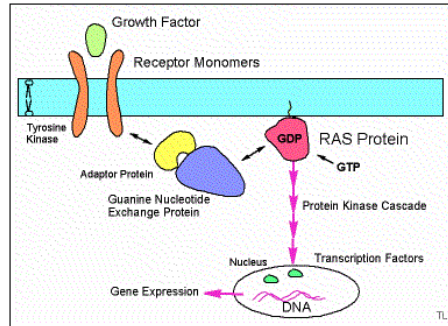
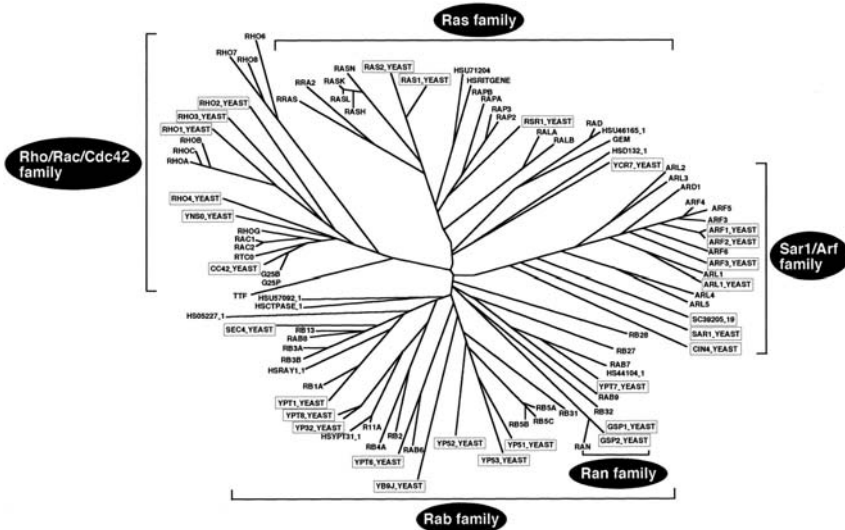


Small G proteins GTP/GDP binding sites



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 Christian Geest

Dendrogram of small G protein family



**Conserved
GTP-GDP
Binding seq** →

G1	G2	G3	
AQRKLVVVGDAVGKTCLLISYTTNAPPEEYVPTVFENYVADVEVD--GKPVGLMDT	58	Consensus	
AIRKKLVIVGDVACGKTCLLIVFSKDPPEVYVPTVFENYVADIEVD--GKVELALMDT	61	RhoA	
MQTIKCVVVGDAVGKTCLLISYTTNKPpseYVPTVFENYAVTVMIG--GEPYTLGLFDT	58	Cdc42	
MQAIRCVVVGDAVGKTCLLISYTTNAPpgeYIPTVFENYANVMVD--GKPVNLGLMDT	58	Rac1	
AIRKKLVIVGDVACGKTCLLIVFSKDPPEVYVPTVFENYVADIEVD--GKVELALMDT	61	RhoA	
ELRRKLVIVGDVACGKTCLLIVFSKGTTPpevYVPTVFENYVADVEVD--GRHVELALMDT	61	Rho1	
ETSKKLVVVGDCGCKTCLLIVFSSGTPperYVPTVFENYITDITYGpnsKVIELALMDT	73	Rho1-like protein	

Sequence alignment of Rho subfamily members

G4	
AGQEDYDRLRPLSYPPADVFLICFSVSVSPSPFENKKEKWPVEVTHFCNPFIILVGTKLD	118 Consensus
AGQEDYDRLRPLSYPPDVLVILMCPSIDSPDLENIPKWTPEVKHFCNPVILVGNKDK	121 RhoA
AGQEDYDRLRPLSYPQTDVFLVCPFSVSPSPFENKKEKWPETHHCNTPFLVGTQID	118 Cdc42
AGQEDYDRLRPLSYPQTDVFLICFSLVSPASFPENVRKWPVEVRHHCNPFIILVGTKLD	118 Rac1
AGQEDYDRLRPLSYPPDVLVILMCPSIDSPDLENIPKWTPEVKHFCNPVILVGNKDK	121 RhoA
AGQEDYDRLRPLSYPPDVLVILMCPSIDSPDLENIPKWTPEVKHFCNPVILVGNKDK	121 Rho1
AGQEDYDRLRPLSYPPDVLVILMCPSIDSPDLENIPKWTPEVKHFCNPVILVGNKDK	121 Rho1-like protein

G5	
LRDDPSTIEELAKQKQKPVTYEQEKLAKRIGAVKYLECSALTQEGKQVDFEAIRAA	176 Consensus
LRNDEHTRRELAKMGEQPKPEGRDMANRIGAFGMESAKTKDGVREVFEMATRAA	179 RhoA
LRddpstielaaknkgkpiTPETAELARDLkAVKYLECSALTQGLKNVDFEAILAA	176 Cdc42
LRddkdiiekkekkltpiTYPQLAMAKEIGAVKYLECSALTQGLKTVDFEIRAV	176 Rac1
LRNdehtrrelakmgepVKPEGRDMANRIGAFGMESAKTKDGVREVFEMATRAA	179 RhoA
LRndpkiielaktngpvtTEEQVAQKIGAVKYLECSAKTNEGVRVFEATRAA	179 Rho1
LRkdrnatelrvrtggltpvTYQQAQSVALSMAA-PYVECSAKENTGVNEVFQLAVGLT	190 Rho1-like protein

AVGKTC----YV-T---DT-G--K-D---AL

Sequence alignment of Ran family

In red : amino acids involved in the binding of GDP/GTP

consensus	1	-----AQRKLVVVGDC AVGKTC LLISYTTNAPPEE YVPT VFENYVADVEVDCK--PV
RAB9	1	---MCGSSIFRKLILICD GVGR SSLENRYVINKRFS GLFHT IGVFFIMRDEVDG-HFV
RAB7-like	1	---MNPRAKVDLKLILVCA ICVGR SLDHYVHKTFE EQT ICASTISKIILDD-TTL
RAB7	1	---MCSDDHLFRVILVGC AVGK SLDQRYSDS SEK KRS IV GVDFALKVILQWSDSHV
Ran	1	MAAQEPQVCFKVVVWDC GT TRFRRHIL GE EEKE VA ICVYVHTLRFHTNR-CPI

consensus	52	EL Q MD T AG Q EDMDL R PLSYPPADVFLICFSVSVSPSPFENKKEKWPVEVTHFC----P
RAB9	57	TL Q MD T AG Q ERFSL E TP Y RG D CLL T FS D DS S Q S F Q ML-SM W R R FF Y Y A D V K E P E
RAB7-like	58	EL Q MD T AG Q ERF S W S T Y RG D CL L AF D V T D P ES F EAL-D I R D D V LAK I IP M E T
RAB7	58	EL Q MD T AG Q ERF S W S T Y RG D CL L AF D V T W A T S S S -Q R R D D V D S KL L P S GE
Ran	60	RF V MD T AG Q ER F CG L ED C Y I CA Q CA T IM F D V T S R V T Y RM L -P S W R D L W R V C ---- E

consensus	107	MT P IL V GT L LD L LD---DPSTIEELAKQKQKPVTYEQEKLAKRIGAVKYLECSALTQEGKQVDFEAIRAA
RAB9	116	S F P F W L GN T LD L DR W S T EAQA Q CK MG D Y PE T EA D ST W AA F EA V P W AT
RAB7-like	116	S P W L GN T LD L DR W S T EAQA Q CK MG D Y PE T EA D ST W AA F EA V P W AT
RAB7	117	P W CL L AN S LS P W A FR D Q D RES K MG F CT C HT S URE N K R IN E RM R LV E RM IN
Ran	114	N I D V LC E V V W W IR W AK P L F HR Q W---L Q MD T EA S SN Y IF E K P W W AR K CG D

consensus	164	-GLK Q VD E AR AA -----
RAB9	176	-ED R SE H L I Q T D T -- W MD H R K PK P NS CC -----
RAB7-like	175	-Y Q CT A EN H L D S-- R LS P C - Q P KS CC -----
RAB7	177	-S R ED W MS L ST Q GN V MD Q AK P SS G W TC -----
Ran	172	P N LE F W A MP A L A PP W W D P A L A A Q Y E H D L E V A Q T T A L P D E E D L

SMALL GTPase Arf

