# The Crystal Structure of the RhoA : AKAP-Lbc DH-PH Domain Complex

## Supplementary Material

## Contents

# Protein sequences of the constructs used

## RhoA

SMAAIRKKLVIVGDGACGKTCLLIVFSKDQFPEVYVPTVFENYVADIEVDGKQVELALWDTAGQEDYDRLRPLSYPDTD
VILMCFSIDSPDSLENIPEKWTPEVKHFCPNVPIILVGNKKDLRNDEHTRRELAKMKQEPVKPEEGRDMANRIGAFGYM
ECSAKTKDGVREVFEMATRAALQARRG

## AKAP-Lbc DH-PH domain

SMSKQLEAESWSRIIDSKFLKQQKKDVVKRQEVIYELMQTEFHHVRTLKIMSGVYSQGMMADLLFEQQMVEKLFPCL
DELISIHSQFFQRILERKKESLVDKSEKNFLIKRIGDVLVNQFSGENAERLKKTYGKFCGQHNQSVNYFKDLYAKDKRFQA
FVKKKMSSSVVRRLGIPECILLVTQRITKYPVLFQRILQCTKDNEVEQEDLAQSLSLVKDVIGAVDSKVASYEKKVRLNEIYT
KTDSKSIMRMKSGQMFAKEDLKRKKLVRDGSVFLKNAAGRLKEVQAVLLTDILVFLQEKDQKYIFASLDQKSTVISLKKLI
VREVAHEEKGLFLISMGMTDPEMVEVHASSKEERNSWIQIIQDTINTLNRD

## AKAP-Lbc DH domain

SMEAESWSRIIDSKFLKQQKKDVVKRQEVIYELMQTEFHHVRTLKIMSGVYSQGMMADLLFEQQMVEKLFPCLDELISI
HSQFFQRILERKKESLVDKSEKNFLIKRIGDVLVNQFSGENAERLKKTYGKFCGQHNQSVNYFKDLYAKDKRFQAFVKKK
MSSSVVRRLGIPECILLVTQRITKYPVLFQRILQCTKDNEVEQEDLAQSLSLVKDVIGAVDSKVASYEKKVRLNEIYTK

## **Figure S1 -** Sequence alignment of selected RhoGEF domains

```
p115-RhoGEF      ---------------------------------------DEGEPGRSGLELEPE-EPPGW 413
PDZ-RhoGEF       ---------------------------------------LLEDDLGQLSDLEPEPDAQNW 716
LARG             ---------------------------------------GESQSEDEQFENDLETDPPNW 769
AKAP-Lbc         ---------------------------------------------------SKQLEAESW 1980
                                                                    . : :. .*

p115-RhoGEF      RELVPPDTLHSLPKSQVKRQEVISELLVTEAAHVRMLRVLHDLFFQPMAECLFFPLEELQ 473
PDZ-RhoGEF       QHTVGKDVVAGLTQREIDRQEVINELFVTEASHLRTLRVLDLIFYQRMKKENLMPREELA 776
LARG             QQLVSREVLLGLKPCEIKRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSPSELR 829
AKAP-Lbc         SRIIDSKFLKQQKKDVVKRQEVIYELMQTEFHHVRTLKIMSGVYSQGMMADLLFEQQMVE 2040
                  . :  . :       :.***** **: **  *:* *:::  :: * :    ::  . :

p115-RhoGEF      NIFPSLDELIEVHSLFLDRLMKRRQES-------GYLIEEIGDVLLARFDGAEGSWFQKI 526
PDZ-RhoGEF       RLFPNLPELIEIHNSWCEAMKKLREE--------GPIIKEISDLMLARFDGPAREELQQV 828
LARG             KIFSNLEDILQLHIGLNEQMKAVRKRNE------TSVIDQIGEDLLTWFSGPGEEKLKHA 883
AKAP-Lbc         KLFPCLDELISIHSQFFQRILERKKESLVDKSEKNFLIKRIGDVLVNQFSGENAERLKKT 2100
                 .:*. * :::.:*    : :   ::.           :*..*.: ::  *.*   . :::

p115-RhoGEF      SSRFCSRQSFALEQLKAKQRKDPRFCAFVQEAESRPRCRRLQLKDMIPTEMQRLTKYPLL 586
PDZ-RhoGEF       AAQFCSYQSIALELIKTKQRKESRFQLFMQEAESHPQCRRLQLRDLIISEMQRLTKYPLL 888
LARG             AATFCSNQPFALEMIKSRQKKDSRFQTFVQDAESNPLCRRLQLKDIIPTQMQRLTKYPLL 943
AKAP-Lbc         YGKFCGQHNQSVNYFKDLYAKDKRFQAFVKKKMSSSVVRRLGIPECILLVTQRITKYPVL 2160
                  . **. :  ::: :*    *: **  *::.  * .  *** : : *    **:****:*

p115-RhoGEF      LQSIGQNTEEPT-EREKVELAAECCREILHHVNQAVRDMEDLLRLKDYQRRLDLSHLRQS 645
PDZ-RhoGEF       LESIIKHTEGGTSEHEKLCRARDQCREILKYVNEAVKQTENRHRLEGYQKRLDATALERA 948
LARG             LDNIAKYTEWPT-EREKVKKAADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLS 1002
AKAP-Lbc         FQRILQCTKDNEVEQEDLAQSLSLVKDVIGAVDSKVASYEKKVRLNEIYTKTDSKSIMRM 2220
                 :: * : *:    *:*.:  : .  ::::  *:. * . *.  **:    : * . :

p115-RhoGEF      SDPMLSEFKNLDITKKKLVHEGPLTWRVTKDKAVEVHVLLLDDLLLLLQRQDERLLLKSH 705
PDZ-RhoGEF       SNPLAAEFKSLDLTTRKMIHEGPLTWRISKDKTLDLHVLLLEDLLVLLQKQDEKLLLKCH 1008
LARG             EYPNVEELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLLQKQDDRLVLRCH 1062
AKAP-Lbc         KS--GQMFAKEDLKRKKLVRDGSVFLKNAAGRLKEVQAVLLTDILVFLQEKDQKYIFASL 2278
                 .      : . *:. :*::::*.:  :   .:  :: .:** *:*::**.:*:: :: .

p115-RhoGEF      SRTLTPTPDGKTMLRPVLRLTSAMTREVATDHKAFYVLFTWDQ-EAQIYELVAQTVSERK 764
PDZ-RhoGEF       SKTAVGSSDSKQTFSPVLKLNAVLIRSVATDKRAFFIICTSKLGPPQIYELVALTSSDKN 1068
LARG             SKILASTADSKHTFSPVIKLSTVLVRQVATDNKALFVISMSDN-GAQIYELVAQTVSEKT 1121
AKAP-Lbc         DQKST-----------VISLKKLIVREVAHEEKGLFLISMGMT-DPEMVEVHASSKEERN 2326
                 .:  .           *: *.  : *.** :.:.::::       .:: *: * : .::.

p115-RhoGEF      NWCALITETAGSLKVPAPASRPKPRPSPSSTREPLLSSSE------------NGNGGRET 812
PDZ-RhoGEF       TWMELLEEAVRNATRHPGAAPMPVHPPPPGPREPAQQGPTPSRVELDDSDVFHGEPEPEE 1128
LARG             VWQDLICRMAASVKEQSTKPIPLPQSTPGEGDNDEEDPSKLKEEQHG--ISVTGLQSPDR 1179
AKAP-Lbc         SWIQIIQDTINTLNRD
                  *  ::     . .
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| Protein | Official Symbol | Genbank ID |
|---|---|---|
| p115-RhoGEF | ARHGEF1 | NP_945353.1 |
| PDZ-RhoGEF | ARHGEF11 | NP_055599.1 |
| LARG | ARHGEF12 | NP_056128.1 |
| AKAP-Lbc | AKAP13 | NP_006729.4 |