DBD

```
ARF17        MSPPSATAGDINHREVDPTIWRACAGASVQIPVLHSRVYYFPQGHVEHCCP------LLSTLPSSTSP--VPCIITSIQLLADPVTDEVFAHLILQ  88
ARF10        ME--QEKSLDPQLWHACAGSMVQIPSLNSTVFYFAQGHTEHAH-------APPDFHAPRVPPLILCRVVSVKFLADAETDEVFAKITLL         80
ARF16        MINVMNPMKGGTEKGLDPQLWHACAGGMVRMPPMNSKVFYFPQGHAENAY-------DCVDFGNLPIPPMVLCRVLAIKYMADAESDEVFAKLRLI   89
Os ARF10     MITFVDSAAKERERESDKCLDPQLWHACAGGMVQMPPVSSKVYYFPQGHAEHAQGHG----PVEFPGGRVPALVLCRVAGVRFMADPDTDEVFAKIRLV 95
Os NP_922010 MKEVGEVEEVRCLDPQLWHACAGGMVQMPAPRSRVYYFAQGHAEHADGGGGAAAAAAELGPRALPPLVLCRVEGVQFLADRDSDEVYAKIRLA    93
Os XP_466861 MITFADLAEPAPG-AERCVDRQLWLACAGGMCTVPPVGAAVYYFPQGHAEHALGL-----AAPELSAARVPALVPCRVASVRYMADPDTDEVFARIRLV 93
Os XP_473206 MELAGPTEGDGGGSVDSQLWAACAGSMSSVPPVGAAVYYFPQGHAEQAS------AAVDLSSARVPPLVPCRVAVRFMADAESDEVFAKIRLV    88

ARF17        PMTQQQFTP---TNYSRFGRFDGDVDDNNKVT---TFAKILTPSDANNGGGFSVPRFCADSVFPLLNFQIDPPVQKLYVTDIHGAVWDFRHIYRGTPRRH 182
ARF10        PLPGNDLDLENDAVLGLTPPSSDGNGNGKEKP--ASFAKTLTQSDANNGGGFSVPRYCAETIFPRLDYSAEPPVQTVIAKDIHGETWKFRHIYRGTPRRH 178
ARF16        PLK-DDEYVDHEYGDGED---SNGFESNSEKT--PSFAKTLTQSDANNGGGFSVPRYCAETIFPRLDYNAEPPVQTILAKDVHGDVWKFRHIYRGTPRRH 183
Os ARF10     PVRANEQGYAG-DADDGIGAAAAAAAQE-EKP--ASFAKTLTQSDANNGGGFSVPRYCAETIFPRLDYSADPPVQTVLAKDVHGVVWKFRHIYRGTPRRH 191
Os NP_922010 PVAPGEAEFREPDELCPLGAAGDAAEPSPEKP--TSFAKTLTQSDANNGGGFSVPRFCAETIFPKLDYRADPPVQTVLAKDVHGVVWKFRHIYRGTPRRH 191
Os XP_466861 PLRAAEDG------DVEEDGAAAG---EEHEKP--ASFAKTLTQSDANNGGGFSVPRYCAETIFPRLDYAADPPVQTVVAKDVHGVAWNFRHIYRGTPRRH 183
Os XP_473206 PLRPGDAVV----DVGEAAAAEARREEENSRPRPTSFAKTLTQSDANNGGGFSVPRFCAETIFPELDYSSEPPVQSVCAKDVHGVEWTFRHIYRGTPRRH 184

ARF17        LLTTGWSKFVNSKKLIAGDSVVFMRKSADEMFIGVRRTPISSSD--GGSSYYGG----DEYNGYYS----QSSVAK-EDDGS-------PKKTFRRS--- 261
ARF10        LLTTGWSTFVNQKKLIAGDSIVFLRSESGDLCVGIRRAKRGGLG--SN---AGS------DNPYP-----GFSGFLRDDESTTTTSKLMMMKRNGNNDGNA 263
ARF16        LLTTGWSNFVNQKKLVAGDSIVFMRAENGDLCVGIRRAKRGGIG--NGPEYSAG-----WNPIGGS--CGYSSLLREDESNS-------LRRS--NCSLA  265
Os ARF10     LLTTGWSTFVNQKKLVAGDSIVFMRTENGDLCVGIRRAKKGGVG---GPEFLPPPPPPPTPAAGGNYGGFSMFLRGDDDGN-------KMAAAARG---  278
Os NP_922010 LLTTGWSTFVNQKKLVAGDSIVFLRTRHGELCVGIRRAKMACG----GMECMSG-----WNAPGYGG--GGFSAFLK-EEESK-------LMKGHGGGGYM 274
Os XP_466861 LLTTGWSTFVNQKKLVAGDSIVFLRGDGGDLHVGIRRAKRGFCGGGGGAEEAS-------LPGWDQ----YGGLMR--GNAS-------PCAAAK-----  258
Os XP_473206 LLTTGWSPFVNKKQLTAGDSIVFMRDEGGNIHVGLRRAKRGFCSIGGDDESLSS------IPGWDQ----YRGLMR--RNAT-------ATATGGRT---  262

ARF17        -GNGKLTAEAVTDAINRASQGLPFEVVFYPAAGWSEFVVRAEDVESSMSMYWTPGTRVKMAMETEDSSRITWFQGIVSSTYQETG-PWRGSPWKQLQITW 359
ARF10        AATGRVRVEAVAEAVARAACGQAFEVVYYPRASTPEFCVKAADVRSAMRIRWCSGMRFKMAFETEDSSRISWFMGTVSAVQVADPIRWPNSPWRLLQVAW 363
ARF16        DRKGKVTAESVIEAATLAISGRPFEVVYYPRASTSEFCVKALDARAAMRIPWCSGMRFKMAFETEDSSRISWFMGTVSAVNVSDPIRWPNSPWRLLQVAW 365
Os ARF10     KVRARVRPEEVVEAANLAVSGQPFEVVYYPRASTPEFCVKAGAVRAAMRTQWFAGMRFKMAFETEDSSRISWFMGTVSAVQVADPIRWPNSPWRLLQVSW 378
Os NP_922010 GKGKGKVRMADVVEAASLASSGQPFEVAYYPRASTPDFVVKAASVQAAMRIQWCSGMRFKMAFETEDSSRISWFMGTISSVQVADPNRWPNSPWRLLQVTW 374
Os XP_466861 -GRGKVRAEDLVEAARLANGGQPFEVVYYPRASTPEFCVRAAAVRAAMRVQWCPGMRFKMAFETEDSSRISWFMGTVASVQVADPIRWPQSPWRLLQVTW 357
Os XP_473206 PPKGKVPPENVLTAATRATTGQPFEVLYYPRASTPEFCVRAAAVRTAMAVQWCPGMRFKMAFETEDSSRISWFMGTVAGVQASDPVRWPQSPWRLLQVTW 362
```

miR160

```
ARF17        DEPEILQNVKRVNPWQVEIAAHATQLHT-PFPP-AKRLKYPQPGGGFLSGDDGE--IL-YPQSGLSSAAAPD-----PSPSMFSYSTFPAGMQGARQ---  446
ARF10        DEPDLLQNVKRVSPWLVELVSNMPTIHLSPFSP-RKKIRIPQPFEFPFHGTKFPIFSPGFANNGGGESMC-------YLSNDNNNAP--AGIQGARQ-AQ  452
ARF16        DEPDLLQNVKRVNPWLVELVSNVHPIPLTSFSPPRKKMRLPQHPDYNNLINSIPVES--FPSNP-LIRSS-------PLSSVLDNVP--VGLQGARHNAH  453
Os ARF10     DEPDLLQNVKRVSPWLVELVSNMPAIHLAPFSPPRKKLCVPLYPELPIDGQFPT-PM--FHGNPLARGVG-------PMCYFPDGTP--AGIQGARH---  463
Os NP_922010 DEPDLLQNVKCVSPWLVELVSSIPPIHLGPFSSPRKKLRVPPHPDFPFEGHLLN-PI--FHGNPLGPSNS-------PLCCYPDTAP--AGIQGARH---  459
Os XP_466861 DEPDLLQNVKRVSPWLVELVSSMPAINLSSFSPPRKKPRILAYPEFPFEGQLLN-PA--FPNPLAHGHHHYHHNHPSFFPFPDVSAP-AGIQGARH---   450
Os XP_473206 DEPELLQNVKRVCPWLVELVSSMPNLHLPSFSPPRKKPRNPPYAELPLEGQIFTGPV--FPNPMAHDHHHHHG--FPFLPFPDSSAQPAGIQGARH---  455

ARF17        YDFG---------------------------------SFNP------TGFIGGNP----------------------------P--QLFTNNFL        471
ARF10        QLFGSPSPSLLSDLNLSSYTGNNKLHSP------AMFLSSFNPR----HHHYQARDSENSNNISCSLTMG--NPAMVQDKKKSVGSVKTHQFVLFGQPIL 540
ARF16        QYYG------LSSSDLHHYYLNRPPPPP------PPSSLQLSP-----SLGLRNIDTKNEKGF-CFLTMG---TTPCNDTKSK------KSHIVLFGKLIL 527
Os ARF10     AQFGIS----LSDLHLNKLQS-SLSPHG------FHQLDHGMQP----RIAAGLIIGHPAARDDISCLLTIGSPQNNKKSDGKKA-----PAQLMLFGKPIL 545
Os NP_922010 AQFGLP----LTDHQLNKLHL-GLLHSGS-----FNRLDAITPPS--RISKGFVVSSAPAHDNISCLLSISTPQVAEKSDDRKT-----TPHIMLFGKAIF 543
Os XP_466861 AQFGPS----LSDLHLTHLQS-SLMYPGLRRP--DHVGPTSIPP-PRISTDLTMGSS----PPARALSMG-----AKKPDDAK------PPGLMLFGQRIL 528
Os XP_473206 AQFASP----FPEFHIGNLQPNLMLYAGIRLPPADRAAPAPRPPRIIISTDLTIGSPGKPDDAACSPSSG-----GKKIDDTK------PRGFLLFGQAIL 541
```

III

```
ARF17        SPLPD-LG-----------------------------KVSTEMMNFGSPPSDNLSPN----------SNTTNLSSG-------NDLVGNRGPLSKKVNSI 524
ARF10        TEQQVMNR-----------------------KRFLEEEAEAE---EEKGLVARGLTWN----------YSLQGLETGHCKVFMESEDVGRTLDLSVIGSYQ 605
ARF16        PEEQLSEKGST-----------------DTANIEKTQISSGGSNQNGVAGREFSSSDEGSPCSKKVHDASGLETGHCKVFMESDDVGRTLDLSVLGSYE  609
Os ARF10     TEQQISLGDAASVDVKKS----SSDGNAENTVNKSNSDVSSPRSNQNGT-TDNLSCGGVP-LCQDNKVLDVGLETGHCKVFMQSEDVGRTLDLSVVGSYE 639
Os NP_922010 TEQQITSSGST--ET-------LSPGVTGNSSPNGNAHKTGNASDGSGS-SICIGFS-----SQGHEASDLGLEAGHCKVFMESEDVGRTIDLSVFGSYE 628
Os XP_466861 TERQMSLSGTTSPAATGNSSLNWNTEKG--ASEGSGSGVIQNSPTDNTS-SERLQWFRE---N--STVSELGLEPGQCKVFIESDTVGRNLDLSSLASFE 620
Os XP_473206 TEEQIKNGNSDGRPASPN----WDAEKAPNTSEGSDSGVTQGSPTKNTTPSWSLPYFGG---NNISRASEYELNPGQCKVFVESETVGRSLDLSALSSFE 634
```

III   IV

```
ARF17        QLFGKIITVEEHSESGPAESGLCEEDGSKESSDNETQLSLSHAPPSVPKHSNSNAGSSSQG                                   585
ARF10        ELYRKLAEMFHIEERSDLLTHVVYRDANGVIKRIGDEPFSDFMKATKRLTIKMDIGGDNVRKTWITGIRTGENGIDASTKTGPLSIFA       693
ARF16        ELSRKLSDMFGIK-KSEMLSSVLYRDASGAIKYAGNEPFSEFLKTARRLTILTEQGSESVVV                                 670
Os ARF10     ELYRRLADMFGIE-KAELMSHVFYRDAAGALKHTGDEPFSEFTKTARRLNILTDTSGDNLAR                                 700
Os NP_922010 ELYGRLADMFGIE-KEEIINHLHFRDAAGVVKHPGEVPFSDFMKAARRLTIIAGDR-ERIERPLIECLVEQA                       698
Os XP_466861 QLYGRLSEMFCID-SAELRSRVLYRGATGEVRHAGDEPFSEFIKLARRLTILTDAGSDNLGS                                 681
Os XP_473206 ELYACLSDMFSIG-SDELRSHLVYRSPAGEVKHAGDEPFCAFVKSARKLRILTDAGSDNLGD                                 695
```