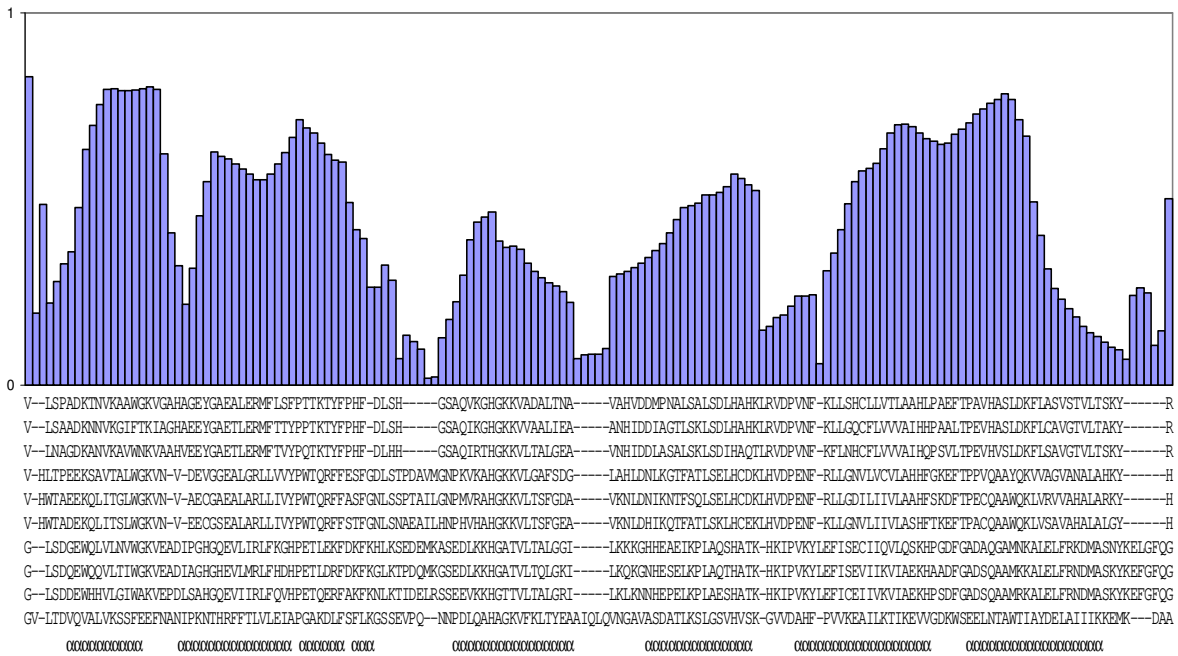
1
0
V--LSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHF-DLSH-----GSAQVKGHGKKVADALTNA-----VAHVDDMPNALSALSDLHAHKLRVDPVNF-KLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKY------R
V--LSAADKNNVKGIFTKIAGHAEEYGAETLERMFTTYPPTKTYFPHF-DLSH-----GSAQIKGHGKKVVAALIEA-----ANHIDDIAGTLSKLSDLHAHKLRVDPVNF-KLLGQCFLVVVAIHHPAALTPEVHASLDKFLCAVGTVLTAKY------R
V--LNAGDKANVKAVWNKVAAHVEEYGAETLERMFTVYPQTKTYFPHF-DLHH-----GSAQIRTHGKKVLTALGEA-----VNHIDDLASALSKLSDIHAQTLRVDPVNF-KFLNHCFLVVVAIHQPSVLTPEVHVSLDKFLSAVGTVLTSKY------R
V-HLTPEEKSAVTALWGKVN-V-DEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDG-----LAHLDNLKGTFATLSELHCDKLHVDPENF-RLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKY------H
V-HWTAEEKQLITGLWGKVN-V-AECGAEALARLLIVYPWTQRFFASFGNLSSPTAILGNPMVRAHGKKVLTSFGDA-----VKNLDNIKNTFSQLSELHCDKLHVDPENF-RLLGDILIIVLAAHFSKDFTPECQAAWQKLVRVVAHALARKY------H
V-HWTADEKQLITSLWGKVN-V-EECGSEALARLLIVYPWTQRFFSTFGNLSNAEAILHNPHVHAHGKKVLTSFGEA-----VKNLDHIKQTFATLSKLHCEKLHVDPENF-KLLGNVLIIVLASHFTKEFTPACQAAWQKLVSAVAHALALGY------H
G--LSDGEWQLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDKFKHLKSEDEMKASEDLKKHGATVLTALGGI-----LKKKGHHEAEIKPLAQSHATK-HKIPVKYLEFISECIIQVLQSKHPGDFGADAQGAMNKALELFRKDMASNYKELGFQG
G--LSDQEWQQVLTIWGKVEADIAGHGHEVLMRLFHDHPETLDRFDKFKGLKTPDQMKGSEDLKKHGATVLTQLGKI-----LKQKGNHESELKPLAQTHATK-HKIPVKYLEFISEVIIKVIAEKHAADFGADSQAAMKKALELFRNDMASKYKEFGFQG
G--LSDDEWHHVLGIWAKVEPDLSAHGQEVIIRLFQVHPETQERFAKFKNLKTIDELRSSEEVKKHGTTVLTALGRI-----LKLKNNHEPELKPLAESHATK-HKIPVKYLEFICEIIVKVIAEKHPSDFGADSQAAMRKALELFRNDMASKYKEFGFQG
GV-LTDVQVALVKSSFEEFNANIPKNTHRFFTLVLEIAPGAKDLFSFLKGSSEVPQ--NNPDLQAHAGKVFKLTYEAAIQLQVNGAVASDATLKSLGSVHVSK-GVVDAHF-PVVKEAILKTIKEVVGDKWSEELNTAWTIAYDELAIIIKKEMK---DAA