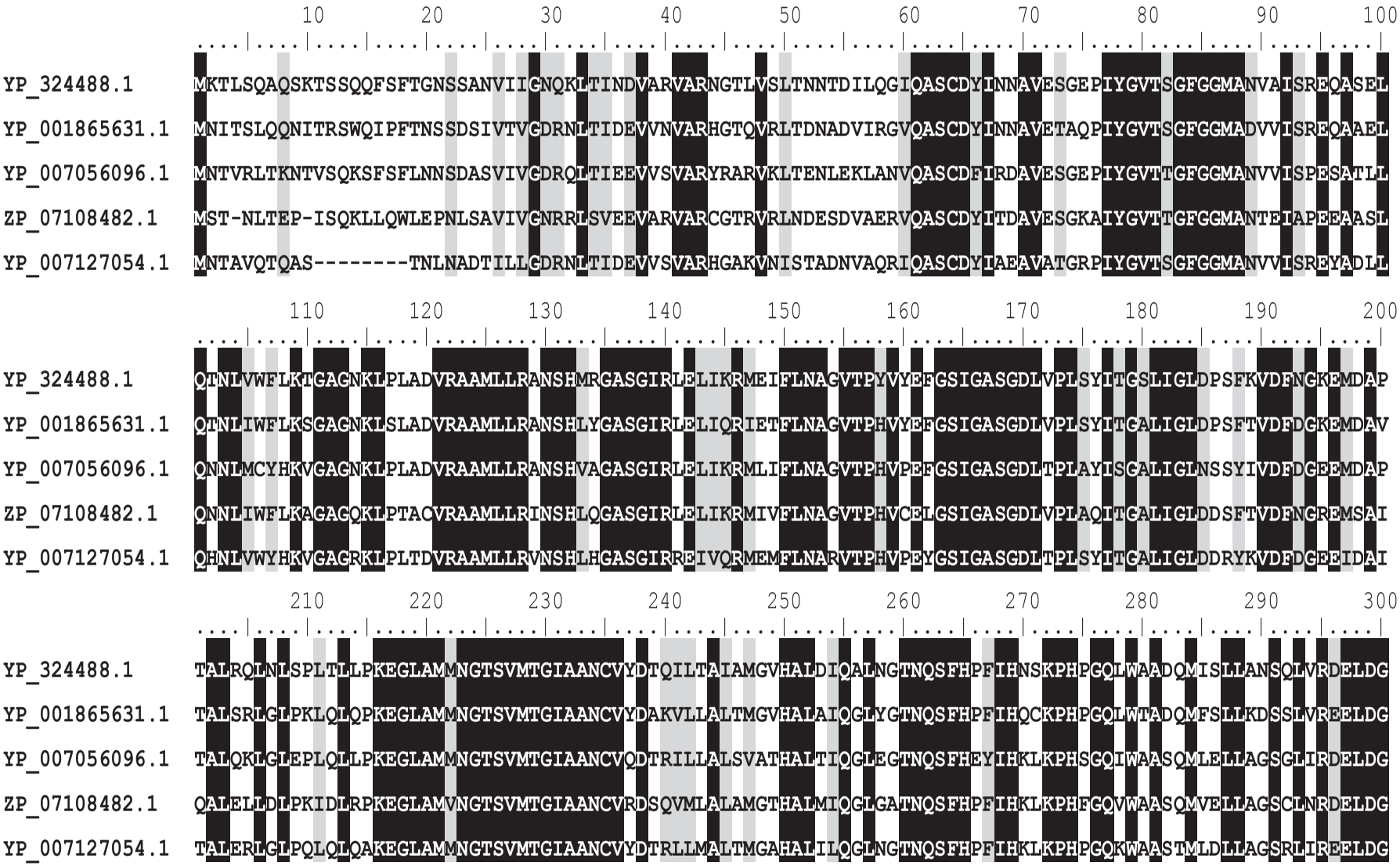

10 20 30 40 50 60 70 80 90 100
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YP_007056096.1 MNTVRLTKNTVSQKSFSFLNNSDASVIVGDRQLTIEEVVSVARYRARVKLTENLEKLANVQASCDFIRDAVESGEPIYGVTTGFGGMANVVISPESATLL
ZP_07108482.1 MST-NLTEP-ISQKLLQWLEPNLSAVIVGNRRLSVEEVARVARCGTRVRLNDESDVAERVQASCDYITDAVESGKAIYGVTTGFGGMANTEIAPEEAASL
YP_007127054.1 MNTAVQTQAS--------TNLNADTILLGDRNLTIDEVVSVARHGAKVNISTADNVAQRIQASCDYIAEAVATGRPIYGVTSGFGGMANVVISREYADLL
110 120 130 140 150 160 170 180 190 200
YP_324488.1 QTNLVWFLKTGAGNKLPLADVRAAMLLRANSHMRGASGIRLELIKRMEIFLNAGVTPYVYEFGSIGASGDLVPLSYITGSLIGLDPSFKVDFNGKEMDAP
YP_001865631.1 QTNLIWFLKSGAGNKLSLADVRAAMLLRANSHLYGASGIRLELIQRIETFLNAGVTPHVYEFGSIGASGDLVPLSYITGALIGLDPSFTVDFDGKEMDAV
YP_007056096.1 QNNLMCYHKVGAGNKLPLADVRAAMLLRANSHVAGASGIRLELIKRMLIFLNAGVTPHVPEFGSIGASGDLTPLAYISGALIGLNSSYIVDFDGEEMDAP
ZP_07108482.1 QNNLIWFLKAGAGQKLPTACVRAAMLLRINSHLQGASGIRLELIKRMIVFLNAGVTPHVCELGSIGASGDLVPLAQITGALIGLDDSFTVDFNGREMSAI
YP_007127054.1 QHNLVWYHKVGAGRKLPLTDVRAAMLLRVNSHLHGASGIRREIVQRMEMFLNARVTPHVPEYGSIGASGDLTPLSYITGALIGLDDRYKVDFDGEEIDAI
210 220 230 240 250 260 270 280 290 300
YP_324488.1 TALRQLNLSPLTLLPKEGLAMMNGTSVMTGIAANCVYDTQILTAIAMGVHALDIQALNGTNQSFHPFIHNSKPHPGQLWAADQMISLLANSQLVRDELDG
YP_001865631.1 TALSRLGLPKLQLQPKEGLAMMNGTSVMTGIAANCVYDAKVLLALTMGVHALAIQGLYGTNQSFHPFIHQCKPHPGQLWTADQMFSLLKDSSLVREELDG
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YP_007127054.1 TALERLGLPQLQLQAKEGLAMMNGTSVMTGIAANCVYDTRLLMALTMGAHALILQGLNGTNQSFHPFIHKLKPHPGQKWAASTMLDLLAGSRLIREELDG

FIG. 1

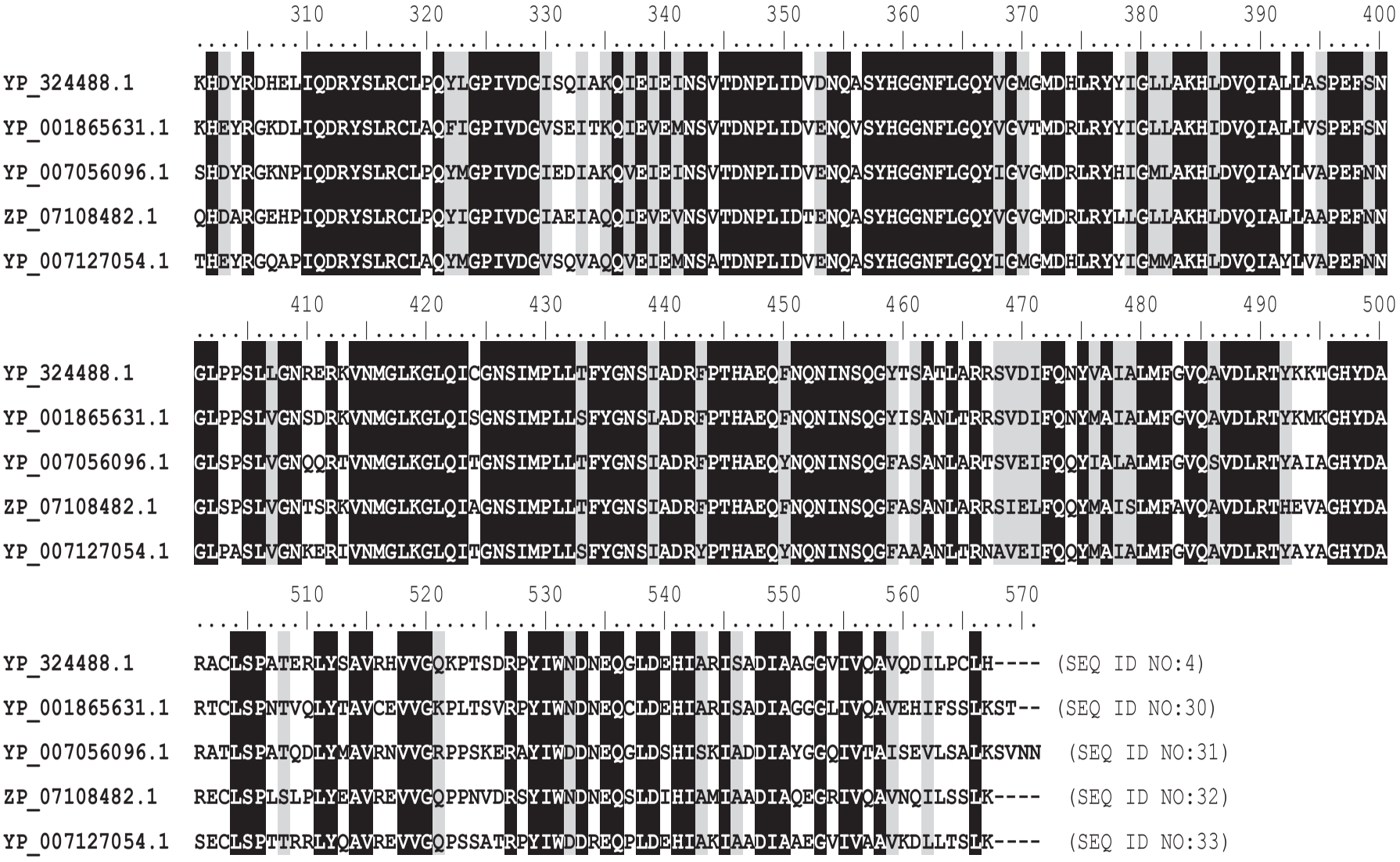

310 320 330 340 350 360 370 380 390 400
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YP_001865631.1 KHEYRGKDLIQDRYSLRCLAQFIGPIVDGVSEITKQIEVEMNSVTDNPLIDVENQVSYHGGNFLGQYVGVTMDRLRYYIGLLAKHIDVQIALLVSPEFSN
YP_007056096.1 SHDYRGKNPIQDRYSLRCLPQYMGPIVDGIEDIAKQVEIEINSVTDNPLIDVENQASYHGGNFLGQYIGVGMDRLRYHIGMLAKHLDVQIAYLVAPEFNN
ZP_07108482.1 QHDARGEHPIQDRYSLRCLPQYIGPIVDGIAEIAQQIEVEVNSVTDNPLIDTENQASYHGGNFLGQYVGVGMDRLRYLLGLLAKHLDVQIALLAAPEFNN
YP_007127054.1 THEYRGQAPIQDRYSLRCLAQYMGPIVDGVSQVAQQVEIEMNSATDNPLIDVENQASYHGGNFLGQYIGMGMDHLRYYIGMMAKHLDVQIAYLVAPEFNN
410 420 430 440 450 460 470 480 490 500
YP_324488.1 GLPPSLLGNRERKVNMGLKGLQICGNSIMPLLTFYGNSIADRFPTHAEQENQNINSQGYTSATLARRSVDIFQNYVAIALMEGVQAVDLRTYKKTGHYDA
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YP_007056096.1 GLSPSLVGNQQRTVNMGLKGLQITGNSIMPLLTFYGNSIADRFPTHAEQYNQNINSQGFASANLARTSVEIFQQYIALALMEGVQSVDLRTYAIAGHYDA
ZP_07108482.1 GLSPSLVGNTSRKVNMGLKGLQIAGNSIMPLLTFYGNSIADRFPTHAEQENQNINSQGFASANLARRSIELFQQYMAISLMEAVQAVDLRTHEVAGHYDA
YP_007127054.1 GLPASLVGNKERIVNMGLKGLQITGNSIMPLLSFYGNSIADRYPTHAEQYNQNINSQGFAAANLTRNAVEIFQQYMAIALMEGVQAVDLRTYAYAGHYDA
510 520 530 540 550 560 570
YP_324488.1 RACLSPATERLYSAVRHVVGQKPTSDRPYIWNDNEQGLDEHIARISADIAAGGVIVQAVQDILPCLH---- (SEQ ID NO:4)
YP_001865631.1 RTCLSPNTVQLYTAVCEVVGKPLTSVRPYIWNDNEQCLDEHIARISADIAGGGLIVQAVEHIFSSLKST-- (SEQ ID NO:30)
YP_007056096.1 RATLSPATQDLYMAVRNVVGRPPSKERAYIWDDNEQGLDSHISKIADDIAYGGQIVTAISEVLSALKSVNN (SEQ ID NO:31)
ZP_07108482.1 RECLSPLSLPLYEAVREVVGQPPNVDRSYIWNDNEQSLDIHIAMIAADIAQEGRIVQAVNQILSSLK---- (SEQ ID NO:32)
YP_007127054.1 SECLSPTTRRLYQAVREVVGQPSSATRPYIWDDREQPLDEHIAKIAADIAAEGVIVAAVKDLLTSLK---- (SEQ ID NO:33)

FIG. 1 (Cont.)