

SEQUENCES OF THE HUMAN ARF FAMILY MEMBERS

(Sequences shown in red are those for which we conclude that errors were made in the determination of intron/exon boundaries in the public databases, and so our predicted protein sequences are shown)

>ARF1 (181AA)

MGNIFANLFK GLFGKKEMRI LMVGLDAAGK TTILYKCLKG EIVTTIPTIG FNVETVEYKN
ISFTVWDVGG QDKIRPLWRH YFQNTQGLIF VVDSNDRERV NEAREELMRM LAEDELDAV
LLVFANKQDL PNAMNAEIT DKLGLHSLRH RNWYIQATCA TSGDGLYEGL DWLSNQLRNQ
K

>ARF3 (181AA)

MGNIFGNLLK SLIGKKEMRI LMVGLDAAGK TTILYKCLKG EIVTTIPTIG FNVETVEYKN
ISFTVWDVGG QDKIRPLWRH YFQNTQGLIF VVDSNDRERV NEAREELMRM LAEDELDAV
LLVFANKQDL PNAMNAEIT DKLGLHSLRH RNWYIQATCA TSGDGLYEGL DWLANQLKNK
K

>ARF4 (180AA)

MGLTISSLFS RLFGKKQMRI LMVGLDAAGK TTILYKCLKG EIVTTIPTIG FNVETVEYKN
ICFTVWDVGG QDRIRPLWKH YFQNTQGLIF VVDSNDRERI QEVADELQKM LLVDELDAV
LLLAFANKQDL PNAMAISEMT DKLGLQLSRN RTWYVQATCA TQGTGLYEGL DWLSNELSKR

>ARF5 (180AA)

MGLTVSALFS RIFGKKQMRI LMVGLDAAGK TTILYKCLKG EIVTTIPTIG FNVETVEYKN
ICFTVWDVGG QDKIRPLWRH YFQNTQGLIF VVDSNDRERV QESADELQKM LQEDELDAV
LLVFANKQDM PNAMPVSELT DKLGLQHLRS RTWYVQATCA TQGTGLYDGL DWLSHELKSR

>ARF6 (175AA)

MGKVLKIFG NKEMRILMLG LDAAGKTIL YKCLKGQSVT TIPTVGFNVE TVTYKNVKFN
VWDVGGQDKI RPLWRHYTYG TQGLIFVDC ADRDRIDEAR QELHRIINDR EMRDAIILIF
ANKQDLPDAM KPHEIQEKLK LTRIRDRNWY VQPSCATSGD GLYEGLTWT SNYKS

>ARL1 (181AA)

MGGFFSSIFS SLFGTREMRI LILGLDGAGK TTILYRLQVG EVVTTIPTIG FNVETVITYKN
LKFQVWDLGG QTSIRPYWRC YYSNTDAVIY VVDSNDRDRI GISKSELVAM LEEEELRKAI
LVVFANKQDM EQAMTSSEMA NSLGLPALKD RKWQIFKTSK TKGTLDEAM EWLIVTLKSR
Q

>ARL2 (184AA)

MGLLTILKKM KQKERELRL MLGLDNAGKT TILKKFNGED IDTISPTLGF NIKTLEHRGF
KLNIWVWVGG QSLRSYWRNY FESTDGLIIV VDSADRQRMQ DCQRELQSL VEEERLAGATL
LIFANKQDLP GALSSNAIRE ALELDSIRSH HWCIQGCSAV TGENLLPGID WLLDDISSRI
FTAD

>ARL3 (182AA)

MGLLSILRKL KSAPDQEVRI LLLGLDNAGK TLLKQLASE DISHITPTQG FNIKSVQSQG
FKLNVDVIGG QRKIRPYWKN YFENTDILYI VIDSADRKRK EETGQELAE LEEELKSCVP
VLIFANKQDL LTAAPASEIA EGLNLHTIRD RVWQIQSCSA LTGEGVQDGM NWVCKVNAK
KK

>ARL4A (200AA)

MGNGLSDQTS ILSNLPSFQS FHIVILGLDC AGKTTVLYRL QFNEFVNTVP TKGFNTEKIK
VTLGNSKTVT FHFWDVGGQE KLRPLWKSYP RCTDGIVFV DSVDERMEE AKTELHKITR
ISENQGPVL IVANKQDLRN SLSLSEIEKL LAMGELSSST PWHLQPTCAI IGDGLKEGLE
KLHDMIIKRR KMLRQKQKRR

>ARL4P (234AA) PSEUDOGENE

MGNGLSDQTS ILSNLPSFQS FHIVMLGLDC AGKTTVLYRL QFNEFVNTVP TKAFNTEKIK
VNLRNKTVT FHFWDVGGQE KLMLWKSYP RCTDGILFLM DSVDERMEE AKTELHKITR
LSENGGPVL TVANKQDLEN SLSLSEIEKL LATGELSSST PWHLQPTCAI IGDGLKEGLE
KLHDMIIKEK MNINTYYICV EEVFSGLILT NGKVSTAWFA CLPSWMLLKL CIVQ

>ARL4C (192AA)

MGNISSNISA FQSLHIVMLG LDSAGKTTVL YRLKFNFEVN TVPTIGFNTE KIKLSNGTAK
GISCHFWDVG GQEKLRPLWK SYSRCTDGI YVVDSDVDVDR LEEAKTELHK VTKFAENQGT
PLLVIANKQD LPKSLPVAEI EKQLALHELI PATTYHVQPA CAIIGEGLTE GMDKLYEMIL
KRRKSLKQKK KR

>ARL4D (201AA)

MGNHLTEMAP TASSFLPHFQ ALHVVVIGLD SAGKTSLLYR LKFKEFVQSV PTKGFNTEKI

RVPLGGSRGI TFQVWDVGGQ EKLRPLWRSY NRRTDGLV FV VDAAEAERLE EAKVELHRIS
RASDNQGV PV LVLANKQDQP GALSAAEVEK RLAVRELAAA TLTHVQGC SA VDGLGLQQGL
ERLYEMILKR KKAARGGKKR R
>ARL5A (179AA)
MGILFTRIWR LFNHQEHKVI IVGLDNAGKT TILYQFSMNE VVHTSPTIGS NVEEIVINNT
RFLMWDIGGQ ESLRSSWNTY YTNTEFVIVV VDSTDRERIS VTREELYKML AHEDLRKAGL
LIFANKQDVK ECMTVAEISQ FLKLTSIKDH QWHIQACCAL TGEGLCQGLE WMSRLKIR
>ARL5B (179AA)
MGLIFAKLWS LFCNQEHKVI IVGLDNAGKT TILYQFLMNE VVHTSPTIGS NVEEIVVKNT
HFLMWDIGGQ ESLRSSWNTY YSNTEFIILV VDSIDRERLA ITKEELYRML AHEDLRKAAV
LIFANKQDMK GCMTAAEISK YLTLSSIKDH PWHIQSCCAL TGEGLCQGLE WMTSRIGVR
>ARL5C (179AA)
MGQLIAKLMS IFGNQEHTVI IVGLDNEGKT TILYRFLTNE VVHMCPTIGS NVEEIIIPKT
HFFMWDIVRP EALSFIWNTY YSNTEFIILV IDSTDRDRLL TTREELYKML AHEALQDASV
LIFANKQDVK DSMRMVEISH FLTLSTIKDH SWHIQGCCAL TREGLPARLQ WMESQAAAN
>ARL6 (186AA)
MGLLDRLSVL LGLKKKEVHV LCLGLDNSGK TTIINKLKPS NAQSQNILPT IGFSIEKFKS
SSLSFTVFD M SGQGRYRNLW EHYYKEGQAI IFVIDSSDRL RMVVAKEELD TLLNHPDIKH
RRIPILFFAN KMDLRDAVTS VKVSQLLCLE NIKDKPWHIC ASDAIKGEGL QEGVDWLQDQ
IQTVKT
>ARL8A (186AA)
MIALFNKLLD WFKALFWKEE MELTLVGLQY SGKTTFVNVI ASGQFNEDMI PTVGFNMRKI
TKGNVTIKLW DIGGQPRFRS MWERYCRGVS AIVYMVDAAD QEKIEASKNE LHNLLDKPQL
QGIPVLVLGN KRDLPGALDE KELIEKMNLS AIQDREICCY SISCKEKDNI DITLQWLIQH
SKSRRS
>ARL8B (186AA)
MLALISRLLD WFRSLFWKEE MELTLVGLQY SGKTTFVNVI ASGQFSEDMI PTVGFNMRKV
TKGNVTIKIW DIGGQPRFRS MWERYCRGVN AIVYMIDAAD REKIEASRNE LHNLLDKPQL
QGIPVLVLGN KRDLPNALDE KQLIEKMNLS AIQDREICCY SISCKEKDNI DITLQWLIQH
SKSRRS
>ARL9 (123 AA)
MEFLEIGGSK PFRSYWEMYL SKGLLLIFVV DSADHSRLPE AKKYLHQLIA ANPVLPLVVF
ANKQDLEAAY HITDIHEALA LSEVGNDRKM FLFGTYLTKN GSEIPSTMQD AKDLIAQLAA
DVQ
>ARL9 (265AA)
MERGKVKKKE KEKETQEEKI GEKGREEKVK RKEVEQKIKQ KQEKQERRKG KEKEEKRTKQ
GKETNKEKEQ FKGQEEKGEN KDSTLTRTPL EPLEKNKQIL VLGLDGAGKT SVLHSLASNR
VQHSVAPTQG FHAVCINTED SQMEFLEIGG SKPFRSYWEM YLSKGLLLIF VVDSADHSRL
PEAKKYLHQL IAANPVLPLV VFANKQDLEA AYHITDIHEA LALSEVGNDR KMFLFGTYLT
KNGSEIPSTM QDAKDLIAQL AADVQ
>ARL10 (244AA)
MAPRPLGPLV LALGGAAAVL GSVLFILWKT YFGRGRERRW DRGEAWWGAE AARLPEWDEW
DPEDEEDEEP ALEELEQREV LVLGLDGAGK STFLRVLSGK PPLEGHIPTW GFNSVRLPTK
DFEVDLLEIG GSQNLRFYWK EHVSEVDVLV FVVD SADRLR LPWARQELHK LLDKDPDLPV
VVVANKQDLS EAMSMGELQR ELGLQAIDNQ REVFLLAASI APAGPTFEPE GTVHIWKL LLL
ELLS
>ARL11 (196AA)
MGSVNSRGHK AEAQVMMGL DSAGKTTL LY KLKGHQLVET LPTVGFNVEP LKAPGHVSLT
LWDVGGQAPL RASWKDYLEG TDILVYVLDS TDEARLPESA AELTEVLNDP NMAGVPFLVL
ANKQEAPDAL PLLKIRNRLS LERFQDHCWE LRGCSALTGE GLPEALQSLW SLLKSRSCMC
LQARAHGAER GDSKRS
>ARL13A (297AA)
MFRLSSCCS CLRTEEETRR NVTIPIIGLN NSGKTVLVEA FQKLLPSKTD HCMKSEL TTL
LLDEYELSIY DLNGDLKGRE AWPNYAQAH GLVFLVLDSSD IRRMQEVKII LTHLLSDKRV
AGKPILILAN QDKKKALMP CDIIDYLLK KLVKENKCPC RVEPCSAIRN LERRNHQPIV
EGLRWLLAVI DTCQLPPTSS ISISKNN TGS GERCSSHSFS TRTGMSKEKR QHLEQCSIEA
KPLKSILQIL AIKSILYSLR GSRRVRWHPL RMKTTLVKKN RDFTSLYRDA ADKACGQ
>ARL13B (428AA)
MFSLMASCCG WFKRWREPVR KVTLLMVGLD NAGKTATAKG IQGEYPEDVA PTVGFSKINL

RQGFVETIF DLGGGIRIRG IWKNYYAESY GVIFVVDSSD EERMEETKEA MSEMLRHPRI
SGKPILVLAN KQDKEGALGE ADVIECLSLE KLVNEHKCLC QIEPCSAISG YGKKIDKSIK
KGLYWLLHVI ARDFDALNER IQKETTEQRA LEEQEKQERA ERVRKLREER KQNEQEQAEL
DGTSGLAELD PEPTNPFQPI ASVIEENEGK LEREKKNQKM EKSDSGCHLK HKMEHEQIET
QGQVNHNGQK NNEFGLVENY KEALTQQLKN EDETDRPSLE SANGKKKTKK LRMKRNHRVE
PLNIDDCAPE SPTPPPPPPP VGGWTPKVTR LPKLEPLGET HHNDFYRKPL PPLAVPQRPN
SDAHDVIS

>ARL14 (192AA)

MGSLGSKNPQ TKQAQVLLLG LDSAGKSTLL YKLKLAKDIT TIPTIGFNVE MIELERNLSL
TVWDVGGQEK MRTVWGCYCE NTDGLVYVVD STDKQRLEES QRQFEHILKN EHIKNVPVVL
LANKQDMPGA LTAEDITRMF KVKKLCSDRN WYVQPCCALT GEGLAQGFRK LTGFVKSHMK
SRGDTLAFKK QN

>ARL15 (204AA)

MSDLRITEAF LYMDYLCFRA LCCKGPPPAR PEYDLVCIGL TGSGKTSLLS KLCSESPDNV
VSTTGFSIKA VPFQNAILNV KELGGADNIR KYWSRYYQGS QGVIFVLDSA SSEDLEAAR
NELHSALQHP QLCTLPFLIL ANHQDKPAAR SVQEIKKYFE LEPLARGKRW ILQPCSLDDM
DALKDSFSQL INLLEEKDHE AVR

>ARL16 (173AA)

MCLLLGATGV GKTLLVKRLQ EVSSRDGKGD LGEPPTTRPT VGTNLTDIVA QRKITIRELG
GCMGPIWSSY YGNCRSLLFV MDASDPTQLS ASCVQLLGLL SAEQLAEASV LILFNKIDLP
CYMSTEEMKS LIRLPDIIAC AKQNITTAEI SAREGTGLAG VLAWLQATHR AND

>ARFRP1 (201AA)

MYTLLSGLYK YMFQKDEYCI LILGLDNAGK TTFLEQSKTR FNKNYKGMSL SKITTTVGLN
IGTVDVGKAR LMFWDLGGQE ELQSLWDKYY AECHGVYIYVI DSTDEERLAE SKQAFEKVVT
SEALCGVPVL VLANKQDVET CLSIPDIKTA FSDCTSKIGR RDCLTQACSA LTGKGVREGI
EWMVKCVVRN VHRPPRQRDI T

>SAR1A (198AA)

MSFIFEWIYN GFSSVLQFLG LYKKSGLKLV LGLDNAGKTT LLHMLKDDRL GQHVPTLHPT
SEELTIAGMT FTTFDLGGHE QARRVWKNYL PAINGIVFLV DCADHSRLVE SKVELNALMT
DETISNVPIL ILGNKIDRTD AISEEKLREI FGLYGQTTGK GNVTLKELNA RPMEVFMCSV
LKRQGYGEGF RWLSQYID

>SAR1B (198AA)

MSFIFDWIYS GFSSVLQFLG LYKKTGKLV LGLDNAGKTT LLHMLKDDRL GQHVPTLHPT
SEELTIAGMT FTTFDLGGHV QARRVWKNYL PAINGIVFLV DCADHERLLE SKEELDSLMT
DETIANVPIL ILGNKIDRPE AISEERLREM FGLYGQTTGK GSISLKELNA RPLEVFMCSV
LKRQGYGEGF RWMAQYID

>TRIM23 (574AA) (ARD1)

MATLVVKNLG AGVDSGRQGS RGTAVVKVLE CGVCEDVFSL QGDKVPRLLL CGHTVCHDCL
TRLPLHGRAI RCPFDRQVTD LGDSGVWGLK KNFALLELLE RLQNGPIGQY GAAEESIGIS
GESIIRCDDED EAHLASVYCT VCATHLCSEC SQVTHSTKTL AKHRRVPLAD KPHEKTMCSQ
HQVHAIEFVC LEEGCQTSPL MCCVCKEYGK HQGHKHSVLE PEANQIRASI LDMAHCIRTF
TEEISDYSRK LVGIVQHIEG GEQIVEDGIG MAHTEHVPGT AENARSCIRA YFYDLHETLC
RQEEMALSVV DAHVREKLIW LRQQQEDMTI LLSEVSAACL HCEKTLQDD CRVVLAKQEI
TRLLETLQKQ QQQFTEVADH IQLDASIPVT FTKDNRVHIG PKMEIRVVTL GLDGAGKTTI
LFKLLQDEFM QPIPTIGFNV ETVEYKNLKF TIWDVGGKHK LRPLWKHYL NTQAVVAVVD
SSHRDRISEA HSELAKLLTE KELRDALLI FANKQDVAGA LSVVEITELL SLHKLCCGRS
WYIQGCDARS GMGLYEGLDW LSRQLVAAGV LDVA

(FOR COMPARISON)

>H-RAS (189AA)

MTEYKLVVVG AGGVGKSALT IQLIQNHFVD EYDPTIEDSY RKQVVIDGET CLLDILDITAG
QEEYSAMRDQ YMRTGEGFLC VFAINNTKSF EDIHQYREQI KRKDSDDVP MVLVGNKCDL
AARTVESRQA QDLARSYGIP YIETSAKTRQ GVEDAFYTLV REIRQHKLRK LNPPDESGPG
CMSCKCVLS