

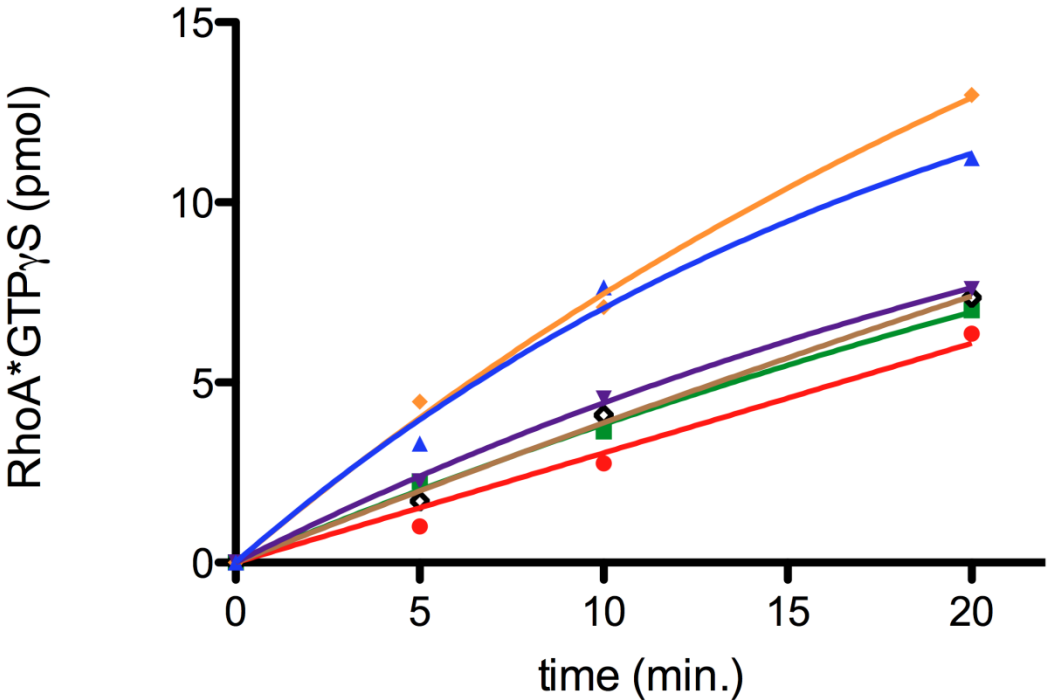
Supplemental Figure Legends

Supplemental Figure 1: The T274E mutation in G α 13 impairs RhoA activation *in vitro*. GTP γ S binding to RhoA (final concentration 500 nM) was measured in the presence of buffer, 5 nM p115RhoGEF, or 5 nM p115RhoGEF and 100 nM AlF $_4^-$ -activated G α 13 (wild-type or mutant). Samples were incubated at 30 °C and quenched in ice-cold buffer containing 10 mM MgSO $_4$ at the indicated times. Samples are: RhoA only (●); p115RhoGEF (■); p115RhoGEF + G α 13 T274E/N278A (□); p115RhoGEF + G α 13 T274E (◇); p115RhoGEF + G α 13 N278A (□); p115RhoGEF + G α 13 (▲). Data presented are from a single experiment.

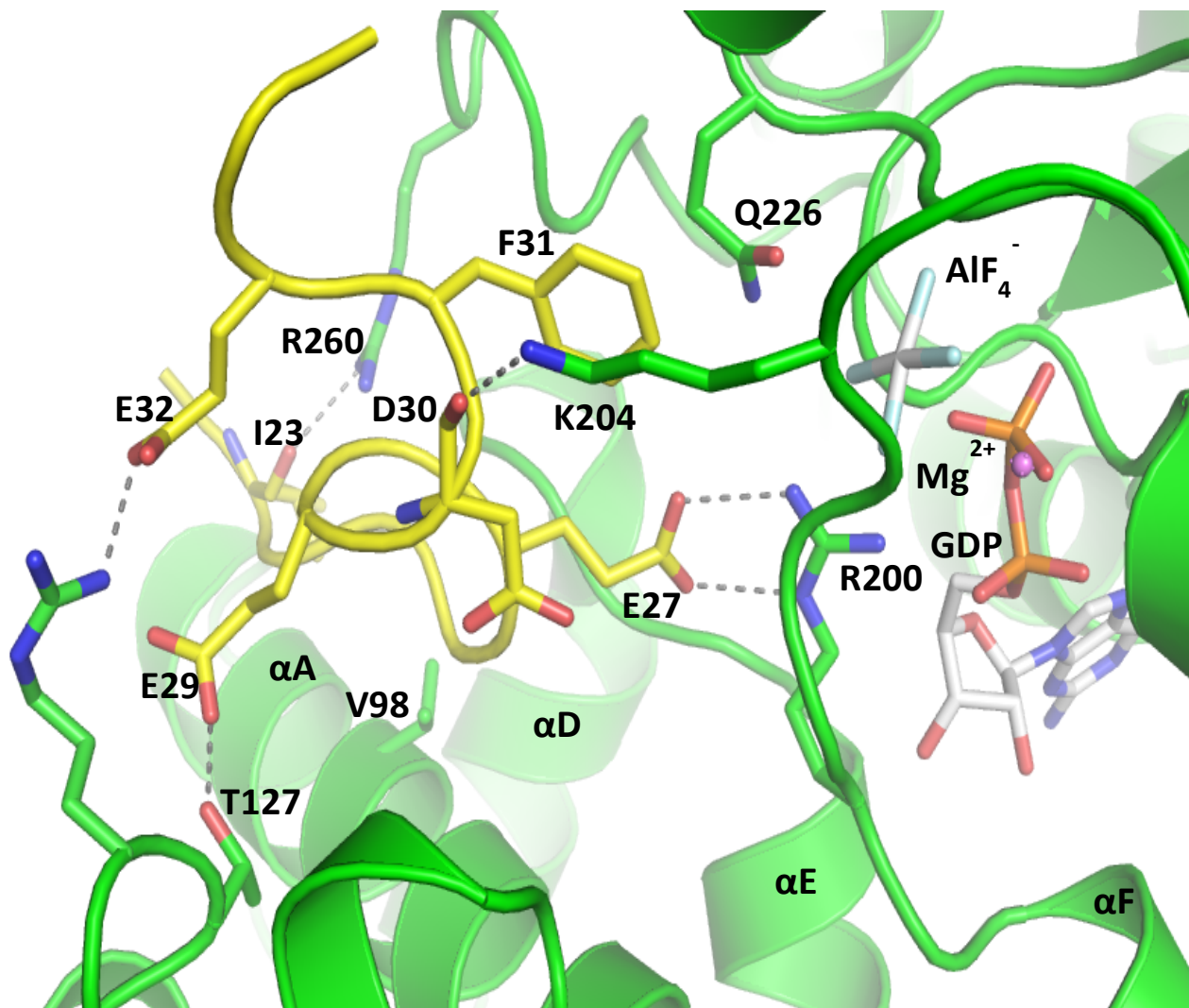
Supplemental Figure 2: A detailed view of the G α 13-p115 RH GAP interface. The complex is shown as a ribbon diagram with G α 13 colored in green and the RH domain of p115RhoGEF colored in yellow. Oxygen and nitrogen atoms are colored red and blue, respectively. Phosphate atoms are colored orange, while aluminum and fluoride atoms are light grey and light blue, respectively. GDP and AlF $_4^-$ are depicted as stick models, while the Mg $^{2+}$ co-factor is a purple sphere. Hydrogen bonds are depicted as dashed lines.

Supplemental Figure 3: Mutational analysis of the G α 12-RH-RhoGEF effector interface. **Upper panel:** The T277E and N281A mutations in G α 12 impair Rho activation in cells. HeLa cells were transiently transfected with empty vector or the indicated G α 12 QL construct. The luciferase activity of cell lysates was determined as described in Materials and Methods. Data are presented as the mean (\pm S.E.M.) of triplicate determinations from a single experiment, representative of two independent experiments with similar results. Total cell lysate was immunoblotted for either G α 12 or GAPDH. Data were analyzed by one-way ANOVA, followed by Dunnett's post-test. Statistically significant difference from G α 12 QL: ns, not significant; **, $p < 0.01$. **Lower panel:** The T277E mutation in G α 12 impairs binding to the RH domain of p115RhoGEF. HEK293 cells were transiently transfected with wild-type G α 12 or the indicated mutant. Detergent-soluble cell extracts were incubated with 250 pmoles of GST-p115 RH in the presence or absence of AlF $_4^-$ and GST-p115 RH was pulled down with glutathione Sepharose beads. Bound proteins were released by the addition of SDS-PAGE sample buffer and boiling, and separated by SDS-PAGE. G α 12 was detected by immunoblotting, and GST-p115 RH was stained with Coomassie Brilliant blue. Data presented are from one experiment, representative of two independent experiments with similar results.

Supplemental Figure 1



Supplemental Figure 2



Supplemental Table I

p115RhoGEF residues (Chain B)

	S22	I23	I24	G25	A26	E27	D28	E29	D30	F31	E32	A67	L68	Q69	F70	K160	M163	M165	T166	E169	E171	L172	E176	T207	I208
V98					hydrophobic contact(s)																				
D101			M-S hydrogen bond(s)																						
A102																									
K105	M-S hydrogen bond(s)	hydrophobic contact(s)																							
L106																									
T127								S-S hydrogen bond(s)																	
R128								hydrophobic contact(s)			S-S hydrogen bond(s)														
F168																									
R200								S-S hydrogen bond(s)																	
P202						hydrophobic contact(s)																			
K204									M-S hydrogen bond(s)	hydrophobic contact(s)															
Q226										hydrophobic contact(s)															
S228																									
R230																	M-S hydrogen bond(s)	hydrophobic contact(s)							
K231																					hydrophobic contact(s)				
F234																			hydrophobic contact(s)	hydrophobic contact(s)					
F237																									
M257										hydrophobic contact(s)															
R260		M-S hydrogen bond(s)																							
E267																									
N270																	M-S hydrogen bond(s)	hydrophobic contact(s)							
I271																			hydrophobic contact(s)						
E273																S-S hydrogen bond(s)									
T274														M-S hydrogen bond(s)											
I275																			hydrophobic contact(s)						
N278													hydrophobic contact(s)												
R279												M-S hydrogen bond(s)	M-M hydrogen bond(s)		M-S hydrogen bond(s)										
V280												hydrophobic contact(s)												hydrophobic contact(s)	
S282																									
N283																									
R335															hydrophobic contact(s)										

Residues involved in

hydrophobic contact(s)	M-S hydrogen bond(s)	S-S hydrogen bond(s)	M-M hydrogen bond(s)
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M- main chain
S- side chain

Supplemental Table II

p115RhoGEF residues (Chain D)

	S22	I23	I24	G25	A26	E27	D28	E29	D30	F31	E32	A67	L68	Q69	F70	K160	M163	M165	T166	E169	E171	L172	E176	T207	I208	
V98			hydrophobic contact(s)	hydrophobic contact(s)																						
D101			M-S hydrogen bond(s)																							
A102		hydrophobic contact(s)																								
K105	M-S hydrogen bond(s)																									
L106		hydrophobic contact(s)																								
T127								S-S hydrogen bond(s)																		
R128								hydrophobic contact(s)			S-S hydrogen bond(s)															
F168		hydrophobic contact(s)																								
R200						S-S hydrogen bond(s)																				
P202						hydrophobic contact(s)																				
K204									M-S hydrogen bond(s)	hydrophobic contact(s)																
Q226										hydrophobic contact(s)																
S228																										
R230																	M-S hydrogen bond(s)	hydrophobic contact(s)								
K231																										
F234																			hydrophobic contact(s)	hydrophobic contact(s)						
F237																										
M257																										
R260	M-S hydrogen bond(s)						S-S hydrogen bond(s)																			
E267																										
N270																		hydrophobic contact(s)								
I271																			hydrophobic contact(s)							
E273																S-S hydrogen bond(s)										
T274														M-S hydrogen bond(s)		S-S hydrogen bond(s)		hydrophobic contact(s)								
I275																										
N278														hydrophobic contact(s)												
R279												M-S hydrogen bond(s)	M-M hydrogen bond(s)		M-S hydrogen bond(s)											
V280													hydrophobic contact(s)											hydrophobic contact(s)		
S282																										
N283																										
R335															hydrophobic contact(s)											

Residues involved in
 hydrophobic contact(s)
 M-S hydrogen bond(s)
 S-S hydrogen bond(s)
 M-M hydrogen bond(s)





M- main chain
S- side chain

Supplemental Table III

PDZ-RhoGEF residues

	L307	I308	I309	G310	P311	E312	.	E313	D314	Y315	D316	L349	S350	Q351	A352	K439	L442	L444	G445	.	S446	L447	N451	K480	IY481
V98																									
D101																									
A102																									
K105																									
L106																									
T127																									
R128																									
F168																									
R200																									
P202																									
K204																									
Q226																									
S228																									
R230																									
K231																									
F234																									
F237																									
M257																									
R260																									
E267																									
N270																									
I271																									
E273																									
T274																									
I275																									
N278																									
R279																									
V280																									
S282																									
N283																									
R335																									

Residues involved in

 hydrophobic contact(s)	 M-S hydrogen bond(s)	 S-S hydrogen bond(s)	 M-M hydrogen bond(s)
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M- main chain
S- side chain