAL     [A0A182FD52] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:AALB004439-PA};  81..95
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KTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVTTGPNGLPIHHSRA
HSSPASLGKIPASLVGLGSGAVAAAAAAAAAAAAAGGGAGAGGGGGGGGGASAGGAAAAAGAGAGTAGAAGVKQQ
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DGRIYYIK    PYRMRNLPESFFLPP

tr:X5J6X0_BLAGE   [X5J6X0] SubName: Full=Yorkie-S
{ECO:0000313|EMBL:CCX34982.1};>gp:HF969253_1 [HF969253] Yorkie-S [Blattella
germanica]  45..59
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SISHSRENSADSAFGTASVGAGPGATTTTTSAASASGLQVNHPRAHSSPASLQQTYASAQPQQHQQHSHLKQRSY
DITTVDELGPLPPGWEQARTPEGQVYYLNHITRTTTWEDPRKTLAAQVAQSQQQQQTSADLISNVAGSPLSSSSP
QPQGTKSVDAANLGPLPEGWEQATTQEGEVYFINHQTRTTSWFDPRIPLQLQKSPANSSMMPQQSSSWIQPLTSQ
SLQACQQKLRLQSLQMERERLKLRQQEIMRQEMMMRQQSTTDLPPGANSAGMDPFLSGPTDHSRQESADSGLGMC
SYSLPHTPEDFLANMDDNMDGVSEGGNPSDMATLDGPDISSLSDNIDSTDDLVPSLQLSEEFSSDILDDVQSLIN
PNSRPGNGLTWL      PLRMRKLPNSFFNPP

tr:A0A2P8Z9J9_BLAGE     [A0A2P8Z9J9] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PSN53170.1};      45..59
      MALNPDSEQHKGNLVVRIDQDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGATTTTTSAASASGLQVNHPRAHSSPASLQQTYASAQPQQHQQHSHLKQRSY
DITTVDELGPLPPGWEQARTPEGQVYYLK PLRMRKLPNSFFNPP

tr:A0A2P8Y267_BLAGE     [A0A2P8Y267] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PSN38352.1};      121..135
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AVYPILPPLSSLGTTKDDVENIAAGMRSTASPEEGQAPRREVSVANTDLLFSLFRTVEDETPKVAVVLAMVSLKD
GDKSVSLPSLNVEHNYSQILSELVIKL   PMKLRALPQSFWQQP

tr:A0A1B6DK87_9HEMI     [A0A1B6DK87] SubName: Full=Uncharacterized protein
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SISHSRENSADSAFGTTTTTTTASGLQVNHPRAHSSPASLQQTYASAQQQQQHQQHLKQRSYDITALDELGPLPP
GWEQARTPEGQVYFLNHVTRTTTWEDPRKTLAAQVQNQQQRSAELLNTVATSPHPSSSPQPQAAHLQRTPGAGSV
LPQGLSSWIQPQTIQVCQQKLRLQSLQMERERLKMRQQEIMRQQELMLRQSSADGASSGMDPFLSGLTDHSRQES
ADSGLGMGNNYSLPHTPEDFLSTMDDNMDGVSEGGTPGPDMSALDSHDMTSLSDNIDSTDDLVPSLQLAEEDPIF
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tr:A0A1B6BY62_9HEMI     [A0A1B6BY62] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAS06213.1};      45..59
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SISHSRENSADSAFGTTTTTTTASGLQVNHPRAHSSPASLQQTYASAQQQQQHQQHLKQRSYDITALDELGPLPP
GWEQARTPEGQVYFLNHVTRTTTWEDPRKTLAAQVQNQQQRSAELLNTVATSPHPSSSPQPQAAHLQRTPGAGSV
LPQGLSSWIQPQTIQVCQQKLRLQSLQMERERLKMRQQEIMRQQELMLRQSSADGASSGMDPFLSGLTDHSRQES
ADSGLGMGNNYSLPHTPEDFLSTMDDNMDGVSEGGTPGPDMSALDSHDMTSLSDNIDSTDDLVPSLQLGEEFSSD
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SISHSRENSADSAFGTTTTTTTASGLQVNHPRAHSSPASLQQTYASAQQQQQHQQHLKQRSYDITALDELGPLPP
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APLGPLPEGWEQAATPEGEIYFINHQTRTTSWFDPRIPAHLQRTPGAGSVLPQGLSSWIQPQTIQVCQQKLRLQS
LQMERERLKMRQQEIMRQQELMLRQSSADGASSGMDPFLSGLTDHSRQESADSGLGMGNNYSLPHTPEDFLSTMD
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tr:A0A1B6D5S2_9HEMI     [A0A1B6D5S2] SubName: Full=Uncharacterized protein
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LQMERERLKMRQQEIMRQQELMLRQSSADGASSGMDPFLSGLTDHSRQESADSGLGMGNNYSLPHTPEDFLSTMD
DNMDGVSEGGTPGPDMSALDSHDMTSLSDNIDSTDDLVPSLQLAEEDPIFAANIFGGSIL
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tr:X5J6P8_BLAGE   [X5J6P8] SubName: Full=Yorkie-L
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germanica]  45..59
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AGMDPFLSGPTDHSRQESADSGLGMCSYSLPHTPEDFLANMDDNMDGVSEGGNPSDMATLDGPDISSLSDNIDST
DDLVPSLQLSEEFSSDILDDVQSLINPNSRPGNGLTWL    PLRMRKLPNSFFNPP

tr:A0A1E1X4E4_9ACAR     [A0A1E1X4E4] SubName: Full=Putative transcriptional
coactivator {ECO:0000313|EMBL:JAT94124.1}; Flags: Fragment;      47..61
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tr:A0A2M4A1L2_9DIPT     [A0A2M4A1L2] SubName: Full=Putative transcriptional
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EIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGDNLETPDE
FMLDDPLLLEKIDAVTNLNLIDPTSSKPDNTLYDII      PYRMRNLPESFFLPP

tr:A0A1B0A976_GLOPL     [A0A1B0A976] SubName: Full=Uncharacterized protein
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tr:A0A2M3YY54_9DIPT   [A0A2M3YY54] SubName: Full=Putative transcriptional
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tr:A0A0P6E261_9CRUS   [A0A0P6E261] SubName: Full=65 kDa yes-associated
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KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANELSSNTA
DPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDFHARQESADSGLGMGGSYSLPHTPEDFLAS
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tr:A0A0A1WYQ7_ZEUCU   [A0A0A1WYQ7] SubName: Full=Protein yorkie
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tr:A0A0P5X705_9CRUS   [A0A0P5X705] SubName: Full=65 kDa yes-associated
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tr:A0A0P5Z949_9CRUS     [A0A0P5Z949] SubName: Full=65 kDa yes-associated
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tr:A0A0P6IXI8_9CRUS     [A0A0P6IXI8] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAN68476.1};    46..60
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tr:A0A0P5D7J6_9CRUS     [A0A0P5D7J6] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAJ63320.1};    46..60
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KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQXILLH    PFRLRNLPDSFFKPP

tr:A0A0P5DEV6_9CRUS     [A0A0P5DEV6] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAJ66074.1}; Flags: Fragment;    46..60
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tr:A0A0P5IUG7_9CRUS     [A0A0P5IUG7] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAK41373.1};    46..60
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ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANEL
SSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLAGLGMGGSYSLPHTPEDFLASMDDTMDT
TLDCPASVGTVDMNDMNDMNGGLETGDLPAHMDTTDDLVPTLDLGEELSTDILNDVLLNSNKVDNVLTWL
      PFRLRNLPDSFFKPP

tr:A0A0P5M8R9_9CRUS     [A0A0P5M8R9] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAK88401.1}; Flags: Fragment;    46..60
      MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
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GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGEDSSSL
NSNASMHPCLYKDLVSIHKMVCVGTSQPTLTPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENN
SGSQQQTE   PFRLRNLPDSFFKPP

tr:A0A0P5IC55_9CRUS   [A0A0P5IC55] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAK36224.1};   46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPPSSLATDFHARQESADS
GLGMGGSYSLPHTPEDFLASMDDTMDTTLDCPASVGTVDMNDMNDMNGGLETGDLPAHMDTTDDLVPTLDLGEEL
STDILNDVLLNSNKVDNVLTWL PFRLRNLPDSFFKPP

tr:A0A0P6ASK4_9CRUS   [A0A0P6ASK4] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAM72512.1};   46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLRKEIFYFMFFLLSCFLSCFLSCFYLFFYLFFYLFFYFFLLF
LLLTNLLLLLLLLLLSPFAMTFTFSPIIAIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGEDSSSLNSNASM
HPCLYKDLVSIHKMVCVGTSQPTLTPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQ
TEFAMRRNPLHSQSNSNSSAANELSSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDF
HARQESADSGLGMGGSYSLPHTPEDFLASMDDTMDTTLDCPASVGTVDMNDMNDMNGGLETGDLPAHMDTTDDLV
PTLDLGEELSTDILNDVLLNSNKVDNVLTWL   PFRLRNLPDSFFKPP

tr:A0A0P5TJ82_9CRUS   [A0A0P5TJ82] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAL76676.1};   46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANEL
SSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDFHARQESADSGLGMGGSYSLPHTPE
DFLASMDDTMDTTLDCPASVGTXXXXXXXXXXXXXXXXXXXXXXXXPKIFWPLWMTQWTLPSIVLLL
PFRLRNLPDSFFKPP

tr:A0A0P6D628_9CRUS   [A0A0P6D628] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAN12140.1}; Flags: Fragment;   46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLRKEIFYFMFFFLSCFLSCFYLFFYLFFYLFFYFFLLFLLLT
NLLLLLLLLLLSPFAMTFTFSPIIAIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTLTPAQAAQQQL
RLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQ PFRLRNLPDSFFKPP

tr:A0A0P5GW87_9CRUS   [A0A0P5GW87] SubName: Full=Putative 65 kDa yes-
associated protein {ECO:0000313|EMBL:JAK16128.1}; Flags: Fragment;
46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQXXXXXXXXGSNAAAVLAASQQALTQALGPLPEGWEQAVTPEGELYF
IDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTLTPAQAAQQQLR
PFRLRNLPDSFFKPP

tr:A0A0N8CTS7_9CRUS   [A0A0N8CTS7] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAM04084.1};   46..60
MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA

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KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANEL
SSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLAXXXXXXXXXXXXXXXLAPMGQAMEQLP
ASRRIRRCHRRL      PFRLRNLPDSFFKPP

tr:A0A0P5ZQ45_9CRUS     [A0A0P5ZQ45] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAM62768.1};   46..60
      MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEDSSSLNSNASM
HPCLYKDLVSIHKMVCVGTSQPTLTPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMVF PFRLRNLPDSFFKPP

tr:A0A0P5TNU9_9CRUS     [A0A0P5TNU9] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAL76677.1};   46..60
      MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLRKEIFYFMFFLLSCFLSCFLSCFYLFFYLFFYLFFYFFLLF
LLLTNLLLLLLLLLLSPFAMTFTFSPIIAIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTLTPAQAA
QQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANELSSNTAD
PFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDFHARQESADSGLGMGGSYSLPHTPEDFLASM
DDTMDTTLDCPASVGTXXXXXXXXXXXXXXXXXXXXXXXPKIFWPLWMTQWTLPSIVLLL
      PFRLRNLPDSFFKPP

tr:A0A0P4XE70_9CRUS     [A0A0P4XE70] SubName: Full=Putative 65 kDa yes-
associated protein {ECO:0000313|EMBL:JAI80311.1};    46..60
      MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLK PFRLRNLPDSFFKPP

tr:A0A0P5N888_9CRUS     [A0A0P5N888] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAL02098.1};   46..60
      MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLRKEIFYFMFFFLSCFLSCFYLFFYLFFYLFFYFFLLFLLLT
NLLLLLLLLLLSPFAMTFTFSPIIAIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTLTPAQAAQQQL
RLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANELSSNTADPFLS
AASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDFHARQESADSGLGMGGSYSLPHTPEDFLASMDDTM
DTTLDCPASVGTVDMNDMNDMNGGLETGDLPAHMDTTDDLVPTLDLGEELSTDILNDVLLNSNKVDNVLTWL
      PFRLRNLPDSFFKPP

tr:A0A0P5QN37_9CRUS     [A0A0P5QN37] SubName: Full=65 kDa yes-associated
protein {ECO:0000313|EMBL:JAL39744.1};   46..60
      MSKNPEVVEHKERNQIVHIRGDSDSELQALFDSVLKPDAHRPLQLPFRLRNLPDSFFKPPPTGSKSPSV
ASNSHSRENSTDSGHFALNPSPSANIHHSRAHSSPASLQQTLAAGQQRPVHQHLKQQSCDLSLDHFPLPEGWEQA
KTPQGQVYFLNHLTQTTTWEDPRKKLLQQQIQPLSPAPPPNMVAPPLLSAVTTPVAGSNAAAVLAASQQALTQAL
GPLPEGWEQAVTPEGELYFIDHHTRKTSWFDPRLPIHMQKPPMVHAAGAQSVAALQQQQQITQQPAASGTSQPTL
TPAQAAQQQLRLQKLQQEQDRLRQRQQEIIAMMERETRVRQQENNSGSQQQTEFAMRRNPLHSQSNSNSSAANEL
SSNTADPFLSAASATTTAVVSHPCANGAGNGAATSIAQNSTVPPSSLATDFHARQESADSGLGMGGSYSLPHTPE
DFLASMDDTMDTTLDCPASVGTVDMNDMNDMNGGLETGDLPAHMDTTDDLVPTLDVKKIFKYIYISV
      PFRLRNLPDSFFKPP

tr:A0A131XMV1_9ACAR     [A0A131XMV1] SubName: Full=Putative transcriptional
coactivator {ECO:0000313|EMBL:JAP67555.1}; Flags: Fragment;      47..61
      ATNGRGEMIEQKGPNHIVRIRSDSDINLDDLFKAVMQPGDRVPLSVPMRLRNLPASFFQQPERSKSASH
SRESSADATYSPSVSEASAAAAAAAAAAAAPPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQQSFDLVDDLPPGW
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EMAKTSTGQRYFLNHLTQTTTWDDPRKKTPSTKHHATPPPPPHTAAPPAGPFKNLGPLPDGWEQATTAEGEVYFI
NHIERTTSWFDPRIPAHAQKPLLQSHASQLPGHQQSQGSGNAVNSTGPASPDTMNSISAVVAATSSLTLQQQRQQ
KMRLQQLQMERERLKIRQQEILRQTAFLGNSARNEMMLRRTLTEEILPSPTSPTASDVVGVGPTTDPFLGGDFHS
RQESADSGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPNHQNSELSLDGLQGTGIDLGTENMDSDDLVPSLQE
ELQGDLLSDMEALLTSSKDSVLTWL   PMRLRNLPASFFQQP

tr:A0A1Z5L713_ORNMO   [A0A1Z5L713] SubName: Full=ATP synthase-coupling factor 6 mitochondrial ATPase subunit F6 {ECO:0000313|EMBL:JAW02844.1}; Flags: Fragment; 52..66
MSSQQQQQSNRDVIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNLPASFFQQPERS
KSASHSRESSNDATFPDTAGQTPLPISHPRAHSSPASLQRTYSSPQQQPQQHLRQRSYDLADEGSLPPGWEMAKT
ASGQRYFLNHLTQTTTWEDPRKKTPGGPKQQTAPPPPHTAAPVLPNFKDLGPLPDGWEQATTAEGEVYFINHIER
TTSWFDPRIPIHLQKPSLQGTSAQPTQGNTDISAVVAATSSLTLQQQRQQKLRLQQLQRERERLKFRHHEILRQT
AFLGNPARNQEMLVRRTLTEEILSNPTSPSDPFLGGDFHTRQESADSGLGLGPSLPHTPEDFLSTMDDSTMDGLN
DDASQRDMSLESLQGTAIDLGAENMDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL
PMRLRNLPASFFQQP

tr:A0A293M1B4_ORNER   [A0A293M1B4] SubName: Full=YAP65-like protein {ECO:0000313|EMBL:MAA33871.1}; Flags: Fragment;50..64
MSSQPPNSRDVIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNLPASFFQQPERSKS
ASHSRESSSDATFPETTGPAISHPRAHSSPASLQQTYNNPPQQQHLRQRSYDLADEGSLPPGWEMAKTATGQRYF
LNHLTQTTTWEDPRKKSPGGTKQQTPPPPPHTAAPVLPHFKNLGPLPDGWEQATTSEGEVYFINHIERTTSWFDP
RIPIHLQKPSIQGTSAPPTQGTADISAVVAATSSLTLQQQRQQKLRLQQLQRERERLKLRQQEILRQTAFLGNPA
RNQEMLLRRTLTEEILSNPTSPSDPFLGGDFHTRQESADSGLGLGPSLPHTPEDFLSTMDDSTMDGLNDDASQRD
VSLESLQGTGLDLGTENMDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL   PMRLRNLPASFFQQP

tr:A0A293LX93_ORNER   [A0A293LX93] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:MAA32388.1}; Flags: Fragment;34..48
MTSPPPGETAQRLSDEKSDSTSSADDRDLPFPLPLRLRQLPASFWQEPKTQPAATSSCSLYPPQEYSCT
QYCPLCPACSFYPGFSLPPIYLIPERVPIPYSVRELVPAVALPDMYQMGSSTRGHRTRRSSRYHPML
PLRLRQLPASFWQEP

tr:A0A293MZB2_ORNER   [A0A293MZB2] SubName: Full=YAP65-like protein {ECO:0000313|EMBL:MAA45268.1}; Flags: Fragment;50..64
MSSQPPNSRDVIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNLPASFFQQPERSKS
ASHSRESSSDATFPETTGPAISHPRAHSSPASLQQTYNNPPQQQHLRQRSYDLADEGSLPPGWEMAKTATGQRYF
LNHLTQTTTWEDPRKKSPGGTKQQTPPPPPHTAAPVLPHFKNLGPLPDGWEQATTSEGEVYFINHIERTTSWFDP
RIPIHLQKPSIQGTSAPPTQGTADISAVVAATSSLTLQQQRQQKLRLQQLQRERERLKLRQQEILRQQEMLLRRT
LTEEILSNPTSPSDPFLGGDFHTRQESADSGLGLGPSLPHTPEDFLSTMDDSTMDGLNDDASQRDVSLESLQGTG
LDLGTENMDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL   PMRLRNLPASFFQQP

tr:A0A182PJT4_9DIPT   [A0A182PJT4] SubName: Full=Uncharacterized protein {ECO:0000313|VectorBase:AEPI007200-PA}; 74..88
MAFNGGAGGNGGGSAASAAAAAAVAAGSAPTDENEPTGASKKKNLIILVDKDSNDKLNELFDKTLSNKL
PLQIPYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVATGPNGLPIHHSRAHSSPASLG
KIPVGLGGLGGGAVAAAAAAAAAAAAAGNGTGAAGGGGGGGGSSGGGGSGGTGAGKAAQAAAAAAQNDASSLGAA
VLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIK PYRMRKLPESFFMPP

tr:A0A2P2ID39_9CRUS   [A0A2P2ID39] SubName: Full=Transcriptional coactivator YAP1-like {ECO:0000313|EMBL:LAB71856.1}; Flags: Fragment;
62..76
FLLNAVIGSPLTMDTTENDDKLVGEPQKGSHVLHVRADSDSELQALFDCVLKPSKQMPLQKPFKMRNLP
ASFFNPPAHRQSPAPTVSHSRESSADSTYGGGGPPGLRVGGAMSPAGIQPPPAPQHFRHHSSPATLQQTFAVAQT
TPIGGHAKQHSYDALAEDTSPLPDGWEQARTPQGQLYYL   PFKMRNLPASFFNPP

tr:H9J2E4_BOMMO   [H9J2E4] SubName: Full=Uncharacterized protein {ECO:0000313|EnsemblMetazoa:BGIBMGA003681-TA}; 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH

SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLK PLRMRQLPKSFFNPP

tr:W6FTH1_BOMMO [W6FTH1] SubName: Full=YKI2
{ECO:0000313|EMBL:AHJ26003.1};>gp:KF904340_1 [KF904340] YKI2 [Bombyx mori]
44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAQHLQRTPVGATGV
AGGGWANASTQACQQKLRLQSLQLERDRLKQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGL
TDHQRQESADSGLGMAVPQSYSMPHTPEDFLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLLNEFTNDILL
DDVQSLINSTPSKPDNVLTWL PLRMRQLPKSFFNPP

tr:W6FGB5_BOMMO [W6FGB5] SubName: Full=YKI1
{ECO:0000313|EMBL:AHJ26002.1};>gp:KF904339_1 [KF904339] YKI1 [Bombyx mori]
44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGTSTVSHSRAHSSPASLQQTYTAGQQSQQPPLHHQHTKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQNVANTVQHQAAEALLNQNAQQTITNTATPAAKSTSNTTTDPLG
PLPEGWEQATTAEGEIYSINHAARTTSWFDPRIPQHLQRTPVSATGVAGGGWANASIQACQQKLRLQSLQLERDR
LKQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLPGLTDHQRQESADSGLGMAVPQSYSMPHTPE
DFLSGMDDRMDCTSEAGANMDSTDITLGDNIGSTDDLLNEFTNDILLDDVQSLINSTPSEPDNVLTWL
PLRMRQLPKSFFNPP

tr:A0A182KPB2_9DIPT [A0A182KPB2] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:ACOM024764-PA}; 74..88
MAFNGGAAGSGNGSAAAAAAAAAAAVAAVAADENESTGANKKKNLIILVDKDSNDKLNELFDKALSNKV
PLQIPYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVAGVAATGPNGLPIHHSRAHSSPASL
GKIPGGMSGLGGAXXXXXXXIVLQVGGKNQGQLPTRRQFGGFVEDEMQKVCISLSRFM
PYRMRKLPESFFMPP

tr:A0A087UBV3_9ARAC [A0A087UBV3] SubName: Full=Yorkie-like protein
{ECO:0000313|EMBL:KFM74842.1}; Flags: Fragment;47..61
MSQQRDVIEQQGPNQIVRIRSDSGTNLDDLFKAVMEPKGNQVHQSIPMRLRNLPPSFFQQPERGSKSAS
HSRESSTDNTYSSPPPQPVSQNNNSSNNVNTSSNQGNNNNSVSSPPPQHPSGLPINHPRAHSSPASLQQTYTNAS
QHQHLRQQSYDITDSIPLPLGWERAKTATGQLYFLNHLTKTTTWEDPRKKLSLGSLSNSSGITCSSPSTSPASSI
LNVQNLGPLPEGWDQATTAEGEVYYINHKTRTTSWYDPRIPIQLQQPPLVPILGYGSVTGQSQNPVSLSGQQTQS
SVVTSGSGASVLPTLSSQTLQQQQQNLRLQRLQMERERLRLRQQEILREEMMRRTLREEGSLPTSPTNSSSDGTS
STHTNIDPFLGGDSDFHSRQESGDSGLGLGTNYSLPNTPEDYLMGMEEGAEDVLLDIAELNLEPIPGAALGIVPE
NMDSEDLVPSLQEEFNADILSDVEAILTKESGMKWL PMRLRNLPPSFFQQP

tr:A0A087U4J8_9ARAC [A0A087U4J8] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KFM72287.1}; Flags: Fragment;27..41
MNSPPVVPSKISESVSDTESDPKPMVPLRQRRLPASFWQEPCIAPSASHQDIAHQIPGMSSNQTAPGSS
LHPWTMNTTNAVFPTFMSQRLSVPNALVLAQNTSPFWLRSPFSCCGCATCLNYSYAIPRIPDVYGNLRYRQPVNI
PCCPSLNSVDQSCKLCCTSDSWHPERLRQLRLRSARYNALID PLRQRRLPASFWQEP

tr:A0A087UE32_9ARAC [A0A087UE32] SubName: Full=Yorkie-like protein
{ECO:0000313|EMBL:KFM75621.1}; Flags: Fragment;48..62
MSQQQQDVIEQKGPNQVVHIRSDSETKLDELFNAVIHPKDYQVPLTVPMRLRNLPPSFFQQPEKGSKSA
SHSRESSADGSSYPPGGGSDTPSQPQTQQQLPSGLQINHPRAHSSPASLQQAYNKSISSSHHQHPRQRSYGDLLD
DDDNTPLPLGWEKAKTSAGQTYFL PMRLRNLPPSFFQQP

tr:A0A1I8IM79_9PLAT [A0A1I8IM79] SubName: Full=Uncharacterized protein
{ECO:0000313|WBParaSite:maker-uti_cns_0014022-snap-gene-0.2-mRNA-1};
99..113
CTVKGIPGIELEASATTNQRLVWDWAGLHGLAFNRGFGEKKPTPWNFSGSRTDTSRSFFRLNWHCGSAA
TPSTSSSSGGIQRRRQLRVRVRPLYPITVPLRDRRLPASFWTHPNRRPQTEAASLPAPQYSVASSQSHLTALTAS
WAAAAAAAAA PLRDRRLPASFWTHP

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tr:A0A1I8GK67_9PLAT     [A0A1I8GK67] SubName: Full=Uncharacterized protein
{ECO:0000313|WBParaSite:maker-uti_cns_0002291-snap-gene-0.2-mRNA-1};
      52..66
      CTVKGIPGIELEASATTNQRLATPSTSSSSGGIQRRRQLRVRVRPLYPITVPLRDRRLPASFWTHPNRR
PQTEAASLPAPQYSVASSQSHLTALTASWAAAAAAAAA    PLRDRRLPASFWTHP

tr:A0A195F1G8_9HYME     [A0A195F1G8] SubName: Full=Yorkie like protein
{ECO:0000313|EMBL:KYN34313.1};      46..60
      MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPE
GQIYFLNHLTRTTTWEDPRKTAAAASVAAVAAAVESSKSNALGPLPDGWEQARTAEGEIYFINHQTRTTSWFDPR
IPSHLQRTPASGAMLPQNWQLQQPAGIQSNQNLQACQKQKIRLQSLQLERERLKQRQQEIMRQQQEMMLRQSTTD
AVMDPFLSGINEQHARQESADSGLGLGSAYSLPQASDDFLNIDENMDSTSDGGTPMEPDLSTLSDNIDSTDDLLP
SLQLNEEFSTDILDDVQSLINPNTTKPENVLTWL  PLRLRNLPDSFFNPP

tr:A0A1B6G6L8_9HEMI     [A0A1B6G6L8] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAS58077.1};      45..59
      MALNPDVEQLKGNLVVRIDQDSDSELQALFDSVLKPDSRRPLQVPFRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGNNTTTTTTTGLQVNHPRAHSSPASLQQTYASAHQQQQQHIKQRSCDMTALEQDLGPLPAG
WEQARTLEGQVYFLNHITRTTTWEDPRKTIAAQVANQQQRSAELLNTPHPATSPQPQGKGSSPATSPAPLGPLPE
GWEQAATPEGEIYFINHQTRTTSWFDPRIPTHLQRPPTSGALLPAALSSWLPQVQSSASQQKLRLQSLQLERERL
KLRQQEIMRQQELMMRQSTTDSGMDPFLSGLTDHARQESADSGLGMSNNYSLPHTPEDFLSTMDDNMDGISEGGT
PGPADIALDSHEMTSLTDNIDSTDDLVPSLQLAADDPIFPANIFGGSIL    PFRMRKLPNSFFNPP

tr:A0A1B6G5W6_9HEMI     [A0A1B6G5W6] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAS57830.1};      45..59
      MALNPDVEQLKGNLVVRIDQDSDSELQALFDSVLKPDSRRPLQVPFRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGNNTTTTTTTGLQVNHPRAHSSPASLQQTYASAHQQQQQHIKQRSCDMTALEQDLGPLPAG
WEQARTLEGQVYFLNHITRTTTWEDPRKTIAAQVANQQQRSAELLNTPHPATSPQPQGKGSSPATSPAPLGPLPE
GWEQAATPEGEIYFINHQTRTTSWFDPRIPTHLQRPPTSGALLPAALSSWLPQVQSSASQQKLRLQSLQLERERL
KLRQQEIMRQQELMMRQSTTDSGMDPFLSGLTDHARQESADSGLGMSNNYSLPHTPEDFLSTMDDNMDGISEGGT
PGPADIALDSHEMTSLTDNIDSTDDLVPSLQLGEEFSSDILDEVQALINPKVDNGLTWL
      PFRMRKLPNSFFNPP

tr:A0A1I8IES8_9PLAT     [A0A1I8IES8] SubName: Full=Uncharacterized protein
{ECO:0000313|WBParaSite:maker-uti_cns_0011849-snap-gene-0.3-mRNA-1};
      101..115
      SKCTVKGIPGIELEASATTNQRLVWDWAGLHGLAFNRGFGEKKPTPWNFSGSRTDTSRSFFRLNWHCGS
AATPSTSSSSGGIQRRRQLRVRVRPLYPITVPLRDRRLPASFWTHPNRRPQTEAASLPAPQYSVASSQSHLTALT
ASWAAAAAAAA PLRDRRLPASFWTHP

tr:A0A182KD48_9DIPT     [A0A182KD48] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:ACHR008685-PA};   65..79
      MAFNGGAAGSGGSSAAAAVATDENEPTGANKKKNLIIILVDKDSNDKLNELFDKTLSNKLPLQIPYRMR
KLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVATGPNGLPIHHSRAHSSPASLGKIPVGLGGL
GGGVVAAAAAAAAAAAAAGGNGAGGGGGGGGGGGGGGTGAGNTAAGAGGSKSAAAQAAAAAAAAQNDASSLGAAV
LQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIK   PYRMRKLPESFFMPP

tr:A0A2M4CYC1_ANODA     [A0A2M4CYC1] SubName: Full=Putative transcriptional
coactivator yorkie {ECO:0000313|EMBL:MBW70332.1};     82..96
      MAFNGSTPGVSGNGNAAAAAAAVAAAVAVGASAAGASEENDPTASATKKKNLIIILVDKDSNDKLNELF
DKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVVTTGPNGLPIHHS
RAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAGGGAGAGAGGGASVGGGGGGGAAGTGTGAAGVKQQQSA
AQQQQQNAAAAAAAAAAAASDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAKTQDGR
IYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTPNNVVFPDAIQMTNEIVPPSN
AAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLRK
RQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGDNLET
PDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII   PYRMRNLPESFFLPP
```

tr:A0A2M4CYV0_ANODA [A0A2M4CYV0] SubName: Full=Putative transcriptional coactivator yorkie {ECO:0000313|EMBL:MBW70477.1}; 82..96

```
      MAFNGSTPGVSGNGNAAAAAAAAVAAAVAVGASAAGASEENDPTASATKKKNLIILVDKDSNDKLNELF
DKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVVTTGPNGLPIHHS
RAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAASGGAGAGAGGGASVGGGGGGGAAGTGTGAAGVKQQQSA
AQQQQQQNAAAAAAAAAAAASDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAKTQDG
RIYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTPNNVVFPDAIQMTNEIVPPS
NAAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLR
KRQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGDNLE
TPDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII  PYRMRNLPESFFLPP
```

tr:A0A2M4CYR8_ANODA [A0A2M4CYR8] SubName: Full=Putative transcriptional coactivator yorkie {ECO:0000313|EMBL:MBW70476.1}; 82..96

```
      MAFNGSTPGVSGNGNAAAAAAAAVAAAVAVGASAAGASEENDPTASATKKKNLIILVDKDSNDKLNELF
DKTLSNKLPLQIPYRMRNLPESFFLPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVVTGVVTTGPNGLPIHHS
RAHSSPASLGKIPAGLVGLGGGAVAAAAAAAAAAAAAGGGAGAGAGGGASVGGGGGGGAAGTGTGAAGVKQQQSA
AQQQQQQNAAAAAAAAAAAASDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHVTFGELPPGWEQAKTQDG
RIYYINHNTRTTTWEDPRITAMQESLFQQQSSVETLFNTGSQTLLSPTISSPTPTPNNVVFPDAIQMTNEIVPPS
NAAPPAAMLTGSNADLGPLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLR
KRQQEIKSHMGDDPFLSGIADHTRQESGDSGLSESSMTQSMPHTPDFLSSIDDSMDGLSMTDNTMDTIAFGDNLE
TPDEFMLDDPLLLEKIDAVTNLNLIDPTSSKPENTLYDII  PYRMRNLPESFFLPP
```

tr:A0A194PPP3_PAPXU [A0A194PPP3] SubName: Full=Protein yorkie {ECO:0000313|EMBL:KPI94943.1}; 44..58

```
      MALNTDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLKQAGDMRLRCLAGRAPPSVRRAARRSLQPCERDGPSRARLPRQQIDSYHFLIASWVDVL
      PLRMRQLPKSFFNPP
```

tr:A0A2S2NBW4_SCHGA [A0A2S2NBW4] SubName: Full=Yorkie {ECO:0000313|EMBL:MBY14704.1}; 66..80

```
      MSGLQQQQQEQHQQVSIKMEPTGPSSPTPAVNSNLVVRVDQNSETDLQALFDTVLKPDGKKPLQLPLRM
RQLPKSFFNPPSTGSKSPSISHSRENSGDSAFGTTAAGQSCTGGPVPMHSRAHSSPASLQQTYAVGAAKQQQQQQ
QHAKQRSYDVSSAIDELGPLPQGWEQARTPEGQIYYLNHLTRTTQWEDPRKSLAAQAANQHQRSAEQLLSPGNDS
GSSTNATSTPTNSPPHIHSTLQGTNKNVTLGPLPDGWEQAVTGDGETYFINHIARTTSWFDPRIPVHLQRAPTSG
AVLPSGSASWLLNGASGLSQSLQVTQQKLRLHSLQLERERLKSRQQEIIRQQDLMSRSGHTNNDLDPFLSCSSSS
VDHSRQESADSGLGLGNNYSLPHTPEDFLSSNMDDNMDCTSESDNPGPSSDMSVVDSQEMATLDVTDDLVPSLQL
GDEFGNDILDEVQLLIDPNNKPGSILTWL PLRMRQLPKSFFNPP
```

tr:A0A1B6LNH3_9HEMI [A0A1B6LNH3] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:JAT25208.1}; 45..59

```
      MALNPDVEQLKGNLVVRIDQDSDSELQALFDSVLKPDSRRPLQVPFRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTNTTTTTTATGLQVNHPRAHSSPASLQQTYASAHQQQQQHIKQRSCDMSVLEQDLGPLPA
GWEQARTLEGQVYFLNHITRTTTWEDPRKTIAAQVANQQQRSAELLNTPHPATSPQPQGKGSSPATSPAPLGPLP
EGWEQAATPEGEIYFINHQTRTTSWFDPRIPTHLQRPPTSGALLPAALSSWLPQVQSSASQQKLRLQSLQLERER
LKLRQQEIMRQELMMRQSTTDSGMDPFLSGLTDHARQESADSGLGMSNNYSLPHTPEDFLSTMDDNMDGVSEGGT
PGPADITLDSHEMTSLTDNIDSTDDLVPSLQLGEEFSSDILDDVQALINPKVDNGLTWL
      PFRMRKLPNSFFNPP
```

tr:A0A1B6L2C5_9HEMI [A0A1B6L2C5] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:JAT17848.1}; 45..59

```
      MALNPDVEQLKGNLVVRIDQDSDSELQALFDSVLKPDSRRPLQVPFRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTNTTTTTTATGLQVNHPRAHSSPASLQQTYASAHQQQQQHIKQRSCDMSVLEQDLGPLPA
GWEQARTLEGQVYFLNHITRTTTWEDPRKTIAAQVANQQQRSAELLNTPHPATSPQPQGKGSSPATSPAPLGPLP
EGWEQAATPEGEIYFINHQTRTTSWFDPRIPTHLQRPPTSGALLPAALSSWLPQVQSSASQQKLRLQSLQLERER
LKLRQQEIMRQELMMRQSTTDSGMDPFLSGLTDHARQESADSGLGMSNNYSLPHTPEDFLSTMDDNMDGVSEGGT
PGPADITLDSHEMTSLTDNIDSTDDLVPSLQLAADDPIFPANIFGGSIL    PFRMRKLPNSFFNPP
```

tr:A0A1B6MVB7_9HEMI [A0A1B6MVB7] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAT39875.1}; 45..59
MALNPDVEQLKGNLVVRIDQDSDSELQALFDSVLKPDSRRPLQVPFRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTNTTTTTTATGLQVNHPRAHSSPASLQQTYASAHQQQQQHIKQRSCDMSVLEQDLGPLPA
GWEQARTLEGQVYFLNHITRTTTWEDPRKTIAAQVANQQQRSAELLNTPHPATSPQPQATHLQRPPTSGALLPAA
LSSWLPQVQSSASQQKLRLQSLQLERERLKLRQQEIMRQELMMRQSTTDSGMDPFLSGLTDHARQESADSGLGMS
NNYSLPHTPEDFLSTMDDNMDGVSEGGTPGPADITLDSHEMTSLTDNIDSTDDLVPSLQLGEEFSSDILDDVQAL
INPKVDNGLTWL PFRMRKLPNSFFNPP

tr:T2MG76_HYDVU [T2MG76] SubName: Full=Yorkie homolog
{ECO:0000313|EMBL:CDG70925.1}; 43..57
MDMNSTQRQGNFVLHVRQDSDTDLEQLFKNSVSTNKDIPRSKPFRDRKLPASFFRPPPSLETDQTAPIH
TRARSLPSNIGQIAQDQVILQQQQLQQQHPQNNFLLTPSHQRTQSYGTLESNYLPSGCEMRTTASGQKYYINHQN
QSTSWQDPRKAQSMTVLPANPQNLLMDDLPEGWERAVTAEGEVYFINHQTKTTSWFDPRLNRPNNNLLLGGTNIQ
YYQQEKRHRQQQIQNQLLEREFLIHQRMNGQHTDSVLNNNSLINNLVREKYTAHMNSSVLGRGSSVDSGLDGMES
YLTSTSTDGLNDMDTADVDRNNQFDKNTSMEQGICFNNRLPEFFDSLQASNVDLDILEDGSELSSDLEAINTEAL
NDVDMILSPNNKPNAYMTWL PFRDRKLPASFFRPP

tr:A0A1B0D0M3_PHLPP [A0A1B0D0M3] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:PPAI000895-PA}; 65..79
MALNNSNSSGSNNNLSNNNNNNNESDNTKQGNLVVRMDEDSATKLQALFDTVLKPSEQNRPLQIPLRMR
KLPNSFFNPPSTGSKSPSVSHSRENSIDSAFGSGTTIVYAPGGGSGSGTGTASSVLTQRLSISHSRAHSSPATLE
QTHAAGLKSVTGATGSGNSTSQTQAQTPLKAVHASQRSYDVISAIQLQDELGDLPPGWEQARTAEGQIYYLKLVL
SPCRQFIIPMVCFKNSFSTLHKSQLLADKSALIY PLRMRKLPNSFFNPP

tr:F6WJM1_CIOIN [F6WJM1] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSCINP00000022513};50..64
MDMEENNEPTTQTTFTHHNQIIHVRQDSASELEALFNTVMNPNFKSKSLPMKARNLPKSFFTQPDKPRQ
QAAYHHGHSQSVGGLVAPNSVSHSRSKSSPASLQLMDIGSLSVKASDIPHDMPLPHGWSAAKTADGQQYYMNHND
RSTTWEDPRIGILKQQRQNQVVMQNQSIATNIHQQQIPLPSGWEQAATPQGEIYFINHQTKSTSWVDPRFQGKKY
WLKERNVTENRVSFFPESNFTPEINLCGKSGNQQLCLGRLSPEKHRLKLKRRTHSNSRRDYQEIILRLGITPTNN
NNPPNNSQLQQQLMKQLSNPGMENFMGGGNPSFHQRDASLDSGVGMGSNYSLPRTPDGFLNNVEEMETAQPATQQ
HTHTNNQRFPDFLDTLPASSVDFTSSPVPTSGGQRVCTTSASLDGSELVPSLQDSLPQDFDVESMLNHVKTENMD
NGMIWL PMKARNLPKSFFTQP

tr:A0A067QNF7_ZOONE [A0A067QNF7] SubName: Full=65 kDa Yes-associated
protein {ECO:0000313|EMBL:KDR09902.1}; 45..59
MALNPDSEQHKGNLVVTIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSTGSKSPSVS
SISHSRENSADSAFGTASVGAGPGGTTTTSAAGANGLQVNHPRAHSSPASLQQTYASAQQQQHGHLKQRSYDITT
VDELGPLPPGWEQARTREGQVYYLNHITRTTTWEDPRKTLAAQVAQSQQQTSADLISNVAGSPHSSSSPQPQVDG
SSLGPLPEGWEQATTQEGEVYFINHQTRTTSWFDPRIPMHLQKSPAGTILPQHSASWIQPLSTQSQLCQQKIRLQ
SLQMERERLKLRQQEIMRQQGIMLRQASTTDLPPGANSAGMDPFLSGLTDHSRQESADSGLGMCNSYSLPHTPED
FLANMDDNMDGVSEGGNPADMATLDGPDISSLSDNIDSTDDLVPSLQLSEEFSSDILDDVQSLINPNSRPDNVLT
WL PLRMRKLPNSFFNPP

tr:A0A1D2NI00_ORCCI [A0A1D2NI00] SubName: Full=Transcriptional
coactivator YAP1 {ECO:0000313|EMBL:ODN04606.1};54..68
MAASGNNGPGSGALPSHKSQQIIHMRGDSDSELQALFDSVLQPGIAGRRPNGVPLRLRKLPDSFFKPPS
TGSKSPSVSVSHSRENSVDSTLNPMRRSPMTSNGAMGAGGHHRAHSSPATLEQTYSVAQSHVSQASPSLQSGSSG
NLSEDPLPPGWEQACTAEGQVYFINHITRSTTWEDPRKAQHQQILAAVGGEPPNTGSNPSLSAMGIAQGMANGPL
PEGWEQAITPEGEVYFINHQARTTSWFDPRLPAHLQRPPVLQQQLNAAALAQAAANAAALGNGATAQLLQMPKQQ
ELRLQQLQLERERLKLRQQEIMRQMEQEQARLARQQPARAPPTQMDDGLELDPFLSGSTMGNPSTPSSDFHSRQE
SADSGLGMGNSYSLPNTPEDFLSTMDDNMDTISENGLGGASLDTGDIPILGSDPVDSTDDLVPSLLPDELSSELL
DEMQSIINSKSDNGMTWL PLRLRKLPDSFFKPP

tr:A0A0M9A5Y1_9HYME [A0A0M9A5Y1] SubName: Full=Yorkie like protein
{ECO:0000313|EMBL:KOX77897.1}; 46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFAVASLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPH

GWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAANVAAAAAAVDNGKSTTGATNSLGPLPDGWEQARTPEGEIYF
INHQTRTTSWFDPRIPTHLQRPPTSGAMLPQSWLQQPTGGGIQSNQTLQACQQKLRLQSLQMERERLKQRQQEII
RQQELMLRQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDL
STLSDNIDSTDDLVPSLQLSEDFSSDILDDVQSLINPNTTKPENVLTWL   PLRMRNLPDSFFNPP

tr:A0A1J1ITS4_9DIPT   [A0A1J1ITS4] SubName: Full=CLUMA_CG015352, isoform
A {ECO:0000313|EMBL:CRL02510.1};   65..79
MAFNNSSQTRQSTQLSATNEDETNLQQQQQQKKNNLIILVEKDSNDKLDELFDKTLSNKLPLQVPYHMR
NLPASFFKPPSSGSKSPSVSHSRENSADSAFGSGTTIGAGVQSTATPVVAPSAIPSGLTIHHSRAHSSPASLGKL
PLNINLNLSALNLGSVTPTNSSPSPNHSSSNISSISSNNSSKQQQSGISVNIASNSTNSTNNTNNNLLNNNGTGS
NQSTNNNLPHNILDKTLQHIHSRGRSYDIPSLQHQIHFGELPTGWEQAKTHEGKIYYINHNTRTTQWEDPRIQAA
TTALSNGNLFSSSEHSSVETLFSSPTHLSSLGSTQNVTDTQSQTQTAAITAPSVPLGNNTTNLGPLEWPWEEGVT
ENGERYYINHITRTTTWRDPRLSNQDWADQEQSVRIFNLHLERERLKRRQQEIAKLNIGEDPFLSGMTDHARQES
SDSGLSVSLSHTPDFLSTIDDSMDGLSSTVNDSMDTITFNEAMETPDEFMLNDPLLLDKIDELI
PYHMRNLPASFFKPP

tr:A0A182YR17_ANOST   [A0A182YR17] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:ASTEI10903-PA}; 72..86
MAFNGGAAGGNGSAAAAAAVAAGAANNATDENEPTGANKKKNLIILVDKDSNDKLNELFDKTLSNKLPL
QIPYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVATGPNGLPIHHSRAHSSPASLGKI
PVGLGGLGGGVVAAAAAAAAAAAAASGNAGGGGGGGGGGGGGGGTGGAGAGSAGGAGGSKSAAAAAQAAAVAAAQ
NDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIK
PYRMRKLPESFFMPP

tr:T1HC02_RHOPR   [T1HC02] SubName: Full=Uncharacterized protein
{ECO:0000313|EnsemblMetazoa:RPRC001564-PA};   44..58
MAGNPDVEFKSSLVVRIDQDSDSELQALFDSVLKPGSKRPLQVPLRMRKLPDSFFNPPSTGSKSPSVSS
ISHSRENSADSAFGNATTTVTGLQVNHPRAHSSPASLQQTYASAQQTQPQHLKQRSYDITALDELGPLPPGWEQA
RTSEGQVYFLKVVSFVGVDGNCNQGEHNLIAGASSFGGCDIVVFGEGPAA   PLRMRKLPDSFFNPP

tr:J3RGB6_9EUKA   [J3RGB6] SubName: Full=Yorkie-like protein
{ECO:0000313|EMBL:AER13454.1};>gp:JN202490_1 [JN202490] Yorkie-like protein
[Capsaspora owczarzaki] 113..127
MQQQQQQQSQQSQLQHHPHSHNSLYSLSQSSHSQPHSRHSSMHVRKSSMDSVSSASQHGSGKYLAMDTT
GRGSTVDPLYAPVLPHNRSQSESNQYHISQPSLDSLHSTLSMPPLRDRNLPASFFRSPSSAAADRIDSSAMSEAG
ASHSRDSSLDSGISFVPHQPQLIMNGSTFPPVAFHSRQSSAGSSEPTSQSHNLQQQQLLLLQQQQQQQQQLLYQQ
QQQQLSLPQQSGQMPGQSPGLLVPMYNQLQHSYQTSQSSPFPPATPSSAHSSTFFSREPSISSFLEMSLHFEQQQ
QQPQQHSRPLSHSNSGNVLSAQANNPGLPASGNSSNSLQRLSASSLDESPLPPGWEKGIKDGLPFFIDHNNKTTT
WVDPRTDRATPGTQGLSERKRVPDVLSDPLLNPTLNPLPAGWEMAMHSDGIPYFINHRKRTTTWIDPRTDVDMQE
YFRNQTYSAATSVRRRDSGRSAHALSFGNGASPSPAPGLENGPPSELRVHASTMTRISPRNTPFSSFDSALPDPG
YDQMTGNSSPLASFNLTSPPPPVSPGITGMDSQSLAGLSQRELQARRMMLQKEQIRLKQMQLLQEELEIQRAQRN
LAVLETTTRGGSAKLPPPQLTVSECLTTTTATATADVTSRRSVSDTSMPEPVVVATKANRSSSTAGSTLYSPMQQ
LVLRLGHSQPQQQFGFSPASTRRSTCNTSRC   PLRDRNLPASFFRSP

tr:A0A2J7PQI8_9NEOP   [A0A2J7PQI8] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PNF18603.1};   45..59
MALNPDSEQHKGNLVVRIDEDSDSDLQALFDSVLKPDSKRPLQVPLRMRKLPNSFFNPPSPASLQQTYA
SAQQQQHGHLKQRSYDITPVDELGPLPPGWAQARTPEGQVYYLK   PLRMRKLPNSFFNPP

tr:W4YAW0_STRPU   [W4YAW0] SubName: Full=Uncharacterized protein
{ECO:0000313|EnsemblMetazoa:SPU_012881-tr};   45..59
MEPAGGRKQNAVVHVRGDSGAELDDLFRNVLNTPEAADKVPSQVPWRKRNMPASFFQEPRISHSRESSA
DSTNYSGNMSNASHEIASRSLGPQGMTIAHSRAHSSPASLQEMRNINPQDVIRNQHLRQQSYDISDTDNPNLPSG
WEMAVTPTGQKYFLDFDDKRHDVKTVCVSFITVRG PWRKRNMPASFFQEP

tr:A0A0J7KY09_LASNI   [A0A0J7KY09] SubName: Full=Yorkie-like protein
{ECO:0000313|EMBL:KMQ95206.1};   46..60
MALNQDVDQLSKSNLVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPNSFFNPPSTGGSKSPS
ISHSRENSADSAFGTAVAATPSGGGGGGGGGAPNVSANGNGSGGGTTTGAGGGGGGAGGGGGAGGGGGANSTAGA

VAAAAAVAAAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHG
WEQARTSEGQIYFLNQVAISTAEIDKMSVSDIALNIVKPINNRQDILEIQGNLGDNGLITL
PLRMRNLPNSFFNPP

tr:W4Y1C6_STRPU [W4Y1C6] SubName: Full=Uncharacterized protein
{ECO:0000313|EnsemblMetazoa:SPU_009506-tr}; 139..153
MDKLVKPSASTSPPTANNGKRGPTCSLSGSSSSEGEGSDHEEIPPSPCSSTSSGPTYVRPPGFKHHGQE
IKVQEQRPKVNTSVRIKRKIKRQSMMKDVLPLSHVTSHPVTKVTMEEKTTGVQVLPPSGMKTKVRKEPIPMRLRA
LPQSFWQQPNTVNSASPGSMYSVLPPLCKMEQSNSDLAGKVP PMRLRALPQSFWQQP

tr:A0A2A3EAS4_APICC [A0A2A3EAS4] SubName: Full=WW domain-containing
transcription regulator protein {ECO:0000313|EMBL:PBC28574.1}; 46..60
MALNQDVDQLSKSNLVVRIDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTVGGGGPT
PGGNATGTPATGAAGAATGGSGNSAGSGSNAAGAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHH
HHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLKHAPLRGSIQESVSFLLIDIAVATHLQRAPTSGAMLPQ
NWLQQQQPTGGGIQNNQTLQACQQKLRLQSLQMERERLKQRQQEIIRQQELMLRQSTTDAAMDPFLSGINEQHAR
QESADSGLGLGSAYSLPHTPEDFLANIDDNMDGTSDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSEDFSSDILD
DVQSLINPNTTKPENVLTWL PLRMRNLPDSFFNPP

tr:A0A023F3K9_TRIIF [A0A023F3K9] SubName: Full=Putative ww domain-containing transcription regulator protein 1 {ECO:0000313|EMBL:JAC15946.1};
44..58
MAGNPDVEFKSSLVVRIDQDSDSELQALFDSVLKPGSKRPLQVPLRMRKLPDSFFNPPSTGSKSPSVSS
ISHSRENSADSAFGNATTTVSGLQVNHPRAHSSPASLQQTYASAQQTQPQHLKQRSYDITALDELGPLPPGWEQA
RTSEGQVYFLNHITQTTTWEDPRKANAVAQQRASDLLNAAASSPGHSTSPQPHQGKNGSGGSGSGSNSGSSNGGA
APTGLGPLPDGWEQAATAEGEIYFINHQTKTTSWFDPRIPVHLQRAPSTTGALPSWLQPVVTQSQTLQATQQKLR
LQSLQMERERLKIRQQEIMRQQELMLRDAPATTGLDPFLPGVTDHSRQESADSGLGLGNSYSLPQTPDDFLTSMD
MDASVSDGGTASEMAGLDSHEITSLSDNIDSTDDLVPSLQLGEEFTSDILDDVQALINPTSKGGNSLTWL
PLRMRKLPDSFFNPP

tr:A0A1E1WGE3_PECGO [A0A1E1WGE3] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAT86052.1}; 44..58
MALNSDGEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHSKQRSYDVGTHIPDDLGPLPAGW
EQARTPEGQIYYLNHITKTTTWEDPRKSLAAQAVAQAQHQSAETLLSQTPAQTIPSPTTPAKSTSSSTPSDPLGP
LPEGWEQAATPEGEIYFINHAARTTSWFDPRIPQHLQRTPAANAGAAGGGWANASIQACQQKLRLQSLQLERERL
KQRQQEIRLQQELMARQASSIVSSLASSTGAVASTELPLDPFLSGLTDHQRQESADSGLGMAVSQSYSMPHTPED
FLAGMDDRMDCTSEAGANIDSTDIALGDNIDSTDDLVPSLQVTVAY PLRMRQLPKSFFNPP

tr:A0A0K8T4K1_LYGHE [A0A0K8T4K1] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAG60336.1}; 48..62
MSGNPDGRGVQQGSNLVVRIDHDSETELQALFDSVLKPEAKQRPQSKPFRMRNLPNSFFNPPSTGSKSP
SVSSISHSRENSADSAFGTTTTTMGGLTVNHPRAHSSPASLQQTYASASVVASSPQHLKQRSYDISSLDDLGPLP
LGWEQARTSEGQIYFLNHMTQTTTWEDPRKTAAAQQQAAQQRSQELLNTVATSPHPSTSPQPHQGKNGGVSPGST
AGLGPLPDGWEQAQTLEGEVYFINHRTKTTSWFDPRIPVHLQRAPAAGNVLPSWLQQSLSPSANIAASQQQKLRL
QSLQQERERLKVRQAEIMRQELMLRDAPATTGLDPFLSGLADHSRQESADSGLGLGNNYSLPHTPDDFLSTMDDN
MDGVSEAGAEMGSLDSHELTISDNIDSTDDLVPSLQLGEEFSSDILDDVQALINPNSKPGNSLTWL
PFRMRNLPNSFFNPP

tr:A0A146KK45_LYGHE [A0A146KK45] SubName: Full=Yorkie
{ECO:0000313|EMBL:JAP96953.1}; Flags: Fragment;13..27
VLKPDSKRPLQVPWSMRKLPDSFFNPPPTGSKSINHSRENSVDSAFGSSSGGGGSGTGATAVSTAALQN
QHHRAHSSPASLQQTYAVGQQTAPTHHHIKQRSYDVASKSSEDSTPLPPGWEQARTPEGQVYYLNHLTRTTTWED
PRKSLVSQGAVQQHQSAEQLLTSHQVSQTQTPSQSPACTAKANTDVDLGPLPEGWEQAQTPEGG
PWSMRKLPDSFFNPP

tr:A0A182IXU2_9DIPT [A0A182IXU2] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:AATE007567-PA}; 65..79
MAFNTSGAGGSAAAAAAAAVASEENEPTGASKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQIPYRMR

KLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVTTGPNGLPIHHSRAHSSPASLGKIPVGMGGL
GGGVVAAAVAAAAAAAAAANGSGGGGGGGGGGGGAGGSGAVNGSKANAAAVAAAQNAAAAGNDASSLGAAVLQQAAL
SKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIKPGVMVMVLLRFSAAVESEKHAAWKDTSNKK
SNKPAPATQNQQK PYRMRKLPESFFMPP

tr:B4GCJ5_DROPE [B4GCJ5] SubName: Full=GL10424
{ECO:0000313|EMBL:EDW32472.1}; 61..75
MSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMRKLPN
SFFTPPAPSHSRANSADSTYDAGSQSNINKTAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLQQNYNVRS
RSDANPGPSGQGPTYPENSAEFPNSAANTIELDGMNTCMGGQDMPMSTQTVHKKQRSYDVVSPIQLQSQLGALPP
GWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSESGLTGLDCPDNLVSSLQIEDNICTNLFN
DAQTIVNPPSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

tr:A0A1Q3FK93_CULTA [A0A1Q3FK93] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAV27997.1}; Flags: Fragment; 66..80
MAFNSNSSSASNNNNNNTASNTSASEENDGASKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQIPYRM
RKLPDSFFKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVNPVTGPNGLPIHHSRAHSSPASLGKIPAGLISS
LTGGSGSGVAQATGNSSKAQQQADSSSLGASSVAQQQQQQQQQAQQGLPKQAIQHL PYRMRKLPDSFFKPP

tr:A0A195B2H4_9HYME [A0A195B2H4] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:KYM78480.1}; 46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVPATPNGGGSGVPNGGTNGSGGSGGGGGXXXXSPPRPASPFLIPAPTAAQPPSSRRTRRH
SKRRNTRRSRTRVTTIIRSSAATTSSARSTTWARCRTDGSKRAPPRARSTSSRLPQTGKTGKIQGN
PLRLRNLPDSFFNPP

tr:A0A131YDR7_RHIAP [A0A131YDR7] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:JAP76600.1}; 59..73
MSSSPSQPNNGAATNGRGEMIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSDRVPLSVPMRLRNLPASF
FQQPDRSKSASHSRESSSDATFSPSEASAAAAAAAAAAAAVAAPPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQ
QSYDLVDDLPPGWEMAKTSTGQRYFLNHLTQTTTWDDPRKKTPSTKHHATPPPPPHTAAPPAGPFKNLGPLPDGW
EQATTAEGEVYFINHIERTTSWFDPRIPAHAQKPLLQSHASPLPGHQQSQGSGNAVSSTGPTSPDTMNSISAVVA
ATSSLTLQQQRQQKMRLQQLQMERERLKIRQQEILRQTAFLGNSARNEMMLRRTLTEEILPSPTSPTASDVAGVG
PTTDPFLGGDFHSRQESADSGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPNNQNSELSLDGLQGTGIDLGTE
NMDSDDLVPSLQLSTNFFLGLSPF PMRLRNLPASFFQQP

tr:A0A131YJL0_RHIAP [A0A131YJL0] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:JAP79484.1}; 59..73
MSSSPSQPNNGAATNGRGEMIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSDRVPLSVPMRLRNLPASF
FQQPDRSKSASHSRESSSDATFSPSEASAAAAAAAAAAAAVAAPPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQ
QSYDLVDDLPPGWEMAKTSTGQRYFLNHLTQTTTWDDPRKKTPSTKHHATPPPPPHTAAPPAGPFKNLGPLPDGW
EQATTAEGEVYFINHIERTTSWFDPRIPAHAQKPLLQSHASPLPGHQQSQGSGNAVSSTGPTSPDTMNSISAVVA
ATSSLTLQQQRQQKMRLQQLQMERERLKIRQQEILRQTAFLGNSARNEMMLRRTLTEEILPSPTSPTASDVAGVG
PTTDPFLGGDFHSRQESADSGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPNNQNSELSLDGLQGTGIDLGTE
NMDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL PMRLRNLPASFFQQP

tr:A0A182V6X1_ANOME [A0A182V6X1] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:AMEM009880-PA}; 24..38
MDSNDKLNELFDKALSNKVPLQIPYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGV
AGVAATGPNGLPIHHSRAHSSPASLGKIPGGMSGLGGGAVAAAAAAAAAAAAAGGNGAGGGSGGGGGGGGGTGG
TGAAGASKSAAAQAAAAAVAAQNDATSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQ
DGRIYYIK PYRMRKLPESFFMPP

tr:A0A0B6YQ79_9EUPU [A0A0B6YQ79] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:CEK58307.1}; 38..52
MSQDRTGPIVHVRENSDTELEALFNHAMNPSETNKYVPLRERKLPASFFCPPEPPKPMQQQMGVGKDNP
TDAPVFHGAVNPNMNIAHMRAHSSPASLQQSLSAAPPPTSSSHVRQHSYDALDEQPLPAGWDMAKTPQGQRYYLN
HVLQITTWNDPRKTHGTGNPATISSSNNNNNANTTNLNSLSQTGVSSIPIHSSPGTTPVNVDKVPLPPGWERAYT
ADLEVYFINHIDRTTSWFHPSLPTHLQRPGMKFQQQLTSGPMSPQQDRLKHLKLQQLQMEQERLKKRQDEIALQE

MALRAQVGETVIGTSGDITAISQSSEITSITDPFFGQTGTSDHHSRQESADSGLGGMGTNYSLPRTPDFLGNMED
MDTQDGGQKLQGQSDFGSMDMASVNDVVDHLTMDSEDLVPSLQEEINSELLKDVETVLGSKDNPLTWL
PLRERKLPASFFCPP

tr:A0A0B6YR91_9EUPU [A0A0B6YR91] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:CEK58306.1}; 38..52
MSQDRTGPIVHVRENSDTELEALFNHAMNPSETNKYVPLRERKLPASFFCPPEPPKPMQQQMGVGKDNP
TDAPVFHGAVNPNMNIAHMRAHSSPASLQQSLSAAPPPTSSSHVRQHSYDALDEQPLPAGWDMAKTPQGQRYYLN
HVLQITTWNDPRKTHGTGNPATISSSNNNNNANTTNLNSLSQTGVSSIPIHSSPGTTPVNVDKVPLPPGWERAYT
ADLEVYFINHIDRTTSWFHPSLPTHLQRPGMKFQQQLTSGPMSPQQDRLKHLKLQQLQMEQERLKKRQDEIALQE
MALRAQVGETVIGTSGDITAISQSSEITSITDPFFGQTGTSDHHSRQESADSGLGGMGTNYSLPRTPDFLGNMED
MDTQDGGGNQQ PLRERKLPASFFCPP

tr:T1E377_9DIPT [T1E377] SubName: Full=Putative yorkie
{ECO:0000313|EMBL:JAA94768.1}; Flags: Fragment; 62..76
MAFNSSSSNNNNSASNTANSSEENDGSSKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQIPYRMRKLP
DSFFKPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTTGPNGLPIHHSRAHSSPASLGKIPAGLVASLTAANS
QQQSSNNSSNGNNSSKTQQGGNGEGASAVAVAQQTQQQQQQQQSLTRQAILHSRGRSYDVSNQHANYGELPPGW
EQAKTQDGRIYYINHNTRTTTWEDPRITAALQQQESLFQQQSSVETLFNTGSQTLLSSAISSPTPN
PYRMRKLPDSFFKPP

tr:A0A182R0B2_9DIPT [A0A182R0B2] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:AFAF020431-PA}; 72..86
MAFNGGNGSSAAAAAAAAAAVAAATNATTDENESTGANKKKNLIILVDKDSNDKLNELFDKTLSNKLPL
QIPYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVGVTGPNGLPIHHSRAHSSPASLGK
IPVGLGGLGGGAVAVAAAAAAAAAAAGGGNAAAGGAGGGGGGGGGGGGGSGGAGSGASTSTGGGVKSAAAAQAAA
QNDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIK
PYRMRKLPESFFMPP

tr:A0A0K8W0H5_BACLA [A0A0K8W0H5] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:JAI44579.1}; 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACLQDGIGPVFTTGAVPFPPSVNAGAAVRMEQGEQPVPKDAPNIQTFHMKQRSYDVVSTIQ
LQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKGKESVNLADNLGPLPEGW
EQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQM
DPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISGNYSESGSLNALSGIDCPDNLVSSLQVT
PFRMRQLPESFFKPP

tr:A0A1A9UJ16_GLOAU [A0A1A9UJ16] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:GAUT006492-PA}; 63..77
MSLSKSSANDENKCSVKTDDSSTTAKTSNNLVVRINQDSDENLQALFDSVLNPHESKRPLQVPFRMRKL
PNSFFNPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQASVATSLSDLQSTTAVVQQPTTTAITQQQPPPPPPE
TQRLQICHSRAHSSPASLQQSYNLHGGNISDDATTSFIQQQQQPQGDGSTGTVAGTGFTNNMVGFTAAAAAAGLN
ANSIIGLVNQANAGATGSGGPLQTYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKTTQWED
PRIQFKQQQALNAAANARLNNKTGGNAASLLNGDLGPLPEGWEQALTETGDVYFINHIDRTTSWNDPRIPILFQK
AVKAKNEMSWVNAVEVDKDNDIFKQKTIQKPLNKHNVSLHMDPFLSGDNHARQESSDSGLSLSSNSFAVNTDFIT
HMDNNMDCISENGSIIDNLDTTLQLNDNICMLSDVLNSPSTKPDNLEWYKLN PFRMRKLPNSFFNPP

tr:A0A0K8TY67_BACLA [A0A0K8TY67] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:JAI19030.1}; 59..73
MSLSKTVGSLNKGNAKEKSTSKESNNLVVRIDQDSDNNLQALFDSVLNPTESKCPLQVPFRMRQLPESF
FKPPATASRSPSVAHSRANSADSAYDTGSQPNVSQGNISTSSVAAVPATITQPQVTANRLSISHSRAHSSPASLQ
QTYNVHIGNVMETSACLQDGIGPVFTTGAVPFPPSVNAGAAVRMEQGEQPVPKDAPNIQTFHMKQRSYDVVSTIQ
LQNELGPLPPGWEQAKTNDGQIYYLNHTTKSTQWEDPRIQLKQQIFQDGLSHNVNLKGKESVNLADNLGPLPEGW
EQAYTESGDVYFINHVNRTTSWNDPRIPDFLQKPVKSQKPGPSWLNIQHIEKEQDYFKPSSEQSSLTRQNGSLQM
DPFLSGDNHARQESSDSGLSLSSNTFSTTADLMPNIDDSMDCISGNYSGCV PFRMRQLPESFFKPP

tr:A0A0P4VUL1_9HEMI [A0A0P4VUL1] SubName: Full=Putative ww domain-containing transcription regulator protein 1 {ECO:0000313|EMBL:JAI56237.1};
44..58
MAGNPDVEFKSSLVVRIDQDSDSELQALFDSVLKPGSKRPLQVPLRMRKLPDSFFNPPSTGSKSPSVSS
ISHSRENSADSAFGNATTTVTGLQVNHPRAHSSPASLQQTYASAQQTQPQHLKQRSYDITALDELGPLPPGWEQA
RTSEGQVYFLNHITQTTTWEDPRKANAVVQQRASDLLNAAASSPGHSTSPQPHQAVHLQRAPSTTGALPSWLQPV
VTQSQTLQATQQKLRLQSLQMERERLKIRQQEIMRQQELMLRDAPATTGLDPFLPGVTDHSRQESADSGLGLGNS
YSLPQTPDDFLTSMDMDASVSDGGTASEMTGLDSHEITSLSDNIDSTDDLVPSLQLGEEFTSDILDDVQALINPT
SKGGNSLTWL PLRMRKLPDSFFNPP

tr:V5HBD0_IXORI [V5HBD0] SubName: Full=Putative yorkie
{ECO:0000313|EMBL:JAB80740.1}; Flags: Fragment;39..53
IEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNLPASFFQQPERSKSASHSRESSNDA
TFSPSSEATAAVVAAAAAVPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQQSYDLADEGSLPPGWEMAKTSTGQR
YFLNHLTQTTTWEDPRKKSSGAGPKHHATPPPPPHTAAPAALHFKNLGPLPDGWEQATTGEGEVYFINHIERTTS
WFDPRIPIHLQKPLLQNQGSVPGISGPSPNQLPGSGNPAAIGGPNSPESMNAISAVVAATSSLTIQQQRQQKLRL
QQLQMERERLKLRQQEILRQTAFLGNPRNEMLLRRNLTEEILPSPTSPPTSDGGVGPTTDPFLGGDFHSRQESAD
SGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPSHQNSELSLDGLQGTGIDMGTENMDSDDLVPSLQEELQGDL
LSDMEALLTSSKDSVLTWL PMRLRNLPASFFQQP

tr:A0A131XWQ1_IXORI [A0A131XWQ1] SubName: Full=Putative transcriptional coactivator {ECO:0000313|EMBL:JAP70722.1}; 63..77
MSSPSQPNIAAAAAAAAANSRGDLIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNL
PASFFQQPERSKSASHSRESSNDATFSPSSEATAAVVAAAAAVPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQQ
SYDLADEGSLPPGWEMAKTSTGQRYFLNHLTQTTTWEDPRKKSSGAGPKHHATPPPPPHTAAPAALHFKNLGPLP
DGWEQATTGEGEVYFINHIERTTSWFDPRIPIHLQKPLLQNQGSVPGISGPSPNQPRPPPPQLPGSGNPAAIGGP
NSPESMNAISAVVAATSSLTIQQQRQQKLRLQQLQMERERLKLRQQEILRQTAFLGNPRNEMLLRRNLTEEILPS
PTSPPTSDGGVGPTTDPFLGGDFHSRQESADSGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPSHQNSELSLD
GLQGTGIDMGTENMDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL PMRLRNLPASFFQQP

tr:V5GZ01_IXORI [V5GZ01] SubName: Full=Putative yorkie
{ECO:0000313|EMBL:JAB69599.1}; 63..77
MSSPSQPNIAAAAAAAAANSRGDLIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNL
PASFFQQPERSKSASHSRESSNDATFSPSSEATAAVVAAAAAVPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQQ
SYDLADEGSLPPGWEMAKTSTGQRYFLNHLTQTTTWEDPRKKSSGAGPKHHATPPPPPHTAAPAALHFKNLGPLP
DGWEQATTGEGEVYFINHIERTTSWFDPRIPIHLQKPLLQNQGSVPGISGPSPNQLPGSGNPAAIGGPNSPESMN
AISAVVAATSSLTIQQQRQQKLRLQQLQMERERLKLRQQEILRQTAFLGNPRNEMLLRRNLTEEILPSPTSPPTS
DGGVGPTTDPFLGGDFHSRQESADSGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPSHQNSELSLDGLQGTGI
DMGTENMDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL PMRLRNLPASFFQQP

tr:A0A1Y3BEU9_EURMA [A0A1Y3BEU9] SubName: Full=Yorkie-like protein
{ECO:0000313|EMBL:OTF79451.1}; 61..75
MHLKPDSETTNHTNNNNNSNNNANGNAIVRVETAADEGLDELFKAVMSPNDGQSRLPQQVPMRQRRLPP
SFFRPPSAASSINSLASASHSRESSLDGGYQSQGQTPIASNGQNKINNSPLIGYSAANGLAIIHPRANSSPAALP
PASLNTGSTSGNASLNGGQGTFGSNDIKSPNDSATNQISHYRQMSYDLDQIRLPDGWEMSYTASGERYFLNHKEK
TTTWEDPRKKIVEEMLRRSTPPPPHQPSQQPQQPIIQPSTPTAVPLQASTTPAVVEPEQLSYIDPSIVPLPDGWE
QAQTSSGDIYFISHVDQTTTWFHPSIPRNLQMKRIQQQTCSIQPPPFQNSTNIPPELVVALKNMNTSGQAQAPPV
AVTATATSTTQNQHLRDLELERERMKQRQEELLQSSLLSSTASNIMLSSSSETAASPFLPLPNGCHSRQESFDSG
LDLGNSSNFSMPHTPDNFLRLSNNAAQQSSSMAAAVVAPTNTPATISDDLAFENMQISGLDLDSESMDFMQGLDM
DLLSNVEELLNSNKDNIMTWL PMRQRRLPPSFFRPP

tr:A0A1Y3B4I1_EURMA [A0A1Y3B4I1] SubName: Full=Yes-associated protein 1-like protein {ECO:0000313|EMBL:OTF74823.1}; Flags: Fragment; 46..60
MAENMSHESTMYVAPNPETHFEELFRVVQQNANNSNNNNQQSTNVPMRQRNFPDSFFRPPSSSSSASHS
RDSSLDASFNSNFIVKNISNPSNSAKPPATPIQSNSSHRNGRHVSPSPPFVHQKAHSLPASLSNQKLVTSSIINL
DDNNSKNSVIISQQQTPPPPPPPQQYRHQQLKLPNHNITNSNNNNFHFRQQSYDIDKIPLPNGWSMSFDSNGERY
FIDHKHKITTWDDPRIKITQQNFTTLAQTSNSNINHPVPFDRQSQQQIQPKSIPMRQRNFPDSFFRPP

tr:H2Z0P5_CIOSA [H2Z0P5] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSCSAVP00000011157}; 34..48
GHNQIIHVRQDSASELEALFNTVMNPNFKSKSLPMKARNLPKSFFTQPDKPRQTSISSSSDSNTSHASS
ILAPNANNNNGSSVGSVSMAPGSPMNGNISHKSNYPMSPAQRLKASDIPADMPLPAGWSAAKTADGQQYYMNHND
RSTTWEDPRIPIIKQQRQSQPIYPHLQHISLPPGWEQATTPQGEIYFIDHQTKTTSWVDPRFQGRFYVNQMDMSS
VGQSRPTPMPPQQQSMLKHLVQEKEHLMRRQLLKQKIHPNPRNFTPTPEISPQPQKFHPNPRNSPQPQKFTPTPE
IHPSPPFGNPSFHQRDASLDSGVGMGSNYSLPRTPDGFLNNVEEMETGTTQPQSTHHAANQRFPDFLDTLPASSV
DFNGSPVPTSGGQRAGGNMDGSELVPSLQDTLPQDFDVESMLNHVKTENIDNSMIWL PMKARNLPKSFFTQP

tr:H2Z0P4_CIOSA [H2Z0P4] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSCSAVP00000011156}; 34..48
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ILAPNANNNNGSSVGSVSMAPGSPMNGNISHKSNYPMSPAQRLKASDIPADMPLPAGWSAAKTADGQQYYMNHND
RSTTWEDPRIPIIKQQRQSQPIYPHLQHISLPPGWEQATTPQGEIYFIDHQTKTTSWVDPRFQGRFYVNQMDMSS
VGQSRPTPMPPQQQSMLKHLVQEKEHLMRRQLLKQKIHPNPRNFTPTPEISPQPQKFHPNPRNSPQPQKFTPTPE
IHPSPPFVPQLSNPGMDGFMGQGNPSFHQRDASLDSGVGMGSNYSLPRTPDGFLNNVEEMETGTTQPQSTHHAAN
QRFPDFLDTLPASSVDFNGSPVPTSGGQRAGGNMDGSELVPSLQDTLPQDFDVESMLNHVKTENIDNSMIWL
PMKARNLPKSFFTQP

tr:H2Z0P3_CIOSA [H2Z0P3] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSCSAVP00000011155}; 46..60
NNDSPTQTTITQGHNQIIHVRQDSASELEALFNTVMNPNFKSKSLPMKARNLPKSFFTQPDKPRQTSMY
HHGHSHNFHFRSKSSPASLQLMDVGNLTVKASDIPADMPLPAGWSAAKTADGQQYYMNHNDRSTTWEDPRIPIIK
QQRQSQVAVMQSQSVSGNLLPPPAHSNPGHNIQTDHSVTPTDPHVPSQVNQMDMSSVGQSRPTPMPPQQQSMLKH
LVQEKEHLMRRQLLKQKFHPNPRNSPQPQKFTPTPEIHPSPPFVPQLSNPGMDGFMGQGNPSFHQRDASLDSGVG
MGSNYSLPRTPDGFLNNVEEMETGTTQPQSTHHAANQRFPDFLDTLPASSVD PMKARNLPKSFFTQP

tr:H2Z0P6_CIOSA [H2Z0P6] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSCSAVP00000011158}; 34..48
GHNQIIHVRQDSASELEALFNTVMNPNFKSKSLPMKARNLPKSFFTQPDKPRQTSISSSSDSNTSHASS
ILAPNANNNNGSSVGSVSMAPGSPMNGNISHKSNYPMSPAQRLKASDIPADMPLPAGWSAAKTADGQQYYMNHND
RSTTWEDPRIPIIKQQRQTPTDPHVPSQVNQMDMSSVGQSRPTPMPPQQQSMLKHLVQEKEHLMRRQLLKQKIHP
NPRNFTPTPEISPQPQKFHPNPRNSPQPQKFTPTPEIHPSPPFGNPSFHQRDASLDSGVGMGSNYSLPRTPDGFL
NNVEEMETGTTQPQSTHHAANQRFPDFLDTLPASSVDFNGSPVPTSGGQRAGGNMDGSELVPSLQDTLPQDFDVE
SMLNHVKTENIDNSMIWL PMKARNLPKSFFTQP

tr:A0A2T7PTI5_POMCA [A0A2T7PTI5] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:PVD36736.1}; 49..63
MLVFTSTLHVKGCLLEIVDNGNLAAMPYPRYPSYPIHTPDRVILVPSTPMKLRALPQSFWQQPNLAQQV
SPATMYPLLPPLCNKDTEEDIAEVRPVTPPNESGAETKRLAPERKISVANTDLLFKLFENISDEKKTATVHLKRG
RPRRMPIKSCTKGLLFGNDPYLVDAIADTLFPQLSIESSRFGGNTSLQLVTLGTGDKTVTLPSLTLEQNYPQMLS
ELVTHI PMKLRALPQSFWQQP

tr:H2Z0P2_CIOSA [H2Z0P2] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSCSAVP00000011154}; 51..65
MDVDENNDSPTQTTITQGHNQIIHVRQDSASELEALFNTVMNPNFKSKSLPMKARNLPKSFFTQPDKPR
QTSMYHHGHSQSVGGLVAPNSVQINHSRSSSSDSNTSHASSILAPNANNNNGSSVGSVSMAPGSPMNGNISHKSN
YPMSPAQRRVAHSAFVNSQGHNSLQIPQVSHSRSKSSPASLQLMDVGNLTVKASDIPADMPLPAGWSAAKTADGQ
QYYMNHNDRSTTWEDPRIPIIKQQRQSQVAVMQSQSVSGNLLPPPAHSNPGHNIQTDHSHISLPPGWEQATTPQG
EIYFIDHQTKTTSWVDPRFQGISPQTNNNPPNNSQLQQQLMKVNQMDMSSVGQSRPTPMPPQQQSMLKHLVQEKE
HLMRRQLLKQLSNPGMDGFMGQGNPSFHQRDASLDSGVGMGSNYSLPRTPDGFLNNVEEMETGDGNRRVHGSQQH
IGSSTQPQSTHHAANQRFPDFLDTLPASSVDFNGSPVPTSGGQRAGGNMDGSELVPSLQDTLPQDFDVESMLNHV
KTENIDNSMIWL PMKARNLPKSFFTQP

tr:A0A3B0JPZ1_DROGU [A0A3B0JPZ1] SubName: Full=Blast:Protein yorkie {ECO:0000313|EMBL:SPP73228.1}; 65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKSAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLMQNY
NVRSRSEANPGASSQGPSYPESSAEFPNSAANTIELDGMSTCMEGQDMQTVHKKQRSYDVVSPIQLQSQLGALPP

GWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSDVLQTTKQTTTSTIANSLGPLPDGWEQAV
TESGDIYFINHIDRTTSWIDPRMQSGLTVLDCPDNLVSSLQIEDNICTNLFNDAQTIVNPPSSHKPDDLEWYKIN
PFRMRKLPNSFFTPP

tr:A0A3B0JII2_DROGU [A0A3B0JII2] SubName: Full=Blast:Protein yorkie
{ECO:0000313|EMBL:SPP73229.1}; 65..79
MLTTMSTSNTNNIIEKEIDDEDMLSPIKSSNNLVVRVNQDTDDNLQALFDSVLNPGDAKRPLQLPFRMR
KLPNSFFTPPAPSHSRANSADSTYDAGSQSNINKSAQPVDVQQPAISQIQPSQQSRLAIHHFRARSSPASLMQNY
NVRSRSEANPGASSQGPSYPESSAEFPNSAANTIELDGMSTCMEGQDMQTVHKKQRSYDVVSPIQLQSQLGALPP
GWEQAKTNDGQIYYLNHTTKSTQWEDPRIQYRQQQQRLMAERIKQSESGLTVLDCPDNLVSSLQIEDNICTNLFN
DAQTIVNPPSSHKPDDLEWYKIN PFRMRKLPNSFFTPP

tr:A0A2Y9D1E4_9DIPT [A0A2Y9D1E4] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:ADIR016051-PA}; 83..97
MAFNGGAAGGNGSAAAAAAAVAAAVAAGAGGGGAANNNATDENESTGANKKKNLIILVDKDSNDKLNEL
FDKTLSNKLPLQIPYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVAGVTGPNGLPIHH
SRAHSSPASLGKIPVGLGGLGGGVVAAAAAAAAAAAAAGGNGAGGGGGGGGGGGGGAGSGAAAGSSAAVKSAAAQ
AAAQNDASSLGAAVLQQAALSKAAIQHLHSRGRSYDVSNLNANFGELPPGWEQAKTQDGRIYYINHNTRTTTWED
PRIIALQESLFQQQSSVETIYNTGSQTLLSPTISSPTPTNNVVFPDAIQMTNDNLAPSNAAPPAAMLTGSNVDLG
PLPEGWEEGITEKGERYYINHATRSTTWRDPRLSNQDWAVQEQTVRLYNLQLERERLRKRQQEIKSHMGDDPFLS
GIADHTRQESGDSGLSESSMTQSMPHTPEFLSSIDDSMDGLSMTDNTMDTIAFGDNLETPDEFMLDDPLLLEKID
AVTNLSLMDPTSSKPDNTLYDII PYRMRKLPESFFMPP

tr:A0A0L8FZ90_OCTBM [A0A0L8FZ90] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KOF69904.1}; 42..56
MSQQRTEQKGNQVVHVRGDSDSDLEALFKAAMNPSEVPHQLPLRMRNLPASFFTPPDPTQQKQHSREGS
TDSTGAGSGSVLNSPGLTIAHPRAHSSPASLAQTMSAAPPPSSQHVRQHSYDLTDEQPLPPGWEMAKTNQGHRYY
LK PLRMRNLPASFFTPP

tr:A0A0L8FXC6_OCTBM [A0A0L8FXC6] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KOF69030.1}; 67..81
MIENSRNFPSSGNTAFLVPSISATPMPPSLTSFSQSQSMTAPLLTTSSIDGALSYSDNKHHPYPPIPLR
QRDLPASFWQEPNSQTRQRCLDHLAAAAAGLSHTSLQSRSSTLSGSSQLASNSFLSSSPMSSSNSHFLPFLALYP
DLMLSNTAFNRYVRRPSQLNPAGDLASSTPLNRLKGGTLNSSIGDAVQQNGRLNPYSAQRTQSRFPITEYLYNMY
GSKYRYANPVVLQQTPPLSEKTWDDVRIKMIEANSRSNTHHSTEANEKLNSNKNSKHDDIVNNPINSQIYLKRRA
SDNHIKSLDDSVLPLLSLQSLQTSSSSSSPTDKNATIKTAGTALSERAADFSLRLSDCYKSSTKHSPHSRLSDGM
LFDNSVNDSDQLNNARCVCCDVLKDSCPNQPKRNNSNSLSQTNNGTSVSTATNDNATLATTNNSSNPGELGFLPY
FQVFPHLWPPFPPPLPPSASLSLAATATARERYLPDNIYAYSNQERSIRLMRPRSTLGARYHPFGDVR
PLRQRDLPASFWQEP

tr:A0A226EVH2_FOLCA [A0A226EVH2] SubName: Full=Transcriptional
coactivator YAP1 {ECO:0000313|EMBL:OXA60841.1};51..65
MATGGSGGGLPNGQSHKNQVIHIRGDSDSELQALFDSVLAPNANRRPKQVPLRLRNLPDSFFNPPSIGS
KSPSCSVSHSRENSVDSTLNPVRRSPLSTAGASHSRAHSSPATLEQTYSVAAALPGLSLSQSGSANNLSDDPLPP
GWEQACTPEGQIYFINHITRSTTWEDPRKAQTQQILAAIGNGTGSLSSQANHSGNVIQAVGSAVGPLPEGWEQAI
TPEGEIYFIDHMNRTTSWFDPRIPMHLQRPQVLQHQINAAALAQASALAAASAAAISASSNVNTAVTSAAGTASL
LNNNTSIQLSRQQEVRLQQLQLERERLKLRQQEIMQQMEKEQARLRQQNRLQQMEDGEIDPFLGGSMVNPSTPSS
DFHSRQESADSGLGMGNSYSLPNTPEDFLSNMDDNMDTISGLFYPRVYYPSETE PLRLRNLPDSFFNPP

tr:U4UWQ5_DENPD [U4UWQ5] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:ERL94741.1}; 41..55
MARNQDEAKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFTPPSTGSKSINHSRENS
VDSAFDVSGPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQPPAHHHIKQRSYDVASKSEDNTPLPPGWEQARTPE
GQVYYLE PWSMRKLPDSFFTPP

tr:A0A1A9Y6J1_GLOFF [A0A1A9Y6J1] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:GFUI033359-PA}; 63..77
MSLSKSSANDENKCSVKTDDSSTTAKTSNNLVVRINQDSDENLQALFDSVLNPHESKRPLQVPFRMRKL
PNSFFNPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQASVATSLSDLQSTTAVVQQPTTTTITQQQPPPPPPE

TQRLQICHSRAHSSPASLQQSYNLHGGNISDDATTSFIQQQQQQGDSSTGAVAGTGFTNNMVGFTAAAAAGLNAN
SIIGLVNQANAGATGAGGPLQTYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKTTQWEDPR
IQFKQQQALNAAANARLNNKTGGNAASLLNGDLGPLPEGWEQALTETGDVYFINHIDRTTSWNDPRIPILFQKAV
KAKNEMSWVNAVEVDKDNDIFKQKTIQKPLNKHNVSLHMDPFLSGDNHARQESSDSGLSLSSNSFAVNTDFITHM
DSSMDCISENGSIIDNLDTTLQLNDNICMLNDVLNSPSTKPDNLEWYKLN PFRMRKLPNSFFNPP

tr:A0A194QUS4_PAPMA [A0A194QUS4] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:KPJ08730.1}; 44..58
MALNSDSEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGAAPVSHSRAHSSPASLQQTYAAGQQTQQAPLHHQHSKQRSYDVGTHMQDDLGPLPSGW
EQARTPEGQIYYLKLEVRIQSVPVSAIVSRPPRRDDRSGRGLKPMRHQSFCHLVNNPTGVTNMVNNKNSKMNIIS
PLRMRQLPKSFFNPP

tr:A0A182R729_ANOFN [A0A182R729] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:AFUN001978-PA}; 70..84
MAFNGGAAGGNGSAAAAVAAGAANNASDENESTGANKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQI
PYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVATGPNGLPIHHSRAHSSPASLGKIPV
GLGGLGGGVVAAAAAAAAAAAAAGGNGAGGGGGGGGGNSGGGAGNNAGASGSKSAAAAAQAAAAAAAAAQNDASS
LGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIK PYRMRKLPESFFMPP

tr:V5GQC1_ANOGL [V5GQC1] SubName: Full=Yorkie protein
{ECO:0000313|EMBL:JAB63817.1}; 41..55
MALNQDEAKQEVRVNQDSETDLQALFDTVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATAAAPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQAPVHHIKQRSYDVASKTEDNTPLPPGWEQAR
TPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAQQHQSAEQLLTAHQISHPQSPNPNTAKVNSDVDLGPLPEGWEQA
QTPEGEIYFINHQTRTTSWFDPRIPTHLQQRPAGANLVGSTWHSQALSSSPSKAQQIRLQQLRMERERLKQRQQE
IMRQQDIMMRSSSDLPVMDPFLSSLTDHSRQEYRGVVGLVWGQHTRCHTHLKIF PWSMRKLPDSFFNPP

tr:V5I8I0_ANOGL [V5I8I0] SubName: Full=WW domain-containing transcription
regulator protein 1 {ECO:0000313|EMBL:JAB63816.1}; 41..55
MALNQDEAKQEVRVNQDSETDLQALFDTVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSRENS
VDSAFGGGATAAAPVNSVPLQTAHHRAHSSPASLQQTYAVGQQQAPVHHIKQRSYDVASKTEDNTPLPPGWEQAR
TPEGQVYYLNHTTRTTTWEDPRKSLAAQAAAQQHQSAEQLLTAHQISHPQSPNPNTTHLQQRPAGANLVGSTWHS
QALSSSPSKAQQIRLQQLRMERERLKQRQQEIMRQQDIMMRSSSDLPVMDPFLSSLTDHSRQEYRGVVGLVWGQH
TRCHTHLKIF PWSMRKLPDSFFNPP

tr:A0A183R065_9TREM [A0A183R065] SubName: Full=Uncharacterized protein
{ECO:0000313|WBParaSite:SROB_0000934101-mRNA-1}; 38..52
MEGYDSRKPPSVRVTVLEDPNSSLQELFNPASQRQQVPLHQRNLPKSFFVPPGDVNDNSRLSKLNSVNC
NERNSTDFVVFHGKANSSPACLDAALRTSISANVPNHSHQKSLDVASKYKTDFNPDFAFSGSCGPGIFQGQRNSQ
QTALLYGPTMTFAISELPVGYDMAINESNQVYFLNHQTQETTWFDPRIPEKFQKWGMTPEELEQVHLRYAKQFLC
TTPSSNLNVCVQQMPFFAQTGIHYVDTYQMQSFSVWLI PLHQRNLPKSFFVPP

tr:T1IUK9_STRMM [T1IUK9] SubName: Full=Uncharacterized protein
{ECO:0000313|EnsemblMetazoa:SMAR004835-PA}; 47..61
MSEDELEIHEQKGNHVLHIRGDSDSDLEALFKSVINPTDTQVSLIVPMRLRKLPKSFFKPPETGSRTPP
QQTSTSSRSGLPASGGTTTGLQIHHPRARSSPASLQQSLIPNEPPPQQHARQQSYDISDDLPLPPGWEMSKTLTG
QRYFLK PMRLRKLPKSFFKPP

tr:T1JIB8_STRMM [T1JIB8] SubName: Full=Uncharacterized protein
{ECO:0000313|EnsemblMetazoa:SMAR013599-PA}; 47..61
MTQQQRDLLEQKCNQIVHIRGDSDSDLEALFNAVMNPSDTQVQLTVPMRLRKLPNSFFKPPNAGSKTLP
QIQPSSPAALSREANPESSIPSPPQTTSAGLQIHHLRAHSSPASLTQNIVAPAQHQHLRQQSYDITDDIPLPPGW
EMARTTSGLRYFLK PMRLRKLPNSFFKPP

tr:A0A369SJ87_9METZ [A0A369SJ87] SubName: Full=Transcriptional
coactivator YAP1 {ECO:0000313|EMBL:RDD46562.1};35..49
MDQKPQPVVHERHDSKEELERLFNVLNSQNNPTVPMRDRRLPYSFFQGPTRPYDSNNTTATLSTDNNFG
VGDSIVHPRIKSSPASFPYHNNNSDMTNSNNSAFQHRNQPLHPKHHSSSAAFRNENAHSNKSFPADVNYKNLINP
NVAMRQLPMASPVQQNGLHIRGGSGSGLHPNNGPMQAKLPDGWEKAFTPEGQVYFVNHITRTTSWNDPRRSMMQA

QSPNPVIQSPLKTTYDLPNDKAMQELQMMQLERKHLEQKREEMLRKESEIKRQIETYQRQQIPVGRTEQLLHRPG
LATTAAPNGIPNHNPGLIKREPSSPSPMQIDYPTPQHNSLPTDIQANLSQGQMLNYRGGNISINNQLANGGFNNQ
IISENNEPDIEELIQSLSTSAQDLDIEATLIDRDAIAKIESDLVNTEPDWY   PMRDRRLPYSFFQGP

tr:A0A154P2I5_9HYME   [A0A154P2I5] SubName: Full=Yorkie like protein
{ECO:0000313|EMBL:KZC06149.1};   46..60
MALNQDVDQLSKSNLVVRMDQNSESDLQALFDSVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGTAPGAGAVAAAAAAGLTVAHPRAHSSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDV
ISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAAAANVAAVAAAVDNGKTTSAATNSLGPLPDGW
EQARTPEGEIYFINHQTRTTSWFDPRIPTHLQRAPTSGAMLPQNWLQQPTGGGIQSNQTLQACQQKLRLQSLQME
RERLKQRQQEIMRQQELMLRQSTTDAAMDPFLSGINEQHARQESADSGLGLGSAYSLPHTPEDFLANIDDNMDGT
SDGGAPMETPDLSTLSDNIDSTDDLVPSLQLSEDFSSDILDDVQSLINPNTTKPENVLTWL
PLRMRNLPDSFFNPP

tr:A0A2A4J152_HELVI   [A0A2A4J152] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PCG65254.1};   44..58
MALNSDAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAGQQNQQPPLHHQHTKQRSYDVGTHIPDDLGPLPPGW
EQARTPEGQIYYLNHITKTTTWDDPRKTLAAQSVAGSVQHQSTDALLTQAASPQNIPSTPAPAAKSTSSNTTTDP
LGPLPEGWEQAATAEGEIYFINHAARTTSWFDPRIPQHLQRTPAAGGAVPDGGWANASLQACQQKLRLQSLQLER
ERLKQRQQEIRLQQELIMARQSSSIVSSLANSTGVASTDLPLDPFLSGLSDHQRQESADSGLGMGVPHSYSMPHT
PEGFLAGMDDRMDCTSEAGANLDSTDITLADNLDSTDDLVPSLQLNEFTNDILLDDVQSLINSTPSKPDNVLTWL
PLRMRQLPKSFFNPP

tr:E9IY16_SOLIN   [E9IY16] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:EFZ14541.1}; Flags: Fragment;47..61
MALNQDVVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGVAVTGGTPNGGGGAGGSGGVTGTGSGNAGAGGGANGTANAIAAAAAVAAAAGLTVSHPRAH
SSPASLQQTYASAQQAPQHAPQPHARHHHHQKQRSYDVIAPTVDDLGPLPTGWEQARTQEGQIYFL
PLRMRNLPDSFFNPP

tr:A0A1B0FBE8_GLOMM   [A0A1B0FBE8] SubName: Full=Vismay
{ECO:0000313|VectorBase:GMOY000857-PA};   63..77
MSLSKSSANDENKCSVKTDDSSTTAKTSNNLVVRINQDSDENLQALFDSVLNPHESKRPLQVPFRMRKL
PNSFFNPPAASPKSPTVSHSRANSVDSAYDCGSQPNINQASVATSLSDLQSTTAVVQQPTTTTITQQQPPPPPPP
ETQRLQICHSRAHSSPASLQQSYNLHGGNISDDATTSFIQQQQQPQGDGSTGTVAGTGFTNNMVGFTAAAAAAGL
NANSIIGLVNQANAGASGSGGPLQTYHMKQRSYDVISPIQLQNELGPLPPGWEQAKTNDGQIYYLNHTTKTTQWE
DPRIQFKQQQALNAAANARLNNKTGGNAASLLNGDLGPLPEGWEQALTETGDVYFINHIDRTTSWNDPRIPILFQ
KAVKAKNEMSWVNAVEVDKDNDIFKQKTIQKPLNKHNVSLHMDPFLSGDNHARQESSDSGLSLSSNSFGVNTDFI
THMDNMDCISENGSIIDNLDTTLQLNDNICMLNDVLNSPSTKPDNLEWYKLN PFRMRKLPNSFFNPP

tr:A0A224YXB1_9ACAR   [A0A224YXB1] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:MAA22247.1};   59..73
MSSSPSQPNNGAATNGRGEMIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSDRVPLSVPMRLRNLPASF
FQQPDRSKSASHSRESSSDATFSPSEASAAAAAAAAAAAVAAPPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQQ
SYDLVDDLPPGWEMAKTSTGQRYFLNHLTQTTTWDDPRKKTPSNKHHATPPPPPHTAAPPAGPFKNLGPLPDGWE
QATTAEGEVYFINHIERTTSWFDPRIPAHAQKPLLQSHASPLPGHAQSQGSGNAVSSTGPTSPDTMNSISAVVAA
TSSLTLQQQRQQKMRLQQLQMERERLKIRQQEILRQTAFLGNSARNEMMLRRTLTEEILPSPTSPTASDVAGVGP
TTDPFLGGDFHSRQESADSGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPNNQNSELSLDGLQGTGIDLGTEN
MDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL   PMRLRNLPASFFQQP

tr:A0A2R5LJ54_9ACAR   [A0A2R5LJ54] SubName: Full=Putative transcriptional
coactivator yap1 {ECO:0000313|EMBL:MBY09455.1}; Flags: Fragment; 41..55
DVIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSNRVPLSVPMRLRNLPASFFQQPERSKSASHSRESSS
DATFPDTAGPPLAINHPRAHSSPASLQQTYSSPQQQHLRQRSYDLADEASLPPGWEMAKTATGQRYFLNHLTQTT
TWEDPRKKTPGGSKQQTPPPPPHTAAPVLPNFKNLGPLPDGWEQATTSEGEVYFINHIERTTSWFDPRIPIHLQK
PSLQGTSAQPSEGNADISAVVAATSSLTIQQQRQQKLRLQQLQRERERLKLRQQEILRQTAFLGNPARNQEMLLR
RTLTEEILSNPTSPSDPFLGGDFHTRQESADSGLGLGPSLPPEDFLSTMDDSTMDGLNDDASQRDISLESLQGTG
LDLGAENMDSDDLVPSLQEELQGDLLSDMEALLTSSKDSVLTWL   PMRLRNLPASFFQQP

tr:A0A224YX93_9ACAR [A0A224YX93] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:MAA22248.1}; 59..73
MSSSPSQPNNGAATNGRGEMIEQKGPNHIVRIRSDSDINLDDLFKAVMQPSDRVPLSVPMRLRNLPASF
FQQPDRSKSASHSRESSSDATFSPSEASAAAAAAAAAAVAAPPSLPVNHPRAHSSPASLQQSYNAPSPQHLRQQ
SYDLVDDLPPGWEMAKTSTGQRYFLNHLTQTTTWDDPRKKTPSNKHHATPPPPPHTAAPPAGPFKNLGPLPDGWE
QATTAEGEVYFINHIERTTSWFDPRIPAHAQKPLLQSHASPLPGHAQSQGSGNAVSSTGPTSPDTMNSISAVVAA
TSSLTLQQQRQQKMRLQQLQMERERLKIRQQEILRQTAFLGNSARNEMMLRRTLTEEILPSPTSPTASDVAGVGP
TTDPFLGGDFHSRQESADSGLGLGPNYSLPHTPEDFLSSMDDSIDAGLNDDPNNQNSELSLDGLQGTGIDLGTEN
MDSDDLVPSLQLSTNFFVGLSPF PMRLRNLPASFFQQP

tr:A0A0L7LBH0_9NEOP [A0A0L7LBH0] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KOB72745.1}; 44..58
MALNSEAEQKSNLVLRVDQDSDSVLQSLFDTVLKPDSKRPLQVPLRMRQLPKSFFNPPSTGSKSPSVSH
SRENSADSAFGSSSATGASPVSHSRAHSSPASLQQTYAAAGQQNQQQPPLHHQHAKQRSYDVPHIPDDLGPLPPG
WEQARTPEGQIYYLK PLRMRQLPKSFFNPP

tr:A0A3Q0KCM0_SCHMA [A0A3Q0KCM0] SubName: Full=Uncharacterized protein
{ECO:0000313|WBParaSite:Smp_014840.1}; 38..52
MEGYDSRKPPSVRVTVLEDPNSSLQELFNPASQRQQVPLHQRNLPKSFFVPPGDVNDNSRLSKLNSVNC
NERNSTDFVVFHSKANSSPACLDAALRTSISANVPNHSHQKSLDVASKYKTDFSPDFAFSGSCGPGFFQGQRNSQ
QTALLYGPTMTFAISELPVGYDMAINESNQVYFLNHQTQETTWFDPRIPEKFQKWGMTPEELEQVHLRYAKQFLC
TTPSSNLNVCVQQVDRISPSLVPSPTACVSASSPSGFLSKNQSGVPSPMVSISVSPNSSTSGLPLHNLPLSSSST
CTNVQNRLRSTTAVNNNNSNNNNNGNNGNNNQNIAANHRAHPNQLPYPHHQHSHQVNEQLQTSGGIQHQRQHSQG
LPVQSQPTSQSLVTHFRSCSQPVSMSSGRDCGSSTGIILSSNSSGVSTATTTVTGTLGHTQLRIPGSLSGILSSS
SSLTGLCGSNVNTGQQGCVTGSISTSSGQLVQGLECLRLNASVTSTNALNNSNHVLLDQQQIPKTQRVQQPQFIL
SASSGIVYGSNINAAAARLVGTVLPNTPQPGNQHSHQSSMDSGVGQSLTGQSNPSANQTPEHTVMLFCDPSIGAC
GAEHMEGIAYPNEELICTGFNDFDNIDISDMST PLHQRNLPKSFFVPP

tr:A0A195E7L9_9HYME [A0A195E7L9] SubName: Full=Yorkie like protein
{ECO:0000313|EMBL:KYN20824.1}; 46..60
MALNQDVDQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRLRNLPDSFFNPPSTGSKSPSI
SHSRENSADSAFGAAVPATPNGDQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLNHLTRTTTWEDPRKTAA
AASVAAVAAAVESSKSNALGPLPDGWEQARTAEGEIYFINHQTRTTSWFDPRIPSHLQRTPASGAMLPQNWQLQQ
PTGIQSNQNLQACQKQKIRLQSLQLERERLKQRQQEIMRQQQEMMLRQSTTDAVMDPFLSGINEHARQESADSGL
GLGSAYSLPQASDDFLNIDENMDGTSDGGAPMDTPDLSTLSDNIDSTDDLLPSLQLNEEFSTDILDDVQSLINPN
TTKPENVLTWL PLRLRNLPDSFFNPP

tr:A0A1B1JCF7_SACKO [A0A1B1JCF7] SubName: Full=Yes-associated protein
1-like protein {ECO:0000313|EMBL:ANS11592.1};>gp:KU359113_1 [KU359113] yes-associated protein 1-like protein [Saccoglossus kowalevskii] 45..59
MTMDPKGHQIVHVRGDSDTDLEDLFRAVMNPTGIVKEPLPQHPVPLRMRKLPPSFFKEPDKPMASSPSG
SHSRESSTDSTNPGGPFGAQTLGLPVNHPRAHSSPASLQQMQAAAASQQQQQTVTPQHTRHTSYDVTTIEDLPLP
PGWEVARTPSGQRYFLNHMDQTTTWNDPRKNLTQAQLAQLQQAQQARALLQQQQQPQQQQQPDLGPLPATWEQAS
TPEGLRATAGQTVGLSGTQLNRNQQIQQALQQQQLQAQQQGPLSRQQQHPQKERLQQLQLEREKLRRRQLEIQQQ
EMLIRKEIVGEDGQPVSKSNQQSQDREMTSVSTTGVDPFLSGGTYHSRDESGDSGLGMSSNYSLPRTPDDMLSNV
DEMDTSDGERKPDMNAATPIQTPMNDYLESMQGTNVDIGSLEDEEGDDLVPSLQEALSSDILTDVEAVLSPHKIE
NFLTWL PLRMRKLPPSFFKEP

tr:A0A195CJ14_9HYME [A0A195CJ14] SubName: Full=Protein yorkie
{ECO:0000313|EMBL:KYN00059.1}; 47..61
MALNQDVVEQLSKSNPVVRVDQNSESDLQALFDTVLKPDSKRPLQVPLRMRNLPDSFFNPPSTGSKSPS
ISHSRENSADSAFGAAVPATPNGGSVPNGGTNGTANAIAAAAAVAAAAGLTVSHPRAHSSPASLQQTYASAQQAP
QHAPQPHARHHHHQKQRSYDVISTVDDLGPLPHGWEQARTPEGQIYFLK PLRMRNLPDSFFNPP

tr:A0A182M3F8_9DIPT [A0A182M3F8] SubName: Full=Uncharacterized protein
{ECO:0000313|VectorBase:ACUA008517-PA}; 70..84
MAFNGGAAGGNGSAAGAVAAGAANNASDENESTGANKKKNLIILVDKDSNDKLNELFDKTLSNKLPLQI
PYRMRKLPESFFMPPSSGSKSPSVSHSRENSADSAFGSGTTILGGVTGVATGPNGLPIHHSRAHSSPASLGKIPV

GLGGLGGGAVAAAAAAAAAAAAAGGNGAGGGGGGGGGNGGGGAGNNAGASGSKSAVAAAQAAAAAAAAAQNDASS
LGAAVLQQAALSKAAIQHLHSRGRSYDVSNLHANFGELPPGWEQAKTQDGRIYYIK PYRMRKLPESFFMPP

tr:A0A3M7PAX5_BRAPC [A0A3M7PAX5] SubName: Full=E3 ubiquitin-ligase BRE1A-like {ECO:0000313|EMBL:RMZ96251.1}; 341..355
MDDSKSQLPTVQPQVRKLYFKSSATEALHSAILLKSRNSNQKSKHVTKMPSIGTAATPKTESDDHELES
PLKIKENLQTSAKTIKSGLDMLRSSSDDEDSHSDNLERKKPDIILLDINKSLRKRGKEEALSNSSSDEEDSSLRT
NKQTSLNLNLKPIGNKPPYITPVVSANYSANYLDNELVASPNSLSCPSGFSSPHSVKSQKSCSDQEFSSSLASIS
SPTSCCSSLTTNDGLLDFDDSSSTASGPVYVRQPGFEHHAHEVLKQDVKLNNLKNFVINDKSKSKFQKKLNGSSS
TGALVENCEAKPKAKKKMCVMNPDYLTENSESSIMLKPIRQKREPLPLRLRALPASFWEQPNLPNISPATMYLPP
LHRNEIENDLGEHLNEDYVHSSSVLREREVRVSPANTELLFKLFDNIEQCKDKKQVQLILNSRGHSKVKAMTKAL
IKGEDPCIQDAEGLFPQLKLDSKTETNYISNSVSSSNLPLIEQNYSQILSEIVASL PLRLRALPASFWEQP

tr:A0A2L2YT68_PARTP [A0A2L2YT68] SubName: Full=Yorkie-like protein {ECO:0000313|EMBL:LAA11274.1}; Flags: Fragment; 48..62
MSQQRDVIEQKQGHNKILRIRGDSETNLDDLFNAVMHPKGNQAHQSKPMRSRNLPKSFFQQPERGSKSA
SHSRESSTDNTFSSPPPQQVPQSNNNNNNRSAASPGISNSNNAVSPPPAHPNGLVINHPRAHSSPASLQQTYNAA
QHQHLRQQSYDITDIIPMPAGWEMARTENGQRYFLNHLTKTTTWEDPRKNLSTGSLSSSSGVTSLSPSTSPASSL
INLQLVNNLAQGPLPDGWEQATTPDNEIYYINHRTQTTSWYDPSLPPQLQNTPVVPILGYGAHSQSVLGLSSQQS
QASAASVTTSLTAASNQTLQQQQQQLRLQRLQMERERLRLRQQEILRNSNLGNSSPTLNEYLMRKTLQEEGVANS
SSSNRHTDASQSNSTNLDPFISAD PMRSRNLPKSFFQQP

tr:A0A2B4S6G3_STYPI [A0A2B4S6G3] SubName: Full=Protein **FAM181**B {ECO:0000313|EMBL:PFX24075.1}; 244..258
MKHCRNDTSGISSLSDEKGNKVSAPDQLANILNTQFQSVFSIEIPAPQDLLPPISPFPRMPDILISKSG
VLKLLQELKVHKADGPDQEMNSLGEESVATPTSLLNFVSNATSALKFALDKPIKPKRKVNHRKYLQRQLSGRSSS
AATSSFDGSWISQGEILFDHVLKSGQRGSASAVARAEKSSTAIPWKNRSEETQALGTDNVLDVFQKKRAQGKEKN
WKITRSQQINDTKTSQALFSQPSQPLKKRKLPESFWTEPSPKASRKPLQATRNSKTNLATNELQRSELEILDWLR
PELDDFIERWSEESECASNNSSRPDSLSDSPSTIDPHSPYSDESENVGLMDEFFEQRVPFSFDSSTKNGECTSNI
PSTRNYANANINFVNNRTYNVPQDYVQRPLNHSVSCYGGQYGFSANEWSANPVQPNYFETGYNVLS
PLKKRKLPESFWTEP

tr:A0A210QKD5_MIZYE [A0A210QKD5] SubName: Full=Yorkie-like {ECO:0000313|EMBL:OWF49209.1}; 43..57
MSQDQTERKGTQVVHVREDSGSELDALFNAVMNPKSGQSGQIPLRMRNLPASFWKPPDQPQRPVQHMKQ
GSNDSTGGYPGHPSGVGPSQGNLQIAHMRAHSSPASLQQTLSTVPQGPPQAPAHHARQHSCDALLDNEPLPPGWE
IAKMPDGQRYYLKQNPPPDIFNKASSPNSNHLTQSTTWQDPRKAVSTTALNSQQSPPSSQQSPNVSMQNLNLDSL
PQGWEQASTPEGDIYYINHHERTTSWYDPRIPERMRQQARINSVGPGPGQRQMGQQLAPPPQHPQQNGGTQRSQQ
ANLQFSKLQMEKERLRKRQEEIARQQQLQQQQQQQQDAIPVSQSINISQANEMTSVTDPFLGQTNSSDHSRQES
TDSGVGGMGTGTNYSMPRTPEDFLSNVDEMDTQEGGHRQGDFNNMDIGGNIGESGEPSNMDSEDLVPSLQEDISN
ELLNDMENVLNSNKLEDNLLTWL PLRMRNLPASFWKPP

tr:A0A1L8DHT7_9DIPT [A0A1L8DHT7] SubName: Full=Putative transcriptional coactivator yorkie {ECO:0000313|EMBL:JAV06022.1}; Flags: Fragment;
102..116
DCVWDFFCTTNPWNCASARDSVISWKAESGCFRTLAMALNNSNSSGSSNNLSNTPNNNNNESENVKQGN
LVVRMDEDSATKLQALFDTVLKPSEQNRPLQIPLRMRKLPNSFFNPPSTGSKSPSVSHSRENSIDSAFGSGTTIV
YAPGGGASGAANSVLTQRLSISHSRAHSSPATLEQTHAASLKSAAAAASVATANAAQNTQAQPQTPLKAVHASQR
SYDVISAIQLQDELGDLPPGWEQARTAEGQIYYLNHNTRTTQWEDPRKQLAAHQALVSHQSADSLLRSQPPQQQQ
PPIQQNSGNPVTKLSSATSVSSDPLLGPLPDGWEQAVTSAGETYFINHFNRTTSWFDPRIPEHFQRSEMSRTAGG
WLNIHNLEKEREYLKQRQQEIQHQTMGLQMDPFLPGVTDHSRQESSDSGLSLTSNHYSLPQNSDFMSVDDSMDCI
SESGTLETSTLENTDDLVPSLQLGEGFNNDILDDVHSLMDSEVKTDSLTWI PLRMRKLPNSFFNPP

tr:A0A1L8DFT9_9DIPT [A0A1L8DFT9] SubName: Full=Putative transcriptional coactivator yap1 isoform x1 {ECO:0000313|EMBL:JAV05247.1}; Flags: Fragment;
102..116
DCVWDFFCTTNPWNCASARDSVISWKAESGCFRTLAMALNNSNSSGSSNNLSNTPNNNNNESENVKQGN
LVVRMDEDSATKLQALFDTVLKPSEQNRPLQIPLRMRKLPNSFFNPPSTGSKSPSVSHSRENSIDSAFGSGTTIV
YAPGGGASGAANSVLTQRLSISHSRAHSSPATLEQTHAASLKSAAAAASVATANAAQNTQAQPQTPLKAVHASQR

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SYDVISAIQLQDELGDLPPGWEQARTAEGQIYYLNHNTRTTQWEDPRKQLAAHQALVSHQSADSLLRSQPPQQQQ
PPIQQNSGNPVTKLSSATSVSSDPLLGPLPDGWEQAVTSAAEHFQRSEMSRTAGGWLNIHNLEKEREYLKQRQQE
IQHQTMGLQMDPFLPGVTDHSRQESSDSGLSLTSNHYSLPQNSDFMSVDDSMDCISESGTLETSTLENTDDLVPS
LQLGEGFNNDILDDVHSLMDSEVKTDSLTWI     PLRMRKLPNSFFNPP

tr:A0A1L8DFM1_9DIPT     [A0A1L8DFM1] SubName: Full=Putative transcriptional
coactivator yap1 isoform x1 {ECO:0000313|EMBL:JAV05248.1}; Flags: Fragment;
      128..142
      LCRNAKVSDRKKKSVEHRKGFRETLETVCGIFFCTTNPWNCASARDSVISWKAESGCFRTLAMALNNSN
SSGSSNNLSNTPNNNNNESENVKQGNLVVRMDEDSATKLQALFDTVLKPSEQNRPLQIPLRMRKLPNSFFNPPST
GSKSPSVSHSRENSIDSAFGSGTTIVYAPGGGASGAANSVLTQRLSISHSRAHSSPATLEQTHAASLKSAAAAAS
VATANAAQNTQAQPQTPLKAVHASQRSYDVISAIQLQDELGDLPPGWEQARTAEGQIYYLNHNTRTTQWEDPRKQ
LAAHQALVSHQSADSLLRSQPPQQQQPPIQQNSGNPVTKLSSATSVSSDPLLGPLPDGWEQAVTSAAEHFQRSEM
SRTAGGWLNIHNLEKEREYLKQRQQEIQHQTMGLQMDPFLPGVTDHSRQESSDSGLSLTSNHYSLPQNSDFMSVD
DSMDCISESGTLETSTLENTDDLVPSLQLGEGFNNDILDDVHSLMDSEVKTDSLTWI  PLRMRKLPNSFFNPP

tr:A0A0K2UK18_LEPSM     [A0A0K2UK18] SubName: Full=Putative LOC100881892
[Megachile rotundata] {ECO:0000313|EMBL:CDW38385.1}; 163..177
      MSCATAPVMYQPYSPYNNSSPSATMPPQGFHSSPDRVPPSQQSGIVEDNNNRSHLENKHHVQQVFKVEH
LHSTPPQDLSSYQPNNVSNTSSCNNSQSSPPTSRPPSHLNQHDEDSSDSTISAHRLSSNIVVFTHYVGNASSVVE
DHFSRALSSYERDETSYKPMSARNLPASFWTAPSDYTPPSPRHSASATACNLLNQSSTVPYGDIYPESITGALHQ
LAADWQYPHASVGHTPSSSSYSSNYSNYAARFQSANYWSPRLVGSSSTTSSVKSEWSPEPPYSDFSSHPHHLSHH
PYHHYSNIAAVAAVGLESNPSSDASLVNKPHHTAPGPATTAGTDLFWTTTF  PMSARNLPASFWTAP

tr:A0A2G8K7X8_STIJA     [A0A2G8K7X8] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PIK44110.1};     93..107
      MGNRYGRSVSSEQNDYQKEKSTQGKGYEITPPCKRRKISGNFEVDKTFHVSKDDVVARATCSPKAERAP
CTKDKDANFSTTNDKTDSATNPLPLRKRRLPASFWQEPGKSEIKPPIKVESSPRQTAFLPISPRQSSSFGRYVKD
FLGSNLSASEKLELLRLNSLERDSYNHLCSTREISGRRCPSYPCVLMHCKNQHEEIHFRDFPPFYPRNDYPFLHP
TQGASLPFPARNAFSSNHERHANVLGMPYPPSFPPYYPDLLRHNEVIDSNYGSRFIFPMETNVSPLFPLSSHFNP
SVVRPVPKKHLSNISRSFHPSFDVR    PLRKRRLPASFWQEP

tr:A0A2G8L677_STIJA     [A0A2G8L677] SubName: Full=Putative transcriptional
coactivator YAP1 isoform X1 {ECO:0000313|EMBL:PIK55763.1}; 48..62
      MTSVDMVDAEDRKTQVISHMKGDSATELEHLFQRVLHPSADKEELPKPMKERNLPPSFFSQPGPRLSPN
GNHRRDSSQDESHYSDSPTDSGITSPPSGPQSLSTHGLNIVHQRARSSPAILQEMRSAVGQQSLQVQHLKQQSYD
ITDNADILSSIPLPPGWEVAHTPNGQQYFLE     PMKERNLPPSFFSQP

tr:A0A2G8LFH1_STIJA     [A0A2G8LFH1] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PIK58900.1};     234..248
      MANRRPRVRRLAPSWGLSAVLHALAGPPYEPMANASLAALTKKTLFLIAVASARRRSCLHALTTKPNHI
RFEGHGVRMVPDPAFIAKNQALTFLPGDIFIPEIKTLSSVAEDKRWCPVRALKWYLSRTEKLRQTTSLFILPRPP
YTSASKDTLSRWLVETIRPFTTGAARPRAHDIRGISASTALFAGIPIEDILKAAAWKTPTTFVACYLTDTLHAEA
AFGSAVMRGPADPLPMKLRALPQSFWQQPNSVNTMSPGNMYLPVLPPLCKSEHSNVDPSEIRPISPTLEDDMTRP
KLEDHNYTTMEVHPKTSILNNNSNKVKDRNSESYTVESTGKSVLSSPRERDLFLCKDSVQESSSPLVVRRHHPGR
PTARILKVSPASQELLMKLFEGVEGGEKGPKKVTGPNIPRKFRQRQDSKLSQPTSNKHLIKDPYMINAVTDGLLP
MLSLETSKQSTAPSSQLALVALKAGDKTLTLPSLSVEQNYPAVLSELVKAL  PMKLRALPQSFWQQP

tr:A0A1Y1JY79_PHOPY     [A0A1Y1JY79] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAV54274.1};     42..56
      MALSQDESSKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSREN
SVDSAFGSSSGGGGSGTGATAVSTVPLQNQHHRAHSSPASLQQTYAVGQQTAPSHHHVKQRSYDVATKSSEDSTP
LPPGWEQARTPEGQVYYLNHLTRTTTWEDPRKTLVTQAAVQQHQSAEQLLPAHQVAQSQSPTQSSACTAQHLQRT
PGGTSILQQPWQHTSTLSPQSSPAKQQQLRLQLLQLERERLKQRQQEIRRQQELMLRGSNTELPMDPFLSSLTDH
SRQESADSGLGMGTTYSMPHTPEDFLSNMDDNMDVASESHTMDTPDISSLSDNIDSTDDLVPTLQLGEEFPNVML
DDVQSLINAPTTKPDNVLIWL   PWSMRKLPDSFFNPP

tr:A0A1Y1K3R9_PHOPY     [A0A1Y1K3R9] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:JAV54275.1};     42..56
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MALSQDESSKQVVRVDQDSETDLQALFDSVLKPDSKRPLQVPWSMRKLPDSFFNPPSTGSKSINHSREN
SVDSAFGSSSGGGGSGTGATAVSTVPLQNQHHRAHSSPASLQQTYAVGQQTAPSHHHVKQRSYDVATKSSEDSTP
LPPGWEQARTPEGQVYYLNHLTRTTTWEDPRKTLVTQAAVQQHQSAEQLLPAHQVAQSQSPTQSSACTAKANTDV
DLGPLPEGWEQAQTPEGEIYFINHQSRTTSWFDPRIPQHLQRTPGGTSILQQPWQHTSTLSPQSSPAKQQQLRLQ
LLQLERERLKQRQQEIRRQQELMLRGSNTELPMDPFLSSLTDHSRQESADSGLGMGTTYSMPHTPEDFLSNMDDN
MDVASESHTMDTPDISSLSDNIDSTDDLVPTLQLGEEFPNVMLDDVQSLINAPTTKPDNVLIWL
PWSMRKLPDSFFNPP

tr:U3FU04_CALJA [U3FU04] SubName: Full=Protein **FAM181**B
{ECO:0000313|EMBL:JAB51546.1}; 218..232
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGMPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAAPGPPSPSAADTPAKRPLAAPGAPTVAAPAHSK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVVTPAAGLGAGGAGGDAAGLAGGAAVPGAKKVPL
RARNLPPSFFTEPSRAGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPTGASVLR
GPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKPPLTVPRGGLTLNEPLRPLYPAAADSPGGEDGPGHLASF
APFFPDCALPPPPPPHQVPYDYSAGYSRTAYSSLWRPDGVWEGEPGEEGAHRDPLRARNLPPSFFTEP

tr:D2HNZ1_AILME [D2HNZ1] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSAMEP00000020920}; Flags: Fragment;
159..173
QVSSVPFPGAASHPQSPRSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRK
YLQKQLKRFSQKYPRLPRGLPGRGAETHLRRGADHRPGRLPLEAGHDSSPSGGGGCKEKALGNPYREECLSKEQT
LQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYEGKKHWKGLEPLDPEMAPVPASPR
ALAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYAGPPGALPQSSVPGLGLWRKSPAPPGELAHFCKDVDGPGQ
KVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:H2NM42_PONAB [H2NM42] SubName: Full=**FAM181**A isoform 2
{ECO:0000313|EMBL:PNJ33980.1}; SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSPPYP00000006927};
191..205
MPLEERRPSGERNDAAHTKHRRPGEKRASTAKQVSSVPFLGAAGHQQSLPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPETTPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGTLP
QSPVPSLGLWRKSPAFPGELTHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A2F0B0K3_ESCRO [A0A2F0B0K3] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:MBV96545.1}; Flags: Fragment;197..211
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ASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGSEDRP
GRLPLDSGHSSSPSGGGCCKEKALGNPYREECLSKEQTLHGPDPEAARPGQVPMRKRQLPASFWEEPRPTHSYPV
GLEGGLGPREGPPYEGKKHRKGLEPLGPETAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPVYPG
PPGALPQSPLPSLGLWRKSSASPGELAHFCKDVEGPGQKVYRPVVLKPIPTKPALPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A384AAL9_BALAS [A0A384AAL9] SubName: Full=LOW QUALITY PROTEIN:
protein **FAM181**A {ECO:0000313|RefSeq:XP_007184309.1}; 226..240
MLCIWRGAPDWPEGPPSSGDSSSIQPARGLHNCLQPDHGACRPRRAWPRSAAGTLPGHLGGARGPAPSV
SSVPCPGAASRLQSXPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKR
FSQKYSRLPRGLPGRGAEPHLKRGSEDQPGRLPLDSGHSSSPSGGGCCKEKALGNPYREECLSKEQTLHGPDPEA
ARPGQVPMRKRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHRKGLEPLGPETAPVPASPRAPAEKEPL
KMPGVSLVGRVNAWSCCPFQYHGQPVYPGPAGALPQSPLPSLGLWRKSSASPSELAHFCKDVEGPGQKVYRPVVL
KPIPTKPAMPPPIFNVFGYL PMRKRQLPASFWEEP

tr:A0A2K6TRB4_SAIBB [A0A2K6TRB4] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSSBOP00000022186};80..94
AGPGELEAPFPSSGGEGPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMN
PKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVS

GPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNM
MNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSS
SNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGM
SQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYL
EAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A2K6TR83_SAIBB [A0A2K6TR83] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSSBOP00000022163}; 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2K6TRA6_SAIBB [A0A2K6TRA6] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSSBOP00000022197}; 66..80
PAQPPQGQGPPSAPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRL
RKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLRQS
SFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASAMNQRISQS
APVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELA
LRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDE
MDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDK
ESFLTWL PMRLRKLPDSFFKPP

tr:A0A2K6G6P6_PROCO [A0A2K6G6P6] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSPCOP00000021907};
191..205
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KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLKRGSEDRPGRLLLD
PGPESSPGGGGGCKEKAPGSPYGEECLSKEQVLQGQSPEATRPGQVPMRKRQLPASFWEEPRPTHSYPMGLEGGL
GPREGPPYEGKKHCKGLEPLGPEVALVPMSPRALAEKEPLEMPGVSLVGRGNAWSCCPLQYHGQPIYPGLPGALP
QSPVPSLGLWRKSPAFPGELAHLCKDVDGLGQVCRPVVLKPIPTKPAMAPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A2K6TR76_SAIBB [A0A2K6TR76] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSSBOP00000022158}; 13..27
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SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A2K6FBU1_PROCO [A0A2K6FBU1] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSPCOP00000011450}; 85..99
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NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLNP
TGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQ
AMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLS
MSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEAL
SSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2K6SBJ8_SAIBB [A0A2K6SBJ8] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSSBOP00000004756};
186..200

LPLGERRSSGRQEGCRPHRTPMACYVPQVSSVSFLGAASHQQSPPSSWKALCGGPLVMASDSDVKMLLN
FVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGPEDRPGRLLLDLGPES
SPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAAQAGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREG
PPYEGKKNCKGLEPLGPETASVPMSPSALAEKESLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVP
SLGLWRKSPAFPGELAYLCKDADGLGQKVCRPMVLKPIPTKPAVPPPVFNVFGYL PMRKRQLPASFWEEP

tr:F7EAB4_MACMU [F7EAB4] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSMMUP00000016280}; 184..198
RSSGERNDAAYRKHRRPGEKKAGHSKVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVKMLLNFV
NLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDLGPDSSP
GGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPP
YEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSL
GLWKKSPAFPGELAHLCKDADSLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYLPMRKRQLPASFWEEP

tr:H9F9V4_MACMU [H9F9V4] SubName: Full=Yorkie homolog isoform 3 {ECO:0000313|EMBL:AFE71413.1}; Flags: Fragment;20..34
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQL
GAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQ
MNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPP
LAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELR
TMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPG
TNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:H9F9V3_MACMU [H9F9V3] SubName: Full=Yorkie homolog isoform 2 {ECO:0000313|EMBL:AFE71412.1}; Flags: Fragment;20..34
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQL
GAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQ
MNVTAPTSPPVQQNMMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKQ
QELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTP
DDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMES
VLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:F7HRP8_CALJA [F7HRP8] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSCJAP00000017662}; 189..203
MPLEERRSSRDSDDAATECRPGRKGRSTEKQVSSVSFPGAASHQQSPPSSWKASCSGPLVMASDSDVKM
LLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGPEDRPGRLLLDLG
PDSSPSGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLQGGLGP
REGPPYEGKKNCKGLEPLGPETASVPMSPSALVEKESLKMPGVSLVGRVNAWSCCPLQYHGQPIYPGPLGALPQS
PVPSLGLWRKSPAFPGELAHLCKDADGLGQKVCRPMVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:G7MW15_MACMU [G7MW15] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:EHH28130.1}; Flags: Fragment;190..204
PLEEKRSSGERNDAAYRKHRRPGEKKAGHSKAVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDL
GPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLG
PREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQ
SPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A2K5IFP6_COLAP [A0A2K5IFP6] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSCANP00000015376}; 60..74
XXXXXXXXXXXXPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDS
FFKPPEPKSHSRQASTDAGTAGAVTPQHVGVHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQSLQQSSFEIPD
DVPLPADWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDG
EIYYINHKNKTTSWLDPRLDPRFAMNQRISQSDPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLR
LKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDAGTPNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSR
DESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEE
LMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2K5IG17_COLAP [A0A2K5IG17] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSCANP00000015402}; 48..62
PAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSR
QASTDAGTAGAVTPQHVGVHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQSLQQSSFEIPDDVPLPADWEMAK
TSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASAMNQRISQSDPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDAGTPNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A2K5IFJ4_COLAP [A0A2K5IFJ4] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSCANP00000015390}; 60..74
XXXXXXXXXXXXPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDS
FFKPPEPKSHSRQASTDAGTAGAVTPQHVGVHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQSLQQSSFEIPD
DVPLPADWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDG
EIYYINHKNKTTSWLDPRLDPRFAMNQRISQSDPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLR
LKQQELLRQVRPQELALRSQLPTLEQDAGTPNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSS
YSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSD
ILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2K5I8C1_COLAP [A0A2K5I8C1] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSCANP00000012883};
190..204
TPLEEKRSSGERNNAAYRKHRRPGEKKAGTAKQVSLPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRATEPYLKRGSEDRPGRLLLDL
GPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLG
PREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQ
SPVPSLGLWKKSPAFPGELVHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A2K5PHS9_CEBCA [A0A2K5PHS9] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSCCAP00000003177};
190..204
MPLEERRSSRDRKDAAHIECRPGWKGQSTEKQVSSVSFPGAASQQQSPPSSWKASCGGPLVMASDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRATEPYLKRGPDNQPGRLLLDL
GPDSSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAARPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLG
PREGPPYEAKKNCKGLEPLGPETASVSMSPSALAEKESLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQ
SPVPSLGLWRKSPTFPGELAYLCKDADGLGQKVCRPMVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:L8YB02_TUPCH [L8YB02] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:ELV12145.1}; 160..174
MAAGRDANGPFVPQALSVPFPGAAGHQHSPPSSWKVPCGGPLVMASDSDVKMLLNFVNLASSDIKAALD
KSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPSRVAEPHLKRGPQDRHPGGGGGCKEKALGSPYGEECLSKEQ
TLRGQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPMGLEGGLGPREGPPYEGKKNCKGLEPLGPETAPMPVSP
RALAEKEPLKMPGVSLVGRVNAWSCCPFQCHGQPLYPGPPGALPQSPVPSLGLWRKNPTSPGEPGEPAPFCKDVD
SLGQKVHRPVVLKPSPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:G3MYF5_BOVIN [G3MYF5] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSBTAP00000054587}; 161..175
RQVGSVLFPGAASCLENPASSWKARCSGALVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHR
KYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRPLPLESGHGSSPGGGGGCKEKALGNLDREESLSKE
RTLHGPDPGAARPGQVPMRKRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTPVPTS
PRAPAEKEPLKMPGVSLVGRVSAWSCCPFQYHGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGP
GQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:W5PX95_SHEEP [W5PX95] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSOARP00000015079}; 217..231
MPWEGGGEREKERERERQTGRVSHSTLKDSGESSPPWLTPSDCLSALEHGSCRPGVLGVGSVLFPGAAS

CLENPASSWKARGSGALVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPR
GLPGRGAEPHLKRGPEDRPGRPLHLESGHGSSPSGGGGYKEKALGNPDREESLSKERTLHGPDPGAARPGQVPMR
KRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETAPVPTSPRAPAEKEPLKMPGVSLVG
RVSAWSCCPFQYHGQPIYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGPGQKVYRPVVLKPIPTKPAV
PPPIFNVFGYL PMRKRQLPASFWEEP

tr:H0X0L5_OTOGA [H0X0L5] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSOGAP00000008466}; 170..184
PGEIPMACCISQVSSVPFRGVADHQQNPPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKS
APCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHLKRGPEDRPGRLLLDPGPESSPGGGGGYKEKALGNP
YSEECLSKEQVLQGQSPEAARPGQVPMRKRQLPASFWEEPRPTHSYSMGLEGGLGPREGPPYEGKKNCKGLESLG
PEAAPVPMSPRALAEKEPLKMPGVSLVGRSSAWSCCPLQYHGQPIYPGLSGTLPQSPIPSLGLWRKSPAFPGELA
HFCKEVDGLGQVYRPVVLKPIPTKPAMAPPIFNVFGYL PMRKRQLPASFWEEP

tr:H2NET4_PONAB [H2NET4] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSPPYP00000004258};181..195
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSAASQSRSLIVLFDSMRHVPGGAEPAGG
AVAAPAAGLGGAGTGGAGGDVAGPAGATAIPGARKVPLRARNLPPSFFTEPSRAGGGGCVPSGPDVSLGDLEKGA
EAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGASVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKK
SPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGHLASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWR
SDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

tr:H2NFY0_PONAB [H2NFY0] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSPPYP00000004665};172..186
LLSGAEGGEVREATRDLLSFIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSP
SAADTPAKRPLAAPSAPTVAAPAHGKAAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVAAPAAGL
GGAGTGGAGGDVAGPAGATAIPGARKVPLRARNLPPSFFTEPSRAGGGGCVPSGPDVSLGDLEKGAEAVEFFELL
GPDYGAGTEAAVLLAAEPLDVFPAGASVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGG
LTL PLRARNLPPSFFTEP

tr:A0A2J8TLZ9_PONAB [A0A2J8TLZ9] SubName: Full=**FAM181**A isoform 5
{ECO:0000313|EMBL:PNJ33983.1}; Flags: Fragment;129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPGRLLLDLGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGTLP PMRKRQLPASFWEEP

tr:A0A2J8QMV0_PANTR [A0A2J8QMV0] SubName: Full=**FAM181**A isoform 5
{ECO:0000313|EMBL:PNI97569.1}; Flags: Fragment;129..143
MASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLK
RGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPR
PTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETTLVPMSPRALDEKEPLKMPGVSLVGRVNAWSCCPFQYH
GQPIYPGPLGALP PMRKRQLPASFWEEP

tr:A0A2K5KWF0_CERAT [A0A2K5KWF0] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSCATP00000005007};
191..205
MPLEEKRSSGERNDAAYRKHRRPGEKKAGTAKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKALRNPYREECLAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAAPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A337SBL9_FELCA [A0A337SBL9] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSFCAP00000047839};
221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGTPAGELLAGNEGGDMREATRDLLSF

IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADTPAKRPLAAPSAQAVAVPPHGK
AVPRREASQAAAAASLQSRSLAALFDSLRHVPGDTEGAGGSLAAPAAGLGGAGAGGSGGEAAGTAGGTAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPGVSLGDLEKGAEALEFFELLGPDYGAGTEASVLLAAEPLDVFPTGA
AVLRGPPELEPGLFEPPPAMVGSLLYSESWSAPGCPQTKKPPLAAPRGGLTLNEPLRPLYPSAADSPGAEDGPGL
LASFAPFFSDCALPAPPPPHQVSYDYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

tr:A0A337SGJ8_FELCA   [A0A337SGJ8] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSFCAP00000049727};82..96
WTPGRRPHSPRPPPAPRAPPPAQPPPGQGPPPAPGPAAPPGPQPPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALAPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPVQQ
NMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAVNQRVGQSAPAKQPPPLAPQSPPGGVLGS
GGSNQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSSANSPKCQELALRSQLPTLDQEGGTQNPVPSPGM
SQELRTMTTTSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNPIPGTN
VDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A337S1H6_FELCA   [A0A337S1H6] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSFCAP00000040424};
190..204
LGYGGIRTLAEPCDLAPKQGAHPGDLRAALCRVSSVPSPGAASHEQNPPASWKAPCSGLLVMANDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDS
GRDSSPGGGGGCKEKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPRATHSYPLGLEGGPG
PREGPPYEGKKHCKGLEPLDPETAPVPASPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYPGPPGALPQ
SPVPGLSLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A2I2UR01_FELCA   [A0A2I2UR01] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSFCAP00000034850};82..96
WTPGRRPHSPRPPPAPRAPPPAQPPPGQGPPPAPGPAAPPGPQPPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALAPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPVQQ
NMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAVNQRVGQSAPAKQPPPLAPQSPPGGVLGS
GGSNQQMRLQQLQMEKERLRLKQQELLRQVRPQELALRSQLPTLDQEGGTQNPVPSPGMSQELRTMTTTSSDPFL
NSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNPIPGTNVDLGTLEGDGMNIEGE
ELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

tr:A0A337S140_FELCA   [A0A337S140] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSFCAP00000042260};82..96
WTPGRRPHSPRPPPAPRAPPPAQPPPGQGPPPAPGPAAPPGPQPPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGSAGALAPQHVRAHSSPASLQLGAVSPGTLTPTGV
VSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPVQQ
NMMNSASAVNQRVGQSAPAKQPPPLAPQSPPGGVLGSGGSNQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNI
NPSSANSPKCQELALRSQLPTLDQEGGTQNPVPSPGMSQELRTMTTTSSDPFLNSGTYHSRDESTDSGLSMSSYS
VPRTPDDFLNSVDEMDTGDTINQSTLPSQQNPIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVL
AATKLDKESFLTWL   PMRLRKLPDSFFKPP

tr:A0A2K6P1K7_RHIRO   [A0A2K6P1K7] SubName: Full=Family with sequence
similarity 181 member A
{ECO:0000313|Ensembl:ENSRROP00000010416};>tr:A0A2K6JWU0_RHIBE [A0A2K6JWU0]
SubName: Full=Family with sequence similarity 181 member A
{ECO:0000313|Ensembl:ENSRBIP00000003484};191..205
TPLEEKRSSGERNDVAYRKHRRPGEKKAGTAKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

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tr:A0A2K6Q6P6_RHIRO     [A0A2K6Q6P6] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSRROP00000024452};221..235
      MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAVPPGPPSPSAADTPAKRPLAAPCAPTVAAPAHCK
AVPRREAAQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGAVVAPVAGLGGAGTGGAGGDAVGPAGATAVPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELESGLFDPAPAVVGNLLYPEPWSVPGCPPTKKPPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGH
LASFSPFFPDCALPPPPPPHQVSYDYSAGYSRNAYSSLWRPDGVWEGAPGEEGAHRD  PLRARNLPPSFFTEP

tr:F6R5L7_MONDO   [F6R5L7] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSMODP00000005604};     222..236
      MAVQAAILSPHHFIPFCFPGSPGALGMDFGDLDKGCCYEEDEAGGTGAALLGGGGGGDFREATRDLLSF
IDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGMMTSSPASASGPAPSASPSPGPAAAVSVGALEAPTKSK
APPKREGSQAAASLQSKSLAALFDSLHQVRGGGGEKGGAGTLAAVTGGGGGGGSGGAGVEGGVPAVAPPGAGGNK
KVPLRNRNLPPSFFTEPSRAGSCGPSGGGVTLRELEKGGEAVEFFELLGPDYCAGGEVGGLLPSEPLDLFPAAVR
PPQELEHILYDPHPTLVAGLLYSEPWSTPCPPAKKPAPVSNRGGGGLTLNETLRPLYSSTSDS
      PLRNRNLPPSFFTEP

tr:A0A096NJH4_PAPAN     [A0A096NJH4] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSPANP00000013125};
      191..205
      TPLEEKRSSGERNDAAYRKHRRPGEKKAGTAKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAPEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
      PMRKRQLPASFWEEP

tr:A0A2K5CEF3_AOTNA     [A0A2K5CEF3] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSANAP00000007036};
      190..204
      MPLKERRSSRDGKDAAHTECRPGWKGQSTEKQVSSVSFPGAASHQQSPPSSWKASCGGPLVMASDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAESYLKRGPENRPGRLLLDL
GPDSSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAARPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLG
PREGPPYEGKKNCKGLEPLGPETASGPMSPSALAEKESLKMPEVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQ
SPVPSLGLWRKSPAFPGELAHLCKDADGLGQKVCRPMVLKPIPTKPAVPPPIFNVFGYL
      PMRKRQLPASFWEEP

tr:A0A2K5CEB8_AOTNA     [A0A2K5CEB8] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSANAP00000007038};
      225..239
      MLCIWRGAPDWPEGPPSSGELSSIQPTQGLHNCFQPDGAQPAVPGPVPGLQRGTCRATLVGPRPAPSVS
SVSFPGAASHQQSPPSSWKASCGGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRF
SQKYSRLPRGLPGRAAESYLKRGPENRPGRLLLDLGPDSSPGGGGGCKEKVLRNPCREECLAKEQLPQGQHPEAA
RPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPETASGPMSPSALAEKESLK
MPEVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLCKDADGLGQKVCRPMVLK
PIPTKPAVPPPIFNVFGYL     PMRKRQLPASFWEEP

tr:A0A2K5CZ67_AOTNA     [A0A2K5CZ67] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSANAP00000013999};
      218..232
      MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAAGHARQTAAGRPGRPDSRGPSPRQ
GCPPAGGVAGRGGRQLASRSLAALFDSLRHVSGGAEPAGGAVLAPAAGLGAGGAGGDTAGPAGGAAVPGARKVPL
RARNLPPSFFTEPSRGGGSGCGRVGAGRELGRPGEGRGGRGVLRAAGARLRRRHRGGRLAGRREPLDVFPAGASV
LRGPPELEPGLFEPPPSVVGNLLYPEPWSVPGCPPTKKPPLTAPARLDLERALAPLYPAASDSPGGEDGPGHLAS
FAPFFPDCALPPPPPPHSGPHRLLQPWRPDGVWEGAPGEEGAHR    PLRARNLPPSFFTEP
```

tr:G3W8G2_SARHA [G3W8G2] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSSHAP00000011717}; 82..96
MDPGQQPPQPPSQGQGQPPSQPPQGQGQGPPTGPGPAGTSAAPPPPAGHQIVHVRGDSETDLEALFNAV
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLSPSGV
VSAPGAAPSGQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
NIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGSVMGG
GSSNQQQQMRLQQLQVEKERLRLKHQELLRQALRNVNPSTANSPKRQEIALRSQLPTMEQDGGTQNPVSSPGMNQ
ELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSQQNRFPDYLEA
IPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:G3W7G9_SARHA [G3W7G9] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSSHAP00000011374}; 217..231
REEMAAGVIRNLCDFRLQAAFHQPFLPTSGHRDPDFPETSEEEEEDGEEEEEGEKLGDNLELAGSNPGC
QRSDQNLITGPTRSSPSSAEMTLQLLRFSELISCDIQKYFGQKTKDDDPDACNIYEDCRPPGKSARELYYADLMQ
IVQSGDQEDEDTDVVGLPKGLDCPARFISSRDRSQKLGPLVELFEYGLCQYARQRVSDSRRLRLEKKYGHITPMH
KRKLPQSFWKEPAPSSLCLLNTSTPDFSDLLANWTSDVAQELHGVGGRELDRQALE PMHKRKLPQSFWKEP

tr:A0A2R9CPZ2_PANPA [A0A2R9CPZ2] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSPPAP00000040677}; 89..103
MGFYHISQAGRKLLTSGDPPPLASQSGGTTGGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDL
EALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPG
TLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGT
QNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPS
QQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A2R9CFK0_PANPA [A0A2R9CFK0] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSPPAP00000040720}; 70..84
XXXXXXXXXXXQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASAMNQR
ISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKC
QELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLN
SVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAAT
KLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2R9CFQ0_PANPA [A0A2R9CFQ0] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSPPAP00000040719}; 70..84
XXXXXXXXXXXQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGPLPD
GWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQ
QLQMEKERLRLKQQELLRQVRPQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDE
STDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELM
PSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2R9CFK2_PANPA [A0A2R9CFK2] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSPPAP00000040679}; 79..93
AGPGELEAPFPSTGGEKGPSGGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNP
KTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSG
PAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMM
NSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNS
NQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMS
QELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLE
AIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2R9CI69_PANPA [A0A2R9CI69] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSPPAP00000040718}; 70..84
XXXXXXXXXXXQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGPLPD
GWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQ
QLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTN
SSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDL
GTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2R9APL7_PANPA [A0A2R9APL7] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSPPAP00000019316}; 148..162
NPLSPSPPPPGRSPPAPSLRPLLTRPNELPREAAQPARPGASRLRRARRAGAGAGPXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXAAAASLQSRSLAALFDSLRHVPGGAEPVAAPAAGLGGAGTGGAGGDVAGPAGATAIPGA
RKVPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPA
GASVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGP
GHLASFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD
PLRARNLPPSFFTEP

tr:F7DKK6_HORSE [F7DKK6] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSECAP00000015981}; 118..132
VMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHL
KRGPEDRPGRLPLALAGKALGNPYREECLSKEQTLQGQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEG
GLGPREGPPYEGKKHCKGLEPTAPVPASPRAPAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPPGALPQS
PVPSLGLWRKSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:U6DXK6_NEOVI [U6DXK6] SubName: Full=Chromosome 14 open reading frame 152, isoform CRA_a {ECO:0000313|EMBL:CCP87720.1}; Flags: Fragment;
30..44
LGNPYREECLSKEQSLQRQNPEAARPGQVPMRKRQLPASFWEEPRPAHSYSLGLEGELGPREGSPYEGK
KPCKGLEPWDPEMAPVPASPRAPAGKEPLKMSGVSLVGRVNAWGYCPFQYHGQPIYAGPPGALPQSPVPNLGLWR
KSPASPGELAHFCKDVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:U6DAP2_NEOVI [U6DAP2] SubName: Full=Yes-associated protein 1 {ECO:0000313|EMBL:CCP79172.1}; Flags: Fragment; 44..58
QAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQAST
DGGTGGALTPQHVRAHSSPASLQLGAASPGSLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSG
QRYFLNHIDQTTTWQDPRKAMLSQMSVTAPTSPPVQQSLMTSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLD
PRLDPRF PMRLRKLPDSFFKPP

tr:G3TYB5_LOXAF [G3TYB5] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSLAFP00000020573}; 131..145
VMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPHL
KRGPEDRLSRLPLDSHDPSPSGVGGCKEKALGNPGREECLSRQQEQTLQGQNPEAAQPGQVPMRKRQLPASFWEE
PRPAHSFPLGLEGGLGAREGPPYEGKKTCQGLEPLGPETAPVPMSPRALAEKEPLKMPGVSLMGQVNAWSCCPFQ
YHGQPIYPGPPGALPQGSVPNLGLWRTSPASTGELTPFCKDADGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A0D9RF42_CHLSB [A0A0D9RF42] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSCSAP00000007231};
191..205
TPLEEKRSSGERNDAGYRKHRRPGEKKAGHSKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKAPRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A286ZNK4_PIG [A0A286ZNK4] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSSSCP00000033204}; 13..27

MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAISPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A287AIA3_PIG [A0A287AIA3] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSSSCP00000043628}; 13..27

MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAISPGT
LTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQ
GGVMGGGSSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSS
DPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGT
LEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2K6A3S4_MANLE [A0A2K6A3S4] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSMLEP00000034725}; 74..88

GGRTSCGQGRPRSPQRPQFGPGMDPAFVVLFCSFFAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANV
PQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATP
TAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASG
PLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQ
MRLQQLQMEKERLRLKQQELLRQVRPQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRT
MTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGT
NVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A287BCL2_PIG [A0A287BCL2] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSSSCP00000054260}; 171..185

MIVPPLCSENVLKVSSVAFPGAASRLQNSPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDK
SAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDTGHNSSPSGGGGCKEKASGN
PYREESLPKEQTLHGQDPEAARPGQVPMRKRQLPASFWEEPQPTHSYPVGLEGGWAPGRDLPTTGRNTAKAWSPW
GPRHPPGRPLRRSHSRCPGSPWGAVSVPGAAAPSSTTDSPSTQAHQGPCLRARSPAWACGGRARLPPASWPTSAR
MRRAQGRKCTDP PMRKRQLPASFWEEP

tr:A0A2K6A3X1_MANLE [A0A2K6A3X1] SubName: Full=Yes associated protein 1 {ECO:0000313|Ensembl:ENSMLEP00000034770}; 39..53

APPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTA
GALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFL
NHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDP
RFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLE
QDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQ
STLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A2K5YCV9_MANLE [A0A2K5YCV9] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSMLEP00000013386};
191..205

TPLEEKRSSGERNDAAYRKHRRPGEKKAGTAKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKALRNPYREECLAKEQLLQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWKKSPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A287BEM1_PIG [A0A287BEM1] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSSSCP00000054978}; 226..240

MLCIWRGAPDWPEGPPSSGDSSSIQPTRGLHNCLQPDHGARRPRGAWPRSAAGNLPGHLGRAPGPAPSV
SSVAFPGAASRLQNSPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKR
FSQKYSRLPRGLPGRGAEPHLKRGPEDRPGRLPLDTGHNSSPSGGGGCKEKASGNPYREESLPKEQTLHGQDPEA
ARPGQVPMRKRQLPASFWEEPQPTHSYPVGLEGGWAPGRDLPTTGRNTAKAWSPWGPRHPPGRPLRRSHSRCPGS
PWGAVSVPGAAAPSSTTDSPSTQAHQGPCLRARSPAWACGGRARLPPASWPTSARMRRAQGRKCTDP
PMRKRQLPASFWEEP

tr:A0A2K6A3U6_MANLE [A0A2K6A3U6] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSMLEP00000034745}; 74..88
GGRTSCGQGRPRSPQRPQFGPGMDPAFVVLFCSFFAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANV
PQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATP
TAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASA
MNQRISQSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLPTLEQDG
GTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTL
PSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:L8IIT5_9CETA [L8IIT5] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:ELR56048.1}; Flags: Fragment;161..175
RQVGSVLFPGAASCLENPASSWKARCSGALVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHR
KYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGPEDRSGRPLPLESGHGSSPGGGGGCKEKALGNLDREESLSKE
RTLHGPDPGAARPGQVPMRKRQLPASFWEEPRPTHSYPVGLEGGLGPREGPPYEGKKHCKGLEPLGPETTPVPTS
PRAPAEKEPLKMPGVSLVGRVSAWSCCPFQYHGQPVYPSPPGALPQSPMPSLGLWRKSAASPGELAHFCKDAEGP
GQKVYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:G1S3Q5_NOMLE [G1S3Q5] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSNLEP00000020143}; 219..233
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGDLDKGCCFEDDETGAPAGALLSGVEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AAPRREASQAAAAAFLQSLAALFDSLHHVPGGAEPAGGAVAAPAAGLGGAGTGGAGGDAAGPAGATAIPGARKVP
LRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGASV
LRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCPPTKKSPLTAPRGGLTLNEPLRPLYPAAADSPGGEDGPGHLA
SFAPFFPDCALPPPPPPHQVSYDYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

tr:G1S5Y3_NOMLE [G1S5Y3] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSNLEP00000020921}; 167..181
TPLEERRSSGESNDAAHTKHRRPGEKRAEHSKVSSVPFLGAAGHQQSLPSSWKASCSGPLVMASDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRNPYRE
ECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGPET
TPVPMSPRVLVEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAHLC
KDAGGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:J9NZN3_CANLF [J9NZN3] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSCAFP00000038753}; 221..235
MAVQAALLSTHPFVPFGFGGSPDALGGAFGALDKGCCFEDDEPGPPAGALLAGAEGGDVREATRDLLSF
MDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAADAPAKRPLGAAGAQAVAGPPPGK
AAPRREASQAAAANSLQSRSLAALFDSLRHVPAGDERPGASGAAPAAALGAAGAGGSGGDAAGPAGGTAGPGARK
VPLRARNLPPSFFTEPSRAGRGCGPSGPGVSLGDLEKGADALEILELLAAGSGTGAGAGAGVLLAAEPLEVFPAG
AAVLRGPPELEPGLFEPPAATVGALLYPEPWSAPGCPPAKRPPPAAPRGGLALTEPLRPAYPAAADCQGGEDAPG
LLASFAPFFSDCALPPQPPPHQVSYEYGAGYGRSGYAGLWRPDAAWEGAPGEEGAPRD PLRARNLPPSFFTEP

tr:J9NTW6_CANLF [J9NTW6] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSCAFP00000036602}; 193..207
MPRQEERGLGLLEKGSGRPAQKNKNLAAKCGTWERVSSVPFPGAASHQQSPPSSWKAPCSGPLVMASDS
DVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGAEDRPGRLP
LGSGHDSSTGEGGGCKEKALGNPYREECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEG
GLGPREGPPYESKKHCKGLEPLDPETAPVPTSPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYAGPPGA
LPQSPVPGLGLWRKSPASPGELAHFCKHVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:F1PKW9_CANLF   [F1PKW9] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSCAFP00000025965};   169..183
MAAVGLESLGEVSSVPFPGAASHQQSPPSSWKAPCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSA
PCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPHLKRGAEDRPGRLPLGSGHDSSTGEGGGCKEKALGNPY
REECLSKEQTLQRQNPEAARPGQVPMRKRQLPASFWEEPRPTHSYPLGLEGGLGPREGPPYESKKHCKGLEPLDP
ETAPVPTSPRAPAEKEPLKMSGVSLVGRVNAWSCCPFQYHGQPVYAGPPGALPQSPVPGLGLWRKSPASPGELAH
FCKHVDGPGQKVYRPVVLKPIPTKPAVPPPIFNVFGYL   PMRKRQLPASFWEEP

tr:A0A2I2Y768_GORGO   [A0A2I2Y768] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSGGOP00000030748};
191..205
TPLEERRSSGERNDAAHTNHRRPGEKRASTAKQVSSVSFLGAASHQQSLSSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPYLKRGSEDRPRRLLLD
LGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPETTLVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWRKSPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:D2HS97_AILME   [D2HS97] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:EFB15216.1}; Flags: Fragment;70..84
EGGDVREATRDLLSFIDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPGAAKV
PLRARNLPPSFFTEPSRAGGGGXGAAGPGVSLGDLEKGAEAVEFFELLGPDYGAGTEASVLLAAEPLDVFPTGAA
VLRGPPELEPGLFEPPPAMVGSLLYSESWSAPGXPSAKKPPLAAPRGGLTLNEPLRPLYPSAADSPGGEDGPGLL
ASFAPFFSDCALPPPPPPHQVSYEYSAGYSRTAYSSLWRPDGVWEGAPGEEGAHRD   PLRARNLPPSFFTEP

tr:G3RHC5_GORGO   [G3RHC5] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSGGOP00000015043};   169..183
MAAVGLESLGEVSSVSFLGAASHQQSLSSSWKASCSGPLVMASDSDVKMLLNFVNLASSDIKAALDKSA
PCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRGAEPYLKRGSEDRPRRLLLDLGPDSSPGGGGGCKEKVLRNPY
REECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLGPREGPPYEGKKNCKGLEPLGP
ETTLVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQSPVPSLGLWRKSPAFPGELAH
LCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL   PMRKRQLPASFWEEP

tr:K9ITQ5_DESRO   [K9ITQ5] SubName: Full=Putative ubiquitin protein ligase
rsp5/nedd4 {ECO:0000313|EMBL:JAA51862.1}; Flags: Fragment; 45..59
SQAAPQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQAS
TDAGSAGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSS
GQRYFLNHIDQTTTWQDPRKAMLSQLNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWL
DPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRS
QLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDT
GDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESF
LTWL PMRLRKLPDSFFKPP

tr:K9ISJ3_DESRO   [K9ISJ3] SubName: Full=Putative ubiquitin protein ligase
rsp5/nedd4 {ECO:0000313|EMBL:JAA51843.1}; Flags: Fragment; 40..54
QAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGS
AGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDQTTTWQDPRKAMLSQLNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLD
PRFGKAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQELALRSQLP
TLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDT
INQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTW
L   PMRLRKLPDSFFKPP

tr:K9J2W4_DESRO   [K9J2W4] SubName: Full=Putative ubiquitin protein ligase
rsp5/nedd4 {ECO:0000313|EMBL:JAA51926.1}; Flags: Fragment; 40..54
QAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGS
AGALTPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDQTTTWQDPRKAMLSQLNVTAPTSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLD
PRFGKAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQMRLQQLQMEKERLRLKQQELLRQVRPQAMRNI

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NPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYS
VPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDIL
NDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

tr:G7PBC7_MACFA   [G7PBC7] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:EHH63846.1}; Flags: Fragment;190..204
      PLEEKRSSGERNDAAYRKHRRPGEKKAGHSKAVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDVK
MLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLDL
GPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGLG
PREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALPQ
SPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAMPPPIFNVFGYL
      PMRKRQLPASFWEEP

tr:A0A2K5V0J7_MACFA     [A0A2K5V0J7] SubName: Full=Family with sequence
similarity 181 member A {ECO:0000313|Ensembl:ENSMFAP00000018250};
      191..205
      TPLEEKRSSGERNDAAYRKHRRPGEKKAGTAKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKALRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKIPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
      PMRKRQLPASFWEEP

tr:G1QDK3_MYOLU   [G1QDK3] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSMLUP00000021786};     174..188
      MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDEPGMPAGALLAGTEGGDAREATRDLLSF
IDSASSNIKLALDKPSKSKRKVNHRKYLQKQIKRCSGLMGAAPAGPPSPGAADTPAKRALGTPGAQTAAVPAPRQ
GPPRERALGVREEMLPALRGTAAPGARKVPLRARNLPPSFFTEPSRASGGGCGPSGCSVNLCDLEKGPETLEFLE
LLGPDYGAGSEAGVLLPAEPLDVFPTGATVLRGPPELEPGLFEPPPAMGGSLPYPEPWSAPACPATKKPSLAPPR
GGSTLTEPLRLLYPAAVNSPGGEDGPGPLASFGPFFSDCVLPQPPPPPQPRQVAYDVCAGYGRTAYSSLWRPDGL
WEGDPGEEGAPRD     PLRARNLPPSFFTEP

tr:G1PSC1_MYOLU   [G1PSC1] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSMLUP00000014064};     221..235
      MVTICDGKECGNGALPLGCFVSGEALLIGLRPQLWGLVLHSAHSRAAQLLPAGQPELAGRAGLTQVSPV
PFPGAARTSRPPSSWKARCSGLVMASDSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKY
SRLPRGLPGRGAEPPLRRGPEDRPGRLPLNPGPDASPSGGGDCKEKALGNPYREECLSREQTLQGQNPGAARPGQ
VPMRKRQLPASFWEEPRPTHSYPVALEGVLGPREGPPYECKKHCRGLELFGPDMALIPMSPRALAEKEPPKLPGV
SLVGRVNAWSCCPFQYHGQPIYPGPPGALPPGPVPSLGLWRKSPASPGELAHLAKDVDGPGQKVHRPVVLKPIPT
KPAMPPPIFNVFGYL   PMRKRQLPASFWEEP

tr:G1U198_RABIT   [G1U198] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSOCUP00000023132};13..27
      MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPTGVVSGPAATPTTQQHLQQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAP
TSPPVQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSP
QGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPV
SSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSSLPSQQNR
FPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
      PMRLRKLPDSFFKPP

tr:L5L0E6_PTEAL   [L5L0E6] SubName: Full=65 kDa Yes-associated protein
{ECO:0000313|EMBL:ELK16513.1};     298..312
      METATLMRSQYHDGSRGAGGFGRLLLQIPASENLPIFEHAGDNQPAPPVVRGRGARREEPLGLGGCGDV
GQASRPRGLDRPHPESMLGRIQAQAFGFDQKFQAYRKDDFVMVGTEVKKIEAINVPCTQLSMSFFNRLYDENIVR
DSGHIVKCLDSFCDPFLISDELRKVLLVEDSEKYEVFSQPDREEFLFCLFKHLCLGGALCQYEDVLNPYLETTKL
IYKDLVSVRKNPQTKKIQITSSIFKVTAYPAPPGSQAASQAPPAGHQIVHVRGDSETDLEALFNAVMNPKTANVP
QTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGALTPTGVVSGPAPTPT
AQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNMMNSASGP
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LPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGVMGGGNSNQQQQM
RLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNS
SDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSINQSTLPSQQNRFPDYLEAIPGTNVDLG
TLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A2K6BGS7_MACNE [A0A2K6BGS7] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSMNEP00000010610};
191..205
TPLEEKRSSGERNDAAYRKHRRPREKKAGTAKQVSLVPFLGAAGHQQSPPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPGRLLLD
LGPDSSPGGGGGCKEKVLRNPYREECLAKEQLPQGQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPEIVPVPMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWKKSPAFPGELAHLCKDADGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A091CSR7_FUKDA [A0A091CSR7] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFO21372.1}; 298..312
MRRRKRRRNKKRKKKAGQGSWLPKKPHGALPFLESHRYRAPSVYQPYATCFLYISSLSSPQPADILVSS
FTIGQNGPPVDGKHQPDDARRSWKEGAGPGTNLLDPGTSTVSDFGGSAWWKSRAVERLPKTEFDSQEAPDQGQPR
TLLRAASPLQRAPSSWKAPHPGPLVMASDTDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQ
KYSRLPRGLPGRAAEPHLKRGPEDRPGRLLLHPGPDSGPGGGGGCKEKALGSPFGEECLSKEQILQGQGLGAAKP
GQVPMRKRQLPASFWEEPRPTHSYPMGLEGGLGPREGSPYESKKNCKGLESSVPEAAPGPMSPRVLANKEPLKMP
GVSLVGCVDAWSCCPFQYHGQPIYPSPPGALPPSPLPSLGLWRKSPALPAELAHFCKHVDSPGQKVYRPMVLKPI
PTKPAVPPPIFNVFSYL PMRKRQLPASFWEEP

tr:R9PXS9_RAT [R9PXS9] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|Ensembl:ENSRNOP00000007866}; 70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQVRPQEVLNGISSPQPVALTGAGWRDSECSVFSRDDSGIEDNDNQ
PMRLRKLPDSFFKPP

tr:A0A0G2K0Y6_RAT [A0A0G2K0Y6] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|Ensembl:ENSRNOP00000071631}; 13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTA
SGVVSGPAATPAAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPA
VPQTLMNSASGPLPDGWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGV
LGGGSSNQQQQIQLQQLQMEKERLRLKQQELFRQAIRNINPSTANAPKCQELALRSQLPSLEQDGGTQNAVSSPG
MTQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSIPRTPDDFLNSVDEMDTGDTISQSTLPSQQSRFPDY
LEALPGTNVDLGTLEGDAMNIEGEELMPSLQEALSSEILDVESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A250Y0P1_CASCN [A0A250Y0P1] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|EMBL:JAV37197.1};13..27
MNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPAGGVSGPAATPTAQHLRQPSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVPQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDSRFAMNQRISQSAPVKQPPPMAPQSPQ
GGVMGGGNSSQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEPDGGTQNPVSS
PGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFP
DYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:G5AXI8_HETGA [G5AXI8] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:EHB01749.1}; Flags: Fragment;151..165
LLRAASPLQKAPSSWKAPCSGPLVMASDTDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQL
KRFSQKYSRLPRGLPGRAAEPHLRRGPQDRPGRLALHPGPDSSPGGGGGCKEKALGSPFGEECLSKEQNLQGPGA
AKPGQVPMRKRQLPASFWEEPRPTHSYAMGLEGGLGPRERSPYESKKNCKGLESMVPEAAPGPMSPRALADKEPL

KMPGVSLVGCVDAWSCCPFQYHRQPIYPGPPGALPPSPMPSLGLWRKSPALPPEQAHFCKRVDGPGQKVYRPVVL
KPIPTKPAMPPPIFNIFGYL PMRKRQLPASFWEEP

tr:A0A1A6HND2_NEOLE [A0A1A6HND2] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OBS79237.1}; 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVTEPHLQ
RGPEERPGQLPLHSCPESSPGGGGICKEKVLGTPFREDCLSKEQSFGGLNPEAARPGQLPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPREASLYENKKNCKGLESLGPETAPLPMSPRVLADMEPLKMSGVSLVGSLDAWSYCPFQYH
GQPIFPSLPGVLPQGPVPSLGLWRKSPASPVELTHFCKDVDSPGPKVYRPVVLKPIPTKPAMPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A1A6HHX5_NEOLE [A0A1A6HHX5] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OBS78168.1}; Flags: Fragment;218..232
MAVQAALLTSHPFIPFGFGGSADGLVSSFGSLDKGCCFEDDESGAPAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPGPPSPSTADAPVKRPPGAQGAPTVAAPAHCK
ATPRREATQAAAAASLQSRSLAALFDSLHHVPGGAEPAGGAVAVSVPGLGAASPAGDGAGTSGSSAASGTRKVPL
RARNLPPSFFTEPSRVGGSGSSGGGCGPSGQAVSLGDLEKGAEAVEFFELLAPXFGAGNDSGALLAAEPLDAFPA
GATVLRGPLELESGPFEQPAMVGNLLYPEPWSAPSCPQTKKPPLASVRGGVTLNEPVRLLYPTALDSPDCALPPP
HQMSYDYSAGYSRAVYPSLWRPDGVTNLPE PLRARNLPPSFFTEP

tr:G3UYA6_MOUSE [G3UYA6] SubName: Full=Transcriptional coactivator YAP1
{ECO:0000313|Ensembl:ENSMUSP00000134007};70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQTVRLGISSAQPVAYTGAGWRDSECSVFSWDVSGIENNDNQ
PMRLRKLPDSFFKPP

tr:G3UYV4_MOUSE [G3UYV4] SubName: Full=Transcriptional coactivator YAP1
{ECO:0000313|Ensembl:ENSMUSP00000134237};70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQAIRNINPSTANAPKCQTVRLGISSAQPVAYTGAGWRDSECSVFSWDVSGIENNDNQ
PMRLRKLPDSFFKPP

tr:G3UY62_MOUSE [G3UY62] SubName: Full=Transcriptional coactivator YAP1
{ECO:0000313|Ensembl:ENSMUSP00000133959};70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQH
LRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPAPASPAVPQTLMNSASGPLPD
GWEQAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQ
QLQMEKERLRLKQQELFRQEVPKTVRLGISSAQPVAYTGAGWRDSECSVFSWDVSGIENNDNQ
PMRLRKLPDSFFKPP

tr:A0A140LHM6_MOUSE [A0A140LHM6] SubName: Full=Protein **FAM181**B
{ECO:0000313|Ensembl:ENSMUSP00000146473};215..229
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGATAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGTAPPRPASPSAADAPAKRPPGAPTVATPAHCKAAP
RREATQAAAAASLQSRSLAALFDSLRHIPGGAETAGGAEAVSVPGLGAASAVGDGAGTAVSSVAPGTRKVPLRAR
NLPPSFFTEPSRVGCGGASGVPSGQGVSLGDLEKGAEAVEFFELLAPDFGSGNDSGVLMAADPLDPFPAGATVLR
GPLELESGPFEQPAMVGNLLYPEPWNTPELSSDQEASCGWRSRRRDLERACAPPVPHSLGLSRWGGRASLVFFHP
LLPRLCVAAAPSGVL PLRARNLPPSFFTEP

tr:Q3U046_MOUSE [Q3U046] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:BAE34009.1}; Flags: Fragment;>gp:AK157234_1 [AK157234]
Mus musculus activated spleen cDNA, RIKEN full-length enriched library,

clone:F830207J03 product:yes-associated protein, full insert sequence. [Mus musculus] 138..152
LGVWSQSFCLSWDAAAAGGKEREEGRSSRRGGEERGGGLGQGVQGDAGPRRSPPNLSAVPRASNEAAAM
EPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTVPMRLRKL
PDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTASGVVSGPAAAPAAQHLRQSSFE
IPDDVPLPAGWEMAKTSSGQRYFLK PMRLRKLPDSFFKPP

tr:A0A087WP32_MOUSE [A0A087WP32] SubName: Full=Family with sequence similarity 181, member A {ECO:0000313|Ensembl:ENSMUSP00000139607}; Flags: Fragment; 129..143
MAADSDVKMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRVAEPHLQ
RGPEERPGRPPLHPCPQSSPGGGGSCTEKALGTPFREECLSKDQGFRGLNPEAARPGQVPMRKRQLPASFWEEPR
PTLSYPMGLEVGLAPR PMRKRQLPASFWEEP

tr:A0A1A8AEC2_NOTFU [A0A1A8AEC2] SubName: Full=Family with sequence similarity 181, member B {ECO:0000313|EMBL:SBP53442.1}; 148..162
MNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTGIITPGHVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAKEVRGEKA
KKPPLRHRNLPPSFFTEPANCSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPLRAQPDLG
GLDPVSYDAHHLVGGLLYSEPWTSCSGPPKKLGESLRTGLAQPPIYSQSEEASGSIDDSGLSSLAFSNFFTDCSI
PQVTYDLNCGYSKANYSSP PLRHRNLPPSFFTEP

tr:A0A1A8G386_9TELE [A0A1A8G386] SubName: Full=Family with sequence similarity 181, member A {ECO:0000313|EMBL:SBQ64819.1}; 98..112
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHAHRSADHRC
LKSPGTAAQETASHEQDVENVGIEVEQVPMRKRQLPASFWEEPRQTKAKRDKTGLGLKKSAIGSSDGSKNEMRKA
ALDDGANASSSRRNSADKEVLKLDVTSHHSVSVCGCCPLQYHGHHVLHSHIVVPHPPLWSKAAAGTESEHPFGPR
IHTHVVVKPIPTKPTPQSPIFSVFGFI PMRKRQLPASFWEEP

tr:A0A1A8HK71_9TELE [A0A1A8HK71] SubName: Full=Family with sequence similarity 181, member B {ECO:0000313|EMBL:SBQ83826.1}; 155..169
MAVQTAIMNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAK
EIRGEKAKKPPLRHRNLPPSFFTEPANCSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPL
RAQPDLGGLDPVSYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGLAQPPVYSQSEEASGSIDDSGLSTLAFSN
FFTDCSIPQVTYDLNCGYSKANYSSP PLRHRNLPPSFFTEP

tr:A0A1A7Z0A9_9TELE [A0A1A7Z0A9] SubName: Full=Family with sequence similarity 181, member A {ECO:0000313|EMBL:SBP36317.1}; 106..120
MKSTTDFVNMANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCH
AHRSADYRCLKPPGTAAQEKATAQDVENVGSEVEQVPMRKRQLPASFWEEPRQTKAKRDKSYLGLKKSTTGPSEG
SENEKRKPPLDDGAKASSSRRNSADKEVLKLDVTSHHSVSVCGCCPLQYHGHHVLHGHIVVPHQPLGLWSKAATG
TESEHPFGPRIHTHVVVKPIPTKPTPQSPIFSVFGFI PMRKRQLPASFWEEP

tr:A0A1A7X5B1_9TELE [A0A1A7X5B1] SubName: Full=Yes-associated protein 1 {ECO:0000313|EMBL:SBP13302.1}; 45..59
MDPSQHNPPVGHQIVHVRGDSETDLETLFNIVMNPNSANIPHSVPMRQRKLPDSFFNPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSAGSLSGLAPAGASPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQTSPPSSVPVPQQNLMNPTSGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
EPRYGLNQQRITQSAPGKQGGPLPPNTHGGVNPMRLQQIEKERLRLKQHEVLRQRPQELALRNQLPTSMEQDGPT
NPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDQLPPSMATQPN
RFPDYLDTIPGTDVDLGTLESESMAVEGEELMPSLHEPLSSDILSDMESVLAATKIDKESFLTWL
PMRQRKLPDSFFNPP

tr:A0A0S7FXX3_9TELE [A0A0S7FXX3] SubName: Full=YAP1 {ECO:0000313|EMBL:JAO19315.1}; 45..59
MDAHRGAPPAGQQIVHVRGDSKTELEALFNAVMNPSKATRQQSVPMRMRKFPDSFFKPPEPRGHSRQAS
SDGGVCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPEGWEMAKTSTGQRYFINHVHRTTTWQ

DPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETAPKVNPAILTLAMQQRLEKLRLKQGIPPQFVPQ
VRENTKLERVVPKISNVILNFCFL   PMRMRKFPDSFFKPP

tr:A0A0S7F445_9TELE   [A0A0S7F445] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO09842.1}; Flags: Fragment;56..70
TSPLVLIWWGNMDPNQLNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKP
PEPKSHSRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPSGWE
MAKTSSGQRYFLNHNEKSTTWQDPRKSLLQMNQPPPPSSVPVQPQTLISPANGSLPEGWEQAITQEGEIYYINHT
NKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQELALRNQLPTSMD
QDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPASI
ASQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

tr:A0A0S7F337_9TELE   [A0A0S7F337] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO09840.1}; Flags: Fragment;56..70
TSPLVLIWWGNMDPNQLNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKP
PEPKSHSRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPSGWE
MAKTSSGQRYFLNHNEKSTTWQDPRKSLLQMNQPPPPSSVPVQPQTLISPANGSLPEGWEQAITQEGEIYYINHT
NKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQVHRPQELALRNQL
PTSMDQDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDP
LPASIASQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

tr:A0A0S7FZJ3_9TELE   [A0A0S7FZJ3] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO19322.1};   45..59
MDAHRGAPPAGQQIVHVRGDSKTELEALFNAVMNPSKATRQQSVPMRMRKFPDSFFKPPEPRGHSRQAS
SDGGVCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPEGWEMAKTSTGQRYFINHVHRTTTWQ
DPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETAPKVNPAILTLAMQQRLEKLRLKQGIPPQFVPQ
VQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDT
GDSSDPPSMGLQESMPVLPINEDLMPGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

tr:A0A1A8LRE1_9TELE   [A0A1A8LRE1] SubName: Full=Family with sequence
similarity 181, member B {ECO:0000313|EMBL:SBR47157.1};   148..162
MNSQFMSFCFPDSVMEYDAEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTGIIAPGNVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAKEVRGEKA
KKPPLRHRNLPPSFFTEPANCSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPLRAQPDLG
GLDPVSYDAHHLVGGLLYSEPWTSCSGPSKKLGESLPTGLAQPPIYSQSEEASGSIDDSGLSTLAFSNFFTDCSI
PQVTYDLNCGYSKANYSSP   PLRHRNLPPSFFTEP

tr:A0A1A8PAY9_9TELE   [A0A1A8PAY9] SubName: Full=Yes-associated protein 1
{ECO:0000313|EMBL:SBR78413.1};>tr:A0A1A8SGI5_9TELE [A0A1A8SGI5] SubName:
Full=Yes-associated protein 1 {ECO:0000313|EMBL:SBS16675.1};   45..59
MDPSQHNPPAGHQIVHVRGDSETDLETLFNIVMNPSSTNIPHSVPMRQRKLPDSFFNPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSAGSLSGLAPAGASPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQTSPPSSVPVPQQNLMNPTSGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
EPRYGLNQQRNTQSAPGKQGGPLPTNSHGGVNQMRLQQIEKERLRLKQHDVLRQRPQELALRNQLPTSMEQDGPT
NPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDQLPPSMATQPN
RFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEPLSSDILSDMESVLAATKIDKESFLTWL
PMRQRKLPDSFFNPP

tr:A0A1A8NTF5_9TELE   [A0A1A8NTF5] SubName: Full=Family with sequence
similarity 181, member A {ECO:0000313|EMBL:SBR72002.1};>tr:A0A1A8SN00_9TELE
[A0A1A8SN00] SubName: Full=Family with sequence similarity 181, member A
{ECO:0000313|EMBL:SBS19074.1};   98..112
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHAHKSADHRC
LKPPGTAAQETASHAQDVENVGIEVEQVPMRKRQLPASFWEEPRQTKAKRDKTGLGLKKSAIGSSDGNKNEMRKA
ALDDGANASSSRRNSADKEVLKLDVTSHHFVSVCGCCPLQYHGHHVLHSHIVVPHPPLWSKAAAGTESEHPFGPK
IHTHVVVKPIPTKPTPQSPIFSVFGFI   PMRKRQLPASFWEEP

tr:A0A1A8JU42_NOTKU [A0A1A8JU42] SubName: Full=Family with sequence similarity 181, member B {ECO:0000313|EMBL:SBR23665.1}; 148..162
MNSQFMSFCFPDSVVEYDVEKSLDGSLLCEAEIDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTSIITPGHVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAKEIRGEKA
KKPPLRHRNLPPSFFTEPANCSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPLRAQPDLG
GLDPVSYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGLAQPPIYSQSEEASGSIDDSGLSSLAFSNFFTDCSI
PQVTYDLNCGYSKANYSSP PLRHRNLPPSFFTEP

tr:A0A1A8JCC2_NOTKU [A0A1A8JCC2] SubName: Full=Family with sequence similarity 181, member A {ECO:0000313|EMBL:SBR07473.1}; 98..112
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHAHRSADHRC
LKPPGTAAQETASHAQDVENVGIEVEQVPMRKRQLPASFWEEPRQTKAKRDKTGLGLKKSAIGSSDGSKNEMRKA
ALDDGANASSSRRNSADKEVLKLDVTSHHFVSVCGCCPLQYHGHHVLHSHIVVPHPPLWSKAAAGTESEHPFGPR
IHTHVVVKPIPTKPTPQSPIFSVFGFI PMRKRQLPASFWEEP

tr:A0A1A8QZZ7_9TELE [A0A1A8QZZ7] SubName: Full=Family with sequence similarity 181, member B {ECO:0000313|EMBL:SBR98783.1}; 148..162
MNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTGIIAPGNVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAKEVRGEKA
KKPPLRHRNLPPSFFTEPANSSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPLRAQPDLG
GLDPVSYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGLAQPPIYSQSEEASGSIDDSGLSTLAFSNFFTDCSI
PQVTYDLNCGYSKANYSSP PLRHRNLPPSFFTEP

tr:H0ZR92_TAEGU [H0ZR92] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSTGUP00000013135}; 38..52
PPAGHQIVHVRGDSETDLEALFNAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAG
ALTPQHVRAHSSPASLQLGAVSPGTLTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNH
IDQTTTWQDPRKAMLSQMNVTAPTSPSVQQNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRF
AMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPK
PMRLRKLPDSFFKPP

tr:H0Z1D1_TAEGU [H0Z1D1] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSTGUP00000004369}; 58..72
SPRSAEAVPEASRGSPGAAHRLGPLAELFEYGVHRCLPARAAGGKTQRLERKYGHITPMHRRKLPPSFW
KEPGPGPASLLHTGTPDFSDLLANWTVEPGPELPGRPGLEAEPFAG PMHRRKLPPSFWKEP

tr:A0A1A7Y3K7_9TELE [A0A1A7Y3K7] SubName: Full=Family with sequence similarity 181, member B {ECO:0000313|EMBL:SBP24868.1}; 148..162
MNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTGIITPGNVTDGPVKRQGFPGTQPGPLQSKTLPKRDGVQASLQSKSLAALFSPVKEIRGEKA
KKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMISDQDLYQGAPLRAQPDLG
GLDPISYDTHHLVGGLLYSEPWTSCSGPSKKLGESLRTGLAQPPVYSQSEEASGPIDDIGLSTLAFSNFFTDCSI
PQVTYDLNCGYNKTNYSSL PLRHRNLPPSFFTEP

tr:A0A1A7XQJ1_9TELE [A0A1A7XQJ1] SubName: Full=Family with sequence similarity 181, member B {ECO:0000313|EMBL:SBP20372.1}; 148..162
MNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTGIITPGNVTDGPVKRQGFPGTQPGPLQSKTLPKRDGVQASLQSKSLAALFSPVKEIRGEKA
KKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMISDQDLYQGAPLRAQPDLG
GLDPISYDTHHLVGGLLYSEPWTSCSGPSKKLGESLRTGLAQPPVYSQSEEASGPIDDSGLSTLAFSNFFTDCSI
PQVTYDLNCGYNKTNYSSL PLRHRNLPPSFFTEP

tr:A0A3P8SX74_AMPPE [A0A3P8SX74] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSAPEP00000016920};
155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQGSPLTQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMSLKDLERGNPEAADFFELLGPDYSNMVSDQDLYQGMPF

RVQPELGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKLGETLRTGPAQPPAYCHSEAASGPIEDNALCTLAFPN
FFTDCAIPQVTYDLSGGSFINILTWRQISSW PLRHRNLPPSFFTEP

tr:A0A1A8V5Z3_NOTFU [A0A1A8V5Z3] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:SBS55226.1}; 47..61
MDAHRGGAPPAGQQVVHVRGDSKTELEALFSAVMDPGKASRQPQSLPMRMRKLPDSFFKPPEPRGHSRQ
ASSDGGVCGSLAPHHVRAHSSPASLPVNSLTAQADADVAATPIIPDDVPLPDGWELAKTLTGQRYFINHLEKTTT
WLDPRLSQLQSAAAQHPISCAPIHTHSFSNPAPTTQAQHIHPETAQKMNPAILGLAMQQRQEKERLRCKQGLPPQ
ITPQDAAGRNQIPRGMDHDRSAQMLVPSVDARIRALNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHLLSSVDHM
DTGDSSEPSSVTMQETMPVLPITEGEELMPCIPDGLNSDLLMDMETVLSGPHMDRDSLLTWL
PMRMRKLPDSFFKPP

tr:S4RVF5_PETMA [S4RVF5] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSPMAP00000009195}; 52..66
KTPTKSLQPMELGGDHQLGPMGQQVLHVRGDSETDLETLFNTVMNPQGGALPWRYRKLPPSFFREPDSG
SHSRQSSADSTSPCGIVPQHSRSHSSPANLQQIQGGLGGFGPLQLSCSELQQATLAVAEPPLPPGWEVATTPSGQ
RYYI PWRYRKLPPSFFREP

tr:A0A091QPY5_9GRUI [A0A091QPY5] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KFQ29233.1}; Flags: Fragment; 56..70
SPQHTEAEAPCASPRGIHRLGPLAGLFEYGVHRCLSPQAAGGKTQQLERKYGHITPMHRRKLPPSFWRE
PGPSPAGLLHTGIPDFSDLLANWTVEPGLDAGRELPPELGRPGLESEPFAG PMHRRKLPPSFWREP

tr:A0A3B4C0E7_PYGNA [A0A3B4C0E7] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSPNAP00000004365};
156..170
MAVQAAIMNSQFLNFCFPGSVMEYEVEKGLDGSLLGEADCEDDFRETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIIASGNAATQEPCKGQDSPQAPTSTLQSKTPTKRDGSQANLQSKSLAALFNPA
KDLRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGNPDAAEFFELLGPDYSNMVSEQELFQSTP
IRVQQEGTGGPEPGSFDSHPFVTGGFLYAEPWDTSSNVAKKTGDMRTVPGQPHLYGNTDSSGPVQVEQSSPCALT
FPNFFTDCSVSQVSYDLASGYSRALLKKKRTAWPAQPG PLRHRNLPPSFFTEP

tr:A0A2G9QIE7_LITCT [A0A2G9QIE7] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PIO15402.1}; 115..129
MASDNEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRCHSSKNVDLRKG
LVERINLATHSKGLSEKVMATLDENTDGNACSREIGAEGEKPDQVPMRKRQLPPSFWEEPRPSTSLLEMSCPSKL
DLLYKERTSVTGTTLSSFDNKKLKNVVIQETSSPSCLEKEAGKVPSVTPLAGRVNVCSCCPLQYHGQQMLYHHSH
HGTLPPDPFAALALWSKSTTIPTVEIQHLCKDSGQRIYRHVVFKPIPTKPAMPASIFNVFGYI
PMRKRQLPPSFWEEP

tr:A0A091EZF7_CORBR [A0A091EZF7] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KFO63283.1}; Flags: Fragment; 60..74
SPQSTEAVPEAVVPRRSPGATHMLGPLAELFEYGVHRCLPARVAGSKTQRLERKYGHITPMHHRKLPPS
FWKEPGPGPASLLHAGTPDFSDLLANWTVEPGPELPGTGRELPGRLGLEAEPFAG PMHHRKLPPSFWKEP

tr:A4IGV8_XENTR [A4IGV8] SubName: Full=LOC100038276 protein
{ECO:0000313|EMBL:AAI35265.1}; Flags: Fragment;>gp:BC135264_1 [BC135264]
LOC100038276 protein [Xenopus tropicalis] 144..158
CTLAGWIILSNGIACIDFVWKSVFLNIMASDSEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQ
KQLKRFSQKYSRLPRCTPSKSVDLRKGLLDRQNNTSLNNGLSEKAMHALETEESIIKDTFTQENSSEAGRPDQVP
MRKRHLPASFWEEPRPSSSLLELHCPSRPDIFKESTDTLLPLYETKRGKNLAIHESHSSSSFYPSEDKESGKLPS
VASLTELVNACSCCPFQYHGQAMYQHYPGELSSNPFTALALWSKSTVPTLELQHLCKESGQRIYRHVVLKPIPTK
PAVHSSLFNVFGYI PMRKRHLPASFWEEP

tr:F6YXE9_XENTR [F6YXE9] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSXETP00000058802}; 144..158
CTLAGWIILSNGIACIDFVWKSVFLNIMASDSEVKTLLNFVNLASCDIKAALDKSAPCRRSVDHRKYLQ
KQLKRFSQKYSRLPRCTPSKSVDLRKGLLDRQNTTSLNNGLSEKSMHALETEESIIKDTFTQENSSEAGRPDQVP
MRKRHLPASFWEEPRPSSSLLELHCPSRPDIFKESTDTLLPLYETKRGKNLAIHESHSSSSFYPSEDKESGKLPS

VASLTELVNACSCCPFQYHGQAMYQHYPGELSSNPFTALALWSKSTVPTLELQHLCKESGQRIYRHVVLKPIPTK
PAVHSSLFNVFGYI   PMRKRHLPASFWEEP

tr:A0A2P4T9W7_BAMTH   [A0A2P4T9W7] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:POI33134.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPTKTPECGPR
RGAEDRARSCQPDVPDPGPHNGAATEKVLQAAEAEESLKREQAVPEQNPETNRPDQVPMRKRQLPASFWEEPRPP
QSLPARGFPPGPEGLPVPRDPPPFEGKKSKRSQDTIGPESHEPSLNAGEKDPTGVLAGRVGAWTCCPFPCPGPAV
YQPPGTLPPSPFPGLGLWRKGNATLPAEAQPFCKDAEGTGQKLYRPVVLKPIPTKPTIPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A2P4SF16_BAMTH   [A0A2P4SF16] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:POI22702.1};   166..180
MAVPAALLSPHHLLSFCFPAGGLLGYADLEKGYEGGGGGGGGGGGGCEAGDFKEATRDLLSFIDSASSN
IKLALDKPVKSKRKVNHRKYLQKQIKRCTGIIAPPPAAPPPSACPKPPPPPRREGSQAGSSLQSRSLAALFGSLQ
PGRGSAGSDGGGAAGGGPRKVPLRDRNLPPSFFTEPGAKETEKGGGPEAAEFFELLGPEYGALLPEHAAPPQDAF
PAARPPAELGLEHGLYEAAPLPAAPHPLLGGLLYPEPPWSPPGPCSPAKKAPPEPLRPLYPEPAAGGDAFGPFFP
ECPLPPPQMPYDYGGGFHRAAYTGL   PLRDRNLPPSFFTEP

tr:A0A2P4SIM1_BAMTH   [A0A2P4SIM1] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:POI23956.1};   202..216
MHGRAAAPRVSPGPGLSLCTDMAAGVIQPLAKLRLPSPFPHGLLLPARPEPDFPDLSEEDDEEEEEEED
EEEAAEESAGCSGPEPAGPNAAETTLRLLRFSELISCDIQRYFGQRGREEAAGGHGMPEDCSSPRSSPRDASLGH
MARGGRAQPEAALGGHGAAHRLGPLAELFEYGVHRCLAPRVVSGKTQRLERKYGHITPMHRRKLPPSFWREPGPG
PGSLLHAGTPDFSDLLAHWTVEPGPELPGSGRELPPVLGHAGLEAEPYGGL   PMHRRKLPPSFWREP

tr:H2LC86_ORYLA   [H2LC86] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSORLP00000003522};   155..169
MAVQTAIMNPQFMSFCFPGSVMEFDVEKSLDGSLLCEAEQDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNGAETPVKRQSSPVSQQSSLQNKVLPKRDGVQANLQSKSLAALFSPVK
ELRGERAKKPPLRHRNLPPSFFTEPANCSKVSPTSEVTLKDLERGSPDFFELLGPDYSSMVSDQDLYPSVPLRMQ
SELGGLDPASYDAHVVAHHLYTADPWTSCSGPSKKLGENPRAGPVQPPAYFQSEEASGGMDDNALCTLAFPNFFP
DCSLPQVTYDLNSGYNRSKRERGGGGYKC PLRHRNLPPSFFTEP

tr:A0A3P9L0R8_ORYLA   [A0A3P9L0R8] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSORLP00020014325};
155..169
MAVQTAIMNPQFMSFCFPGSVMEFDVEKSLDGSLLCEAEQDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNGAETPVKRQSSPVSQQSSLQNKVLPKRDGAQANLQSKSLAALFSPVK
DIRGERAKKPPLRHRNLPPSFFTEPANCSKVSPTSEVTFKDLERGSPDFFELLGPDYSSMVSDQELYPSVPLRMQ
SELGVLDPASYDAHVVAHHLYTADPWTSCSGPSKKLGENPRAGPVQPPAYFQSEEASGGMDDNALCTLAFPNFFP
DCSLPQVTYDLNSGYNRSMFVVLWEDAF PLRHRNLPPSFFTEP

tr:A0A3P9IJ23_ORYLA   [A0A3P9IJ23] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSORLP00015019934};
155..169
MAVQTAIMNPQFMSFCFPGSVMEFDVEKSLDGSLLCEAEQDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNGAETPVKRQTSPVSQQSSLQNKVLPKRDGVQANLQSKSLAALFSPVK
EIRGERAKKPPLRHRNLPPSFFTEPANCSKVSPTSEVTLKDLERGSPDFFELLGPDYSSMVSDQDLYPSVPLRMQ
SELGGLDPASYDAHVVAHHLYAADPWTSCSGPSKKLGENPRAGPVQPPTYFQSEEASGGMDDNALCTLAFPNFFP
DCSLPQVTYDLNSGYNRSGARQGPAAPAEEGSTPGRKGAHQGCC   PLRHRNLPPSFFTEP

tr:A0A3P9I183_ORYLA   [A0A3P9I183] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSORLP00015013735};42..56
MDAHRSGRQVVHVRGDSQKELEALFSRVMNPSEASRQPSSVPMRMRKLPDSFFKPPEPRGHSRQASSDG
GVCGSLTPHHSRTVSAPAALPVNSLSTQAADVAATSIIPDDVPLPPGWEMAKTPTGQRYFLNHLDKTTTWLDPRL
SQLQSAQHPIANAPVHSHSFSNPAPTTQAQSVNPESGPLPEGWEQAVTPEGEMYYIDHINKTTTWVDPRLGPPPQ
VTQQVRGQINQAAAPKRTDSRTFWVVACMAVDHMKNQMSAGLDHDRSGQVLVPSVDARIRHFNIIAHSRNESTDS

GLSVSSLPRTNDHMLSPVDHMDTGNALKHTKLFFPLNAVPVELGPMLPMSEGEELMPCIPEGLSSDLLMDMETVL
SGSHMDRDNLLTWL PMRMRKLPDSFFKPP

tr:A0A3P9L293_ORYLA [A0A3P9L293] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSORLP00020014834};45..59
MDPSQHNPPVGHQIVHVRGDSETDLEALFNAVMNPKGAVVPQSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYF
LNHIDQTTTWQDPRKALLQLNQATPPSTVPVQQQNLLSPASGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
ETRYALNQQRITQSAPVKQGGPLPPNPHGGVMGGNNQMRLQQMEKERIRLKQQELLRQSQRPQVLDEFLALRNQL
PTSMDQDGSSNPVSSPMAQDARTMTANSNDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDP
LAPSMATQPSRFPDYLDTIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

tr:W5L798_ASTMX [W5L798] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSAMXP00000015710};45..59
MDPGQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAAVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLTGLPQPGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LKKAMLQMNQPPPGSPVPVQQQNLLNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRLDPRFALNQQRIS
QSAPVKPGPPLPSSPPNAGVIGGSCQMRLQQLQMEKERLRLKHQELLRRPQELALRNQLPTSMEQDGGTQNPVSS
PGMGQDARSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLVPASMATQPRGFP
DYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

tr:A0A3B1JDI6_ASTMX [A0A3B1JDI6] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSAMXP00000040328};45..59
MDPGQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAAVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGTLTGLPQPGTSPQHLRQPSYEIPDDVPLPPGWEMAKTASGQRYF
LNHIDQSTTCPVPVQQQNLLNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRLDPRFALNQQRISQSAPV
KPGPPLPSSPPNAGVIGGSCQMRLQQLQMEKERLRLKHQELLRRPQELALRNQLPTSMEQDGGTQNPVSSPGMGQ
DARSMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETSDSLVPASMATQPRGFPDYLDA
IPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL PMRMRKLPDSFFKPP

tr:W5LT58_ASTMX [W5LT58] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSAMXP00000026269}; 156..170
MAVQAAIMNSQFLNFCFPGSVMEYEVEKGLDGGLLGEADCERDFRETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISSGTAATQEPCKRQDSPQTPTSTLQSKTPPKRDGAQANLQSKSLAALFNPA
KDLRGERAKKPPLRHRNLPPSFFTEPANCSRVTSTSGMSLKDLERGNPDAAEFFELLGPDYSNMVTEQELFHTTT
PVRVQQEGTGGPEPGAFDHFVTGGFLYAEPWGTTGSGASKKTGDMRTVPGQPPLYGSTDSSGPAPAEQSSPCSSL
TFPNFFTDCPVSQVSYDLASGYTRGNKDDNGVSLDTAMVPPRECLALVKGHTIPLRHRNLPPSFFTEP

tr:A0A2U9B3Z1_SCOMX [A0A2U9B3Z1] SubName: Full=Putative transcriptional
coactivator YAP1 {ECO:0000313|EMBL:AWO98672.1};>gp:CP026245_269 [CP026245]
putative transcriptional coactivator YAP1 [Scophthalmus maximus] 45..59
MDPSQPNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGVALTPHHVRAHSSPASLQLGAVSGGSLSGMVPAGSPSHLRQSSYEIPDDVPLPPGWEMAKTSSGQRYFL
NHIDQTTTWQDPRKALLQMNQAAPANSVPVQQQNLMNPTSGSLPDGWEQAITSEGEIYYINHKNKTTSWLDPRLD
QRYALNPQRITQSAPVKQGGQLPPSAHTGVLGGNNQMRLQQIEKERLRLKQQELLRQRPQELALRNQLPMDQDGS
TNPVSSPMAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSMATQP
SRFPDYLDAIPGTDVDLGTLEGESMVVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

tr:A0A091T886_PHALP [A0A091T886] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KFQ70649.1}; Flags: Fragment;6..20
RPDQVPMRKRQLPASFWEEPRPAQSLPTRAFPTGPEGLPAPRDPPPYEGKKSKRSSDTAGPESPPESAP
HTGDKDSTGVLSGQVGSWTCCPFPCPGPGVYQPPGALPPSPFPGLGLWRKSTAALPAEVPHFCKEADSTGQKLYR
PVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:A0A2U9B4K8_SCOMX [A0A2U9B4K8] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:AWO98678.1};>gp:CP026245_275 [CP026245] putative protein

FAM181B [Scophthalmus maximus]   155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLSFIDTASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNGAEAPVKRQGSPMAQPSPLQNKTLPKRDGLQANLQSKSLAALFSPVK
EVRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMSLKDLERGNPEAAEFFELLGPDYSNMVSDQDLYQSVPL
RVQPELGGPDPASYDTHHLVGGLLYSEPWTSCSGPSKKPGDSLRTGPAQPPVYCQSEAAAGPVEDNALCTLAFPN
FFTDCSLPQVTYDLGGGYNRANYSSL   PLRHRNLPPSFFTEP

tr:A0A2U9CK07_SCOMX   [A0A2U9CK07] SubName: Full=**FAM181** domain containing
protein {ECO:0000313|EMBL:AWP16523.1};>gp:CP026259_639 [CP026259] **FAM181**
domain containing protein [Scophthalmus maximus]   152..166
MSMFDALCACENTQWSNVPMSRNLDGEAGALTWTDSKVLAKKQKTKKMANADSEVKTLLNFVNLASSDI
KAALDKSAPCRRSVDHRKYLQKQLKRFSQRYSRGPRCHTHRPGEYGRGRPGGAARQGPKDAEQAGGSEARGGDDD
GSAVEQVPMRKRLLPASFWEEPKLTPAKRERTHLGLKRGSSAGAPEGGDNDKRKRSCGDDAKAALSAAGRRSSAD
REALKVDLSSHHCVSVCGCCPFQYHGHQGLHSHIVVPHPAMALWGEAAGAEAEGPEHPYGQKIHTHVVVKPIPTK
PAVQSPIFSVFGFI   PMRKRLLPASFWEEP

tr:A0A1A8IR53_NOTKU   [A0A1A8IR53] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:SBQ99822.1}; Flags: Fragment;32..46
VHVRGDSKTELEALFSAVMDPGKASRQPQSLPMRMRKLPDSFFKPPEPRGHSRQASSDGGVCGSLAPHH
VRAHSSPASLPVNSLTAQADADVAATPIIPDDVPLPDGWELAKTLTGQRYFINHLEKTTTWLDPRLSQLQSAAAQ
HPISCAPIHTHSFSNPAPTTQAQHIHPETAQKMNPAILGLAMQQRQEKERLRCKQGLPPQITPQDAAGRNQMPRG
MDHDRSTQMLVPSVDARIRALNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLCSV PMRMRKLPDSFFKPP

tr:A0A1A8JKU0_NOTKU   [A0A1A8JKU0] SubName: Full=Yes-associated protein 1
{ECO:0000313|EMBL:SBR09786.1};   45..59
MDPSQHNPPAGHQIVHVRGDSETDLETLFNIVMNPSSANIPHSVPMRQRKLPDSFFNPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSAGSLSGLAPAGASPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQTSPPSSVPVPQQNLMNPTSGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
EPRYGLNQQRNTQSAPGKQGGPLPTNSHGGVNQMRLQQIEKERLRLKQHEVLRQRPQELALRNQLPTSMEQDGPT
NPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDESTDSGLSMSSYSVPRT
PDDFLNSVDEMDTGDQLPPSMATQPNRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEPLSSDILSDMES
VLAATKIDKESFLTWL PMRQRKLPDSFFNPP

tr:A0A1A8JN51_NOTKU   [A0A1A8JN51] SubName: Full=Yes-associated protein 1
{ECO:0000313|EMBL:SBR21534.1};>tr:A0A1A8CUN3_9TELE [A0A1A8CUN3] SubName:
Full=Yes-associated protein 1 {ECO:0000313|EMBL:SBP82406.1};   45..59
MDPSQHNPPAGHQIVHVRGDSETDLETLFNIVMNPSSANIPHSVPMRQRKLPDSFFNPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSAGSLSGLAPAGASPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQTSPPSSVPVPQQNLMNPTSGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
EPRYGLNQQRNTQSAPGKQGGPLPTNSHGGVNQMRLQQIEKERLRLKQHEVLRQRPQELALRNQLPTSMEQDGPT
NPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDQLPPSMATQPN
RFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEPLSSDILSDMESVLAATKIDKESFLTWL
PMRQRKLPDSFFNPP

tr:A0A091MVH1_APAVI   [A0A091MVH1] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KFP81473.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPSECGWR
RGPEDQGRGPQPEAPDPSPHGGATAEKVLLTAEVEESLAGERVLQEQNPEATRPDQVPMRKRQLPASFWEEPRPA
QSLPARVFPASPEGLPAPRDPPPHEGKKSKRSLDSAGPESPPEPAPHTGEKDPAGVFSGRVGAWTCCPFSCPGPG
VYQPPGALPPSPFPGLGLWRKSGAKLPAEVPQPVVLKPIPTKPAIPPPIFNVFSYL   PMRKRQLPASFWEEP

tr:A0A315VJ38_GAMAF   [A0A315VJ38] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PWA23163.1};   46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKAARQPPSVPMRMRKFPDSFFKPPQPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPVNSLSAQADADADAAATPIIPDDVPLPDGWEMAKTPTGQRYFINHVHRTT
TWQDPRLAQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIITETGPLPEGWEQAVTAEGEMYYIDHINQATTWD
DPRLAPKVNPAIHSLAMQQRLEKLRLKQGVLPQFAPQFDEIKHTRIQVQEAGGSNQMPGGMDHDRSAQMLVPSVD
IRIRALNQEPNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGDSSEPPSMGLQESMPVLPINEDLMPGI
PDSLTTDMLMEMDTVLSGPHMDRDSLLTWL   PMRMRKFPDSFFKPP

tr:A0A099ZW71_CHAVO [A0A099ZW71] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KGL86061.1}; Flags: Fragment;127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPGKPPESGWR
RVAEDRGRVPQPELPDPSPHGGAATEKVLRTTEAEESLAGERVLQEQNPEASRPDQVPMRKRQLPASFWEEPRPA
QSLPTRAFPPGLEGLPAPRDPPPYEGKKSKRSSDTTGPESPPDAAPHGREKDPTGVLSGRVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLRLWRKRAS PMRKRQLPASFWEEP

tr:A0A0Q3MCH6_AMAAE [A0A0Q3MCH6] SubName: Full=Yorkie isoform X1
{ECO:0000313|EMBL:KQK80359.1}; 84..98
MDPGQTQQQQPPQASQPPASQQAPPQPPGAVSGAPSGAAQPPGAAPPPAGHQIVHVRGDSETDLEALFN
AVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPS
GVVTGPGAPASQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPSVQ
QNIMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRS
QLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDT
GDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESF
LTWL PMRLRKLPDSFFKPP

tr:A0A0Q3PKI1_AMAAE [A0A0Q3PKI1] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KQK76684.1}; 178..192
MAVPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGDAAGDFKEATRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIIAAAPPPPPAPPAPSASSPPASCPAKPPPRREGSQGASSLQSKSLAALFGSL
QHGPGPAGGGEVAGGGGGATGGGGAAGGGPRKVPLRDRNLPPSFFTEPALPAAARGPVPGAKEPEKGGGDAVEFF
ELLGPEYSALLPEHGAPQDAFPGGAAARLPAELALEHGLYDAALPLPSAHHPLLGGLLYPEPWSPPGPCSPGKKA
PSEALRPLYPGGGEPAPSGGSEEPGGHLPAGFASFFPECPLPPPQVPYEYSAGFPRAAFPGM
PLRDRNLPPSFFTEP

tr:A0A1A8C8U4_9TELE [A0A1A8C8U4] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:SBP75140.1}; 47..61
MDAHRGGAPPAGQQVVHVRGDSKTELEALFSAVMDPGKASRQPQSLPMRMRKLPDSFFKPPEPRGHSRQ
ASSDGGVCGSLAPHHVRAHSSPASLPVNSLTAQADADVAATPIIPDDVPLPDGWELAKTLTGQRYFINHLEKTTT
WLDPXLSQLQSAAAQHPISCAPIHTHSFSNPAPTTQAQHIHPETAQKMNPAILGLAMQQRQEKERLRCKQGLPPQ
ITPQDAAGRNQMPRGMDHDRSAQMLVPSVDARIRALNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHM
DTGDSSEPSSVTMQETMPVLPITEGEELMPCIPDGLNSDLLMDMETVLSGPHMDRDSLLTWL
PMRMRKLPDSFFKPP

tr:A0A1A8EFM5_9TELE [A0A1A8EFM5] SubName: Full=Family with sequence
similarity 181, member B {ECO:0000313|EMBL:SBQ44452.1}; 148..162
MNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTGIITPGHVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAKEVRGEKA
KKPPLRHRNLPPSFFTEPTNCSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPLRAQPDLG
GLDPVSYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGLAQPPIYSQSEEASGSIDDSGLSSLAFSNFFTDCSI
PQVTYDLNCGYSKANYSSP PLRHRNLPPSFFTEP

tr:A0A1A8C923_9TELE [A0A1A8C923] SubName: Full=Family with sequence
similarity 181, member B {ECO:0000313|EMBL:SBP75588.1}; 148..162
MNSQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDDDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKV
NHRKYLQKQIKRCTGIITPGHVAEGPVERQGSPGMQPGPLQSKTPPKRDEVQASLQSKSLAALFSPAKEIRGEKA
KKPPLRHRNLPPSFFTEPANCSKVISTSGMTLKDLERGNPEAAEFFELLGPDYSNMIGDQDLYQGAPLRAQPDLG
GLDPVSYDAHHLVGGLLYSEPWTSCSGPSKKLGESLRTGLAQPPIYSQSEEASGSIDDSGLSSLAFSNFFTDCSI
PQVTYDLNCGYSKANYSSP PLRHRNLPPSFFTEP

tr:A0A093CA05_9AVES [A0A093CA05] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KFV09112.1}; 108..122
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWR
RGAEDRGHGPQPAEAEESLTGERVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPAQSLPARAFPAGPEGLLAPK
DPPPYEGKKSKWSSDTASPESPPESAPHAGEKDPAGGLLGGVGAWTCCPFPCPGPGVYQPPGTLPPSPFPGLGLW
RKSAATLPAEVPHFCKEADGMGQNLYRPVVLKPIPTKPAVPPPIFNVFSYL PMRKRQLPASFWEEP

tr:A0A3B3ZMU0_9GOBI [A0A3B3ZMU0] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSPMGP00000005977}; 46..60
MDAHYGAPPAGQQVVHVRGDSQTELEALFNAVMNPSKVQRQPTSVPMKDRKLPKSFFTQPEPRGHSRQA
SSDGGVSNTLTPRHVRAHSSPAILPPQADVTTAPIIPDDMPLPHGWEMAQTPSGQRYFLNHVDKTTTWHDPRLAQ
LQSAAAQHPLSAAGPPAHSHSLSPLPEGWEQAVTGDGEVYYIDHINKITTWVDPRLGSTLSNLYMKILRNRMPGG
MDHDRNTQTLVPPLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTTDHMLSPVDHMDTGDSGESSSLTLQE
SMPPVLPMSEGDELMGLSSDLLMDMETVLSGSHMDRDSLLTWL PMKDRKLPKSFFTQP

tr:A0A3B4AU07_9GOBI [A0A3B4AU07] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPMGP00000019821}; 13..27
MNPKSTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQASTDAGSGASQTPHHVRAHSSPANLQLGAVSAGS
LSGMGSAGASPQHLRQSSYEIPDDVPLPPGWELAKTASGQRYFLNHIEQTTTWQDPRKALLQLNQPAPASTVPVQ
QQNLMNPATGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRLDPRFGLNQQRISQSAPVKPTGQLPPHSAVMGG
NNQMRLQQLEKERLRLKQQELLRQRPQELALRNQLPMDQDGGSNPVSSPMAQDTRTMTANSSDPFLNSGTYHSRD
ESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGTSMASQPSRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQ
EALSSDIFNDMESVLTGKIDKESFLTWL PMRMRKLPDSFFKPP

tr:A0A3B4AT14_9GOBI [A0A3B4AT14] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSPMGP00000019860};
161..175
MAVQAAIMNPQFLNFCFPGSVMEYDVEKSLDDSSILGEAETEEDYKETTRDLLSFIDSASSNIKLALDK
PVKSKRKVNHRKYLQKQIKRCTGIIALSNAAEPPPPGKRHGSPPMAQTSSTLHTKNLPKRDGVHANLQSKSLAAL
FSPVQDVRGGDKAKKPPLRHRNLPPSFFTEPANCSRVSPTAGTMLKELERGNAEHVDFFELLGPDYSSMVSEQDL
YQTLPVREHSEMGGLETTSYDSQHLVGNLLYSAEPKLTNTQAPGFCHSDATSGPIEDGSLCTLAFPNFFTDCSIP
QVTYDTSGAFSRPNYSSL PLRHRNLPPSFFTEP

tr:A0A3B3ZMV8_9GOBI [A0A3B3ZMV8] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSPMGP00000005978}; 46..60
MDAHYGAPPAGQQVVHVRGDSQTELEALFNAVMNPSKVQRQPTSVPMKDRKLPKSFFTQPEPRGHSRQA
SSDGGVSNTLTPRHVRAHSSPAILPPQADVTTAPIIPDDMPLPHGWEMAQTPSGQRYFLNHVDKTTTWHDPRLAQ
LQSAAAQHPLSAAGPPAHSHSLSPLPEGWEQAVTGDGEVYYIDHINKITTWVDPRLDFLMIFMCYLRAHSRNEST
DSGLSVSSLPRTTDHMLSPVDHMDTGKTESCVFDAISSSLTLQESMPPVLPMSEGDELMGLSSDLLMDMETVLSG
SHMDRDSLLTWL PMKDRKLPKSFFTQP

tr:U3JNH0_FICAL [U3JNH0] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSFALP00000004324}; 57..71
PPPPPAGAVAPRDSPGATHRLGPLAELFEYGVHRCLPARAAGGRTQRLERKYGHITPMHRRKLPPSFWK
EPGPGPASLLHTGTPDFSDLLANWTVEPGPELPGRPGLEAEPFAG PMHRRKLPPSFWKEP

tr:A0A093GY73_DRYPU [A0A093GY73] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:KFV74321.1}; Flags: Fragment; 59..73
PQCAEAQPEAEALQGSPAAVHRLGPLAELFEYGVHRCLPPRGAGSKTQRLERKYGHITPMHRRKLPPSF
WREPGPGPTGLLHTSTPDFSDLLANWTVEPGLELPGTGRELPSDPGRPGLEAEPFTG PMHRRKLPPSFWREP

tr:I3JBA7_ORENI [I3JBA7] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSONIP00000006147}; 45..59
MDAHRGAPPAGQQIVHVRGDSQTELEALFTAVMNPNAAKQPSSLPMRMRKLPDSFFRQPDPRGHSRQAS
SDGGVCGSQAPHHVRAHSSPASLPVNSLSTQAADVAATPIIPDDMPLPRGWEMAKTPTGQRYFLNHLDKTTTWHD
PRLAQLQSAAAQHPISGPPVHAHSLSNPAPSPLPEGWEQAVTADGEMYYIDHINKTTTWVDPRLEKNFKKKDRKV
LKSFPHNCNSQKASLPVVFCVTAQKMNPSILGMAMQQSQEKDRLRCKQGIPQQIPPQDVGGRSQMPGGMDHDRSA
QTLIPSLDVRIRASNHEPTLNGAHSRNESTDSGLSVSSLPRTTDHMLSSVEHMDTGNVPKHTTSTTQKHRLGFLC
WGDSEPPSMALQDSMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

tr:I3KYB3_ORENI [I3KYB3] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSONIP00000026110}; 103..117
NMANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHTHRSAEYR
CAKPMGTVHQSVTEKASSGAQDVDHLGSSVEQVPMRKRQLPASFWEEPKLTPTKREHSYLGMKRSHAGTSEGTEN

EKRKRSYDDDGAKAAISACSRRSSTDKETLKLDVTSHHCVSVCGCCPFQYHGHQILHNHIFVPHPPLGLWSKASG
TETERSEHPYGQKIHTHVVVKPIPTKPTAQSPIFSVFGFI PMRKRQLPASFWEEP

tr:A0A3P9PTW4_POERE [A0A3P9PTW4] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSPREP00000025143}; 46..60
MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCSSLAPHHVRAHSSPASLPINSVNAVATPIIPDDVPLPEDWEMAKTPTGQRYFINCFIFLIVNKIKQLF
ISLPKICKLQTFLSTLHLAPATICLLTLYFYCCSGPLPKGWEQAVTAEGEVYYIDHIKQETTWDDPRLAKTRKAQ
TEARRPSTICPTGQREYQAGASRSINIQCYPKLLLSLKSNEIKHTRIQVQEAGGSNQMPGGMDHDRSAQMLVPSV
DIRIRTLNQESNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDIGDSSEPPSMGLQESMPVLPINEELMSG
IPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

tr:Q4TA32_TETNG [Q4TA32] SubName: Full=Chromosome undetermined SCAF7454, whole genome shotgun sequence {ECO:0000313|EMBL:CAF90250.1}; Flags: Fragment; 131..145
DEEKGLDESLLCEAENEEDYRETTRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGII
TPGNVAEAPVKRQVSPLAQSSPLQSKTPPKREGLQASLQSKSLAALFSPVRDVKGEKTKKPPLRHRNLPPSFFTE
PVSYSKVSSTSGMTLRDLERANPETADFFDLLGPEYGGMVSEQDLYQGIPLRVQPDLGGLDPNCYDAHHLVGGLL
YPEPWTSCSGTSRKAGSGPRSGPHQSPAYCPPEASGPMEEHSLCTLAFPNLFTDCSTPQVTYDLNGACNRPHYSC
L PLRHRNLPPSFFTEP

tr:H3DJ10_TETNG [H3DJ10] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSTNIP00000020504}; 105..119
GRKMASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHMHRSTE
HVCAKPAGGVYQRVAAKSDSEVPAAENAAAAAEQTPMRKRQLPASFWEEPKLGQTRGQRLALGTDAGGDPEVSQD
EPRKSADRSALKLDLSSHRCASVCGCCPFQYHGHHILHGHIVLPPPPPWSKAAVSDAGRAAHPYAPQIHTHVVVK
PIPTKPAVQSSIFSVFGFI PMRKRQLPASFWEEP

tr:Q4THS3_TETNG [Q4THS3] SubName: Full=Chromosome undetermined SCAF2719, whole genome shotgun sequence {ECO:0000313|EMBL:CAF87559.1}; Flags: Fragment; 47..61
ATWTRTTAPPAGQQIVHVRGDSQTELEALFSAVMNPSKAARQPSSLPMRMRKLPDSFFRQPDSRGHSRK
PMRMRKLPDSFFRQP

tr:Q4RM11_TETNG [Q4RM11] SubName: Full=Chromosome 10 SCAF15019, whole genome shotgun sequence {ECO:0000313|EMBL:CAG10571.1}; Flags: Fragment; 105..119
GRKMASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHMHRSTE
HVCAKPAGGVYQRVAAKSDSEVPAAENAAAAAEQTPMRKRQLPASFWEEPKLGQTRGQRLALGTDAGGDPEVSQD
EPRKRSRAGDAPASLAASGRRGCADRSALKLDLSSHRCASVCGCCPFQYHGHHILHGHIVLPPPPPWSKAAVSDA
GRAAHPYAPQIHTHVVVKPIPTKPAVQSSIFSVFGFI PMRKRQLPASFWEEP

tr:H3CX97_TETNG [H3CX97] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSTNIP00000012882}; 40..54
APPAGQQIVHVRGDSQTELEALFSAVMNPSKAARQPSSLPMRMRKLPDSFFRQPDSRGHSRKASSDGGV
CNSLTPHHIRAHSSPASLPVNSLSSQAPDVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWHDPRIAQ
LQSAAAQRPIASTPVHTHSLSNPAQRPLPEGWEQAVTADGEVYYIDHINKTTTWVDPRLGSTLSNMSIRETFVPS
RSVFQIMTQKMNPNILGLALQQRQEKERMRQQQGLPPQLPPQEAAGRNQMPGGLDHDRNAQMLVPPLDVRIRAPN
HEPTLNGAHSRNESTDSGLSHSLPRTSDHMLSSVDHMDTGDSGDASSMTLQESMPVLPMSEGEELIPCIPEGLGS
DLLMDMETVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

tr:Q4SFS1_TETNG [Q4SFS1] SubName: Full=Chromosome 7 SCAF14601, whole genome shotgun sequence {ECO:0000313|EMBL:CAG00511.1}; 46..60
MDAHHGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKAARQPSSLPMRMRKLPDSFFRQPDSRGHSRKA
SSDGGVCNSLTPHHIRAHSSPASLPVNSLSSQAPDVAATPIIPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWH
DPRIAQLQSAAAQRPIASTPVHTHSLSNPAQPTTQPQNSISPEPGPLPEGWEQAVTADGEVYYIDHINKTTTWVD
PRLAQKMNPNILGLALQQRQEKERMRQQQGLPPQLPPQSPLTQREHRQRPERHSLPRTSDHMLSSVDHMDTGNVL
YIFHEAFSKKQNSFAFGTKKNPLSQFHSSRLVPSGDSGDASSMTLQESMPVLPMSEGEELIPCIPEGLGSDLLMD
METVLSGSHMDRDSLLTWL PMRMRKLPDSFFRQP

tr:A0A1D5NXI5_CHICK [A0A1D5NXI5] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|Ensembl:ENSGALP00000045081}; 83..97
MDPGQPQPQQPPQAAQPPAPQQAAPQPGRGSGAPGGAAQPPGAGPPPAGHQIVHVRGDSETDLEALFNA
VMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTPSG
VVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQ
NLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQ
LPTMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTG
DSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFL
TWL PMRLRKLPDSFFKPP

tr:A0A1D5PM63_CHICK [A0A1D5PM63] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|Ensembl:ENSGALP00000053936}; 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTS
PPVQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A1A8L4M2_9TELE [A0A1A8L4M2] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:SBR39331.1}; Flags: Fragment;34..48
QVVHVRGDSKTELEALFSAVMDPGKASRQPQSLPMRMRKLPDSFFKPPEPRGHSRQASSDGGVCGSLAP
HHVRAHSSPASLPVNSLTAQADADVAATPIIPDDVPLPDGWEMAKTLTGQRYFINHLEKTTTWLDPRLSQLQSAA
AQHPISCAPIHTHSFSNPAPTTQAQNIHPETAQKMNPAILGLAMQQRQEKERLRCKQGLPPQITPQDAAGRNQMP
RGMDHDRSAQMLVPSVDARIRALNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSSEPSSVTM
QETMPVLPITEGEELMPCIPDGLNSDLLMDMETVLSGPHMDRDSLLTWL PMRMRKLPDSFFKPP

tr:A0A1D5NUE6_CHICK [A0A1D5NUE6] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSGALP00000043963};156..170
MAAGVIQPLAELRLPSPFPHGLLLPARPEPDFPDLSEEDDEEEEEEEDEEEAAEESAGCSGPEPAGPNA
AETTLRLLRFSELISCDIQRYFGRRGREEAAGGHSVPEDCSSPHSSPRDRLGPLAELFEYGVHRCLAPRVVSGKT
QRLERKYGHITPMHRRKLPPSFWREPGPGPGSLLHASTPDFSDLLAHWTVEPGPELPGSGRELPPVLGHAGLEAE
PYSGL PMHRRKLPPSFWREP

tr:A0A1L1RVL6_CHICK [A0A1L1RVL6] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSGALP00000062873};
142..156
MAVPAALLSPHHLLSFCFPAGGLLGYADLEKGYEGGGGVGGGGGGGGCEAGDFKEATRDLLSFIDSASS
NIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIIAGSSLQSRSLAALFGSLQPGRGSAGSDGGGAAGGGPRKVPLR
DRNLPPSFFTEPGAKETEKGGGPEAAEFFELLGPEYGALLPEHAAPPQDAFPAGRPPAELGLEHGLYEAAPLPAA
PHPLLGGLLYPEPPWSPPGPCSPAKKAPPEALRPLYPEPAAGGDAFGPFFPECPLPPRRCPTTTAAASTGRPTPG
C PLRDRNLPPSFFTEP

tr:R4GJN3_CHICK [R4GJN3] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSGALP00000042353}; 111..125
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPTKPPESEDR
ARSCHGAATEKVLQAAEAEESLTREQAVPEQNPETNRPDQVPMRKRQLPASFWEEPRPPQSLPAGGFPPGPEGLP
VPRDPPPFEGKKSKRSQDTIGPESHEPALNAGEKDPTGVLSGRVGAWTCCPFPCPGPAVYQPPGTLPPSPFPGLG
LWRKGTATLPAEAQPFCKDAEGTGQKLYRPVVLKPIPTKPTIPPPIFNVFGYLPMRKRQLPASFWEEP

tr:A0A1A8MTN2_9TELE [A0A1A8MTN2] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:SBR60250.1}; Flags: Fragment;34..48
QVVHVRGDSKTELEALFSAVMDPGKASRQPQSLPMRMRKLPDSFFKPPEPRGHSRQASSDGGVCGSLAP
HHVRAHSSPASLPVNSLTAQADADVAATPIIPDDVPLPDGWEMAKTLTGQRYFINHLEKTTTWLDPRLSQLQSAA
AQHPISCAPIHTHSFSNPAPTTQAQNIHPETGPLPEGWEQAVTADGEVYYIDHINKNTTWVDPRLAQKMNPAILG
LAMQQRQEKERLRCKQGLPPQITPQDAAGRNQMPRGMDHDRSAQMLVPSVDARIRALNQEPTLNGAHSRNESTDS
GLSVSSLPRTSDHMLSSVDHMDTGDSSEPSSVTMQETMPVLPITEGEELMPCIPDGLNSDLLMDMETVLSGPHMD
RDSLLTWL PMRMRKLPDSFFKPP

tr:A0A3P9ACG0_ESOLU [A0A3P9ACG0] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSELUP00000038723}; 48..62
MDARQGQGAPPVGQQIVHVRGDSQTDLEALFNAVINPKTATLPPSSLPMRMRKLPDSFFRQPDPRSHSR
QASSDGNMVGSLAPHHVRAHSSPASLPINTLVTPATNSMATQPLPDDMPLPPGWEMAKTTSGQPYFLNHLEQTTT
WHDPRLSHLQTTAAPHPLSAPPPHTHTLAHPGPLPEGWEQAVTPEGEVYYINHTTKTTSWLDPRLGKTPTSSSGS
KYLMPTTLTSDPVGVVTQRRQQLQAEKDRLRRKQQDLVRPIRAQVRAKTSYNVFIYLDRFGYCTSQYRNFYYISI
NCAALLTSRLFCDWTLPSYYPVFCVMIGDSGAAQPMAFLEAGPGVCMAMDGEELMPSIQEALSSELLSDMDTVLW
L PMRMRKLPDSFFRQP

tr:A0A3P8Z603_ESOLU [A0A3P8Z603] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSELUP00000024251};
173..187
MAVQTAVMNSPFINFCFPGAVLMEYDMDKSLDGSLLGEMGSEEGGDFRETTRDLLSFIDSASSNIKLAL
DKPVKSKRKVNHRKYLQKQIKRCTGIISPLGNPAPAAPGPGLGPNKRQGSGSPTQAQPHTSPFQPGKPILKRDGL
QANLQSKSLAALFKPVKDPVKGERAKKPPLRHRNLPLSFFTEPANSPTTATNTPGVTSTSGMFLEDLERGGGNPE
AADFFELLGPDYSQMLGDQDLFQPQSRAGRVFQHLNPDINGPDQALPPSYDPQQLVGGFLYAEPWSTTSCTGPSK
KGGENTRNSLGPQTMLYSHSDPPMTGSGEDNTLCALAFSNYFPDCSVPQVSYDLSGGDVHSLLCQSGTGEPCFGG
VKNLL PLRHRNLPLSFFTEP

tr:G1K8Z4_ANOCA [G1K8Z4] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSACAP00000000911}; 209..223
MAVQAAPLAPHGHPFLPFGFSALPAGSLGDFGDLEKGFEEGSTLLLDGGTADGDPGDFKELLSFIDSAS
SNIKLALDKPVKSKRKVNHRKYLQKQIKRCNGIIGGTSGTQESSPNPSSQPSSVTAAHCKPPFQQQKRTNPSLSP
SSGGAVHCKPPQPSKRDASAATLVQSQSLAALFDSLQPSGVGLSSMQPEGGLGSSVPHVVGKKVPLRHRNLPPSF
FTEPSHS PLRHRNLPPSFFTEP

tr:G1KYC8_ANOCA [G1KYC8] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSACAP00000020801}; 140..154
SADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYARLPRCHHHHHPHHMQQP
SSLRERKAELEGKSRGLNTSESPEASEGRVAVVATTSASILAQSDKACKADHERQQQQGTSEALARPDQVPMRKR
QLPASFWEEPRPTQGPLSLFASSPLSSSKDLLPLYEGKKSLKGPDGFASLKNLVPLYEGKKSHKGPDRRPDAEAL
QVLSTWGCWPFQCHGPQTSPGLYVPPLPLAAALPSPAAPFPALGLWRKNGGSSMEGEAFGKLGGMGQKVYHRPVV
WKPIPTKPAAPPATLFSVFGYI PMRKRQLPASFWEEP

tr:A0A1A8EM70_9TELE [A0A1A8EM70] SubName: Full=Yes-associated protein 1 {ECO:0000313|EMBL:SBQ46838.1}; 45..59
MDPSQHNPPAGHQIVHVRGDSETDLETLFNIVMNPSSTNIPHSVPMRQRKLPDSFFNPPEPKSHSRQAS
TDAGSGGVLIPHHVRAHSSPASLQLGAVSAGSLSGLAPAGASPQHLRQSSYEIPDDVPLPAGWEMAKTSSGQRYF
LNHIDKTTTWQDPRKPLLQMNQTSPPSSVPVPQQSLMNPTSGPLPEGWEQAITPEGEIYYINHKNKTTSWLDPRL
EPRYGLNQQRNTQSAPGKQGGPLPTNSHGGVNQMRLQQIEKERLRLKQHEVLRQRPQELALRNQLPTSMEQDGPT
NPVSSPLAQDARTMTANSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDQLPPSLATQPN
RFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEPLSSDILSDMESVLAATKIDKESFLTWL
PMRQRKLPDSFFNPP

tr:A0A1A8EXZ4_9TELE [A0A1A8EXZ4] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:SBQ50724.1}; Flags: Fragment; 39..53
PPAGQQVVHVRGDSKTELEALFSAVMDPGKASRQPHSLPMRMRKLPDSFFKPPEPRGHSRQASSDGGVC
GSLAPHHVRAHSSPASLPVNSLTAQADADVAASPIIPDDVPLPDGWELAKTLTGQRYFINHLEKTTTWLDPRLSQ
LQSAAAQHPISCAPIHTHSFSNPAPTTQAPNIHPETAQKMNPAILGLAMQQRQEKERLRCKQGLPPQITPQDAAG
RNQMPRGMDHDRSAQMLVPSVDARIRALNQEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSSEP
SSVTMQETMPVLPITEGEELMPCIPDGLNSDLLMDMETVLSGPHMDRDSLLTWL PMRMRKLPDSFFKPP

tr:A0A3B3CWB4_ORYME [A0A3B3CWB4] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSOMEP00000022098}; 69..83
QKALKGIKRQQAALNPASQSACGTMDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKGAVVPQSVP
MRMRKLPDSFFKPPEPKSHSRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSY
EIPDDVPLPPGWEMAKTTSGQRYFLNHIDQTTTWQDPRKALLQLNQATPPSTVPVQQQNLISPASGPLPEGWEQA
ITPEGEIYYINHKNKTTSWLDPRLETRYALNQQRITQSAPVKQGGPLPPNPHGGVMGGNSQMRLQQLEKERMRLK
QQELLRQRPQELALRNQLPTSMDQDGSSNPVSSPMAQDARTMTANSTDPFLNSGTYHSRDESTDSGLSMSSYSVP

RTPDDFLNSVDEMDTVSTFTIPPSRFPDYLDTIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMETVL
AATKIDKESFLTWL   PMRMRKLPDSFFKPP

tr:A0A3B4UIT5_SERDU   [A0A3B4UIT5] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSSDUP00000018277};>tr:A0A3B4YF40_SERLL [A0A3B4YF40] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSSLDP00000029230}; 155..169
      MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAENDEDYKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQGSPLAQPSPLQSKTLPKRDGVQANLQSKSLAALFSPVK
DIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSDQDLYHSMPL
RVQPEMGGPDPASYDAHHLVGGLLYSEPWTSCSGPSKKQGESLRTGPAQPPVYCHSEAATGPIEDNALCTLAFPN
FFTDCSIPQVTYDLSAGSICFGLRCWWSGAISSSSDDCLQNL   PLRHRNLPPSFFTEP

tr:A0A1V4KB13_PATFA   [A0A1V4KB13] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:OPJ81531.1};   167..181
      MSDAAAASTGEKSRRTPGLSRLVRRIIIFSWETLHSASSEMASDSEVKTLLNFVNLASSDIKAALDKSA
PCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPPECGWRRGPEDRGHGPQPEAPDPSPHGGAATEKVLRTAELE
ESLTGERVLQEQNPEASRPDQVPMRKRQLPASFWEEPRPAQSLPARAFPSNSEGLPVSRDPPPYEGKKSKRSSDT
TGPESPPESALHTGEKDPARVISGRVGTWTCCPFPCPRPGVYQPLGSLPPSPFLGLGLWRKSAATLPVEVPNFCK
EADGTGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:A0A1V4KTG3_PATFA   [A0A1V4KTG3] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:OPJ87712.1};   187..201
      MHGRAAAPRVSPGPRVPLCANMAAGVIQPLAKLQLPSPFRHNLLLPTRPEPDFPDLSEEEEEEEEEDDE
EETAEENVGPELAIPSAAETTLQLLKFSELISCDIQRYFGRRGQEEATGSRGVPEDCGSPQCAKAHPDATTLQGG
PGAMHRLGPLAELFEYGVHRCLPPQAASGKTQRLERKYGHITPMHRRKLPPSFWREPGPGPTSLLHTSTPDFSDL
LANWTVEPGQELPGTGQEPPSEPGRPGLEAEPFTGL   PMHRRKLPPSFWREP

tr:A0A060VV16_ONCMY   [A0A060VV16] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:CDQ56195.1};   103..117
      MASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRMPRCHTHRSADMTP
INEKGGSGAQDEVNVRMGQNPIADSANSKQDQVPMRKRQLPASFWEEPRLAQTNTEPSLYGWKKSQGVTRINRVE
KKIKNHQEPKPTLFQSNRLGSIEKEPLNVDLVSHNVSVCGCCPFQYHGHHVFQSHIVVPHSTVGLWGKASVAEIE
TPDMAHGHNNQTHVVVKPIPTKPTVPSSIFSVFGFI   PMRKRQLPASFWEEP

tr:A0A060Z9U1_ONCMY   [A0A060Z9U1] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:CDR00833.1};   158..172
      MAVQTAIMNSPFVNFCFPGSVMMEETTRSLDGSPLEESEERGEYRETTRNLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGFISPTGNPAAAPGANKRKLQTQPSPFQQGKPVHKRDGLQANLQTKSLAALFNS
VKEPVKGERAKKPPLRHRNLPPSFFTEPANTTTTSRVTSTRACSWVIWNGERGTQTSLTCWGRTTVTCSVIRTCF
RLAACPVGLGPLLLLRRQGRAAYGRAQEHRHPCTVTLCPTPLRQGLQRIVTHCALWPFQLLPRLLCVSGLICGGY
NTKDFSSL   PLRHRNLPPSFFTEP

tr:A0A060XRJ6_ONCMY   [A0A060XRJ6] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:CDQ79555.1};   48..62
      MDARQGQCAPPVGQQIVHVRGDSQTDLEALFNSVMNPKTSALPPSSLPMRMRKLPDSFFRQPDPRSHSR
QASSDGTIVGSLTPHHVRAHSSPASLPINALSAPATSAMATQPLPDDVPLPPGWEMTKTPSGQCYFLNHLDQTTT
WHDPRLSHLQTNAAAHLLSAPPPHTHTLAHPAPNTHTQSNTSSNTGTTLFFSLSVSVSPSLSLSLSRERERERET
QTDRQTDRQTDRQTDRQTDISVQPLDN   PMRMRKLPDSFFRQP

tr:A0A0P7WT42_9TELE   [A0A0P7WT42] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:KPP66915.1};   75..89
      MLRMASADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKCARMPRWHAHRAPD
AGEQVPMRKRQLPASFWEEPSAARGRRETGPGAWRKCHAASSLLQQERRKSSSEEPASDAAVSTQQRLTLTETEP
PVLHMMSSGSVNVCGCCPSFQFHGHHVFQSHVVLPPSAFSHVGLWSKAREAADGASHGQKRQSHAVLKPIPTKPP
GPSPVFSVFGFI   PMRKRQLPASFWEEP

tr:A0A0P7XD32_9TELE   [A0A0P7XD32] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:KPP73128.1};   70..84

MQQAEFFVPEKPISTFWSNNNSVKDFQLSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNAIVPHSV
PMRMRKLPDSFFKPPEPKSHSRQASTDAGTAGSLTPQHVRAHSSPASLQLGAVSPASMASMTPPGGPPQHLRQSS
YEIPDDVPLPPGWEMAKTSSGQRYFLNHLEQSTTWQDPRKTMLQMNTSPNSSVSVQQGIMGTASGPLPEGWEQAV
TTDGEIYYINHKNKTTSWLDPRLDPRYALNQQRIGQSATVKQAPALPSSPQGGVMGGGGSQLRLQQLQMEKERVR
LKQQELLRQRPQVGVLPTLHA   PMRMRKLPDSFFKPP

tr:A0A0P7XN64_9TELE   [A0A0P7XN64] SubName: Full=Protein **FAM181**B-like
{ECO:0000313|EMBL:KPP78288.1};   214..228
MSPSVQLGGVQKCPCQWQDQGFAHLPPEQEDAACFCEAPPPGTAVDAVGEGAGCDAVMAVQAALMTPQF
ANFCFPPPVLEYEAEKPFDGSLLGEGACEGDFREATRDLLSFIDSASSNIKLALDKPVKSRRKVNHRKYLQKQIK
RCAGIAGTLGAAQDLGKRPGSSPPTHPGGCVPARPPSKRDGLQANLQSRSLAALFEPMRDARGDKARKPPLRQRN
LPPSFFTEPAHCARVTSTSGVTLKDLERGNPEAADFLELLGPDYSGMLTGEQETVPPCASGQSARTEAPQPPPYC
PSDSSVSSTLEEAAPCALAFHSFFTECSIPPGAYDFGAGYSRAAFPSL   PLRQRNLPPSFFTEP

tr:A0A3N0YHY1_ANAGA   [A0A3N0YHY1] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:ROL45481.1};   154..168
MAASVIRTLSNLGFTKPFPPSFFPAEDEEETEEEYEEELREDSLEEEEDGVASESQEEEPWSFDLTPNN
TEMTNQLLRFAELISNDVQRYFGRSQDPDACDIYAERPCPKVGGRQRYYADFIKVASSGQVEEPESLGPLAELFQ
DAQRKGRGLPMSQRRLPISFWTEPFAHQLDVLSDANTQENSLSMIDTSESSINISTSLSMFSNTSVCTMTSSSVS
GTLSSSSTPDFSDLLAHWAMDRENPSEFNCDYQLS PMSQRRLPISFWTEP

tr:A0A3N0YL46_ANAGA   [A0A3N0YL46] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:ROL46601.1};   107..121
MANSDSEVKTLLNFVNLASSDIKAALDRSAPCRRSVDHRKYLQKQLKRFSHRYSKVPRCHPHRTSDPTC
AKAGVFARDGPSGNGTEARLATDLSPNSEDDARAGHVPMRKRQLPASFWKEPQSSTGSRECLEHFLKTNANGTVN
VRSHGERRKMIHDNPLLSSNAEPPRRSAACACCPLQYHALHSRFLLPQADAAYRNKTTETHNFIDGLHNNSSHVV
IKPIPTKPAISSSIFSVFGFI   PMRKRQLPASFWKEP

tr:A0A3N0YUP0_ANAGA   [A0A3N0YUP0] SubName: Full=Protein **FAM181**B
{ECO:0000313|EMBL:ROL49926.1};   156..170
MAVQAAIMNSQFLNFCFPGSVMDYEVEKGLEGGLLGEVDCDGDFRETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIISPGTTPVQEPCKRQGSPQNPTSNLSSKTPPKKDGMQANLQSKSLAALFNPA
KDVRGERAKKPPLRHRNLPPSFFTEPANSSRVTSTSGMSLKDLERGTPEAAEFLELLGPDYSNMVSEQDLFHTAP
IRIQQEVSMGPEPYDSHHFVTGGFLYTEPWGTCSDTPKKSGDMRTLPVQPNLYTHTDLSGSLPVEQSSPCALTFS
NFFTDCSTPPVSYDLANGYNRGSFSSL   PLRHRNLPPSFFTEP

tr:A0A3N0YBQ8_ANAGA   [A0A3N0YBQ8] SubName: Full=Transcriptional
coactivator YAP1 {ECO:0000313|EMBL:ROL43198.1};45..59
MDPSQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGTAGTLTPQHVRAHSSPASLQLGAVSPGNLSSMGPANAPPQHLRQSSYEIPDDVPLPPGWEMAKTPSGQRYF
LK   PMRMRKLPDSFFKPP

tr:A0A096M0A1_POEFO   [A0A096M0A1] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSPFOP00000024842};45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPASLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LNHNDKSTTWQDPRKALLQTSQPAPPSSVPVQPQNLMNPANGPLPEHWEQAITSEGEIYYINHEKRTTSWLDPRL
EPRYAALNQQRMTQSAPGKQSGQLPPSTHGGVMAGNNQLRLQQIEKDRLRLQQHRPQRPQELALRNQLPTSMDQD
GSTNPISSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSLPASMAS
QPSRFPDYLDGIPGTDVDLGTLEGESMAVESEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRNLPDSFFKPP

tr:A0A087X9W3_POEFO   [A0A087X9W3] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSPFOP00000002566};45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPASLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LKLQKSEREQDISSHNDKSTTWQDPRKALLQTSQPAPPSSVPVQPQNLMNPANGPLPEHWEQAITSEGEIYYINH
EKRTTSWLDPRLEPRYALNQQRMTQSAPGKQSGQLPPSTHGGVMAGNNQLRLQQIEKDRLRLQQHRPQELALRNQ
LPTSMDQDGSTNPISSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGD

SLPASMASQPSRFPDYLDGIPGTDVDLGTLEGESMAVESEELMASLQEPLSSDILSDMESVLAATKIDKENFLTW
L PMRMRNLPDSFFKPP

tr:A0A087YKH0_POEFO [A0A087YKH0] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSPFOP00000018523}; 46..60
MDAHRGAPPAGQQVVHVRGDSNTELEALFNAVMNPGKAARQTQSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGVCGSLAPHHVRAHSSPASLPINSVNVAATPVIPDDVPLPEDWEMAKTPTGQRYFINHAQRSTTWQDPRLS
QLQSAAAHNPAPTTQPKNIIPETGPLPKGWEQAVTAEGEVYYIDHIKQETTWDDPRLVQCALLEQLNLWQQDSKK
EGSQAPKVNPAGLPLAIQQRLEKLRLKHPVPPQFAPQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQES
NLNGRFVNNCRAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDTGIDVSCPGYCKSHSVPVICSGDSSEPPSMGL
QESMPVLPINEELMSGIPDSLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

tr:A0A087YS39_POEFO [A0A087YS39] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSPFOP00000020842};
155..169
MAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQGSPVSQQGPLQSKTLQKREGGQANLQSKSLAALFSPVK
EIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPDYSNMVNEQDIYQGVPL
RGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGPCKKPSEGLRTGPPQPPVYSQAEDTSVPLDDNGLCTLTFPNFF
PDCSISQVTYDLNGGYNKTNFSCL PMRHRNLPPSFFTEP

tr:A0A087YQW4_POEFO [A0A087YQW4] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSPFOP00000020417};
108..122
KELLVKMSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQTLT
SADYRCARGAERQRVTVTDEASSDAQLAQSVGGVMDQVPMRKRQLPASFWEEPRLTKARRDKPCLDLRRSSSSGT
SDDGENERRRSQEDAQKTANSSSGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQFQGHQVLHSQIVVPHPPFGLWS
KAAEPERSEHPYGQKLHTHVVVKPIPTKATAQSPILSVFGFI PMRKRQLPASFWEEP

tr:U3ITU9_ANAPL [U3ITU9] SubName: Full=Family with sequence similarity 181 member A {ECO:0000313|Ensembl:ENSAPLP00000010672}; 109..123
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHPEVPDPGPHS
GAAAEKVLQAAEAVESLAGERALPEQNPEAGRAEQVPMVPMRKRQLPASFWEEPRPAQSLPSRGFPPGPECAAPR
DTPPFEGKKSKRSLDTAGPESPPEPALQAGEKDPAGVLSGRVGTWTCCPFPCPGPAVYQPPGTLPPSPFPGLGLW
RKSAATLPAEAQPFCKEAEGAGQKLYRPVVLKPIPTKPAVPPPIFNVFGYL PMRKRQLPASFWEEP

tr:A0A0A1CTT9_ANAPL [A0A0A1CTT9] SubName: Full=Yes-associated protein 1 {ECO:0000313|EMBL:AIX99598.1}; Flags: Fragment;>gp:KM924429_1 [KM924429] Yes-associated protein 1 [Anas platyrhynchos] 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTS
PPVQQNLMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQG
GVMGGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQELALRSQLPTMEQDGGSQNPVSSPGMSQELRTMTTNSSD
PFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTL
EGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A087V9J2_BALRE [A0A087V9J2] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFO09284.1}; 112..126
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKPSETGWR
RGVGDRGPATEKVLRTAEVEEGLTGELVLQEQNPEAGRPDQVPMRKRQLPASFWEEPRPAPSLPARAFPTGAEGL
PSPRDPPPYEGKKSKRSSDTAGPESPPEPAPHAGEKDPAGVLSGRVGVWTCCPFPCPGPGVYQPPGTLPPSPFPG
LGLWRKSAATLPVEVPHFCKEADGMGQKLYRPVVLKPIPTKPAIPPPIFNVFGYL PMRKRQLPASFWEEP

tr:A0A3B5MWC4_9TELE [A0A3B5MWC4] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSXCOP00000023934}; 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPSKATRQPPSVPMRMRKFPDSFFKPPEPRGHSRQA
SSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTSTGQRYFINHVHRTTTW
QDPRLSQLQSAAAQHQIACPLPEGWEQAVTTDGEMYYIDHINQATTWDDPRLAQTEAGHPSTICPTGHRERQAGA
SRSINIQCYPKLLLSLKLNETKHTRIQVQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNLNGAHSRNE

STDSGLSVSSLSRTSDHMLSSVDHMDTGIVPYSCFYQLPSQIHDIFNFIFPPSMGLQESMPVLPINEDLMPGIPD
SLTSDMLMEMDTVLSGPHMDRDSLLTWL PMRMRKFPDSFFKPP

tr:A0A3B5LC93_9TELE   [A0A3B5LC93] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSXCOP00000008462};
155..169
MAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPLKRQGSPVNQQGPVQSKTLQKREGGQANLQSKSLAALFSPVK
EIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPDYSNMVNEQDIYQGVPL
RGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGQCKKPSEGLRSGPPQPPVYSQAEDTSVPLDDNGLCTLTFPNFF
PDCSISQVTYDLNGGYNKTHFSCPGFFF PMRHRNLPPSFFTEP

tr:K7FW09_PELSI   [K7FW09] SubName: Full=Yes associated protein 1
{ECO:0000313|Ensembl:ENSPSIP00000012219};73..87
MDPGQPQQAQPPAQQQAPQPPGAQSGAGQPPGAGPPPAGHQIVHVRGDSETDLEALFNAVMNPKGANVP
HTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQVGAVSPGTLTPSGVVTGPGAAPS
SQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAILSQMNVTAPTSPPVQQSIMNSASAM
NQRISQSAPVKQPPPLAPQSPQGGVMGGGSSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKRQ
ELALRSQLPSMEQDGGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNS
VDEMDTGDISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKL
DKESFLTWL   PMRLRKLPDSFFKPP

tr:G3PEP3_GASAC   [G3PEP3] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSGACP00000016067};38..52
PPVGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQASTDAGTGG
VLTPHHVRAHSSPASLQLGAVTGGSMSGMPPPSPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYFLKTTAWQDP
RKALLQMNQAPPPSTGPVQQQNIMNPASGPLPEAWEQAITSDGEIYYINHKNKTTSWLDPRLDPRFALNQQRISQ
SAPVKQGGQLPPGFAVGNSQMRLQQMEKERLRQKQQELLRQRPQVRNREEKSRKKWKKRRNELSIRNQLPTSMDQ
DGGTNPVSSPMAQDARTMTANSTDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDALPPSMA
TQPSRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

tr:A0A226P518_COLVI   [A0A226P518] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OXB74499.1};>tr:A0A226MFB5_CALSU [A0A226MFB5] SubName:
Full=Uncharacterized protein {ECO:0000313|EMBL:OXB53971.1};   179..193
MAAGVIQPLAELRLPSPFPHSLLLPRRTEPEFPDLSEEDDEEEEEEDEEEAAEESTGCSEPELASPNAA
ETTLRLLRFSELISCDIQRYFGQRGREEAAGGHSVPEDCSSPRSSPRDTDLEHTARAGQAQAVLGGGHGAAHRLG
PLAELFEYGVHRCLAPQAAGGKTQRLERKYGHITPMHRRKLPPSFWREPAPGPASLLHAGTPDFSDLLAHWTAEP
GPELPGSGRELPPAQGHAGMEAEPYGGL PMHRRKLPPSFWREP

tr:A0A226P454_COLVI   [A0A226P454] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OXB74169.1};   164..178
MAVPAALLSPHHLLSFCFPAGGLLGYADLEKGYEGGGGGGGGGGGGEDFKEATRDLLSFIDSASSNIK
LALDKPVKSKRKVNHRKYLQKQIKRCTGIIAPPPAAPPPAPCPKPPPPPRRDGSQAGSSLQSRSLAALFGSLRPG
RGSAGSDGGGAAGGGPRKVPLRDRNLPPSFFTEPGAKEAEKAGGQEAADFLELLGPEYGALLPEHACPPRDAFPA
ARPPAELGMEHGMYEAAPHPLLGGLPYPEPPWSPPGPCSPAKKAPSEALRPLYPEPSVGGDAFGPFFPECPLQLP
YEYGAGFHRAAYSGL   PLRDRNLPPSFFTEP

tr:A0A226P1D5_COLVI   [A0A226P1D5] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OXB73199.1};   127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHATKPLECGPR
RGAEDRARSCQPEVPDPSPHSGAATEKVLQAAEAEESLAGEQAVPEQNPEDSRPDLVPMRKRQLPASFWEEPRPA
QSIPARGFPLGTEGLPVPRDPPPFEGKKSKRSQDAAGPESHEPALHAGEKDPTSVLSGRVGAWTCCPFPCPGPAV
YQPPGTLPPSPFPGLGLWRKDAASLPAEAQPFSKEAEGTGQKLYRPVVLKPIPTKPTIPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:G3PED8_GASAC   [G3PED8] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSGACP00000015962};   153..167
MAVQTAIMNPQFMNFCFPGSVMEYDVEKSLDGSLLGEAETEEDYRETTSDLLSFIDSASSNIKLALDKP

VKSKRKVNHRKYLQKQIKRCTGIITPANTAEAPVKRQGSPAAQPSQSKTPPKRDGVQASLQSKSLAALFSPVKDI
RGERTRKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVSEQDLYQSVRVQP
EMGGPDPTSYEAQHLVGGLLYSEPWTSYSGPCKKVGASQPPVYCPSEAASVSVEDNALCTLAFPNYFTDCSAPQA
TYDLSGGYNRANYSSL PLRHRNLPPSFFTEP

tr:G3NZF7_GASAC [G3NZF7] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSGACP00000010729}; 104..118
MANADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRVPRCHAHRSGDYGC
TEPMGAARLRADVTKKAASDAPRAEDAGSAAEQVPMRKRQLPASFWEEPKLSPAKREAPHLGLKRSHAGAAEGSE
NEKRRRGCDKDDARAALSASSWRSGADREALKLDVTSRHCANACGCCPFQYHGHQVLHSHIVVPHPQLGLWSKAA
EAERPEHPYGAKIHTHVVVKPIA PMRKRQLPASFWEEP

tr:G3PEN8_GASAC [G3PEN8] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSGACP00000016062}; 38..52
PPVGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRMRKLPDSFFKPPEPKSHSRQASTDAGTGG
VLTPHHVRAHSSPASLQLGAVTGGSMSGMPPPSPQHLRQSSYEIPDDVPLPPGWEMAKTASGQRYFLKAILIRTT
AWQDPRKALLQMNQAPPPSTGPVQQQNIMNPASGPLPEAWEQAITSDGEIYYINHKNKTTSWLDPRLDPRFALNQ
QRISQSAPVKQGGQLPPGFAVGNSQMRLQQMEKERLRQKQQELLRQRPQVRNREEKSRKKWKELSIRNQLPTSMD
QDGGTNPVSSPMAQDARTMTANSTDPFLNSYVSSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDAL
PPSMATQPSRFPDYLDAIPGTDVDLGTLESESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKESFLTWL
PMRMRKLPDSFFKPP

tr:G3QBL9_GASAC [G3QBL9] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSGACP00000027285}; 49..63
LGDMDAHRGAPPVGQQIVHVRGDSQTELEALFSAVMNPNKSARQPSSLPMRMRKLPDSFFRQPDSRGHS
RQASSDGGVCGSLTPHHVRAHSSPASLPVNSLSTQAADVAAATVVPDDVPLPHGWEMAKTPTGQRYFLNHLDKTT
TWHDPRLSQLQSAAAQHPIAGTPVHAHSLSNPAPTTQQQNTNPETGIAPPPSHSRRTSLPTFLYSFHLYNRNNRP
LKRNQRQEKERLRCKQGLPPQITQEAGGRNQMPGGMDHDRNAQTLVPPLDVRIRASSHEPTLNGAHSRNESTDSG
LSVSSLPRSSDHMLSSVGDSGETSSMTVQESMSVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLT
WL PMRMRKLPDSFFRQP

tr:M4B0N5_XIPMA [M4B0N5] SubName: Full=Family with sequence similarity
181 member B {ECO:0000313|Ensembl:ENSXMAP00000020280}; 155..169
MAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQGSPVSQQGPVQSKTLQKREGGQANLQSKSLAALFSPVK
EIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPDYSNMVNEQDIYQGVPL
RGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGQCKKPSEGLRSGPPQPPVYSQAEDTSVPLDDNGLCTLTFPNFF
PDCSISQVTYDLNGGYNKTHFSYGSNGSWKGFPTTPIWP PMRHRNLPPSFFTEP

tr:A0A3M0K2T0_HIRRU [A0A3M0K2T0] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:RMC07463.1}; 171..185
MAVPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGDDAGDFREATRDLLSFIDSASSNIKLALDRP
VKSRRKVNHRKYLQKQIKRCTGIIAAAAPPPAACPPAACPARPPPRREPAQAAGSSLQSKSLAALFGSLQRGRGA
AGGAEAKAGGGGAGGGEKAAGGPRKVPLRDRNLPPSFFTEPALPGPAARGPPAKEPEKGGGSGGAEAAEFFELLC
PEYGALLPEHAAPTDAFGGRLPAELGLEHGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPAEPPRPLF
PGGAEPVPGGGGGGDEPGGHLPAGFAPFFPECPLPPPQPPYDYGGGFHRGGYPGL PLRDRNLPPSFFTEP

tr:A0A3M0JCV9_HIRRU [A0A3M0JCV9] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:RMB98792.1}; 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKAPECGWR
RGAEDRARGPQPEAPDPSPHGGAAAEKVVRTAEAEESLTGEMGLQEQKPEAARPDQVPMRKRQLPASFWEEPRPA
RSLTAGAFPASPEGLQAPRDPPPYEGKKNKRSPDAAGPESPPDTVPHAGEKDPAGALSGRVGAWTCCPFPCPGPG
VYQPPGALPPSPFPGLGPWRKSAATLPAEVPHFCKEADGPGQKLYRPMVLKPIPTKPAIPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A3M0K235_HIRRU [A0A3M0K235] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:RMC07369.1}; 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGT

LTPSGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLKSGKLVSKIAVLLEAKTVATAFDVLLH
FGRPSVAEFCL PMRLRKLPDSFFKPP

tr:A0A3M0KX01_HIRRU [A0A3M0KX01] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:RMC17829.1}; 165..179
MAAGVIQPLAELRLPSPFPHGLLLPMHPEPDFPDLSEEEEEEEEEEEEEEDVEAVEESVRPELAGVSST
AESTLRLLKFSELISCDIQRYFGRRGREEAGSRAVPEDCGSPQGAEAVPEAAAPGATHRLGPLAELFEYGVHRCL
PARAAGGKTQRLERKYGHITPMHRRKLPPSFWKEPGPGPASLLHAGTPDFSDLLANWTVEPGPELPGTGREPPGR
PGLEAEPFAGL PMHRRKLPPSFWKEP

tr:A0A0S7IVU8_9TELE [A0A0S7IVU8] SubName: Full=F181A
{ECO:0000313|EMBL:JAO56122.1}; Flags: Fragment;102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQSLTSADYRC
ARGAERKRAAATDQASSDAQHAQSDGGVMDQVPMRKRQLPASFWEEPRLTKARRDKPFLDLIRSSSSSEGGENEK
RRRSQEDAQKTANSSFGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQLQGQQLLHSQIVVPHPPFGLWSKAAEPQR
PEHPHGQKLHTHVVVKPIPTKATAQSPVS PMRKRQLPASFWEEP

tr:A0A0S7FQL2_9TELE [A0A0S7FQL2] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO19316.1}; 45..59
MDAHRGAPPAGQQIVHVRGDSKTELEALFNAVMNPSKATRQQSVPMRMRKFPDSFFKPPEPRGHSRQAS
SDGGVCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPEGWEMAKTSTGQRYFINHVHRTTTWQ
DPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETGITLQCCTLFVVICLPLTWSVLGVVPLGFSLGC
LH PMRMRKFPDSFFKPP

tr:A0A0S7F408_9TELE [A0A0S7F408] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO09838.1}; Flags: Fragment;56..70
TSPLVLIWWGNMDPNQLNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKP
PEPKSHSRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPSGWE
MAKTSSGQRYFLNHNEKSTTWQDPRKSLLQMNQPPPPSSVPVQPQTLISPANGSLPEGWEQAITQEGEIYYINHT
NKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQVHRPQELALRNQL
PTSMDQDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGPK
RSQ PMRMRKLPDSFFKPP

tr:A0A0S7EM87_9TELE [A0A0S7EM87] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO03874.1}; Flags: Fragment;45..59
MDAHRGAPPAGQQIVHVRGDSKTELEALFNAVMNPSKATRQQSVPMRMRKFPDSFFKPPEPRGHSRQAS
SDGGVCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPEGWEMAKTSTGQRYFINHVHRTTTWQ
DPRLSQLQSAAAQHQIACTPSHAHSFSNPAPTTQPKNIIPETAPKVNPAILTLAMQQRLEKLRLKQGIPPQFVPQ
VQEAGGSNQMPGGMDHDRSAQMLVPSVDIRIRALNQEPNLNGAHSRNESTDSGLSVSSLSRTSDHMLSSVDHMDT
GIVPLLTTNPNSLHFLRIFLLICSFLNA PMRMRKFPDSFFKPP

tr:A0A0S7F1Z1_9TELE [A0A0S7F1Z1] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO09835.1}; Flags: Fragment;56..70
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PEPKSHSRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPSGWE
MAKTSSGQRYFLNHNEKSTTWQDPRKSLLQMNQPPPPSSVPVQPQTLISPANGSLPEGWEQAITQEGEIYYINHT
NKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQVHRPQELALRNQL
PTSMDQDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEW
YV PMRMRKLPDSFFKPP

tr:A0A0S7EXX9_9TELE [A0A0S7EXX9] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO09841.1}; Flags: Fragment;56..70
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PEPKSHSRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPSGWE
MAKTSSGQRYFLNHNEKSTTWQDPRKSLLQMNQPPPPSSVPVQPQTLISPANGSLPEGWEQAITQEGEIYYINHT
NKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQELALRNQLPTSMD
QDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEWYV
PMRMRKLPDSFFKPP

tr:A0A0S7IV94_9TELE [A0A0S7IV94] SubName: Full=F181A
{ECO:0000313|EMBL:JAO56123.1}; 102..116
MSSADSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRGQSLTSADYRC
ARGAERKRAAATDQASSDAQHAQSDGGVMDQVPMRKRQLPASFWEEPRLTKARRDKPFLDLIRSSSSSEGGENEK
RRRSQEDAQKTANSSFGRRSSAEKEVLKLDLTSHRSVSFCSCCPFQLQGQQLLHSQIVVPHPPFGLWSKAAEPQR
PEHPHGQKLHTHVVVKPIPTKATAQSPIFSVFGFI PMRKRQLPASFWEEP

tr:A0A0S7MHU2_9TELE [A0A0S7MHU2] SubName: Full=F181B
{ECO:0000313|EMBL:JAP01008.1}; Flags: Fragment;196..210
KLHEQHQEQVFIHRTKSCFEETFSSGITVDATGVAAGLDRVMAVQTAIMNPQFMSFCFPDSVMEYDVEK
SLDGSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPV
KRQGSPVSQQGPLQSKTLQKREGGQANLQSKSLAALFSPVKEIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSST
SGMTLKDLERGNPEAADFFELLGPDYSNMVNEQDIYQGVPLRGQPDMGGLDPASYDHLVGGLLYTEPWTNCSGPS
KKPSEGLRSGPPQPPVYSQAEDTSVPLDDNGLCTLTFRTSSQTAPYLRLPMT PMRHRNLPPSFFTEP

tr:A0A0S7F5E5_9TELE [A0A0S7F5E5] SubName: Full=YAP1
{ECO:0000313|EMBL:JAO09837.1}; Flags: Fragment;56..70
TSPLVLIWWGNMDPNQLNPPAGHQIVHVRGDSQTDLELLFNSVMNPKTSNVPPSVPMRMRKLPDSFFKP
PEPKSHSRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPSGWE
MAKTSSGQRYFLNHNEKSTTWQDPRKSLLQMNQPPPPSSVPVQPQTLISPANGSLPEGWEQAITQEGEIYYINHT
NKTTSWLDPRLEPRYALNQQRLTQSAPGKQSGQLPSSTHGGVMGGNNQLRLQQIEKERLRLQELALRNQLPTSMD
QDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGPKRSQ
PMRMRKLPDSFFKPP

tr:A0A218V6B6_9PASE [A0A218V6B6] SubName: Full=Protein **FAM181**B
{ECO:0000313|EMBL:OWK61122.1}; 150..164
MAVPAALLSPHHLLSFCFPAAGGLLGYADLEKGYEGGGGDAGDFREATRDLLSFIDSASSNIKLALDRP
IKRCTGIIAAAAPPPAACPPAACPARPPPRREPAQAAGSSLQSRSLAALFGFLPRGRAAAGGAEPKAGGGEKAAG
GPRKVPLRDRNLPPSFFTEPALPGPAARGPPAKEPEKGGGSAEAAEFFELLCPEYGALLPEHAAATDAFGGRLPA
ELGLEPGLYELPLPAGPHPLLGGLLYPEPPWSPAAPCSPPRKAPAEPLRPIYPGGAEPVPGGGGSEEPGGHLPAG
FAPFFPECPLPPPQPPYDYGGGYHRGGYPGL PLRDRNLPPSFFTEP

tr:A0A218U9Q2_9PASE [A0A218U9Q2] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OWK50230.1}; 171..185
MAGRQRQGVIQPLAELRLPSPFPHGLLLPTHPEPDFPDLSEEEEEEEEEEEEEDVEAVEESVRPELAGV
SSTAETTLRLLRFSELISCDIQRYFGRRGREEAASSRPVPQDCGSPPSAEAVPEAPRGSPGATHRLGPLAELFEY
GVHRCLPARAAGGKTQRLERKYGHITPMHRRKLPPSFWKEPGPGPASLLHSGTPDFSDLLANWTVEPGPELPGAG
RELLGRPGLEAEPFAGL PMHRRKLPPSFWKEP

tr:A0A218UEN4_9PASE [A0A218UEN4] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:OWK52237.1}; 172..186
MVILMWGQLKAALPGAACALSKCRGCQVQVQPWLGCGTGPCPVRRCRQHREMASDSEVKTLLNFVNLAS
SDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKAPECGWRRGAEDRARGPQPEAPEPSPHKVVQ
TAEAEESLTGERVLQEQKPEAARPDQVPMRKRQLPASFWEEPRPAQSLAARAFAASPEGLQAPRDPPPYEGKKSK
RSPDAAGPESPPDSAPHAGEKEPAGPLSGRVGAWTCCPFPCPGPGVYQPPGALPPSPFPGLGLWRKSAATLPAEV
PHFCKEADGQGQKLYRPMVLKPIPTKPAIPPPLFNVFGYL PMRKRQLPASFWEEP

tr:A0A091LX75_CARIC [A0A091LX75] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KFP62949.1}; 110..124
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKTPECGWG
PPGGGPATEKVLQTAEEEDSLSGERVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPAQSLPARAFPTIPEGLPA
PRDPPPYEAKKSKQSLDAVGPESPPEPVPHAGEKDPAGVLSGRVGAWTCCPFPCPGPGVYQPPGPLPPSPFPGLG
LWRKSAAALPAEVPRFCKEADGTGQKLYRPVVLKPIPTKPAIPPPIFNVFGYLPMRKRQLPASFWEEP

tr:A0A091UR35_NIPNI [A0A091UR35] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KFQ93176.1}; Flags: Fragment;60..74
SPQCAEAQPEAVAPRGSPGAMHRLGPLAELFEYGVHRCLPPRAAGGKTQRLERKYGHITPMHRRKLPPS
FWREPGPGPAGLLHAGTPDFSDLLANWTVEPGPELPGTGRELPPEPDRPGLEAEPFAG PMHRRKLPPSFWREP

tr:A0A093PGK4_9PASS   [A0A093PGK4] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KFW76013.1}; Flags: Fragment;80..94
FAQKYSRMPRCHPSKPPECGWRRGAEDRGRGPQLEAPDPSPHGGAATEKVMQTAEAEETLTGERVLQEQ
KPEAVRPDQVPMRKRQLPASFWEEPRPAQNLTARAFPASPEGLPAPRDPPPYEGKKSKWSPDAAGPESPPDPAPH
AGEKDPAGVLSGRVGAWTCCPFPCPGTGVYQPPGALPPSPFPGLGLWRKSAATLPAEVPHFCKEADGTGQKLYRP
MVLKPIPTKPTIPPPIFNVFGYL PMRKRQLPASFWEEP

tr:W5N5Z2_LEPOC   [W5N5Z2] SubName: Full=Family with sequence similarity
181 member A {ECO:0000313|Ensembl:ENSLOCP00000016051};   90..104
MACTDSEVKTLLNFVNLASSDIKAALDKSAPCRRYSRIPRCQSYRTSESGIGKALEDKSGTYPLETVNR
NLSLAHLSEKIGSDLRQDQVPMRKRQLPASFWEEPRSSKSKHETFQAVWRKNQAVGGSGLSGSVEQIRKKCSEGP
KTTSVHINRQSVAEKEPLTVEMTSLTGSASLCGCCPFQYHGQHVYQSHVVLPQSGFSDSSMWGKPSVAQTEGLDS
CKDVAINGQKSHTHVVVKPIPTKPTVPSPIFSVFGFI   PMRKRQLPASFWEEP

tr:A0A3L8SGS6_CHLGU   [A0A3L8SGS6] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:RLW01486.1};   170..184
MAAGVIQPLAELRLPSPFPHGLLLPTHPEPDIPDLSEEEEEEEEEEEEEEDVEAVEESERPELASVSST
AETTLRLLKFSELISCDIQRYFGRRGREEAASSHPVPQDCGSPQSAEAVPEVVAPRGSPGTTHQLGPLAELFEYG
VHRCLPARAAGGKTQRLERKYGHITPMHRRKLPPSFWKEPGPGPASLLHTGTPDFSDLLANWTVEPGPELPGTGR
ELLGRPGLEAEPFAGL PMHRRKLPPSFWKEP

tr:A0A226MJJ1_CALSU   [A0A226MJJ1] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OXB55378.1};   160..174
MAVPAALLSPHHLLSFCFPAGGLLGYADLEKGYEGGGGGGGGGEDFKEATRDLLSFIDSASSNIKLALD
KPVKSKRKVNHRKYLQKQIKRCTGIIAPPPAAPPPAPCPKPPPPPRRDGSQAGSSLQSRSLAALFGSLRPGRGSA
GSDGGGAAGGGPRKVPLRDRNLPPSFFTEPGAKEAEKAGGQEAADFLELLGPEYGALLPEHACPPRDAFPAARPP
AELGMEHGMYEAAPHPLLGGLPYPEPPWSPPGPCSPAKKAPSEALRPLYPEPSVGGDAFGPFFPECPLQLPYEYG
AGFHRAAYTGL PLRDRNLPPSFFTEP

tr:A0A226MRB7_CALSU   [A0A226MRB7] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OXB57873.1};   85..99
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NAVMNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
SGVVTGPGAPSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNLDSNTHAELYLAIALALITTALCWENDGD
QSKGSENMSHIDQTTTWQDPRKAMLSQMNVTAPTSPPVQQNLMNSASAMNQRISQSAPVKQPPPLAPQSPQGGVM
GGSSSNQQQQMRLQQLQMEKERLRLKHQELLRQAMRNPSTANSPKHQELALRSQLPTMEQDGGSQNPVSSPGMSQ
ELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEA
IPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL PMRLRKLPDSFFKPP

tr:A0A226NKW2_CALSU   [A0A226NKW2] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OXB68018.1};   127..141
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RGAEDRARSCQPEVPDPGPHSGAATEKVLQAAEAEESLAGEQAVPEQNPEASRPDLVPMRKRQLPASFWEEPRPA
QSIPARGFPLGTEGLPVPRDPPPFEGKKSKRSQDAAGPESHEPALHAGEKDPTSVLSGRVGAWTCCPFPCPGPAV
YQPPGTLPPSPFPGLGLWRKDAASLPAEAQPFSKEAEGTGQKLYRPVVLKPIPTKPTIPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A151P7M0_ALLMI   [A0A151P7M0] SubName: Full=Transcriptional
coactivator YAP1 isoform B {ECO:0000313|EMBL:KYO44970.1}; 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGPASSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQPNIMNSASAMNPRITQSAPVKQPPSLAPQSPQGGVMGSGNSNQQQQMRLQQLQMEKERLRLKHQELLRQA
LRNINPSTANSPKHQELALRSQLPTMEQDSGSQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSM
SSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRFPDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALS
SDILNDMESVLAATKLDKESFLTWL   PMRLRKLPDSFFKPP

tr:A0A151NHH5_ALLMI   [A0A151NHH5] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:KYO35955.1};   130..144
MTLQLLRFSELISSDIQRYFGRKDKEEDPDSCNIYEDCFSPQRSGRELYYADLMHIAQSGELDDEDSHS

AQVPLGQLDQQVWRSICNKDGGQKLGPLAELFEYGLRQYIKQTVSDSRRLRLEKKYAHITPMHRRKLPPSFWKEP
SPGPAGILNTNTPDFSDLLANWTVEPGQELPNASRELAGELGRQAMEADQFNVL PMHRRKLPPSFWKEP

tr:A0A151P7T5_ALLMI [A0A151P7T5] SubName: Full=Transcriptional
coactivator YAP1 isoform A {ECO:0000313|EMBL:KYO44969.1}; 13..27
MNPKGANVPHTLPMRLRKLPDSFFKPPEPKAHSRQASTDAGSAGALTPQHVRAHSSPASLQLGAVSPGT
LTPSGVVTGPGPASSSQHLRQSSFEIPDDVPLPPGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPT
SPPVQPNIMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNPRITQSAPVKQPPSLAPQSPQ
GGVMGSGNSNQQQQMRLQQLQMEKERLRLKHQELLRQALRNINPSTANSPKHQELALRSQLPTMEQDSGSQNPVS
SPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDSISQSNIPSHQNRF
PDYLEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL
PMRLRKLPDSFFKPP

tr:A0A091GQR5_BUCRH [A0A091GQR5] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:KFO85936.1}; 124..138
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RDRGRGPQPETPDPGPHGGAAAEKVLQTSEVEESLTGERVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPAQSL
PAGAFPTSPEGFPAPRDPPHYEGKKSKRSPGAASPESPPESVPHAREKDPARVLSGRVGAWTCCPFPCPGPGVYQ
PPGALPPSPFPGLGLWRKSVATLPAEGPRFCKEAEGAGQKLFRPVVLKPIPTNPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A2I0TS16_LIMLA [A0A2I0TS16] SubName: Full=Sentrin-specific
protease 3-like {ECO:0000313|EMBL:PKU36598.1}; 166..180
MAAGIIRPLAELRLPSPFPHSLLLPTRPEPDFPDLSEEEEEEEEEDEEEVAEESVKPELAVPSAAETT
LRLLKFSELISCDIQRYFGRQGQEEATGSHGVPEDCGSPRHAEGQPEAVAPRGSPGATHRLGPLAELFEYGVHRC
LPPRAAGGKTQRLERKYGHITPMHRRKLPPSFWREPAPVPTGLLHTGTPDFSDLLANWTVEPGPELPGTGRELPP
EPGHPGLEAEPFAGL PMHRRKLPPSFWREP

tr:A0A2I0UHA0_LIMLA [A0A2I0UHA0] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:PKU45414.1}; 127..141
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRIPRCHPSKAPESGWR
RVVEDRGRGPQPELPDPSPHGGAVTEKVLRTGEAEESLAGEGVLQEQNPEAARPDQVPMRKRQLPASFWEEPRPA
PSLPARAFPAGIEGLPAPRDPPPYEGKKSKRSSDTASPESPPEPAPHAGDKEPAGVLSGRVGAWTCCPFPCPGPG
VYQAPGALAPSPFPGLGLWRKSVAALPGEVPHFCKEADGMGQKLYRPMVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

tr:A0A3B3WPM6_9TELE [A0A3B3WPM6] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSPMEP00000004758}; 45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPASLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LNYLKINLKLIFAYKCLGRYNTESLIATYANLVSVLVCNPPGPLPEHWEQAITSEGEIYYINHEKRTTSWLDPRL
EPRYALNQQRMTQSAPGKQSGQLPPSTLGGVMAGNNQLRLQQIEKDRLRLQQHRPQVSHQFGLGAFISEGGDGRG
TFPFCIRFMCKRQSPKIKEIGTDLIVGTSEVMNKKPTVVTKIT PMRMRNLPDSFFKPP

tr:A0A3B3WZA6_9TELE [A0A3B3WZA6] SubName: Full=Family with sequence
similarity 181 member B {ECO:0000313|Ensembl:ENSPMEP00000008073};
155..169
MAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQGSPVSQQGPLQSKTLQKREGGQANLQSKSLAALFSPVK
EIRGEKAKKPPMRHRNLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAADFFELLGPDYSNMVNEQDIYQGVPL
RGQPDLGGLDPASYDHLVGGLLYTEPWTNCSGPCKKPSEGLRTGPPQPPVYSQAEDTSVPLDDNGLCTLTFPNFF
PDCSISQVTYDLNDGSNNPSGHIDSHTN PMRHRNLPPSFFTEP

tr:A0A3B3Y9M5_9TELE [A0A3B3Y9M5] SubName: Full=Yes-associated protein 1
{ECO:0000313|Ensembl:ENSPMEP00000024061}; 45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPASLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LNHNDKSTTWQDPRKALLQTSQPAPPSSVPVPPQNLMNPANGPLPEHWEQAITSEGEIYYINHEKRTTSWLDPRL

EPRYALNQQRMTQSAPGKQSGQLPPSTLGGVMAGNNQLRLQQIEKDRLRLQQHRPQVSHQFGLGAFISEGGDGRG
TFPFFSQRLILVLPSSSNRKRDFRCWMESMPCQSN PMRMRNLPDSFFKPP

tr:A0A3B3WPN1_9TELE [A0A3B3WPN1] SubName: Full=Yes-associated protein 1 {ECO:0000313|Ensembl:ENSPMEP00000004763}; 45..59
MDPNQHNPPAGHQIVHVRGDSQTDLELLFNSVMNPKSSNVPASLPMRMRNLPDSFFKPPEPKSHSRQAS
TDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSLSGMASAGASPQHLRQSSYEIPDDVPLPAGWEMAKTTSGQRYF
LNHNDKSTTWQDPRKALLQTSQPAPPSSVPVPPQNLMNPANGPLPEHWEQAITSEGEIYYINHEKRTTSWLDPRL
EPRYALNQQRMTQSAPGKQSGQLPPSTLGGVMAGNNQLRLQQIEKDRLRLQQHRPQVSHQFGLGAFISEGGDGRG
TFPFCIRFMCKRQSPKIKEIGTDLIVGTSEVMNKKPTVVTKIT PMRMRNLPDSFFKPP

tr:A0A091K654_COLST [A0A091K654] SubName: Full=Protein **FAM181**A {ECO:0000313|EMBL:KFP32510.1}; 108..122
MASDSEVKTLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKGGWRRGAEERGRGPQPEAPDPGP
HGRAAAEKVLQAGEAEETLARERVLQEQNPEASRPDQVPMRKRQLPASFWEEPRPVQSLPARVFPEGLPSPRDPL
LYEGKKSKRSPDIAGPESSPEPSSHAGEKDPAEVLSSRVGSWTCCPFPCPGPGVYQPPGALPPAPFPGLGLWTKS
AALLPAEVPHFCKEADSVGQKLYRPVVLKPIPTKPTIPSPIFNVFGYL PMRKRQLPASFWEEP

tr:A0A3B4Y209_SERLL [A0A3B4Y209] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSSLDP00000021918}; 46..60
MDAHRGAPPAGQQIVHVRGDSQTELEALFSAVMNPSKATRQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGSLTPHHVRAHSSPASLPDVGQILLFTLSTPCTPSTSLTVYFHCCSGPLPEGWEQAVTADGEVYYIDH
INKTTAWVAPRLGKTFCSNVHHHKLLFSNKNKKDRKSFDNFCSYMSLLKCFTFWKYLLNGQKGLFSMNFMFPAQK
MNPGILGLALQQRQEKERLRCKGLPPQITPQDQELRNIFVRVFLCSAHSRNESTDSGLSVSSLPRTSDHMLSSVD
HMDTGDSGDNSSMTLQESMPVLPMSEGEELMPCIPEGLSSDLLMDMETVLSGSHMDRDSLLTWL
PMRMRKLPDSFFRQP

tr:A0A146RFW2_FUNHE [A0A146RFW2] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:JAQ66927.1}; 204..218
MAVQTAIMNPQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNTSEAPVKRQSSPVSQQGPLQSKNLKRKVNHRKYLQKQIKRCTGIITP
GNTSETPVKRQSSPVSQQGPLQSKNLQKREGGQANLQSKSLAALFSPEKEIRGEKAKKPPLRHRNLPPSFFTEPA
NCSRVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVTEQDVYQGVSPRVQPDLGGLDSTSYDHLVSGLLYPEP
WTNCLGPCKKPGDGLRTGPPQPPVYGQAEDPSGPLDDSGLCTLAFPNFFPDCSIPQAAYDLNGGYSKTSYSCL
PLRHRNLPPSFFTEP

tr:A0A146Y1A6_FUNHE [A0A146Y1A6] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|EMBL:JAR47983.1}; 46..60
MDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPGKAARQPHSLPMRMRKLPDSFFKPPEPRGHSRQA
SLDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTPTGQRYFINHVHKTTTW
QDPRLSQLQSAAAQHQIACTPIHAHSFSNPAPTTQPKNIIPETAQKVNPANLGLAMQQRQEKLRLKHSILPQFVP
QESGGSNQMPGGMDHDRTAQMLVPSVDVRIRALKQEPNLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTG
DSSEPPSMSLQESMPVLPMNDELMPGIPDGLTSDILMDMDTVLSGSHMDRDSLLTWL PMRMRKLPDSFFKPP

tr:A0A146NMN4_FUNHE [A0A146NMN4] SubName: Full=Transcriptional coactivator YAP1 {ECO:0000313|EMBL:JAQ32692.1}; 45..59
MDPNQHNPPAGHQIIHVRGDSQTDLELLFNSVMNPKNSNVPASLPMRMRKLPDSFFKPPEPKSHSRQAS
TDAGSGGVLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRQASTDAGSGGVLTPHHVRAHSSPASLQLGAVSGGSL
SGMASAGASPQHLRQSSYEIPDDMPLPAGWEMAKTHSGQRYFLNHIDKTTTWQDPRKSLLQMNQPAPPSSVPVPQ
QNLMNPASGALPEGWEQAITPEGEIYYINHKNKTTSWLDPRYAQNQQRITQSAPVKQSGQLPPSTHGGVMGGNNQ
LRLPQIEKERLRLQQHRPQELAVRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLRLQQHRPQELAVRNQLPTSMD
QDGSTNPVSSPLAQDARTMTVNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDPLPPSI
ATQPNRFPDYLDAIPGTDVDLGTLESESMVVEGEELMASLQEPLSSDILSDMESVLAATKIDKENFLTWL
PMRMRKLPDSFFKPP

tr:A0A146S711_FUNHE [A0A146S711] SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:JAQ76422.1}; Flags: Fragment; 215..229
RPLSTDKHLLPTPNLDCLWKLHERDQEQVFICGRKSCSEETLSSRITVDATGVAAGLDRVMAVQTAIMN
PQFMSFCFPDSVMEYDVEKSLDGSLLCEAENDEDFKETTRDLLSFIDSASSNIKLALDKPVKSKRKVNHRKYLQK

QIKRCTGIITPGNTSEAPVKRQSSPVSQQGPLQSKNLQKREGGQANLQSKSLAALFSPEKEIRGEKAKKPPLRHR
NLPPSFFTEPANCSRVSSTSGMTLKDLERGNPEAAEFFELLGPDYSNMVTEQDVYQGVSPRVQPDLGGLDSTSYD
HLVSGLLYPEPWTNCLGPCKKPGDGLRTGPPQPPVYGQAEDPSGPLDDSGLCTLAFPNFFPDCSIPQAAYDLNGG
YSKTSYSCL   PLRHRNLPPSFFTEP

tr:A0A147ARY4_FUNHE   [A0A147ARY4] SubName: Full=Protein **FAM181**A
{ECO:0000313|EMBL:JAR81187.1}; Flags: Fragment; 90..104
VNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKFSRVPRCQTLRSADYRCARAAGAERQSAAVV
DEAGSDAQHAQNVGGVTEQVPMRKRQLPASFWEEPRLTKTKRDKSCLDLRRSSSGTSEGTENEKRRRSQDDALKT
AISSSSRRSSADKDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRSSVDKDVLKLDL
TSHHSVSFCGCWPFQFHGNQVLHSQIVVPHPPVSLWSKAAGPEPERPEHPYGQKLHTHVVVKPIPTKPTAQSPIF
SVFGFI   PMRKRQLPASFWEEP

tr:A0A1L8HJ61_XENLA   [A0A1L8HJ61] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OCT96130.1};   54..68
MEPGSQQQPSAPAQQPPPVGHQVVHVRTDSETDLEALFNAVMNPKNANLPQTLPMRMRKLPDSFFKQPQ
PEAKSHSRQASTDGGSAGALTPQHVRAHSSPASLQLAAVSPGALSPQGVVTGLAPPSAPHLRQSSYEIPDDVPLP
PGWEMAKTPSGQRYFLNHIDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTGPLPDGWEQALTPEGEAYFIN
HKNKSTSWLDPRLDPRFAMNQQRLSQNAPVKAPPALPPPSPQTGVLGSGGNQQMRLQQLQMEKERLRLKHQELLR
QVRPQELALRSQIPPMEQDGGTQNPVCTTGISQELRTMTMNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPD
DFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAMNVEGEELMPSLQEALSSDILNDMETV
LAATKLDKESFLTWL   PMRMRKLPDSFFKQP

tr:A0A1L8HAV2_XENLA   [A0A1L8HAV2] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OCT93186.1};   54..68
MEPGSQQQPSAPGQQPPPVGHQIVHVRTDSETDLETLFNAVMNPKNANVPQTLPMRMRKLPDSFFKQPE
PKSHSRHVDQTTTWQDPRKAMLSQINVTAPTSPPVQQNIMTPTAMNQQRLSQSAPVKSPPALQPQSPPSGVLGSG
GNQQMRLQQLQMEKERLRLKHQELLRQVRPQELALRSQIPPMEQDSGPPNPVCSSGISQELRTMTMNSSDPFLNS
GTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGEAITQSTIPTQQNRFPDYLETLPGTNVDLGTLEGEAM
NVEGEELMPSLQEALSSDILNDMETVLAATKLDKESFLTWL PMRMRKLPDSFFKQP

tr:A0A147AQR8_FUNHE   [A0A147AQR8] SubName: Full=Transcriptional
coactivator YAP1 {ECO:0000313|EMBL:JAR80920.1}; Flags: Fragment; 126..140
RSSRPLSCVRALPRLVKRVFCTPCREKRDTGGLFFFFFLLWPFFPAGIHRGGGGGAAAGGGGGGTLWLL
EDLFRLQTLGDMDAHRGAPPAGQQVVHVRGDSKTELEALFNAVMNPGKAARQPHSLPMRMRKLPDSFFKPPEPRG
HSRQASSDGGLCGSLAPHHVRAHSSPASLPVNSLSAQADADAAATPIIPDDVPLPDGWEMAKTPTGQRYFINHVH
KTTTWQDPRLSQLQSAAAQHQIACTPIHAHSFSNPAPTTQPKNIIPETGPLPEGWEQAVTADGEMYYIDHINKTT
TWDDPRLAQKVNPANLGLAMQQRQEKLRLKHSILPQFVPQESGGSNQMPGGMDHDRTAQMLVPSVDVRIRALKQE
PNLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSSEPPSMSLQESMPVLPMNDELMPGIPDGLTSDIL
MDMDTVLSGSHMDRDSLLTWL   PMRMRKLPDSFFKPP

tr:A0A1L8HB22_XENLA   [A0A1L8HB22] SubName: Full=Uncharacterized protein
{ECO:0000313|EMBL:OCT93300.1};   151..165
MNHQFLSLYIPGSIVDYEKRYQEGVDYLGAVESGDFKETTKDLLSFINTASSNIKLALDKPGKSKRKVN
HRKYLQKQIKRCTGLMGSGNINQGSPKRSPTSPGNSSMTPSGFPWKPPTKRDSTQSNLQSKSLAALFDNVKEIRD
ERCKKVPLRNRNLPPSFFTEPESPCSGLLSNSGVALRDLGKCNQETLELFDFLGSDYNNMSEQEIIQGASVRLHQ
DVSVEQSLYEPHHLLNGLFYSDMWNPCNQVKKSSVGTGNLGLNETLKSAPLQGALYTNNQDPTMDSTMDESCPSL
TTYTPCFPSDCSLPQIFYDYNTQNCNRISYPVM   PLRNRNLPPSFFTEP

tr:A0A3B5KEE0_TAKRU   [A0A3B5KEE0] SubName: Full=Uncharacterized protein
{ECO:0000313|Ensembl:ENSTRUP00000053746}; 155..169
MLTLISDSEAAFKWLSFDFRARGPVFFPQSIKSPRCYGSKQTRKDTKVQKGGCWGGGGGVLVGTEIVNK
SDQNRSAPASTSNAPRLCALLVSFCVSKLRFLAATPNFGDMDAHHGAPPAGQQIVHVRGDSQTELEALFSAVMNP
SKASRQPPSLPMRMRKLPDSFFRQPDSRGHSRQASSDGGVCSSLTPHHIRAHSSPASLPVNSLSAQAPDVAAAPI
IPDDVPLPHGWEMAKTPTGQRYFLNHLDKTTTWHDPRIAQLQSAAAQRPIAGTPVHTHSLSNPAQPATQPQNNMS
PETGPLPEGWEQAVTADGEVYYIDHINKTTTWVDPRLAQKMNPNILGLSLQQRQEKERMRQQQGLPPQLPPQEAA
GRNQVSGGLDHDRNTQMLVPPLDVRIRAPNHEPTLNGAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGD
ASSMTLQESMPVLPMSEGEELIPCIPEGLGSDLLMDMETVLSGSHMDRDSLLTWL   PMRMRKLPDSFFRQP

tr:H2UEB8_TAKRU [H2UEB8] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSTRUP00000035287}; 155..169
MAVQTAIMNPQFMNFAFPGSVMGYDMEKGLDEGLLCEADNEEDYRETTRDLLSFMDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGNVAEAPVKRQVSPLTQSSPLQSKTPPKREGIQASLQSKSLAALFSPVK
DVRGEKTKKPPLRHRNLPPSFFTEPVSCSKVSSTSGMTLRDLERANPETADFFDLLGPDYSSMVSEQDLYQGIPL
RVQPDLGGLDPACYDTHHLVGGLLYPEPWTSCSDTSKKAGSGPRSGPHQLPAYCPSDPCGPMEDHSLCTLAFPNL
FTDCSTPQVTYDLNGASEQTLHTEGIWIFCP PLRHRNLPPSFFTEP

tr:A0A3P8VK80_CYNSE [A0A3P8VK80] SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSCSEP00000015683}; 46..60
MDAHRGAPPAGQQVVHVRGDSQTELEALFSAVMNPNKAVRQPASLPMRMRKLPDSFFRQPDPRGHSRQA
SSDGGVCGTLTPHHVRAHSSPASLPVNSLSTQTADVAATPIIPDDVPLPHGWEMAKTSTGQRYFLNHHDKTTTWH
DPRLSQLQSPAAQHPIAGPPLHAHSLSNPAQTTQQQNINPETGPLPEGWEQAVTADGEVYYIDHINKSTTWVDPR
LAQNMNPGILGMVMQQRQEKERLRCKQGHPPQAAPQEVGGRNQMSGGIDHDRNSQTLVPNLDVRIRSSNHEPTLN
GAHSRNESTDSGLSVSSLPRTSDHMLSSVDHMDTGDSGENSSITLQESMPVMPMSEGDELMPCIPEGLSSDLLMD
METVLSGSHMERDSLLTWL PMRMRKLPDSFFRQP

tr:A0A3P8V3D9_CYNSE [A0A3P8V3D9] SubName: Full=Family with sequence similarity 181 member B {ECO:0000313|Ensembl:ENSCSEP00000008629};
155..169
MAVQTAIMNPQFMNFCFPGSVMEYDVDKSLDGSLLGEAENDEDYKETTRDLLNFIDSASSNIKLALDKP
VKSKRKVNHRKYLQKQIKRCTGIITPGTGAEPPGKRQGSPLAQPSPLQNKTLPKRDGVQANLQSKSLAALFSPAK
EIRGEKAKKPPLRHRNLPPSFFTEPANCSKVSSTSGMTLKDLERGNPEAVEFFELLGPDYSNMVSDQDLYPNSSL
RLQPEMGTLDPACYDSHHLVGGLLYSEPWTSCSGPSKNLRASPAQPPVYCQSEAAAAAAAAAGNMDDNALCTLTF
PNFFTDCSIPQVTYDLNGETDDAVETRLPGENMEPQN PLRHRNLPPSFFTEP

gp:AK141493_1 [AK141493] Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530038J03 product:hypothetical Alanine-rich region profile containing protein, full insert sequence. [Mus musculus] 128..142
KRKVNHRKYLQKQIKRCSGLMGTAPPRPASPSAADAPAKRPPGAPTVATPAHCKAAPRREATQAAAAAS
LQSRSLAALFDSLRHIPGGAETAGGAEAVSVPGLGAASAVGDGAGTAVSSVAPGTRKVPLRARNLPPSFFTEPSR
VGCGGASGVPSGQGVSLGDLEKGAEAVEFFELLAPDFGSGNDSGVLMAADPLDPFPAGATVLRGPLELESGPFEQ
PAMVGNLLYPEPWNTPSCPQTKKPPVAGVRGGVTLNEPVRLLYPTALDSPGGEDAPALSSFTPFFPDCALPPPHQ
VSYDYSAGYSRAVYPSLWRPDGVWEGASGEEGGHPD PLRARNLPPSFFTEP

gp:BT029961_1 [BT029961] IP17673p [Drosophila melanogaster] 88..102
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPIAA
IPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAP
ASSAIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWED
PRIQYRQQQQILMAERIKQNDVLQTTKQTTTSTC PLRMRKLPNSFFTPP

gp:BT029965_1 [BT029965] IP17873p [Drosophila melanogaster] 88..102
MCACLIAKIILCSFRLYTISAFYMLTTMSASSNTNSLIEKEIDDEDMLSPIKSNNLVVRVNQDTDDNLQ
ALFDSVLNPGDAKRPLQLPLRMRKLPNSFFTPPAPSHSRANSADSTYDAGSQSSINIGNKASIVQQPDGQSPIAA
IPQLQIQPSPQHSRLAIHHSRARSSPASLQQNYNVRARSDAAAANNPNANPSSQQQPAGPTFPENSAQEFPSGAP
ASSAIDLDAMNTCMSQDIPMSMQTVHKKQRSYDVISPIQLNRQLGALPPGWEQAKTNDGQIYYLNHTTKSTQWED
PRIQYRQQQQILMAERIKQNDVLQTTKQTTTSTMLTIWVHCRMVGSRQLPSPEIFTL PLRMRKLPNSFFTPP

gp:AK093387_1 [AK093387] Homo sapiens cDNA FLJ36068 fis, clone TESTI2019352. [Homo sapiens] 191..205
MPLEERRSSGERNDAAPTNHRRPGEKRTSTAKQVSSVPFLGAAGHQQSLPSSWKASCSGPLVMASDSDV
KMLLNFVNLASSDIKAALDKSAPCRRSVDHRKYLQKQLKRFSQKYSRLPRGLPGRAAEPYLKRGSEDRPRRLLLD
LGPDSSPGGGGGCKEKVLRSPYREECLAKEQLPQRQHPEAAQPGQVPMRKRQLPASFWEEPRPTHSYHVGLEGGL
GPREGPPYEGKKNCKGLEPLGPETTLVSMSPRALAEKEPLKMPGVSLVGRVNAWSCCPFQYHGQPIYPGPLGALP
QSPVPSLGLWRKSPAFPGELAHLCKDVDGLGQKVCRPVVLKPIPTKPAVPPPIFNVFGYL
PMRKRQLPASFWEEP

gp:BC150621_1   [BC150621] family with sequence similarity 181, member B
[Homo sapiens]   221..235
MAVQAALLSTHPFVPFGFGGSPDGLGGAFGALDKGCCFEDDETGAPAGALLSGAEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIKRCSGLMGAAPPGPPSPSAADTPAKRPLAAPSAPTVAAPAHGK
AAPRREASQAAAAASLQSRSLAALFDSLRHVPGGAEPAGGEVAAPAAGLGGAGTGGAGGDVAGPAGATAIPGARK
VPLRARNLPPSFFTEPSRAGGGGCGPSGPDVSLGDLEKGAEAVEFFELLGPDYGAGTEAAVLLAAEPLDVFPAGA
SVLRGPPELEPGLFEPPPAVVGNLLYPEPWSVPGCSPTKKSPLTAPRGGLTLNEPLSPLYPAAADSPGGEDGRGH
LASFAPFFPDCALPPPPPPHQVSYNYSAGYSRTAYSSLWRSDGVWEGAPGEEGAHRD PLRARNLPPSFFTEP

gp:AB041569_1   [AB041569] Mus musculus brain cDNA, clone MNCb-1231. [Mus
musculus]   215..229
MAVQAALLSSHPFIPFGFGGSADGLVSAFGSLDKGCCFEDDESGATAGALLSGSEGGDVREATRDLLSF
IDSASSNIKLALDKPGKSKRKVNHRKYLQKQIRRCSGLMGTAPPRPASPSAADAPAKRPPGAPTVATPAHCKAAP
RREATQAAAAASLQSRSLAALFDSLRHIPGGAETAGGAEAVSVPGLGAASAVGDGAGTAVSSVAPGTRKVPLRAR
NLPPSFFTEPSRVGCWLAPAASHRARA   PLRARNLPPSFFTEP

gp:DQ186896_1   [DQ186896] neuron-specific YAPdeltaC insert13 isoform
[Rattus norvegicus]   70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQTVRAGISSPQPVALTGAGWRDSECSVFSRDDSGIEDNDNQ   PMRLRKLPDSFFKPP

gp:DQ186897_1   [DQ186897] neuron-specific YAPdeltaC insert25 isoform
[Rattus norvegicus]   70..84
MEPAQQPPPQPAPQGPAPPSVSPAGTPAAPPAPPAGHQVVHVRGDSETDLEALFNAVMNPKTANVPQTV
PMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAGTLTASGVVSGPAATPAAQHLRQ
SSFEIPDDVPLPAGWEMAKTSSGQRYFLNHNDQTTTWQDPRKAMLSQLNVPTSASPAVPQTLMNSASGPLPDGWE
QAMTQDGEVYYINHKNKTTSWLDPRLDPRFAMNQRITQSAPVKQPPPLAPQSPQGGVLGGGSSNQQQQIQLQQLQ
MEKERLRLKQQELFRQVRPQTVRAGISSPQPVALTGAGWRDSECSVFSRDDSGIEDNDNQ
PMRLRKLPDSFFKPP

gp:KJ898207_1   [KJ898207] YAP1 [synthetic construct]   85..99
MDPGQQPPPQPAPQGQGQPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRGDSETDLEALF
NAVMNPKTANVPQTVPMRLRKLPDSFFKPPEPKSHSRQASTDAGTAGALTPQHVRAHSSPASLQLGAVSPGTLTP
TGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNVTAPTSPP
VQQNMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQRISQSAPVKQPPPLAPQSPQGGV
MGGSNSNQQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPG
MSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDY
LEAIPGTNVDLGTLEGDGMNIEGEELMPSLQEALSSDILNDMESVLAATKLDNESFLTWL
PMRLRKLPDSFFKPP

gp:BC129216_1   [BC129216] Yes-associated protein 1 [Danio rerio]
45..59
MDPNQHNPPAGHQIVHVRGDSETDLEALFNAVMNPKNTIVPPSVPMRLRKLPDSFFTPPEPKSHSRQAS
TDAGTAGTVTPHHVRAHSSPASLQLGAVSPGALTSMGPANAPPQHLRQSSYEIPDDMPLPPGWEMAKTPSGQRYF
LNHNDQTTTWQDPRKALLQMNQAAPASPVPVQQQNIMNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRL
DPRFAMNQQRISQSAPVKQGSQLPSSPQSGVMSGNNPIRLQQIHIEKERLRIKQELLRQRPQELALRNQLPTSME
QDGGTQNPVSSPGMGQDARNMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVPRTPDDFLNSVDEMETGDTLGP
SSMATQPSRFPDYLDAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDILNDMESVLAATKIDKENFLTWL
PMRLRKLPDSFFTPP