

Mannheimia_haemolytica	-----MNYTKFDVKNWVRREHFEFYRHRLPCGFSLTSKIDITTLKKSLLD
Aeromonas_salmonicida	-----MNFTRIDLNTWNRREHFAFYRQQIKCGFSLTTKLDTALRTALAE
Photorhabdus_luminescens	-----MNYSKVDIDLWDRKEHFLHYRNVVQCGFSLTAKIDITHLLSSLVE
Yersinia_pestis_biovar	MEKKITGYTTVDISQWHRKEHFEAFQSVACQTYNQTVQLDITAFLLKTVKK
Salmonella_typhimurium	-----NQTVQLDITAFLLKTVKK
Neisseria_meningitidis	-----MVFEKIDKNSWRKEYFDHYFASVPCTYSMTVKVDITQIK-----E
Streptococcus_suis	-----MNFNKIDLDNWKKEIFNHYLN-QQTTFSITTEIDISVLYRNIKQ
Enterococcus_faecium	-----MTFNIINLETWDRKEYFNHYFN-QQTTYSVTKELDITLLKSMIKD
	xxxxxx31455554455551525545455434555555555345542345
Mannheimia_haemolytica	SAYKFYPVMIYLIAQAVNQFDELMAIK-DDELIVWDSVDPQFTVFHQET
Aeromonas_salmonicida	TGYKFYPLMIYLIISRAVNQFPEFRMALK-DNELIYWDQSDPVFTVFHKEK
Photorhabdus_luminescens	KQYKFYPTMIYLISTVNSYSEFRMAIK-DEELIVWDGVPAYTIFHKEK
Yersinia_pestis_biovar	NKHKFYPAFIHILARLMNAHPEFRMAMK-DGELVIWDSVHPCYTVFHEQT
Salmonella_typhimurium	NKHKFYPAFIHILARLMNAHPEFRMAMK-DGELVIWDSVHPCYTVFHEQT
Neisseria_meningitidis	KGMKLYPAMLYYIAMIVNRHSEFRTAINQDGELGIYDEMI PSYTI FHNDT
Streptococcus_suis	KRYKFYPAFVFLVTRVINSNTAFRTGYNSEGELGYWDKLDPLYTIFDSVS
Enterococcus_faecium	KGYELYPALIIHIVSVINRNKVFRGTGINSEGNLGYWDKLEPLYTVFNKET
	2255155555455555125454355145x254531354314525145353
Mannheimia_haemolytica	ETFSALSCPYSDDIDQFMVNYLSVMERYKSDTKLFPQGVTPENHLNISAL
Aeromonas_salmonicida	ETFSALSCRYFPDLSEFMAGYNAVTAEYQHDTRLFPQGNLPENHLNISSL
Photorhabdus_luminescens	ETFSAIWTEFNSDLAEFMKNYSADYETYKDDLCCFFSKPELPENHFHISSV
Yersinia_pestis_biovar	ETFSSLWSEYHDDFRQFLHIYSQDIACYGENLAYFPKG-FIENMFFVSAN
Salmonella_typhimurium	ETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKG-FIENMFFVSAN
Neisseria_meningitidis	ETFSSLWTECKSDFKSLADYESDTQRYGNHRMEGKPNAPENIFNVSMI
Streptococcus_suis	KTFSGIWT PARND FKEFYDLYLSDVEKYNGSGKLPKTPIPENAFSISII
Enterococcus_faecium	EKFSNIWTESNASFNSFYNSYKNDLFKYKDKNEMFPKKPI PENTVPI SMI
	5435555451235453514355354553554525251415534524154
Mannheimia_haemolytica	PWVNFDSFNLNVANFTDYFAPIITMAKYQQEGDRLLLPLSVQVHHAVCDG
Aeromonas_salmonicida	PWVSFDGFNLNITGNDYFAPVFTMAKFQQEGDRVLLPVSVQVHHAVCDG
Photorhabdus_luminescens	PWVSFDGFNLNMAVMDYFPPIFTMGKFYQNGNQTLPLAIQVHHATCDG
Yersinia_pestis_biovar	PWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDVLMPLAIQVHHAVCDG
Salmonella_typhimurium	PWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDVLMPLAIQVHHAVCDG
Neisseria_meningitidis	PWSTFDGFNLNLQKGYDYLIPIFTMGKYYKEDNKIILPLAIQVHHAVCDG
Streptococcus_suis	PWTSFTGFNLNINNNNSNYLLPIITAGKFINKGNSIYLPPLSLQVHHSVCDG
Enterococcus_faecium	PWIDFSSFNLNIGNNSRFLLPITITIGKFYSKDDKIYLPFSLQVHHAVCDG
	55555535354555545554153535554545543545555445555355
Mannheimia_haemolytica	FHVARFISRLQELCNSKLK---
Aeromonas_salmonicida	FHAARFINTLQLMCDNILK---
Photorhabdus_luminescens	FHVGRVINNLQELCNDFI----
Yersinia_pestis_biovar	FHVGRMLNELQQYCDEWQGGA-
Salmonella_typhimurium	LHVGRMLNELQQYCDEWQ----
Neisseria_meningitidis	FHICRFVNELQELINS-----
Streptococcus_suis	YHAGLFMNSIQELADRPNDWLF
Enterococcus_faecium	YHVSFLFMNEFQNIIDNVNEWI-
	1545554445453242xxxxxx

Figure A2

Multisequence alignment of the chloramphenicol acetyltransferase protein family

Predicted RCRRs (red) and experimentally examined regions (green) are marked. The rare codon score S is displayed for each column.

Table A2

Organisms and GenBank identifiers of the chloramphenicol acetyltransferase protein family

<i>Mannheimia haemolytica</i>	GenBank: NP_073222
<i>Aeromonas salmonicida</i>	GenBank: CAD57199
<i>Photobacterium luminescens</i>	GenBank: NP_929686
<i>Yersinia pestis</i> biovar	GenBank: ZP_01174255
<i>Salmonella typhimurium</i>	GenBank: ABA56511
<i>Neisseria meningitidis</i>	GenBank: AAC14400
<i>Streptococcus suis</i>	GenBank: BAC11901
<i>Enterococcus faecium</i>	GenBank: NP_863168