

Large Nucleotide-Dependent Conformational Change in Rab28

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RAB28[INP_004240] 1-----MSDSEESQDRQLKIVLIGDGTSGKTSLTTGFAQE--TF--GKQYKQTIQLDFL51
RAB1A[INP_004152] 1-----MSMNP EYD-YLFKLLLI GDSGVGKSSCLLRFADD--TY--TESYI STIGVDFK1 47
RAB1B[INP_112243] 1-----MNP EYD-YLFKLLLI GDSGVGKSSCLLRFADD--TY--TESYI STIGVDFK1 47
RAB2A[INP_002856] 1-----MAYA-YLFKYLII GDTGVGKSSCLLQFTDK--RF--QPVHDLTIGVEFGA 45
RAB2B[INP_116235] 1-----MTYA-YLFKYLII GDTGVGKSSCLLQFTDK--RF--QPVHDLTIGVEFGA 45
RAB3A[INP_002857] 1-----MASATDSRYGQKESSDQNF--YMFKILII GNSVVGKTSFLRYADD--SF--TPAFVSTVGI DFKV 61
RAB3B[INP_002858] 1-----MASVTDGKTGVKDDASDQNF--YMFKLLII GNSVVGKTSFLRYADD--TF--TPAFVSTVGI DFKV 61
RAB3C[INP_612462] 1-----MRHEAPMQMASQADARYGQKDS SDQNF--YMFKLLII GNSVVGKTSFLRYADD--SF--TSAFVSTVGI DFKV 69
RAB3D[INP_004274] 1-----MASAGDTPQAGPRDAADQNF--YMFKLLII GNSVVGKTSFLRYADD--SF--TPAFVSTVGI DFKV 61
RAB4A[INP_004569] 1-----MSQTAMS ETYD-FLFKFLVI GNACTGKSSCLLHQFIEK--KF--KDDSNHTIGVEFGS 52
RAB4B[INP_057238] 1-----MAETYD-FLFKFLVI GSAGTGSCLLHQFIEK--KF--KDDSNHTIGVEFGS 47
RAB5A[INP_004153] 1-----MASRGTARPNGPNTGNKIQCFKLVLLGESAVGKSSVLRVFKG--QF--HEFQESTIGAAFLT 59
RAB5B[INP_002859] 1-----MTRSTARPNQGPQASKIQCFKLVLLGESAVGKSSVLRVFKG--QF--HEFQESTIGAAFLT 59
RAB5C[INP_958842] 1-----MAGRGAARPNAGNKKIQCFKLVLLGESAVGKSSVLRVFKG--QF--HEFQESTIGAAFLT 60
RAB5C[INP_004574] 1-----MAGRGAARPNAGNKKIQCFKLVLLGESAVGKSSVLRVFKG--QF--HEFQESTIGAAFLT 60
RAB6A[INP_002860] 1-----MSTGGDFGNPLRKFVFLGEGSVAKTSLITRFMYD--SF--DNTYQATIGIDFLS 52
RAB6A[INP_942599] 1-----MSTGGDFGNPLRKFVFLGEGSVAKTSLITRFMYD--SF--DNTYQATIGIDFLS 52
RAB6B[INP_057661] 1-----MSAGGDFGNPLRKFVFLGEGSVAKTSLITRFMYD--SF--DNTYQATIGIDFLS 52
RAB6C[INP_115520] 1-----MTRSKKYLKVIILGDSGVGKSSLMNQYVNK--KF--SNOYKATIGADFLT 47
RAB7[INP_004628] 1-----MNP RKKVLDKLIIVGAI VGKTSLPHQYVHK--TF--YEEYQITLGASJLS 47
RAB7B[INP_796377] 1-----MAKTYD-YLFKLLII GDSGVGKTSCLLRFSEED--AF--NTFISTIGIDFK1 47
RAB8A[INP_005361] 1-----MAKTYD-YLFKLLII GDSGVGKTSCLLRFSEED--AF--NTFISTIGIDFK1 47
RAB8B[INP_057614] 1-----MAGKSSLFKVIILGDSGVGKSSLMNRYVTN--KF--DTQLFHTIGVEFLN 46
RAB9A[INP_004242] 1-----MAGKSSLFKVIILGDSGVGKSSLMNRYVTN--KF--DTQLFHTIGVEFLN 46
RAB9B[INP_057454] 1-----MAKKTVDY-LFKVLLI GDSGVGKSNLRSFTRN--EF--NLESKSTIGVEFAT 50
RAB10[INP_057215] 1-----MGRDDEYD-YLFKVLLI GDSGVGKSNLRSFTRN--EF--NLESKSTIGVEFAT 50
RAB11[INP_004654] 1-----MGRDDEYD-YLFKVLLI GDSGVGKSNLRSFTRN--EF--NLESKSTIGVEFAT 50
RAB11B[INP_004209] 93 P HACMDP GAALQRRRAAGGGGLGAGSPALSGGQRRRKP RPAD-FKLOVILII GSRGVGKTSLMEFTDD--TF--CEACKTIGVDFK1 177
RAB12[INP_113967] 1-----MAKAYD-HLFLKLLI GDSGVGKTSCLIRFAED--NF--NNTYI STIGIDFK1 47
RAB13[INP_002861] 1-----MATAPYNS-YIFKYLII GDMVGKSSCLLHQFTTEK--KF--MADCPHTIGVEFGT 50
RAB14[INP_057406] 1-----MAQYD-VLFRLLI GDSGVGKTSCLLRFADD--EF--HSSHLSTIGVDFKM 47
RAB15[INP_941959] 1-----MAQHRTPQRPADYVFKVLLI GDSGVGKSSLLRFTDN--DF--KSLIPTVGCARFV 57
RAB17[INP_071894] 1-----MAQHRTPQRPADYVFKVLLI GDSGVGKSSLLRFTDN--DF--KSLIPTVGCARFV 57
RAB18[INP_067075] 1-----MDEDLV-TTLKLLII GDSGVGKSSLLRFTDN--DF--KSLIPTVGCARFV 57
RAB21[INP_055814] 1-----MAAGCGGGGAAAGRAYSFKVVLLGCECGVCKTSLVLRYCN--KF--NDKHITTLQOASFLT 58
RAB22[INP_065724] 1-----MALRELKCVLLGDTGVGKSSIVRFEED--SF--DPNINPTIGASFMT 44
RAB22[INP_065724] 1-----MLEEDME-VAILKMWVVGNGAVGKSSIMQRYCKG--IF--TKDYKTI GVDLFE 48
RAB23[INP_057361] 1-----MSGQRVDVKVVMKCKEYVGTSLVRYVHD--RF--LVGPYQNTIGAIFA 47
RAB24[IAAH21263] 1-----MNGT EEDYN-FVFKVLLI GDSGVGKSNLRSFTRN--EF--SHDRTTIGVEFST 51
RAB25[IAAH3322] 18 ST LP TANGARPARSGTALSGDPARPNGP LQPGRP S LGGGVDFYD-VAFKVMLV GDSGVGKTSCLLRFKIDG--AF--LAGTFISTVGI DFRN 103
RAB26[INP_055168] 1-----MSDGYD-YLIFKFLV GDSGVGKTSVLYQYTDG--KF--NSKFIITVGI DFR 48
RAB27[INP_899059] 1-----MTDGYD-YLILKLLA GDSGVGKTSFLRYFTDN--KF--NPKFIITVGI DFR 48
RAB27B[INP_004154] 1-----MSMEDYD-FLFKVLLI GNAVGKTSCLVRRFTDQ--LF--PPGQCATIGVDFM1 48
RAB30[INP_055303] 1-----MMAIRELKVLLIGDGVGKSSIVCRFVDD--HF--DHNISPTIGASFMT 45
RAB31[INP_006859] 1-----MAGCGAGDPGLGAAAPAPETREHLFKVLI GELGVGKTSIKRYVHQ--LF--SQHRATIGVDFAL 64
RAB32[INP_006825] 1-----MAQPI LCHGSLQPAASAGLASLELDSLDQYD IRIFKIIVIGDSNVGKTSCLLRFKCGG--TF--PDKTEATIGVDFRE 75
RAB33[INP_004785] 1-----MAEMESSLEASAFSSGAVSGASGLPPARSRIKIIIVIGDSNVGKTSCLLRFKCGG--RF--PDRTEATIGVDFRE 72
RAB33B[INP_112886] 6 P VRRDRVLAELPQCLRKEAALHGKHD FHPRVTCACQEHRTGTGVFKSIIIV GDL SVGKTSCLINRFCKD--TF--DKNYKATIGVDFEM 91
RAB34[INP_114140] 1-----MARDYD-HLFLKLLI GDSGVGKSSLLRFADN--TF--SGSYITTI GVDFK1 47
RAB35[INP_006851] 1-----MARDYD-HLFLKLLI GDSGVGKSSLLRFADN--TF--SGSYITTI GVDFK1 47
RAB36[INP_004905] 77 P VSRDRV IASFRKWYTP EACLQ LREHFHGQVSAACQRNTGTVGLKSVVV GDLVYVGTSLIHRFKCN--VF--DRDYKATIGVDFE1 162
RAB37[INP_783865] 1-----MDLQRPDSYQGGAGP DFNHVLKHTLLV GDSGVGKTSVLYQFDQK--KF--IPGSFATVGI GFTN 62
RAB38[INP_071732] 1-----MQAPHK EHL YKLLVI GDLGVGKTSIKRYVHQ--NF--SHYRATIGVDFAL 48
RAB39[INP_059986] 1-----MEIWI-YQFRLIIVIGDSTVGKSSCLLHRTQG--RF--PGLRSPADPTVGVDF 51
RAB39B[INP_741995] 1-----MSAPGSPDQAYD-FLKFLV GDRDVGKSEILESLODG--AA--ESPYSHLGGIDYKT 53
RAB40A[INP_543155] 1-----MSALGSPVRAVD-FLKFLV GDRDVGKSEILESLODG--AA--ESPYSHLGGIDYKT 53
RAB40B[INP_006813] 1-----MGSQGS P V KSYD-YLLKFLV GDSDVGKCEILASLDG--AA--ESPYAY SNGIDYKT 53
RAB40C[INP_066991] 1-----MAGP GP GP DQEQYD-FLKFLV GDA SVGKTSVQRFKTDG--AF--SEROGTTIGVDF 57
RAB43[INP_940892] 1-----MGSRD-HLFLKVLV GDAAVGKTSLVQRYSD--SF--SKHYKTVGVDFAL 46
RAB71[INP_003920] 1-----MVKLAKCII LADPAVGRK TALAQIFRISDGAHE---OKSYTITITIGMDI VV 45
RABL4[INP_006851]

P-loop

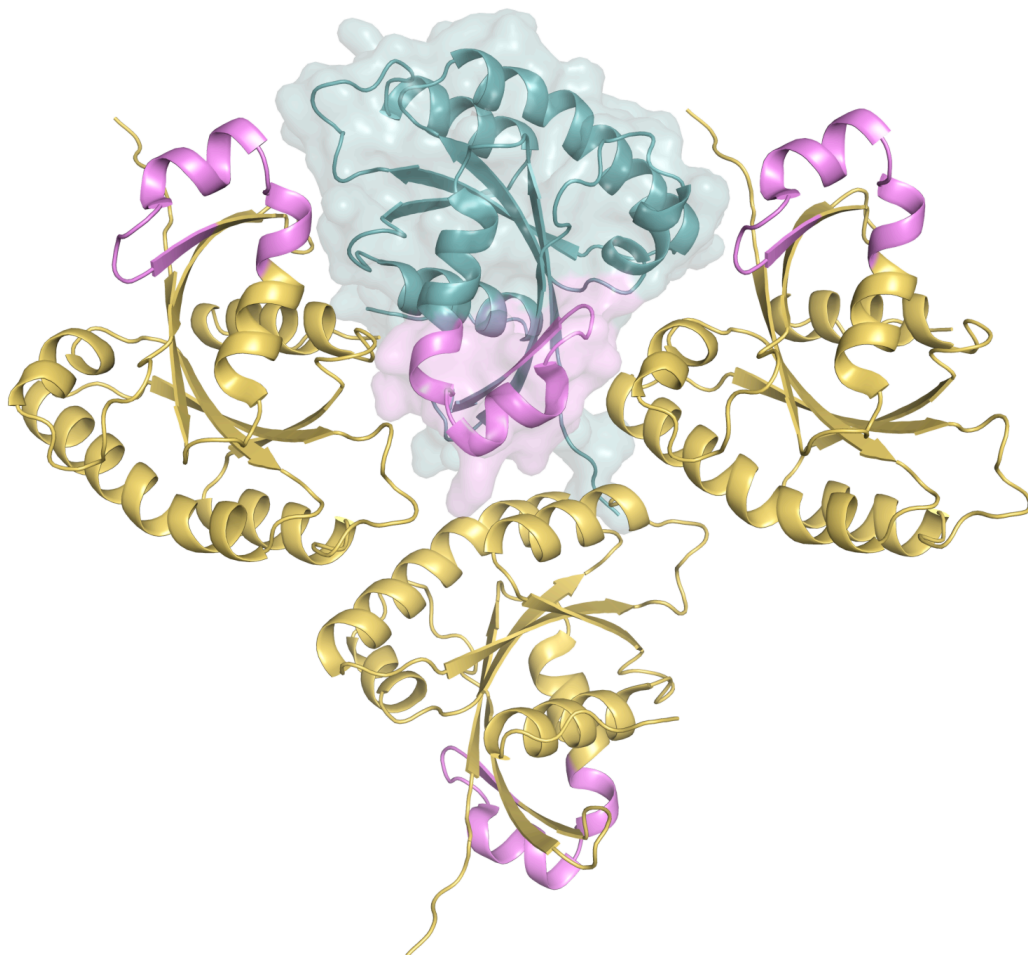
Switch I

RAB28[INP_004240] TLRPGLNVTLQIWDI **GGQ**TIIGC-KMLDKYIYGAQ GVLVLYDITNYQSFENLEDWYTVYVKKVSSESE-TQP LVALVGNKID 132
 RAB1A[INP_004152] ELD-GKTIKLIQIWDI **AGQ**ERFR-TITSSYYRGAHGIIVVYDVTQDESYANVKKQWLQEI DRYAS-EN---VNKLLVGNKSD 127
 RAB1B[INP_112243] ELD-GKTIKLIQIWDI **AGQ**ESFR-TITSSYYRGAHGIIVVYDVTQDESYANVKKQWLQEI DRYAS-EN---VNKLLVGNKSD 124
 RAB2A[INP_002856] TID-GKQIKLIQIWDI **AGQ**ESFR-SITRSYRGAAGALLVYDITRRDIFNHLTQWLEDARQHSN-SN---MVMIMLIGNKSD 122
 RAB2B[INP_116235] NID-GKQIKLIQIWDI **AGQ**ESFR-SITRSYRGAAGALLVYDITRRDIFNHLTQWLEDARQHS-SN---MVMIMLIGNKSD 122
 RAB3A[INP_002857] YRN-DKRIKLIQIWDI **AGQ**ERYR-TITTAAYRGAHCFILMYDITNEESFNVAQDWTQIKTYSW--DN---AQLVGNKCD 138
 RAB3B[INP_002858] YRN-DKRIKLIQIWDI **AGQ**ERYR-TITTAAYRGAHCFILMYDITNEESFNVAQDWTQIKTYSW--DN---AQLVGNKCD 138
 RAB3C[INP_612462] FKN-EKRIKLIQIWDI **AGQ**ERYR-TITTAAYRGAHCFILMYDITNEESFNVAQDWTQIKTYSW--DN---AQLVGNKCD 146
 RAB3D[INP_004274] YRH-DKRIKLIQIWDI **AGQ**ERYR-TITTAAYRGAHCFILMYDITNEESFNVAQDWTQIKTYSW--DN---AQLVGNKCD 138
 RAB4A[INP_004569] NVG-CKYVKLIQIWDI **AGQ**ERFR-SVTRSYRGAAGALLVYDITSRETYNALTNWLTARMLAS-QN---IVILCGNKKD 129
 RAB4B[INP_005238] NVG-GKTVKLIQIWDI **AGQ**ERFR-SVTRSYRGAAGALLVYDITSRETYNALTNWLTARMLAS-QN---IVILCGNKKD 124
 RAB5A[INP_004153] CLD-DTTVKFEIWDI **AGQ**ERYH-SLAPMYRGAQAAIIVYDITNQETFARAKTWKELQKQAS-PN---IVIALSGNKAD 136
 RAB5B[INP_002859] CLD-DTTVKFEIWDI **AGQ**ERYH-SLAPMYRGAQAAIIVYDITNQETFARAKTWKELQKQAS-PN---IVIALSGNKAD 136
 RAB5C[INP_958842] CLD-DTTVKFEIWDI **AGQ**ERYH-SLAPMYRGAQAAIIVYDITNQETFARAKTWKELQKQAS-PN---IVIALSGNKAD 137
 RAB5D[INP_004574] CLD-DTTVKFEIWDI **AGQ**ERYH-SLAPMYRGAQAAIIVYDITNQETFARAKTWKELQKQAS-PN---IVIALSGNKAD 137
 RAB6A[INP_002860] YLE-DRTVRLQIWDI **AGQ**ERFR-SLIPSYIRDSTVAVVYDITNVNSFQQTQKIIDVYTERG-SD---VIMLVGNKTD 129
 RAB6B[INP_942599] YLE-DRTVRLQIWDI **AGQ**ERFR-SLIPSYIRDSTVAVVYDITNVNSFQQTQKIIDVYTERG-SD---VIMLVGNKTD 129
 RAB6C[INP_115520] YLE-DRTVRLQIWDI **AGQ**ERFR-SLIPSYIRDSTVAVVYDITNVNSFQQTQKIIDVYTERG-SD---VIMLVGNKTD 129
 RAB7[INP_004628] MVD-DRLVTMQIWDI **AGQ**ERFR-SLIPSYIRDSTVAVVYDITNVNSFQQTQKIIDVYTERG-SD---VIMLVGNKTD 128
 RAB7B[INP_796377] LG-DTTLKLIQIWDI **AGQ**ERFR-SMSTYRGAAGALLVYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 124
 RAB8A[INP_005361] ELD-GKRIKLIQIWDI **AGQ**ERFR-TITTAAYRGAHCFILMYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 124
 RAB8B[INP_057614] ELD-GKRIKLIQIWDI **AGQ**ERFR-TITTAAYRGAHCFILMYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 124
 RAB9A[INP_004242] EVD-GHFVTMQIWDI **AGQ**ERFR-SLRTPFYRGAAGALLVYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 127
 RAB9B[INP_057454] EVD-CRFVTLQIWDI **AGQ**ERFR-SLRTPFYRGAAGALLVYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 127
 RAB10[INP_057215] ELQ-GKIKLIQIWDI **AGQ**ERFR-TITTAAYRGAHCFILMYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 125
 RAB11A[INP_004654] QVD-GKTIKLIQIWDI **AGQ**ERYR-AITSAAYRGAAGALLVYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 127
 RAB11B[INP_004209] QVD-GKTIKLIQIWDI **AGQ**ERYR-AITSAAYRGAAGALLVYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 127
 RAB12[INP_113967] ELR-GKKIKLIQIWDI **AGQ**ERFR-TITTAAYRGAHCFILMYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 124
 RAB13[INP_002861] DLE-GKKIKLIQIWDI **AGQ**ERFR-TITTAAYRGAHCFILMYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 124
 RAB14[INP_057406] EVS-GQIKLIQIWDI **AGQ**ERFR-AVTRSYRGAAGALLVYDITRSTYHNSLSWLTARNLTN-PN---TVILIGNKAD 127
 RAB15[INP_941959] EVD-GIKVRQIWDI **AGQ**ERYQ-TITKQYRRAQGIIFLYDITNKSFDNIKNIRNIEHAS-SD---VERMILGNKCD 125
 RAB17[INP_071894] DVG-ATSKLEIWDI **AGQ**EKYL-SVCHLYRGAAGALLVYDITRKSDFLKAQWLKDEELHPGE---VLMVGNKTD 135
 RAB18[INP_067075] SVD-GNKAKLAIWDI **AGQ**ERFR-TLPSYRGAAGALLVYDITRKSDFLKAQWLKDEELHPGE---VLMVGNKTD 135
 RAB21[INP_055814] NIC-CKRVNLAIWDI **AGQ**ERFR-ALGPIYRDSNGAILVYDITDEDSFQVKNWVWELRKLMLG-NE---ICLCVGNKID 135
 RAB22A[INP_065724] QYQ-NEHLKLIWDI **AGQ**ERFR-ALAPMYRGAAGALLVYDITRSTYHNSLSWLTARNLTN-PN---TVILIGNKAD 127
 RAB22B[INP_057611] QVN-DEDLRLMLWDI **AGQ**EFD-AITKAYYRGAAGALLVYDITRSTYHNSLSWLTARNLTN-PN---TVILIGNKAD 124
 RAB24[IAH21263] SVG-DRTVTLGIWDI **AGS**ERYE-AMSRYYRGAAGALLVYDITDSSSFERAKFWKELRSLEG---COIYLCGTGKSD 123
 RAB25[IAH3322] MLG-TAAVKAQIWDI **AGL**ERYR-AITSAAYRGAAGALLVYDITRKSDFLKAQWLKDEELHPGE---VLMVGNKTD 138
 RAB26[INP_055168] DVD-CVKVKLQMWDT **AGQ**ERFR-SVTHAYRDAHALLVYDITNKASFDNIQAWLTEIHEYAQ-HD---VALMLGNKSD 120
 RAB27A[INP_899059] KRVVYRASGPDGATGRGQRIHLQIWDI **AGQ**ERFR-SLTAFRDAHALLVYDITNKASFDNIQAWLTEIHEYAQ-HD---VALMLGNKSD 120
 RAB27B[INP_004154] KRVVYNAQCPNCGSSGKAFKVLQIWDI **AGQ**ERFR-SLTAFRDAHALLVYDITNKASFDNIQAWLTEIHEYAQ-HD---VALMLGNKSD 120
 RAB30[INP_055303] EIN-GEKVKLIQIWDI **AGQ**ERFR-SITQSYRGAAGALLVYDITCEESFRCLPWLREIEQYASNK---VITVLVGNKID 125
 RAB31[INP_006859] PCG-NEHLKLIWDI **AGQ**ERFR-SLAPMYRGAAGALLVYDITKQDSFYTLKWKVLEKEHGP-EN---IVMAIAGNKKD 146
 RAB32[INP_006825] NWDSTRTLVRLQIWDI **AGQ**ERFR-SLAPMYRGAAGALLVYDITKQDSFYTLKWKVLEKEHGP-EN---IVMAIAGNKKD 146
 RAB33A[INP_004785] EIE-GEKIKVQIWDI **AGQ**ERFR-SMVEHYRNVHAVVYDITKMTSFTNLKMWIECKNGHAYVP-L---VPKVLVGNKCD 154
 RAB33B[INP_112586] EID-GERIKIQLWDT **AGQ**ERFR-FRKSVMQHYRNVHAVVYDITKMTSFTNLKMWIECKNGHAYVP-L---VPKVLVGNKCD 154
 RAB34[INP_114140] EVL-GIPFSLQIWDI **AGQ**ERFR-CIASTYRGAQAIIVFNLNDVASLEHTKQWLADALKEKNDP-S---VLLFLVGSKKD 169
 RAB35[INP_006852] EIN-GEKVKLIQIWDI **AGQ**ERFR-TITTAAYRGAHCFILMYDITNKASFDNIQAWLTEIHEYAQ-HD---VALMLGNKSD 120
 RAB36[INP_004905] TVD-GVRVLIQIWDI **AGQ**ERFR-CIASAYRGAQAIIVFNLNDVASLEHTKQWLADALKEKNDP-S---VLLFLVGSKKD 169
 RAB37[INP_783865] TAD-GVRVLIQIWDI **AGQ**ERFR-SVTHAYRDAHALLVYDITNKASFDNIQAWLTEIHEYAQ-HD---VALMLGNKSD 139
 RAB38[INP_071732] HMDPETVRLQIWDI **AGQ**ERFR-NMTRVYRKEAFVAFVFDISRSSTFEAVLKWKSDLSKVLHPNGSP IPAVLLANKCD 146
 RAB39A[INP_059986] EIEPGRKIKLIQIWDI **AGQ**ERFR-SITRSYRGAAGALLVYDITNRSSFHVKDWLEEAQMYVQPF-R---VFLVLVGHKCD 130
 RAB39B[INP_741995] EIEPGRKIKLIQIWDI **AGQ**ERFR-SITRSYRGAAGALLVYDITNRSSFHVKDWLEEAQMYVQPF-R---VFLVLVGHKCD 130
 RAB40A[INP_543155] LLD-GQRVKLIQIWDI **SCQ**GRFC-TIFRSYRGAQCVILVYDIANRWSFEGMDRWIKIEEHAP-G---VPKILVGNRLLH 129
 RAB40B[INP_006813] LLD-GQRVKLIQIWDI **SCQ**GRFC-TIFRSYRGAQCVILVYDIANRWSFEGMDRWIKIEEHAP-G---VPKILVGNRLLH 129
 RAB41[INP_940892] LLD-GRRVLELQIWDI **SSQ**GRFC-TIFRSYRGAQCVILVYDIANRWSFEGMDRWIKIEEHAP-G---VPKILVGNRLLH 129
 RAB43[INP_940892] EIQ-GKRVKLIQIWDI **AGQ**ERFR-TITQSYRGAAGALLVYDITRKSDFLSPVHWIEDVRKYAG-SN---IVQLLIGNKSD 134
 RAB71[INP_003920] QWSDYEIVRLQIWDI **AGQ**ERFR-SMTRLVYRDAACVIMFDVNTNATTFNSQKQDLSDSKLTPNCGEPVPCLLANKCD 128
 RABL4[INP_006851] PVPDTGDSVELFI **FD**SAKLELS-EMLDKLEWESPVLVCLVYDVTNEESFNKCSKWLKARSAQAPGIS---LPQVLYVGNKTD 125

Switch II

RAB28[NP_004240] 133 L--- EHM-RTIKPE-KHLRFQEN-GFSS-HFVSAK---TGDSVFLCFQKVAAEILGICKLNKAEIEQSQRIVRA---EIVKYPE
RAB1A[NP_004152] 128 L--- TTK-KVVVDYT-TAKEFADSL-GIPF-LETSAK---NATNVEQSFMTMAAEIKKRMGPATAGAEK-----SNVKIQS
RAB18[NP_112243] 125 L--- TTK-KVVVDYT-TAKEFADSL-GIPF-LETSAK---NATNVEQSFMTMAAEIKKRMGPATAGAEK-----SNVKIQS
RAB2A[NP_002856] 123 L--- ESR-RVKKKE-EGEAFARH-GLIF-METSAK---TASNVEAFINTAKIYEKIQEGVFINNEA-----NGIKIGP
RAB21[NP_116231] 123 L--- ESR-RDVKRE-EGEAFARH-GLIF-METSAK---TASNVEAFINTAKIYEKIQEGVFINNEA-----NGIKIGP
RAB3A[NP_002857] 139 M--- EDE-RVVSSE-RCQLADHL-GFEF-FEASAK---DNINVKQTFERLVDVICKEMSEGLTDVHNEA-----TGAKQGP
RAB38[NP_002858] 139 M--- EEE-RVVPTE-KGQLAEQL-GFDF-FEASAK---ENISVRQAFERLVDVICKEMSDSLDTPSMLGSS---KNTRLSD
RAB3C[NP_612462] 147 M--- EDE-RVISTE-RCQHLCEQL-GFEF-FETSAK---DNINVKQTFERLVDVICKEMSELETDPAI-----TAAKQNT
RAB3D[NP_004274] 139 L--- EDE-RVVP AE-DGRFLADDL-GFEF-FEASAK---ENINVKQFERLVDVICKEMSELETDPAI-----TAAKQNT
RAB4A[NP_004569] 130 L--- DAD-REVTFL-EASRFAQEN-ELMF-LETSAL---TGENVEAEFLKCAKRTLNKIDSCGLDPERMG---SGIQYGD
RAB48[NP_057238] 125 L--- DP-E-REVTFL-EASRFAQEN-ELMF-LETSAL---TGENVEAEFLKCAKRTLNKIDSCGLDPERMG---SGIQYGD
RAB5A[NP_004153] 137 L--- ANK-RAVDFO-EAQYAADN-SLFF-METSAK---TSMNVNEIFMAIAKRLPKSEPNLGGAGARS---RGVDLHE
RAB5B[NP_002859] 137 L--- ANK-RAVDFO-EAQYAADN-SLFF-METSAK---TSMNVNEIFMAIAKRLPKSEPNLGGAGARS---RGVDLHE
RAB5C[NP_958842] 138 L--- ASK-RAVEFO-EAQYAADN-SLFF-METSAK---TAMNVNEIFMAIAKRLPKSEPNLGGAGARS---RGVDLHE
RAB5C[NP_004574] 138 L--- ASK-RAVEFO-EAQYAADN-SLFF-METSAK---TAMNVNEIFMAIAKRLPKSEPNLGGAGARS---RGVDLHE
RAB6A[NP_002860] 130 L--- ADK-RQVSI-EGERKAKEL-NVMF-IETSAK---AGYNVKQLFRVAALPQMGESTQDRSREDM---IDIKLEK
RAB6A[NP_942599] 130 L--- ADK-RQVSI-EGERKAKEL-NVMF-IETSAK---AGYNVKQLFRVAALPQMGESTQDRSREDM---IDIKLEK
RAB6B[NP_057661] 130 L--- ADK-RQVSI-EGERKAKEL-NVMF-IETSAK---AGYNVKQLFRVAALPQMGESTQDRSREDM---IDIKLEK
RAB6C[NP_115520] 130 L--- ADK-RQVSI-EGERKAKEL-NVMF-IETSAK---AGYNVKQLFRVAALPQMGESTQDRSREDM---IDIKLEK
RAB7[NP_004628] 129 L--- EN-ROVATK-RAQAWCYSKNINIPY-FETSAB---EAINVEQAFQTLARNALQOETVELYNEFP---EPICKLDK
RAB7B[NP_796377] 128 L--- AD- RKPVE-VAQGWCREK-DIPY-FEVSAB---NDINVQAFEMLASRALRYQSILENHLLT---ESIKLSP
RAB8A[NP_005361] 125 V--- NDK-RQVSE-RGCKLALDY-GIKF-METSAB---ANINVEAEFLLARDIIMKAKMDKICENSPQGSN---QGVKITE
RAB8B[NP_057614] 125 M--- NDK-RQVSE-RGCKLALDY-GIKF-METSAB---ANINVEAEFLLARDIIMKAKMDKICENSPQGSN---QGVKITE
RAB9A[NP_004242] 128 L--- SE-RQVSTE-EAQWCRDNGDYPY-FETSAB---DATNVAAEFAVRRYLATEDRSIDLITQ---DTVNLHR
RAB9B[NP_057454] 128 K--- ED-ROVTE-EAQTWCMGNDYPY-FETSAB---DDNTVVAFEAVRQYLAVEQLHECMLG---HTIDLNS
RAB10[NP_057215] 126 M--- DDK-RVVPKG-KGGQIAREH-GIRF-FETSAB---ANINIKAKFLAEDILRKTYPKEPNS---ENVDISS
RAB11[NP_004654] 128 L--- RHL-RAVPTD-EARAFAEKN-NLSE-IETSAL---DSTNVEAEFKNLTLEIYRIVSQKQIADRAAHDESPGN-NVVDISV
RAB11B[NP_004209] 128 L--- RHL-RAVPTD-EARAFAEKN-NLSE-IETSAL---DSTNVEAEFKNLTLEIYRIVSQKQIADRAAHDESPGN-NVVDISV
RAB12[NP_113961] 225 C--- ET-DREITRQ-QGKFAQITGMR-FCEASAB---DNFNVDIEFLKLVLDILKMPLDILRNLNSN---SILSLQP
RAB13[NP_002861] 125 M--- EAK-RKVQKE-EAKQFAEEN-GLLF-LEASAB---TGENVEDAEFLAARKIYQNIQDGSLDLNAE---SGVQHKP
RAB14[NP_057406] 126 L--- EQ-RDVTYE-EAKQFAEEN-GLLF-LEASAB---TGENVEDAEFLAARKIYQNIQDGSLDLNAE---SGVQHKP
RAB15[NP_941959] 126 K--- ARRGPDGKAN-ASRKLCLPO---PW-METSAB---HQAQSERVNLGI-LRMLSRNGRWEESKSSWR---RSMAWTS
RAB17[NP_071894] 126 L--- SQE-REVTFO-EGKEEADSO-KLFF-METSAB---LNHQVSEFNTVAQELLQORSDDEQALRGD---AAVALNK
RAB18[NP_067075] 126 K--- EN-REVDNR-EGKFAARKH-SMLF-I-EASAB---TCDGVQCAFELVEKIIQTPGLWESENQ---KGVKLSH
RAB21[NP_055814] 136 L--- EKE-RHVS IQ-EAESYAESV-GAKH-YHTSAB---QNKGI EELFLDLCKRMI-ETAQVDERAKKNGSSQPGTARRGVQIID
RAB22A[NP_065724] 122 L--- IDV-REVMER-DAKDYADSI-HAIF-FETSAB---NAININELFIEISRRIPSTDANLPISGG---GFKFLSR
RAB23[NP_057361] 125 L--- LDD-SCIKNE-EAEALAKR-LKRF-YRTSAB---EDLNVNEFVLYLAEKYLOK LKQOIAEDPELTHSSSNKIGVFTLSG
RAB24[AAH21263] 124 LLEDRRRRVDFH-DVQDYADNI-KAQL-FETSAB---TQGSVDELFOKVAEDVSVAAFOYMTED---KQVDLQ
RAB25[AAH3322] 129 L--- SQA-REVPTE-EARMAEENN-GLLF-LETSAL---DSTNVELAFETVLKELFAKQSMKAPSE---PRFRLHD
RAB26[NP_055168] 181 S--- AHE-RVVKRE-DGCKLAKEY-CLPF-METSAB---TGLNVDLAFTAIKELKORSMKAPSE---PRFRLHD
RAB27A[NP_899059] 137 L--- AER-REVSRQ-RAEESQAQ-DMYY-LETSAB---ESDNVEKFLDLACRLI SEARQNTLV---NNVSSPL
RAB27B[NP_004154] 126 L--- AER-REVSRQ-RAEESQAQ-DMYY-LETSAB---ESDNVEKFLDLACRLI SEARQNTLV---NNVSSPL
RAB30[NP_055303] 137 L--- SDI-REVLK-DAK EYAESI-GAIV-VETSAB---NAINIEELFOGSRQIP LDPHENGNN---GTIKVEK
RAB31[NP_006859] 147 Q--- NKD-SSQSP S-QVDFCKEH-CFACGFETSAB---DNINIEAARFLVEKILVNHQSPNEENDY---DKIKLDQ
RAB32[NP_006825] 152 L--- R EQ- IQVPSN-LALKFADAH-NMPL-L-FETSABKPEESQNSIFMGLACRLKAKQ5LYLRDAERQ---GKVKQLE
RAB33A[NP_004785] 155 L--- R SA- IQVPTD-LAQKFAADH-SMPL-L-FETSABKPNNDNDHVEAIFMTLAHKLSHKP LMLSOPD---NGCIIKP
RAB33B[NP_112586] 170 L--- STPQAQYALMEKDALQVAQEM-KA EY-WAVS SL---TGENVREFFRVAALTFEANYLAELEKSGARRIG---DVRINS
RAB34[NP_114140] 124 D--- P ER-KVETE-DAVKFAGQM-GIQL-FETSAB---ENVNVEEMFNCTIELVLRKADNLAKOQQOQN---DVKLTK
RAB35[NP_006852] 241 L--- LSGAAC EQAEADAVHLAREM-QA EY-WSVSAB---TGENVKAFFRVAALAEQSVLQDLERQSSARLQVNGDILQMEG
RAB36[NP_004905] 140 M--- SSE-RVIRSE-DGETLAREY-GVPF-LETSAB---TGMNVELAFIAKELKRYRAGHQADE---PSFOIRD
RAB37[NP_783865] 131 Q--- CKD-VLMNGLKMDQFEKHEH-GFVGWFETSAB---ENINIDEASRCLVKHII LANECDLMESEIP---DVKVPHL
RAB38[NP_071732] 131 L--- ASQ-RQVTRH-EAEKLSADC-GMKY-IETSAB---DATNVEESTITLTRDIYELIYKGEICIQDQW---EGVKSGF
RAB39A[NP_059986] 127 L--- DTQ-RQVTRH-EAEKLSADC-GMKY-IETSAB---DAINVEKAFITLTRDIYELIYKGEICIQDQW---EGVKSGF
RAB39B[NP_741995] 130 L--- AFK-RQVPR-DAQAYAEERL-GVTF-FEVSPL---CNFNIESFTELARIVLRLHRMNWLGRPS---KVLSLQD
RAB40A[NP_543155] 130 L--- AFK-RQVPR-DAQAYAEERL-GVTF-FEVSPL---CNFNIESFTELARIVLRLHRMNWLGRPS---KVLSLQD
RAB40B[NP_006813] 130 L--- AFK-RQVPR-DAQAYAEERL-GVTF-FEVSPL---CNFNIESFTELARIVLRLHRMNWLGRPS---KVLSLQD
RAB40C[NP_066991] 135 L--- SEL-REVSLA-EAQSLAEHY-DI LCAIETSAB---DSSNV EAEFLRVATELIMRHGGLFSEKSP---DHIQLNS
RAB43[NP_940892] 129 L--- SP---WAVSRD-QIDRSKEN-GFTGWTETSAB---ENKNI NEAMRVLIEKMMRNSTEDIMSLSTQ---DYINLQT
RAB71[NP_003920] 126 L--- AGR-RAVDSA-EARAWALCO-GLEC-FETSAB---EMENFEAPFHLAKQFHQLYREKV---EVFRALA
RAB4A[NP_006851] 185

Supplementary Fig. 1. Alignment of human Rab GTPases. The order of the sequences is according to their numerical classification, except for Rab28, which is shown on top. The accession numbers of the sequences are indicated next to their names. Highly conserved amino acids, based on an overall identity threshold of 90%, are highlighted (blue background). The regions corresponding to the P-loop, switch 1 and switch 2 are boxed red. Phylogenetic analysis of the Rab family suggests that Rab28 is at the periphery of this family [1-3]. Among all the members of the Rab family, only Rab28 and Rab7B (whose structure is still unknown) present a double-glycine motif at the beginning of switch 2 (red). We propose that the presence of the double-glycine motif explains, in part, the large conformational change observed in the switch region of Rab28. The position corresponding to Rab28 Gly70 is typically occupied by Ala in other members of the Rab family, whereas the double-glycine motif is found in members of the Arf GTPase family [2,3]. The alignment was generated with the program MUSCLE [4] and edited with the program Jalview [5].



Supplementary Fig. 2. Crystal packing contacts near switch 1 in the structure of GDP-3'P-Rab28. Crystal packing contacts may help stabilize the conformation of switch 1 (pink) in the structure of GDP-3'P-Rab28 (cyan, reference molecule; yellow, symmetry-related molecules).

Supplementary Movie 1. Nucleotide-dependent conformational change in Rab28. The movie illustrates a linear interpolation between the atomic coordinates of the GppNHp-bound and GDP-3'P-bound structures of Rab28. The C α -trace and transparent surface representations are colored according to displacement, using a color ramp from blue (minimum displacement) to red (maximum displacement). Note that the nucleotide moves slightly after hydrolysis, a fact hardly ever noticed but which probably contributes to the conformational change.

Supplementary Table 1. Structures of Rab GTPases

Name	PDB	Nucleotide	Complex	Resolution (Å)	Reference	Comments
h-Rab1A	2FOL	GDP	No	2.63	Structural Genomics	
cp-Rab1A	2RHD	GDP	No	2.06	Structural Genomics	
h-Rab2A	1Z0A	GDP	No	2.12	[6]	
r-Rab3A	3RAB	GppNHp	No	2.00	[7]	
r-Rab3A	1ZBD	GTP	rabphilin-3A (effector)	2.60	[8]	
h-Rab3D	2GF9	GDP	No	1.53	Structural Genomics	
h-Rab4A	1Z0K	GTP	Rabenosyn-5 (effector)	1.92	[6]	Q67L mutant
h-Rab4A	1YU9	GppNHp	No	2.07	[6]	
h-Rab5A	1N6H	GppNHp	No	1.51	[9]	
h-Rab5A	1N6R	GppNHp	No	1.55	[9]	A30L mutant
h-Rab5A	1N6P	GppNHp	No	1.54	[9]	A30E mutant
h-Rab5A	1N6O	GppNHp	No	1.80	[9]	A30K mutant
h-Rab5A	1N6N	GppNHp	No	1.60	[9]	A30R mutant
h-Rab5A	1N6L	GTP	No	1.60	[9]	A30P mutant
h-Rab5A	1N6K	GDP-AIF ₃	No	1.55	[9]	A30P mutant
h-Rab5A	1N6I	GDP	No	1.55	[9]	A30P mutant
h-Rab5A	1TU3	GppNHp	Rabaptin-5 (effector)	2.31	[9]	
h-Rab5A	1TU4	GDP	No	2.20	[9]	Co ²⁺ in catalytic site
h-Rab5A	1R2Q	GppNHp	No	1.05	[10]	
m-Rab5C	1HUQ	GppNHp	No	1.80	[11]	
m-Rab5C	1Z07	GppNHp	No	1.81	[6]	G55Q mutant
m-Rab5C	1Z0D	GDP	No	2.20	[6]	
h-Rab6A	1YZQ	GppNHp	No	1.78	[6]	
h-Rab6A	3BBP	GTP	GCC185	3.00	[12]	Q72L mutant
h-Rab6A	2GIL	GTP	No	1.82	[13]	Slow GTPase activity
h-Rab6B	2FE4	GDP	No	2.30	[14]	
pf-Rab6	1D5C	GDP	No	2.30	[15]	
h-Rab7A	1T91	GTP	No	1.90	[16]	Q67L mutant
h-Rab7A	1YHN	GppNHp	RILP (effector)	3.00	[16]	
r-Rab7A	1VG0	GDP	Rab escort protein 1	2.20	[17]	
r-Rab7A	1VG9	GDP	Rab escort protein 1	2.50	[17]	
r-Rab7A	1VG8	GppNHp	No	1.70	[17]	
r-Rab7A	1VG1	GDP	No	1.90	[17]	
h-Rab8A	2FU5	None	MSS4 (GEF)	2.00	[18]	
h-Rab9A	1WMS	GDP	No	1.25	[19]	
h-Rab9B	2OCB	GppNHp	No	2.20	Structural Genomics	
m-Rab9A	1YZL	GppNHp	No	1.85	[6]	
c-Rab9A	1S8F	GDP	No	1.77	[20]	
h-Rab11A	1YZK	GppNHp	No	2.00	[6]	
h-Rab11A	2GZD	GTP	FIP2 (effector domain)	2.44	[21]	Q70L mutant
h-Rab11A	2GZH	GTP	FIP2 (effector domain)	2.47	[21]	Q70L mutant
h-Rab11A	2HV8	GTP	FIP3 (effector domain)	1.86	[22]	Q70L mutant
h-Rab11A	2D7C	GTP	FIP3 (effector domain)	1.75	[23]	Q70L mutant
h-Rab11A	1OIX	GDP-Pi	No	1.70	[24]	
h-Rab11A	1OIW	GTP _γ S	No	2.05	[25]	
h-Rab11A	1OIV	GDP	No	1.98	[25]	
pf-Rab11A	3BFB	GDP	No	1.80	Structural Genomics	
h-Rab11B	2F9M	GppNHp	No	1.95	[26]	
h-Rab11B	2F9L	GDP	No	1.55	[26]	
h-Rab12	2IL1	GDP	No	2.10	Structural Genomics	
h-Rab14	2AED	GDP	No	2.30	Structural Genomics	
h-Rab14	1Z0F	GDP	No	2.15	[6]	
h-Rab18	1X3S	GppNHp	No	1.32	Structural Genomics	

Supplementary Table 1 Continued

h-Rab21	1YZT	GppNHp	No	2.05	[6]	
h-Rab21	1YZU	GppNHp	No	2.50	[6]	
h-Rab21	1Z08	GppNHp	No	1.80	[6]	Q53G mutant
h-Rab21	1Z0I	GDP	No	2.33	[6]	
h-Rab21	2OT3	None	VPS9 (GEF domain)	2.10	[26]	
m-Rab22A	1YVD	GppNHp	No	1.93	[6]	
m-Rab22A	1Z0J	GTP	Rabenosyn-5 (effector)	1.32	[6]	V22M, Q64L mutants
m-Rab23	1Z22	GDP	No	2.06	[6]	
m-Rab23	1Z2A	GDP	No	1.90	[6]	
h-Rab25	2OIL	GDP	No	2.30	Structural Genomics	
h-Rab26	2G6B	GppNHp	No	2.00	Structural Genomics	
m-Rab27B	2IEZ	GDP	No	2.80	[27]	Q78L mutant
m-Rab27B	2IF0	GDP	No	2.80	[27]	Q78L mutant
m-Rab27B	2IEY	GDP	No	3.18	[27]	Q78L mutant
h-Rab28	2HXS	GDP-3 ^o P	No	1.10	This work	
h-Rab28	3E5H	GppNHp	No	1.50	This work	
h-Rab30	2EW1	GppNHp	No	2.00	Structural Genomics	
h-Rab31	2FG5	GppNHp	No	2.80	Structural Genomics	
m-Rab33B	1Z06	GppNHp	No	1.81	[6]	
m-Rab33B	2G77	GDP-AIF ₃	Gyp1 TBC domain (GAP)	2.26	[28]	
h-Rab43	2HUP	GDP	No	2.05	Structural Genomics	
h-Rab45	2P5S	GDP	No	2.15	Structural Genomics	h-RasEF (aa 533-712)
Sc-Sec4	1G16	GDP	No	1.80	[29]	
Sc-Sec4	1G17	GppNHp	No	2.00	[29]	
Sc-Sec4	2EQB	Phosphate	Sec2 GEF domain	2.70	[30]	PO ₄ in nucleotide pocket
Sc-Sec4	2OCY	None	Sec2 GEF domain	3.30	[31]	
Sc-Ypt1	1UKV	GDP	GDI	1.50	[32]	
Sc-Ypt1	1YZN	GppNHp	No	2.06	[6]	
Sc-Ypt7	1KY2	GppNHp	No	1.60	[33]	
Sc-Ypt7	1KY3	GDP	No	1.35	[33]	
Sc-Ypt51	1EK0	GppNHp	No	1.48	[34]	

h, human; r, rat; m, mouse; c, canine; Sc, *Saccharomyces cerevisiae*; pf, *Plasmodium falciparum*; cp, *cryptosporidium parvum*

Supplementary Table 2. Structures of Arf GTPases

Name	PDB	Nucleotide	Complex	Resolution (Å)	Reference	Comments
r-Arf1	1RRF	GDP	No	3.00	[35]	
r-Arf1	1RRG	GDP	No	2.40	[35]	
b-Arf1	1R8S	GDP	Sec7 (GEF domain)	1.46	[36]	Sec7 catalytic E->K mutant
b-Arf1	1R8Q	GDP-3'P	Sec7 (GEF domain)	1.86	[36]	With inhibitor brefeldin A
b-Arf1	1S9D	GDP	Sec7 (GEF domain)	1.80	[36]	With inhibitor brefeldin A
h-Arf1	1RE0	GDP	Sec7 (GEF domain)	2.40	[37]	With inhibitor brefeldin A
m-Arf1	1J2J	GTP	GGA1 fragment	1.60	[38]	Q71L mutant
m-Arf1	1O3Y	GTP	No	1.50	[38]	Q71L mutant
m-Arf1	2J59	GTP	ARHGAP21 (GAP)	2.10	[39]	
h-Arf1	1U81	GDP	No	NMR	[40]	
Sc-Arf1	1MOZ	GDP	No	3.17	[41]	Also known as ARL1
Sc-Arf2	1MR3	GDP-3'P	No	1.60	[41]	
h-Arf4	1Z6X	GDP	No	2.70	Structural Genomics	
h-Arf5	2B6H	GDP	No	1.76	Structural Genomics	
h-Arf6	2J5X	GTP _γ S	No	2.80	[42]	
h-Arf6	1E0S	GDP	No	2.28	[43]	
h-Arf6	2A5D	GTP	Cholera toxin A1	1.80	[44]	
h-Arf6	2A5F	GTP	Cholera toxin A1	2.02	[44]	
h-Arf6	2A5G	GTP	Cholera toxin A1	2.66	[44]	Q67L mutant
h-SAR1a	2GAO	GDP	No	2.00	Structural Genomics	
Ch-SAR1	2FA9	GDP	No	2.50	[45]	Not in PubMed
Ch-SAR1	1F6B	GDP	No	1.70	[46]	
Ch-SAR1	2FMX	GDP	No	1.82	[45]	
Sc-SAR1	1M2O	GppNHp	Sec23	2.50	[47]	
Sc-SAR1	2QTV	GppNHp	Sec23 and Sec31 domain	2.50	[48]	
h-Arf5	1ZJ6	GDP-3'P	No	2.00	[49]	

h, human; r, rat; m, mouse; b, bovine; Sc, *Saccharomyces cerevisiae*, Ch, Chinese hamster

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