Fig. S9.

Secondary structure labels (block 1): PD β1, α1, TT, α2, PD β2

		Sequence
Escherichia	1	MAMKKLLIASLLF..............SSATVYGAEGFVVKDIHFEGLQRVAVGAALLSMPVRTGDTVNDEDISNTIRALFATGNFEDVRVLR.DGDTLL
Salmonella	1	MAMKKLLIASLLF..............SSATVYGAEGFVVKDIHFEGLQRVAVGAALLSMPVRTGDTVNDEDISNTIRALFATGNFEDVRVLR.DGNTLL
Aggregatibacter	1	MTMKKLLIASLLF..............SSTAA.LAGPFVVQDIRVDGVQAGTESNIIASLPVKVGQKINDANIAGVVRNLFLTGQYEDVKASQ.QGNTLV
Haemophilus	1	M...KKLLLSSLLV..............ANGVIAAPFVVKDIRIDGVQTETGNAIIASLPVKVGQTATDGDVTNIVKQLFSQNRFENVSAAR.EGQTLV
Pasteurella	1	M..KKLLLASLLF..............GSTTA.FAAPFVVKDIRVDGVQAGTEGSVLATDVNDIANVVRKLFLSGQYDDVKASR.EGNTLV
Vibrio	1	MAMKQILLATLLA..............TSVSANGAEKFVVQDIQIDGLQRVALGAALLKMPVRVGDSVDSQDVANIIKALYSSGNFEDVKVLR.DGNTLM
Pseudomonas	1	M..KRFLLPALLS..............ALMIAEVHAESFTVSDIRVNGLQRVSAGSVFAALPLNVGETVDDQSLVQATRSLFKTGFFQDIQLGR.DGNVLV
Xylella	1	M..TRFYTRHLLTLTIAA......NFSLPVLTQAAESFVANDIRVDGLQRIASGTVFTYLPVNRGDTVDDAKVADAIRALYRTGFFENVRIDR.QGNILV
Neisseria	1	MKLK..QIASA..........LMMLGISPLAFADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVET.ADGQLL
Agrobacterium	1	MKAGSRFLNAVSAVALSAGVSSVAGLGVLASAGVANAAVISKIDVRGAERSGADSVRSNITIAPGKNFSNSDIDESVKRLYATGYFSNVSMRV.SGSTLV
Rickettsia	1	MK..IISISKLTILL..............LTIFYYHISFADYVIRKITIEGNHRVERSTIESYLKLNVGETYNNSKEDEAIKRLYATSLFRNINMYITNDGNLI
Caulobacter	1	MA...LLLGSTALVAP..............QQAFAQAAQTGVVQRTLVQGNERIEQGTVLSYLPIQPGDTVDSQRLDLALKTLARTDLFADVKIEM.LGGDLV

Secondary structure labels (block 2): PD β3, PD β4, TT, α3, α4, PD β5, TT, PD β6, PD β7

		Sequence
Escherichia	86	VQVKERPTIASITFSGNKSVKDDMLKQNLEASGVRVGESLDRTTIADIEKGLEDFYYSVGKYSASVKAVVTPLPRNRVDLKLVFQEGVSAEIQQINIVGN
Salmonella	86	VQVKERPTIASITFSGNKSVKDDMLKQNLEASGVRVGESLDRTTLSDIEKGLEDFYYSVGKYSASVKAVVTPLPRNRVDLKLVFQEGVSAKIQQINIVGN
Aggregatibacter	85	ISVVPKAIISDVVLDGNKSIPNDALKQNLNANGFQKGDILNREKLEAFRKSLEDHYYSVGRYNAKVETIVNPLPRNRAEVKIQIKENDVALLKGVTFVGN
Haemophilus	82	IKVAERPLINNLTIKGNNAIPKNALEQNLKANLIVAGEVYDKAKLEAFKQALVDHYHTMGRYQADIQTITTPNNNGSINVELNITEGEIAYVKKINFEGN
Pasteurella	83	VTVMPKPVISNVVIVGNKSIPDEAIKQNLDANGFKVGDVLNRAKLEEFRKGIVEHYNSVGRYNAKVDAIVNTLPNSAEIKIQINEDDVALFKEITFEGN
Vibrio	86	VQVKERPTISSVSFSGNKAIKEEQLKQNLEASSIRVGEALDRTTLSNIEKGLEDFYYSVGKYNATVKAVVTPLPRNRADLKFVFTEGVSAKIQQINFIGN
Pseudomonas	85	VTVVERPSISSIEIEGNKAISKEDLLKGLKQSGLAEGEIFQRATLEGVRNELQRQYVAQGRYSAEINAEVIPQPRNRVALKININEGTVAAISHINVVGN
Xylella	92	VKVKERPAINKLTITGNKDIKSEELLKGLSEIGLSEGGTFDRLSLDRVTQELKRQYNNRGKYNVQMTTTTTTPLDRNRVDVTIAIKEGKAAKIRHINLIGT
Neisseria	85	LTVIERPTIGSLNITGAKMLQNDAIKNNLESFGLAQSQYFNQATLNQAVAGLKEEYLGRGKLNIQITPKVTKLENNRVKVDIDITIDEGKSAKITDIEFEGN
Agrobacterium	100	VTVNENQLVNQVVFNGNKKIDDKLAGVVQTQP...LGPFNQAIVTADIARIKEAYSAIGRSDVEITTQTVSVGQGRVNIAFVINEGERTKIGRIDFVGN
Rickettsia	89	VNVTETPFISSVVFSGNSKIKTNILAKEIYT...MSGESLSQAKIELDVKKILEIYKRSGRFSTKVTPKIKSLENNRVKVIFDIAEGPKTVIKSIYFSGN
Caulobacter	86	VKVVENPIINQVVFEGNSSLKEDKLKDEVQI...RPRGIFTRAKVQADVQRIIELYRRSGRISATVTPKVVELPQKRVDLVFEINEGAKSGVLGINFLGN

Secondary structure labels (block 3): α5, TTT, α6, PD β8, TT, PD β9, PD β10

		Sequence
Escherichia	186	HAFTTDELISHFQLRDEVPWWNVV.GDRKYQKQKLAGDLETLRSYYLDRGYARFNIDSTQVSLTPDKKGIYVTVNITEGDQYKLSGVEVSGNL.AG.HSA
Salmonella	186	HAFSTEELISHFQLRDEVPWWNVV.GDRKYQKQKLAGDLETLRSYYLDRGYARFNIDSTQVSLTPDKKGIYITVNITEGDQYKLSGVQVSGNL.AG.HSA
Aggregatibacter	185	QVFSDDRLQDKQMELQPD.AWWKLF.G.NKFDSTQFSKDLETIQNYYLDRGYAKAQIVNDVQLNDEKTEARVTINVSEGEKYTVNGARIVGDV.GG.MSE
Haemophilus	182	NAFSYDELIKELEIKPNAPWWNIF.ESSKFQQQEYNKDIEILRDFYMDHGYAKFTLKDTDVKFNENKTEVDLTYKINEGSQYNISEMRIGDI.QK.LDN
Pasteurella	183	EAFSSGKLADQMELQTD.SWWKLF.G.NKFDQTQFNKDLETLRSYYLDRGYAQFQILDTDVKLSDDKKEPCLI..SEEGDLYTVKT.RVSGGMWGG.MSA
Vibrio	186	QVFSDEELSRFNLNVDVAWWNFL.ADDKYKKQVLAGDIEALRTYYLDRGYLKFQVDSTQVAISPDKKGVYITLNLNEGEPYTVSKVQFRGEL.MG.KEA
Pseudomonas	185	TVFSEEDLTDLFELKTT.NWLSFFKNDDKYAREKLSGDLERLRSYYLDRGYINMDIASTQVSITPDKKHVYITVNINEGEKYTIRDVKLTGDL.KV.PEE
Xylella	192	EKFNNKDVMSAWESKEH.NWASWYRRDDQYSKEKLSGDLEKLNSWYLDRGYVDFNIDSTQVSISPEKHNMFITAGVTEGDQYKISSIKVTGNT.VL.PQE
Neisseria	185	QVYSDRKLMRQMSLTEGGIWTWL.TRSDRFDRQKFAQDMEKVTDFYQNNGYFDFRILDTDIQTNEDKTRQTIKITVHEGGRFRWGKVSIEGDT.NEVPKA
Agrobacterium	197	NSYSDGRLAAVINTKKS.NMLSFLTRKDVYNEDKLRADEEALRQFYYNRGYADFRVVSSDAVLDESKNEYTISITVDEGKKYDFGNVAVESTV.PGIDGS
Rickettsia	186	EHYSDSELKSIVLTKES.RWFRFLESNDTYDPDRVEYDKELLREFYQSVGFADFRVISASVALNDTKEYFTITYSIEEGEKYRFGNVTIDNKL.TNINIK
Caulobacter	183	AEYSDNDLRDVIVTKES.RWYKILTSNDNYDPDRIEYDREQLRKHYRNRGYFDFRVISSVAELAPDKNGFAVTYTLEEGPKYKFGKITVETEL.KKLDGN

Secondary structure labels (block 4): α7, α8, PD β11, PD β12, PD β13, α9, TT

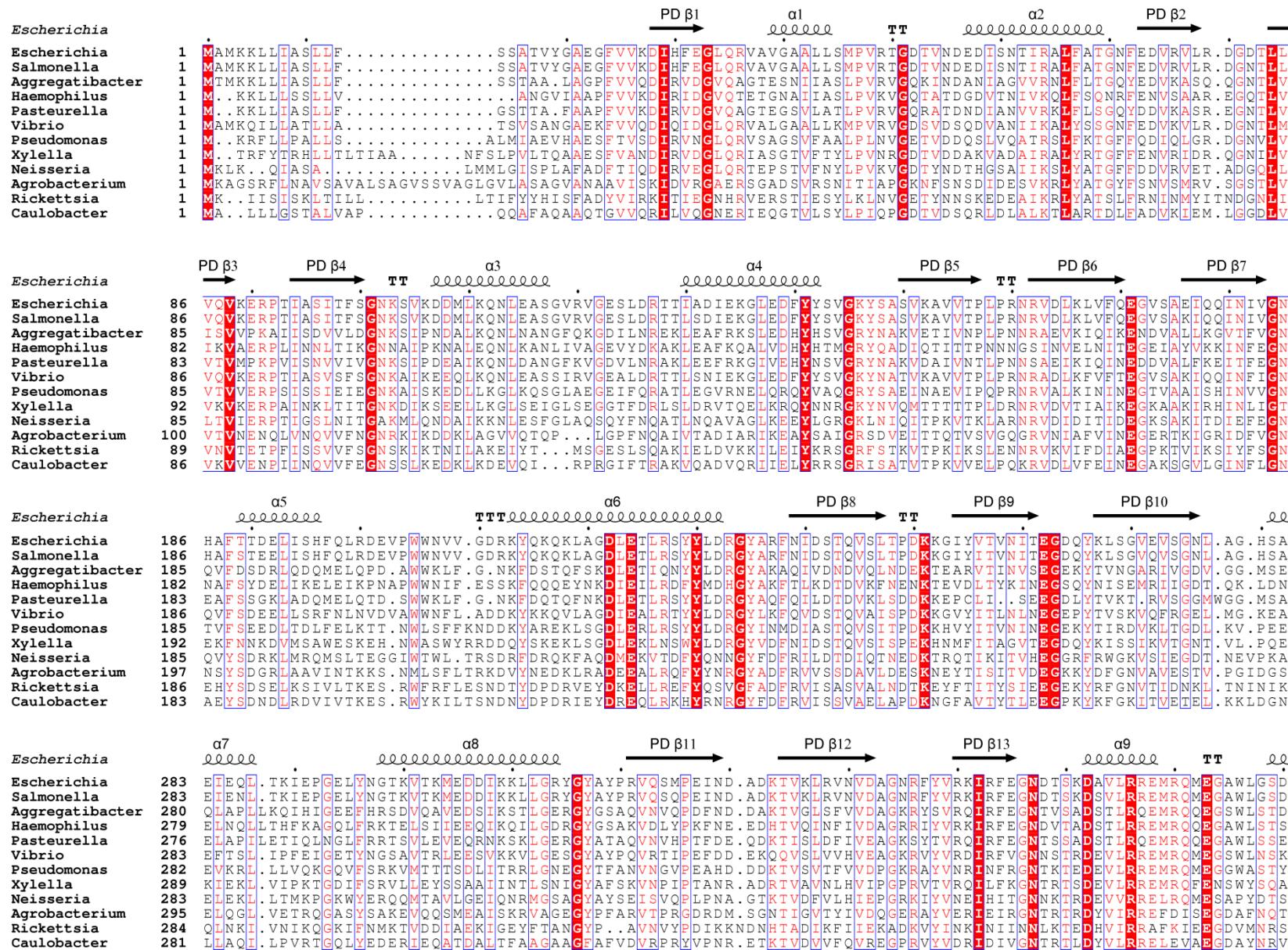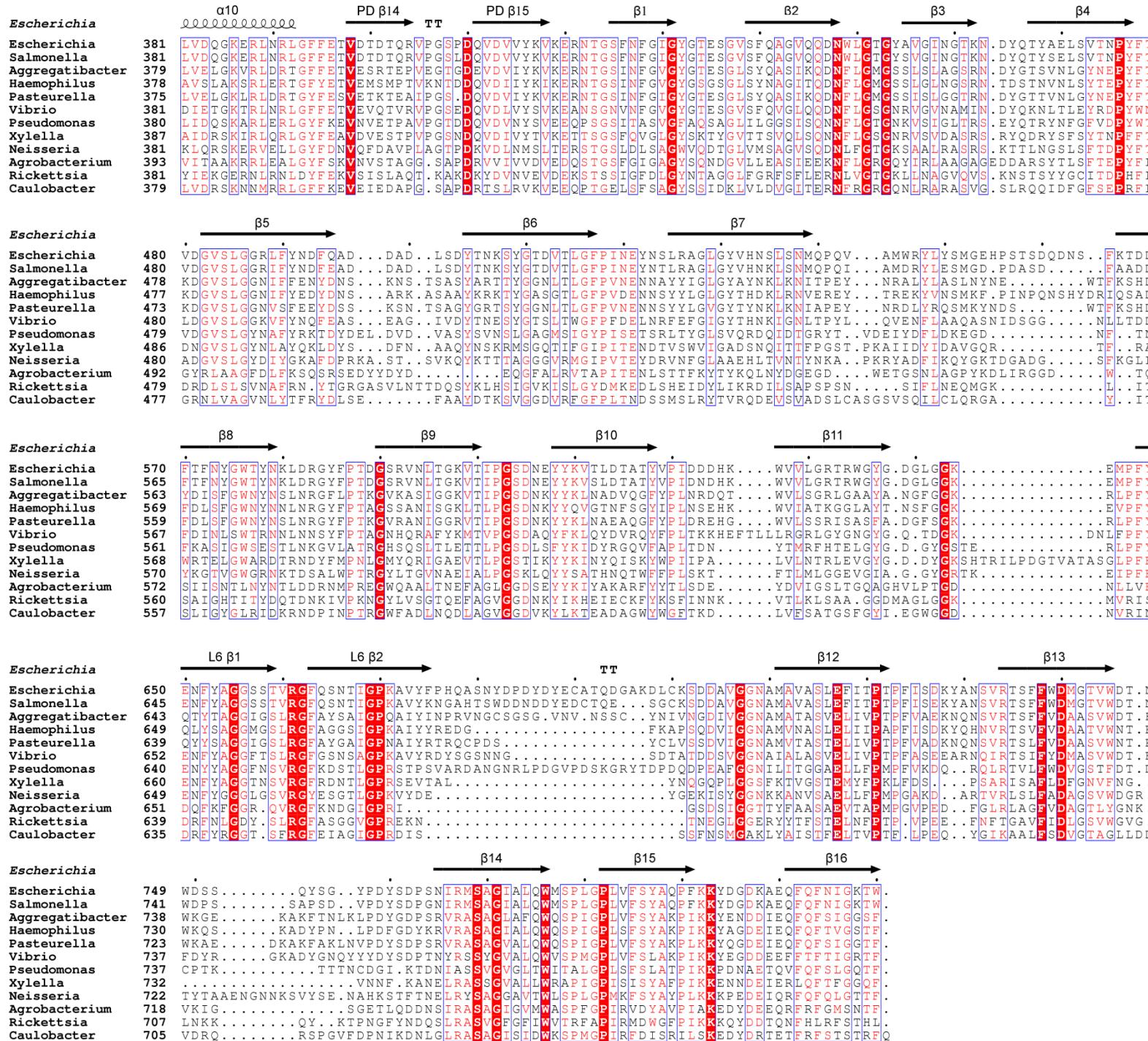|		Sequence
Escherichia	283	ETEQL.TKIEPGELYNGTKVTKMEDDIKKLLGRYGYAYPRVQSMPEIND.ADKTVKLRVNVDAGNRFYVRKIRFEGNDTSKDAVLRREMRQMEGAWLGSD
Salmonella	283	EIENL.TKIEPGELYNGTKVTKMEDDIKKLLGRYGYAYPRVQSQPEIND.ADKTVKLRVNVDAGNRFYVRKIRFEGNDTSKDSVLRREMRQMEGAWLGSD
Aggregatibacter	280	QLAPLLKQIHIGEEFHRSDVQAVEDIKSTLGERGYGGSAQVNVQPDFND.DAKTVGLSFVVDAGKRYSVRQIRFEGNTVSADSTLRQEMRQQEGSWLSTD
Haemophilus	279	ELNQLLTHFKAGQLFRKTELSIIEEQIKQILGDRGYGGSAKVDLYPKFNE.EDHTVQINFIVDAGRRIYVRKIRFEGNDVTADSTLRREMRQQEGAWLSSE
Pasteurella	276	ELAPILETIQLNGLFRRTSVLEVEQRNKSKLGERGYATAQVNVHPTFDE.QDKTISLDFIVEAGKSYTVRQIRFEGNTSSADSTLRQEMRQQEGAWLSSE
Vibrio	283	EFTSL.IPFEIGETYNGSAVTKITLEESVKKVLGESGYAYPVRTIPEFDD.EKQQVSLVVHVEAGKRYVNIRFEGNNSTRDEVLRREMRQMEGSWLNSK
Pseudomonas	282	EVKRL.LLVGKGQVFSRKVMTTTSDLITRRLGNEGYTFANVNGVPEAHD.DDKTVSVTFVVDPGKRAYVNRINFRGNTKTEDEVLRREMRQMEGGWASTY
Xylella	289	KIEKL.VIPKTGDIFSRVLLEYSSAAIINTLSNIGYAFSKVNPIPTANR.ADRTVAVNLHVIPGPRVTVRQILFKGNTRTSDEVLRREMRQFENSWYSQA
Neisseria	283	ELEKL.LTMKPGKWYERQQMTAVLGEIQNRMGSACGYAYSEIVPKVHIEPGRKIYVNIHITGNNKTRDEVRRRELEKMEGSAPYDTS
Agrobacterium	295	ELQGL.VETRQGASYSAKEVQQSMEAISKRVAGEGYFARVTPRGRDM.SGNTIGVTYIVDQGKRAYVERIEIRGNTRTRDYVIRREFDISEGDAFNQT
Rickettsia	284	QLNKI.VNIKQGKIFNMKTVDDIAEKIGEYFTANGYP..AVNVYPDIKKNDNHTADIKFIIEKADKVYINKININNLKTEDHVIRRAFKIEEGDVMNRS
Caulobacter	281	LLAQI.LPVRTGQLYEDERIEQATDALTFAAGAAGFAVDVRPRYVPNR.ETKTVDVVFQVREGPRVYVDRIDIVGNTRTLDYVLRRELEVAEGDAYNRV

Fig. S9. continued.

Figure S9. Alignment of BamA/ Omp85 orthologues. The figure shows the alignment of *E. coli* K-12 BamA (GenBank AAC73288) with the BamA/ Omp85 orthologues from *Salmonella enterica serovar* Typhi (GenBank CAD08682), *Aggregatibacter actinomycetemcomitans* (GenBank ACX81664), *Haemophilus ducreyi* (GenBank AAP96041), *Pasteurella multocida* (GenBank AAC44600), *Vibrio cholerae* (GenBank AAF95396), *Pseudomonas aeruginosa* (GenBank ABR83527), *Xylella fastidiosa* (GenBank AAF83856), *Neisseria gonorrhoeae* (GenBank ACF31073), *Agrobacterium tumefaciens* (WP003512849), *Rickettsia prowazekii* (GenBank CAA14627), *Caulobacter crescentus* (GenBank AAK23890). Secondary structure, derived from our model predications (Fig. 2), is indicated above the alignment. POTRA domain β-strands are designated PD β1 to PD β15, whilst those in the β-barrel are labelled β1 to β16. Predicted β-strands in loop L6 are labelled as L6 β1 and L6 β2.