

The Ras superfamily at a glance

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The Ras superfamily of small guanine triphosphatases (GTPases) comprise

over 150 human members (Table S1 in supplementary material), with evolutionarily conserved orthologs found in *Drosophila*, *C. elegans*, *S. cerevisiae*, *S. pombe*, *Dictyostelium* and plants (Colicelli, 2004). The Ras oncogene proteins are the founding members of this family, which is divided into five major branches on the basis of sequence (Fig. S1 in supplementary material) and functional similarities: Ras, Rho, Rab, Ran and Arf. Small GTPases share a common biochemical mechanism and act as binary molecular switches (Vetter and Wittinghofer, 2001). Although similar to the heterotrimeric G protein α subunits in biochemistry and function, Ras family proteins function as monomeric G proteins. Variations in structure (Biou and Cherfils, 2004), post-translational modifications that dictate specific

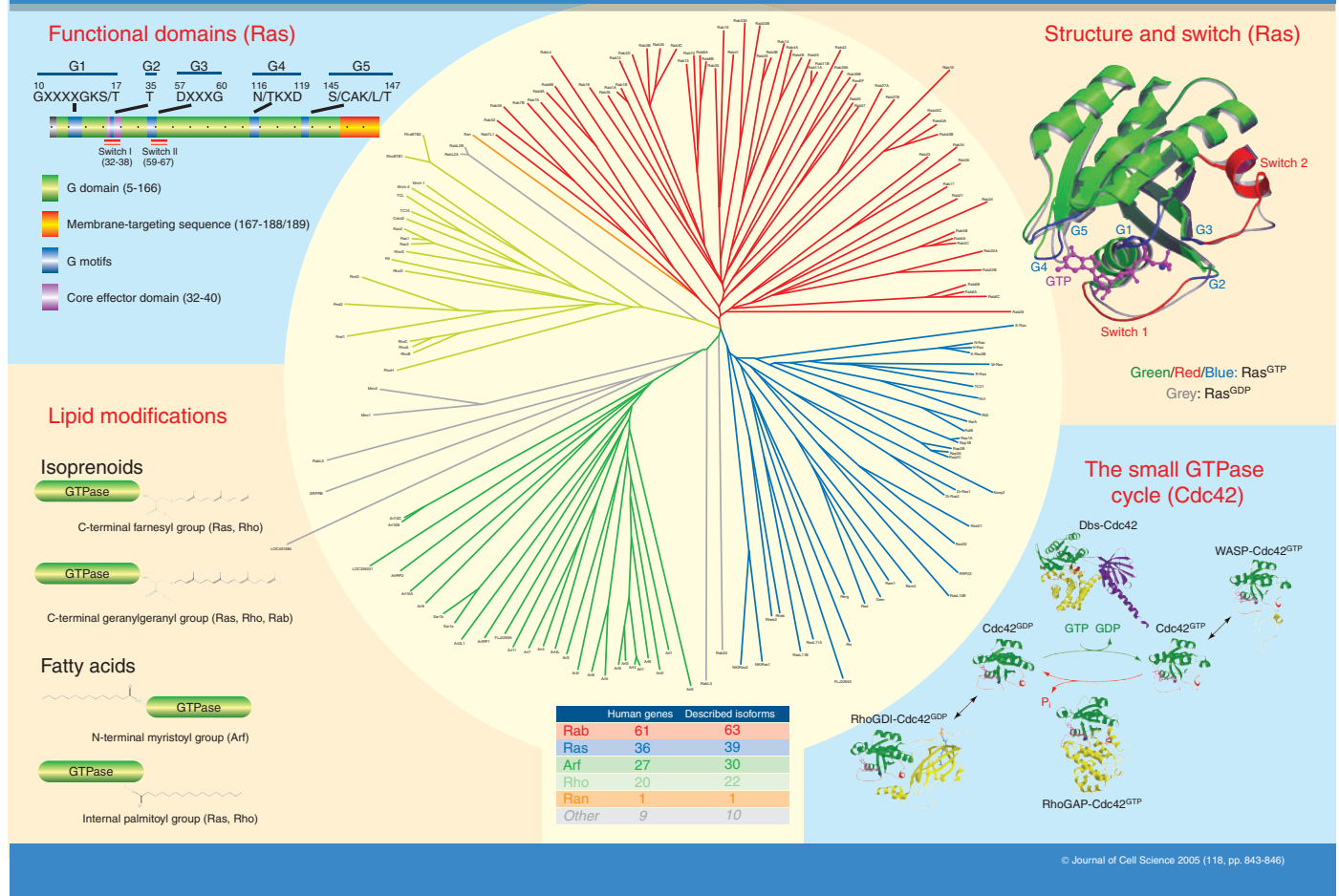
subcellular locations and the proteins that serve as their regulators and effectors allow these small GTPases to function as sophisticated modulators of a remarkably complex and diverse range of cellular processes. Here, we present the basic structural features of Ras proteins, with respect to specific Ras sequences, to highlight the general properties of this family of proteins and discuss features that distinguishes the various branches of the superfamily from Ras.

Ras superfamily structure

Ras superfamily GTPases function as GDP/GTP-regulated molecular switches (Vetter and Wittinghofer, 2001). They share a set of conserved G box GDP/GTP-binding motif elements beginning at the N-terminus: G1,

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(See poster insert)

GXXXXGKS/T; G2, T; G3, DXXGQ/H/T; G4, T/NKXD; and G5, C/SAK/L/T (Bourne et al., 1991) (Fig. S1 in supplementary material). Together, these elements make up an ~20 kDa G domain (Ras residues 5-166) that has a conserved structure and biochemistry shared by all Ras superfamily proteins, as well as G α and other GTPases.

Ras superfamily GTPase biochemistry and regulation

Small GTPases exhibit high-affinity binding for GDP and GTP, and possess low intrinsic GTP hydrolysis and GDP/GTP exchange activities. GDP/GTP cycling is controlled by two main classes of regulatory protein. Guanine-nucleotide-exchange factors (GEFs) promote formation of the active, GTP-bound form (Schmidt and Hall, 2002), whereas GTPase-activating proteins (GAPs) accelerate the intrinsic GTPase activity to promote formation of the inactive GDP-bound form (Bernards and Settleman, 2004). GTPases within a branch use shared and distinct GAPs and GEFs. GTPases in different branches exhibit structurally distinct but mechanistically similar GAPs and GEFs. The two nucleotide-bound states have similar conformations but these have pronounced differences corresponding to the switch I (Ras residues 30-38) and switch II (59-67) regions: the GTP-bound conformation possessing high affinity for effector targets (Bishop and Hall, 2000; Repasky et al., 2004). It is mainly through the conformational changes in these two switches that regulatory proteins and effectors 'sense' the nucleotide status of the small GTPases. Arf proteins contain additional N-terminal sequences, whereas Ran has additional C-terminal sequences that undergo significant conformational changes during GDP/GTP cycling. Although the GTP-bound form is the active form for all Ras superfamily GTPases, the cycling between the GDP-bound and GTP-bound states, in which distinct functions are associated with each nucleotide-bound form, is also critical for the activities of Rab, Arf and Ran GTPases. The core effector domain (Ras residues 32-40) includes the switch I domain and is critical for direct association with effectors (Herrmann, 2003).

Lipid modification and membrane targeting

A second important biochemical feature of a majority of Ras superfamily proteins is their post-translational modification by lipids. The majority of Ras and Rho family proteins terminate with a C-terminal CAAX (C=Cys, A=aliphatic, X=any amino acid) tetrapeptide sequence (Cox and Der, 2002). This motif, when coupled together with residues immediately upstream (e.g. cysteine residues modified by the fatty acid palmitate), comprises the membrane-targeting sequences that dictate interactions with distinct membrane compartments and subcellular locations. The CAAX motif is the recognition sequence for farnesyltransferase and geranylgeranyltransferase I, which catalyze the covalent addition of a farnesyl or geranylgeranyl isoprenoid, respectively, to the cysteine residue of the tetrapeptide motif. Rab family proteins terminate in a distinct set of cysteine-containing C-terminal motifs (CC, CXC, CCX, CCXX, or CCXXX) that are similarly modified by geranylgeranyltransferase II, which also attaches geranylgeranyl groups. Some members of the Arf family are modified at their N-termini by a myristate fatty acid. These modifications are essential for facilitating membrane association and subcellular localization critical for biological activities. Rho and Rab GTPases are regulated by a third class of proteins, guanine nucleotide dissociation inhibitors (GDIs), which mask the prenyl modification and promote cytosolic sequestration of these GTPases (Seabra and Wasmeier, 2004). Some Ras superfamily members do not appear to be modified by lipids, but still associate with membranes (e.g. Rit, RhoBTB, Miro and Sar1). Others (e.g. Ran and Rerg) are not lipid modified and are not bound to membranes.

Subgrouping of the Ras superfamily

The Ras superfamily has traditionally been divided into five different major branches. The classification of some less-studied proteins into these major subfamilies is arbitrary, and sequence comparisons of the G domains suggest that they may define distinct subfamilies.

In the absence of any functional data, a definitive classification of these GTPases is not yet possible. Here, we group the proteins that, on the basis of structure, function or both, clearly belong to a specific subfamily. In cases where neither structural nor functional data support putting a protein in one of the major subfamilies, we leave the protein as 'Unclassified' even though some of these proteins have previously been labeled as belonging to a certain subfamily. In the human genome, there are also a large number of *Ras* superfamily pseudogenes. We have chosen not to include gene sequences from databases where no evidence of transcription has been found. Furthermore, in addition to the proteins listed here, there are many genes that have regions predicted to encode sequences similar to parts of a small GTPase domain, but we have chosen only to include proteins that contain complete Ras-like GTPase domains.

The Ras family

The *Ras* sarcoma (Ras) oncoproteins are the founding members of the Ras family (36 members) and have been the subject of intense research scrutiny, in large part because of their critical roles in human oncogenesis (Repasky et al., 2004). Ras proteins serve as signaling nodes activated in response to diverse extracellular stimuli. Activated Ras interacts with multiple, catalytically distinct downstream effectors, which regulate cytoplasmic signaling networks that control gene expression and regulation of cell proliferation, differentiation, and survival.

The best characterized Ras signaling pathway is activation of Ras by the epidermal growth factor receptor tyrosine kinase through the RasGEF Sos (Repasky et al., 2004). Activated Ras binds to and promotes the translocation of the Raf serine/threonine kinase to the plasma membrane, where additional phosphorylation events promote full Raf kinase activation. Raf phosphorylates and activates the MEK1/2 dual specificity protein kinase, which phosphorylates and activates the ERK1/2 mitogen-activated protein (MAP) kinase. Activated ERK translocates to the nucleus, where it

phosphorylates Ets-family transcription factors, which in turn activate Ets-responsive promoters.

Other Ras family proteins, including Rap, R-Ras, Ral and Rheb proteins, also regulate signaling networks. Finally, although biochemically similar to Ras, several Ras family proteins appear to act as tumor suppressors, rather than as oncogenes (e.g. Rerg, Noey2 and D-Ras), in cancer development (Colicelli, 2004).

The Rho family

Like Ras, Ras homologous (Rho) proteins also serve as key regulators of extracellular-stimulus-mediated signaling networks that regulate actin organization, cell cycle progression and gene expression (Etienne-Manneville and Hall, 2002). Twenty members have been identified, RhoA, Rac1 and Cdc42 being the best studied. Rho GTPases are key regulators of actin reorganization. RhoA promotes actin stress fiber formation and focal adhesion assembly; Rac1 promotes lamellipodium formation and membrane ruffling; and Cdc42 promotes actin microspikes and filopodium formation. Consequently, Rho GTPases have been implicated in the regulation of cell polarity, cell movement, cell shape, and cell-cell and cell-matrix interactions, as well as in regulation of endocytosis and exocytosis (Ridley, 2001). Reflecting their involvement in such a diversity of cellular processes, RhoA, Rac1 and Cdc42 proteins are each regulated by a surprising diversity of GEFs and GAPs (Schmidt and Hall, 2002; Moon and Zheng, 2003) and utilize a similarly diverse set of downstream effectors (Bishop and Hall, 2000). Actin reorganization functions have also been observed for other Rho family GTPases, in particular Rnd proteins, which antagonize RhoA.

Although the Miro proteins were first described as Rho proteins, these atypical GTPases instead appear to form their own subgroup of the Ras superfamily (Wennerberg and Der, 2004). In addition to their N-terminal GTPase domain, they contain EF-hand domains and one C-terminal GTPase-like domain. They lack the insert domain that is characteristic of

Rho GTPases (Fig. S1 in supplementary material). The Miro proteins do not regulate the cytoskeleton; instead they are localized to mitochondria and regulate the integrity of these cellular compartments.

The Rab family

First described as Ras-like proteins in brain (Rab), Rab proteins comprise the largest branch of the superfamily, with 61 members (Pereira-Leal and Seabra, 2001). Rab GTPases are regulators of intracellular vesicular transport and the trafficking of proteins between different organelles of the endocytic and secretory pathways (Zerial and McBride, 2001). Rab proteins facilitate vesicle formation and budding from the donor compartment, transport to the acceptor compartment, and vesicle fusion and release of the vesicle content into the acceptor compartment.

Rab proteins localize to specific intracellular compartments consistent with their function in distinct vesicular transport processes (Zerial and McBride, 2001). This localization is dependent on prenylation, and specificity is dictated by divergent C-terminal sequences. For example, Rab1 is located in the intermediate compartment of the cis-Golgi network and is involved in ER-to-Golgi transport. By contrast, Rab5 is located in early endosomes and regulates clathrin-coated-vesicle-mediated transport from the plasma membrane to early endosomes. Similar distinct intracellular locations and roles in vesicular transport have been established for other Rab members.

The Ran family

The Ras-like nuclear (Ran) protein is the most abundant small GTPase in the cell and is best known for its function in nucleocytoplasmic transport of both RNA and proteins (Weis, 2003). Although related to the Rab proteins in sequence, it has features that distinguish it. Unlike other small GTPases, Ran function is dependent on a spatial gradient of the GTP-bound form of Ran. There is a single human Ran protein that is regulated by a Ran-specific nuclear GEF and cytoplasmic GAP activities. This results in a high concentration of

Ran-GTP in the nucleus, which facilitates the directionality of nuclear import and export. Nuclear Ran-GTP interacts with importin to promote cargo release, and with exportin-complexed cargo, to facilitate nuclear import and export of cargo, respectively. By a similar mechanism, Ran GDP/GTP cycling also regulates mitotic spindle assembly, DNA replication and nuclear envelope assembly (Li et al., 2003).

The Arf family

Like the Rab proteins, the ADP-ribosylation factor (Arf) family proteins are involved in regulation of vesicular transport, Arf1 being the best characterized (Memon, 2004). Arf GDP/GTP cycling is regulated by distinct GEFs and GAPs (Nie et al., 2003). Arf-GTP, the active form, interacts with effectors including vesicle coat proteins. Conformational differences between the two nucleotide-bound forms include not only the switch I and II regions, but also changes in the N-terminal region that allow the myristate group to interact with membranes in their GTP-bound state (Pasqualato et al., 2002).

Arf1 regulates the formation of vesicle coats at different steps in the exocytic and endocytic pathways (Nie et al., 2003; Memon, 2004). GTP- and donor-membrane-bound Arf associates with and activates coat proteins. The Arf-coat-protein complex then facilitates cargo sorting and vesicle formation and release. GAP-mediated formation of Arf-GDP is required for dissociation of the Arf-coat-protein complex and subsequent vesicle fusion with acceptor membranes. In contrast to Rab proteins, which function at single steps in membrane trafficking, Arf proteins can act at multiple steps. For example, Arf1 controls the formation of coat protein I (COPI)-coated vesicles involved in retrograde transport between the Golgi and ER, of clathrin/adaptor protein 1 (AP1)-complex-associated vesicles at the trans-Golgi network (TGN) and on immature secretory vesicles, and of AP3-containing endosomes. Arf6 is functionally distinct from Arf1 and can regulate actin organization as well as endocytosis. Regulation and function of Sar1 is

similar to that of Arf1, controlling the assembly of the COPII-coated vesicles at the ER. Arf1 also functions in membrane trafficking. Other family members exhibit different or poorly characterized cellular functions.

The complex modes of regulation of Ras superfamily small GTPases facilitate their key involvement in an amazingly diverse spectrum of biochemical and biological processes. The extent of this superfamily, when combined with G α subunits and up to 50 other human GTPases (Colicelli, 2004), reveal the versatile role of GTPase switches in the control of cellular processes.

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Supplemental figure. Alignment of the GTPase domain of the Ras superfamily members

		<u>G1</u>	<u>Core effector domain/G2</u>	
Arf1	18	MRILMVGLDAAGKT	TILYKCLKLG-----EIVTTIP----	TI--GFNVET 55
Arf3	18	MRILMVGLDAAGKT	TILYKCLKLG-----EIVTTIP----	TI--GFNVET 55
Arf4	18	MRILMVGLDAAGKT	TILYKCLKLG-----EIVTTIP----	TI--GFNVET 55
Arf5	18	MRILMVGLDAAGKT	TILYKCLKLG-----EIVTTIP----	TI--GFNVET 55
Arf6	18	MRILMLGLDAAGKT	TILYKCLKLG-----QSVTTIP----	TV--GFNVET 55
Ard1	405	IRVVTGLDAGGKT	TILFKLQD-----EFMQPIP----	TI--GFNVET 442
Arl1	18	MRILILGLDAGGKT	TILYRLOVG-----EVVTTIP----	TI--GFNVET 55
Arl5	17	HKVIVGLDNAGKT	TILYQFSMN-----EUVHTSP----	TI--GSNVEE 54
Arl8	16	HKVIVGLDNAGKT	TILYQFLMN-----EUVHTSP----	TI--GSNVEE 53
Arl2	17	LRLMLGLDNAGKT	TILKKFNGE-----DIDTISP----	TL--GFNIKT 54
Arl3	18	VRILLGLDNAGKT	TLLKQLASE-----DISHITP----	TQ--GFNIKS 55
Arl6	19	VHVLCLGLDNSGKT	TIINKLKPSNA-----QSONILP----	TI--GFSIEK 58
Arl4	21	FHIVILGLDCAGKT	TVLYRLOFN-----EFVNTVP----	TK--GFNTEK 58
Arl7	14	LHIVMLGLDSAGKT	TVLYRLKFN-----EFVNTVP----	TI--GFNTEK 51
Arf4L	22	LHVVVIGLDSAGKT	SLLYRLKFK-----EFVQSVV----	TK--GFNTEK 59
Arl11	13	AQVVMGLDSAGKT	TLLYKCLKGH-----QLVETLP----	TV--GFNVEP 50
FLJ22595	14	AQVLLGLDSAGKS	TLLYKCLKLA-----KDITITP----	TI--GFNVEM 51
ArfRP1	18	YCILILGLDNAGKT	TFLEQSKTRFNKNYKGM	SLSKITT-----TV--GLNIGT 63
Arl2L1	22	VTLLMVGLDNAGKT	ATAKGIQGEY-----PEDVAP----	TV--GFSKIN 59
Arl9	19	KQILVLGLDAGGKT	SVLHSLASNR-----VQHSVAP----	TQ--GFHAVC 57
Arl10A	78	REVLVLGLDAGGKS	TLLHMLSGKP-----PLEGHIP----	TW--GFNSVR 116
Sarla	26	GKLVFLGLDNAGKT	TLLHMLKDD-----RLGQHVP----	TL--HPTSEE 63
Sar1b	26	GKLVFLGLDNAGKT	TLLHMLKDD-----RLGQHVP----	TL--HPTSEE 63
Arl10B	21	MELTLVGLQYSGKT	TFVNVIASG-Q-----FNEDMIP----	TV--GFNMRK 59
Arl10C	21	MELTLVGLQYSGKT	TFVNVIASG-Q-----FSEDMIP----	TV--GFNMRK 59
LOC339231	24	GMCLLLGATGVGKT	LLVKRLOEVSSRDGKGD	LGEPPPTRP-----TV--GTNLTD 71
RhoA	6	KKLVIVGDGACGKT	CLLIVFSKDQ-----FPEVYVP----	TVF--ENYVAD 45
RhoC	6	KKLVIVGDGACGKT	CLLIVFSKDQ-----FPEVYVP----	TVF--ENYIAD 45
RhoB	6	KKLVVVGDGACGKT	CLLIVFSKDE-----FPEVYVP----	TVF--ENYVAD 45
Rnd2	8	CKIVVVGDAECGKT	ALLQVFAKDA-----YPGSYVP----	TVF--ENYTAS 47
Rnd3	24	CKIVVVGDSQCGKT	ALLHVFAKDC-----FPENYVP----	TVF--ENYTAS 63
Rnd1	14	CKLVVLGDVQCGKT	AMLQVLAKDC-----YPETYVP----	TVF--ENYTAC 53
RhoD	18	VKVVLVGDGGCGKT	SLLMVFADGA-----FPESYTP----	TVF--ERYMVN 57
Rif	20	LKIVIVGDGGCGKT	SLLMVYSQGS-----FPEHYAP----	SVF--EKYTAS 59
Rac1	4	IKCVVVGDGAVGKT	CLLISYTTNA-----FPGEYIP----	TVF--DNYSAN 43
Rac2	4	IKCVVVGDGAVGKT	CLLISYTTNA-----FPGEYIP----	TVF--DNYSAN 43
Rac3	4	IKCVVVGDGAVGKT	CLLISYTTNA-----FPGEYIP----	TVF--DNYSAN 43
RhoG	4	IKCVVVGDGAVGKT	CLLICYTTNA-----FPKEYIP----	TVF--DNYSAQ 43
TC10	18	LKCVVVGDGAVGKT	CLLMSYANDA-----FPEEYVP----	TVF--DHYAVS 57
TCL	22	LKCVVVGDGAVGKT	CLLMSYANDA-----FPEEYVP----	TVF--DHYAVT 61
Cdc42	4	IKCVVVGDGAVGKT	CLLISYTTNK-----FPSEYVP----	TVF--DNYAVT 43
Wrch-2	32	IKCVLVGDGAVGKS	SLIVSYTCNG-----YPARYRP----	TAL--DTFSVQ 71
Wrch-1	50	VKCVLVGDGAVGKT	SLVVSYTTNG-----YPTEYIP----	TAF--DNFSAV 89
RhoH	5	IKCVLVGDGAVGKT	SLLVRFSTSET-----FPEAYKP----	TVY--ENTGVD 44
RhoBTB1	15	IKCVVVGDNAVAGKT	RLICARACNATLTQY---QLLATHVP----	TVWAIQYRV 61
RhoBTB2	15	IKCVVVGDNAVAGKT	RLICARACNATLTQY---QLLATHVP----	TVWAIQYRV 61
H-Ras	4	YKLVVVGAGGVGKS	SALTIQLIQNH-----FVDEYDP----	TIED--SYRKQ 43
K-Ras2B	4	YKLVVVGAGGVGKS	SALTIQLIQNH-----FVDEYDP----	TIED--SYRKQ 43
N-Ras	4	YKLVVVGAGGVGKS	SALTIQLIQNH-----FVDEYDP----	TIED--SYRKQ 43
R-Ras	30	HKLVVVGAGGVGKS	SALTIQFIQSY-----FVSDYDP----	TIED--SYTKI 69
TC21	15	YRLVVVGAGGVGKS	SALTIQFIQSY-----FVTDYDP----	TIED--SYTKQ 54
M-Ras	14	YKLVVVGAGGVGKS	SALTIQFFQKI-----FVPDYDP----	TIED--SYLKH 53
Rit1	22	YKLVMLGAGGVGKS	SAMTMQFISHR-----FPEDHDP----	TIED--AYKIR 61
Rit2	21	YKVVMLGAGGVGKS	SAMTMQFISHQ-----FPDYHDP----	TIED--AYKTQ 60
Rap1A	4	YKLVVLGSGGVGKS	ALTVOFVQGI-----FVEKYDP----	TIED--SYRKQ 43
Rap1B	4	YKLVVLGSGGVGKS	ALTVOFVQGI-----FVEKYDP----	TIED--SYRKQ 43
Rap2A	4	YKVVVLGSGGVGKS	ALTVOFVTGT-----FIEKYDP----	TIED--FYRKE 43
Rap2C	4	YKVVVLGSGGVGKS	ALTVOFVTGT-----FIEKYDP----	TIED--FYRKE 43

Rap2B	4	YKVVVLGSGGVGKS	ALTVQFVTGS-----FIEKYDP-----	TIED-FYRKE	43		
RalA	15	HKVIMVGS	GGVGSALTLQFMYDE-----FVEDYEP-----	TKAD-SYRKK	54		
RalB	15	HKVIMVGS	GGVGSALTLQFMYDE-----FVEDYEP-----	TKAD-SYRKK	54		
E-Ras	42	YKAVVVGAS	GVGKSALTIQLNHQC-----FVEDHDP-----	TIQD-SYWKE	81		
Gem	76	YRVVLI	GEQGVGKSTLANIFAGVH-----DSMDSCEV---	LGED-TYERT	117		
Rad	92	YKVVLLG	GAPGVGKSALARIFGGVE-----DGPEAEA----	AGH--TYDRS	130		
Rem1	81	YRVVLLG	DPGVGKTSLASLFAGKQ-----ERDLHEQ-----	LGED-VYERT	120		
Rem2	105	FKVMLV	GESGVGKSTLAGTFGGLO-----GDSAHEP-----	ENPEDTYERR	145		
Rerg	7	VKLAIF	GRAGVGKSALVVRFLTKR-----FIWEYDP-----	TLES-TYRHQ	46		
Ris	21	VNLAIL	GRRGAGKSALTVKFLTKR-----FISEYDP-----	NLED-TYSSE	60		
RasL11A	28	IKLAVL	GAGRVGKSAMIVRFLTKR-----FIGDYEP-----	NTGK-LYSRL	67		
RasL11B	34	VKIAVV	GASGVGKTALVVRFLTKR-----FIGDYER-----	NAGN-LYTRQ	73		
FLJ22655	5	LHLKYNE	KSVSVTKALTVRFLTKR-----FIGEYAS-----	NFES-IYKKH	44		
Di-Ras1	8	YRVVVF	GAGGVGKSSLVLRVFKGT-----FRDTYIP-----	TIED-TYRQV	47		
Di-Ras2	8	YRVAVF	GAGGVGKSSLVLRVFKGT-----FRESYIP-----	TVED-TYRQV	47		
Noey2	38	YRVVVV	GTAGVGKSTLLHKWASGN-----FRHEYLP-----	TIEN-TYCQL	77		
RasD1	25	YRMVIL	GSSKVGKTAIVSRFLTGR-----FEDAYTP-----	TIED-FHRKF	64		
RasD2	20	YRMVVL	GASRVGKSSIVSRFLNGR-----FEDQYTP-----	TIED-FHRKV	59		
RRP22	5	LRVAVL	GAPGVGKTAIIROFLFGD-----YPERHRP-----	TDGPRLYRPA	45		
RasL10B	5	YRVAVL	GARGVGKSAIVRQFLYNE-----FSEVCVP-----	TTARRLYLPA	45		
Rheb	7	RKIAIL	GYRCVGKSSLTIQFVEGO-----FVDSYDP-----	TIEN-TFTKL	46		
RhebL1	7	RKVVIL	GYRCVGKSTLAHQFVEGE-----FSEGYDP-----	TVEN-TYSKI	46		
NKIRas1	5	CKVVVC	GLLSVGKTAILEQLLYGN-----HTIGMEDCE---	TMED-VYMAS	46		
NKIRas2	5	CKVVVC	GQASVGKTSILEQLLYGN-----HVVGSEMIE---	TQED-IYVGS	46		
Rab40A	15	LKFLLV	GDRDVGKSEILESLODGA-----AESPY-----	SHLGGIDYKTTT	55		
rab40B	15	LKFLLV	GDSDVGKGEILASLODGA-----AESPY-----	GHPAGIDYKTTT	55		
Rab40C	15	LKFLLV	GDSDVGKGEILESLODGA-----AESPY-----	AYSNGIDYKTTT	55		
Rab1A	12	FKLLL	IGDSGVGKSCLLLRFADDT-----YTESY-----	ISTIGVDFKIRT	52		
Rab1B	9	FKLLL	IGDSGVGKSCLLLRFADDT-----YTESY-----	ISTIGVDFKIRT	49		
Rab35	9	FKLLI	IGDSGVGKSSLLLRFADNT-----FSGSY-----	ITTIGVDFKIRT	49		
Rab3A	23	FKILII	IGNSSVGKTSFLFRYADDS-----FTPAF-----	VSTVGIDFKVKT	63		
Rab3C	31	FKLLII	IGNSSVGKTSFLFRYADDS-----FTSAF-----	VSTVGIDFKVKT	71		
Rab3B	23	FKLLII	IGNSSVGKTSFLFRYADDT-----FTPAF-----	VSTVGIDFKVKT	63		
Rab3D	23	FKLLL	IGNSSVGKTSFLFRYADDS-----FTPAF-----	VSTVGIDFKVKT	63		
Rab8A	9	FKLLL	IGDSGVGKTCVLFRFSEDA-----FNSTF-----	ISTIGIDFKIRT	49		
Rab8B	9	FKLLL	IGDSGVGKTCVLFRFSEDA-----FNSTF-----	ISTIGIDFKIRT	49		
Rab10	10	FKLLL	IGDSGVGKTCVLFRFSDDA-----FNSTF-----	ISTIGIDFKIKT	50		
Rab13	9	FKLLL	IGDSGVGKTCVLFRFSDDA-----FNSTF-----	ISTIGIDFKIKT	50		
Rab13	9	FKLLL	IGDSGVGKTCVLFRFSDDA-----FNSTF-----	ISTIGIDFKIKT	50		
Rab12	139	LQVII	IGSRGVGKTSLMEFRFTDDT-----FCEAC-----	KSTVGVDFKIKT	179		
Rab18	9	LKILII	IGESGVGKSSLLLRFTDDT-----FDPEL-----	AATIGVDFKIKT	49		
Rab19	18	FKIIL	IGDSNVGKTCVVFHFKSGV-----YTETQ-----	QNTIGVDFTVRS	58		
Rab41	19	FKLVL	VGDA	SVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59	
Rab30	10	FKIVL	IGNAGVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab30	10	FKIVL	IGNAGVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab33A	37	FKIIV	IGDSNVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab33B	34	FKIIV	IGDSNVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab2A	7	FKYIII	IGDTGVGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab2B	7	FKYIII	IGDTGVGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab2B	7	FKYIII	IGDTGVGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab4A	14	FKFLV	IGNAGTGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab4B	44	FKFLV	IGNAGTGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab14	12	FKYIII	IGDMVGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab11A	12	FKVVL	IGDSGVGKSNLLSRFTRNE-----FNLES-----	KSTIGVEFATRS	52		
Rab11B	12	FKVVL	IGDSGVGKSNLLSRFTRNE-----FNLES-----	KSTIGVEFATRS	52		
Rab25	13	FKVVL	IGESGVGKSNLLSRFTRNE-----FNLES-----	KSTIGVEFATRS	52		
Rab39A	9	FRLIV	IGDSTVGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab39B	9	FRLIV	IGDSTVGKSCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab42	9	FRVAL	LGDAAVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59		
Rab26	64	FKVML	VGD	SGVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59	
Rab37	23	HKTIL	VGD	SGVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59	
RasEF	542	YKIVL	AGDA	AVGKSNLLSRFTRNE-----FNLES-----	KSTIGVEFATRS	52	
Rab27A	10	IKFLA	L	GD	SGVGKTSVLYQYTDGK-----FNSK-----	FITTVGIDFREKR	50
Rab27B	10	IKLLA	L	GD	SGVGKTCVVFQRFKGTGA-----FSERQ-----	GSTIGVDFTMKT	59

Rab23	10	IKM VVV NGAVGKSSMIQRYCKG-----IFTKD---YK K TIGVDFLERO	50
RabL4	5	AAK C ILADPAVGK T ALAQIFRSDG-----AHFQ K S---Y T LT T GM D LVV K T	47
Rab9A	8	FKV I LLGDGGVGK S SLMNRYVTN-----KF D T Q ---L F H T IGV E FLN-K	47
Rab9B	8	LKV I LLGDGGVGK S SLMNRYVTN-----KF D S Q ---A F H T IGV E FLN-R	47
Rab7A	9	LKV I LLGD S GVGK T SLMNQYV N K-----K F S N Q---Y K A T IG A D F L T -K	48
Rab7B	9	L K L I IV G AIGVGK T SLPHQYV H K-----T F Y E E---Y Q T L G A S I L S -K	48
Rab32	26	FKV L VI G ELVGK T SIIKRYV H Q-----L F S Q H---Y R A T IGV D F A L-K	65
Rab38	10	Y K LL V IGDLVGK T SIIKRYV H Q-----N F S S H---Y R A T IGV D F A L-K	49
Rab7L1	8	FKV L V V GDAAVGK T SLVQRY S QD-----S F S K H---Y K S T V G V D F A L-K	47
Rab5A	21	FK L V L LG S AVGK S SLVLR F V K G-----Q F H E F---Q E S T IG A A F L T -Q	60
Rab5C	21	FK L V L LG S AVGK S SLVLR F V K G-----Q F H E Y---Q E S T IG A A F L T -Q	60
Rab5B	21	FK L V L LG S AVGK S SLVLR F V K G-----Q F H E Y---Q E S T IG A A F L T -Q	60
Rab22A	6	L K V C LL G D T GVGK S SIVWR F V E D-----S F D P N---I N P T IG A S F M T -K	45
Rab22B	7	L K V C LL G D T GVGK S SIVCR F V Q D-----H F D H N---I S P T IG A S F M T -K	46
Rab24	8	V K V V M L G K EYVGK T SLV E R V H D -----R F L V G P ---Y Q N T IG A A F V A -K	48
Rab21	20	FKV V LL G E G CVGK T SLVLR Y C E N-----K F N D K---H I T L Q A S F L T -K	59
Rab17	29	FK L V L LG S GS V GK S SLALR Y V K N-----D F K S I---L P T V G C A F F T -K	67
Rab6A	14	FK L V F L G E Q SVGK T SLI T R F M Y D-----S F D N T---Y Q A T IG I D F L S -K	53
Rab6C	14	FK L V F L G E Q SV A K T SLI T R F R Y D-----S F D N T---Y Q A T IG I D F L S -K	53
Rab6B	14	FK L V F L G E Q SVGK T SLI T R F M Y D-----S F D N T---Y Q A T IG I D F L S -K	53
Rab28	13	L K I V V L G D G T SGK T SL T T C F A Q E -----T F G K Q---Y K Q T IG L D F F L -R	52
Rab15	9	F R LL L IG D SGVGK T CL L CR F T D N E -----F H S S H I S---T I G V D F K M K T	49
Rab34	53	S K I I V V G D L S VGK T CL I N R F C K D T-----F D K N Y K A---T I G V D F E M E R	93
Rab36	124	S K V V V V G D L Y VGK T SLI H R F C K N V -----F D R D Y K A---T I G V D F E I E R	164
Ran	11	FK L V L V G D G G T GK T TFV K R H L T G-----E F E K K---Y V A T L G V E V H P-L	50
RabL2A	22	V K I I C L G D S A VGK S K L M E R F L M D G -----F Q P Q Q L ---S T Y A L T L Y K H T	62
RabL2B	22	V K I I C L G D S A VGK S K L M E R F L M D G -----F Q P Q Q L ---S T Y A L T L Y K H T	62
Miro1	5	V R I L L V G E P R VGK T SL I M S L V S E E-----F P E E V P P R A E E I T I P A D V T P E R	50
Miro2	5	V R I L L L G E A Q VGK T SL I L S L V G E E-----F P E E V P P R A E E I T I P A D V T P E K	50
Rab20	6	S K I V LL G D M N V GK T SL L Q R Y M E R R-----F P D T V S -----T V G G A F Y L K Q	45
RabL3	7	V K V L V L G D SGVGK S SL V H L L C Q N Q V L G -----N P S W T V -----G C S V D V R V H D	49
Arfrp2	33	Y D L V C I G L T G SGK T SL L S K L C S E -----S P D N V V S---T T --G F S I K A	70
RabL5	4	A K I L F V GP C ES G K T V L A N F L T E S S -----D I T E Y S P T --Q G V R I L E F E N P H	47
SRPRB	65	R A V L L V G L C D SGK T LL F V R LL T G L -----Y R D T Q T S---I T D--S C A V Y R	104
LOC401884	1	M V S G G A G E G T R V W G T G T P A Q R-----P L V G L G R---G L P A E W E G L	39

Arf1	VEYKN-----	ISFTV	65
Arf3	VEYKN-----	ISFTV	65
Arf4	VEYKN-----	ICFTV	65
Arf5	VEYKN-----	ICFTV	65
Arf6	VTYKN-----	VKFNV	65
Ard1	VEYKN-----	LKFTI	452
Arl1	VTYKN-----	LKFQV	65
Arl5	IVINN-----	TRFLM	64
Arl8	IVVKN-----	THFLM	63
Arl2	LEHRG-----	FKLNI	64
Arl3	VQSQG-----	FKLNV	65
Arl6	FKSSS-----	LSFTV	68
Arl4	IKVTLGNSKT-----	VTFHF	73
Arl7	IKLSNGTAKG-----	ISCHF	66
Arf4L	IRVPLGGSRG-----	ITFQV	74
Arl11	LKAPG---H-----	VSLTL	61
FLJ22595	IELER---N-----	LSLTV	62
ArfRP1	VDVGK-----	ARLMF	73
Arl2L1	LRQ GK-----	FEVTI	69
Arl9	INTED-----	SQMEF	67
Arl10A	LPTKD-----	FEVDL	126
Sarla	LTIAG-----	MTFTT	73
Sar1b	LTIAG-----	MTFTT	73
Arl10B	ITKGN-----	VTIKL	69
Arl10C	VTKGN-----	VTIKI	69
LOC339231	IVAQR-----	KITI	80
RhoA	IEVDGKQ-----	VELAL	57
RhoC	IEVDGKQ-----	VELAL	57
RhoB	IEVDGKQ-----	VELAL	57
Rnd2	FEIDKRR-----	IELNM	59
Rnd3	FEIDTQR-----	IELSL	75
Rnd1	LETEEQR-----	VELSL	65
RhoD	LQVKGKP-----	VHLHI	69
Rif	VTVGSKE-----	VTLNL	71
Rac1	VMVDGKP-----	VNLGL	55
Rac2	VMVDSKP-----	VNLGL	55
Rac3	VMVDGKP-----	VNLGL	55
RhoG	SAVDGRT-----	VNLNL	55
TC10	VTVGKQ-----	YLLGL	69
TCL	VTVGKQ-----	HLLGL	73
Cdc42	VMIGGEP-----	YTLGL	55
Wrch-2	VLVDGAP-----	VRIEL	83
Wrch-1	VSDGRP-----	VRLQL	101
RhoH	VFMDGIQ-----	ISLGL	56
RhoBTB1	CQEVLSRDRVVDEVS-----	VSLRL	82
RhoBTB2	CQEVLSRDRVVDDVS-----	VSLRL	82
H-Ras	VVID-GETCL-----	LDI	55
K-Ras2B	VVID-GETCL-----	LDI	55
N-Ras	VVID-GETCL-----	LDI	55
R-Ras	CSVD-GIPAR-----	LDI	81
TC21	CVID-DRAAR-----	LDI	66
M-Ras	TEID-NQWAI-----	LDV	65
Rit1	IRID-DEPAN-----	LDI	73
Rit2	VRID-NEPAY-----	LDI	72
Rap1A	VEVD-CQOCM-----	LEI	55
Rap1B	VEVD-AQOCM-----	LEI	55
Rap2A	IEVD-SSPSV-----	LEI	55
Rap2C	IEVD-SSPSV-----	LEI	55

Rap2B	IEVD-SSPSV-----LEI	55
RalA	VVLD-GEEVQ-----IDI	66
RalB	VVLD-GEEVQ-----IDI	66
E-Ras	LTLD-SGDCI-----LNV	93
Gem	LMVD-GESAT-----IIL	129
Rad	IVVD-GEEAS-----LMV	142
Rem1	LTVD-GEDTT-----LVV	72
Rem2	IMVD-KEEVT-----LVV	157
Rerg	ATID-DEVVS-----MEI	58
Ris	ETVD-HQPVH-----LRV	72
RasL11A	VYVE-GDQLS-----LQI	79
RasL11B	VQIE-GETLA-----LQV	85
FLJ22655	LCLC-RKQLN-----LEI	56
Di-Ras1	ISCD-KSVCT-----LQI	59
Di-Ras2	ISCD-KSICT-----LQI	59
Noey2	LGCS-HGVLS-----LHI	89
RasD1	YSIR-GEVYQ-----LDI	76
RasD2	YNIR-GDMYQ-----LDI	71
RRP22	VLLD-GAVYD-----LSI	57
RasL10B	VVMN-GHVHD-----LQI	57
Rheb	ITVN-GQEYH-----LQL	58
RhebL1	VTLG-KDEFH-----LHL	58
NKIRas1	VETDRGVKEQ-----LHL	59
NKIRas2	IETDRGVREQ-----VRF	59
Rab40A	ILLD-GQVVK-----LKL	67
rab40B	ILLD-GRRVK-----LQL	67
Rab40C	ILLD-GRRVR-----LEL	67
Rab1A	IELD-GKTIK-----LQI	64
Rab1B	IELD-GKTIK-----LQI	61
Rab35	VEIN-GEKVK-----LQI	61
Rab3A	IYRN-DKRIK-----LQI	75
Rab3C	VFKN-EKRIK-----LQI	83
Rab3B	VYRH-EKRVK-----LQI	75
Rab3D	VYRH-DKRIK-----LQI	75
Rab8A	IELD-GKRIK-----LQI	61
Rab8B	IELD-GKKIK-----LQI	61
Rab10	VELQ-GKKIK-----LQI	62
Rab13	VDIE-GKKIK-----LQV	61
Rab12	VELR-GKKIR-----LQI	191
Rab18	ISVD-GNKAK-----LAI	61
Rab19	LDID-GKKVKNSSASIIITFASIQIHGOTQKMSPQIWTKSSHYLWEPLIWTLLPVLLQMQV	117
Rab41	LEIQ-GKRVK-----LQI	71
Rab30	VEIN-GEKVK-----LQI	62
Rab33A	VEIE-GEKIK-----VQV	89
Rab33B	VEID-GERIK-----IQL	86
Rab2A	ITID-GKQIK-----LQI	59
Rab2B	VNID-GKQIK-----LQI	59
Rab4A	INVG-GKYVK-----LQI	66
Rab4B	VNVG-GKTVK-----LQI	96
Rab14	IEVS-GQKIK-----LQI	64
Rab11A	IQVD-GKTIK-----AQI	64
Rab11B	IQVD-GKTIK-----AQI	64
Rab25	VMLG-TAAVK-----AQI	65
Rab39A	LEIEPGKRIK-----LQL	66
Rab39B	VEIEPGKRIK-----LQI	62
Rab42	LQLRAGPRVK-----LQL	67
Rab26	LDVDGV-----KVKLQ	117
Rab37	VTVDGV-----RVKLQI	76
RasEF	LIVDGE-----RTVLQ	594
Rab27A	VVYRASGPDGATGRGQ-----RIHLQ	72
Rab27B	VVYNAQGPNGSSGKAF-----KVHLQ	72

Rab23	IQVNDE--D-----	VRLML	62
RabL4	VPVPDTGDS-----	VELFI	61
Rab9A	DLEV D-GHF-----	VTMQI	60
Rab9B	DLEV D-GRF-----	VTLQI	60
Rab7A	EVMVD-DRL-----	VTMQI	61
Rab7B	IIILG-DTT-----	LKLQI	61
Rab32	VLNWD SRTL-----	VRLQL	79
Rab38	VLHWD PETV-----	VRLQL	63
Rab7L1	VLQWSDY EI-----	VRLQL	61
Rab5A	TVCLDDTT-----	VKFEI	73
Rab5C	TVCLDDTT-----	VKFEI	73
Rab5B	SVCLDDTT-----	VKFEI	73
Rab22A	TVQYQNEL-----	HKFLI	58
Rab22B	TVPCGNEL-----	HKFLI	59
Rab24	VMSVGDRT-----	VTLGI	61
Rab21	KLNIGGKR-----	VNLAI	72
Rab17	VVDVGATS-----	LKLEI	80
Rab6A	TMYLEDRT-----	IRLQL	66
Rab6C	TMYLEDGT-----	IGLRL	66
Rab6B	TMYLEDRT-----	VRLQL	66
Rab28	RITLPGNLN-----	VTLQI	66
Rab15	IEVDGIKVR-----	IQI	61
Rab34	FEVLGIPFS-----	LQL	105
Rab36	FEIAGIPYS-----	LQI	176
Ran	VFHTN-RGP-----	IKFNV	63
RabL2A	ATVDGKT-----	ILVDF	74
RabL2B	ATVDGRT-----	ILVDF	74
Miro1	VPT-----	HI	55
Miro2	VPT-----	HI	55
Rab20	WRSYN-----	ISI	53
RabL3	YKEGTPEEKT-----	CYIEL	64
ArfRP2	VPFQN-----	AILNV	80
RabL5	VTSNNKGTG-----	CEFEL	61
SRPRB	VNNNRGNS-----	LTL	115
LOC401884	AARGAGRGRG-----	RGR	52

G3

Arf1	WDVGGQ	-----DKIRPLWRHYFQNTQGLIFVVDSND-RERVNEAREELMRMLAEDE	115
Arf3	WDVGGQ	-----DKIRPLWRHYFQNTQGLIFVVDSND-RERVNEAREELMRMLAEDE	115
Arf4	WDVGGQ	-----DRIRPLWKHYFQNTQGLIFVVDSND-RERIQEVADELQKMLLVDE	115
Arf5	WDVGGQ	-----DKIRPLWRHYFQNTQGLIFVVDSND-RERVQESADELQKMLQEDE	115
Arf6	WDVGGQ	-----DKIRPLWRHYTGTQGLIFVVDCAD-RDRIDEARQELHRIINDRE	115
Ard1	WDVGGK	-----HKLRPLWKHYLNTQAVFVVDSSH-RDRISEAHSELAKLLTEKE	502
Arl1	WDLGGQ	-----TSIRPYWRCYYSNTDAVIYVVDSCD-RDRIGISKSELVAMLEEEE	115
Arl5	WDIGGQ	-----ESLRSSWNTYYTNTFEFVIVVVDSTD-RERISVTREELYKMLAHED	114
Arl8	WDIGGQ	-----ESLRSSWNTYYSNTEFIIILVVDSID-RERLAITKEELYRMLAHED	113
Arl2	WDVGGQ	-----KSLRSYWRNYFESTDGLIWWVDSAD-RQRMQDCQRELOSLLEVEER	114
Arl3	WDIGGQ	-----RKIRPYWKNYFENTDILIIYVIDSAD-RKRFEETGQELAELEEEK	115
Arl6	FDMSGQ	-----GRYRNLWEHYKQAIIFVIDSSD-RLRMVVAKEELDTLLNHPD	118
Arl4	WDVGGQ	-----EKLRPLWKS YTRCTDGIIVVVDSD-VERMEEAKTELHKITRISE	123
Arl7	WDVGGQ	-----EKLRPLWKSYSRCTDGIIVVVDSD-VDRLEEAKTELHKVTKFAE	116
Arf4L	WDVGGQ	-----EKLRPLWRSYTRRTDGLVVFVDAAE-AERLEEAKVELHRISRASD	123
Arl11	WDVGGQ	-----APLRASWKDYLEGTDILVYVLDSTD-EARLPESAALTEVLNDPN	111
FLJ22595	WDVGGQ	-----EKMRTVWGCYCENTDGLVYVVDSTD-QORLEESQRQFHEHILKNEH	112
ArfRP1	WDLGGQ	-----EELQSLWDKYIAECHGVYVIDSTD-EERLAESKQAFEKVVTSEA	123
Arl2L1	FDLGGG	-----IRIRGIWKNYAESYGVIFVVDSSD-EERMEETKEAMSEMHRHPR	119
Arl9	LEIGGS	-----KPFRSYWEMYLSKGLLLIFVVDSAD-HSRLPEAKKYHLQLIAANP	117
Arl10A	LEIGGS	-----QNLRFYWKFEVSEVDVLFVVDSD-RLRLPWARQELHKLLDKDP	176
Sarla	FDLGGH	-----EQARRVWKNYLPAINGIVFLVDCAD-HSRLVESKVELNALMTDET	123
Sar1b	FDLGGH	-----VQARRVWKNYLPAINGIVFLVDCAD-HERLLESKEELDLSMTDET	123
Arl10B	WDIGGQ	-----PRFRSMWERYCRGVSAIVYMVDAAD-QEKIEASKNELHNLLDKPQ	119
Arl10C	WDIGGQ	-----PRFRSMWERYCRGVNAIVYMIDAAD-REKIEASRNELHNLLDKPQ	119
LOC339231	RELGGC	-----MGPIWSSYYGNCRSLLFVMDASD-PTQLSASCVQLLGLLSAEQ	128
RhoA	WDTAGQ	-----EDYDRLRPLSYPD TDVILMCFSDS-PDSLENIPEKWTPVVKHFC	107
RhoC	WDTAGQ	-----EDYDRLRPLSYPD TDVILMCFSDS-PDSLENIPEKWTPVVKHFC	107
RhoB	WDTAGQ	-----EDYDRLRPLSYPD TDVILMCFSDS-PDSLENIPEKWTPVVKHFC	107
Rnd2	WDTSGS	-----SYDNRPLAYPDSDAVLICFDISR-PETLDSVLKWKQGETQEF	109
Rnd3	WDTSGS	-----PYDNRPLSYPDSDAVLICFDISR-PETLDSVLKWKQGETQEF	125
Rnd1	WDTSGS	-----PYDNRPLCYSDSAVLLCFDISR-PETVDSALKKWRTEILDYC	115
RhoD	WDTAGQ	-----DDYDRLRPLFYPDASVLLLCFDVTS-PNSFDNIFNRWYPEVNHFC	119
Rif	YDTAGQ	-----EDYDRLRPLSYQNTHLVLCYDVMN-PTS YDNVLIKWFPEVTHFC	121
Rac1	WDTAGQ	-----EDYDRLRPLSYPQTDVFLICFSLVS-PASFENVRAKWYPEVRHHC	105
Rac2	WDTAGQ	-----EDYDRLRPLSYPQTDVFLICFSLVS-PASYENVRAKWYPEVRHHC	105
Rac3	WDTAGQ	-----EDYDRLRPLSYPQTDVFLICFSLVS-PASFENVRAKWYPEVRHHC	105
RhoG	WDTAGQ	-----EEYDRLRPLSYPQTNVVICFSIAS-PPSYENVRHKWHPEVCHHC	105
TC10	YDTAGQ	-----EDYDRLRPLSYPMTDVFLICFSVFN-PASFQNVKEEWVPELKEYA	119
TCL	YDTAGQ	-----EDYNQLRPLSYPNTDVFLICFSVFN-PASYHNVQEEWVPELKDCM	123
Cdc42	FDTAGQ	-----EDYDRLRPLSYPQTDVFLVCFVSVS-PSSFENVKEKWPEITHHC	105
Wrch-2	WDTAGQ	-----EDFDRLRSLCYPD TDVFLACFSVVO-PSSFQNI TEKWLPEIRTHN	133
Wrch-1	CDTAGQ	-----DEFDKLRPLCYTNTDIFLLCFVSVS-PSSFQNVSEKWWPEIRCHC	151
RhoH	WDTAGN	-----DAFRSIRPLSYQQADVLLMCYSVAN-HNSFLNLKKNKWI GEIRSNL	106
RhoBTB1	WDTFGD	-----HHKDRRFAYGRSDVVVLCFSIAN-PNSLNHVKSMWYPEIKHFC	130
RhoBTB2	WDTFGD	-----HHKDRRFAYGRSDVVVLCFSIAN-PNSLHHVKT MWYPEIKHFC	130
H-Ras	LDTAGQ	-----EEYSAMRDQYMRTGEGFLCVFAINN-TKSFEDIHQYREQIKRVKD	105
K-Ras2B	LDTAGQ	-----EEYSAMRDQYMRTGEGFLCVFAINN-TKSFEDIH HYREQIKRVKD	105
N-Ras	LDTAGQ	-----EEYSAMRDQYMRTGEGFLCVFAINN-SKSFADINLYREQIKRVKD	105
R-Ras	LDTAGQ	-----EEFGAMREQYMRAGHGFLLVFAIND-RQSFNEVGKLF TQILRVKD	131
TC21	LDTAGQ	-----EEFGAMREQYMRRTGEGFLLVFSVTD-RGSFEEIYKFQ RQILRVKD	116
M-Ras	LDTAGQ	-----EEFSAMREQYMRGEGFLIVYSVTD-KASFHEVDRFHQLILRVKD	115
Rit1	LDTAGQ	-----AEFTAMRDQYMRAGEGFIICYSITD-RRSFHEVREFKQLIYRVRR	123
Rit2	LDTAGQ	-----AEFTAMREQYMRGEGFIICYSVTD-RQSFQEA AKFKELIFQVRH	122
Rap1A	LDTAGT	-----EQFTAMRDLYMKNGQGFALVYSITA-QSTFNLDQLDREQILRVKD	105
Rap1B	LDTAGT	-----EQFTAMRDLYMKNGQGFALVYSITA-QSTFNLDQLDREQILRVKD	105
Rap2A	LDTAGT	-----EQFASMRDLYIKNGQGFILVYSLVN-QQSFQDIKPMRDQIIRVKR	105
Rap2C	LDTAGT	-----EQFASMRDLYIKNGQGFILVYSLVN-QQSFQDIKPMRDQIIRVKR	105

Rap2B **LDTAGT**-----EQFASMRDLYIKNGQGFILVYSLVN-QQSFQDIKPMRDQIIRVKR 105
 RalA **LDTAGQ**-----EDYAAIRDNYFRSSEGFLCVFSITE-MESFAATADFREQILRVKE 116
 RalB **LDTAGQ**-----EDYAAIRDNYFRSSEGFLLVFSITE-HESFTATAAEFREQILRVKA 116
 E-Ras **LDTAGQ**-----AIHRALRDQCLAVCDGVLGVFALDD-PSSLIQL----QQIWATWG 139
 Gem **LDMWEN**-----KGE-NEWLHDHCMQVGDAYLIVYSITD-RASFEKASELRIQLRRARQ 180
 Rad **YDIWEQ**-----DGGRWLPGHCMAMGDAYVIVYSVTD-KGSFEKASELRLVQLRRARQ 192
 Rem1 **VDTWEA**-----EKLDKSWSQESCLQGG SAYVIVYSIAD-RGSFESASELRIQLRRTHQ 184
 Rem2 **YDIWEQ**-----GDA-GGWL RDHCLQGTGDAFLIVFSVTD-RRSFSKVPETLLRLRAGR 208
 Rerg **LDTAGQ**-----EDTIQREGHMRWGEFVFLVYDITD-RGSFEEVLPLKNILDEIKK 107
 Ris **MDTADL**-----DTPRNCERYLNWAHAFVLYSVDS-RQSFDS SSSYLELLALHAK 121
 RasL11A **QDTPGGV**--QIQDSL PQVVDSL SKCVQWAEGLLVYSITD-YDSYLSIRPLYQHIRKVHP 136
 RasL11B **QDTPGI**---QVHENS LSCSEQLNRCIRWADAVVIVFSITD-YKSYELISQLHQHVQQLHL 141
 FLJ22655 **YDPCSQ**-----TQKAKFSLTSELHWADGFVIVYDISD-RSSF AFAKALIYRIREPQT 107
 Di-Ras1 **TDTTGS**-----HQFPAMQRLSISKGHAFILVFSVTS-KQSL EELGPIYKLIVQIKG 109
 Di-Ras2 **TDTTGS**-----HQFPAMQRLSISKGHAFILVYSITS-RQSL EELKPIYEQICEIKG 109
 Noey2 **TDSKSG**-----DGNRALQRHVIARGHAFVLYSVTK-KETLEELKAFYELICKIKG 139
 RasD1 **LDTSGN**-----HPFPAMRRLSILTGDFVILVFSLDN-RDSFEEVQRLRQOILDTKS 126
 RasD2 **LDTSGN**-----HPFPAMRRLSILTGDFVILVFSLDN-RESFDEVKRLQKQILEVKS 121
 RRP22 **RDGDVAG**PGSSPGGPEEWPDAKDWLQD TDAFVLVYDICS-PDSFDYVKALRQRI AETR- 115
 RasL10B **LDFPPI S**-AFPVNTLQEWADTCCRGLSRHAYILVYDICC-FDSFEYVKTIROQILETR- 114
 Rheb **VDTAGQ**-----DEYSIFPQTSYIDINGYILVYSVTS-IKSFEVIKVIHGKLLDMVG 108
 RhebL1 **VDTAGQ**-----DEYSILPYSFIIGVHG YVLVYSVTS-LHSFQVIESLYQKLHEGHG 108
 NKIRas1 **YDTRGL**-----QEGVELPKHYFSFADGFVLYSVNN-LESFQRV ELLKKEIDKFKD 109
 NKIRas2 **YDTRGL**-----RDGAELPRHCF SCTDGYVLVYSTDS-RESFQRV ELLKKEIDKSKD 109
 Rab40A **WDTSGQ**-----GRFCTIFRSYSRGAQGVILVYDIAN-RWSFEGMDRWIKKIEEHAP 117
 rab40B **WDTSGQ**-----GRFCTIFRSYSRGAQGVILVYDIAN-RWSFDGIDRWIKEIDEHAP 117
 Rab40C **WDTSGQ**-----GRFCTIFRSYSRGAQGILLVYDITN-RWSFDGIDRWIKEIDEHAP 117
 Rab1A **WDTAGQ**-----ERFR-TITSSYYRGAHGIIVVYD VTD-QESFN NVKQWLQ EIDRYA- 113
 Rab1B **WDTAGQ**-----ERFR-TITSSYYRGAHGIIVVYD VTD-QESYANVKQWLQ EIDRYA- 110
 Rab35 **WDTAGQ**-----ERFR-TITSTYYRGT HGVIVVYDVTS-AESFVNVKRWLHEINQN-- 109
 Rab3A **WDTAGQ**-----ERYR-TITTAYYRGAMGFILMYDITN-EESFNAVQDWSTQIKTYS- 124
 Rab3C **WDTAGQ**-----ERYR-TITTAYYRGAMGFILMYDITN-EESFNAVQDWSTQIKTYS- 132
 Rab3B **WDTAGQ**-----ERYR-TITTAYYRGAMGFILMYDITN-EESFNAVQDWATQIKTYS- 124
 Rab3D **WDTAGQ**-----ERYR-TITTAYYRGAMGFLLMYDIAN-QESFAAVQDWATQIKTYS- 124
 Rab8A **WDTAGQ**-----ERFR-TITTAYYRGAMGIMLVYDITN-EKSF DNIRNWIRNIEEHA- 110
 Rab8B **WDTAGQ**-----ERFR-TITTAYYRGAMGIMLVYDITN-EKSF DNIKNWIRNIEEHA- 110
 Rab10 **WDTAGQ**-----ERFH-TITTSYYRGAMGIMLVYDITN-GKSFENISKWLRNIDEHA- 111
 Rab13 **WDTAGQ**-----ERFK-TITTAYYRGAMG IILVYDITD-EKSFENIQNWMSIKENA- 110
 Rab12 **WDTAGQ**-----ERFN-SITSAYYRS AKG IILVYDITK-KETFDDL PKWMMKIDKYA- 240
 Rab18 **WDTAGQ**-----ERFR-TLTPSYRGAQGVILVYDVTR-RDTFVKLDNWLNELETYCT 111
 Rab19 **WDTAGQ**-----ERFR-TITQSYRS AHAAILAYDLTR-RSTFESIPHWIHEIEKYGA 167
 Rab41 **WDTAGQ**-----ERFR-TITQSYRS ANGAILAYDITK-RSSFLSVPHWIEDVRKYAG 121
 Rab30 **WDTAGQ**-----ERFR-SITQSYRSANALILTYDITC-EESFRCLPEWLREIEQYAS 112
 Rab33A **WDTAGQ**-----ERFRKSMVEHYRNVHAVVFVYDVTK-MTSFTNLKMWIQECNGHAV 140
 Rab33B **WDTAGQ**-----ERFRKSMVQHYRNVHAVVFVYDMTN-MASFHSLPSWIEECKQHLL 137
 Rab2A **WDTAGQ**-----ESFR-SITRSYYRGAAGALLVYDITR-RDTFNHLTTWLEDARQHSN 109
 Rab2B **WDTAGQ**-----ESFR-SITRSYYRGAAGALLVYDITR-RETFNHLTSWLEDARQHSS 109
 Rab4A **WDTAGQ**-----ERFR-SVTRSYYRGAAGALLVYDITS-RETYNALTNWLT DARM LAS 116
 Rab4B **WDTAGQ**-----ERFR-SVTRSYYRGAAGALLVYDITS-RETYN SLAAWLT DART LAS 146
 Rab14 **WDTAGQ**-----ERFR-AVTRSYYRGAAGALM VYDITR-RSTYNHLS SWLT DARNL TN 114
 Rab11A **WDTAGQ**-----ERYR-AITSAYYRGAVGALLVYDIAK-HLTYENVERWLKELRDHAD 114
 Rab11B **WDTAGQ**-----ERYR-RITSAYYRGAVGALLVYDIAK-HLTYENVERWLKELRDHAD 114
 Rab25 **WDTAGL**-----ERYR-AITSAYYRGAVGALLVFDLTK-HQTYAVVERWLKELYDHA E 115
 Rab39A **WDTAGQ**-----ERFR-SITRSYYRNSVGGFLVFDITN-RRSFEHV KDWLEEAKMYVQ 116
 Rab39B **WDTAGQ**-----ERFR-SITRAYYRNSVGG LLLFDITN-RRSFQNVHEWLEETKVHVQ 112
 Rab42 **WDTAGH**-----ERFR-CITRSFYRNVGVLLVFDVTN-RRSFEHIQDWHQEV MATQG 117
 Rab26 **WDTAGQ**-----ERFR-SVTHAYYRDAHALLLLYDV TN-KASFDNIQAWLTEIHEYAQ 167
 Rab37 **WDTAGQ**-----ERFR-SVTHAYYRDAQALLLLYDITN-KSSFDNIRAWLTEIHEYAQ 126
 RasEF **WDTAGQ**-----ERFR-SIAKSYFRKADG VLLLLYDVTC-EKSFLNIREWVDMIEDAAH 644
 Rab27A **WDTAGQ**-----ERFR-SLTTAFFRDAMGFLLLFDL TN-EQSFLNVRNWSQLQMHAY 122
 Rab27B **WDTAGQ**-----ERFR-SLTTAFFRDAMGFLLMFDL TS-QQSFLNVRNWSQLQANAY 122

Rab23	WDTAGQ -----	EEFDAITKAYYRGAQACVLVSTTD-RESFEAVSSWREKVVAEVG	112
RabL4	FDSAGK -----	ELFSEMLDKLWESPVLCLVYDVTN-EESFNNSCKWLEKARSQAP	111
Rab9A	WDTAGQ -----	ERFRSLRTPFYRGSDCCLLTFSVDD-SQSFQNLNWKKEFIYYAD	110
Rab9B	WDTAGQ -----	ERFKSLRTPFYRGADCCLLTFSVDD-RQSFENLGNWQKEFIYYAD	110
Rab7A	WDTAGQ -----	ERFQSLGVAFYRGADCCVLVFDVTA-PNTFKTLDSWRDEFLIQAS	111
Rab7B	WDTGGQ -----	ERFRSMVSTFYKGS DGCILAFDVTD-LESFEALDIWRGDVLAKIV	111
Rab32	WDIAGQ -----	ERFGNMTRVYYKEAVGAFVVDISR-SSTFEAVLKWKSDLDKSVH	129
Rab38	WDIAGQ -----	ERFGNMTRVYYREAMGAFIVFDVTR-PATFEAVAKWKNLDLDSKLS	113
Rab7L1	WDIAGQ -----	ERFTSMTRLYYRDASACVIMFDVTN-ATTFSNSQRWKQDLDSKLT	111
Rab5A	WDTAGQ -----	ERYHSLAPMYRGAQAIIVVDITN-EESFARAKNWKELQR---	120
Rab5C	WDTAGQ -----	ERYHSLAPMYRGAQAIIVVDITN-TDTFARAKNWKELQR---	120
Rab5B	WDTAGQ -----	ERYHSLAPMYRGAQAIIVVDITN-QETFARAKTWKELQR---	120
Rab22A	WDTAGQ -----	ERFRALAPMYRGSAAAIIVVDITK-EETFSTLKNWKELRQ---	105
Rab22B	WDTAGQ -----	ERFHSLAPMYRGSAAAVIVVDITK-QDSFYTLKKWKELKE---	106
Rab24	WDTAGS -----	ERYEAMSRIYYRGAKAAIVCYDLTD-SSSFERAKFVWKELRS---	108
Rab21	WDTAGQ -----	ERFHALGPIYYRDSNGAILVYDITD-EDSFQKVKVWKELRK---	119
Rab17	WDTAGQ -----	EKYHSVCHLYFRGANAALLVYDITR-KDSFLKAQQWLKLEEE--	128
Rab6A	WDTAGQ -----	ERFRSLIPSYIRDSAAAVVVDITN-VNSFOQTTKWIDDVRT---	113
Rab6C	WDTAGQ -----	ERLRSIIPRYIRDSAAAVVVDITN-VNSFOQTTKWIDDVRT---	113
Rab6B	WDTAGQ -----	ERFRSLIPSYIRDSTVAVVVDITN-LNSFOQTSKWIDDVRT---	113
Rab28	WDIGGQ -----	TIGGKMLDKYIYGAQGVLLVYDITN-YQSFENLEDWYTVVKKVSE	116
Rab15	WDTAGQ -----	ERYQTITKQYYRRAQGIFLVYDISS-ERSYQHIMKWVSDVDEVD	111
Rab34	WDTAGQ -----	ERFKCIASTYYRGAQAIIIVFNLND-VASLEHTKQWLADALKEND	155
Rab36	WDTAGQ -----	EKFKCIASAYYRGAQVIITAFDLTD-VQLEHTROWLEDALRENE	226
Ran	WDTAGQ -----	EKFGGLRDGYIIQAQCAIIMFDVTS-RVITYKNVFNWHRDLVRVCE	113
RabL2A	WDTAGQ -----	ERFQSMHASYYHKAHACIMVFDIQR-KVTYRNLS-TWYTELREFR	123
RabL2B	WDTAGQ -----	ERFQSMHASYYHKAHACIMVFDVQR-KVTYRNLS-TWYTELREFR	123
Miro1	VDYSEA -----	EQSDEQLHQEISQANVICIVYAVNN-KHSIDKVTSRWIPLINERT	105
Miro2	VDYSEA -----	EQTDEELREEIHKANVVCVVDVSE-EATIEKIRTKWIPLVNGGT	105
Rab20	WDTAGR -----	EQFHGLGSMYCRGAAAILTYDVNH-RQSLVELEDRLFGLTDTAS	103
RabL3	WDVGGSVG -----	SASSVKSTRAVFYNSVNGIIFVHDLTN-KKSSQNLRRWSLEALNRDL	118
Arfrp2	KELGGA -----	DNIRKYWSRYYQGSQGVIFVLDSASSEDLEAARNELHSALQHPQ	131
RabL5	WDCGGD -----	AKFESCWPALMKDAHGVIIVFNADI-PSHRKEMEMWYSCFVQOPS	111
SRPRB	IDLPGH -----	ESLRLQFLERFKSAGAIVFVDSAAFQREVKDVAEFLYQVLIDSM	167
LOC401884	GAELGA -----	PGRAEVGRDTAERKGSRI PRGAPPEASRAAAAAGAPALSPRALPS	103

G4

Arf1	LRD-----AVLLVFANKQDLPN-----AMNAAE-----I	139
Arf3	LRD-----AVLLVFANKQDLPN-----AMNAAE-----I	139
Arf4	LRD-----AVLLLIFANKQDLPN-----AMAISE-----M	139
Arf5	LRD-----AVLLVFANKQDMPN-----AMPVSE-----L	139
Arf6	MRD-----AIIILIFANKQDLPD-----AMKPHE-----I	139
Ard1	LRD-----ALLLIFANKQDVAG-----ALSVEE-----I	526
Arl1	LRK-----AILVVFANKQDMEQ-----AMTSSE-----M	139
Arl5	LRK-----AGLLIFANKQDVKE-----CMTVAE-----I	138
Arl8	LRK-----AAVLIFANKQDMKG-----CMTAAE-----I	137
Arl2	LAG-----ATLLIFANKQDLPG-----ALSSNA-----I	138
Arl3	LSC-----VPVLIFANKQDLLT-----AAPASE-----I	139
Arl6	IKHR-----RIPILFFANKMDLRD-----AVTSVK-----V	144
Arl4	NQG-----VPVLIIVANKQDLRN-----SLSLSE-----I	147
Arl7	NQG-----TPLLVIANKQDLPK-----SLPVAE-----I	140
Arf4L	NQG-----VPVVLVANKQDQPG-----ALSAAE-----V	148
Arl11	MAG-----VPFVLVANKQEAPD-----ALPLLK-----I	135
FLJ22595	IKN-----VPVLLANKQDMPG-----ALTAED-----I	136
ArfRP1	LCG-----VPVVLVANKQDVET-----CLSIDP-----I	147
Arl2L1	ISG-----KPILVLANKQDKEG-----ALGEAD-----V	143
Arl9	VLP-----LVVFANKQDLEA-----AYHITD-----I	139
Arl10A	DLP-----VVVVANKQDLSE-----AMSMGE-----L	198
Sar1a	ISN-----VPILILGNKIDRTD-----AISEEK-----L	147
Sar1b	IAN-----VPILILGNKIDRPE-----AISEER-----L	147
Arl10B	LQG-----IPVVLVGNKRDLPG-----ALDEKE-----L	143
Arl10C	LQG-----IPVVLVGNKRDLPN-----ALDEKQ-----L	143
LOC339231	LAE-----ASVLIILFNKIDLPCY-----MSTEEMKSLIR-L	158
RhoA	PN-----VPIILVGNKKDLRNDDEHTRRELAK-MKQEPVK-----P	141
RhoC	PN-----VPIILVGNKKDLRQDEHTRRELAK-MKQEPVR-----S	141
RhoB	PN-----VPIILVANKKDLRSDEHVRTELAR-MKQEPVR-----T	141
Rnd2	PN-----AKVVLVGCKLDMRTDLATLRELSK-ORLIPVT-----H	143
Rnd3	PN-----TKMLLVGCKSDLRTDVTSTLVELSN-HRQTPVS-----Y	159
Rnd1	PS-----TRVLLIGCKTDLRDTLSTLMELSH-QKQAPIS-----Y	149
RhoD	KK-----VPIIVVGCKTDLRKDKSLVNKLRR-NGLEPVT-----Y	153
Rif	RG-----IPMVLIGCKTDLRKDKQLRKLRA-AQLEPIT-----Y	155
Rac1	PN-----TPIILVGTKLDLRDDKDTIEKLKE-KKLTPIT-----Y	139
Rac2	PS-----TPIILVGTKLDLRDDKDTIEKLKE-KKLAPIT-----Y	139
Rac3	PH-----TPILLVGTKLDLRDDKDTIERLRD-KKLAPIT-----Y	139
RhoG	PD-----VPILLVGTKKDLRAQPDTLRRLKE-QSQAPIT-----P	139
TC10	PN-----VPFLLIGTQIDLRDDPKTLARLND-MKEKPIC-----V	153
TCL	PH-----VPYVLLIGTQIDLRDDPKTLARLLY-MKEKPLT-----Y	157
Cdc42	PK-----TPFLLVGTQIDLRDDPSTIEKLAK-NKQKPIT-----P	139
Wrch-2	PQ-----APVLLVGTQADLRDDVNVLIQLDQGGREGPVP-----Q	168
Wrch-1	PK-----APIILVGTQSDLREDVKVLIELDK-CKEKVPV-----E	185
RhoH	PC-----TPVLLVATQTDQR-----EMGP-HRASCVN-----A	133
RhoBTB1	PR-----TPVILVGCQLDLRYADLEAVNRARRPLARPIKRGDILPP	171
RhoBTB2	PR-----APVILVGCQLDLRYADLEAVNRARRPLARPIKNEILPP	171
H-Ras	SDD-----VPMVLVGNKCDLAA-----RTVESR-----	128
K-Ras2B	SED-----VPMVLVGNKCDLPS-----RTVDTK-----	128
N-Ras	SDD-----VPMVLVGNKCDLPT-----RTVDTK-----	128
R-Ras	RDD-----FPVVLVGNKADLES-----QRQVPRS-----	155
TC21	RDE-----FPMILIGNKADLDH-----QRQVTQE-----	140
M-Ras	RES-----FPMILVANKVDLMH-----LRKITRE-----	139
Rit1	TDD-----TPVVLVGNKSDLKQ-----LRQVTKE-----	147
Rit2	TYE-----IPLVLVGNKIDLEQ-----FROVSTE-----	146
Rap1A	TED-----VPMILVGNKCDLED-----ERVVGKE-----	129
Rap1B	TDD-----VPMILVGNKCDLED-----ERVVGKE-----	129
Rap2A	YEK-----VPVILVGNKVDLES-----EREVSSS-----	129
Rap2C	YEK-----VPLILVGNKVDLEP-----EREVMSS-----	129

Rap2B	YER-----VPMILVGNKVDLEG-----EREVSYG-----	129
RalA	DEN-----VPFLLVGNKSDLED-----KROVSVE-----	140
RalB	EEDK-----IPLLVVGNKSDLEE-----RRQVPVE-----	141
E-Ras	PHPA-----QPLVLVGNKCDLVT-----TAGDAHA-----	164
Gem	T-----EDIPIILVGNKSDLVR-----CREVSVS-----	204
Rad	T-----DDVPIILVGNKSDLVR-----SREVSVD-----	216
Rem1	A-----DHPVPIILVGNKADLAR-----CREVSVE-----	208
Rem2	H-----HDLPVILVGNKSDLAR-----SREVSLE-----	232
Rerg	P-----KNVTLILVGNKADLDH-----SRQVSTE-----	131
Ris	ET-----Q-----RSIPALLLGNKLDMAQ-----YRQVTKA-----	157
RasL11A	-----D-----SKAPVIVGNKGDLLH-----ARQVQTQ-----	160
RasL11B	-----G-----TRLPVVVVANKADLLH-----IKQVDPQ-----	165
FLJ22655	SHC---KRA-----VESAVFLVGNKRDLCHE-----VREVGWE-----	136
Di-Ras1	-----SV-----EDIPVMLVGNKCDDET-----QREVDTR-----	133
Di-Ras2	-----DV-----ESIPIMLVGNKCDESP-----SREVQSS-----	134
Noey2	N-----NL-----HKFPIVLVGNKSDDT-----HREVALN-----	164
RasD1	CLKNKTKEN-----VDVPLVICGNKGDRLD-----FYREVDQRE-----	159
RasD2	CLKNKTKEA-----AELPMVICGNKNDHGE-----LCRQVPTTE-----	155
RRP22	-----PAGA-----PEAPILVVGNKRDRLQ-----RLRFGPRRA-----	143
RasL10B	-----VIGT-----SETPIIVGNKRDLLQ-----RGRVIPRWN-----	142
Rheb	KVQ-----IPIMLVGNKDDLHM-----ERVISYE-----	142
RhebL1	KTR-----VPVVLVGNKADLSP-----EREVQAV-----	142
NKIRas1	KKE-----VAIVVLGNKIDLSE-----QRQVDAE-----	143
NKIRas2	KKE-----VTIVVLGNKCDLQEQ-----QRRVDPD-----	143
Rab40A	G-----VPKILVGNRLHLAF-----KROVPRE-----	139
rab40B	G-----VPKILVGNRLHLAF-----KROVPTTE-----	139
Rab40C	G-----VPRILVGNRLHLAF-----KROVPTTE-----	139
Rab1A	SE-----NVNKLVLVGNKCDLTT-----KKVVDYT-----	137
Rab1B	SE-----NVNKLVLVGNKSDLTT-----KKVVDNT-----	134
Rab35	CD-----DVCRIILVGNKNDPE-----RKVVETE-----	133
Rab3A	WD-----NAQVLLVGNKCDMED-----ERVVSSE-----	148
Rab3C	WD-----NAQVILVGNKCDMED-----ERVISTE-----	156
Rab3B	WD-----NAQVILVGNKCDMEE-----ERVVPTTE-----	158
Rab3D	WD-----NAQVILVGNKCDLED-----ERVVPAE-----	158
Rab8A	SA-----DVEKMILGNKCDVND-----KRQVSKE-----	134
Rab8B	SS-----DVERMILGNKCDMND-----KRQVSKE-----	134
Rab10	NE-----DVERMLLGNKCDMDD-----KRVVPKG-----	135
Rab13	SA-----GVERLLLGNKCDMEA-----KRKVOKE-----	134
Rab12	SE-----DAELLLVGNKLDCE-----DREITRQ-----	264
Rab18	RN-----DIVNMLVGNKID-KE-----NREVDRN-----	134
Rab19	A-----NVVIMLIGNKCDLWE-----KRHVLFE-----	190
Rab41	S-----NIVQLLIGNKSDLSE-----LREVSLA-----	144
Rab30	N-----KVITVLVGNKIDLAE-----RREVSQQ-----	135
Rab33A	PP-----LVPKVLVGNKCDLRE-----QIQVPSN-----	164
Rab33B	AN-----DIPRILVGNKCDLRS-----AIQVPTD-----	161
Rab2A	S-----NMVIMLIGNKSDLES-----RREVKKE-----	132
Rab2B	S-----NMVIMLIGNKSDLES-----RRDVKRE-----	132
Rab4A	Q-----NIVIILCGNKDLDA-----DREVTFL-----	139
Rab4B	P-----NIVVILCGNKDLDP-----EREVTFL-----	169
Rab14	P-----NTVIILIGNKADLEA-----QRDVTYE-----	137
Rab11A	S-----NIVIMLVGNKSDLRH-----LRVPTD-----	137
Rab11B	S-----NIVIMLVGNKSDLRH-----LRVPTD-----	137
Rab25	A-----TIVVMLVGNKSDLSEQ-----AREVPTTE-----	138
Rab39A	PF-----RIVFLLVGHKCDLAS-----QRQVTR-----	140
Rab39B	PY-----QIVFVLVGHKCDLDT-----QRQVTRH-----	136
Rab42	PD-----KVIFLLVGHKSDLQES-----TRCVSAQ-----	141
Rab26	HD-----VA-LMLLGNKVDSAH-----ERVVKRE-----	190
Rab37	RD-----VV-IMLLGNKADMSS-----ERVIRSE-----	149
RasEF	ET-----VP-IMLVGNKADIRDTAATE-----GQKCVPGH-----	673
Rab27A	CE-----NPDIVLVCGNKSDLED-----QRVVKEE-----	146
Rab27B	CE-----NPDIVLIGNKADLPD-----QREVNER-----	146

Rab23	-----DIPTVLVQNKIDLLD-----DSCIKN-----	133
RabL4	GI-----SLPGVLVGNKTDLAG-----RRAVDS-----	134
Rab9A	VKEP-----ESFPFVILGNKIDISE-----RQVSTE-----	136
Rab9B	VKDP-----EHFPFVVLGNKVDKED-----RQVTTE-----	136
Rab7A	PRDP-----ENFPFVVLGNKIDLEN-----RQVATK-----	137
Rab7B	PME-----QSYPMVLLGNKIDLAD-----RKVPQE-----	137
Rab32	LPNG-----SPIPAVLLANKCDQNK-----DSSQSP-----	155
Rab38	LPNG-----KPVSVVLLANKCDQK-----DVLMMNG-----	140
Rab7L1	LPNG-----EPVPCLLLANKCDLSP-----WAVSRD-----	137
Rab5A	-QAS-----PNIVIALSGNKADLAN-----KRAVDFQ-----	146
Rab5C	-QAS-----PNIVIALAGNKADLAS-----KRAVEFQ-----	146
Rab5B	-QAS-----PSIVIALAGNKADLAN-----KRMVEYE-----	146
Rab22A	-HGP-----PNIVVAIAGNKCDLID-----VREVMER-----	131
Rab22B	-HGP-----ENIVMAIAGNKCDLSD-----IREVPLK-----	132
Rab24	-LEE-----G-CQIYLCGTKSDLLEEDR-----RRRRVDFH-----	137
Rab21	-MLG-----NEICLCIVGNKIDLEK-----ERHVS IQ-----	145
Rab17	-LHP-----GEVLVMLVGNKTDLSQ-----EREVTFQ-----	154
Rab6A	-ERG-----SDVIIMLVGNKTDLAD-----KROVSIE-----	139
Rab6C	-ERG-----SDVIITLVGNRTDLAD-----KROVSVE-----	139
Rab6B	-ERG-----SDVIIMLVGNKTDLAD-----KRQITIE-----	139
Rab28	-ESE-----TQPLVALVGNKIDLEH-----MRTIKPE-----	142
Rab15	ATS-----LPGCGEGASP-----GKARRGPD-----	132
Rab34	PSSV-----LLFLVGSKKDLST-----PAQYALME-----	180
Rab36	AGSC-----FIFLVGTTKDLLS-----GAACEQAE-----	251
Ran	N-----IPIVLCGNKVDIKD-----RKVKAK-----	134
RabL2A	PE-----IPCIVVANKIDDIN-----VT-----	141
RabL2B	PE-----IPCIVVANKIDDIN-----VT-----	141
Miro1	DKDS-----RLPLILVGNKSDLVE-----YSSMET-----	130
Miro2	TQGP-----RVPIILVGNKSDLRS-----GSSMEA-----	130
Rab20	KD-----CLFAIVGNKVDLTE-----EGALAGQ-----	126
RabL3	VPTGVLVTNGDYDQEQFADNQIPLLVIGTKLDQIHET-----KRHEVLTTTAF LAED	170
Arfrp2	LCT-----LPFLILANHQDKPA-----ARVQOE-----I	155
RabL5	LQD-----TQCMLIAHHPGSG-----DDK-----	131
SRPRB	GLKN-----TPSFLLIACNKQDIAMAKS-----AKLIQQOLEK-----E	200
LOC401884	LTMG-----MGQKEAPHCGEVRGG-----FGTGVRGG-----G	131

G5

Arf1	TDKLGHLHLRH-----RNWY IQATCAT SG-----DGLYEGLDWLSNQLRNQ	180
Arf3	TDKLGHLHLRH-----RNWY IQATCAT SG-----DGLYEGLDWLANQLKNK	180
Arf4	TDKLGLOSLRN-----RTWY VQATCAT QG-----TGLYEGLDWLSNELSKR	180
Arf5	TDKLGLOHLRS-----RTWY VQATCAT QG-----TGLYDGLDWLSHELKSR	180
Arf6	QEKLGLTRIRD-----RNWY VQPSCAT SG-----DGLYEGLTWLTSNYKS	179
Ard1	TELLSLHKLCCG-----RSWY IQGCDAR SG-----MGLYEGLDWLSRQLVAA	468
Arl1	ANSLGLPALKD-----RKWQ IFKTSAT KG-----TGLDEAMEWLVTLSKSR	180
Arl5	SQFLKLTSIKD-----HQWH IQACCAL TG-----EGLCQGLEWMSRLKIR	179
Arl8	SKYLTLSIKD-----HPWH IQSCCAL TG-----EGLCQGLEWMTSRIGVR	178
Arl2	REALELDSIRS-----HHWC IQGCSAV TG-----ENLLPGIDWLLDDISSR	179
Arl3	AEGLNLHTIRD-----RVWQ IQSCSAL TG-----EGVQDGMNVVCKNVNAK	180
Arl6	SQLLCLENIKD-----KPWH ICASDAI KG-----EGLQEGVDWLQDQIQTV	185
Arl4	EKLLAMGELSSS-----TPWH LQPTCAI IIG-----DGLKEGLEKLHDMI IKR	189
Arl7	EKQLALHELIPA-----TTYH VQPACAI IIG-----EGLTEGMDKLYEMILKR	182
Arf4L	EKRLAVRELAHA-----TLTH VQGC SAV DG-----LGLQOGLERLYEMILKR	190
Arl11	RNRLSLERFQ-D-----HCWEL RGCSAL TG-----EGLPEALQSLWLSLLKSR	176
FLJ22595	TRMFVKVKKLCS-----RNWY VQPCAL TG-----EGLAQGFRKLTGFVKVSH	178
ArfRP1	KTAFS-DCTSKIG-----RRDCL TQACSAL TG-----KGVREGIEWLTKVVRN	190
Arl2L1	IECLSLEKLVNEH-----KCLC QIEPCS SAISGYGKKIDKSIKGLYWLLHVIARD	193
Arl9	HEALALSEVGN-----RKMFL FGTYLT KNGS--EIPSTMQDAKDLIAQLAAD	185
Arl10A	QRELGLQAINQ-----REV FLLAAS IAPAGPTFEETPGTVHIWKLLELLS	244
Sarla	REIFGLYGOTTGKGNVTLKELNAR PMEVFMCSV LKR-----QGYGEGFRWLSQYID	198
Sarl1b	REMFGLYGOTTGKGSISLKELNAR PLEVFMCSV LKR-----QGYGEGFRWMAQYID	198
Arl10B	IEKMNL SAIQD -----REIC CYSIS CKEK-----DNIDITLQWL IQH SKSR	184
Arl10C	IEKMNL SAIQD -----REIC CYSIS CKEK-----DNIDITLQWL IQH SKSR	184
LOC339231	PDIIACAKQN-----IT TAEI SAREG-----TGLAGVLAWLQATHRAN	190
RhoA	EEGRDMANRIGA-----FGY MECSAK T-----KDG-VREVFEMATRAALQA	181
RhoC	EEGRDMANRISA-----FGY LECSAK T-----KEG-VREVFEMATRAGLOV	181
RhoB	DDGRAMAVRIOA-----YD YLECSAK T-----KEG-VREVFEMATRAALQK	181
Rnd2	EQGTVLAKQVGA-----VSY VECSSR S-----SERSVRDVPHVATVASLGR	184
Rnd3	DQGANMAKQIGA-----ATY IECSAL Q-----SENSVRDIFHVATLACVNK	200
Rnd1	EQGCAIAKQLGA-----EI YLEGSA FT-----SEKSIHSIFRTASMLCLNK	190
RhoD	HRGQEMARSVGA-----VAY LECSAR L-----HDN-VHAVFQEAEEVALSS	193
Rif	MQGLSACEQIRA-----ALY LECSAK F-----REN-VEDVFREAAKVALSA	195
Rac1	POGLAMAKEIGA-----VKY LECSAL T-----QRG-LKTVFDEAIRAVLCP	179
Rac2	POGLALAKEIDS-----VKY LECSAL T-----QRG-LKTVFDEAIRAVLCP	179
Rac3	POGLAMAREIGS-----VKY LECSAL T-----QRG-LKTVFDEAIRAVLCP	179
RhoG	QOQOALAKQIHA-----VR YLECSAL Q-----QDG-VKEVFAEAVRAVLNP	179
TC10	EQGQKLAKAIGA-----CCY VECSAL T-----QKG-LKTVFDEAIIAILTP	193
TCL	EHGVKLAKAIGA-----QCY LECSAL T-----QKG-LKAVFDEAILTIFHP	197
Cdc42	ETAEKLARDLKA-----VKY VECSAL T-----QKG-LKNVFDEAIIAALAP	179
Wrch-2	POAQGLAERIRA-----CCY LECSAL T-----QKN-LKEVFDSAILSATIEH	208
Wrch-1	EAAKLCAEEIKA-----ASY IECSAL T-----QKN-LKEVFDAIIVAGIQY	225
RhoH	MEGKKLAQDVRA-----KG YLECSAL S-----NRG-VQQVFECVAVTAVNQ	173
RhoBTB1	EKGREVAKELG-----LPY YETS VFD-----QFG-IKDVFDNAIRAALIS	210
RhoBTB2	EKGREVAKELG-----IPY YETS VVA-----QFG-IKDVFDNAIRAALIS	210
H-Ras	-QAQDLARSYG-----IPY IETSAK -----TRQGVEDAFYTLVREIROH	166
K-Ras2B	-QAQDLARSYG-----IP FIETSAK -----TRQGVDDAFYTLVREIRKH	166
N-Ras	-QAHELAKSYG-----IP FIETSAK -----TRQGVEDAFYTLVREIROY	166
R-Ras	-EASAFGASHH-----VAY FEASAK -----LRLNVDEAFEQLVRAVRKY	193
TC21	-EGQQLARQLK-----VTY MEASAK -----IRMNVDAQFHELVRVIRKF	178
M-Ras	-QGKEMATKHN-----IPY IETSAK D-----PPLNVDKAFHDLVRVIRQQ	178
Rit1	-EGLALAREFS-----CP FFETSAA -----YRYIIDDFHALVREIRRK	185
Rit2	-EGLSLAQEYN-----CG FFETSAA -----LRFCIDDAFHGLVREIRKK	184
Rap1A	-QOQNARQWCN-----CAF LESSAK -----SKINVNEIFYDLVRQINRK	168
Rap1B	-QOQNARQWCN-----CAF LESSAK -----SKINVNEIFYDLVRQINRK	168
Rap2A	-EGRALAEWEG-----CP FMETSAK -----SKTMVDELFAEIVRQMNIA	167
Rap2C	-EGRALAEWEG-----CP FMETSAK -----SKSMVDELFAEIVRQMNYS	167

Rap2B	-EGKALAE EWS-----	CPFMETS AK -----	NKASVDELFAEIVRQMNYA	167
RalA	-EAKNRAEQWN-----	VNYVETS AK -----	TRANVDKVFDFDLREIRAR	178
RalB	-EARSKAEEWG-----	VQYVETS AK -----	TRANVDKVFDFDLREIRTK	179
E-Ras	-AAAALAHSWG-----	AHFVETS AK -----	TRQGVEEAFSLLVHEIQRV	205
Gem	-EGRACAVVFD-----	CKFIETS AAV -----	QHN-VKELFEGIVRQVRLR	242
Rad	-EGRACAVVFD-----	CKFIETS AAL -----	HHN-VQALFEGVVRQIRLR	254
Rem1	-EGRACAVVFD-----	CKFIETS ATL -----	QHN-VAELFEGVVRQLRLR	246
Rem2	-EGRHLAETLS-----	CKHIETS AAL -----	HHN-TRELFEGAVRQIRLR	270
Rerg	-EGEKLAETELA-----	CAFYEC SACT -----	GEGNITEIFYELCREVRRR	170
Ris	-EGVALAGRFG-----	CLFFEV SACL -----	DFEHVQHVHFHEAVREARRE	186
RasL11A	-DGIQLANELG-----	SLFLEI STSE -----	NYEDVCDVFOHLCKEVSKM	199
RasL11B	-LGLQLASMLG-----	CSFYEV SVE -----	NYNDVYSAFHVLCKEVSHK	204
FLJ22655	-EGQKLALENR-----	QFC ELSAE -----	QSLEVEMMFIRI IKDILIN	175
Di-Ras1	-EAQAVAQEWK-----	CAF METS AKM-----	NYN-VKELFQELLTLETRR	171
Di-Ras2	-EAEALARTWK-----	CAF METS AKL-----	NHN-VKELFQELLNLEKRR	172
Noey2	-DGATCAMEWN-----	CAF MEI SAKT-----	DVN-VQELFHMLLNYYKKP	202
RasD1	IEQLVGDDPQR-----	CAY FEI SAKK-----	NSS-LDQMFRALFAMAKLP	198
RasD2	AELLVSGD-EN-----	CAY FEV SAKK-----	NTN-VDEMFFYVLFMAKLP	193
RRP22	LAALVRRG-WR-----	CGY LECS AKY-----	NWH-VLRLFRELLRCALVR	181
RasL10B	VSHLVRKT-WK-----	CGY VECS AKY-----	NWH-ILLFSELLKSVGCA	180
Rheb	-EGKLAESWN-----	A AFLE SSAK-----	ENQTAVDVFRRILEAEKM	170
RhebL1	-EGKKLAESWG-----	AT FME SSAR-----	ENQLTQGIFTKVIQEIARV	170
NKIRas1	-VAQQWAKSEK-----	VRL WEV TVT-----	DRKTLIEPFTLLASKLSQP	171
NKIRas2	-VAQHWAKSEK-----	VKL WEV SVA-----	DRRSLLEPFVYLASKMTPQ	171
Rab40A	-QAQAYAERLG-----	VT FFEV SPLC-----	NFN-IIESFTELARIVLLR	177
rab40B	-QAQAYAERLG-----	VT FFEV SPLC-----	NFN-ITESFTELARIVLLR	177
Rab40C	-QARAYA EKNC-----	MT FFEV SPLC-----	NFN-VIESFTELSRIVLMR	177
Rab1A	-TAKEFADSL-G-----	IP FLE TSAK-----	NATNVEQSFMTMAAEIKKR	175
Rab1B	-TAKEFADSL-G-----	IP FLE TSAK-----	NATNVEQAFMTMAAEIKKR	172
Rab35	-DAYKFAGQM-G-----	I QLF ETS AK -----	ENVNVEEMFNCITELVLRA	171
Rab3A	-RGRQLADHL-G-----	FE FFE AS AK -----	DNINVKQTFERLVDVICEK	186
Rab3C	-RGQHLGEQL-G-----	FE FFE AS AK -----	DNINVKQTFERLVDIICDK	194
Rab3B	-KGQLLAEQL-G-----	FD FFE AS AK -----	ENISVRQAFERLVDAICDK	186
Rab3D	-DGRRLAADDL-G-----	FE FFE AS AK -----	ENINVQVFERLVDVICEK	186
Rab8A	-RGEKLALDY-G-----	IK FMET SAK-----	ANINVENAFFTLARDIKAK	172
Rab8B	-RGEKLALDY-G-----	IK FLE TS AK -----	SSANVEEAFFTLARDIMTK	172
Rab10	-KGGQIAREH-G-----	IR FFET SAK-----	ANINIEKAFLTLAEDILRK	173
Rab13	-QADKLAREH-G-----	IR FFET SAK-----	SSMNVEAFSSLARDILLK	172
Rab12	-QGEKFAQQITG-----	M RFCE AS AK -----	DNFNVDEIFLKLVDLILKK	303
Rab18	-EGLKFARKH-S-----	ML FI EAS AK -----	TCDGVQCAFEELVEKIIQT	172
Rab19	-DACTLAEKYGL-----	LAV LE TS AK -----	ESKNIEEVFVLMAKELIAR	229
Rab41	-EAQSLAEHYDI-----	LC AI ETS AK -----	DSSNVEEAFLRVATELIMR	183
Rab30	-RAEEFSEAQDM-----	Y- YLE TS AK -----	ESDNVEKLFLDLACRLISE	173
Rab33A	-LALKFADAHNM-----	L- LF ETS AK DPK-----	ESQNVESIFMCLACRLKAQ	205
Rab33B	-LAQKFADTHSM-----	P- LF ETS AK NPN-----	DNDHVEAIFMTLAHKLKSH	202
Rab2A	-EGEAFAREH-G-----	L IFMET SAK-----	TASNVEEAFINTAKEIYEK	170
Rab2B	-EGEAFAREH-G-----	L IFMET SAK-----	TACNVEEAFINTAKEIYRK	170
Rab4A	-EASRFAQEN-E-----	LM FLE TS AK -----	TGENVEEAFVQCARKILNK	177
Rab4B	-EASRFAQEN-E-----	LM FLE TS AK -----	TGENVEEAFKLCARTILNK	207
Rab14	-EAKQFAEEN-G-----	LL FLE AS AK -----	TGENVEDAFLEAAKKIYQN	175
Rab11A	-EARAFAEKN-G-----	LS FI ETS AK -----	DSTNVEEAFQITILTEIYRI	175
Rab11B	-EARAFAEKN-N-----	LS FI ETS AK -----	DSTNVEEAFKNILTEIYRI	175
Rab25	-EARMFAENN-G-----	LL FLE TS AK -----	DSTNVELAFETVLKEIFAK	176
Rab39A	-EAEKLSADC-G-----	M KYI ETS AK -----	DATNVEESFTILTRDIYEL	178
Rab39B	-EAEKLAAAY-G-----	M KYI ETS AK -----	DAINVEKAFTDLTRDIYEL	174
Rab42	-EAEELAASL-G-----	MA FVET SVK-----	NNCNVDLAFDTLADAIQQA	179
Rab26	-DGEKLAKEY-G-----	LP FMET SAK-----	TGLNVDLAFTAIAKELKQR	228
Rab37	-DGETLAREY-G-----	VP FLE TS AK -----	TGMNVELAFLAIAKELKYR	187
RasEF	-FGEKLAMTY-G-----	AL FCET SAK-----	DGSNIVEAVLHLIAKELVKKR	711
Rab27A	-EAIALAEKY-G-----	IP YFET S AA -----	NGTNISQAIEMLLDLIMKR	184
Rab27B	-QARELADKY-G-----	IP YFET S AA -----	TGQNVKAVETLLDLIMKR	184

Rab23	-EEAEALAKRLK-----	LRFYRTSVK	-----	EDLNVNEVFKYLAEKYLQK	172
RabL4	-AEARAWALGQG-----	LECFETSVK	-----	EMENFEAPFHCLAKQFHQL	173
Rab9A	-EAQAWCRDNGD-----	YPYFETSAK	-----	DATNVAAAFEEAVRRVLAT	175
Rab9B	-EAQTWCMENGD-----	YPYLETSAK	-----	DDTNVTVAFEEAVRQVLAV	175
Rab7A	-RAQAWCYSKNN-----	IPYFETSAK	-----	EAINVEQAFQTIARNALKQ	176
Rab7B	-VAQGWCREK-D-----	IPYFEVSAK	-----	NDINVVQAFEMLASRALS	174
Rab32	SOVDQFCKEHGF-----	AGWFETSAK	-----	DNINIEEAARFLVEKILVN	195
Rab38	LKMDQFCKEHGF-----	VGWFETSAK	-----	ENINIDEASRCLVKHILAN	180
Rab7L1	-QIDRFKENG-----	TGWTETSVK	-----	ENKNINEAMRVLIKMMRN	176
Rab5A	--EAQSYADDNS-----	LLFMETSAK	-----	TSMNVNEIFMAIAKKLKPN	184
Rab5C	--EAQAYADDNS-----	LLFMETSAK	-----	TAMNVNEIFMAIAKKLKPN	184
Rab5B	--EAQAYADDNS-----	LLFMETSAK	-----	TAMNVNDLFLAIAKKLKPKS	184
Rab22A	--DAKDYADSIH-----	AIFVETSAK	-----	NAININELFIEISRRIPT	169
Rab22B	--DAKEYAESIG-----	AIVVETSAK	-----	NAINIEELFQGISRQIPPL	170
Rab24	--DVQDYADNIK-----	AQLFETSCK	-----	TGQSVDELFOKVAEDYVSV	175
Rab21	--EAESYAESVG-----	AKHYHTSAK	-----	QNKGIEELFLDLCKRMIET	183
Rab17	--EGKEFADSQK-----	LLFMETSAK	-----	LNHQVSEVFNTVAQELLQR	192
Rab6A	--EGERKAKELN-----	VMFIETSAK	-----	AGYNVKQLFRRVAAALPGM	177
Rab6C	--EGERKAKGLN-----	VTFIETRAK	-----	TGYNVKQLFRRVAAALPGM	177
Rab6B	--EGEQRAKELS-----	VMFIETSAK	-----	TGYNVKQLFRRVAAALPGM	177
Rab28	--KHLRFQENG-----	FSSHVFSAK	-----	TGDSVFLCFQKVAEILGI	180
Rab15	GKANASRKLCLP-----	QPWMKTSKT	-----	HQKASRRSLLGIRLMRSR	171
Rab34	KDALQVAQEMKA-----	EYWAVSSLT	-----	GENVREFFFRVAALTFEA	219
Rab36	ADAVHLAREMQA-----	EYWSV-SAKT	-----	GENVKAFFSRVAALAFEQ	290
Ran	-SIVFHRKKN-----	LQYYDISAK	-----	SNYNFEKPFLLWARKLIGD	171
RabL2A	QKSFNFACKFSL-----	PLYFV-SAAD	-----	GTN-VVKLFNDAIRLAVSY	180
RabL2B	QKSFNFACKFSL-----	PLYFV-SAAD	-----	GTN-VVKLFNDAIRLAVSY	180
Miro1	-ILPIMNQYTEI-----	ETCVECSAKN	-----	LKNISELFYYAQKAVLHP	169
Miro2	-VLPIMSQFPEI-----	ETCVECSAKN	-----	LRNISELFYYAQKAVLHP	169
Rab20	-EKEECSPNMDAG-----	DRVSPRAP	-----	KQVQLEDAVALYKILKYK	165
RabL3	FNPEEINLDCTN-----	PRYLAAGSS	-----	NAVKLSRFFDKVIEKRYFL	210
Arfrp2	KKYFELEPLARG-----	KRWILQPCSLDDM	-----	DALKDSFSQOLINLLEEK	197
RabL5	-GSLSLSPPLNK-----	LKLVHSNLED	-----	DPEEIRMEFIKYLKSIINS	171
SRPRB	LNTLRVTRSAAP-----	STLYSSSTAP	-----	AQLGKKGKEFEFSQLPLKVEFL	244
LOC401884	RCDLGLSPLR-----	SLWLWSWGPLWG	-----	SEVRLRLGSRVKLSPPA	170

Supplemental Table. The Ras superfamily, subfamilies, accession numbers and additional information

Protein	Synonyms	Accession no	Characterized	Comments
Ras family (36)				
H-Ras, isoform 1		NP_005334	yes	
<i>H-Ras, isoform 2</i>	<i>H-RasIDX</i>	<i>NP_789765</i>	yes	
N-Ras		NP_002515	yes	
K-Ras2B		NP_004976	yes	
<i>K-Ras2A</i>		<i>NP_203524</i>	yes	
R-Ras		NP_006261	yes	
TC21	R-Ras2	NP_036382	yes	
M-Ras	R-Ras3	NP_036351	yes	
Rap1A	Krev-1/Smgp21	NP_002875	yes	
Rap1B		NP_056461	yes	
Rap2A		NP_066361	yes	
Rap2B		NP_002877	yes	
Rap2C		NP_067006	yes	
Rit1	Roc1/RibB	NP_008843	yes	
Rit2	Rin/Roc2/RibA	NP_002921	yes	
Rem1	Ges	NP_054731	yes	
Rem2		AAH35663	yes	
Rad	R-Rad/Rem3	NP_004156	yes	
Gem	Kir	NP_859053	yes	
Rheb1	Rheb2	NP_005605	yes	
Rheb2	RhebL1	NP_653194	yes	
Noey2	ARHI/RhoI	NP_004666	yes	
Di-Ras1	Rig/GBTS1	NP_660156	yes	
Di-Ras2		NP_060064	yes	
E-Ras	H-Ras2/H-RasP	NP_853510	yes	
Rerg		NP_116307	yes	
RalA, isoform 1		NP_005393	yes	
<i>RalA, isoform 2</i>		<i>AAA36542</i>	yes	
RalB		NP_002872	yes	
NKIRas1	κB-Ras1	NP_065078	yes	
NKIRas2	κB-Ras2	NP_060065	yes	
RasD1	DexRas/Ags1	NP_057168	yes	
RasD2	Rhes/Tem2	NP_055125	yes	
RRP22	RasL10A	NP_006468	no	
RasL10B		NP_201572	no	
RasL11A		NP_996563	no	
RasL11B		NP_076429	no	
Ris/RasL12		NP_057647	no	
FLJ22655		NP_079006	no	Lacks G1 box.
Rho family (20)				
RhoA	ARHA/Rho H12	NP_001655	yes	
RhoB	ARHB/Rho H6	NP_004031	yes	
RhoC	ARHC/Rho H9	NP_786886	yes	
RhoD	ARHD/RhoHP1	NP_055393	yes	
Rnd3	RhoE/ARHE/Rho8	NP_005159	yes	
Rnd1	ARHS/Rho6	NP_055285	yes	
Rnd2	ARHN/RhoN/Rho7	NP_005431	yes	
Rif	ARHF/RhoF	NP_061907	yes	
RhoG	ARHG	NP_001656	yes	
RhoH	TTF/ARHH	NP_004301	yes	
Rac1	TC25	NP_008839	yes	
<i>Rac1, isoform b</i>		<i>NP_061485</i>	yes	
Rac2		NP_002863	yes	
Rac3		NP_005043	yes	

Protein	Synonyms	Accession no	Characterized	Comments
Cdc42, placental	G25K/Cdc42Hs	NP_001782	yes	
<i>Cdc42, brain</i>		NP_426359	yes	
TC10	RhoQ/ARHQ/RasL7A	NP_036381	yes	
TCL	TC10 β /RhoT/RhoJ/ARHJ/RasL7B	NP_065714	yes	
Wrch-1	RhoU/ARHU/Cdc42L1	NP_067028	yes	
Wrch-2	Chp/RhoV/ARHV	NP_598378	yes	
RhoBTB1		NP_055651	yes	Multi-domain protein
RhoBTB2	DBC2	NP_055993	yes	Multi-domain protein
Arf family (27)				
Arf1		NP_001649	yes	
Arf3		NP_001650	yes	
Arf4		NP_001651	yes	
Arf5		NP_001653	yes	
Arf6		NP_001654	yes	
Sar1a	SARA1/Masra2	NP_064535	yes	
Sar1b	SARA2/Sar1a homolog 2/CMRD	NP_057187	yes	
Arl1		NP_001168	yes	
Arl2		NP_001658	yes	
Arl3		NP_004302	yes	
Arl4		NP_997625	yes	
Arl5, isoform 1		NP_036229	yes	
<i>Arl5, isoform 2</i>		NP_817114		
Arl6	BBS3	NP_816931	yes	
Arl7	LAK	NP_005728	yes	
Arl8		NP_848930	no	
Arl9		AAS07576	no	
Arl10A		NP_775935	no	
Arl10B	Gie2	NP_620150	yes	
Arl10C	Gie1	NP_060654	yes	
Arl11	ArlTS1	NP_612459	no	
Ard1, isoform α	ArfD1/Trim23/RNF46	NP_001647	yes	Multi-domain protein
<i>Ard1, isoform β</i>		NP_150230		
<i>Ard1, isoform γ</i>		NP_150231		
Arf4L		NP_001652	yes	
ArfRP1	Arp	NP_003215	yes	
ArfRP2		NP_061960	no	
Arl2L1, isoform 1		NP_878899	no	Multi-domain protein
FLJ22595		NP_079323	no	
LOC339231		XP_290777	no	
Rab family (61)				
Rab1A		NP_004152	yes	
Rab1B		NP_112243	yes	
Rab2A		NP_002856	yes	
Rab2B		NP_116235	no	
Rab3A		NP_002857	yes	
Rab3B		NP_002858	yes	
Rab3C		NP_612462	yes	
Rab3D	GOV/D2-2/Rab16/Rad3D	NP_004274	yes	
Rab4A		NP_004569	yes	
Rab4B		NP_057238	yes	
Rab5A		NP_004153	yes	
Rab5B		NP_002859	yes	
Rab5C, isoform a	RabL/Rab5CL	NP_958842	yes	
<i>Rab5C, isoform b</i>		NP_004574		
Rab6A, isoform a		NP_002860	yes	
<i>Rab6A, isoform b</i>		NP_942599		

Protein	Synonyms	Accession no	Characterized	Other Comments
Rab6B		NP_057661	yes	
Rab6C	WTH3	NP_115520	yes	
Rab7A		NP_004628	yes	
Rab7B		NP_796377	yes	
Rab8A	MEL	NP_005361	yes	
Rab8B		NP_057614	yes	
Rab9A		NP_004242	yes	
Rab9B	Rab9L	NP_057454	no	
Rab10		NP_057215	yes	
Rab11A	YL8	NP_004654	yes	
Rab11B	H-YPT3	NP_004209	yes	
Rab12		XP_113967	yes	
Rab13		NP_002861	yes	
Rab14	FBP	NP_057406	yes	
Rab15		NP_941959	yes	Lacks G4 box
Rab17		NP_071894	yes	
Rab18		NP_067075	yes	
Rab19	Rab19B	XP_379935	no	
Rab21		NP_055814	yes	
Rab22A		NP_065724	yes	
Rab22B	Rab31	NP_006859	no	
Rab23	HSPC137	NP_057361	yes	
Rab24		AAH21263	yes	
Rab25	CATX-8	AAH33322	yes	
Rab26		NP_055168	yes	
Rab27A	Ram	NP_899059	yes	
Rab27B		NP_004154	yes	
Rab28		NP_004240	yes	
Rab30		NP_055303	yes	
Rab32		NP_006825	yes	
Rab33A	RabS10	NP_004785	yes	
Rab33B		NP_112586	yes	
Rab34	Rah/Rab39	NP_114140	yes	
Rab35	Ray/H-ray/Rab1C	NP_006852	yes	
Rab36		NP_004905	yes	
Rab37		NP_783865	yes	
Rab38	NY-MEL-1	NP_071732	yes	
Rab39A		NP_059986	yes	
Rab39B		NP_741995	no	
Rab40A	Rar2A/Rar-2	NP_543155	no	
Rab40B	Rar/SEC4L	NP_006813	no	
Rab40C	Rar3/RarL/RasL8C	NP_066991	yes	
Rab41	Rab43	NP_940892	no	
Rab42		AK026009 (mRNA)	no	
Rab7L1	Rab29(rat)	NP_003920	yes	
RabL4	RayL	NP_006851	no	
RasEF	Rab45	NP_689786	no	Multi-domain protein
Ran family (1)				
Ran		NP_006316	yes	
Unclassified (9)				
Miro-1	RhoT1	NP_060777	yes	Multi-domain protein
Miro-2	RhoT2	NP_620124	yes	Multi-domain protein
SRPRB	APMCF1	NP_067026	no	
LOC401884		XP_377476	no	No G4 box. G1 & G3 poorly conserved
Rab20		NP_060287	yes	
RabL2A		NP_009013	no	

Protein	Synonyms	Accession no	Characterized	Comments
RabL2B, isoform 2		NP_009012	no	
<i>RabL2B, isoform 1</i>		<i>NP_001003789</i>		
RabL3		NP_776186	no	
RabL5		NP_073614	no	Lacks G4 box