

Supplementary data

Molecular isolation and characterization of the *Rac GTPase* gene from *Oryza sativa indica* cultivar UKMRC9

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Amino acid content of protein:

<u>Ala (A)</u> 23	7.5%	<u>Lys (K)</u> 15	4.9%
<u>Arg (R)</u> 16	5.2%	<u>Met (M)</u> 14	4.6%
<u>Asn (N)</u> 7	2.3%	<u>Phe (F)</u> 10	3.3%
<u>Asp (D)</u> 20	6.5%	<u>Pro (P)</u> 15	4.9%
<u>Cys (C)</u> 3	1.0%	<u>Ser (S)</u> 18	5.9%
<u>Gln (Q)</u> 7	2.3%	<u>Thr (T)</u> 22	7.2%
<u>Glu (E)</u> 22	7.2%	<u>Trp (W)</u> 2	0.7%
<u>Gly (G)</u> 26	8.5%	<u>Tyr (Y)</u> 14	4.6%
<u>His (H)</u> 9	2.9%	<u>Val (V)</u> 20	6.5%
<u>Ile (I)</u> 21	6.8%	<u>Pyl (O)</u> 0	0.0%
<u>Leu (L)</u> 23	7.5%	<u>Sec (U)</u> 0	0.0%

(B) 0 0.0% (X) 0 0.0%

(Z) 0 0.0%

Total number of negatively charged residues (Asp + Glu): 42

Total number of positively charged residues (Arg + Lys): 31

Atomic composition:

Carbon	C	1512
Hydrogen	H	2372
Nitrogen	N	404
Oxygen	O	460
Sulphur	S	17

Formula: C1512H2372N404O460S17

Total number of atoms: 4765

Extinction coefficients:

Extinction coefficients are in units of $M^{-1} \text{ cm}^{-1}$, at 280 nm measured in water.

Ext. coefficient 31985

Abs 0.1% (=1 g/l) 0.938, assuming all pairs of Cys residues form cystines

Ext. coefficient 31860

Abs 0.1% (=1 g/l) 0.934, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).

>20 hours (yeast, in vivo).

>10 hours (Escherichia coli, in vivo).

Instability index:

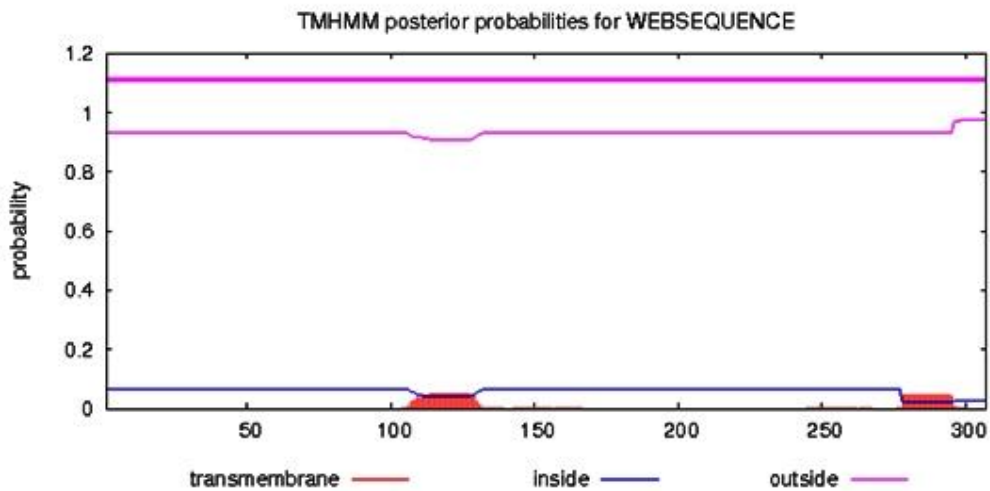
The instability index (II) is computed to be 32.73

This classifies the protein as stable.

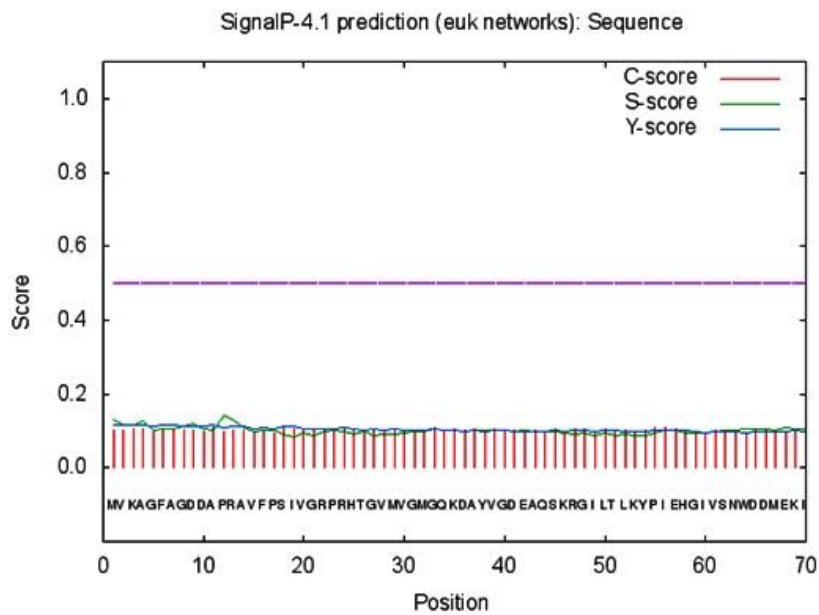
Aliphatic index: 82.28

Grand average of hydropathicity (GRAVY): -0.228

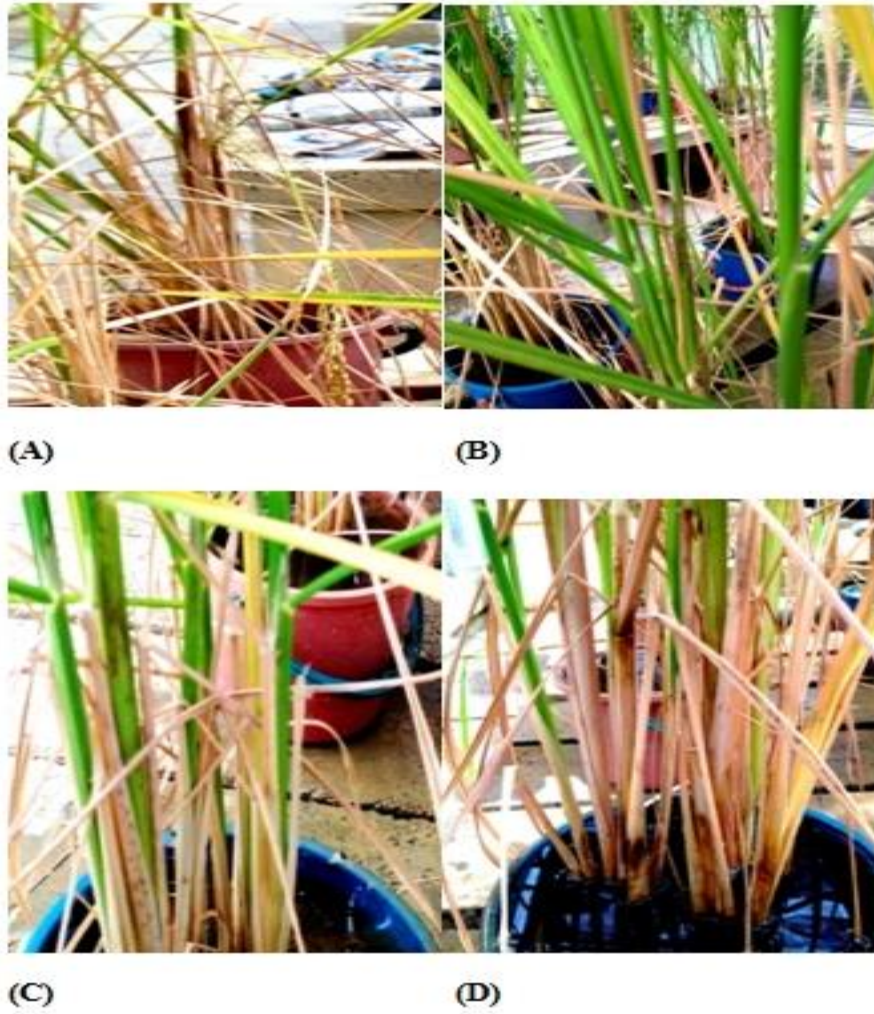
Supplementary Fig 1. Physico chemical analysis of Rac GTPase UKM



Supplementary Fig 3. TMHMM2.0 analysis of the Rac GTPase UKM Protein. The graph indicates that this protein is largely and outer cell membrane protein with some component within the cell. Red is transmembrane, blue: inside cell and magenta: outside cell.



Supplementary Fig 4. The SignalP 4.1 Prediction Network used to predict the presence of signal peptides in protein. Max. C pos. 24 value 0.110; max. Y pos. 11 value 0.115; max. S pos. 12 value 0.142 and D position 1-10 value 0.115 cut off 0.450.



Supplementary Fig 1. The disease symptoms shown by different rice varieties. (A) IR50 as the susceptible line to sheath blight, (B) UKMRC9 as showing moderate resistance. This is followed by (C) UKMRC2 and (D) MR219.

>GTPaseRacUKM

MVKAGFAGDDAPRAVFPISIVGRPRHTGVMVGMGQKDAYVGDQAQSKRGILTLKYPIDIEHGIVSNWDDME
KIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTGI
VLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDMKEKLSYI
ALDYDQEMETAKTSSSVEKSYELPDGQVITIGAERFRCPEVLFPQPSFIGMEAAGIHETTYNSIMKCDV
DIRKDLYGNIVLSGGTTMFPGIADRMSKGDHCLGS*

>AF250327 Oryza sativa small GTP-binding protein RACBP (RACB)

MSASRFIKCVTVGDGAVGKTCMLISYTSNTFPTDYVPTVFDNFSANVVVDGNTVNLGLWDTAGQEDYN
RLRPLSYRGADVFLAFSLISKASYENVSKKWIPELKHYPGVPIILVGTCLDLRDDKQFVDHPGAV
PITTAQGEELRKQIGAPYYIECSSKTQLNVKGVFDAAIKVVLQPPKAKKKKAQRGACSIL

>AB029510 Oryza sativa mRNA for small GTP-binding protein OsRac3

MASSASRFIKCVTVGDGAVGKTCMLICYTSNKFPDYIPTVFDNFSANVVVDSTTVNLGLWDTAGQED
YNRLRPLSYRGADVFLAFSLVSRASYENIMKKWIPELQHYAPGVPIVLVGTCLDLREDKHYLLDHPG
MIPVTTAQGEELRKQIGAAYYIECSSKTQONVKGVFDAAIKVVIQPPTKQREKKKKSRQGCSSMMNMF
RGRKMSCFKS

>AB029509 Oryza sativa mRNA for small GTP-binding protein OsRac2

MSGATKFIKCVTVGDGAVGKTCMLICYTSNKFPDYIPTVFDNFSANVSVDGNIVNLGLWDTAGQEDY
SRLRPLSYRGADIFVLAFLSISRASYENVLKKWMPPELRRFAPNVPIVLVGTCLDLRDRHSYLADHPAA
SAITTAQGEELRKQIGAAAYIECSSKTQONIKAVFDTAIKVVLQPPRRRGETTMARKKTRRSTGCSLK
NLMCGSACVV

>AB029508 Oryza sativa mRNA for small GTP-binding protein OsRac1

MSSAAAATRFIKCVTVGDGAVGKTCMLICYTCNKFPDYIPTVFDNFSANVSVDGSVVNLGLWDTAGQ
EDYSRLRPLSYRGADVFLSFLISRASYENVQKKWMPPELRRFAPGVVVLVGTCLDLREDRAYLADH
PASSIITTEQGEELRKLIGAVAYIECSSKTQONIKAVFDTAIKVVLQPPRHKDVTRKKLQSSSNRPVR
RYFCGSACFA

>AY364311 Oryza sativa (japonica cultivar-group) Rho GTPase
activating protein 2

MEGEVPVSSPLMLPAARGGGGGVSVVETVAAALRRSLLLCSVRAAEDEGAAAAAAAAAGMQIGRPT
DVRHVSHVTFDRFVGLGLPADLEPDVPRPAPSASVSVFVGSPTSMQCSYDNRGNSVPTILLTMQKKL
YQLGGLQAEGIFRINADNSQELHVREQLNMGVVPDGVDMHCLTGLIKAWFRELPSGVLDLSLTPQVMH
CNTEEECALLASTLPPVEAALLDWA INLMADVHEHENYNKMNARNIAMVFAPNMTQADPLTALIHAV
QVMNFKTLILKTVKGREETAMPSSAFPSSSGSPDKDEPQALEHLDKPTICSTQONNDFPMISGATL
DHFLFRAEPLRHNDQAQSAGRPKKRDNDKHDHNSREFPIDSDSSQASNSASKFSNDNVEGLFDRFK
FRKGVGRLCRHPVFQLSRSMKKSGEAGQACV

>AY364310 *Oryza sativa* (japonica cultivar-group) Rho GTPase activating protein 1

MEIGWPTDVRHVAHVTFDRFHGFLGLPVEFEVEMPCRVPSSASASVFGVSAESMQCTYDGGKNSVPTIL
LHMQERLYAQGGKKAEGIFRINPENDQEEHVRDQLNKGVPEDIDVHCLASLIKAWFRELPEGVLDL
SPEQVLQCNSEGEFLELVTLRPTQAALLNWAVELMADVVEEELNKMNARNIAMVFAPNMTQMSDPL
TALMHAVQVMNFKTLILRTLRLRERDDAASGDYTPYSSPASSSQNDAEYYSERDMDRSCMSDMHSE
ISRSGRQVDFLVRYNTCFDSEQEGVDPLSDVEEGFLRQLEHDLKREESAKKQHEISSEIMAVKDV
QAEKVEAKAAGNTQKEEGAGSLQ

>AB047313.1 *Oryza sativa* Japonica Group OsRac1 mRNA for actin

MADAEDIQPLVCDNGTGMVKAGFAGDDAPRAVFPISIVGRPRHTGVMVGMGQKDA YVGDEA QSKRGI LTLKYP IEH
GIVSNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRT
TGIVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDMKEKLSYIALDY
DQEMETAKTSSSVEKSYELPDGQVITIGAERFRCPEVLFQPSFIGMEAAGIHETTYNSIMKCDVDI RDKLYGNIV
LSGGTTFM PGIAD RMSKEIT ALAPSSMKIKV VAPPERKYSVWI GGSILASLSTFQQMWIAKAEYDESGPSIVHRK
CF

>gi|5902926|dbj|BAA84492.1| small GTP-binding protein OsRac1 [*Oryza sativa*]

MSSAAAATRFIKCVTVGDGAVGKTCMLICYTCNKFPDYIPTVFDNFSANVSVDGSSVNLGLWDTAGQ
EDYSRLRPLSYRGADVFLSFLISRASYENVQKKWMPPELRRFAPGVVPLVGTKLDLREDRAYLADH
PASSIITTEQGEELRKLIGAVAYIECSSKTQRNIKAVFDTAIKVVLQPPRHKDVTRKKLQSSSNRPVR
RYFCGSACFA

>gi|5902928|dbj|BAA84493.1| small GTP-binding protein OsRac2 [*Oryza sativa*]

MSGATKFIKCVTVGDGAVGKTCMLICYTSNKFPDYIPTVFDNFSANVSVDGNIVNLGLWDTAGQEDY
SRLRPLSYRGADIFVLAFSLISRASYENVLKKWMPPELRRFAPNVPIVLVGTKLDLDRHRSYLADHPAA
SAITTAQGEELRQIGAAAYIECSSKTQONIKAVFDTAIKVVLQPPRRRGETTMARKKTRRSTGCSLK
NLMCGSACVV

>gi|5902930|dbj|BAA84494.1| small GTP-binding protein OsRac3 [*Oryza sativa*]

MASSASRFIKCVTVGDGAVGKTCMLICYTSNKFPDYIPTVFDNFSANVVVDSTTVNLGLWDTAGQED
YNRLRPLSYRGADVFLVLAFLVSRASYENIMKKWIPELQHYAPGVPIVLVGTKLDLREDKHYLLDHPG
MIPVTTAQGEELRQIGAAAYIECSSKTQONVKGVFDAAIKVVIQPPTKQREKKKKSRQGC SMMNMF
RGRKMSCFKS

>gi|9651980|gb|AAF91343.1|AF250327_1 small GTP-binding protein RACBP
[Oryza sativa]

MSASRFIKCVTVGDGAVGKTCMLISYTSNTFPTDYVPTVFDNFSANVVVDGNTVNLGLWDTAGQEDYN
RLRPLSYRGADVFLLAFLSLISKASYENVSKKIPELKHYPGVPIILVGTKLDRDDKQFFVDHPGAV
PITTAQGEELRKQIGAPYYIECSSKTQLNVKGVFDAAIKVVLQPPKAKKKKKAQRGACSIL

>gi|21902083|dbj|BAC05631.1| putative rac GTPase activating protein
[Oryza sativa Japonica Group]

MDVAGGGEEVEEVEAVDGGEQPPMEIGWPTDVRHVAHVTFDRFHGFQGLPVELQPEVAGNAPSASKT
VFGVSTESMQCSYDARGNSVPSILLMQRRLYEQGGLKAEGIFRIAADDAQEAVREQLNSGVLPEGG
VDVHCLAGLIKAWFRELPGGMIDSLPAAEVTRCQSADDCARLCARLPAKAALLDWAVQLMADVAREE
RSNKMGSRVNMFAPNMTAMDPFTALKHAVHVMNFLTMLIDRALNDVQTCNN

>gi|33354208|dbj|BAC81174.1| rac GTPase activating protein 3 -like
protein [Oryza sativa Japonica Group]

MGEAVLVSNHGCSGGGGRVGVGVRGAGGGGPGEGKAEGQQQVLALLLAALRRSVVLPQOMADADDPA
AVAWGMEIGWPTDVRHVAHVTFDRLNGFLGLPAEFELEIPGHVPSASASVFGVSPESMQCCFDDNGNS
VPKILLMQERLYAQDGLKAEGIFRITPENSQEENVREQLNRGLVPDDIDVHCLASLIKAWFRELPEG
VLDSLSPQVLHCNTEEECVLVRLLPPTQAALLNWVVEFMADVVEEEEENKMNARNVAMVFAPNMTQ
MSDPLTALMHAVQVMNLLKTLILKTLREREHDESEYSAISSQSSSDELDEMHHHVEQGGDSGSDTDN
FGDDGSQSQKDVAKVLQONVVNEQPIGASRRHTSIDFRLPYISYGSDDDVSPNDIEECFLRRLEWNAV
SKDASEIGSITVRSNQEAGQLSFSEENDGYSTDYQSRNILLKDSVGIQSTLPRETESRAEITNDEVQ
DGAEEVETLEQ

>gi|34451566|gb|AAQ72347.1| Rho GTPase activating protein 1 [Oryza
sativa Japonica Group]

MEIGWPTDVRHVAHVTFDRFHGFGLPVEFEVEMPCRVPSASASVFGVSAESMQCTYDGGKNSVPTIL
LHMQRLYAQGGLKAEGIFRINPENDQEEHVRDQLNKGVPEDIDVHCLASLIKAWFRELPEGVLDL
SPEQVLQCNSEGEFLELVTLRPTQAALLNWAVELMADVVEEEELNKMNARNIAMVFAPNMTQMSDPL
TALMHAVQVMNFKTLILRTRLRERDDAASGDYTPYSSPASSSQONDAEYYGSRDMDRSCEMSDMHSE
ISRSGRQVDFLVRYNTCFDSEQEGVDPLSDVEEGFLRQLEHDLKREESAKKQHEISSEIMAVKDV
QAEKVEAKAAGNTQKEEGAGSLQ

>gi|34451568|gb|AAQ72348.1| Rho GTPase activating protein 2 [Oryza sativa Japonica Group]

MEGEVPVSSPILMLPAARGGGGGVSVVETVAAALRRSLLC~~SSVRAAE~~DEGAAAAAAAAAGMQIGRPT
DVRHVSHVTFDRFVGFGLPADLEPDVPRPAPSASVSVFGVSPTSMQCSYDNRGNSVPTILLTMQKKL
YQLGG~~LQ~~AEGI~~FRINADNSQELHVREQLNMGVVPD~~GVD~~MHCLTGLIKAWFREL~~PSGVLD~~SLTPEQVMH~~
CNTEEECALLASTLPPVEAALLD~~WAINLMADVVEHENYNKMNARNIAMVFAPNMTQ~~MADPLTALIHAV
QVMN~~FLKTLILKTVKGREETAMPSSAFSSSGSP~~SDKDEPQALEHLDKPTICSTQ~~QNNDFPMISGATL~~
DHFLFRAEPLRH~~ND~~AQGSAGRPK~~RD~~NDK~~HD~~NS~~S~~REFSPIDSDSSSQASNSAS~~KFSNDNVEGLFDRFK~~
FRKGVGRLCRHPV~~FQLSRSMKKS~~GEAGQACV

>gi|50253132|dbj|BAD29378.1| putative Rho GTPase activating protein 2 [Oryza sativa Japonica Group]

MQCSYDNRGNSVPTILLTMQKKLYQLGG~~LQ~~AEGI~~FRINADNSQELHVREQLNMGVVPD~~GVD~~MHCLTGL~~
IKAWFRELPSGVLD~~SLTPEQVMHCNTEEECALLASTLP~~PVEAALLD~~WAINLMADVVEHENYNKMNARN~~
IAMVFAPNMTQ~~MADPLTALIHAVQVMN~~FLKTLILKTVKGREETAMPSSAFSSSGSP~~SDKDEPQALEH~~
LDKPTICSTQ~~QNNDFPMISGATL~~DHFLFRAEPLRH~~ND~~AQGSAGRPK~~RD~~NDK~~HD~~NS~~S~~REFSPIDSDSS
SQASNSAS~~KFSNDNVEGLFDRFK~~FRKGVGRLCRHPV~~FQLSRSMKKS~~GEAGQACV

>gi|62732732|gb|AAQ94851.1| rac GTPase activating protein 1 [Oryza sativa Japonica Group]

MTTEVALLRGPTNLASPTSSTLRYLANGSDVSLPRRS SREEESPAGLQEEEEEEEEERWSFLALLLE
LLRKSLLRCSTVQEGGGECGMEI~~GWPTDVQHVAVTFDRFHGFLGLPVELEPEVPRRAPSASASVFGV~~
STESMQCSYDSRGN~~SVPTILLMMQRRLYEQGLRAEGI~~FRINAENSQEEFVRDQ~~LNSGIVPDGIDIHC~~
LSGLIKAWFRELPSGVLD~~SIPPEQVMQCQSEEDCARVAKCLPPAE~~AALLEWAVNLMADV~~VQEEQINKM~~
NARNIAMVFAPNMTQ~~MSDPLTALMYAVQVMN~~FLKMLIQKTLKGRQESNLED~~TSLPHKDP~~SDESGHHK~~P~~
CLTLES~~LL~~EEESRRPSFVEEPI~~LNSPAHGTGYNPIEVN~~PVQ~~GKTAASIAQTS~~EVQTIIEGSS~~SCRPS~~
SLTDPATADPVCAEAANSLQ~~RKGS~~RSLSNR~~TRK~~KGKQSGTSATSSAEKSKGTSIVSRINSKIERIE
AWR

>gi|62732733|gb|AAQ94852.1| rac GTPase activating protein 1 [Oryza sativa Japonica Group]

MATAMRSQGEAAARRRALQDSKRRRRRRRRRRGGRSWRCCLSCCGSRCSGAVRCRRAAASAGWRLGGR
RMCSTWHTSPSTGSMDSASPWSSSPRFPAGLPVRESMQCSYDSRGN~~SVPTILLMMQRRLYEQGLRA~~
EGIFRINAENSQEEFVRDQ~~LNSGIVPDGIDIHCL~~SGLIKAWFRELPSGVLD~~SIPPEQVMQCQSEEDCA~~
RVAKCLPPAE~~AALLEWAVNLMADV~~VQEEQINKMNARNIAMVFAPNMTQ~~MSDPLTALMYAVQVMN~~FLKM
LIQKTLKGRQESNLED~~TSLPHKDP~~SDESGHHK~~PCLTLES~~LL~~EEESRRPSFVEEPI~~LNSPAHGTGYN~~P~~
IEVNPVQ~~GKTAASIAQTS~~EVQTIIEGSS~~SCRPS~~SLTDPATADPVCAEAANSLQ~~RKGS~~RSLSNR~~TRK~~
GKQSGTSATSSAEKSKGTSIVSRINSKIERIEAWR

>gi|62733119|gb|AAX95236.1| rac GTPase activating protein 1 [Oryza sativa Japonica Group]

MTTEVALLRGPTNLASPTSSTLRYLANGDSIVSLPRRSREEESPAGLQEEEEEEEEERWSFLALLLE
LLRKSLLRCSSTVQEGGGGECGMEIGWPTDVQHVAHVTFDRFHGFLGLPVELEPEVPRRAPSASASVFGV
STEMQCSYDSRGNVPTILLMMQRRLYEQGGLRAEGIFRINAENSQEEFVRDQLNSGIVPDGIDIHC
LSGLIKAWFRELPSGVLD SIPPEQVMQCQSEEDCARVAKCLPPAEAALLEWAVNLMADVQEEQINKM
NARNIAMVFAPNMTQMSDPLTALMYAVQVMNFKMLIQKTLKGRQESNLEDTSLPHKDPSESGHHKP
CLTLESLLLEESRRPSFVEEEPILNSPAHGTGYNPIEVNPFVQGKTAASIAQTSEVQTIIEGSSSCSRP
SLTDPPATADPVCAEAANSLQRKGSRLNSRRTRKGGKQSGTSATSSAEKSKGTSIVSRINSKIERIE
AWR

>gi|77548721|gb|ABA91518.1| rac GTPase activating protein 1,
putative, expressed [Oryza sativa Japonica Group]

MTTEVALLRGPTNLASPTSSTLRYLANGDSIVSLPRRSREEESPAGLQEEEEEEEEERWSFLALLLE
LLRKSLLRCSSTVQEGGGGECGMEIGWPTDVQHVAHVTFDRFHGFLGLPVELEPEVPRRAPSASASVFGV
STEMQCSYDSRGNVPTILLMMQRRLYEQGGLRAEGIFRINAENSQEEFVRDQLNSGIVPDGIDIHC
LSGLIKAWFRELPSGVLD SIPPEQVMQCQSEEDCARVAKCLPPAEAALLEWAVNLMADVQEEQINKM
NARNIAMVFAPNMTQMSDPLTALMYAVQVMNFKMLIQKTLKGRQESNLEDTSLPHKDPSESGHHKP
CLTLESLLLEESRRPSFVEEEPILNSPAHGTGYNPIEVNPFVQGKTAASIAQTSEVQTIIEGSSSCSRP
SLTDPPATADPVCAEAANSLQRKGSRLNSRRTRKGGKQSGTSATSSAEKSKGTSIVSRINSKIERIE
AWR

Supplementary Fig 5. Sequences of GTPases used for multiple sequence alignment.