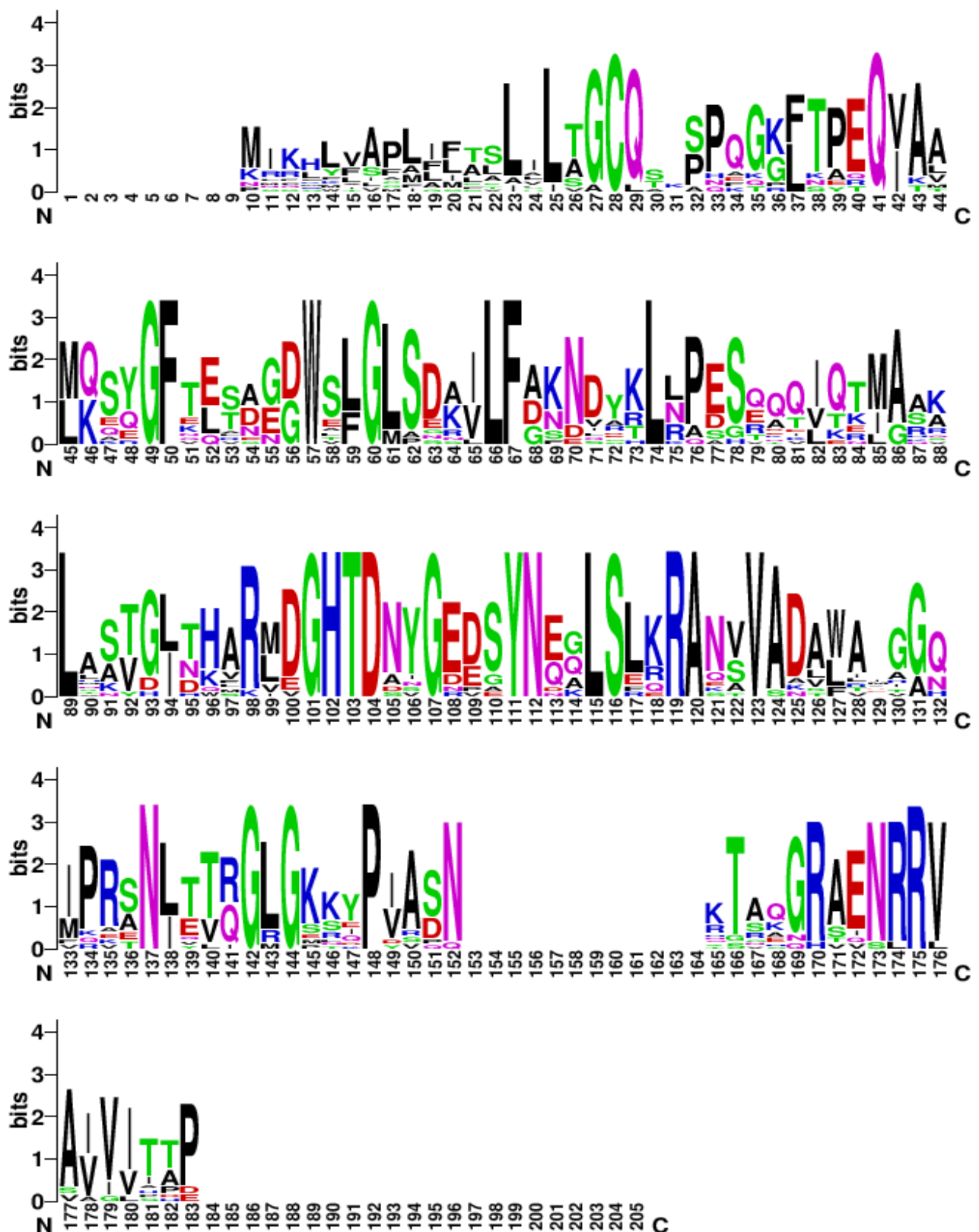


Supplementary Figure S2. The *in-silico* investigation of the YfiB protein. (A) Clustal-Omega multiple sequence alignment of YfiB protein homologs found in various Gram-negative bacteria, showing conserved and non-conserved amino acid residues.

A	YfiB_Citrobacter	-----MKS YGF
	YfiB_Enterobacter	-----MLKRYFAPLLLASLVISGCQT--SPEGKFTPEQIAAMKSYGF
	YfiB_E.coli	-----MIKHLVAPLIFTSLILTGCQ--SPQGKFTPEQVAAMQSYGF
	YfiB_S.dysenteriae	-----MIKHLVAPLIFTSLILTGCQ--SPQGKFTPEQVAAMQSYGF
	YfiB_S.flexneri_X	-----MIKHLVAPLIFTSLILTGCQ--SPQGKFTPEQVAAMQSYGF
	YfiB_S.sonnei	-----MIKHLVAPLIFTSLILTGCQ--SPQGKFTPEQVAAMQSYGF
	YfiB_SFL1613/Y394	-----MIKHLVAPLIFTSLILTGCQ--SPQGKFTPEQVAAMQSYGF
	YfiB_S.boydii	-----MQSYGF
	YfiB_Klebsiella_pneumoniae	-----MIRKYFVPALMAAALLTGCQ--APQGKFTPEQVAAMKSYGF
	YfiB_Xenorhabdus	-----MSKKRSFMFICAFIGTLFLSACQ---NKGGLTAEQITTLKQGGF
	YfiB_Pseudomonas_chlororaphis	-----MQLFTAGLLALLSLTGCQSVPP--KGLTPQQVAVLKQEGF
	YfiB_Pseudomonas_aeruginosa	--MLPQRLHPSRLALALFLSLVLGLAGCQTKPPQTGLSAEQIAVLQEGGF
	YfiB_Yersinia_enterocolitica	MLGLNNNRQKNPLWISFFALCLLVLVGCQAKPH--QGLTPEQIAALQEGGF
	YfiB_Serratia	--MIQQTLLKNRFSLLAMMFIALLALAGCQSKPQ--GLTPEQIALLQSGGF
	YfiB_Aeromonas	-----MGMFALLLAGCQ--SPPAGRLNETQIALLLKARGF
	YfiB_Acinetobacter_baumannii	-----MKLSFIALLCIALAGCLS---FGPLKYRQVKMLKKEGF
		:: **
	YfiB_Citrobacter	TEASGDWSLGLSDNILFDKNDYKLRPESEKQIKEMASKLAATGLNHARLD
	YfiB_Enterobacter	NELNGDWSLGLSDKILFDKNDARLRPESETQITQTHASRLAATGLNHARM
	YfiB_E.coli	TESAGDWSLGLSDAILFAKNDYKLLPESQQQTQTHAAKLASTGLTHARM
	YfiB_S.dysenteriae	TESAGDWSLGLSDAILFAKNDYKLLPESQQQTQTHAAKLASTGLTHARM
	YfiB_S.flexneri_X	TESAGDWSLGLSDAILFAKNDYKLLPESQQQTQTHAAKLASTGLTHARM
	YfiB_S.sonnei	TESAGDWSLGLSDAILFAKNDYKLLPESQQQTQTHAAKLASTGLTHARM
	YfiB_SFL1613/Y394	TESAGDWSLGLSDAILFAKNDYKLLPESQQQTQTHAAKLASTGLTHARM
	YfiB_S.boydii	TESAGDWSLGLSDAILFAKNDYKLLPESQQQTQTHAAKLASTGLTHARM
	YfiB_Klebsiella_pneumoniae	TESNGDWSLGLSDSILFDKNDYRLRPOSQQITTHASRLAATGITHSRLE
	YfiB_Xenorhabdus	QQTDEGWLFMGSEKVLFGNNQSHLRPEGEAKLKEASVLSKVGIHARLD
	YfiB_Pseudomonas_chlororaphis	ELTDEGWAFGLSGKVLFGSDIETLNAASTEIVERIGKALVSVHIDKVRVD
	YfiB_Pseudomonas_aeruginosa	ELRDEGWAFGLSGKVLFGNNLDRLNPDOSRNTLTKEARALLAVDIDKVRLE
	YfiB_Yersinia_enterocolitica	KLTDNGWAFGLANKVLFDSDVRKLNASGVQTVQNTGRALHNVDINHRVD
	YfiB_Serratia	KLTDNGWAFGLSDKVLFGNNVGKLNPESTDVQKMGKRALMSVGITQFRLD
	YfiB_Aeromonas	TQVEEGWSLGLSDRVLFANESRTLNPDOSRAVQKTAHSLLSVGDWARLD
	YfiB_Acinetobacter_baumannii	VLTNEGWTGLPERLLDFDNATLKQSHAEALTRLANQNLNKYDLNKLKIV
		. * : * : . : * : : * : : : : *
	YfiB_Citrobacter	GHTDNYGEDSYNEALS LK RANVVADAWAQGANIPRNLTTQGLGKKYPIA
	YfiB_Enterobacter	GHTDNYGEESYNEALS LK RANVVADAWAKGANIPRNLTTQGLGKKYPVS
	YfiB_E.coli	GHTDNYGEDSYNEGLSLK RANVVADAWAMGGQIPRNLTTQGLGKKYPIA
	YfiB_S.dysenteriae	GHTDNYGEDSYNEGLSLK RANVVADAWAMGGQIPRNLTTQGLGKNIP--
	YfiB_S.flexneri_X	GHTDNYGEDSYNEGLSLK RANVVADAWAIGGQIPRNLTTQGLGKKYPIA
	YfiB_S.sonnei	GHTDNYGEDSYNEGLSLK RANVVADAWAIGGQIPRNLTTQGLGKKYPIA
	YfiB_SFL1613/Y394	GHTDNYGEDSYNEGLSLK RANVVADAWAIGGQIPRNLTTQGLGKKYPIA
	YfiB_S.boydii	GHTDNYGEDSYNEGLSLK RANVVADAWAMGGQIPRNLTTQGLGKKYPIA
	YfiB_Klebsiella_pneumoniae	GHTDNYGEDSYNEALS LK RANVSADAWAEGAHVPSRNLVTRGLGKKIPDR
	YfiB_Xenorhabdus	GHTDNYGEVSYNNQLSLK RANTVADALTDGG--MQRANLTTRGLGPSQPIA
	YfiB_Pseudomonas_chlororaphis	GHTDASGREAYNQQLSLRRAKSVSKVLVATG--HREENIQLRGLGSSEPPA
	YfiB_Pseudomonas_aeruginosa	GHTDNYGDEGYNQKL SERRAESVAAVFREAG--MPAANI EVRGLGMSKPVA
	YfiB_Yersinia_enterocolitica	GHTDAIGEDGYNQQLSFQRASAVADTLAAIG--IPRTNIEVRGRGKLEPVA
	YfiB_Serratia	GHTDNYGEDSYNDQLSLRRANAVADLLASVG--IPRANIETRGMGKRDPA
	YfiB_Aeromonas	GHTDSNGDESYNQQLSRQRAQSVADSLIDAG--MPVANLEVRGLGERYPVA
	YfiB_Acinetobacter_baumannii	GHTDDVGNPEYNQKLSEERAQSVANLFLTHG--FKKENIYVIGRSTQPYV
		**** * ** : * : . * : : * : * *
	YfiB_Citrobacter	SN-----QTSKGRAENRRVAVVITP-----
	YfiB_Enterobacter	SN-----HTAQGRAENRRVAVVISTP-----
	YfiB_E.coli	SN-----KTAQGRAENRRVAVVITP-----
	YfiB_S.dysenteriae	-----
	YfiB_S.flexneri_X	SN-----KTAQGRAENRRVAVVIATP-----
	YfiB_S.sonnei	SN-----KTAQGRAENRRVAVVITP-----
	YfiB_SFL1613/Y394	SN-----KTAQGRAENRRVAVVITP-----
	YfiB_S.boydii	SN-----KTAQGRAENRRVAVVITP-----
	YfiB_Klebsiella_pneumoniae	QQRHGGRRARRKPPGNGGHQHAVSLRLVAGLHHPHCRCRAPAQVVGNEQQ
	YfiB_Xenorhabdus	DN-----RSSKGRAENRRVAIVITAP-----
	YfiB_Pseudomonas_chlororaphis	SN-----STVAGRTEENRRVSIIVIAD-----
	YfiB_Pseudomonas_aeruginosa	DN-----KTRAGRSENRRAVIVPAE-----
	YfiB_Yersinia_enterocolitica	DN-----RTAKGRAENRRVAIVTAP-----
	YfiB_Serratia	DN-----RTSSGRVENRRVAIVVTP-----
	YfiB_Aeromonas	SN-----KTREGRSQNRRAIVITD-----
	YfiB_Acinetobacter_baumannii	PN-----TTNENRAINRRVAIVIIP-----
	YfiB_Citrobacter	-----
	YfiB_Enterobacter	-----
	YfiB_E.coli	-----
	YfiB_S.dysenteriae	-----
	YfiB_S.flexneri_X	-----
	YfiB_S.sonnei	-----
	YfiB_SFL1613/Y394	-----
	YfiB_S.boydii	-----
	YfiB_Klebsiella_pneumoniae	QAGSH
	YfiB_Xenorhabdus	-----
	YfiB_Pseudomonas_chlororaphis	-----
	YfiB_Pseudomonas_aeruginosa	-----
	YfiB_Yersinia_enterocolitica	-----
	YfiB_Serratia	-----
	YfiB_Aeromonas	-----
	YfiB_Acinetobacter_baumannii	-----

Supplementary Figure S2. The *in-silico* investigation of the YfiB protein. (b) Weblogo representations of the YfiB protein amino acid conservation. The height of amino acid code at each position reflects the comparative incidence of the amino acid at that position and the total height of the pile denotes the degree of conservation at each individual locus (measured in bits). The consensus sequence was derived from multiple sequence alignment of YfiB protein sequences from various Gram-negative bacteria.

B



Supplementary Figure S2. The *in-silico* investigation of the YfiB protein. (c) Phylogenetic tree illustrating the evolutionary distance between the YfiB protein homologs from various gram-negative bacteria. Clustal-Omega alignment of the homologs was used to generate this phylogenetic tree and was created using the MEGA software, calculated by the Maximum Composite Likelihood method.

C

