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Helix          AAAAAAAAAAAAAAAAAA   BBBB BBBB BBBB BBBB CCCCCCCCCC
HBA_HUMAN     -----VLSPADKTNVKAAWGKVGAA--HAGEYGAELERMFLSFPTTKTYFPHF
HBB_HUMAN     -----VHLTPEEKSAVTALWGKV-----NVDEVGGEALGRLLLVVYPWTQRFFESF
MYG_PHYCA     -----VLSEGEWQLVLHVWAKVEA--DVAGHGQDILIRLFKSHPETLEKFDRF
GLB3_CHITP    -----LSADQISTVQASFDKVKG-----DPVGILYAVFKADPSIMAKFTQF
GLB5_PETMA    PIVDTGVSAPLAAEKTKIRSAWAPVYS--TYETSGVDILVKFFTSPPAAQEFPPKF
LGB2_LUPLU    -----GALTESQAALVKSSWEEFNA--NIPKHTHRFFILVLEIAPAAKDLFS-F
GLB1_GLYDI    -----GLSAAQRQVIAATWKDIAGADNGAGVGKDCLIKFLSAHPQMAAVFG-F
Consensus     Ls... v a W kv . . g . L. f . P . F F

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Helix          DDDDDDEEEEEEEEEEEEEEEEEEE   FFFFFFFF
HBA_HUMAN     -DLS-----HGSAQVKGHGKVKVADALTNAVAHV---D--DMPNALSALSDLHAHKL-
HBB_HUMAN     -GDLSTPDAVMGNPKVKAHGKVKLGAFSDGLAHL---D--NLKGTFTALSELHCDKL-
MYG_PHYCA     -KHLKTEAEMKASEDLKHHGVTVLTALGAILKK----K-GHHEAELKPLAQSHATKH-
GLB3_CHITP    -AG-KDLESIKGTAFETHANRIVGFPSKIIGEL--P--NIEADVYFVASHKPRG-
GLB5_PETMA    -KGLT'TADQLKKSADVRWHAERIINAVNDAVASM--DDTEKMSMKLRDLSGKHAKSF-
LGB2_LUPLU    -LK-GTSEVPQNNPELQAHAGKVPKLVYEAAIQLQVTGVVVTDATLKNLGSVHVSKG-
GLB1_GLYDI    -SG----AS---DPGVAALGAKVLAQIGVAVSHL--GDEGMVAQMKAVGVRHRKGYGN
Consensus     . t . . . v..Hg kv. a a..l d . a.l.l H .

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Helix          FFGGGGGGGGGGGGGGGGGGG      HHHHHHHHHHHHHHHHHHHHHHHHHHH
HBA_HUMAN     -RVDPVNFLLSHCLVLTAAHLPAEFT'PAVHASLSDKFLASVSTVLT'SKYR-----
HBB_HUMAN     -HVDPENFRLLGNLVCVLAHHFGKEFT'PPVQAAQYKVVAGVANALAHKYH-----
MYG_PHYCA     -KIPIKYLEFISEAIIHVLHSRHPGDFGADAQGMNAKALELFRKDIAAKYKELGYQG
GLB3_CHITP    --VTHDQLNFRAGFVSYMKAHT--DFA-GAEAAGWATLDTFFGMIFSKM-----
GLB5_PETMA    -QVDPQYFKVLAAVIADTVAAG-----DAGFEKLMSMICILRSAY-----
LGB2_LUPLU    --VADAHFPVVKEAILKTIKEVVGAKWSEELNSAWT'IAYDELAIVIKKEMNDAA--
GLB1_GLYDI    -KHIIKAQYFEPGLASLLSAMEHRIGGKMNAAAKDAWAAAYADISGALISGLQS-----
Consensus     v. f l . . . . . . . . f . a a . k . . l sky

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**Figure 5.1** An alignment of seven globins from Bashford, Chothia & Lesk [1987]. To the left is the protein identifier in the SWISS-PROT database [Bairoch & Apweiler 1997]. The eight alpha helices are shown as A–H above the alignment. A consensus line below the alignment indicates residues that are identical among at least six of the seven sequences in upper case, ones identical in four or five sequences in lower case, and positions where there is a residue identical in three sequences with a dot.