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1 -----MRTGPLFDPSFRDGLDAL-----FQWRRDVR-HFR-KDPIDEETVARLLACADLAPSVGNSQ BluB (R. r.)
1 -----MN----FEQTHRDLALTEV-----LRWRRDVR-HFR-PDPIDEAVIDRLRAVMDMAPSVGNAR BluB (R. c.)
1 MLPDPNGCLTAAGAFSSDERAAVYRA-----IETRRDVRDEFL-PEPLSEELIARLLGAAHQAPSVMGFMQ BluB (S. m.)
1 -----MDIISVA-----LKRHSTK-AFDASKKLTPEQAEQIKTLLQYSPSSTNSQ NfnB (E. c.)
1 -----MEATLPVLDAKTAALKRRSIR-RYR-KDPVPEGLLREILEAALRAPSAWNLQ Nox (T. t.)
1 -----MNNTIETI-----LAHRSIR-KFT-AVPI TDEQRQTI IQAGLAASSSSMLQ Frp (V. h.)
1 -----MTHPII HDL-----ENRYTSK-KYDPSKKVSEQEDLAVLLEALRLSASSINSQ FRase (V. f.)

56 PWRFVRVDDGARRGVIIDDF-----RCN-AAARALQPEERQ-----DAYARLKLEGLREAPLQL BluB (R. r.)
52 PWRVIRVDSPALRAEVLANFN-----AAR-AAAGSAYAGEQA-----EAYATLKLQGIDQAPLQL BluB (R. c.)
65 PWNFVLRQDETREKVWQAFQ-----RAN-DEAAEMFSGERQ-----AKYRSLKLEGIRKAPLSI BluB (S. m.)
45 PWHFIVASTEEGKARVAKSAAGNYVFNERKMLDASHVVVFCAKTA-----MDDVWLKLV-VDQEDADG NfnB (E. c.)
51 PWRIVVVRDPATKRALREAAF-----GQAHVEEAPVVLVLYADLE-----DALAHLDEV-IHPGVQGE Nox (T. t.)
45 VVSVIRVTDSEKRNELAQFAG-----NQAYVESAAEFLVFCIDYQRHATINPDVQADF-----Frp (V. h.)
47 PWKFIVIESDAAKQRMHDSFANMHQFNQPHIKACSHVILFANKLS-----YTRDDYDVV-LSKAVADK FRase (V. f.)

110 AVFCDEATDQGHGLG-----QATMPETRRYSVVMAIHTLWLAAARARGLVGWSVLD--PQTVTA BluB (R. r.)
106 AVFTHRDPAAAGHGLG-----RASMPVTLQOSTAMAFTRSGCRAGEN-LGLGMVSVLD--PKAVER BluB (R. c.)
119 CVTCDRTRGGAVVLG-----RTHNPQMDLYSTVCAVQNLWLAAARAEGVGVGWSIFH--ESEIKA BluB (S. m.)
107 RFATPEAKAANDKGRKFFADMHRKDLHDDAEWMAKQVYLVNGVNFLLGVAALGLDAVPIEGFD--AAILDA NfnB (E. c.)
108 RREAQKQAIQRAFAAMG-----QEARKAWASGQSYILLGYLLLEAYGLGSVPMLGFD--PERVRA Nox (T. t.)
98 -----TELTLIGAVDSGIMAQNCLLAAESMGLGGVYIIGGLRNSAAQVDE Frp (V. h.)
109 RITEEQKEAAFASFK--FVELNCDENGEHKAWTKPQAYLALGNALHTLARLNIIDSTTMEGID--PELLSE FRase (V. f.)

168 ALDVPAEAWAFVAYLCIGWPREEHPIPELERLGWQSRRPHP-----VVRR BluB (R. r.)
163 LLNAPPDWDVFAWLCIGVPEFTDDTPLLHRAGWQENLPTTE-----WERR BluB (R. c.)
177 ILGIPDHVEIVAWLCLGFVDRLYQEPELAAGWRQRLPLEDLVFEEGWGVR BluB (S. m.)
175 EFGLKEKGYTSLVVVPVG-HHSVEDFN-ATLP-KSRLPQNIT-----LTEV NfnB (E. c.)
168 ILGLPSRAAIP--ALVALGYPAEEGYPSHRLP-LERVVLR Nox (T. t.)
142 LLGLPENSAVLFGMCLGHPDQNPEVKRPLPAHVVVHENQYQELNLDDIQSYDQTMQAYYASRTSNQKLST Frp (V. h.)
175 IFADELKGYECHVALAIGYHHPSEDYN-ASLP-KSRKAFEDV-----ITIL FRase (V. f.)