

H2B.1.fasta

Canis|545554624|TS_H2B.1
 Homo|24586679|TS_H2B.1
 Mus|28316750|TS_H2B.1
 Rattus|12025524|TS_H2B.1
 consensus

MPELTSKGT TISKKGFKRAVAKTQKKEGKKRRCKESYSIYIYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK

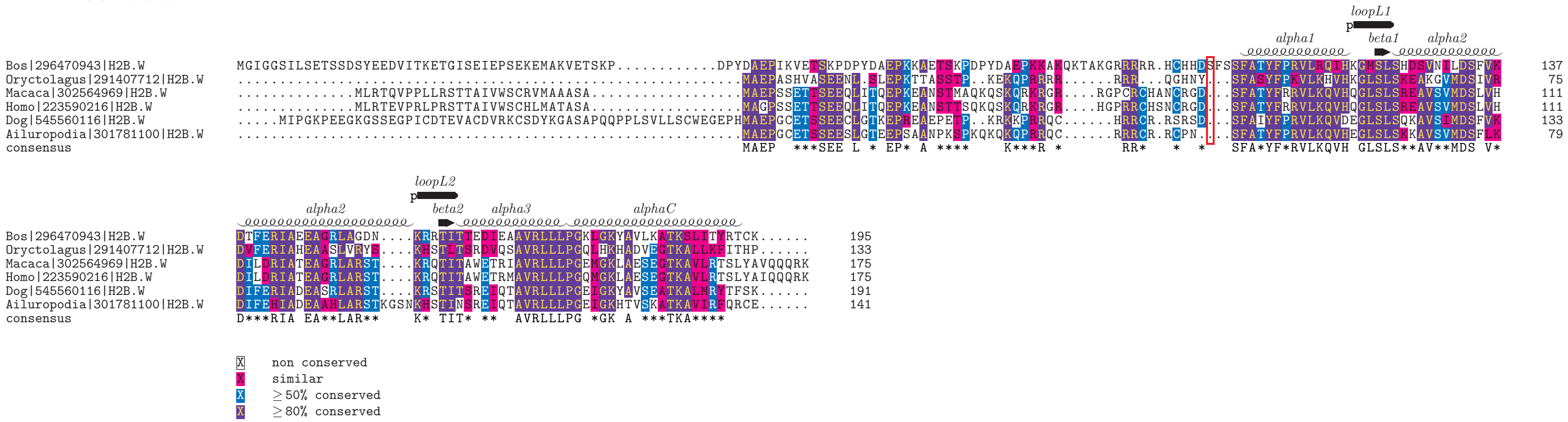
X non conserved
 X similar
 X ≥ 50% conserved
 X ≥ 80% conserved

subH2B.fasta

Accession	Sequence	Position
Monodelphis126320607 subH2B	MTKAM...SNESQKLTNNQEKKK.KKKKLLLSRNSYSLYTHRVLKEVVPQKGISSTYTTIMTSMNNILNFERIAEAGNLLCYKRLHGLGHDIQMAVYRLLPDELAKHVAVFGTRAVITTYND	121
Mus1254588081 subH2B	MAKPTFKKQCYIKRHLRLPLYKKSRCSNNILCHGNYSLYINRVLKEVVPNRCISSYSDIMNILLINDIFERIAEACQQLMLRRKCTLLTPGDIQQAVALHLLPKKLATLAVTFGSKAVHRRFHS	123
Mus1254588081 subH2B	MAKPTFKKQCYIKRHLRLPLYKKSRCSNNILCHGNYSLYINRVLKEVVPNRCISSYSDIMNILLINDIFERIAEACQQLMLRRKCTLLTPGDIQQAVALHLLPKKLATLAVTFGSKAVHRRFHS	123
Cricetulus1354507874 subH2B	MAKSKIKKRYQVVKRRQRRAFKKR.YSSINFGCHGNYSLYINRVLKEVVPNRCISSTYDMMNILLINDIFERIAEACQLMYFRKCTLLTPEDIQKAVYLLVLPKRLAKSAVTFGSKAVHRRFHS	121
Macaca109077646 subH2B	MARSSSTKKHKYKRRHQSPTSEKKR.HSSIDFVHGNSYSFVKNVLYKEVPSHRCCTSTDLMTLLTNINFFGKIMKAYRLLMYFRNRCCTLLTPEDIKLAAAYLLPKRTIYNAVAFGSKVFRFVYHS	122
Cavia1348552306 subH2B	MVSKSLIPRPFYFGCRSTISISKKLS.CLSSNSGVRNYSLYINRVLKEVVPFRAISSTCTVMNMTLLDDTDFERTSEAHNGLMCSQRKCTLLTPEDIQKAVYLLVLPKRLAKYAVAFDGLAVDRVYHS	122
Heterocephalus1512843645 subH2B	MVRSIIQKGYCYSRHLTPITYKKK.YLSTFGCHGNYSLYINRVLKEVVPFRAISSTCTVMNMTLLDDTDFERTSEAHNGLMCSQRKCTLLTPEDIQKAVYLLVLPKRLAKYAVAFDGLAVDRVYHS	122
Equus11497270701 subH2B	MARASTSKKSCSRSLRQSPASKKK.HNSTYGRCHRNYSLYINRVLKEVVPQGISSTRTDMMNILLINDIFERIAEACQLMYFRNRCCTLLTPEDIQKAVYLLVLPKRLAKYAVAFGSKAVQRYVQS	122
Bos145429973 subH2B	MARNITKKNKRCRGKQAIYKKKS.HSSSESLRNYSLYINRVLKEVVPQKGISSTRTDMMNILLINDIFERIAEACQLMYFRNRCCTLLTPEDIQKAVYLLVLPKRLAKYAVAFGSKAVQRYVQS	122
Bos145429973 subH2B	MARNITKKNKRCRGKQAIYKKKS.HSSSESLRNYSLYINRVLKEVVPQKGISSTRTDMMNILLINDIFERIAEACQLMYFRNRCCTLLTPEDIQKAVYLLVLPKRLAKYAVAFGSKAVQRYVQS	122
Loxodonta1344272356 subH2B	MARSIKKRYRNSGHLSSISKKL.HSSINFGCHGNYSLYINRVLKEVVPQKGISSTRTDMMNILLINDIFERIAEACQLMYFRNRCCTLLTPEDIQKAVYLLVLPKRLAKHVAVFGSKAVHRYVHS	122
Sus1311273883 subH2B	MARYITKKNKRCRGKQAIYKKKS.HSSSESLRNYSLYINRVLKEVVPQKGISSTRTDMMNILLINDIFERIAEACQLMYFRNRCCTLLTPEDIQKAVYLLVLPKRLAKHVAVFGSKAVHRYVHS	122
Ailuropoda1301771932 subH2B	MARSTIKKNKRCRGKQAIYKKKS.HSSINFGCHGNYSLYINRVLKEVVPQKGISSTRTDMMNILLINDIFERIAEACQLMYFRNRCCTLLTPEDIQKAVYLLVLPKRLAKYAVAFGSKAVQRYVQS	122
consensus	M**K**K**K**S**NYSLY**RVLKEVVP****S*****N**I**T**F**I**E**A**M***RCTL***D***AV**L*P*KLA*AV*F**G**AV*R***S	122

X	non conserved
X	similar
X	$\geq 50\%$ conserved
X	$\geq 80\%$ conserved

H2B.W.fasta



H2B.Z.fasta

Species	Sequence	Position
Toxoplasma	MSGKGPAAQKSSQAAKKTAGKSLGPHYRKRKRTESFALYIKVLVKQVHPETGVSKKSMIMNSFINDIFDRLADEAVRLIRYNKKRTLSRREIQTAVALLLPGELSKHAYSEGTKAVTKYTTS	123
Plasmodium	MSGKGPAAQKSSQAAKKTAGKTLGPHHKKRRRTESFALYIKVLVKQVHPETGVTKKSMIMNSFINDIFDRLVTEATLIRYNKKRTLSRREIQTAVALLLPGELSKHAYSEGTKAVTKYTTS	123
Plasmodium	MSGKGPAAQKSSQAAKKTAGKTLGPHHKKRRRTESFALYIKVLVKQVHPETGVTKKSMIMNSFINDIFDRLVTEATLIRYNKKRTLSRREIQTAVALLLPGELSKHAYSEGTKAVTKYTTS	123
consensus	MSGKGPAAQKSSQAAKKTAGK*LGPR***RRTESF*LYIKVLVKQVHPETGV*KKSM*IMNSFINDIFDRL**EA*RLIRYNKKRTLSRREIQTAVALLLPGELSKHAYSEGTKAVTKYTTS*A	

X	non conserved
X	similar
X	$\geq 50\%$ conserved
X	$\geq 80\%$ conserved