

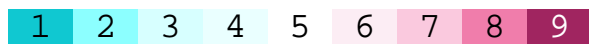
S1A Fig: Evolutionary sequence conservation analysis of ClpB proteins



551 561 571 581 591
 SKMMEGEEKDK LLNMEFLHK RVIGQDQAIK AVSNAVRRSR SGLSDPNRPI
 bebebebebe bbebebebe ebbebebebe bbbbebebe eebebebebe
 s f f f s sf s ff fs s ssffsf ffs sf f
 601 WA2611 621 631 641
 GSFMFLGPTG VGKTELTKAL AEFLFDDEDA MLRVDMSEFM EKHSVARLIG
 bbbbbbebe eeeebbb bbbbebebe bbbbbbbbe eebbbbebe
 sss sssfff fffffs f s s s sf s sssf s fff s fs f
 651 661 671 WB2 681 691
 APPGYVGYEQ GGYLTEHVRR KPYSVILLDE VEKAHADVFN ILLQVLDGR
 bbeebbebe eebeebbe eebbbbbe beeeeebe bbbbebebe
 ssfffssfff ff sff ff fsss s ff ffff fssf ssfssffsf
 701 711 721 731 741
 LTDGQGRVD FKNTVIVMTS NLGSHRIQEM QGDYDTVKD AVMEMVLSHF
 beeeeeeeee bebbbbbbb bbebebebe eeebebebe bbbbebebe
 sfffffffff s s s sss s fs sf s s
 751 Arg2 761 771 781 791
 RPEFVNRVDD AIVFEPLNKE MITEIAKIQT KRLEKRLADL SIGLEVTTEA
 eebebebe bbbbbbebe ebebebebe eebebebe ebebebebe
 ffs ff f ssss s s f f
 801 811 821 831
 MDKLADAGFD PVFGARPLKR AIQNNLENPL ALKLLDGEFK
 bebebebe ebbbebebe bbebebebe bebebebebe
 f f f ssffsf sf ff s f f

Legend:

The conservation scale:



Variable Average Conserved

- e** - An exposed residue according to the neural-network algorithm.
- b** - A buried residue according to the neural-network algorithm.
- f** - A predicted functional residue (highly conserved and exposed).
- s** - A predicted structural residue (highly conserved and buried).
- x** - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

S1B Fig: Evolutionary sequence conservation analysis of DnaK proteins

