

Additional file 2

Figure S2: Sequence comparison of hemocyanin-like proteins of *Biomphalaria glabrata* with hemocyanins of gastropods and cephalopods. The amino acid sequences of functional units included in this multiple sequence alignment come from hemocyanins of Tectipleura, Lepetellida and Cephalopoda (abbreviations see below). Colors indicate conservation scores: Red/blue: conservation of at least 95%/80% over all FUs; grey: FU-specific conservation of 95% (e.g. within FU-a, FU-b, ...); yellow: exception of BgHcl1/2 sequence to conservations described above. "X" symbolizes not known amino acids. Signal peptides as well as tail extensions of FU-h are not included. Included hemocyanins: AcH1+2 (*Aplysia californica*), LsH1+2 (*Lymnaea stagnalis*), BgHcl1+2 (*Biomphalaria glabrata* hemocyanin like proteins), HpHaD + HpHaN + HpHb (*Helix pomatia* alphaD, alphaN, beta), CaHaD CaHaN CaHb (*Cornu aspersum* alphaD, alphaN, beta); HtH1+2 (*Haliotis tuberculata*), KLH1+2 (*Megathura crenulata*), OdHG + OdHA (*Octopus vulgaris*), NpH (*Nautilus pompilius*).

AcH1 - FUE : -----NERQEADGQVGNLYVKNASLSPQELSLKMAAALQADSS-ADGMSIASFHAFPHFC--SBSASKRYA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQTDHGLGLANPTYTDVYTGQTDIPWYKGTIE : 143
AcH2 - FUE : -----NERQESDGLSSYVQVKS DALSPOELSLKMAAALQADSS-ADGMSIASFHAFPHFC--SBSASKRYA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQTDHGLGLANPTYTDVYTGQTDIPWYKGTIE : 143
LsH1 - FUE : -----GERQKSSGEVNTYIVKENSISPRVQSYXAMEALQADSS-ADGMSIASFHAFPHFC--SBSAHNRVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRVSDSLHFIDDENFVDPVVTGQKAMWPKKARIE : 143
LsH2 - FUE : -----SERQEAHGAVSSFVYKNDALSORBALSXYNAMRALQADSS-ADGMSIASFHAFPHFC--SBSAHNRVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
BgH12 - FUE : -----EKSYTSESHVINVRALKERSNFRILSYXAMASLQQDSS-ADGMSIASFHAFPHFC--NREKRYVSPICATLPHNHLTVQVEDAIRRHGSLVGTIYDWSRREGSLSEFLEDDNYHDPITGKTLNPFVHKSIG : 143
HPhAd - FUE : -----KERQAEADGDVKDILVYKNDALSPRILSLHAEALQADSS-ADGMSIASFHAFPHFC--SBSASKRYA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
CaHaD - FUE : -----RERQTEGGDKVHVYVKN DALSFRITLALHAEALQADSS-ADGMSIASFHAFPHFC--SBSASKRYA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
HPhAn - FUE : -----DEVEDQHGSTSTYIVYKNESPLGYYLAALIALAKKTS-ADGMSIASFHAFPHFC--SBSASRYA CIRGTS LQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
CaHaN - FUE : -----DEEQDQLGATTYIVYKNESNPLGYHADALIALAKKTS-ADGMSIASFHAFPHFC--SBSASRYA CIRGTS LQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
HPhb - FUE : -----DEAEHFGHDRAPLIVYKNESPLGKYHVKALITSLNADGS-ADGMSIASFHAFPHFC--SBSASRYA CIRGTS LQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
CaHb - FUE : -----DDVELPHGGRAPSLIVYKNESPLGKYHVKALITSLNADGS-ADGMSIASFHAFPHFC--SBSASRYA CIRGTS LQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
HtH1 - FUE : -----DTHILDHDEEELIVYKNIDLSFRVRSYKALQAKMNRD-ADGMSIASFHAFPHFC--NBSAHRVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
KLH1 - FUE : -----DSAHTDDGHTPEVMIKDTODKROQLSYKALQAKMNRD-ADGMSIASFHAFPHFC--SBSASKRYA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
HtH2 - FUE : -----SSFLRPDGHSDLLIVYKNSITRTTASLHALKSMQDHS-POGMSIASFHAFPHFC--SBSAHRVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
KLH2 - FUE : -----RKNIIYDGLSQHNLIVYKNSITRTTASLHALKSMQDHS-POGMSIASFHAFPHFC--SBSAHRVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
ODG - FUE : -----DHSADIKSEEGNEVIVYKNERSLSBMNSLHFRMRQKRS-SDGMSIASFHAFPHFC--SBSAHRVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 144
OdHA - FUE : -----DHSADIKSEEGNEVIVYKNERSLSBMNSLHFRMRQKRS-SDGMSIASFHAFPHFC--SBSAHRVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 144
NpH - FUE : -----GSKNATHYQEEHEHHFVYKNSRSLIYHIEVYFRMRQKRS-ADGMSIASFHAFPHFC--NREKRYVSPICATLPHNHLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 145
AcH1 - FUF : -----DTHILDHDEEELIVYKNIDLSFRVRSYKALQAKMNRD-ADGMSIASFHAFPHFC--SBSAHRVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 143
AcH2 - FUF : -----DDYVLEKVTPEVMIKDTODKROQLSYKALQAKMNRD-ADGMSIASFHAFPHFC--SBSASKRYA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
LsH1 - FUF : -----RDYDLEKVTPEVMIKDTODKROQLSYKALQAKMNRD-ADGMSIASFHAFPHFC--SBSAHRVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
LsH2 - FUF : -----SDHLDNVTPILTRDSTHERRIQSQALRLDQLQOS-NDGMSIASFHAFPHFC--DPANP-TVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
BgH12 - FUF : -----EDPHLLTVTPILTRDSTHERRIQSQALRLDQLQOS-NDGMSIASFHAFPHFC--DEGN-PTA SAOGLPT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
HPhAd - FUF : -----EDVHVVEATPNIHNSREERIQSQALRLDQLQOS-NDGMSIASFHAFPHFC--SBSAHRVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
CaHaD - FUF : -----EDVHVVEATPNIHNSREERIQSQALRLDQLQOS-NDGMSIASFHAFPHFC--DPDHP-TVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 139
HPhAn - FUF : -----HDVTLKKTVMNHRNDDREERTQSQALRLDQLQOS-NDGMSIASFHAFPHFC--DPDHP-TVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
CaHaN - FUF : -----HDVTLKKTVMNHRNDDREERTQSQALRLDQLQOS-NDGMSIASFHAFPHFC--DPDHP-TVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
HPhb - FUF : -----HDLNLLKVLNHRNDSREERIQSQALRLDQLQOS-NDGMSIASFHAFPHFC--DPDHP-TVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
CaHb - FUF : -----RDIHLRKLKVLNHRNDSREERIQSQALRLDQLQOS-NDGMSIASFHAFPHFC--DPEHP-TVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
HtH1 - FUF : -----HKLNRKHTPVRVHESSREIRIASKALITSLQDNG-TDGMASIAFHAFPHFC--EPGR-EIA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
KLH1 - FUF : -----HDISSHLLSLNHRNDSREIRIASKALITSLQDNG-TDGMASIAFHAFPHFC--EPGR-EIA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
HtH2 - FUF : -----RDINTRSMSPNRVRRESDSARLSSKALRLDQLQOS-PNGMSIASFHAFPHFC--DSRGN-EIA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
KLH2 - FUF : -----HGINVRHVGRNHRNDSREIRIASKALRLDQLQOS-PNGMSIASFHAFPHFC--DDEGH-EIA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 140
ODG - FUF : -----NEDADDITPLNHRNDSREIRIQSMALITRYKEDS-DHGMSIASFHAFPHFC--SPEEP-KVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 139
OdHA - FUF : -----KQCADIDPLNHRNDSREIRIQSMALITRYKEDS-DHGMSIASFHAFPHFC--SPEEP-KVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 139
NpH - FUF : -----EHHEVHPLNHRNDSREIRIQSMALITRYKEDS-DHGMSIASFHAFPHFC--TPEEA-TVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 139
AcH1 - FUG : -----GASEVSSSSSLAGVYKDSSTSEIDNREALRQVADG-PNGMSIASFHAFPHFC--LNGR-RIA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 132
AcH2 - FUG : -----GAEDVSSSTLSGVYKDSSTSAEISNREALRQVADG-PNGMSIASFHAFPHFC--LNGH-PRIA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 131
LsH1 - FUG : -----GVANVDITSAVAGVYKDSSTASSETNREALRQVADG-PNGMSIASFHAFPHFC--YQGH-PPIA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 131
LsH2 - FUG : -----GSTQDAVSTSIAGVYKDSSTLVSEIENREALRQVADG-PNGMSIASFHAFPHFC--YQGH-PPIA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 131
HPhAd - FUG : -----GVKDIHTTAVAGVYKDSSTLVSEIENREALRQVADG-PNGMSIASFHAFPHFC--HENH-SVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 131
CaHaD - FUG : -----GVKDIHTTAVAGVYKDSSTLVSEIENREALRQVADG-PNGMSIASFHAFPHFC--HENH-SVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 131
HPhAn - FUG : -----EGAEVSSSTSIAGVYKDSSTSEIENREALRQVADG-PNGMSIASFHAFPHFC--HDHH-PVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 131
CaHaN - FUG : -----EGAEVSSSTSIAGVYKDSSTSEIENREALRQVADG-PNGMSIASFHAFPHFC--HDHH-PVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 131
HPhb - FUG : -----EAKKTRAVPVGDSYKNDLNSDVANREALRQVADG-PNGMSIASFHAFPHFC--HDHH-PVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 132
CaHb - FUG : -----DEEKAARVAVPVGDSYKNDLNSDVANREALRQVADG-PNGMSIASFHAFPHFC--HDHH-PVA CLRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 132
HtH1 - FUG : -----DHHDDHQSISAGVYKNDLNSDVANREALRQVADG-PNGMSIASFHAFPHFC--MPDG-NYS CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 133
KLH1 - FUG : -----DHHDDHSSMAGVYKNDLNSDVANREALRQVADG-PNGMSIASFHAFPHFC--MPDG-NYS CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 133
HtH2 - FUG : -----GRAADSANSIAGVYKDTTHVSEIENREALRQVADG-PNGMSIASFHAFPHFC--MNGR-KGA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 133
KLH2 - FUG : -----GHTDDHSSDIAGVYKDTTHVSEIENREALRQVADG-PNGMSIASFHAFPHFC--MNGR-KGA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 132
ODG - FUG : -----DFKREVHKKTVGDAITKNNSMPSDIKEDAMARQVADTS-DNGMSIASFHAFPHFC--YENGT-AYA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 133
OdHA - FUG : -----EFTKEIEKAVRGTIKNNSMPSDIKEDAMARQVADTS-DNGMSIASFHAFPHFC--YENGT-AYA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 133
NpH - FUG : -----NTKQAEERRISGGPIIKNNKLSSEIHEDEAMAAGVADHS-SNGMSIASFHAFPHFC--PYA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 129
AcH1 - FUH : -----GYERVAAKTAKSSASLKDNDLHABASNREALRQVADG-PNGMSIASFHAFPHFC--ANED-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 136
LsH1 - FUH : -----RYEKVAERTVVRDDKLIVKNQMLHABASNREALRQVADG-PNGMSIASFHAFPHFC--ATDD-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 136
LsH2 - FUH : -----RYEKVAERTVVRDDKLIVKNQMLHABASNREALRQVADG-PNGMSIASFHAFPHFC--ATDD-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 136
BgH11 - FUH : -----DSEIETQPALLKNSQELDGSNNREALKKLSST-ADNREIAGFHAFPHFC--PHSD-REA SPAGLPT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 128
HPhAd - FUH : -----DYEKIAQKTEAQEDVLLKNNSLEESANREALKKLSST-ADNREIAGFHAFPHFC--QDTE-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 136
CaHaD - FUH : -----DYEKIAQKTEAQEDVLLKNNSLEESANREALKKLSST-ADNREIAGFHAFPHFC--ETAD-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 136
HPhAn - FUH : -----KPLGVAASGFGSVLLKNNSLQSDAVSREDALYQLQDQG-LGMSIASFHAFPHFC--ENED-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 135
CaHaN - FUH : -----KPHGVAASGFGSVLLKNNSLQSDAVSREDALYQLQDQG-LGMSIASFHAFPHFC--ENED-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 135
HPhb - FUH : -----VPOAEQTATTYQSSNLVYKNSHLGASNREALKKLSST-ADNREIAGFHAFPHFC--EKED-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 135
CaHb - FUH : -----VIQPEQEATTSQANLIVYKNSHLGASNREALKKLSST-ADNREIAGFHAFPHFC--EKED-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 135
HtH1 - FUH : -----HRGGKHEDEHDDRLADVLKEDDFSLQANALDLYKLNDS-KGMSIASFHAFPHFC--ERED-KVP CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 138
KLH1 - FUH : -----KHHEKHEDHEDHEDLIVYKNSHLGASNREALKKLSST-ADNREIAGFHAFPHFC--EKED-KVP CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 134
HtH2 - FUH : -----HRGPVEETEVRQTDGNAHFHFKEDSLDANNREALKKLSST-ADNREIAGFHAFPHFC--EKED-KVP CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 130
KLH2 - FUH : -----HHGGTDSGHDSERHDGFFKEDSLDANNREALKKLSST-ADNREIAGFHAFPHFC--EKED-KVA CVRGMAT FQNHLLTVQVEDAIRRHGSLVGTIYDWSRQKSLSEFFSDPTYPDPGGDPVDPWYKANTIE : 137

160 180 200 220 240 260 280 300
AcH1 - Fua : DGQ---VVH...
AcH2 - Fua : DGH---VVH...
LsH1 - Fua : VENSKT...
LsH2 - Fua : KTG---PRF...
BgH11 - Fua : SGV---IHA...
BgH12 - Fua : GDQ---MIR...
HphAd - Fua : PEG---VKN...
CaHaD - Fua : PEG---VKK...
HphAn - Fua : GKR---TYK...
CaHaN - Fua : GAK---TYK...
HphB - Fua : GDK---TYH...
CaHb - Fua : GDQ---TYH...
HtH1 - Fua : I-----NKK...
KLH1 - Fua : L-----DKN...
HtH2 - Fua : E-----NKK...
KLH2 - Fua : L-----NKK...
ODHG - Fua : E-----KKT...
ODHA - Fua : E-----KKT...
Nph - Fua : K-----KMO...
AcH1 - Fub : LNS---GAK...
AcH2 - Fub : LGN---GVV...
LsH1 - Fub : LGD---STK...
LsH2 - Fub : LDN---NVH...
BgH11 - Fub : LRT---GSR...
BgH12 - Fub : L-----NVT...
HphAd - Fub : LGG---DAK...
CaHaD - Fub : LGG---DAK...
HphAn - Fub : LGN---DVK...
CaHaN - Fub : LGN---DVK...
HphB - Fub : LGH---DVK...
CaHb - Fub : LGH---DVK...
HtH1 - Fub : EEG---HHH...
KLH1 - Fub : EEN---APH...
HtH2 - Fub : E-----NKR...
KLH2 - Fub : E-----NNV...
ODHG - Fub : LHN---DVF...
ODHA - Fub : LHN---DVF...
Nph - Fub : LHD---HIT...
AcH1 - Fuc : A-----NAD...
AcH2 - Fuc : V-----DQV...
LsH1 - Fuc : A-----DQV...
LsH2 - Fuc : V-----DHD...
BgH12 - Fuc : X-----XXX...
HphAd - Fuc : V-----NQV...
CaHaD - Fuc : V-----NQV...
HphAn - Fuc : V-----NQD...
CaHaN - Fuc : A-----NQD...
HphB - Fuc : A-----SAD...
CaHb - Fuc : A-----SAD...
HtH1 - Fuc : V-----NQD...
KLH1 - Fuc : V-----DKT...
HtH2 - Fuc : V-----GVD...
KLH2 - Fuc : V-----GHD...
ODHG - Fuc : I-----GHD...
ODHA - Fuc : I-----GHD...
Nph - Fuc : V-----NAD...
AcH1 - Fud : E-----DAV...
AcH2 - Fud : E-----DAV...
LsH1 - Fud : E-----GAV...
LsH2 - Fud : E-----NAV...
BgH12 - Fud : E-----NAV...
HphAd - Fud : E-----NAV...
CaHaD - Fud : E-----NAV...
HphAn - Fud : E-----NAV...
CaHaN - Fud : E-----NAV...
HphB - Fud : E-----NAV...
CaHb - Fud : E-----NAV...
HtH1 - Fud : E-----NAV...
KLH1 - Fud : E-----NAV...
HtH2 - Fud : E-----NAV...
KLH2 - Fud : E-----NAV...
ODHG - Fud : L-----NSB...
ODHA - Fud : L-----NSB...
Nph - Fud : I-----SDY...
AcH1 - Fue : E-----NSV...

AcH2 _ FUE : E-----NTTTEEDVQGYDLFKQGP-HGFDTLFNQAALALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 284
Lsh1 _ FUE : E-----NSPTEDEVSDRLFKRGP-HGWDTLFNQAALALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 284
Lsh2 _ FUE : E-----HAVTEADVKEEFLFKVKG-HGWDTLFNQAALALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-LMRBPLKPPS-FCSPYLNEMKEYSREBET : 284
BgH12 _ FUE : E-----AVYTDADILVDMKMGK-LGWDTLFQQALFALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-MMKRPLKPPS-FCSPYLNEMKEYSREBET : 284
HpHaD _ FUE : E-----HSHHEEDIQSAELFKLGP-HGWDTLFQQALFALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-HKRDPLKPPS-FCSPYLNEMKEYSREBET : 284
CaHaD _ FUE : E-----NSHHEEDIQSAELFKLGP-HGWDTLFQQALFALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-HKRDPLKPPS-FCSPYLNEMKEYSREBET : 284
HpHaN _ FUE : E-----HVDTEEDVQEDKLFKQGP-HGWDTLFYQVFALEQEDPCDFEQLLHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 284
CaHaN _ FUE : E-----HVDTEEDVQEDKLFKSGPH-GWDTLFYQVFALEQEDPCDFEQLLHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 284
HpHb _ FUE : E-----HEDVHADI-QSNLFKRGPHGWDTLFYQVFALEQEDPCDFEQLLHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-KRREPLKPPS-FCSPYLNEMKEYSREBET : 284
CaHb _ FUE : E-----HEDVHADI-QSKDLFKRPHGWDTLFYQVFALEQEDPCDFEQLLHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---YCSLE-KRREPLKPPS-FCSPYLNEMKEYSREBET : 284
HtH1 _ FUE : EGP-----GVHTEHINTERLPHSGDHDGYHNFETVFALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-HMRTPLKPPS-FCSPYLNEMKEYSREBET : 287
KLH1 _ FUE : EGE-----NVHKKADINRDLRFQGST-KTHHNFIEQALFALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCAVN-LMKTPLKPPS-FCSPYLNEMKEYSREBET : 286
HtH2 _ FUE : EGE-----NITHTEVIAIDLKFKVGG-HVFDNFFKQALFALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---HCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 286
KLH2 _ FUE : EGE-----GVTEEDVDAEHLFAKGN-LVYNNFCNQALFALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---HCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 286
OdHG _ FUE : ISE-----DTEKKEV-SEYLEHPV-LGKQTLFDNIALALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---HCALE-LMKVPLKPPS-FCSPYLNEMKEYSREBET : 286
OdHA _ FUE : ISE-----DTEKKEV-SEYLEHPV-LGKQTLFDNIALALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---HCALE-LMKVPLKPPS-FCSPYLNEMKEYSREBET : 286
NpH _ FUE : ISP-----EVMQADV-QDKLQKQP-LGRNTLHDNVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-LNBPPLKPPS-FCSPYLNEMKEYSREBET : 287
AcH1 _ FUF : E-----DVYVADI-REPFRNKQ-AGDHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCALN-YNSOPMRPF-F-EGFLKPKFMDHAVPTVE : 279
AcH2 _ FUF : E-----KAYIVDV-REPFRHLNDR-EGRSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---ACAVN-YNSOPMRPF-F-EGFLKPKFMDHAVPTVE : 279
Lsh1 _ FUF : E-----NTYVADI-REPFRQTSK-DGHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCAVN-YNSOPMRPF-F-EGFLKPKFMDHAVPTVE : 278
Lsh2 _ FUF : E-----KVYVADT-KSELYDKGR-GGKSAIYIYVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCAVN-YNSOPMRPF-F-EGFLKPKFMDHAVPTVE : 279
BgH12 _ FUF : E-----DTYVADI-REPFRHLLKXXX-XXXXXXXXXXXXXXXXXXXXXSTLNSGGDLYSLTTEASAYDFEFLHHSNTDILAVIQAOKYRGYDPNEA---ECCALN-YNSOPMRPF-F-EGFLKPKFMDHAVPTVE : 278
HpHaD _ FUF : E-----DTYVADI-REPFRHRLV-DGKHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCALN-YNSOPMRPF-F-EGFLKPKFMDHAVPTVE : 279
CaHaD _ FUF : E-----DTYVADI-QSPFK-KH-DGKHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCALN-YNSOPMRPF-F-EGFLKPKFMDHAVPTVE : 277
HpHaN _ FUF : E-----KACTVDV-QPELRETTK-DGKHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAVN-ANBPMKPPS-F-ETFTKPKFMDHAVPTVE : 279
CaHaN _ FUF : E-----KACTVDV-QPELRETTK-DGKHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAVN-ANBPMKPPS-F-ETFTKPKFMDHAVPTVE : 279
HpHb _ FUF : E-----GAYIVDV-QHPEFRAYG-DGKHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAVN-ANBPMKPPS-F-ETFTKPKFMDHAVPTVE : 279
CaHb _ FUF : E-----DAYIVDV-YGPEFKSFG-DGKHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAVN-ANBPMKPPS-F-ETFTKPKFMDHAVPTVE : 279
HtH1 _ FUF : K-----DAFVADV-QESLFRKMS-FGKHSALFDLVALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAVN-ANBPMKPPS-F-ETFTKPKFMDHAVPTVE : 278
KLH1 _ FUF : H-----DTYVADV-QEGLHLTS-TGHSALFNQAALALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAVN-LMKTPLKPPS-FCSPYLNEMKEYSREBET : 278
HtH2 _ FUF : A-----NTYVADP-QEMLLQCE-HG-ESIEYQTLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAVN-LMKTPLKPPS-FCSPYLNEMKEYSREBET : 277
KLH2 _ FUF : E-----DAYIVDP-QDILYHLQD-ETGTSVLLDQTLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCALN-MMTRPMRPF-F-EGFLKPKFMDHAVPTVE : 276
OdHG _ FUF : E-----DTYVADV-KPELFE-IG-GGEGSTHYQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---YCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 278
OdHA _ FUF : E-----DTYVADV-KPELFE-IG-GGEGSTHYQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---YCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 276
NpH _ FUF : A-----BTYVADT-QPELREPSK-DCKHSLYDETLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---YCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 277
AcH1 _ FUG : N-----GEVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 270
AcH2 _ FUG : N-----GEVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
Lsh1 _ FUG : N-----GEVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
Lsh2 _ FUG : N-----GEVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
HpHaD _ FUG : N-----GEVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
CaHaD _ FUG : N-----GQVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
HpHaN _ FUG : D-----GHVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
CaHaN _ FUG : D-----GHVTSAL-REQLNDPE-FGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
HpHb _ FUG : L-----DHNVTASL-REQLSDPE-SGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
CaHb _ FUG : L-----DHNVTASL-REQLSDPE-SGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 269
HtH1 _ FUG : L-----NVSTASL-REQLSDPE-SGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 271
KLH1 _ FUG : L-----GVDTASL-REQLSDPE-SGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 271
HtH2 _ FUG : L-----GVTASL-REQLSDPE-SGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 271
KLH2 _ FUG : R-----DMLNDPE-SGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---HCDIQ-VKQPLKPPS-FCSPYLNEMKEYSREBET : 270
OdHG _ FUG : A-----NTDVTASL-RAQLDDPE-KDKSFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 271
OdHA _ FUG : A-----NTDVTASL-RAQLDDPE-KDKSFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 271
NpH _ FUG : I-----NETSAL-REQLSDPE-SGSEFFYRQVLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---NCALE-QKREPLKPPS-FCSPYLNEMKEYSREBET : 267
AcH1 _ FUH : V-----NQDVTADI-QSFLNPT-INGNYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---RCGGA-INEBPLKPPS-Y-SQITNDFRMSQPSKVE : 275
Lsh1 _ FUH : A-----NEKVTQV-QSELYSERK-VHGFYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---SCAGH-INEBPLKPPS-Y-SQITNDFRMSQPSKVE : 275
Lsh2 _ FUH : V-----GKVTADV-KDELNPT-INGNYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---HCGGH-INEBPLKPPS-Y-SQITNDFRMSQPSKVE : 276
BgH11 _ FUH : E-----KEWDEEV-NLKNLLD-PEGTKMLFSALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---CQYVK-HDSDMPPR-N-PDINEMKNDLRENSLPSVE : 265
HpHaD _ FUH : N-----NQRVTADI-QSELYNPHQ-INGNYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---HCGGH-INEBPLKPPS-F-GEINKNDLRENSLPSVE : 275
CaHaD _ FUH : N-----NQRVTADI-QSELYNPHQ-INGNYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---CQGGH-VDDPLKPPS-F-GEINKNDLRENSLPSVE : 275
HpHaN _ FUH : V-----GQRTSNP-LGALFSANT-SAGTSLYQTLDALEDDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---ECGEK-SLHBPPLKPPS---YDINTIALREHAVPTVE : 273
CaHaN _ FUH : A-----GQRTSNP-LGALFSANT-SAGTSLYQTLDALEDDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---ECGEK-SLHBPPLKPPS---YDINTIALREHAVPTVE : 273
HpHb _ FUH : A-----GKVTASL-LEALFSANT-SRGTILYDTHDALEDDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCGGH-TFDKPLKPPS-F-PALNTIALREHAVPTVE : 274
CaHb _ FUH : V-----GQVTASL-LEALFSANT-SRGTILYDTHDALEDDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---SCAGH-KFDKPLKPPS-F-PALNTIALREHAVPTVE : 274
HtH1 _ FUH : V-----QHEVTADV-NQRNLQTK-FGEFDYLYTHDALEDDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---DCAGDLKFDKPLKPPS-Y-ETVNEDEFIRNSLPSVE : 278
KLH1 _ FUH : I-----NQDVTADV-NEALFQTK-FGEFSSYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---SAGD-INEBPLKPPS-Y-ESVNDDFRMSQPSKVE : 273
HtH2 _ FUH : V-----GHDVTADV-NEALFQTK-FGEFSSYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---KAYH-MDEBPLKPPS-Y-ESVNDDFRMSQPSKVE : 279
KLH2 _ FUH : A-----GHDVTADV-NEALFQTK-FGEFSSYLYLALEQEDYCDPEIQPETHNAHSWVGGSQKHSMAHHSYDFAFVHHSNTDILAVIQAOKYRGYDPNEA---KAGH-MDEBPLKPPS-Y-ESVNDDFRMSQPSKVE : 276

AcH2_FUe : DYEGH-DNRR-DNLEFVGMN-PRID-AFKK-RRERSRV-AGFLK-EGFGS-AMVTD-EDCTK----GMES-FQGGYFT-VLGGAAEMPAFDRLFKYELDQ-SEHN-RP--DD-HFHVH-KYIDCFE-DHS-VVNFV-FVLEPAS----- : 419
Lsh1_FUe : NMADH-BHRR-DNLEFVGLS-PQID-AFKK-RHEHDRV-AGFLK-EGFKK-AMVTD-EDCAN----GM-PPGGYFT-VLGGAAEMPAFDRLFKYELDQ-SEHN-RP--DD-HFHVH-KYIDCFE-DHS-VVNFV-FVLEPAS----- : 417
Lsh2_FUe : NYEDH-BHRR-DQFVGMSP-PRID-AFKK-RQEHDRV-AGFLK-EGFGS-AMVTD-EDCAN----DMSN-FEGGYFT-VLGGAAEMPAFDRLFKYELDQ-SEHN-RP--DD-HFHVH-KYIDCFE-DHS-VVNFV-FVLEPAS----- : 419
BgH12_FUe : KYETH-BQR-DNLELAGMNS-QSID-AYTKG-KIKHDRV-AGFOL-EGRLTS-ASVND-EDICTV----RK-TEGGYFAVLG-GAELMPPAFDRLYRYDITQQ-KSRAR-RP--DD-ELKVVH-KSMNSQ-SSS-IASPN-IFVPSK----- : 417
HpHaD_FUe : AYEDH-BMQDSLEFVGMN-PAID-AYTKE-RQEHDRV-AGFLK-EGGLTS-ASVND-EDICA-----FKK-FDGGHFTVLG-GEEMPAFDRLYRYDITQQ-KENH-HY--DD-HFH-H-KALNCTE-DSK-IPEP-IVLVAHA----- : 418
CaHaD_FUe : AYKEH-BMQDSLEFVGMN-PAID-AYTKE-RQEHDRV-AGFLK-EGGLTS-ASVND-EDICA-----FKK-FDGGHFTVLG-GEEMPAFDRLYRYDITQQ-KENH-HY--DD-HFH-H-KALNCTE-DSK-IPEP-IVLVAHA----- : 418
HpHaN_FUe : AYKEH-BMKDALEFVGMN-PTID-AYTKE-RQEHDRV-AGFLK-EGGQASVND-EDICD-----ATGV-FDCGHSILG-SAAEMPAFDRLYRYDITQQ-ESH-HY--DE-HLTVH-KSINGCTE-DSH-IHEP-IVLVPK----- : 419
CaHaN_FUe : AYKEH-BMKDALEFVGMN-PTID-AYTKE-RQEHDRV-AGFLK-EGGQASVND-EDICD-----ATGD-FDCGHSILG-SAAEMPAFDRLYRYDITQQ-ESH-HY--DE-HLTVH-KSINGCTE-DSH-IHEP-IVLVPK----- : 419
HpHb_FUe : DYERH-BHRR-DALEFVGMN-PTID-AYTKE-RQEHDRV-AGFLK-EGHQS-AMVTD-EDCKG----NN-FEGGYFTVLG-PPAEMPAFDRLYRYDITQQ-KHH-HY--DD-NFKIQ-IPADCAI-DSH-LHEP-IVSVPK----- : 417
CaHb_FUe : DYESH-BHRR-DALEFVGMN-PTID-AFKK-RQEHDRV-AGFLK-EGHQS-AMVTD-EDCKG----DTDN-FEGGYFTVLG-PPAEMPAFDRLYRYDITQQ-KHH-HY--DD-HFKIQ-IPADCAI-DSH-LHEP-IVSVPK----- : 419
HtH1_FUe : DYKK-BQR-DNLELEGRS-TRID-ELIQQ-RQEKDRT-AGFLK-EGGTS-ASVSLVQCRV----DHT-KDAGYFTVLG-SAAEMPAFDRLYRYDITQQ-KDMN-RH--DT-SIDVT-TSYNGTV-SGD-IQTPS-IIFVPG----- : 420
KLH1_FUe : DYQK-BGMI-DLEFAGWSR-GRID-HIVRN-RQEHRSV-AGFLK-EGGTS-ASVND-EDVCRV----AGD-EDAGYFTVLG-GEEMPAFDRLYRYDITQQ-KMMN-RH--EISQIEVT-TSYDQTV-DSG-IPTPS-IIYDPA----- : 419
HtH2_FUe : DYRK-BGMI-DNLEFVGMN-VAED-QYIE-HQENDRV-AGFLK-EGGTS-ASVND-EDVCRV----DST-QDAGYFTVLG-SAAEMPAFDRLYRYDITQQ-KMMN-RH--DD-TISVST-TANNCTV-SSS-IPTPS-IVFQRH----- : 419
KLH2_FUe : DYHR-BGMI-DNLEFVGMN-SSIH-NYIKQ-QQEADRV-AGFLK-EGFGS-ASVND-EDICRP----DQS-QEAGYFTVLG-SAAEMPAFDRLYRYDITQQ-KMK-RY--DT-TIKVH-KDIAGAE-SSD-IPTPS-IVLEEGK----- : 419
OdHG_FUe : RYKDN-BHRE-DLIDNSMS-NQIE-SYTRH-QRDHDRV-AGFLK-EGFGS-AMVTD-EDICL-EGE-HEGSHFVLG-GSTMPAFDRLYRYDITQQ-KDMN-RH--SATTIKTK-VAQNCTE-PAS-LPEA-IVIRIPPS----- : 420
ODHA_FUe : RYKDN-BHRE-DLIDNSMS-NQIE-SYTRH-QRDHDRV-AGFLK-EGFGS-AMVTD-EDICL-EGE-HEGSHFVLG-GSTMPAFDRLYRYDITQQ-KDMN-RH--SATTIKTK-VAQNCTE-PAS-LPEA-IVIRIPPS----- : 421
NpH_FUe : NYKDH-BQED-DNLEFVGMN-PTID-DYTK-ELHHR-AGFLK-EGGQASVND-EDICD-----QNH-EDAGYFTVLG-SAAEMPAFDRLYRYDITQQ-TMHN-HY--DN-HINTH-HDMAQND-DSH-LQKAL-ILRQPA----- : 419
AcH1_FUf : DYEH-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----NNV-NYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 419
AcH2_FUf : CHEK-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVND-EDICRP----NNV-NYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 419
Lsh1_FUf : NHEE-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----SQ-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 417
Lsh2_FUf : YEE-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----SE-AFAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 418
BgH12_FUf : NYHD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 420
HpHaD_FUf : NYHD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 420
CaHaD_FUf : NYHD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 418
HpHaN_FUf : NYHD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 418
CaHaN_FUf : NYHD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 418
HpHb_FUf : NYHD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 417
CaHb_FUf : NYHD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 417
HtH1_FUf : NYED-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 417
KLH1_FUf : KYEL-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 417
HtH2_FUf : YET-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 416
KLH2_FUf : YDQ-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 417
OdHG_FUf : DKN-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 414
OdHA_FUf : DYN-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 414
NpH_FUf : NYDD-BGMS-DLDSIGYDLDG-QLIAD-RQSKARV-AGFLK-EGKKS-SSVNLNCLR----QECV-TYAGRNLLG-PTMAMPAFDRLYRYDITQQ-KSAEQS-HPEDVFDSEALFT-DIKVFDVEGHALPVSSVLP-PTII-KAAV----- : 416
AcH1_FUg : DYDR-FNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
AcH2_FUg : DYDR-FNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 402
Lsh1_FUg : DYDR-FNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 402
Lsh2_FUg : DYDR-FNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
HpHaD_FUg : NYDR-LNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
CaHaD_FUg : NYDR-LNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
HpHaN_FUg : NADS-LHQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
CaHaN_FUg : SDDR-LHQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
HpHb_FUg : NYEQ-LHQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
CaHb_FUg : NYEQ-LHQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
HtH1_FUg : EYNR-LSQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 404
KLH1_FUg : EYSR-LNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 404
HtH2_FUg : DYER-LNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 404
KLH2_FUg : DYER-LNQD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 403
OdHG_FUg : DYHK-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 407
OdHA_FUg : DYHK-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 406
NpH_FUg : DYHQ-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 404
AcH1_FUf : DYAH-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 412
Lsh1_FUf : DSER-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 410
Lsh2_FUf : DSER-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 410
BgH11_FUf : DHRH-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 397
HpHaD_FUf : DYTH-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 411
CaHaD_FUf : DYTH-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 411
HpHaN_FUf : DHHH-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 408
CaHaN_FUf : DHHH-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 410
HpHb_FUf : EHDR-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 410
CaHb_FUf : EHDN-LGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 410
HtH1_FUf : DYHR-FNFK-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 415
KLH1_FUf : DSHR-FNFK-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 410
HtH2_FUf : DQHK-FGMD-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 414
KLH2_FUf : DSHK-FNFK-DNLEHGLTISELN-DLEK-RKEEDRV-ABFL-AGFGS-AMVTD-EDICL-EGE-ABAGTFAVLG-GAEMPAFDRLFKYDITQQ-KVFNK-NR-PP--DV-HFEVK-IVAVNCTE-DSG-LRPP-IVQVFPVK----- : 412