

Q-L-K-----GRVAA-EIM--TPAIRNLIRE-K-AQ-YS-IQTG-.-GMQT-DQ-L--L---G-I-----A

Ah QTLLKRIGG....GRVAAHEIMMGIPAVRNLIREDKIAQLYSVIQTGM.THGMQTMDSQLKQLVSRGMVAALDAKAK.AVDPNTI
Av QTLLKRVGG....GRVAAREIMIGTPAIRNLIREDKVAQMYSAIQTTG.SLGMQTLDMALKSLLSRGAIRESAREK.AKIPDSF
Bb QVLLKQEGG....GRCAAWEIMVGTPAIRNLIREDKIAQMVSSIQTGQ.AHGMQTLDDQALQDILLRKKLISAEQALAY.ADRRSLGL
Ca QLLKKKDE....SGRIPAFEIMTFTPAVQNLIREGKTHQIQSLIQTGS.KYGMITMDKCIIDLYKKGIISYETAVQS.SVDKEFVTKMLIL
Cb QLVHKID....GGRIALETMVTNPAIRNLIREDKTYQIESSIQTGS.KYGMKTMDSLAELYKREIISYDTA
Cd QLLPTADG....KGRIAAIELMFATPAIKNLIREGKTYQIPNMIQTGV.KSGMKTMDQDLMELYKNGKITKDMA
Cp QLVETVD....GDRNAALEIMVATPAIKNLIREGKTHQIESSIQTGS.KYGMRTMDMELANLYREGIITQETAMNS.AIDREILSRLLMY
Ct QRLIPDIDN...KGRVAALEIMIVTPAISNLIREGRVAGITSMIQTGA.AQGMKLLDKSIAELYQQGRISKESAYEY.CADRELLKRFIG
Cv QTLLKTKDGQ...GRVAAHEIMIGTPAIRNLIRENKIAQINSMIQTGQ.QHGMQTLDDQCLADLTRRNIVSPAERAK.ASHKDAF
Dh QLLPRKD....QQGRVAAQEILVVTPAVRNLIREDKTHQIANTMOTGG.KLGMQSMEKAIQEHVRAGRISNAVAQEM.IQNMGH
Eca QKLLPAA....QGGRIALYEVLTATAAVSNLIREDKTHQLPGLIQTGA.AAGMOTFEQSYQQRCDGLIS
Ec QKLEVDK....QEGRVALFELLINTPAVGNLIREDKTHQLPHVIQTGQ.QVGMITFQQSYQHRVGEGR
Gm QTLLPKASGT...GRVLAIEVMVNPNAIRNLIREDKIHQIYSQMVQVQEKFGMNTMNQCLYGLLQKRHITMDVGMGR.SPDPDELKQMLTSG**
Gv QTLPADAGSGIQSRCLAQEIMIVTPAIANLIREDKTSQIYSAIQTTG.NLGMKTLETSLRDLYAAGRISYENALAR.TSRPEEFQRIAGAPP**
Ms QVLLKKRGG....GRVAVHEIMLGTGAIKNLIRENQVAQMYSSIQTGR.KLGMQTLQGLQECIQKGLITREQAYEK.ANVKDQ
Md QTLLKKNNG....GRVAAHEIMRGTSAIRNLIREDKVAQMYSAIQTTG.AVGMQTMDDQCLADLVERRIISRDVAKEKAKMPDQF
Ne QALLKTKDGK...GRVAAHEIMIGTPAIRNLIREGKVAQMYSAIQTTG.GVGMQTLDDQNLTDLVKRGVISAVERATK.AMNKDNFRG
Np QTLLVSKNPKPGEYGRVMAQEILVVTPAISNLIREGKTSQIYSAIQTTG.KLGMQTLQGLADFLYKAGTISFEAAMSK.TSKPDEIQRLIGNST**
Pf QTLLIKKIGG....GRVAAHEIMLGTSAIRNLIREDKVAQMYSAIQTTG.SLGMQTLDMCLKDLVTKGLISREHAREK.ARTPDFN
Pp QVLVRRVGG....GRVAAREVLVATPAVRNLIREDGRLAQLSSVMQGG.AEGMLTMEGALRRLRERG.....LIK.GL
Psy QALLKKVGG....GRVAAHEIMMGTPAIRNLIREDKVAQMYSSIQTGQ.SMGMTLDMCLADLVKKGLITRESARER.AKVPDNF
Rm QTLLKTRDGN...GRVAAHEIMIATPAIRHLIRENKIAQMYSSMOTSS.GLGMQTLDDQCLSDLIKRGMINYSARAI.AKNPDAFMG
Sb QKLEADK....LEGRVALFELLINTPATGNLIREDKTHQLPHVIQTGQ.QQGMNT
So QTLLIKKIGG....GRVAAHEIMMGTPAIRNLIREDKVAQMYSAIQTTG.AHGMQTLQCLQNLVNRGLITREDAMAKSSNKQATF
St QKLEVDK....QDGRVALFELLINTPATGNLIREDKTHQLPHVIQTGQ.QQGMNTFAQSAQWRQAQGRLLR
Te QNLVKKTTG....GRCAAHEIMLNTPAIANLIRESKNSQLYSQIQMGA.KLGMQTMEMSLAKLYEKGNTWANAMAK.AVKPDELEALIGPEP**
Tel QTLLVPPKNPKPGEFGRIMAEIMVTPAISNLIREGKTSQIYSAIQTTG.KLGMQTLQGLVADYRAGIITYEAAMAK.SSRQDELQRLIGSGT**
Tm QRLVPPKANG...IGFTPILEIMVGTPAVRNLIRENKHLQLESLIQAGA.RHGMVLFDDALVKAALKGEISRESALQF.ARNQEEVARRLGMKPS
Tte QLIPKKDG....SGRVVATEVMIATPAIRNLIREGKTYQIQSAVQTGG.KFGMITMDMSILHLLKSGVISLEDALTY.CVDQESFSRMI
Vc QKLLKRVGG....GRVACHEIMLATPAIRNLIREDKVAQMYSSIIQTGA.AHGMQTMQNAKQLIARGVVDAQEVQSKIELDLKAF
Vp QKLLKRNNG...GRIACHEIMMATPAIRNLIREDKVAQMYSSIIQTGA.AHGMQTMQNAKQLIARGVVDAQEVQSKIELDLKAF
Vv QKLLKRIGG....GRVACHEIMMATPAIRNLIREDKVAQMYSSIIQTGA.AHGMQTMQNAKQLIARGVVDAQEVQSKIELDLKAF
Ws QVLIPKIGG....GRVCVPEILIGSPAVGNLIRENKIHQIHSQMMIGQNTGMQTTQVIERLYKERLITKEDAFRY.CFRPEELKIKIL
Xa QALLKKVGG....GRVAAHEIMVGTPAIRNLIREDKVAQMYSSIQTGQ.QYGMQTLDDQHLQDLVKRSLITRNQAREY.AKDKRIFE
Xf QMLLKKVGG....GRVAAHEIMVGTPAIRNLIREDKVAQMYSSIQTGQ.QYGMQTLDDQHLQDLIKRNLITRNQAREY.AKDKANF

Alignment of the C-terminal region of a partial list of hypothetical PilT sequences. The following sequences were aligned (organism (strain) accession number): *Aeromonas hydrophila* AAQ95749, *Azotobacter vinelandii* ZP_00089979, *Bordetella bronchiseptica* CAE31290, *Clostridium acetobutylicum* NP_348316, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens* (str.13) BAB81473, *Clostridium thermocellum* (ATCC 27405) ZP_00314371, *Chromobacterium violaceum* (ATCC 12472) AAQ57858, *Desulfotobacterium hafniense* ZP_00097939, *Erwinia carotovora* (CAG76524), *Escherichia coli* (K12) AAC75987, *Geobacter metallireducens* ZP_00079672, *Gloeobacter violaceus* BAC90607, *Magnetococcus sp.* (MC-1) ZP_00044146, *Microbulbifer degradans* (2-40) ZP_00316306.1, *Nitrosomonas europaea* (ATCC 19718) NP_841038, *Nostoc punctiforme* ZP_00111977, *Pseudomonas fluorescens* (PfO-1) ZP_00264682, *Pseudomonas putida* (KT2440) NP_747194, *Pseudomonas syringae* pv. *syringae* (B728a) ZP_00125143, *Ralstonia metallidurans* (CH34) ZP_00272985, *Salmonella bongori*, *Shewanella oneidensis* (MR-1) NP_718905, *Salmonella* serovar Typhimurium (LT2) NP_462015, *Trichodesmium erythraeum* (IMS101) ZP_00072816, *Thermosynechococcus elongatus* (BP-1) NP_680912, *Thermotoga maritima* (MSB8) NP_229163, *Thermoanaerobacter tengcongensis* NP_622883, *Vibrio cholerae* (O1 biovar eltor str. N16961) NP_230116, *Vibrio parahaemolyticus* (RIMD 2210633) NP_798994, *Vibrio vulnificus* (CMCP6) NP_760425, *Wolinella succinogenes* NP_906769, *Xanthomonas axonopodis* (pv. citri str. 306) NP_643233, *Xylella fastidiosa* (Dixon) ZP_00039233. Sequences without accession numbers were obtained from the Sanger Institute website (www.sanger.ac.uk). Sequences were included in the alignment (Clustal W) if they possessed an AIRNLIRE-like motif with greater than 50% identity to the AIRNLIRE consensus sequence. The amino acids of the AIRNLIRE region are shaded black if they are identical in over half of the sequences or grey if they are similar. A consensus sequence is indicated above the alignment, and truncated sequences are marked by asterisks.