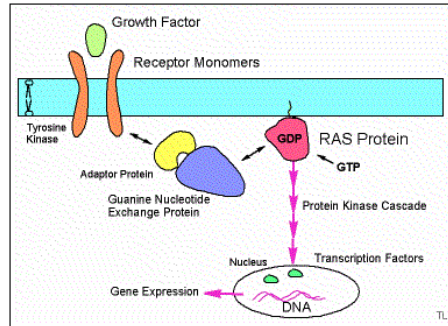
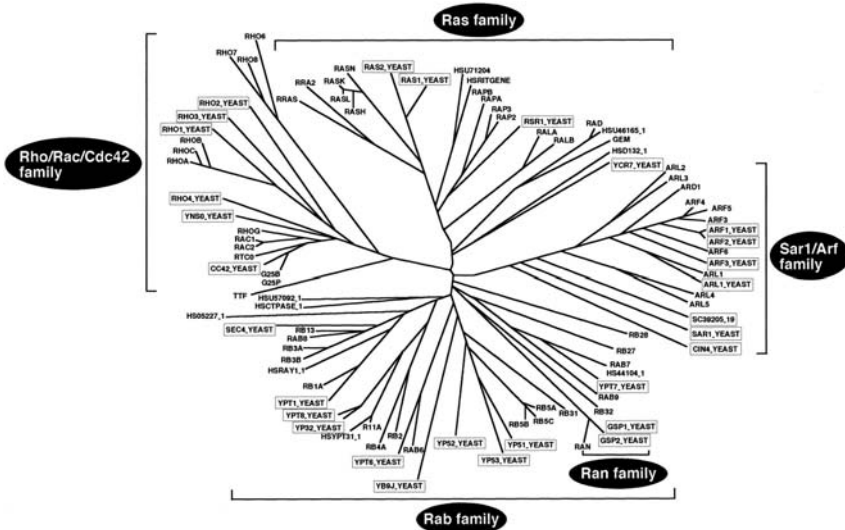


Small G proteins GTP/GDP binding sites



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 Karine Schouwey
 Samantha Fernandez
 Nathalie Leresche
 Christian Geest

Dendrogram of small G protein family



Sequence alignment of Ras family

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*****
H-Ras 1 -----NTYKLVVWCAGGVGVSALTIQFI---QMFV
N-Ras 1 -----NTYKLVVWCAGGVGVSALTIQFI---QMFV
K-Ras 1 -----NTYKLVVWCAGGVGVSALTIQFI---QMFV
Ral-E 1 -----MAAMKGRKSGSIVLHVVVWCAGGVGVSALTIQFI---YDFV
RAP2 1 -----MGLVLRPAKIVVWVWVGVVIGCFALATQFA---CQFP
RAD 1 AACTRTQGRQLDWPFGSSDLSLSCDSEGSDECVYKHAACAPGVCSALTIAGGVG---G
GEM 1 HSTAPEHCRRSWSSDSTDSVSSSESG---NIVYVWVLCGCGVCSSTLHIIAGVGV---C
cons Rho 1 -----AQLRIVVWVGCIVGCFALATQFA---TMAP

***
H-Ras 30 REVDPEEDSYRQVVVDCHCCLLDILFAQGEFTSANDVYHRCGFLVAFINTK
N-Ras 30 REVDPEEDSYRQVVVDCHCCLLDILFAQGEFTSANDVYHRCGFLVAFINTK
K-Ras 30 REVDPEEDSYRQVVVDCHCCLLDILFAQGEFTSANDVYHRCGFLVAFINTK
Ral-E 41 EDVPEKADSYRQVVVDCHERVQDILFAQGEFTSANDVYHRCGFLVAFINTK
RAP2 38 PCEPSEVLESLKQVWVDPALPILITVLESH-LVTLIDVYHRCGFLVAFINTK
RAD 59 PEARAAG-HYDQSHITVDCEASLHVVIVWVDCG-CMLDCHCHANCQAAVIVVSTKRC
GEM 59 SDCBVLGEDVYERTVWVDCESATLITVHWVRCGENMLDCHCHQVAVLVVSTKRA
cons Rho 30 REVDPEEDSYRQVVVDCHCCLLDILFAQGEFTSANDVYHRCGFLVAFINTK

*
H-Ras 89 SFBDIHQVREQIHRVFDSDV-VPIVLVGN-CFLAAL-IVVESHQAQDLASGCHVIFETSA
N-Ras 89 SFADNLVREQIHRVFDSDV-VPIVLVGN-CFLDPT-IVVDHQAEFLASGCHVIFETSA
K-Ras 89 SFBDIHQVREQIHRVFDSDV-VPIVLVGN-CFLDPT-IVVDHQAEFLASGCHVIFETSA
Ral-E 100 SFTATAEVRQIHRVKSERDQVPIVLVGN-SLREEREPQVDPALPILITVLESH-VVETSA
RAP2 97 SFLAARVLEERVCHRCRDA-VPIVLVGN-LADDAEQVLDLQALPILITVLESH-VVETSA
RAD 117 SFBRASERVQLD-ARQDQD-VPIVLVGN-SLWVRSREQVSDGCRACREVDQCFPETS
GEM 119 SFBRASERVQLD-ARQDQD-VPIVLVGN-SLWVRCREQVSDGCRACREVDQCFPETS
cons Rho 89 SFBNORERQVPEVTHFCPNT---PMLVGTDLVLDPPDSTIERELVQRGSPVITYRQGELE

**
H-Ras 147 KTRQVWEDARTLVRETRIQHRRLNPPD---ESGLCCVSCVETFS-----
N-Ras 147 KTRQVWEDARTLVRETRIQHRRLNSSZ---DGTCCGLDDEAH-----
K-Ras 147 KTRQVWEDARTLVRETRIQHRRKSKDGS---KRRKSR-TIDTDM-----
Ral-E 160 KTRQVWEDARTLVRETRIQHRRSENKKNKGRKSSSSSKRKLQGL-----
RAP2 156 ESRITVWVETQVRETEALAPPQRAF---IPANALEWPAERFC-----
RAD 175 ALDHWQALREGVVDTPLDSDSRDNAPDQACTHESVCKRARRFLGRIVANRSMMA
GEM 178 AVQHWKREEGVVDVLDLSDSRKRNREPLAYQREHESIPRSARFVWGIKVAFNKRMIA
cons Rho 147 ERICWVYRECAVTEGELQVDFEATRAA-----

```

Sequence alignment of Arf family

GTP-GDP binding site for the Rho family : AVGKTC---YV-T---DT-G----K-D-----AL
 GTP-GDP binding site for the Arf family : AAGKTT----IP-T---DV-G-----K-D-----AT

```

1      10     20     30     40     50     60     70     80     90     100    110    120    130
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
Cdc42 1  NITIKCVYVGDGKVKTCLLISYTTNMFPCYIPIVDNYSNVHML--GGEPYTLGLDTRAGQEDVDGLRPLSYPIVDFLVCFVSPSSPFENKHPVETI--HCPKTFP
Rac1 1  NRIKICVYVGDGKVKTCLLISYTTNMFPCYIPIVDNYSNVHML--DGPVNLGLDTRAGQEDVDGLRPLSYPIVDFLVCFVSPSSPFENKHPVETI--HCPKTFP
Rac2 1  NRIKICVYVGDGKVKTCLLISYTTNMFPCYIPIVDNYSNVHML--DGPVNLGLDTRAGQEDVDGLRPLSYPIVDFLVCFVSPSSPFENKHPVETI--HCPKTFP
RhoG 1  NRIKICVYVGDGKVKTCLLISYTTNMFPCYIPIVDNYSNVHML--DGRVNLMLDTRAGQEEYDRLRPLSYPIVDFLVCFVSPSSPFENKHPVETI--HCPKTFP
1ARL2 1  HGLLTI---LKKHKQK-ERELRLMLGLDNRGKTTLLKFFMGEDVDIT--SPTLGFNIKILEH----RQFLKLDVGGGKSLRYSNMYFESVIGLLVYVDSADRKQMDQRELQSLVEERLHGLL
2ARL3 1  HGLLSI---LRLKSPDQEWLLLGLDNRGKTTLLKQSRGDSHIT--PTQFNIKSVGS---GQFLKLDVGGGKSLRYSNMYFESVIGLLVYVDSADRKQMDQRELQSLVEERLHGLL
3ARF4 1  HGLTIS---SLFSLFGKQKRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNICFTVHDVGGGKIRPLRHRVYQNTGLLIVVDSNDRERIQEGRAVLLKLELQDVL
4ARF5 1  HGLTVS---ALFSRTFGKQKRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNICFTVHDVGGGKIRPLRHRVYQNTGLLIVVDSNDRERIQEGRAVLLKLELQDVL
5ARF3 1  HGLTFG---MLKSLFGKQKRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNISFTVHDVGGGKIRPLRHRVYQNTGLLIVVDSNDRERIQEGRAVLLKLELQDVL
10ARF1 1  HGLTFG---MLKSLFGKQKRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNISFTVHDVGGGKIRPLRHRVYQNTGLLIVVDSNDRERIQEGRAVLLKLELQDVL
6ARF6 1  HGLTFG---MLKSLFGKQKRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNISFTVHDVGGGKIRPLRHRVYQNTGLLIVVDSNDRERIQEGRAVLLKLELQDVL
7ARL1 1  HGLTFG---SIFSSLFGTRRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNLKFQVHDGQTSIRPYRMYSTDAVLYVDSNDRERIQEGRAVLLKLELQDVL
8ARL5 1  HGLTFG---SIFSSLFGTRRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNLKFQVHDGQTSIRPYRMYSTDAVLYVDSNDRERIQEGRAVLLKLELQDVL
9ARL4 1  HGLTFG---SIFSSLFGTRRLMVLGLDNRGKTTLLYKLGLEIVTI--PTIGFNVETVEY----KNLKFQVHDGQTSIRPYRMYSTDAVLYVDSNDRERIQEGRAVLLKLELQDVL
Consensus 1  .....qg.ril.vGIdagKTCllg.l.....v.t.iPT.gFN.e.....k..f..HD.g60.....rpluc.yg..Tt..i.vvds.dr..tL.....el.....l.....l..s..

131  140  150  160  170  180  190  200  21812
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
Cdc42 1  LLVGTIDLRODPSTIEKLNKQKQIPITPTEAKLRDLKAVKYVCSALTKQGLKNVFDGAILRALEP-PEPKSRRCVLL
Rac1 1  LLVGTIDLRODDKTEKLEKELPTIYPQGLRANKRIGAVKYLECSALTKRGLKTVDEIRAVLCPPTPKRRKRCILL
Rac2 1  LLVGTIDLRODDKTEKLEKELPTIYPQGLRANKRIGAVKYLECSALTKRGLKTVDEIRAVLCPPTPKRRKRCILL
RhoG 1  LLVGTIKDLRQDPTLRLKQGGAPITPQOGLRQKHAVRYLECSALDQDQKVEFIREAVRVLNPTPK-RRGSCILL
1ARL2 1  LIFANKDLPGLSCNRA-----IQEALDLSIKSHI-ARIIGCSAVTGEDLPGDHLLDIISSVFVTRD
2ARL3 1  LIFANKDLPGLSCNRA-----IQEALDLSIKSHI-ARIIGCSAVTGEDLPGDHLLDIISSVFVTRD
3ARF4 1  LIFANKDLPANRASE-----ITDKGLGLSRLRRT-AYVARTCATGTLVGLDHLSELKSR
4ARF5 1  LIFANKDLPANRASE-----ITDKGLGLSRLRRT-AYVARTCATGTLVGLDHLSELKSR
5ARF3 1  LIFANKDLPANRARE-----ITDKGLGLSRLRRT-AYVARTCATGTLVGLDHLSELKSR
10ARF1 1  LIFANKDLPANRARE-----ITDKGLGLSRLRRT-AYVARTCATGTLVGLDHLSELKSR
6ARF6 1  LIFANKDLPANRARE-----ITDKGLGLSRLRRT-AYVARTCATGTLVGLDHLSELKSR
7ARL1 1  YVFNKQDEQHTPSE-----HNRALGLPALKQKQ-HQIFKTSATKGLDERHEMLVETLSRQ
9ARL5 1  LIFANKDQVKECHTVRE-----ISQFLKLSIKDQD-HIQARCCALTEGGLCGLEHMSRLKIR
8ARL4 1  LIFANKDQVKECHTVRE-----TEKLLANGELSSSTPMLQPTCAIGDGLKLEKELHMLIKRRKRLRQKRRK
Consensus 1  1.fanqD9..e..e.....l.gLl..r..s..w.q.cofl..g.Gl..e.gL.....

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SMALL GTPase Arf

