

Supplementary Materials

Plant histone HTB (H2B) variants in regulating chromatin structure and function

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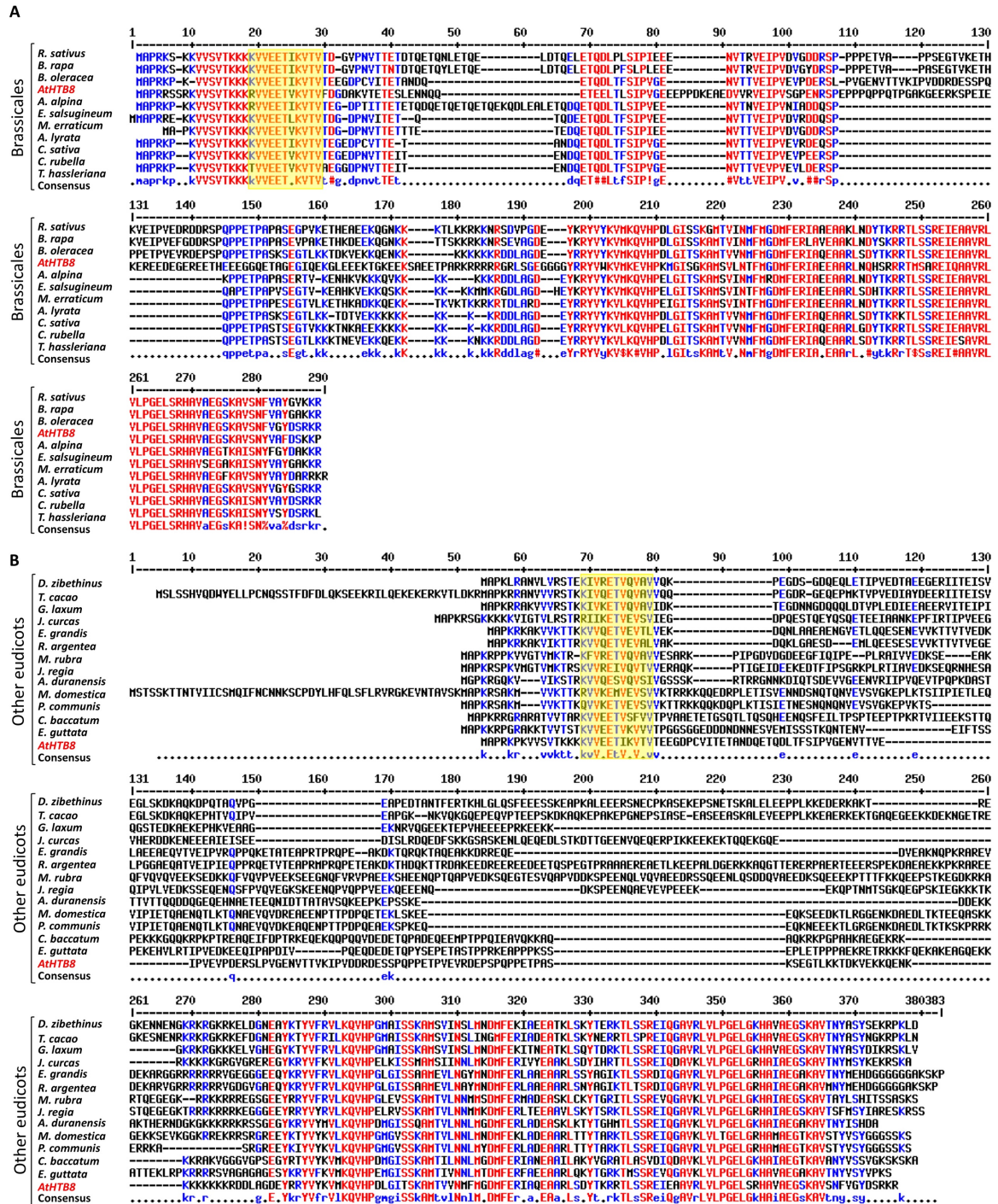


Fig. S1. Amino acid sequence alignments of HTB8-like proteins (Maltin interface; Corpet, 1988). (A) Alignments of HTB8-like proteins in Brassicales. (B) Alignments of HTB8-like proteins in other eudicot species. Note that all HTB8-like proteins share high amino acid sequence similarity of the C-terminal region. The yellow box marks the conserved domain in the N-terminal extension of HTB8 orthologs. Species abbreviations: *C. baccatum*, *Capsicum*; *E. guttata*, *Erythraea*; *T. hassleriana*, *Tarenaya*; *M. erraticum*, *Microthlaspi*; *A. alpine*, *Arabis*; *E. salsugineum*, *Eutrema*; *R. sativus*, *Raphanus*; *B. rapa*, *Brassica*; *B. oleracea*, *Brassica*; *C. sativa*, *Camelina*; *C. rubella*, *Capsella*; *A. lyrata*, *Arabidopsis*; *A. thaliana*, *Arabidopsis*; *J. curcas*, *Jatropha*; *G. laxum*, *Gossypium*; *T. cacao*, *Theobroma*; *D. zibethinus*, *Durio*; *A. duranensis*, *Arachis*; *J. regia*, *Juglans*; *M. rubra*, *Morella*; *M. domestica*, *Malus*; *P. communis*, *Pyrus*; *E. grandis*, *Eucalyptus*; *R. argentea*, *Rhodamnia*.

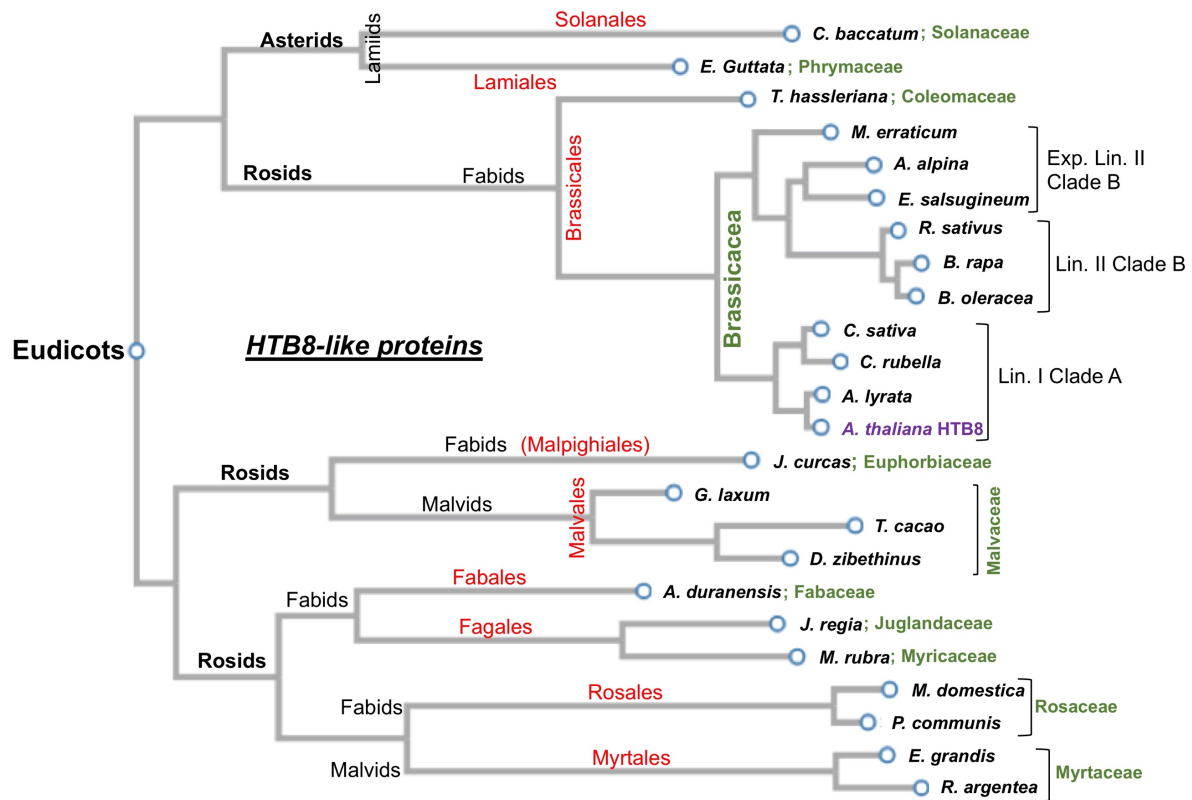


Fig. S2. A phylogenetic tree of HTB8-like proteins within the Eudicot clade of angiosperms. Species within the Rosids clade distributed between Fabids and Malvids and the Asterids clade (Lamiids) are presented. Orders are in red and families are colored green. The Brassicaceae species are clustered according to their phylogeny (Gou et al., 2017) including expanded lineage II (Exp. Lin. II), clade B; Lin II, clade B and Lin I, clade A. Species abbreviation as in Fig. S1.

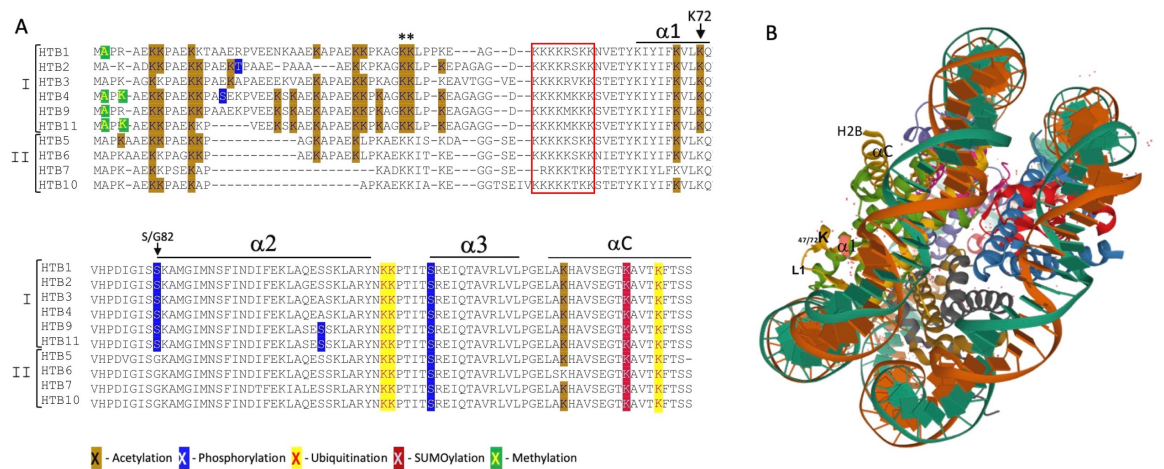


Fig. S4. (A) Posttranslational modifications of *Arabidopsis* HTB variants based on the Plant PTM viewer (<https://www.psb.ugent.be/webtools/ptm-viewer/protein.php>) and Bergmüller et al. [30]. The histone fold helices $\alpha1$ - $\alpha3$ and the C terminal (αC) helices are indicated. PTMs are highlighted as follows: brown, acetylation; green, methylation; blue, phosphorylation; red, SUMOylation and yellow, ubiquitination. Note, K39/K40 (asterisks) and K72 were found to be acetylated in class I HTBs but not in class II. The S to G change at position 82 is indicated. Red box indicates the putative nucleolar localization/retention signal. (B) Nucleosomal disc-like structure modeling the histone fold of the human H2B type 1-J (colored gold) with the $\alpha1$ and αC helices facing outside the nucleosomal disc. The merged position of K47 (human H2B type 1-J) and K72 (HTB9) is indicated (72/47K).

Protein sequences analyzed in this study

Arabidopsis thaliana

>HTB1/At1g07790

MAPRAEKKPAEKKTAAPERVEENKAAEKAPAEKKPKAGKKLPKEAGDKKKRSKKNVETYSKIYIFKVLKQVHPDIGISSKAMGIMNSFINDI
FEKLAQESSKLARYNKKPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

>HTB2/At5g22880

MAKADKKPAEKKPAEKTPAEPAAAAEKKPKAGKKLPKEPAGAGDKKKRSKKNVETYSKI
YIFKVLKQVHPDIGISSKAMGIMNSFINDIFEKLAGESSKLARYNKKPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

>HTB3/At2g28720

MAPKAGKKPAEKKPAEKAPAEEEKVAEKAPAEKKPKAGKKLPKEAVTGGVEKKKKRVKKS
TETYKIYIFKVLKQVHPDIGISSKAMGIMNSFINDIFEKLAQEASKLARYNKKPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

>HTB4/At5g59910

MAPKAEKKPAEKKPAEKPVEEKSAAEKAPAEKKPKAGKKLPKEAGAGDKKKMKKKSVEYSKIYIFKVLKQVHPDIGISSKAMGIMNSFIN
DIFEKLAQEASKLARYNKKPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

>HTB5/At2g37470

MAPKAAEKKPAEKKPAGKAPAEKLPKAEKKISKDAGGSEKKKKSKKSVETYSKIYIFKVLKQVHPDVGISGKAMGIMNSFINDIFEKLAQESS
KLARYNKKPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTS

>HTB6/At3g53650

MAPKAAEKKPAGKKPAEKAPAEKLPKAEKKITKEGGSEKKKKSKKNIETYSKIYIFKVLKQVHPDIGISGKAMGIMNSFINDIFEKLAQESSR
LARYNKKPTITSREIQTAVRLVLPGLSKHAVSEGTKAVTKFTSS

>HTB7/At3g09480

MAPKAEKKPSEKAPKADKKITKEGGSERKKKTKKSTETYSKIYLFKVLKQVHPDIGISGKAMGIMNSFINDTFEKIALESSRLARYNKKPTITS
REIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

>HTB8/At1g08170

MAPRKPVVSVTKKKKVVEETIKVTVTEEGDPCVITETANDQETQDLTFSIPVGENVTVEIPVEVPDERSLPVGENVTTVKIPVDDRDESSP
QPPETPVEVRDEPSQPPETPASKSEGTLLKTKDVEKKQENKKKKKKKKRDDLAGEYRRYVYKVMKQVHPDLGITSKAMTVVNMFMGDMFER
IAQEAAARLSDYTKRRTLSSREIEAAVRLVLPGLSRHAVAEGSKAVSNFVGYSRKR

>HTB9/At3g45980

MAPRAEKKPAEKKPAAEKPVEEKSAAEKAPAEKKPKAGKKLPKEAGAGDKKKMKKKSVEYSKIYIFKVLKQVHPDIGISSKAMGIMNSFIN
DIFEKLASESSKLARYNKKPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

>HTB10/At5g02570

MAPKAEKKPAEKAPAPKAEKKIAKEGGTSEIVKKKKTKKSTETYSKIYIFKVLKQVHPDIGISGKAMGIMNSFINDIFEKLAQESSRLARYN
KPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

>HTB11/At3g46030

MAPKAEKKPAEKKPVEEKSAAEKAPAEKKPKAGKKLPKEAGAGDKKKMKKKSVEYSKIYIFKVLKQVHPDIGISSKAMGIMNSFINDIFEK
LASESSKLARYNKKPTITSREIQTAVRLVLPGLAKHAVSEGTKAVTKFTSS

HTB8 orthologs

Magnoliids

>Cinnamomum micranthum - RWR72246.1 late histone H2B.2.2-like protein; **Lauraceae**

MAPKRSVGVVGSSFVRKTTTKKVQETINVTAADFDPNNTHEEEVEELNESLPTPTTKVKVVEGSPQTSVTPQEDENDTKESTPHPQEEEND
TTESTPHPQEEKNDTTESIPPQVENPPPTKTTEKKLNKEVGKEKEKEKEKKRRKKRRKVGVMGYKRYVMVLKQVHPGGMGISSNAMTVLN
GLMNDMFEKLAEEASKLCLYTKRATMTSREIQGAVRLVLPGLGKHAIAEGTKAVANYMTNDRATSS

28.1 kDa

>Nymphaea colorata - XP_031483632.1 histone H2B-like; **Nymphaeaceae**

MGPRRSGRLVGSVVKETKVVEETVKVVADVDLSSLEPSAISAGIIREIPVVEIKESKTPQKKVEPEAAPFPLEKKQKGIEAKEVEEKEQKGH
VDQKKERKPQELNRRRKLRLRNEEGVGAYRSYVYKVLKQVHPGLGISSKAMDVLNGFMGDMFERLAEEAATLQKHTGRRTLSSREIQMAVRL
VLPGLGKHAISEGSKAITNYYRYPEKKRR

24.45akDa

>Piper nigrum; **Piperaceae**

MASTRQGRNTPEVSTVVKKTTTRKVVNETTIAAVAVVESNEPPIVKTVPVEEESDSVINVEAGTKPPKEVPIARPRSDAAKGTNQRKDGA
ATIAETQQPPEKLREEKHAMEEVKKGSKRRKGERKEGEKKRKRKRKRSYNEEMSGYSRYVFRVLKQVHPDLAISSKAMAVLNAFVWDMFERL
AGEAGKLADYTRRATLSSREIQDAVRLVLPGLGKHAISEGSKAVTNVYTNDD

26.7 kDa

Monocots:

>Elaeis guineensis - XP_010940500.1 histone H2B.11; **Arecaceae**

MAPKRQRRVGTIVKTTTRKVVEETLQVSVEGGEGNGDQNSKESKVVEVEVEEKKAKQESQTSVTHLEDSQAKEKABEEKTNKRNKKSKQAP
KERAEEPPQRDKKQEKDGRREGKDQEEPPVGEKGQKGGGVVEEGEEKKKRGRGGKRRRRKRYGGGVEGIGGGYKRYVFRVLKQVHPGMAVSS
RAMAVLDGMMIDMFERLADEAARLSQYAGKATLSSREIQDAVRLVLPGLGKHAISEGSKAVSKYMSADHGT

28.47 kDa

>Lilium davidii- mgH2B.in; **Liliaceae**

MAPKKKPSKLVGTVTKTRKVTETQTLKVSITKGLKPEDQQTNTNKFVSVTGKQSKTQPLIVSTNTNLVPKKEKEESPTTTLMVKKKRKNRKA
GGEYKRYVYMLVKTVHPDMTVSSKAMVMMEGMMQDMFERLVTEAVRLVQYMKATLTCREIQTAVMLVLPGLGKHAVSEGAKAITNYMAAVG
SGNGGAA/

21.25 kDa

>Ananas comosus - XP_020113371.1 histone H2B.3-like; **Bromeliaceae**

MAPRKPRKMGAVVKTAKVVEETVKVAPVVGVDGDDGDGAEEVEEAAPLKDSKVQVQVVVGGEKGDGEVPEANDGRDEPEKRKEAMEVD
ENQAPKETGEESKRGRGRPLKERGPETPTTEKSEIPPANKKKEKDRGGRSEGEAEEGKGRRRRRRRRRRRFGSAGDAGSGGVGGYKRYVFRVLKQ
VHPELGASARAMQVLDMMMDMFQRLAEEAARLSKYTGRTATLSREIQNAVRLVLPGLGRHAVSEGTKAVTNMASQSS

28.8 kDa

>Brachypodium distachyon; **Poaceae**

MAPKRRVKKVSSVVRKKTKKVQETVQVSTAILPDDSAQPEPEVVVDVSTPATVVKHVEVTSVGDGDDQATAAGATAVNNKPPQSKSPDKPAD
DNQATAPAVPSLQSQETQTDPNKKKTPQQEIVVTTTKGPPGLEPPEKTKKLQPDAPETPKQAGGAGTGGKDEAAAPKKKKKKKKKKRARR
GGGRRRGVPVGDMMGGGKRYVYRVLKQVHPDMGASGRAMEVLDMMGDMFERLADEAARLAKVAGRATLSSREVQNAVRLVLPGLAKHAI
SEGTKAVTSYMSLA

31.27 kDa

>Oryza brachyantha - XP_006661574.1 PREDICTED: late histone H2B.L4-like; **Poaceae**

MAPKQKKKQVVASVVKTKTKVVEETVQVTTAEPSVSGSTVQVEVETDAKKTAVQSQEREFPNAQGRKGGGGGGRRRRSRRGAGAGGGYK
RYVWRVLKQVHPDMGASGRMTDVLDTMMSDMFERLAEEASRLSKVSGRATLTSREVQSAVRLVLPGLDLANHAISEGTKAVSNYLS

19.15 kDa

>Oryza sativa - XP_015612586.1 late histone H2B.L4; **Poaceae**

MAPKQKEAANKKKKKEVAVLVKTKKVQLTTTTAELELEPTVTVQVDDNKTGAAADETPPVVPLQSQETQDPNEPKAAAAKKKKRAGHGRK
RSRRRRGGGALEYGGYKRYVWRVLKQVHPDLGASQTMDVLDMMMDMFERLADEASRLSKLSGRLTLTSREVQSAVRLVLPADLANHAISEGT
KAISNYLS

21.34 kDa

>Panicum hallii - XP_025799366.1 histone H2B.9-like; **Poaceae**

MAPKRRSGGKVVSVVKTKVQETVEVTTAFVADGEPGQRATEDLALAPPAVDASGGSRSRVVHIEQATSKRGRGGRREEKPPAPAEAAQE
PPVAQSQETQDPNEEQEEEEEDAGKKKKKKPPQQLQDEEPPETPRVASERKTAARKTTPQQQKRGGGGAGGGDKTKTKAKKGGRRRLGQA
SPGGDAGMGGVGGYKRYVWRVLKQVHPDLGVSGNAMRVLDMMMDMFERLADEAARLSKVSGRATLSSREVQSAVRLVLPGLSRHAMSEGTK
AISKYMSYDA

30.97 kDa

>Setaria italica; **Poaceae**

MAPKRRSSGKVVSVVKTKVQETVEVTTAIVADGEPEQQQLAPGALALAPRTGEVSRSKVHVHIEITPDSNTTGRSSAKQOPTAKRGRGGR
EEEKPPAPAEAAQEPPQSLQEPNEEEEEEDVDVSKRRKPPPPQRRRDEEPEPETPRVASERKTAGTKTTPQKQKRGGGGGGGGKAKTG
RRRLGGEASPGGDAGMGGGKRYVWRVLKQVHPDLGVSGHAMRVLDMMMDMFERLADEAARLSKAAGRATLSSREVQSAVRLVLPGLGR
HAMSEGTKAISKYMSYDA

32.16 kDa

>Sorghum bicolor - XP_002462010.1 histone H2B.4; **Poaceae**

MAPKRRGNKVVSVVKTKVQETVEVIVADDDTAEEAQQMVPEALAVAPSAVDVSGSTVVHVHVEVTTDPGGDNATGSNVKQPAVAKRGRGR
EEEEKQPPAPPEDSVLPQSQETQDPNEEEEDQEDASKKKKQKQKQRRQDEDEAQPETPRVASERKATPKKAKAKAQPPQQAGGGGDAGKK
RPKARRRLGQASAGGDAGMGGVGGYKRYVWRVLKQVHPDLGVSGHAMQVLDMMMDMFERLADEAARLSKATGRMTLTSREVQSAVRLVLPGLD
LGKHAIAEGTKAISKYMSYA

32.19 kDa

>Zea mays - XP_008670031.1 histone H2B.5; **Poaceae**

MAPKRRGNKVVSVVKTKVQETVEVIVADDDGLHAEQQVPEALALAHPTVDVSGSTVVHVHVEVTAKRGRGGGGGGGGRRNEGKPPPEED
SAAVVPQSQETQDPNEELEFELEDEEEKQPETPRVASEKRKKAATPTKTKTQPPRRRRQLGQASSGGDAGMGGVGGYRRYVWRVLKQVHP
DLGVSGHAMQVLDMMMDMFERLAEEAARLSKATGRATLTSREVQSAVRLVLPGLGRHAISEGTKAISKYMSYA

28.17 kDa

Dicots:

Basal eudicots

>Nelumbo nucifera - XP_010267330.1 late histone H2B.2.2-like; **Nelumbonaceae**

MAPKRSKKVVGTVIKTTTRETIVRVAVVDGKKAEGETEKETIVESTKEPIRVAIEDVRAPEDQLVQKEPRRVVDDKVQEEEDG
AVAVSPETREERGQOEKINQEGKEEKKTEQKGEDKKKKKRERRKGRRRKEGGEEYKRYVFRVLKQVHPGMISSKAMAVLNGF
MNDMFERLAGEATRLSQYTGKMTLSSREIQGAVRLVLPGLGKHAIAEGTKAVTNYSNKTAAQAA

>Aquilegia coerulea - PIA54901.1; **Papaveraceae**

MAPKRSQKKVIGSLVRKTNKVVEETVNITVVEKTKGAEAGNKETEQEETAISTKDPVSTPGEKQQKEQPKKGVGKQLKLEAPT
QKKEETKSKNEKSTTTTTTTSSAKEGEEKKGKSGRKRMLDTGETYNTYVYKVLKQVHPDLGITFKGMMVLNGFMNDMFER
LAREASKLTDYTGKKTMSAREIQGAVRLVLPGLGKHAIVEGTAITTYFSNSS

>Macleaya cordata - OVA17917.1 Histone H2B; **Papaveraceae**

MAPKRKGKVAVVKTTRKVIKETVNVVLETEEPLQAEENEETDEIAVSTKEPVKVVAVKDKTTEEDEDQSVHDQKKKKNQE
EPKATSSNLNLEGPQKKQQQLQDEEKKTAQDGGGEEMEQGPNNQNKENKTTTQDGVEDKEKKKKPGRKSGSRKRNEGGEG
YKRYVFKVLKQVHPGMISSKAMTVLNLMLNDMFERLADEAARLSKYTGRTLSSREIQSAVRLVLPGLGKHAIAEGIKAVT
TYMSEDTKLGSKS

>Papaver somniferum - XP_026418705.1 histone H2B-like; **Papaveraceae**

MAPKRSSGKVVVKATKKVETVDISVDVDEIGEVTNPEETITKDINVVVEETIKKKPQQETAAKVTPLKIEGAKDQTEKKKDG
KEEAKKTQDGEETESQEENEKTKVEKKVKKTQEKGKEEKEKKQRTGRKRKMFTGIEGEYKRYVFKVLKQVHPDLGVSSRAM
VIINGLMNDMFERLAKEAAKLCDYTGRTMSSREIQAARLVLPGLGKHAISEGKAVTNYTSHE

Core eudicots; Asterids

Apiales

>Daucus carota - XP_017234272.1 PREDICTED: late histone H2B.L4-like; **Apiaceae**
MAPKKSPPKKAVGAVVKTITTKVIQETVQVSVIQTTPKPKQQETPQTENNKNKNGPKDIEIQDVTTPPTPKKATKIPTQDTAKKT
KKDSAQGGATKKRKRSEGYKRYVYKVLKQVHPDIGISSKAMTIVNNLMTDMFERLADEAARLTKYTKKMTLSSREIQGAVKLV
LPGLGKHAVAEGAKAVTNYVQYASGPSKP

Lamiales

>Erythranthe guttata - XP_012838320.1 PREDICTED: probable histone H2B.3; **Phrymaceae**
MAPKKRPGRAKKTVVTSTKVVEETVKVVVTPGGSGGEDDDNDNNESVEMISSSTKQNTENVEIFTSSPEKEHVLRTIPVEDKE
EQIPAPDIVPQEQDEDETQPYSEPETASTPPRKEAPPPKSSEPLETPPPAEKRETRKKKFQEKAKEAGQEKKATTEKLRPKRR
RRSVAGAGAGESYKRYVFKVMKQVHPDMGISSKAMTIVNNLMTDMFERFAEEAARLQKYTGRTMSSREVQGAVKLVLPGLG
KHAVAEGAKAVTNYVSYVPSK

Solanales

>Capsicum chinense - PHU15803.1 Histone H2B type 1-M; **Solanaceae**
MAPKRRGRARATVVTARKVVEETVSFVVTPVAAETETGSQTLTQSQHEENQSFEILTPSPTEEPTPKRTVIEEKSTTQPEKK
KGQQRPKPTREAEIIFDPTRKEQEQQPQVDEDETQPADEQEEMPTPPQIEAVQKKAQAQKRKPGPAHKAEGEKRRKKRAK
VGGGVGPSEGYRTYVYKVMKQVHPDMGISSKAMTILNNLMGDMFERIANEAAILAKYVGRATLASVDIQDAVKLVLPGLGKH
AIAEGTKAVANYVSSVGKSKSA

>Solanum tuberosum - XP_006347209.1 PREDICTED: histone H2B.3-like; **Solanaceae**
MAPKRRGGRARATVVTARKVVEETVSVVVSGETETESQTLTEENQSFEILTPPYEEPTPKRTINVQDKSEGKKAQQRKPDPA
QQVDEVEETQPADEPEEMPSPPKKEAVRKKKAQKRKPDPAQRVDEDETQPAEEPEEMPTPPKMEADQKKAQKAKGGGERKKKRA
KVGGVGPSEGYRRYVFRVMKQVHPDMGISSKAMMILNNLMGDMFERIANEAAILTKYAGRATLASVDIQDAVKLVLPGLGKH
HAIAEGTKAVANYVTSVEKSKSKP

Core eudicots; rosids

Brassicales

>Arabidopsis lyrata - XP_002892444.1 histone H2B.2; **Brassicaceae**
MAPRKPKVSVTKKKKVVEETIKVTVTEGEDPCVTTETANDQETQDLTFSSIPVGENVTTVEIPVEVRDEQSPQPPETPASKSE
GTLKKTDTVEKKKKKKKKKKRDDLAGEYRRYVYKVMKQVHPDLGITSKAMTVVNMFMGDMFERIAQEAARLSYTKRKTLS
REIEAAVRLVLPGLSRHAVAEGSKAVSNYVGYGSRKR

>Arabidopsis thaliana - NP_172295.1 HTB8; **Brassicaceae**
MAPRKPKVSVTKKKKVVEETIKVTVTEEGDPCVITETANDQETQDLTFSSIPVGENVTTVEIPVEVPDERSLPVGENVTTVKI
PVDDRDESSPQPPETPVEVRDEPSPPQPPETPASKSEGTLKKTDKVEKKQENKKKKKKKKRDDLAGEYRRYVYKVMKQVHPDL
GITSKAMTVVNMFMGDMFERIAQEAARLSYTKRRTLSSREIEAAVRLVLPGLSRHAVAEGSKAVSNFVGYDSRKR

>Arabis alpina - KFK43131.1; **Brassicaceae**
MAPRKPKVSVTKKKKVVEETIKVTVTEGDPTITTTETETQDQETQETQETQEKQDLEALETQDQETQDLTSLIPVEENVNTNV
EIPVNIADDQSPKPPETPAPASERTVKENHKVKKKQVKKKKKKKKRDDLAGEYKRYVYKVMKQVHPDLGITSKAMSVINMFM
DMFERIAEEAARLNDYTKRRTLSSREIEAAVRLVLPGLSRHAVAEGTKAISNYFGYDAKKR

>Brassica rapa - XP_009148076.1 histone H2B.2; **Brassicaceae**
MAPRKSKVSVTKKKKVVEETIKVTVTDGVPNVTTNTDTQETQYLETQELDTQELDTQDLPPFSLPLEEENVTRVEIPVDVGY
DRSPPPETVPAPASEGTVEKTHKVEIPVEFGDDRSPPQPPETPAPASEVPAKETHKDEEKQGNKKTTSKKRKKNRSEVAGDEYK
RYVYKVMKQVHPDLGISSKAMTVINMFMGDMFERLAVEAAKLNLDYSKRRTLSSREIEAAVRLVLPGLSRHAVAEGSKAVSNF
VAYGAKKR

>Camelina sativa - XP_010475607.1 PREDICTED: histone H2B.2-like; **Brassicaceae**

MAPRKPKVSVTKKKKVVEETVKVTVTEGEDPNVTTEITENDQETQDLTFSIPVGENVTTVEIPVEVPEERSPQPPETPASTS
EGTVKKKTNAEKKKKKKKKKKRDDLAGEYRRYVYKVLKQVHPELGITSKAMTVVNMFMGDMFERIAQEAAARLGDYTKRRT
LSSREIEAAVRLVLPGELSRHAVAEGSKAISNYVAYDSRKR

>Capsella rubella - XP_006306103.1 histone H2B.2; **Brassicaceae**

MAPRKPKVSVTKKKTVEETVKVTVAEGGDPNVTTTEITENDQETQDLTFSIPVGENVTTVEIPVEVLDERSPQPPETPASTS
EGTLKKKTNEVEKKQEKKKKKKKRDDLAGEYRRYVYKVLKQVHPDLGITSKAMTVVNMFMGDMFERIAQEAAARLSDYTKRR
TLSSREIESAVRLVLPGELSRHAVAEGSKAISNYVSYDSRKL

>Eutrema salsugineum - XP_006417719.1 histone H2B.2; **Brassicaceae**

MMAPRREKKVSVTKKKKVVEETLKVTVTDGDPNVITETQTQDEETQDLTFSIPVEENVTTVEIPVDVDRDDQSPQAPETPAPV
SEGTVKEAHKVEKKQSKKKKKMMKRGDLAGEYKRYVYKVMKQVHPELGITSKAMSVINTFMGDMFERIAEEAARLSDHTK
RRTLSSREIEAAVRLVLPGELSRHAVSEGAKAISNYVAYGAKKR

>Microthlaspi erraticum - CAA7033736.1; **Brassicaceae**

MAPKVSVTKKKKVVEETVKVTVTDGDPNVTTTETTTETEDQETQDLTFSIPIEENVTTVEIPVDVGDDRSPPETPAPSESEG
TVLKETHKADKKQEKKTQVTKKRKRTDLARDEYRRYVYKVLKQVHPEIGITSKAMSVINTFMGDMFERIAEEAARLNDYTKR
RTLSSREIEAAVRLVLPGELSRHAVAEGFKAVSNYVAYDARRKR

>Raphanus sativus - XP_018484528.1 histone H2B.2; **Brassicaceae**

MAPRKSKKVSVTKKKKVVEETIKVTVTDGVPNVTTETDTQETQNLLETQELDTQELETQDLPLSIPIEENVTRVEIPVDVGD
DRSPPPPETVAPPSEGTVKETHKVEIPVEDRDRSPQPPETPAPASEGPVKETHEAEEKQGNKKTLKKRKKNRSDVPGDEYK
RYVYKVMKQVHPDLGISSKGMTVINMFMGDMFERIAEEAAKLNDYTKRRTLSSREIEAAVRLVLPGELSRHAVAEGSKAVSNF
VAYGVKKR

>Tarenaya hassleriana - XP_010557373.1 PREDICTED: histone H2B.2; **Cleomaceae**

MAPRRSSRKVSVTKKKKVVEETVKVTVFDGDAKVTTETESLENNQOETEELTSLIPVGEEPPDKEAEDVVRVEIPVSGPENR
SPEPPPQPQTPGAKGEERKSPEIEKEREDEGEREETHEEEGGQETAGEGIEQKGLEEEKTGKEEKSAEETPARKRRRRRGR
LSGEGGGYRRYVWKVMKEVHPKMGISGKAMSVLNTFMGDMFERIAEEAARLNQHSRRRTMSAREIQAAVRLVLPGELSRHAV
AEGSKAVSNYVAFDSKKP

>Carica papaya - XP_021901556.1 histone H2B.8-like; **Caricaceae**

MAPKRSTRLALKTTQKIIIEKVEVSVVPSSGREQEITDVAQKSPVKVIPVEEKSRTKTVRIPEETPSLKTIPVKTPKEQEET
IDDQEPVTTSEEVAADNEQEQEKEEETDQTQEGITSSEPAQTTEEKVEKRPSSRRGRPRRRRKKKGSDEGNKYGYKRYVFKV
LKQVHPELAISSKAMVIINGFMNDMFERLADEAANLSRYSHKATLSSKEIQGAVRLVLPGELSKHATAEGSKAVTNYMSFPLH
NS

Fabales

>Arachis duranensis - XP_015935854.1 histone H2B; **Fabaceae**

MGPKRKGQKVVIKSTRKVVQESVQVSIVGSSSKRTRRGNNKDIQTSDEVVGEENVRIIPVQEVTPQPKDASTTTVTQDDQGE
QEHNAETEEQNIDTTATAVSQKEEPKEPSSKEDDEKKAKTHERNDGKGGKKRRKRSSGEGYKRYVMVLKQVHPDMGISSQAM
TVLNNLMGDMFERLADEASKLKYTGHMTLSSREIQGAVKLVLPGELGKHAI AEGAKAVTNYISHDA

>Glycine max - KRH30545.1 hypothetical protein GLYMA_11G191600; **Fabaceae**

MAPKRAEKLVRSTKKVVSIVQVSVVGKRLTQVIPQAQKVSNSDITTENKAEQENNTHQDGGVQNQEEEQKGVNNEEAKKE
KNKSKTAKEQNGKEKKRGRKKRNIEGYQRYVYGVLKQVHPMGISSKMTALNNLMNDMFERLTFEVSKLTDYTGHMTLSSRE
IQGVVRLVLPGELEKHAIAEGVKAVNNYTSYDA

>Medicago truncatula - Medtr2g084480.1 K11252 histone H2B (H2B); **Fabaceae**

MAPKSARKVVVRSTRKVVQESVQVSVSSHKRSTRGNNDVEIDKDAGNATQQEHVRIIPVQEVTSQTKEDTNTNTNTTTVTS
EDTTNQENTPNDATMEPKTPLSNKEQEKKVRTKEGGNDGKGRKKKRGRRMGEGYQRYVYRVLKQVHPQMGISSQAMTILNNL
MNDMFEKLADA EAKLTAYTKHMTLTSREIQGAVKLVLPGELGKHAI AEGAKAVTNYVSYVA

>Trifolium pratense - PNY02520.1 histone H3-like protein; **Fabaceae**

MAPKRANKKMVVRSTRKVVESVQVSVSSNKRSTRANKDNEIDKDVGSDDHQREEHVRIIPVQEVTPSAKEDSNASTTTFTT
EDKTNQENTPNEATMEPKSENNKKNKEGNYGKEKRKRKRVRMRMGEYQRYVYRVLKQVHPDMGISFKAMTILNNLMNDMFE
KLADA EAKLTYYIGHMTLTSREIQGAVKLVLPGELGKHAI AEGAKAVTNYISSYGA

Fagales

>Juglans regia - XP_035540958.1 histone H2B.2-like isoform X2; **Juglandaceae**

MAPKRS PKVMGTVMKTRSKVVREIVQVTVERAQKPTIGEIDE EKEDTFIPSGRKPLRTIAVEDKSEQRNHESAQIPVLVEDK
SSEQENQSFVQVEGKSKEENQPVQPPVEEKQEEENQDKSPEENQAEVEVP EEEKEKQPTNMTSGKQEGPSKIEGKKKTSTQ
EGEGKTRRRKRRRKEGGGEYRRYVYRV LKQVHPELRVSSKAMTVLNNMMKDMFERL TEEAAVLSKYTSRKTLSSREIQGAVR
LVLPGE LGRHAI AEGSKAVTSFMSYIARESKRSS

>Morella rubra - KAB1227366.1 Histone H2B type 1-A; **Myricaceae**
MAPKRPPKVVGTVMKTRKFVRET VQVAVVESARKPIPGDVDGDEEGFIQIPEPLRAIVVEDKSEEAKQFVQVQVEEKSEDKKQ
FVQVPVEEKSEEGNQFVRVPAEEKSHEENQPTQAPVEDKSQEGTESVQAPVDDKSPEENQLVQVAEEDRSSQEENLQSDQVA
EEDKSQEE EKPTTTFKKQE EPSTKEGDKRKARTQEGEGKRRKKRRRREGSGEYRRYVFRVLKQVHPELVSSKAMTVLNNMMS
DMFERMADEASKLCKYTGRITLSSREVQGAVKLVLPGELGKHAI AEGSKAVTAYLSHITSSASKS

Malpighiales

>Jatropha curcas - XP_012065091.1 histone H2B.2; **Euphorbiaceae**
MAPKRS GKKKKK VIGTVLRSTRRIKETVEVSVIEGDPQESTQEYQSQETEEIAANKEPFIRTIPVEEGVHERDDKENEEEEAI
EISEEDISLRDQEDFSKKG SASKENLQE QEDLSTKDDTTGEE NVQE QERPIKKEEKEKTQ QEKQGERKKRKG RGVGREREGYK
RYVFKVLKQVHPELKISSMAMSIINNLMKDMFERIVYEA AKLSDIYHRTTLSSREIQDAVKLVLPGE LGRHAI AEGSKAVTNY
MSYKEKRSKA

>Manihot esculenta - XP_021629190.1 histone H2B.4-like; **Euphorbiaceae**
MAPKGKRGKKKVLGTVLRSSKRVIKETVKIAVFEGDTQESTQEDQNGDTEELPENEPLVVRTIPVEERVEEEEEAAQTIEVSVK
KPKEEK RQEKIETHEEKQEP AKTTTKTKRTQEEKGQEKRRRRRRRGV EEGGEGYKRYVFRVLKQVHPELRISSMAMSVINS
LMKDMFERIAD EAAKLSQ HSHKMTLSSREIQGAVKLVLPGELGKHAI AEGSKAVTNYMSYEA KGSKA

>Populus alba - XP_034905868.1 histone H2B.2-like; **Salicaceae**
MAPKRRGKEVVGTVLRSTKKVVKETVQVAAIENDNQESTQDQDQNGEPEDIDTPALETFR TIPVDEKVHEEEDRVIEVSVEKP
DKEAAIADSQEHIRGPSKEERQEDQTREVS LRRALKVLIGDISSGAASRGQ QEEPSREDEIRKEDQTGGVSVEEPSKEDPK
EDAASAGDQGKKLGPKKVHPDLGVSSMAMSMINSLMNDMFERIAEEAAKFS DVYRKRTTLSSGEIQGAVKLVLPGELGKHAI A
EGSEAGTNYISHGTRKRSKSWRALS

Malvales

>Durio zibethinus - XP_022731946.1 histone H2B.5-like; **Malvaceae**
MAPKLRANVLVRSTEKIVRET VQVAVVQKPEGDSGDQEQLETIPVEDTAE EGERIITEISVEGLSKDKAQKDPQTAQVPG EAP
EDTANTFERTKHLGLQSFEEESSKEAPKALEEERSNECPKASEKEPSNETSKALELEEPPLKKEDERKAKTREGKENNENGKR
KRGKRKELDGNEAYKTYVFRVLKQVHPGMAISSKAMSVINSLMNDMFEKIAEEATKLSKYTERKTLSSREIQGAVRLVLPGEL
GKHAVAEGSKAVTNYASYSEKRPKLD

>Gossypium laxum - MBA0712944.1; **Malvaceae**
MAPKRRAKVVVRSTKKIVKETVQVAVIDKTEGDNNGDQQQLDTPLEDIEEAEERVITEIPIQGSTEDKAEKEPHKVEAAGEK
NRVQGE EKTEPVHEEEEP RKEEKKGKRKRKGKKELVGHEGYKTYVFRVLKQVHPGMAISSKAMSVINSLMNDMFEKITNEATK
LSQYTDRKTLSSREIQGAVRLVLPGELGKHAVAEGSKAVTNYASYDIKRSKLV

>Herrania umbratica HuH2B8 - XP_021278628.1 histone H2B.2-like; **Malvaceae**
MSKTGETNIKGRKGRKVT LVKRIAPKRPADVVRSTKKIVQETVQVAVVQQPEGDSAEQDPMKTVPVEDIAEDEERIITEIS
AERLSKDKAQKEPHTVQVPVEAPGKNKVQKGQEPQQVSAEEPSKDKAQKEPGNEPSIASEDRSKEAPKALEVEDPPLKKEDEK
KEKTGAQEREVKKEEKGKTRERKESNENRKRKRGRKEFDGNEAYKTYVFRILKQVHPGMAISSKAMSVINSLMNDMFERIA
DEATKLSKCNERRALSPREIQGAVRLVLPGELGKHAVPEGSKAVTNYASYNGKRPKLN

>Theobroma cacao - XP_007016039.2 histone H2B.2; **Malvaceae**
MAPKRRANVVVRSTKKIVQETVQVAVVQQPEGDRGEQEPKMTVPVEDIAYDEERIITEISVEGLSKDKAQKEPHTVQIPVEAP
GKNKVQKGQEP EQVPT EEP SKDKAQKEPAKEPGNEPSIASEEASEEASKALEVEEPPLKKEAERKEKTGAQEGEEKKDEKNGE
TREGKESNENRKRKRGRKEFDGNEAYKTYVFRILKQVHPGMAISSKAMSVINSLINGMFERIAD EATKLSKYNERRTLSPRE
IQGAVRLVLPGELGKHAVAEGSKAVTNYASYNGKRPKLN

Myrtales

>Eucalyptus grandis - XP_010034182.1 PREDICTED: histone H2B.5-like; **Myrtaceae**
MAPKRKAKVVKTTTKVVQETVEVTLVEKDQNLAAEAENG VETLQQESENEVVKTTVTVEDKLAEEAEQVTVEIPVRQPPQKET
ATEAPRTPRQPEAKDKTQ RQKTAQEAKKDRREQEDVEAKNQPKRAREVDEKARGGRRRRRRVGE GGGEEQYKRYVFRVLKQV
HPGLGISSAAMEVLNGYMNDMFERLAAEAARLSSYAGIKTLSSRDIQGAVRLVLPGELGKHAI AEGAKAVTNYMEHDGGGGGG
AKSKP

>Rhodamnia argentea - XP_030522566.1 histone H2B.2-like; **Myrtaceae**
MAPKRRKAKVIKTRKVVQETVEVALVAKDQKLGAESDEMLQEESESEVVKTTVTVEGELPGGAEQATVEIPIEQPPRQETVTE
APRMPRQPETEAKDKTHDQKTTRDAKEEDREEREDEETQSPEGTPRAAAEREATLKEEPALDGERKKAQGTTERERPAERT
EEERSPEKDAAEAKKPKRAREEDEKARVGRRRRRRRVGDGVGAEQYKRYVFRVLKQVHPGLGISSAAMEVLNAYMNDMFERLA
AEAARLSNYAGIKTLTSRDIQGAVRLVLPGELGRHAIAGAKAVMNYMEHDGGGGGAKSKP

Rosales

>Malus domestica - XP_008359166.3 histone H2B.2-like; **Rosaceae**
MAPKRSAMVVKTTKRVVKEMVEVSVVKTRKKQQEDRPLETISVENNDSNQTNVEVSVGKEPLKTSIIPIETLEQVIPIET
QAENQTLKTQNAEVQVDREAEENPTTPDPQETEKLSKEEEKSEEDKTLRGGENKDAEDLTKEEQASKKGEKKSEVKGKKRR
EKRRSRGREEYKTYVYKVLKQVHPGMGVSSKAMTVLNNLMNMFELADEAARLTITYTARKTLSSREIQGAVKLVLGTGELGRH
AMAEGTKAVSTYVSYGGGSSKS

>Pyrus ussuriensis - KAB2606623.1 histone H2B.3; **Rosaceae**
MAPKRSAMVVKTTKQVVKETVEVSVVKTRKKQKQDQPLKTSIETNESNQNNVEVSVGKEPVKTSVIPIETQAENQTLKT
QNAEVQVDKEAQENPTTPDPQEAEEKSPKEQEQKNEEEKTLGRGENKDAEDLTKTTSKPRRKERRKASRGREEYKIYVYKVLKQ
VHPGMGVSSKAMTVLNNLMYDMFERLADEAARLTITYTARKTLSSREIQGAVRLVLPGELGRHAMAEGTKAVSTYVSYGGGSSK
S

Vitales

>Vitis vinifera - XP_002272312.1 PREDICTED: histone H2B; **Vitaceae**
MAPKRSKGTRSKVVVKATRKVVQQTVEVTVLASKQKPPREEQGKKISKDKAPEELQREQVSADEEPPKELPTPVTQEEPPKK
EEEEKTTTTQEGREEKKRGRRRRRRTSGRRRKEGGEGYKRYVYRVLKQVHPGLGVSSKAMTVLSGFMNDMFERIAEEAAKLSK
YTGKTTLSAREIQGAVKLVLPGELQKHAMAEGTKAVSNYMDYAAAGGHKQ