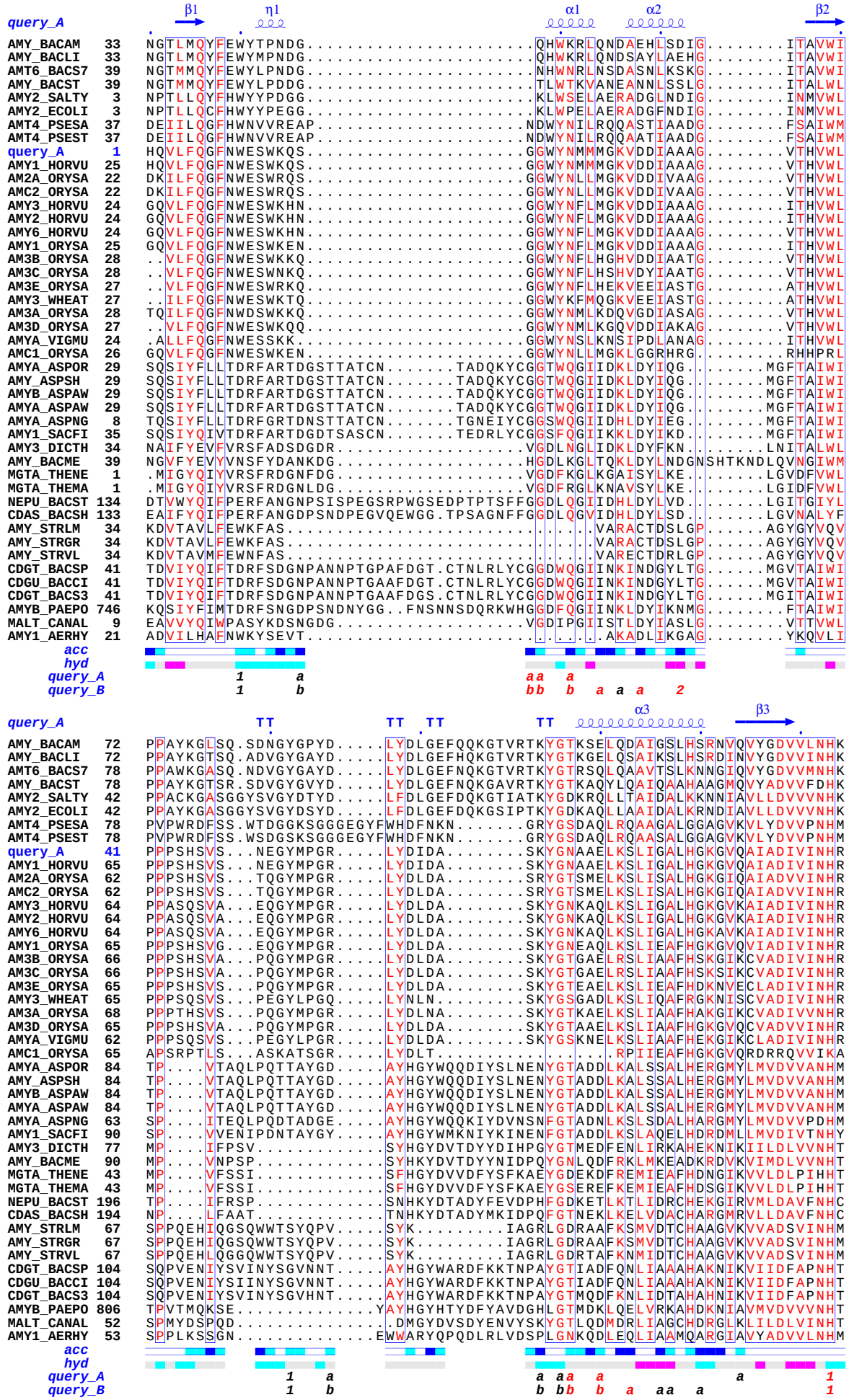
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η1
α1
α2
β2
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AMT6_BACS7 39
AMY_BACST 39
AMY2_SALTY 3
AMY2_ECOLI 3
AMT4_PSESA 37
AMT4_PSEST 37
query_A 1
AMY1_HORVU 25
AM2A_ORYSA 22
AMC2_ORYSA 22
AMY3_HORVU 24
AMY2_HORVU 24
AMY6_HORVU 24
AMY1_ORYSA 25
AM3B_ORYSA 28
AM3C_ORYSA 28
AM3E_ORYSA 27
AMY3_WHEAT 27
AM3A_ORYSA 28
AM3D_ORYSA 27
AMYA_VIGMU 24
AMC1_ORYSA 26
AMYA_ASPOR 29
AMY_ASPSH 29
AMYB_ASPAW 29
AMYA_ASPAW 29
AMYA_ASPNG 8
AMY1_SACFI 35
AMY3_DICTH 34
AMY_BACME 39
MGTA_THENE 1
MGTA_THEMA 1
NEPU_BACST 134
CDAS_BACSH 133
AMY_STRLM 34
AMY_STRGR 34
AMY_STRVL 34
CDGT_BACSP 41
CDGU_BACCI 41
CDGT_BACS3 41
AMYB_PAEPO 746
MALT_CANAL 9
AMY1_AERHY 21
acc
hyd
query_A
query_B
α3
β3
query_A
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AMY_BACLI 72
AMT6_BACS7 78
AMY_BACST 78
AMY2_SALTY 42
AMY2_ECOLI 42
AMT4_PSESA 78
AMT4_PSEST 78
query_A 41
AMY1_HORVU 65
AM2A_ORYSA 62
AMC2_ORYSA 62
AMY3_HORVU 64
AMY2_HORVU 64
AMY6_HORVU 64
AMY1_ORYSA 65
AM3B_ORYSA 66
AM3C_ORYSA 66
AM3E_ORYSA 65
AMY3_WHEAT 65
AM3A_ORYSA 68
AM3D_ORYSA 65
AMYA_VIGMU 62
AMC1_ORYSA 65
AMYA_ASPOR 84
AMY_ASPSH 84
AMYB_ASPAW 84
AMYA_ASPAW 84
AMYA_ASPNG 63
AMY1_SACFI 90
AMY3_DICTH 77
AMY_BACME 90
MGTA_THENE 43
MGTA_THEMA 43
NEPU_BACST 196
CDAS_BACSH 194
AMY_STRLM 67
AMY_STRGR 67
AMY_STRVL 67
CDGT_BACSP 104
CDGU_BACCI 104
CDGT_BACS3 104
AMYB_PAEPO 806
MALT_CANAL 52
AMY1_AERHY 53
acc
hyd
query_A
query_B

β4
β5
η2
query_A
T
T
TT
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AMY_BACLI 136 GGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLN.RIY
AMT6_BACS7 142 GGADATEMVRAVEVNPNNRNQEVTGEYTIEAWTRFDFPGRGNTHSSFKWRWYHFDGVDWDQSRRLNNRIY
AMY_BACST 142 GGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLS.RIY
AMY2_SALTY 107 MGADEKERIRVQRVNQDDRTQIDDNIIECEGWTRYTFPARAGQYSNFIWDYHCFSGIDHIENPDED.GIF
AMY2_ECOLI 107 MGADEKEAIRVQRVNADDRTQIDEEIIECEGWTRYTFPARAGQYSQFIWDFKCFSGIDHIENPDED.GIF
AMT4_PSESA 140 NRGYPDK.....EINLPAGQGFWRNDCADPGNYPNDCDDGDRFIGGES.....
AMT4_PSEST 140 NRGYPDK.....EINLPAGQGFWRNDCADPGNYPNDCDDGDRFIGGDA.....
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AMY1_HORVU 119 CADYKDS.....RGIYCIFEGGTSDGRLDWGPHMICRDDTKYSDGTAN.....
AM2A_ORYSA 116 CADYKDS.....RGIYCIFEGGTPDGRLDWGPHMICRDDTQFSDGTGN.....
AMC2_ORYSA 116 CADYKDS.....RGIYCIFEGGTPDGRLDWGPHMICRDDTQFSDGTGN.....
AMY3_HORVU 118 TAEHKDG.....RGIYCIFEGVTPDARLDWGPHMICRDDRPYADGTGN.....
AMY2_HORVU 118 TAEHKDG.....RGIYCIFEGGTPDARLDWGPHMICRDDRPYADGTGN.....
AMY6_HORVU 118 TAERKDG.....RGIYCIFEGGTPDARLDWGPHMICRDDRPYPDGTGNR....
AMY1_ORYSA 119 TAEHKDG.....RGIYCLFEGGTPDSRLDWGPHMICRDD.PYGDGTGN.....
AM3B_ORYSA 120 CADYKDS.....RGIYCIFEGGTPDSRLDWGPDMICSDDTQYSNGRGH.....
AM3C_ORYSA 120 CADYKDS.....RGIYCIFEGGTPDSRLDWGPDMICSDDTQYSNGRGH.....
AM3E_ORYSA 119 CADYKDS.....RGVYCVFEGGTPDGRLDWGPDMICSDDTQYSNGRGH.....
AMY3_WHEAT 118 CADKKDG.....RGVYCIFEGGTSDNRLDWGPDEICSDDTKYSNGRGH.....
AM3A_ORYSA 122 CADDKDG.....RGVYCIFKGGGPRGCLDWGPSMICCDDTQYSDGTGH.....
AM3D_ORYSA 119 CAEKKDA.....RGVYCVFEGGTPD.RLDWGPGMICSDDTQYSDGTGH.....
AMYA_VIGMU 116 TAERKDG.....RGIYCIFEGGTPDSRQDWGPSFICRDDTAYSDGTGN.....
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AMYA_ASPOR 145 GYDGAGS.....SVDYSVFKPFSSQDYFHPFCFIQN.....
AMY_ASPSH 145 GYDGAGS.....SVDYSVFKPFSSQDYFHPFCFIQN.....
AMYB_ASPAW 145 GYDGAGS.....SVDYSVFKPFSSQDYFHPFCFIQN.....
AMYA_ASPAW 145 GYDGAGS.....SVDYSVFKPFSSQDYFHPFCFIQN.....
AMYA_ASPNG 124 GYAGNGN.....DVDYSVFDPFDSSSYFHPYCLITD.....
AMY1_SACFI 151 GSDGSGD.....SIDYSEYTPFNDQKYFHNYCLISN.....
AMY3_DICTH 130 SSRHPWF.....VSSASSY.NSPYRDYYIWSTEKPEKNSN.....
AMY_BACME 143 SSEHPWF.....QAALKDK.NSKYRDYYIWADKNTDLNEKGSW.G.....
MGTA_THENE 96 GFLHTWF.....QKALKG..DPHYRDYYVWASEKTDLDERREWDN.....
MGTA_THEMA 96 GFLHTWF.....QKALKG..DPHYRDYYVWANKETDLDERREWDG.....
NEPU_BACST 249 GYEFAPF.....QDVWKNGESSKYKDWFHIHEFP.....
CDAS_BACSH 247 GHTFPPF.....VDVLNNGLNSRYADWFHVREWP.....
AMY_STRLM 123 AAGSGTG.....TGGSAYQKYDYPGIWSGADMDDCRSEIN.....
AMY_STRGR 123 AAGSGTG.....TGGSAYQKYDYPGIWSGADMDDCRSEIN.....
AMY_STRVL 123 ANGSGTG.....TGGTSFSKYDYPGLYSGSDMDDCRATIS.....
CDGT_BACSP 169 SPASLDQ.....PSFAENGKLYNNGRDEGGYTNDTHNLFH.....
CDGU_BACCI 169 SPASSDQ.....PSFAENGRLYDNGTLLGGYTNDTQNLFH.....
CDGT_BACS3 169 SPASSDD.....PSFAENGRLYDNGNLLGGYTNDTQNLFH.....
AMYB_PAEPO 862 GDFQPGN.....GFAKAPFDKADWYHHNGDITDGDYN.....
MALT_CANAL 106 SVEHKWFK.....ESRSSKDNPKRDWYIWKPPRIDSNGNKHPPNN...W
AMY1_AERHY 109 ANESWKRND.....LNYPGTELLGQYAANPDYYSRQRLFGDLGQNLLSASDFHPE
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query_A
query_B
α4
β6
η3
query_A
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AMY_BACLI 205 KFQG....KAWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANE.LQLDGFRLDAVKHIKFS.
AMT6_BACS7 212 KFRGH..GKAWDWEVDTENGNYDYLMYADIDMDHPEVVNELRNWGVWYTNT.LGLDGFRIDAVKHIKYS.
AMY_BACST 211 KFRGI..GKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKSWGKWYVNT.TNIDGFRLDAVKHIKFS.
AMY2_SALTY 176 KIVNDYTGDGWNDQVDDEMGNFDYLMGENIDFRNHAVTEEIKYWARWVMEQ.THCDGFRLDAVKHIPAW.
AMY2_ECOLI 176 KIVNDYTGEGWNDQVDDELGNFDYLMGENIDFRNHAVTEEIKYWARWVMEQ.TQCDGFRLDAVKHIPAW.
AMT4_PSESA 183 .....DLNTGHPQIYGMFRDELANLRSG.YGAGGFRFDFVRGYAPE.
AMT4_PSEST 183 .....DLNTGHPQVYGMFRDEFTNLRSQ.YGAGGFRFDFVRGYAPE.
query_A 138 .....LDTGADFAAAPDIDHLNDRVQRELKEWLLWLKSD.LGFDAWRLDFARGYSPE.
AMY1_HORVU 162 .....LDTGADFAAAPDIDHLNDRVQRELKEWLLWLKSD.LGFDAWRLDFARGYSPE.
AM2A_ORYSA 159 .....LDTGADFAAAPDIDHLNGVVQRELTDWLLWLKSDEVGFDAWRLDFARGYSPE.
AMC2_ORYSA 159 .....LDTGADFAAAPDIDHLNGVVQRELTDWLLWLKSDEVGFDAWRLDFARGYSPE.
AMY3_HORVU 161 .....PDTGADFGAAPDIDHLNLRVQKELAEWLNWLKAD.IGFDGWRFDFAKGYSAD.
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AMY6_HORVU 162 .....PTRTRADFGAAPDIDHLNPRVQKELVEWLNWLRTD.DGFDGWRFDFAKGYSAD.
AMY1_ORYSA 161 .....PDTGADFAAAPDIDHLNKRVQRELIGWLDWLKMD.IGFDAWRLDFAKGYSAD.
AM3B_ORYSA 163 .....RDTGADFGAAPDIDHLNTRVQTELSDWLNWLKSD.VGFDGWRLDFAKGYSAA.
AM3C_ORYSA 163 .....RDTGADFGAAPDIDHLNTRVQTELSDWLNWLKSD.VGFDGWRLDFAKGYSAT.
AM3E_ORYSA 162 .....RDTGAGFGAAPDIDHLNPRVQRELTDWLNWLRTD.LGFDGWRLDFAKGYSAP.
AMY3_WHEAT 161 .....RDTGGGFDAAPDIDHLNPRVQRELSAWLNWLKTD.LGFDGWRLDFAKGYSAA.
AM3A_ORYSA 165 .....RDTGADFAAAPDIDHLNPLVQRELSDWLRWLRRD.VGFDGWRLDFAKGYSAA.
AM3D_ORYSA 161 .....RDTGEGFGAAPDIDHLNPRVQRELTDWLNWLKSD.VGFDGWRLDFAKGYSTD.
AMYA_VIGMU 159 .....NDSGEGYDAAPDIDHLNPQVQRELSEWMNWLKTE.IGFDGWRFDFVKGYAPS.
AMC1_ORYSA 152 .....QQARPRSSSAGSTGSRWTSAS.....TRGLDFAKATPPT.
AMYA_ASPOR 176 .....YEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYS.IDGLRIDTVKHVQK..
AMY_ASPSH 176 .....YEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYS.IDGLRIDTVKHVQK..
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AMYA_ASPAW 176 .....YEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYS.IDGLRIDTVKHVQK..
AMYA_ASPNG 155 .....WDNLTMVEDCWEGDTIVSLPDLDTTETAVRTIWYDWVADLVSNYS.VDGLRIDSVLEVQP..
AMY1_SACFI 182 .....YDDQAQVQSCWEGDSSVALPDLRTEDSDVASVFNSWVKDFVGNYS.IDGLRIDSAKHVDQ..
AMY3_DICTH 164 .....LWYKKPTG.YYYALFWSEMPDLNFDNPKVREEVKKIAKFWIEKG..VDGFRLDAAKHIYDDD
AMY_BACME 181 .....QQVWHKAPNGEYFYGTFWEGMPDLNYDNPEVRKEMINVGKFWLKQG..VDGFRLDAALHIFKGQ
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MGTA_THEMA 134 .....EKIWHPLEDGRFYRGLFGPFSPDLNYDNPQVFDEMKRLVLHLLDMG..VDGFRFDAAKHMRDTI
NEPU_BACST 278 .....LQTEP.RPNYDTFRFVPQMPKLNTANPEVKRYLLDVATYWIREFD.IDGWRLDVANEID...
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AMY_STRGR 158 .....DYG..NRANVQN...CELVGLADLDTGEPYVRDRIAAYLNDLLLLG..VDGFRIDAAKHMPAA.
AMY_STRVL 158 .....NYQ..DRANVQN...CELVQLPDLDTGEDHVRGKIAGYLNDLASLG..VDGFRIDAAKHMPAA.
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CDGU_BACCI 204 .....HNGGTDFSTTENGIYKNLYDLADLNHNNSTVDVYLKDAIKMWLDLG..IDGIRMDAVKHMPFG.
CDGT_BACS3 204 .....HYGGTDFSTIENGIYKNLYDLADLNHNNSSVDVYLKDAIKMWLDLG..VDGIRVDAVKHMPFG.
AMYB_PAEPO 894 .....SNNQWKIENGDVAGLDDLNHENPATANELKNWIKWLLNETG.IDGLRLDTVKHVPKG.
MALT_CANAL 147 GSYFSGSAWKYDELTGEYYLHLFAESQPDLNWENKECREAIYNSAIKFWLDKG.VDGFRIDTAGMYSKYQ
AMY1_AERHY 159 G....CITDWSDPGHVQYWRLCGGAGDKGLPDLDPNNWVVSQQQAYLKALKGMGIKGFRVDAVKHMSDY.
acc
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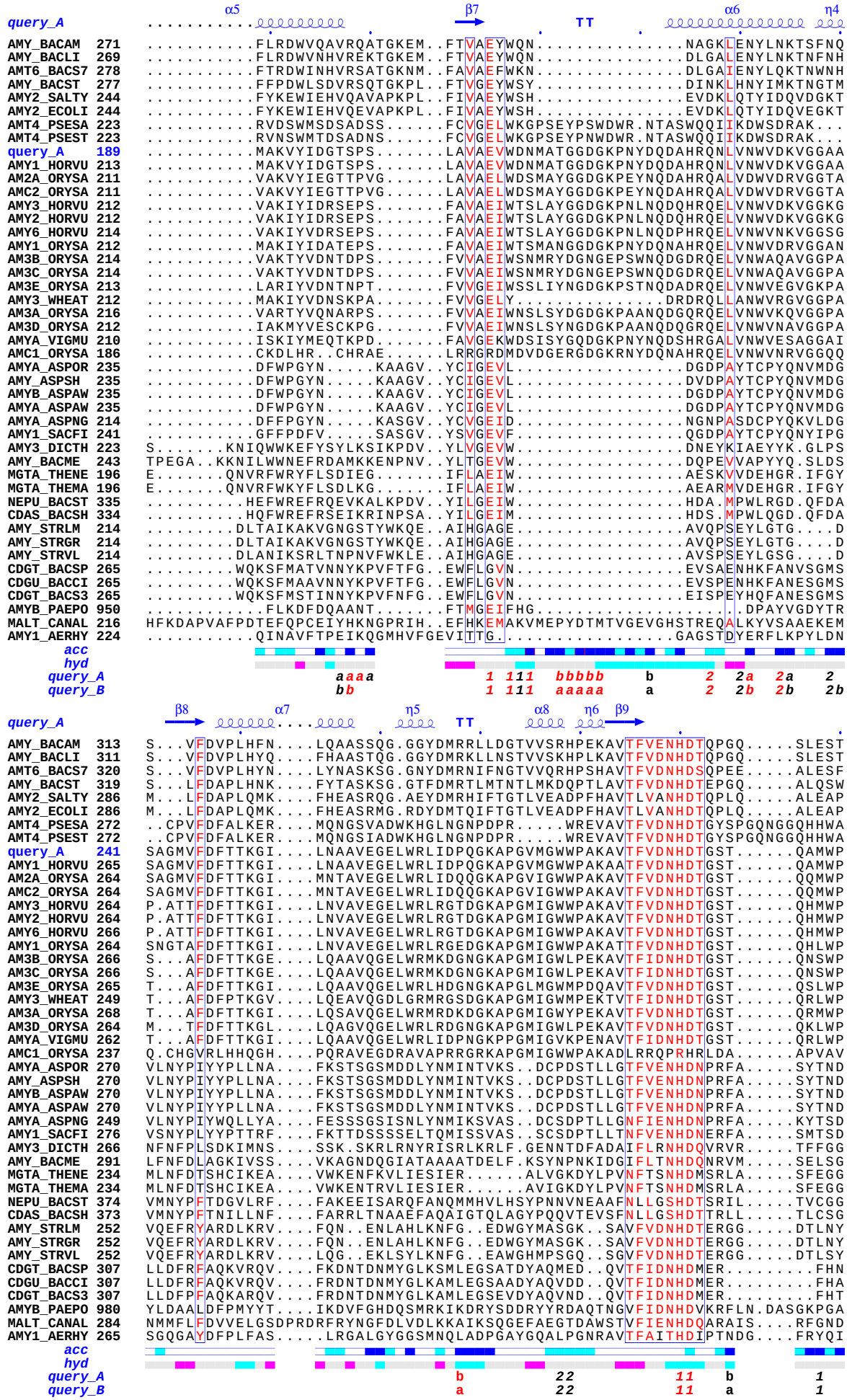
query_A
query_B


α5
β7
α6
η4
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AMY_BACLI 269
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AMY2_SALTY 244
AMY2_ECOLI 244
AMT4_PSESA 223
AMT4_PSEST 223
query_A 189
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AM2A_ORYSA 211
AMC2_ORYSA 211
AMY3_HORVU 212
AMY2_HORVU 212
AMY6_HORVU 214
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AM3B_ORYSA 214
AM3C_ORYSA 214
AM3E_ORYSA 213
AMY3_WHEAT 212
AM3A_ORYSA 216
AM3D_ORYSA 212
AMYA_VIGMU 210
AMC1_ORYSA 186
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AMY_ASPSH 235
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AMYA_ASPNG 214
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AMY3_DICTH 223
AMY_BACME 243
MGTA_THENE 196
MGTA_THEMA 196
NEPU_BACST 335
CDAS_BACSH 334
AMY_STRLM 214
AMY_STRGR 214
AMY_STRVL 214
CDGT_BACSP 265
CDGU_BACCI 265
CDGT_BACS3 265
AMYB_PAEPO 950
MALT_CANAL 216
AMY1_AERHY 224
acc
hyd
query_A
query_B
β8
α7
η5
TT
α8
η6
β9
query_A
AMY_BACAM 313
AMY_BACLI 311
AMT6_BACS7 320
AMY_BACST 319
AMY2_SALTY 286
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AMT4_PSESA 272
AMT4_PSEST 272
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AMY2_HORVU 264
AMY6_HORVU 266
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AM3B_ORYSA 266
AM3C_ORYSA 266
AM3E_ORYSA 265
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AMYA_VIGMU 262
AMC1_ORYSA 237
AMYA_ASPOR 270
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AMY1_SACFI 276
AMY3_DICTH 266
AMY_BACME 291
MGTA_THENE 234
MGTA_THEMA 234
NEPU_BACST 374
CDAS_BACSH 373
AMY_STRLM 252
AMY_STRGR 252
AMY_STRVL 252
CDGT_BACSP 307
CDGU_BACCI 307
CDGT_BACS3 307
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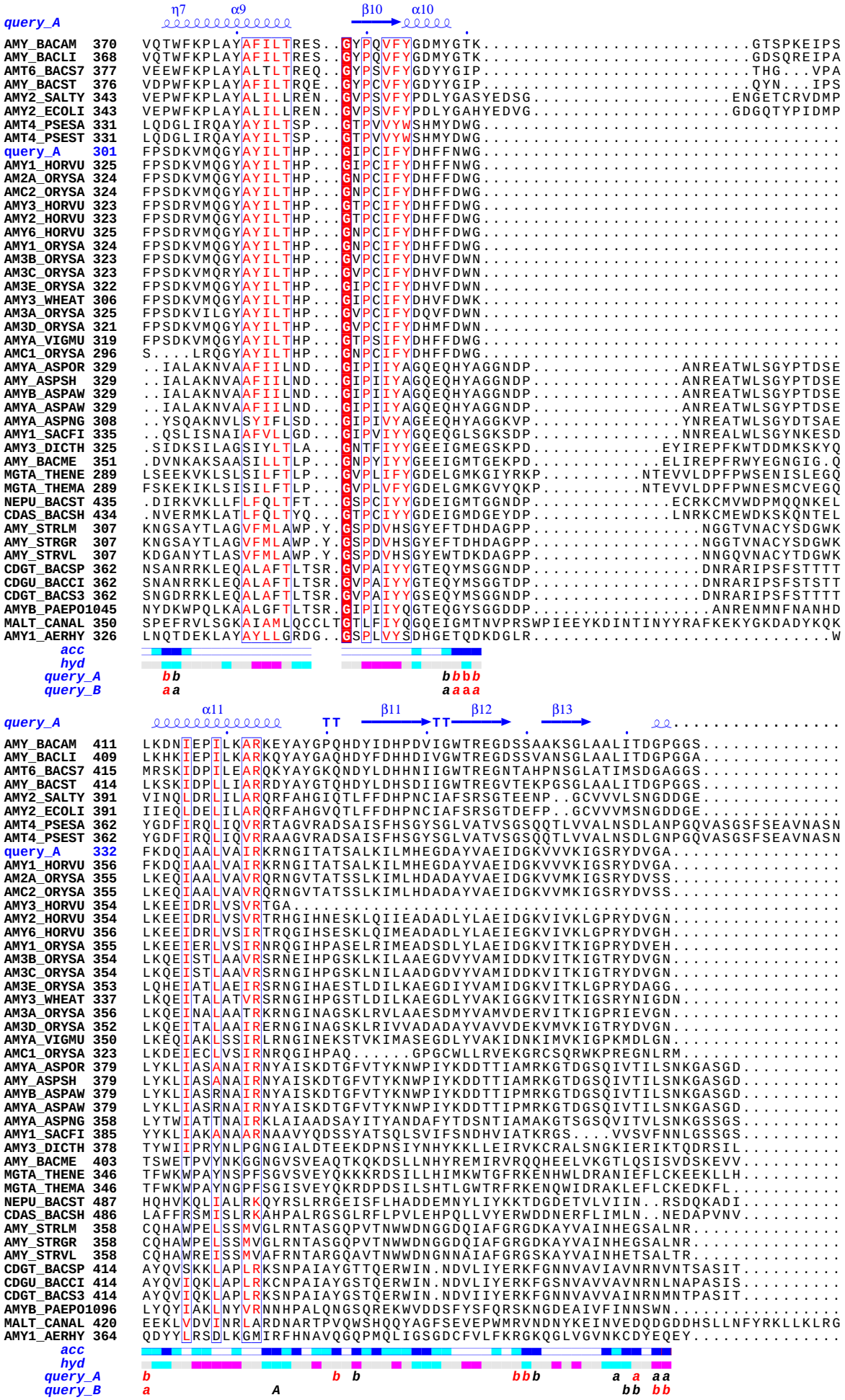
MALT_CANAL 284
AMY1_AERHY 265
acc
hyd
query_A
query_B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AMT6_BACS7 377 VEEWFKPLAYALTLTREQ..GYPSVFYGDYYGIP.....THG...VPA
AMY_BACST 376 VDPWFKPLAYAFILTRQE..GYPCVFYGDYYGIP.....QYN...IPS
AMY2_SALTY 343 VEPWFKPLAYALILLREN..GVPSVFYPDLYGASYEDSG.....ENGETCRVDMP
AMY2_ECOLI 343 VEPWFKPLAYALILLREN..GVPSVFYPDLYGAHYEDVG.....GDGQTYPIDMP
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AMY1_HORVU 325 FPSDKVMQGYAYILTHP...GIPCIFYDHFFNWG.....
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AMC2_ORYSA 324 FPSDKVMQGYAYILTHP...GNPCIFYDHFFDWG.....
AMY3_HORVU 323 FPSDRVMQGYAYILTHP...GTPCIFYDHFFDWG.....
AMY2_HORVU 323 FPSDRVMQGYAYILTHP...GTPCIFYDHFFDWG.....
AMY6_HORVU 325 FPSDRVMQGYAYILTHP...GNPCIFYDHFFDWG.....
AMY1_ORYSA 324 FPSDKVMQGYAYILTHP...GNPCIFYDHFFDWG.....
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AM3C_ORYSA 323 FPSDKVMQRYAYILTHP...GVPCIFYDHVFDWN.....
AM3E_ORYSA 322 FPSDKVMQGYAYILTHP...GIPCIFYDHVFDWN.....
AMY3_WHEAT 306 FPSDKVMQGYAYILTHP...GIPCIFYDHVFDWK.....
AM3A_ORYSA 325 FPSDKVILGYAYILTHP...GVPCIFYDQVFDWN.....
AM3D_ORYSA 321 FPSDKVMQGYAYILTHP...GVPCIFYDHMFDWN.....
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AMC1_ORYSA 296 S....LRQGYAYILTHP...GNPCIFYDHFFDWG.....
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AMYB_ASPAW 329 ..IALAKNVAAFIILND...GIPIIYAGQEQHYAGGNDP.....ANREATWLSGYPTDSE
AMYA_ASPAW 329 ..IALAKNVAAFIILND...GIPIIYAGQEQHYAGGNDP.....ANREATWLSGYPTDSE
AMYA_ASPNG 308 ..YSQAKNVLSYIFLSD...GIPIVYAGEEQHYAGGKVP.....YNREATWLSGYDTSAE
AMY1_SACFI 335 ..QSLISNAIAFVLLGD...GIPVIYYGQEQGLSGKSDP.....NNREALWLSGYNKESD
AMY3_DICTH 325 .SIDKSILAGSIYLTLA...GNTFIYYGEEIGMEGSKPD.....EYIREPFKWTDDMKSKYQ
AMY_BACME 351 .DVNKAKSAASILLTLP...GNPYIYYGEEIGMTGEKPD.....ELIREPFRWYEGNGIG.Q
MGTA_THENE 289 LSEEKVKLSLSIILFTLP...GVPLIFYGDELGMKGIYRKP.....NTEVVLDPFPWSENISLEGQ
MGTA_THEMA 289 FSKEKIKLSISILFTLP...GVPLVFYGDELGMKGVYQKP.....NTEVVLDPFPWNESMCVEGQ
NEPU_BACST 435 .DIRKVKLLFLFQLTFT...GSPCIYYGDEIGMTGGNDP.....ECRKCMVWDPMQQNKEL
CDAS_BACSH 434 .NVERMKLATLFQLTYQ...GTPCIYYGDEIGMDGEYDP.....LNRKCMEWDKSKQNTEL
AMY_STRLM 307 KNGSAYTLAGVFMLAWP.Y.GSPDVHSGYEFTDHDAGPP.....NGGTVNACYSDGWK
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CDGU_BACCI 362 SNANRRKLEQALAFTLTSR.GVPAIYYGTEQYMSGGTDP.....DNRARIPSFSTSTT
CDGT_BACS3 362 SNGDRRKLEQALAFTLTSR.GVPAIYYGSEQYMSGGNDP.....DNRARIPSFSTTTT
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hyd
query_A bb bbbb
query_B aa aaaa
α11 TT β11 TT β12 β13
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AMY_BACLI 409 LKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGA.....
AMT6_BACS7 415 MRSKIDPILEARQKYAYGKQNDYLDHHNIIGWTREGNTAHPNSGLATIMSDGAGGS.....
AMY_BACST 414 LKSKIDPLLILARRDYAYGTQHDYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGS.....
AMY2_SALTY 391 VINQLDRLILARQRFAHGIQTLFFDHPNCIAFSRSGTEENP..GCVVVLSNGDDGE.....
AMY2_ECOLI 391 IIEQLDELILARQRFAHGVQTLFFDHPNCIAFSRSGTDEFP..GCVVVMSNGDDGE.....
AMT4_PSESA 362 YGDFIRQLIQVRRTAGVRADSAISFHSGYSGLVATVSGSQQTLVVALNSDLANPGQVASGSFSEAVNASN
AMT4_PSEST 362 YGDFIRQLIQVRRAAGVRADSAISFHSGYSGLVATVSGSQQTLVVALNSDLGNPGQVASGSFSEAVNASN
query_A 332 FKDQIAALVAIRKRNGITATSALKILMHEGDAYVAEIDGKVVVKIGSRYDVGA.....
AMY1_HORVU 356 FKDQIAALVAIRKRNGITATSALKILMHEGDAYVAEIDGKVVVKIGSRYDVGA.....
AM2A_ORYSA 355 LKEQIAALVAVRQRNGVTATSSLKIMLHDADAYVAEIDGKVVMKIGSRYDVSS.....
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AMY3_WHEAT 337 LKQEITALATVRSRNGIHPGSTLDILKAEGDLYVAKIGGKVITKIGSRYNIGDN.....
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AM3D_ORYSA 352 LKQEITALAAIRERNGINAGSKLRIVVADADAYVAVVDEKVMVKIGTRYDVGN.....
AMYA_VIGMU 350 LKEQIAKLSSIRLRNGINEKSTVKIMASEGDLYVAKIDNKIMVKIGPKMDLGN.....
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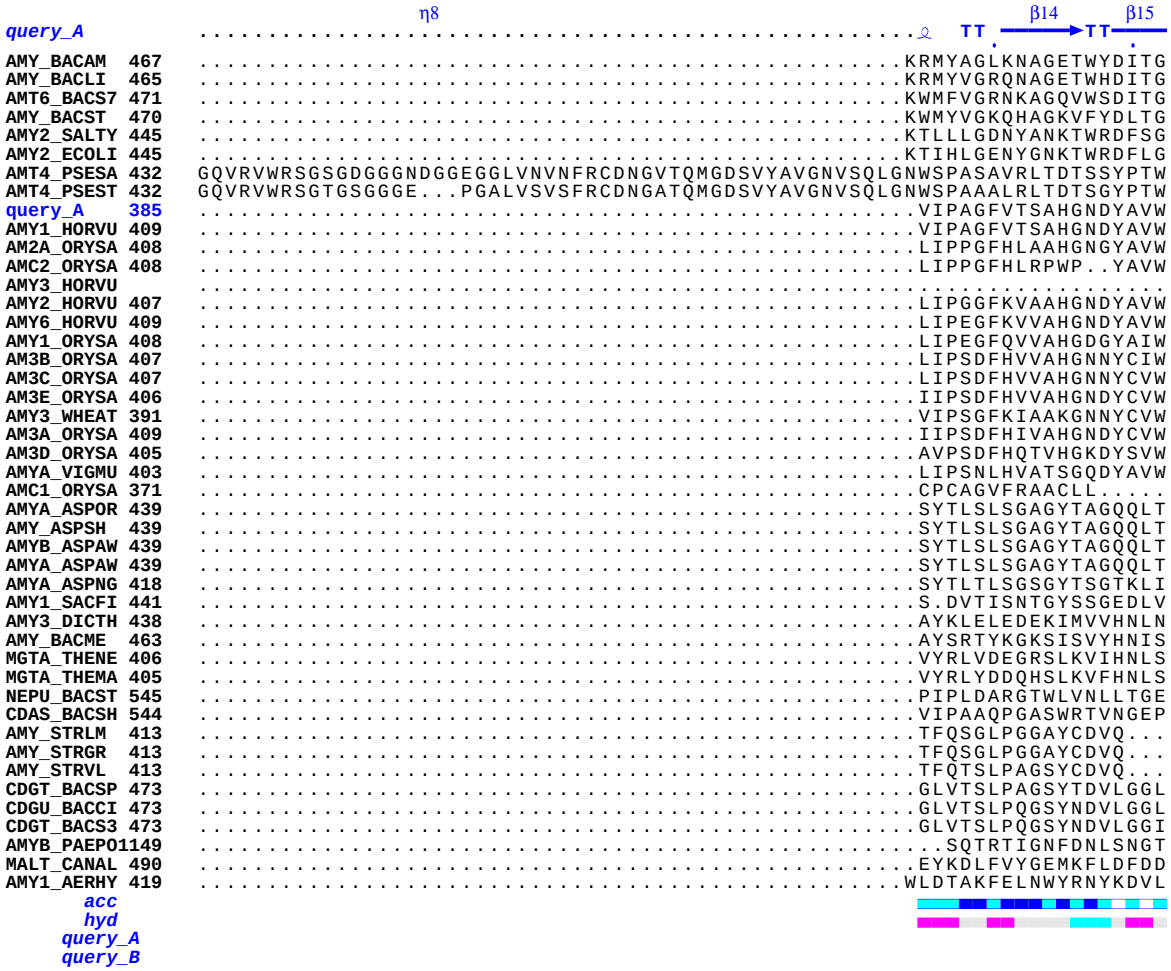
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