

Sequence Alignments

Amino Acid Markers

MAHSADQAPVPRFFARSQPTGCTIRVPQDKSISHRALMLSALCVQSQSRISGLEGEEDVLATAAMRAMGARTIERGADIWTVH
GVSIGLVLQPAQALDAGMLSTRTLLMTLVASHPIITAMFTGDAISLRSPRMARVDTPLGEMGAEASPMFGTLPLMVRGISPAV
PISYRLPVASQAQKSAIILAALNTPTTITTEVPVATDRHAKCKLGGFADLTVEDTADGVRHIIHTVGCDLTAQIDPEVGGDS
SAAFFIVAAILVPGSDLTIENVGMNVRTGTIITVLEQMGQGIERLNARTVGGEPVADLRVRASALSRTIVDPAIVPSMVVDEFF
VVFIAAGMAGMSTVSLGDLDELRVKSDRLTAMARGLEAIGVDPVEEREDGLLTGSGGASLRGGGFVATLLDHRITAMSFAVAGL
VPEEQQVDVDDTAPIATSDPFDIFNLLSRSTGAA

MAHSAQDAPVFRFRASBPGLTQITVRPGQCSHRAALMAHLCVCGS
RTSCGLEDVLTAAHSMAGMARIE-GADGIVTIVGVGVGLGTLIT
AQAQMGNSGTSRLLINGLVAHPITAMTGDASLSRRPMARVTDPI
GEMGAENFSNPETVATMVRGIVSPAVITSLRFLVAQSVQASILLAP
LNTGFTTTPGFTLDRSHSEMLGCGDALTVTDAGDGHVHTHVTG
CDLTAQIEVPGDNPASVGFVIAALVPGSLDTIANGQVNTVTGTS
TVLBQMGGTIERLNARTAAGEFVADRLVASASLSTVDPAIVPMS
DEFVVFTAAAMASTGTSLGDLRLVKESDRLATLARGLEATRGV
EEREDGLITVSGGASLRGGCVATVDLKHRTNDFRAGVLSVGGV

---MDYQTIP---SQLSGEICVPGKRSISHRAVLLAAEGQ
 QVDFGAGDNIALVSA/QMGASIPVIEDENIVLQVWGNGMGLQ
 PEALDCGNSGTAIRLSGLQAGFPNTVLTDSSGLRPMKRIIDPL
 TIMCAKIDST-GNVPKLIPNPLRTGTHYQLVQASQVSLSCG
 LVARGKCTETEPAPBDRTEHLLEHFFHYTLQKQKS---ICVSG
 GKLIKANDISIPGDISAAEFVIAATITPGSAILRKGVGNPTRLGV
 NLLMGKNDIEVTHYTHEKEEPAITDTHVARRLGSLIPDPVQVLT
 DEFFVLLIAAAVQKTVLRDAEALVKETORIAMQVGLKGLTIA
 ESLPDGVITQG---CTLEGGVSYSDERIHAFAVAGTLAKGPV
 IRENQVTSKPSFVPELVAMGVNMGVGRGCGF

MAHSAQDVPPHFAFSGPAGTIRVPGGDSISHRALVSAALCVQGLQ
RISGLCEQDVFLAAMRAAMGARTIRGDCGINTVPGVCGGLQIQA
QALD--MGNSGTSIRLLMGLVASHPITAMFTGDASLRRRMARVTPD
LGEMGAEMASPGCT--FLMVGISPAVPIIRLFPVSAQVKSAIL
AALNFTGTT--VIEPVARDBHE--KMLRGCGADLTVDGAGV
HRTVPGCDLQADIEVPGDSSAFTI/VAALIVPGDGLTITVENGG
VITGTC--ITVLEMGQGIETINARTVGEFVADLRVBSALSRIT
DPAIFPMVDFEVRFTIAANASGTTVSGLELDRVSRKSLORATMA
GLEAQVDFVEEREDGLITGCGASLRGGCVATLLDHRITASFAV

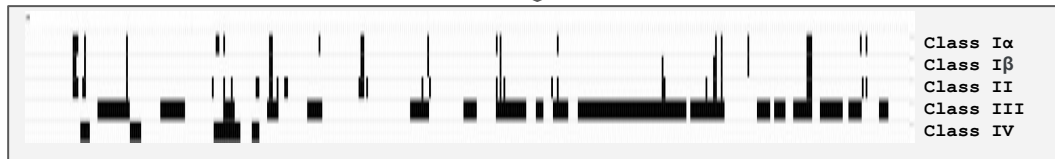
-MSESLTQPIE-----LISGEVNLPGSKSVSNRAILLAAASGTT
 RLTLNLDSDIIRHMLNALTGLVGNVLSADKT--TCEVEGLQGFAP
 QPLEFLPNAGTAMRPLAALCIQGGGVYVLEFGPKMEKRIEGLVDA
 LSQAQGLAYVELENGFFPKIRQTQGLQAGVTVDISQSISQITAFILN
 IRLAQKGVKTTIKGVELSVGLTDLTHIMEQGVGV-----INHRVYR
 FVIYAGQSVTSPPQFLVEGDASBASYFLAAAAI-KGGEVVKVTGICK
 STGGDTQPADALEKMGAKTGGDDTVIA-----RGELNVLVDI
 DFNHIF-----DAAMTIATLAFKGDITAI RNYNVNRVKEITRLAAMG
 ELRKVCAVEGEGEDFIVITPTPKL-----HA-IDTVDHRRMGCSFSL
 AL-SGTFVTEDECKSTKTFVDEKFAALSR-

-MHSDADGVPVPRFARSGPTITRVPGGSHIRHMLSCVGLG
 SRIGLGGEDGLTAAAMRWGACIRERAGDGIWTHVAGVCGV
 AQALEDMGNSGSTRLLMGLVASHPITAMFTGAGLSRRPRMARVTDPI
 GEMGARFNASPGPTFLPWGGLISPAVFIYRLVPAAGVAKSAILLA
 LMTFGPTTVPITVDRHSEKSGCGADITVETADGVRHITVPG
 CDLTADQIEVPG--DPSFAAFITVAALIVPGLSDITINVEGNVTH
 GITVLEQMGQTERIMARVCGEFPVLRHPRASALSRITVDPATV
 -PSMVEFPFVFITAAASGPTTVTSGDLRVKESDRITATHARGLE
 I--GVDDREHRTVLTGGASGLGGCPVATLDRHMTASFAVAGI

MMGGRKLTITPP---GKPLTGRAMPGSGSITNRALLLAGLAKG
SRLTGALRSDTGYRQALSRAMGVITDEPDPTTIVK--GSGKLG
AAPLFGNACTATPTFAAALVDGKVIYVDGAMHKRPGIPVDA
RSLGIDASAETGCP-PYTINGT-----RFEASRVIYDGL-
-----SSQVTSALLMAAGLGRADVVELLIG-ELHIGALG
IDLTVAAMRFAQKVERVSPVAMRPGTCYHAADFVIEPDASAATY
MAAEVLV---GGRIGDTPAEFGSPQCAJYDLSIKFPHL-----PAVIG
SGQMDAIPVLAAFNPMVRFVFGIENLRVCKDRIRALSGSLIS
IVPNLTGEGDGLDLSAPSLAGKILTAETDSFDRIRMTASFLALG
-IKGIGTLIDPDCVAKTFSNGLVLN--SLGVADV

-MAHSDADQVPPFRFARSGPLTGTIRVPGGDSHRAELSCVGLG
 SRIGLLEGGDITLAAAMRANGERTBAGDINTWVHAGCGLV
 AQAELMNCISGTSTRLLMGLVASHFITAMFTGQASLSRRPMARVTDPI
 GENGAEFNASPGGTLFIMVGRVGISYIRLVSFVAGSGKSAITLAL
 LNTFGPTTIVIEPVRDHSEKRLGPGADITVEADQCVRHIVTGL
 CLDTAQDIEVPG--DPSRAAFITVAALIVPGSLDITENVGWGTIR
 GIIITVLEQMGQIKERLNARVGTGEEFVDRVRSALSRISITVDFATV
 -PSMVEFDFFVFTLAAAMASGPTTSGDLRLVKESDRHATMARGLEL
 I--GVVDEERDGLITGSGGASLRGGCVPLTDLRIKMTASFAVAG

-----MFVA-----DTPGSCSITATALFAAAAGDGV
TLIVRFSDTDFGAGBLARLVGRVFPDS--MQVQDFPQGPALVA
DVF--CRDGTATPTLAAAGCHTVKFGD--MGMRRLPLPTALRA
ELCVDLNIHEERDGHPLVTVRAAGVAGGEVTLDAQSSQYLTAALLL
PLTEKGRILHVTDLVSPVPIETSLFMAGRFVGVETG-----RDH
VFGPGVGRATVTAIEPDSATSYFFAAAL--SGEVTVPGLGEALGA
GDLGFDVILRMGAEE-----IGADTPT--VRGTGRLGLTVL
-----MDSIDMTPLLAIAAPFASGPIVDVANTVKKCEKDLAEACNN
RLRGVRFVETGPDWIEIHGPAFTPT--QAEIKTYGDHRIWISFAVTC



CLASS	Class Ia	Class Ib	Class II	Class III	Class IV
IDENTITY	0.76	0.833	1	0.378	0.367

OUTPUT