

Hg 1 -----LIKAFHLLISLPMCASAAISAFAFIDDSEAE
At 1 -----MATHPEALRRERILNSKLYF
Lj 1 -----GPLLLLSPCDSLEPSLPMSSSSSGTDALALARNRIISKLYF
Mt 1 IPDNHHRVKSVMYRWLCHYFIHPSPLKYLHRATPMSSPPSCSAADDTLMRNRIISKLYF
Ce 1 -----MSSDKFKLDTLFDNDDEIIEPD
Gr 1 -----EFLQKHSEMPNVG
Ts 1 -----PRVRGRRSVFKICEVLGIMS

Hg 32 IDWDERCPIVYSEEDYNISFFGIEKCHPFDSNKWGNVFRFLIASGALVESAVLRPIEAKKE
At 21 DVPLSKVSIYSSSYDISFMGIEKLHPFDSKWKGRVCKFLVSDGFLLEKAIVEPLEASKI
Lj 43 DVPPSKVPLIYSESYSYDISFLGIEKLHPFDSKWKGRICGFLVSDVDLDDKKEIVEPLEASKD
Mt 61 DVPPSKVPLIYSDSYDISFLGIEKLHPFDSKWKGRICKFLISFGVLDKNRIVEPLEASKD
Ce 23 GADVKKRNVAIYYHKDVGFHYGQLHPMKPQRLVVCNDLVVSYEMPKYMTVVEVSPKLDAA
Gr 14 VQDHYRKRVAIYYDSNVGNYYYGQGHVMKPHRIRMTHLLLNLCIYRHLDVYRPFPPASLE
Ts 21 RTDDSKRRCVCFYDPDIGNYMFSPNHDMPKIRVRMVHCLVYEQLYRHVTIMEPHRATPD

Hg 92 HLLLVHSSKKYLRSLNGRF----TLTRILEVGLVLLFPICLIDRRIILRPMRIQTGGTVLAA
At 81 DLLVVHSENYLNSLKSSA----TVARITEVAPVAFFPNFLVQKQVLYPFRKQVGGTILAA
Lj 103 DLLVVHSESYLNSLKESS----NVATIEVPPVALFPNCLVQNKVLFPPFRKQVGGTILAV
Mt 121 DLLVVHSESYLNSLKESS----NVAKIIEVPPVALEFPNCLVQRKVLFPFRKQVGGTILAA
Ce 83 DISVFFHTEDYVNFLOTVTPKLGLTMPDDVLRQFNIGEDCPIFAGLWDYCTLYAGGSVEGA
Gr 74 DMTRFHSEDYMKFLRNATPEN-LRQFNKQMLKFNVEDCPVFDGLFEFCQLSSGGSLAAA
Ts 81 EMKIFHDEDYIDMLRRRAKPEH-MNCNLDALSYYNIGDDCPLFDGIFEYCOITGGSTAGA

Hg 148 RVSLIR--GWAINIGGGFHHASEGKGGGFCVYADVTLAIKLIIFANELIKSAMIVDVAHQ
At 137 KLATER--GWAINIGGGFHHCTAERGGGFCAFADISLCHHFAFLRLRISRVMIIDLDAHQ
Lj 159 KLAKER--GWAINVGGGFHHCSAE-----
Mt 177 KLAKER--GWAINVGGGFHHCSAENGGGFCAYADISL CVHFVAVQVQLNISRVIIIDLDAH-
Ce 143 RRLNHKMNDIVINWPGLHHAKKSEASGFCYVNDIVLGILELLEK--YHKRVLYIDIDIHH
Gr 133 VKLNKQKAEIAINWAGGLHHAKKSEASGFCYVNDIVLGILELLEK--YHKRVLYVDIDVHH
Ts 140 QSLNSGEYDIAINWAGGMHHAKWKYKASGFCYVNDIVLAILQLLEK--KHQVLYVDIDCHEM

Hg 206 GNGHETDFASDSRVYIIDL-----
At 195 GNGHETDLGDDNRVYIILDMYNPEIYPFDYRARRFIDQKVEVMSGTTTDEYLRKLDEALEV
Lj -----
Mt -----
Ce 201 GDGVQEAFFNNSDRVMTVSFHRFG-QYFPGSGSIMDKGVGPGKYFAINVPLMAAIRDEPYL
Gr 191 GDGVVEEAFYTTDRVMTVSVSQIPAIFFPGTGELKVIKFL--MNSFLG-----
Ts 198 GMGVEEAFYTTDRVMTISFHKFG-NFFPGTGNYSIGYGKGLHYAVNPFPH-----

Hg -----
At 255 ASRN-----FQPELVIYNAGTDILDGDPLGLLKISPDGITSRDEKVFVRFAREKNIP
Lj -----
Mt -----
Ce 260 KLFESVISGVEENFNPEAIVLQCGSDSLCEDRLGQFALSFNHARAVKYVKS LGKPLMVL
Gr -----
Ts -----

Hg -----
At 306 LVMLTSGGYMKSSARVIADSIENLSRQGLIQTRPE-----
Lj -----
Mt -----
Ce 320 GGGGYTLRNVARCWALETGVILGLRMDDEIPGTSLSYHYFTPRLLRPNLVPMKMDANSAA
Gr -----
Ts -----

Hg -----
At -----
Lj -----
Mt -----
Ce 380 YLASIEKETLACLIRMIRGAPSVQMQRNIVGIRLDEIEQIEENERLQKSSKSSIEYEVGKVS
Gr -----
Ts -----