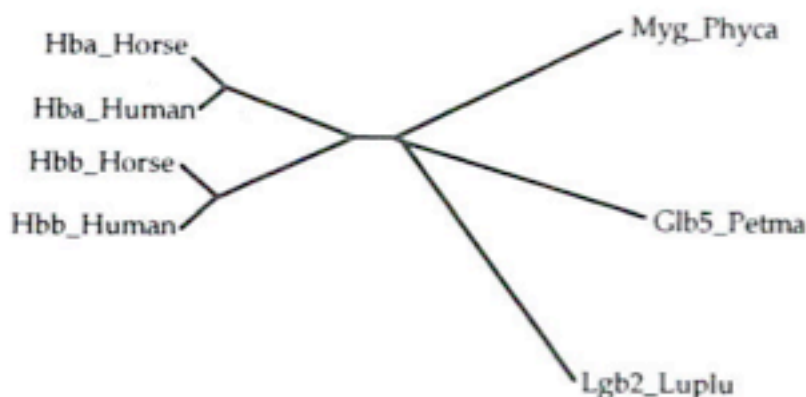


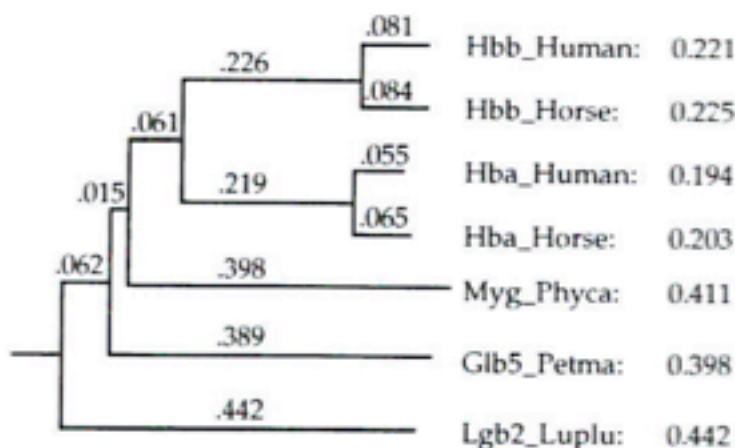
Pairwise alignment:
Calculate distance matrix

Hbb_Human	1	-					
Hbb_Horse	2	.17	-				
Hba_Human	3	.59	.60	-			
Hba_Horse	4	.59	.59	.13	-		
Myg_Phyca	5	.77	.77	.75	.75	-	
Glb5_Petma	6	.81	.82	.73	.74	.80	-
Lgb2_Luplu	7	.87	.86	.86	.88	.93	.90
		1	2	3	4	5	6

Unrooted Neighbor-Joining tree



Rooted NJ tree (guide tree)
and sequence weights



Progressive
alignment:
Align following
the guide tree

```

-----VHLTPEEKSAVTALWGKVN--VDEVGGEALGRLLVVYPNTQRFESFGDLST
-----VQLSDEEKA AVLALWDKVN--EEVVGGEALGRLLVVYPNTQRFESFGDLN
-----VLSPADKTNVKA AWGKVCAHAGEYGAELERMPLSPFTTKTYFPHFDLS--
-----VLSPADKTNVKA AWGKVGGHAGEYGAELERMPLSPFTTKTYFPHFDLS--
-----VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLPKSHPETLEKFD RPKHLKT
PIVDTGSAVPLSAAEKT KIRSAWAPVYSTIYETSGVDILVKPPTSTHAAQEPFPKPKGLTT
-----GALTESQAALVKSSWEEFNANI PKHTRFPFILVLEIAFAAKILFSP LKGTSE
      *      *      *

```

```

PDAVMGNPKVKAHGKKVLGAFSDGLAHLD-----NLKGTFPATLSELHCDK LHVDPENFRL
PGAVMGNPKVKAHGKKVLHSPGEGVHHL D-----NLKGTFAALSELHCDK LHVDPENFRL
----HGSAQVKGHGKKVADALTNVAHV D-----DMPNALSALSDLHAHKL RVDVPNFKL
----HGSAQVKAHGKKVGDALTLAVGHLD-----DLPGALSNLSDLHAHKL RVDVPNFKL
EAEMKASEDLKKHGVTVL TALGAILKKG-----HHEAELKPLAQSHATYHKIPIKYLEF
ADQLKKSADVRWHAERI INAVNDASMDDT--EKEMSKLRDL SGKHAKSPQVLPQYFKV
VP--QNNPELOAHAGKVFKLVYEAMIQLOVTGVVVT DATLKNLGSVHVSKG--VADAHFPV
      *      *      *

```

```

LGNVLVCVLAHHPGKEPTPPVQAAYQKVVAGVANALAHKYH-----
LGNVLVVVLARHFGKDPTPELQAS YQKVVAGVANALAHKYH-----
LSHCLLVTLAAHLP AEPTPAVHASLDKPLASVSTVLTSKYR-----
LSHCLLVTLAVHLPNDFTPAVHASLDKPLSSVSTVLTSKYR-----
ISEAIIHVLHSPHPGDFGADAQGAMNKALELFRKDIAAKYKELGYQG
LAAVIADTVAAG-----DAGPEKLM SMICILLRSAY-----
VKEAIIKTIKEVVGAKWSEELNSAWTIAYDELAIVIKEMNDAA---
      *      *      *

```