Figure S3A

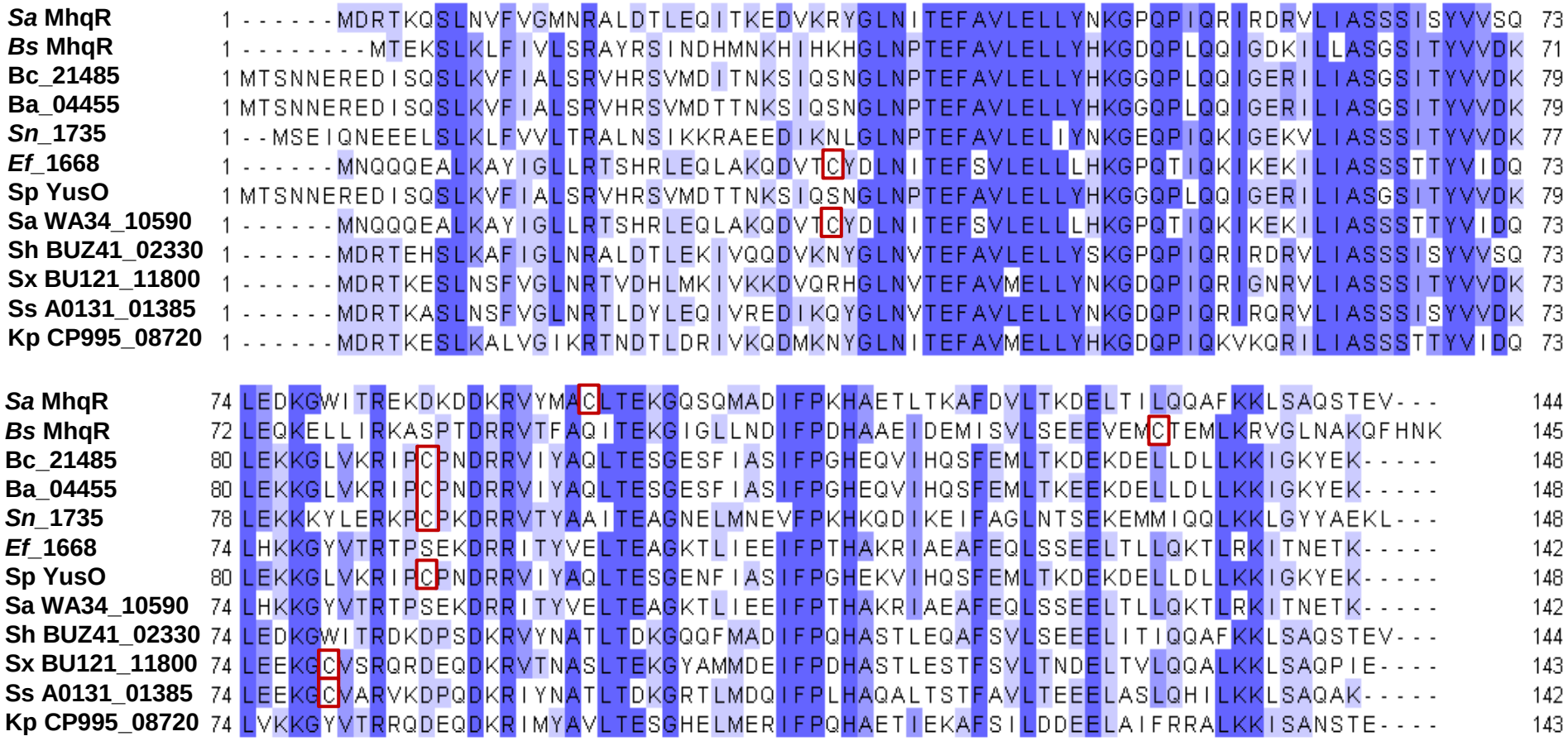

Fig. S3A. Protein sequence alignments of MhqR homologs in bacteria. Alignment was performed with ClustalΩ2 and presented in Jalview. Intensity of the blue color gradient is based on 50% sequence identity. The following protein sequences were aligned and the % identity to MhqR of *S. aureus* is given in parenthesis: MhqR (SACOL2531) of *S. aureus* COL, MhqR (BSU13670) of *B. subtilis* (38.1%), CN491_21485 of *B. cereus* (43.3%), CN907_04455 of *B. anthracis* (42.0%), HMPREF9372_1735 of *Sporosarcina newyorkensis* (43.2%), EF_1668 of *Enterococcus faecalis* (43.8%), YusO of *Streptococcus pneumoniae* (42.0%), WA34_10590 of *S. agalactiae* (43.8%), BUZ41_02330 of *S. haemolyticus* (77.8%), BU121_11800 of *S. xylosus* (66.7%), A0131_01385 of *S. saprophyticus* (67.4%) and CP995_08720 of *Klebsiella pneumoniae* (58.3%). The non-conserved cysteine residues in MhqR homologs are marked in red.

Figure S3B

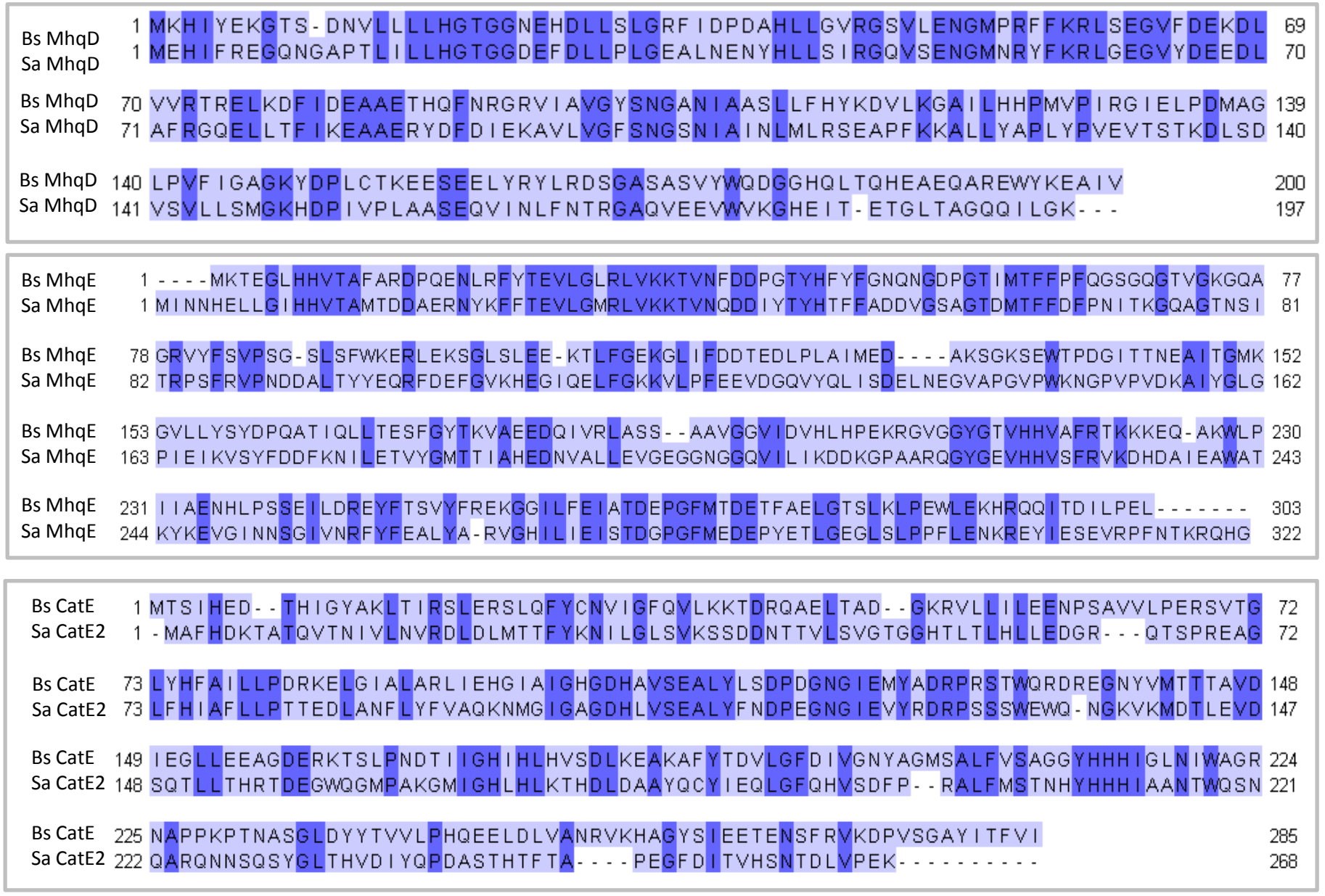
Bs MhqD 1 MKHIYEKGTS-DNVLLLLHGTGGNEHDLLSLGRFIDPDAHLLGVRGSVLENGMPRFFKRLSEGVFDEKDL 69
Sa MhqD 1 MEHIFREGQNGAPTLILLHGTGGDEFDLLPLGEALNENYHLLSIRGQVSENGMNRYFKRLGEGVYDEEDL 70
Bs MhqD 70 VVRTRELKDFIDEAAETHQFNRGRVIAVGYSNGANIAASLLFHYKDVLKGAILHHPMVPIRGIELPDMAG 139
Sa MhqD 71 AFRGQELLTFIKEAAERYDFDIEKAVLVGFSNGSNIAINLMLRSEAPFKKALLYAPLYPVEVTSTKDLSD 140
Bs MhqD 140 LPVFIGAGKYDPLCTKEESEELYRYLRDSGASASVYWQDGGHQLTQHEAEQAREWYKEAIV 200
Sa MhqD 141 VSVLLSMGKHDPIVPLAASEQVINLFNTRGAQVEEVWVKGHEIT-ETGLTAGQQILGK--- 197
Bs MhqE 1 ----MKTEGLHHVTAFARDPQENLRFYTEVLGLRLVKKTVNFDDPGTYHFYFGNQNGDPGTIMTFFPFQGSGQGTVGKGQA 77
Sa MhqE 1 MINNHELLGIHHVTAMTDDAERNYKFFTEVLGMRLVKKTVNQDDIYTYHTFFADDVGSAGTDMTFFDFPNITKGQAGTNSI 81
Bs MhqE 78 GRVYFSVPSG-SLSFWKERLEKSGLSLEE-KTLFGEKGLIFDDTEDLPLAIMED----AKSGKSEWTPDGITTNEAITGMK 152
Sa MhqE 82 TRPSFRVPNDDALTYYEQRFDEFGVKHEGIQELFGKKVLPFEEVDGQVYQLISDELNEGVAPGVPWKNGPVPVDKAIYGLG 162
Bs MhqE 153 GVLLYSYDPQATIQLLTESFGYTKVAEEDQIVRLASS--AAVGGVIDVHLHPEKRGVGGYGTVHHVAFRTKKKEQ-AKWLP 230
Sa MhqE 163 PIEIKVSYFDDFKNILETVYGMTTIAHEDNVALLEVGEGGNGGQVILIKDDKGPAARQGYGEVHHVSFRVKDHDAIEAWAT 243
Bs MhqE 231 IIAENHLPSSEILDREYFTSVYFREKGGILFEIATDEPGFMTDETFAELGTSLKLPEWLEKHRQQITDILPEL------- 303
Sa MhqE 244 KYKEVGINNSGIVNRFYFEALYA-RVGHILIEISTDGPGFMEDEPYETLGEGLSLPPFLENKREYIESEVRPFNTKRQHG 322
Bs CatE 1 MTSIHED--THIGYAKLTIRSLERSLQFYCNVIGFQVLKKTDRQAELTAD--GKRVLLILEENPSAVVLPERSVTG 72
Sa CatE2 1 -MAFHDKTATQVTNIVLNVRDLDLMTTFYKNILGLSVKSSDDNTTVLSVGTGGHTLTLHLLEDGR---QTSPREAG 72
Bs CatE 73 LYHFAILLPDRKELGIALARLIEHGIAIGHGDHAVSEALYLSDPDGNGIEMYADRPRSTWQRDREGNYVMTTTAVD 148
Sa CatE2 73 LFHIAFLLPTTEDLANFLYFVAQKNMGIGAGDHLVSEALYFNDPEGNGIEVYRDRPSSSWEWQ-NGKVKMDTLEVD 147
Bs CatE 149 IEGLLEEAGDERKTSLPNDTIIGHIHLHVSDLKEAKAFYTDVLGFDIVGNYAGMSALFVSAGGYHHHIGLNIWAGR 224
Sa CatE2 148 SQTLLTHRTDEGWQGMPAKGMIGHLHLKTHDLDAAYQCYIEQLGFQHVSDFP--RALFMSTNHYHHHIAANTWQSN 221
Bs CatE 225 NAPPKPTNASGLDYYTVVLPHQEELDLVANRVKHAGYSIEETENSFRVKDPVSGAYITFVI 285
Sa CatE2 222 QARQNNSQSYGLTHVDIYQPDASTHTFTA----PEGFDITVHSNTDLVPEK---------- 268

Figure S3B (continued)

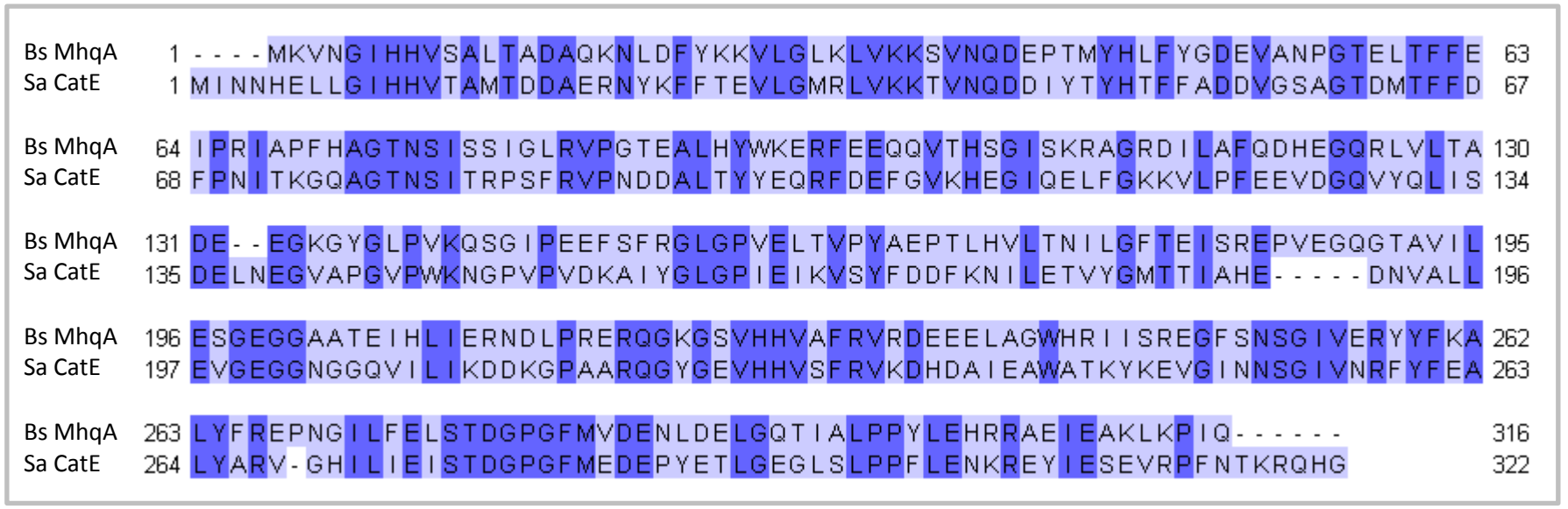

Fig. S3B. Multiple protein sequence alignments of the MhqR and QsrR-regulated phospholipase MhqD and dioxygenases MhqE, CatE and CatE2 of *S. aureus* with homologous enzymes of *B. subtilis*. The alignment was performed with ClustalΩ2 and is presented in Jalview. Intensity of the blue color gradient is based on 50% sequence identity. The following protein sequences were aligned and the % identity between *S. aureus* and *B. subtilis* enzymes is given in parenthesis: MhqE (SACOL2530) of *S. aureus* COL with MhqE (BSU19570) of *B. subtilis* (35.4%), MhqD (SACOL2529) of *S. aureus* COL with MhqD (BSU19560) of *B. subtilis* (38.8%) and CatE2 (SACOL2533) of *S. aureus* COL with CatE (BSU08240) of *B. subtilis* (34.8%) and CatE (SACOL0408) of *S. aureus* COL with MhqA (BSU12870) of *B. subtilis* (35.4%).