

**Supplemental Data Set 1.** Trimmed Sequences of 24 RB-Related Proteins from Green Algae, Moss, and Higher Plants and Animals Corresponding to Alignment in Supplemental Figure 2 Online.

Source organisms: Vc RBR1, *Volvox carteri*; Ci MAT3, *Chlamydomonas incerta*; Cr MAT3, *Chlamydomonas reinhardtii*; Ot RBR, *Ostreococcus tauri*; Pp RBR, *Physcomitrella patens*; Gg RB1, *Gallus gallus*; Mm RB1, *Mus musculus*; Hs RB1 (RB), *Homo sapiens*; Hs RB2 (p130), *Homo sapiens*; Hs RBL1 (p107), *Homo sapiens*; Dm RBF, *Drosophila melanogaster*; Pt RBR, *Populus tremula x Populus tremuloides*; Ee RBR, *Euphorbia esula*; At RBR, *Arabidopsis thaliana*; Nb RBR, *Nicotiana benthamiana*; Nt RBR, *Nicotiana tabacum*; Sb RBR, *Scutellaria baicalensis*; Ps RBR, *Pisum sativum*; Chr RBR, *Chenopodium rubrum*; Zm RBR1, *Zea mays*; Zm RBR2, *Zea mays*; Zm RBR2b, *Zea mays*; Zm RBR3, *Zea mays*; Cn RBR, *Cocos nucifera*. The corresponding GenBank accession numbers are given in the Methods section.

>Ot RBR

TPISQAMASASWLQDIVCASSDLETLHKKVDVLIFFFFLNRIIRAESQVNIALLQSSRF  
TKSLACCMEVIVATYTLTFPATHTLLGIHPFDLTTIIEPFVVRADMDLPREIVRHFNSLE  
EKTLELAWCKGSALFDFLVLQIFFAKVMQLAARRLGDASRLTRDVYALIEHVIYEQTN  
LVYNRHVDQIILASVYGCKDIISFYNKVFVSRVRTFLLA

>Pp RBR

TPVSI TMTTAKWLRTVIAPLSAEPMSKVRANVILYYKVLGAMCTAESHRL-PFLPNERF  
HRCMLACSAELVLASHTMTFFPAVLEPAGITAFDLSKVIEGFVRHEETLPRELKRHLNSIE  
ERLLESMAWEKGSSMFCNLPINVFFQKVLKLA AVRIRNLCERLVERVNRALHHALNHETG  
LFFNRHIDQIILCCVYGICKDIIRFYNEVFVVPSTKSFLLO

>Zm RBR1

TPVTSAMTTAKWLREVISSLPDKPSVTERVSI VLYYRVLEAICRAELQNNLTPLLSNERF  
HRCLLIACSAELVLATHIMMFPVLESTGLTAFDLSKIIENFVRHEETLPRELKRHLNSLE  
EQILLESMAWEKGSSLYNSLP IHIFFSKILKLA AIRIRNLCERVTERVYNVFKQILEQOTT  
LFFNRHIDQLILCCLYGVAKGIITFYNEVFVPAKPFLVS

>Zm RBR2b

TPITSAMTTAKWLREVISSLPEKPSVTERVSI VLYYRVLEAICRAELQNNLTPLLSNERF  
HRCLLIACSAELVLATHIMMFPVLESTGLTSFDLSKIIENFVRHEETLPRELKRHLNSLE  
EQILESMWEKGSSLYNSLP IQIFFSKILKLA AIRIRNLCERITERVYNVFKQILDQOTT  
LFFNRHMHQLILCCLYGVAKDIITFYNEVFVPAKPFLVS

>Zm RBR2

TPITSAMTTAKWLREVISSLPEKPSVTERVSI VLYYRVLEAICRAELQNNLTPLLSNERF  
HRCLLIACSAADVVLATHIMMFPVLESAGLTSFDLSKIIENFVRHEETLPRELKRHLNSLE  
EQILESMWEKGSSLYNSLP IQIFFSKILKLA AIRIRNLCERITERVYNVFKQILDQOTT  
LFFNRHIDQLILCCLYGVAKDIITFYNEVFVPAKPFLVS

>Zm RBR3

TPVSTAMTTAKWLRNTVSPSPSRPSIAHRAGIILYYRVLESMCRAESQINLTSLLSNERF  
HRCMIACSAELVLATHHTMMFPAVLEKTGITAFDLSKVIEGFVRHEDTLPRELKRHLNSLE  
ERLLESMAWEKGSSMYNSLP IGVFFSKISKLAAIRIRSLCERLLERVYSLVQQIILSQQTG  
LFFNRHIDQIILCSIYGVAKDIITFYNEVFIPAVKSLLE

>Chr RBR

TPVSTAMTTAKWLRTYISPLPSKPSVVRRAHIILYYRVLETMCTAEAQLNLTSLLTNERF  
HRCMLACSAELVLATHHTMLFPAVLEKTGITAFDLSKVIESFIRHEDSLPRELRRHLNSLE  
ERLLESMAWEKGSSMDNSLPINIFFSKIVKLA AVRINGMIERLRENVYCRFHIILNQRTS  
LFFNRHIDQIILCAFYGVAKDIITFYNEVFIPSVKPLLGE

>At RBR

TPVSTAMTTAKWLRTVISPLLPKPSVTRRAHIILYYRVLEAMCKAEAQINLNSLLTNERF  
HRCMLACSAELVLATHHTMLFPAVLERTGITAFDLSKVIESFIRHEDSLPRELRRHLNSLE  
ERLLESVMWEKGSSMYNSLPINIFFTKINKLA AVRINGMVERLRESVYCFQHVLAQRTS  
LLFSRHIDQIILCCFYGVAKDIITFYNEIFIPAVKPLLVE

>Nt RBR

TPVSTAMTTARWLRTVIAPLQPKPSVIRRAQIILYYRVLQTMCTAESQINLTSLLTNERF  
HRCMLACSAELVLATHHTMLFPAVLERTGITAFDLSKVIESFIRHEESLPRELRRHLNSLE  
ERLLESVMWEKGSSMYNSLPINVFFGKIVKLA AVRINGMIERLRETVYCLFQKILSQRTS  
LFFNRHIDQIILCSFYGVAKDIITFYNEVFIPSVKPLLVE

>Nb RBR

TPVSTAMTTARWLRTVIAPLQPKPSVIRRAQIILYYRVLQTMCTAESQINLTSLLTNERF  
HRCMLACSAELVLATHHTMLFPAVLERTGITAFDLSKVIESFIRHEESLPRELRRHLNSLE  
ERLLESVMWEKGSSMYNSLPINVFFGKIVKLA AVRINGMIERLRETVYCLFQKILSQRTS  
LFFNRHIDQIILCSFYGVAKDIITFYNEVFIPSVKPLLVE

>Sb RBR

TPVTTAMTTAKWLRTVIAPLPSKPSVTRRAQIILYFRVLQALCTAESQINLTSLLTNERF  
HRCMLACSAELVLATHHTMLFPTVLERTGITAFDLSKVIESFIRHEESLPRELRRHLNSLE  
ERLLESVMWEKGSSMYNSLPVNVFFSKIVKLA AVRINGMVERLRESVYCLFQKILSQRTT  
LFFNRHIDQIILCCFYGVSKDIITFYNEIFVPAVKPLLVE

>Ps RBR

TPVSTAMTTAKWLRTVISPLPSKPSVIRRAQIILYYRVLATMCRAEAQINLTSLLTNERF  
HRCMLACSAELVLATHHTMLFPAVLERTGITAFDLSKVIESFIRYEESSLPRELRRHLNSLE  
ERLLESVWEKGSSMYNSLPISVFFSKIVKLGAVRISGMVERLRENVYCLFQORILNQWTS  
LFFNRHIDQIILCCFYGVAKDIISFYNEVFIPSVKPLLVE

>Ee RBR

TPVTTAMTTAKWLRTVISPLPSKPSVTRRAQIILSYRVLEAMCTAEAQVNLTSLLTNERF  
HRCMLSCSAELVLATHHTMLFPAVLERTGITAFDLSKVIESFIRHEESLPRELRRHLNSLE  
ERLLESVMWEKGSSMYNSLPISIFFCKINKLA AVRINGMIERLRENVYRLFQQIILSHRTS  
LFFNRHIDQIILCCFYGVAKDIITFYNEIFIPAAKPLLVE

>Pt RBR

TPVSTAMTTAKWLRTIISPLPSKPSVIRRAQIILYYRVLESMCTAEAQINLTSLLTNERF  
HRCMLACSAELVVATYHTMLFPAVLERTGITAFDLSKVIESFIRHEESLPRELRRHLNSLE  
ERLLDSMVWEKGSSLYNSLPINVFFTKINKLA AVRINGMIEKLRENVYRLFQLILSHQTS  
LFFNRHIDQIILCCFYGVAKDIITFYNEIFIPAAKPLLVD

>Cn RBR

TPVSTAMTTAKWLRNIISPLPSRPSVTRRASIIILYYRVLETMCRAESHINLTSLLSNDRF  
HRCMLACSAELVLATHMTMMFPAVLEKTGITAFDLKSVIESFVRHEETLPRELKRHLNSLE  
ERLLESMAWERGSSMYNSLPINIFFNKIVKLAAIRIRSLCERLLEWVYCLIQQIILSQRTA  
LFFNRHIDQIILCSFYGVAKDIIITFYNEVFIPSVKPLLVE

>Vc RBR1

TPVSEIMSTSAWLRGITASLAAEPSLNQRVQELVYYLSLERILQAEKNGVTSLLSAGKF  
HRALVACSAEVTACYSCTFPKVLDAALHIKAFDLAKMIQCFVRSITTLPRDLKRHLFLVE  
EKILESLAWHEADSPYSLIKLNHFCKVKLAAFRVAVLDCNDFNTKVYQTIIEHALFFQTH  
LFYNRHIDQIILSALYGFCKDIIAFYNQVVFVPCMKSFLLR

>Ci Mat3

TPISEAMGASAWLRGVTSSMAAEPKMRVRDLYCHSLETIMLNEERTAALALLGSAKF  
QRGLIACCIEVVAACYSCAFPVVDALRIKAFDMASIIIGTFVKSIIATLPRELKRHLFLIE  
EKILECLAWQPGSSLYHLIPLFEFLRKVLKLTSLFRALLCENVSSKVYETIEHALYKQTH  
LFYNRHIDQVMLSTLYGYCKDIIAFYNAVVFVPMKSFLLK

>Cr Mat3

TPISEAMGASAWLRGVTSMVAEPLKMRVRDLYCHSLDTILQNEQRTAALALLGSAKF  
QRGLIACCIEVVAACYSCAFPVVDALRIKAFDMANIIIGTFVKSIIATLPRELKRHLFLIE  
EKILECLAWQPGSSLYHLIPLFEFLRKVLKLTSLFRALLCENFNSKVYEAIEHALYKQTH  
LFYNRHIDQIMLSTLYGYCKDIIAFYNAVVFVPMRNFLLK

>Gg RB1

TPVRAAMNTIQQLMILNSATDKPSILKRVES-LYYRVMESMLKSEEERNFSKLLNDNIF  
HTSLLACALEIVMATYDLSFPWILNVFDLKAADFVKVIESFIKVEPSLTRDMIKHLERCE  
HRIMESLAWQSDSPLFDLIQLSLFYKKVFRLAYLRLHTLFFRLEPLIWTTLFQHTLQNESE  
LMRDRHLDQIMMCSMYGICKSIIVFYNLVFMQKLTNIIQ

>Hs RB1

TPVRTVMNTIQQLMILNSASDQPSILKRVKDILYYRVMESMLKSEEERNFSKLLNDNIF  
HMSLLACALEVVMATYDLSFPWILNVLNLKAADFVKVIESFIKAEGLNTREMIKHLERCE  
HRIMESLAWLSDSPLFDLIQLSLFYKKVYRLAYLRLNTLCERLEHI IWTTLFQHTLQNEYE  
LMRDRHLDQIMMCSMYGICKSIIVFYNSVFMQRLKTNIIQ

>Mm RB1

TPVRTVMNTIQQLMVILNSASDQPSILKRVKDVLYRVMESMLKSEEERNFSKLLNDNIF  
HMSLLACALEVVMATYDLSFPWILNVLNLKAADFVKVIESFIKVEANLTREMIKHLERCE  
HRIMESLAWLSDSPLFDLIQLALFYKKVYRLAYLRLNTLCARLEHI IWTTLFQHTLQNEYE  
LMRDRHLDQIMMCSMYGICKSIIVFYNSVFMQRLKTNIIQ

>Dm RBF

EPVRNATNNVKQLSAF--GRITEPTLLSIIIEIFFFYLLDQILQAEIRNDLKRLLVQKIF  
NITLMACCVELVLEAYELKFPWVLDLDCFSISAFEFQKIIIEIVVRHEGCLNRSIIKHLNSIE  
ETCLERLAWARNSTVWEMIPLQIFLRKVYLLGWLRIQKLCSELPEIWHIFEHSITHETE  
LMKDRHLDQINIMCAIYIYIRDI IHFYNHNTYVPLMRQFVID

>Hs RBL1

TPVASATQSVSRLQSIVAGLKNAPSIMKILKGILYYKILETVMVQETRRDMSVLLLEQDIF  
HRSLMACCLEIVLFAYPRTPFWIIEVLNLQPFYFYKVIIEVVIRSEEGLSRDMVKHLNSIE  
EQILESLAWSHDSALWEALALALFYRKVYHLASVRLRDLCLKLRRKIWTTCFEFTLVHCPD  
LMKDRHLDQLLLCAFYIMAKDLIKFYNTIYVGRVKSFALK

>Hs RB2

TPVSTATHSL SRLHTMLTGLRNAPS IANRLKEMLYYKVLESVIEQEQRDL SGI LEQDAF  
HRSL LACCLEVVTF SYPGNF PFITEIFDVPLYHFYKVIEVFIRAEDGL CREVVKHLNQIE  
EQILDHLAWKPESPLWEKIPLSLFFRKVYHLAAVLRDLCAKLRKKIWT CFEFSIIQCPE  
LMMDRHLDQLLMCAIYVMAKD LIQFYNNIYIKQIKTFAMK