Supplementary Figures

Fig. S1. Conserved cysteine of Rre1. A multiple sequence alignment of cyanobacterial Rre1 orthologues showing the cysteine residues highlighted in red.
Fig. S2. Conserved cysteines of RpaA. A multiple sequence alignment of cyanobacterial RpaA orthologues showing the cysteine residues highlighted in red.
orthologues showing

Fig. S3

1. RQVYKGDERIRLTGMEFSLLELLVSRSGEAFSRSEILQEVWGYTPERHVDTRVVDVHISRLRAKLEDDPSNPELILTARGTGYLFQRILEPEGEEGR---
2. RQVYKGDERIRLTGMEFSLLELLVSRSGEPFSRSEILQEVWGYTPERHVDTRVVDVHISRLRAKLEDDPSNPELILTARGTGYLFQRILEPDEE-----
3. RQVYKGDERIRLTGMEFSLLELLVSRSGEPFSRSEILQEVWGYTPERHVDTRVVDVHISRLRAKLEEDPSNPELILTARGTGYLFQRILEPGEEP----
4. RQVYKRDERIRLTGMEFSLLELLVSRSGEPFSRGEILKEVWGYTPERHVDTRVVDVHISRLRSKLEDDPANPELILTARGTGYLFQRIVDPGEEGR----
5. RQVYRGEERIRLTGMEFSLLELLVGRSGEPFSRGEILKEVWGYTPERHVDTRVVDVHISRLRSKLEDDPANPELILTARGTGYLFQRIVDASGEEGR----
6. RQVFRGDERIRLTGMEFSLLELLVSRSGEPFSRGEILKEVWGYTPERHVDTRVVDVHISRLRSKLEDDPANPELILTARGTGYLFQRIVDSVASEGN------
7. RQVYKGDERIRLTGMEFSLLELLVSRSGEPFSRSEILQEVWGYTPERHVDTRVVDVHISRLRAKLEEDPSNPELILTARGTGYLFQRILEPGEEP-------
8. LETH------KEKILVVDDEASIRRILETRLSMIGYTVVTAADGEEALTKFRQEQPDLVVLDVMMPKLDGYGVCQELRKESDVPIIMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRSVLR---
9. MESH------KEKILVVDDEASIRRILETRLSMIGYDVVTADGEEALETFRKADPDLVVLDVMMPKLDGYGVCQELRKESDIPIIMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRSVLR---
10. LENQ------KEKILVVDDEASIRRILETRLSMIGYEVVTAADGEEALEVFRKQDPDLVVLDVMMPKLDGYGVCQELRKESDIPIIMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRSVLR---
11. MESH------KEKILVVDDEASIRRILETRLSMIGYDVVTAADGEEALDIFHEAVPDLVVLDVMMPKLDGYGVCQELRKESDIPIIMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRSVLR---
12. MEAQR-----KERILVVDDEASIRRILETRLSMIGYDVVTAADGEEALEVFRKQDPDLVVLDVMMPKLDGYGVCQELRKESDIPIIMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRSVLR---
13. VAAPAHN--GKETILVVDDEASIRRILETRLSMIGYNVVTAADGEEALEAFHREPTDLVVLDVMMPKLDGYGVCQELRKESDVPIVMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRCVLR---
14. LSSQT-----KETILVADDEASIRRILETRLSMIGYQVVTADGTEALKLFKDYEPDLVVLDVMMPKLDGYGVCQELRKDSDVPIVMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRCVLRR---
15. TSPS-----KETILVADDEASIRRILETRLSMIGYQVVTACDGNEALDLFRNCEPDLVVLDVMMPKLDGYGVCQELRKDSDVPIVMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRCVLRR---
16. SAPT-----KETILVVDDEASIRRILETRLSMIGYNVVTACDGTEALECFQECEPDLVVLDVMMPKLDGYGVCQELRKESDVPIVMLTALGDVADRITGLELGADDYVIKPFSPKELEARIRCVLRR---
17. TSPS-----KETILVADDEASIRRILETRLSMIGYQVVTACDGNEALDLFRNCEPDLVVLDVMMPKLDGYGVCQELRKDSDVPIVMLTALGDVADRITGLELGADDYVVKPFSPKELEARIRCLLRR---
18. RAEDRDTASG-IPSSGVIHVGDLKIDTNK
19. RVDKTGATG-IPSSGVIHVGNIRIDTNK
20. RVEKTGASG-IPSSGVITINNIRIDTNK
21. RVEKSGANG-IPSSGVIQINSIRIDTNK
22. RVEKNGAPG-IPSSGVIHVGSIKIDTNK
23. RVEKNGAPG-IPSSGVIHVGSIKIDTNK
24. RVEKNGAPG-IPSSGVISIASIKIDTNK
25. RVEKEHGGGSIPNSGVIQVSDLKIDTNK
26. RIDKEQIPG-MPNSGLILVTDIKIDTN
27. RVDKEQVAG-IPNSGVIQVSDLRIDTNK
28. VEKEQVAG-IPNSGVIQVADLRIDTNK
29. VEKEQIAG-LPNSGVIAVMNLKIDTNK

Fig. S3. Conserved cysteines of RpaB. A multiple sequence alignment of cyanobacterial RpaB orthologues showing the cysteine residues highlighted in red.
Fig. S4. Conserved cysteine of RppA. A multiple sequence alignment of cyanobacterial RppA orthologues showing the cysteine residues highlighted in red.
Fig. S5. **Calibration curves of the Superdex 200 column.** Calibration curve was obtained using standard proteins of known molecular mass: thyroglobulin (669 kDa), apoferritin (443 kDa), β-amylase (200 kDa), bovine serum albumin (66 kDa) and carbonic anhydrase (29 kDa). Blue dextran (2000 kDa) was used to determine the void volume (Vo). Ve is the effluent volume. On the y-axis the base-ten logarithm of the protein molecular mass is shown and, on the x-axis, Ve/Vo.

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y = 34665e^{-3.638x} \\
R^2 = 0.9942
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