

Yanagisawa et al., Fig. S2

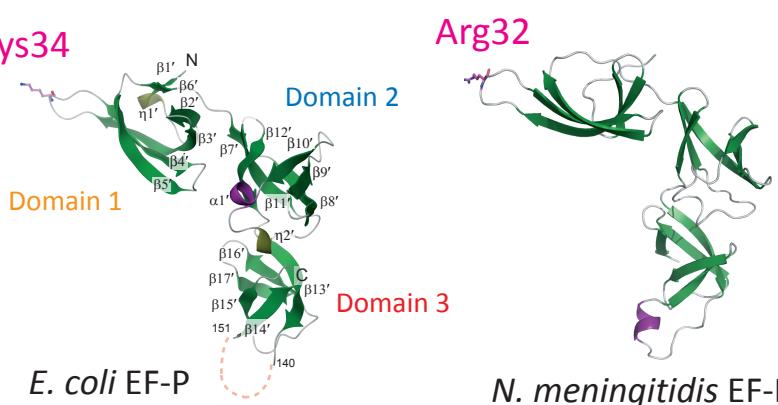
	Domain 1		
	3		
	1 2	β1' β2' β3' β4' β5'	*
NmEFP	MKT -- AQELRA - GNVFMVGNDPMVVQKTEYIKGGRSSAKVSMKLKNLLTGAASETIYKADD	58	
NgEFP	MKT -- AQELRA - GNVFMVGNDPMVVQKTEYIKGGRSSAKVSMKLKNLLTGAASETIYKADD	58	
BcEFP	MKT -- AQELRV - GNVVQIGSEAWVIAKAEYNKSGRNSAVVKMKMKNLLSNAGQESVYKADD	58	
BpEFP	MKT -- AQELRV - GNVIMVGKDPLVVQKTEYNKSGRNAAVVKKFKNLLTGSSESVYKADE	58	
TtEFP	MIS -- VTDLRP - GTKVMDGGLWECVEYQHQKLGRGGAKVVAFKNLETGATVERTFNSGE	58	
DrEFP	MIS -- VTELRN - GTKVQMDGGLWECLDYSHLKMGRGGAKVVTFRNMESGSIVDRTFNSTE	58	
BbEFP	MAVVKSSIEIK - GSFLLIKGAPHIVLEREFSKTGRGGAIVRKLKNLKNKFVIRETLKGAD	60	
EcEFP	MATYYNSNDFRA - GLKIMLDGEPYAVEASEFVKPGKGQAFARVKLRRLLTGTRVEKTFKSTD	60	
HsIF5	TFPMQCSALRKNGFVVLK - GRPCKIVEMSTSKTGHGHAKVHLVGIDIFTGKKYEDICPST	76	
ScIF5	TYPMQCSALRKNGFVVIK - GRPCKIVDMSTSKTGHGHAKVHLVTLDIFTGKKLEDLSPST	77	
MjIF5	TKQVNNGSLKV - GQYVMIDGVPCIEVDISVSKPGKHGGAKARVVGIGIFEKVKKEFVAPTS	63	
	Domain 2		
	64 65	β6' β7' β8' β9' β10' α1' η2' β11'	
NmEFP	KFDVVILSRKNCTSYFADPMYVFMD - EEFNQYEIEADNIGDALKFIVDGMD - QCEVTTF	116	
NgEFP	KFDVVILSRKNCTSYFADPMYVFMD - EEFNQYEIEADNIGDALKFIVDGMD - QCEVTTF	116	
BcEFP	KFEVVMLDRKEVTSYFADPMYVFMD - ADYNQYEVEAEMMGEALNYLEDGMA --- CEVVF	114	
BpEFP	KFDVVVLERKECTSYFGDPMYVFMD - EEYNQYEIEADSMGDALNYLEEAMP --- VEVVF	114	
TtEFP	KLEDIYVETRELQYLYPEGEEMVFMDLETYEQFAVPRSRVVG - AEFFKEGMT --- ALGDM	114	
DrEFP	KLQDIYVEGKKMQYLYPDGDDYVFMDMETFDQVHLGKNIVSDAAKFMKENTE --- VEVAM	115	
BbEFP	TAEAIEIYEVSAQYLYKDKDVLVFMMDLETYDQVSDLKESANLQDKVPFLQESEIYSLVT	120	
EcEFP	SAEGADVDMNLTYLYNDGEFWHFMNNETFEQLSADAKAIGDNAKWLLDQAE --- CIVTL	117	
HsIF5	HNMDVPNIKRNDFQLIGIQDGYLSLLQDSGEVREDLRLPEGDLGKEIEQKYDCGEEILIT	136	
ScIF5	HNLEVPFVKRSEYQLLIDDGYLSLMTMDGETKDDVKAPEGELGDSMQAAFDEGKDLMV	137	
MjIF5	SKVEVPIIDRRKGQVLAIMGDMVQIMDL - - QTYETLELPIPEGIEGLEPGGEVEYIEAVG	121	
	Domain 3		
	128 129	β12' β13' 141 150 β14' β15' β16'	
NmEFP	YEGNPISVELPTIIIVREVEYTEPAVKGDT S - GKVMKTARLVGGTEIQVMSYIENGDKVEI	175	
NgEFP	YEGNPISVELPTIIIVREVEYTEPAVKGDT S - GKVMKTARLVGGTEIQVMSYIENGDKVEI	175	
BcEFP	YNEKAISVELPTVLRREITYTEPAVKGDTSSGKVLKNAKLATGFELQVPLFCNTGDKIEI	174	
BpEFP	YDGRAISVELPTILVREITYTEPAVRGDT S - GKVLKPAKINTGFELSVPLFCAIGDKIEI	173	
TtEFP	YEGQPIKVTPPPTVVELKVVDTPPGVRGDT V - SGGSKPATLETGAVVQVPLFVEPGEVIKV	173	
DrEFP	YGDKALSISLPNQVILKITQTDPGVRGDT V - SGGTKPATLETGAVVQVPLFVEQGTDVKV	174	
BbEFP	FDNVVIDIKLAPKIAFEVVEEAVKGDT V - TNAMKNITLNTGLVVKAPLFINVGDKVLI	179	
EcEFP	WNGQPISVTPPNFVELEIVDTPGLKGDT A - GTGGKPATLSTGAVVQVPLFVQIGEVIKV	176	
HsIF5	VLSAMTEEEAAVAKAMAK	154	
ScIF5	IISAMGEEAAISFKEAPRSD	157	
MjIF5	QYKITRIGGGK	132	
	Lys34		
	187	β17' 188	
NmEFP	DTRTGEFRKRA --	186	
NgEFP	DTRTGEFRKRA --	186	
BcEFP	DTRTNEYRSRA --	185	
BpEFP	DTRTNEYRSRVN-	185	
TtEFP	DTRTGEYVGRA --	184	
DrEFP	DTRTGQYLSRA --	185	
BbEFP	NSETKEYAERIKN	192	
EcEFP	DTRSGEYVSRVK-	188	
	Arg32		
	<i>E. coli</i> EF-P		
	<i>N. meningitidis</i> EF-P (model)		
			

Fig. S2. Structure-based sequence alignment of EF-P and a/eIF5A

The amino acid sequences were aligned using the program CLUSTAL W (56), and then partly optimized and adjusted manually. Highly conserved residues between EF-P and a/eIF5A are colored red. Highly conserved residues in EF-P are colored orange, and those in a/eIF5A are colored sky blue. The rhamnosylated Arg32 of *N. meningitidis* EF-P is highlighted with a purple asterisk above the sequence alignment. Dashes represent breaks in the actual amino acid sequences of the respective proteins, to allow sequence alignment with *N. meningitidis* EF-P. *NmEFP*, *N. meningitidis* EF-P (EFV64285); *N. EcEFP*, *E. coli* EF-P (AAA97046); *NgEFP*, *Neisseria gonorrhoeae* EF-P (YP_208043); *BpEFP*, *Bordetella pertussis* EF-P (NP_880680); *BcEFP*, *Burkholderia cepacia* EF-P (WP_014897640); *BbEFP*, *Borrelia burgdorferi* EF-P (YP_005806412); *TtEFP*, *Thermus thermophilus* EF-P (BAD70948); *DrEFP*, *Deinococcus radiodurans* EF-P (AAF09709); *HsIF5*, *Homo sapiens* eIF5A (AAH80196); *ScIF5*, *Saccharomyces cerevisiae* eIF5A (AAA34425); *MjIF5*, *Methanocaldococcus jannaschii* aIF5A (C64453). An overview of a ribbon diagram of the crystal structure of *E. coli* EF-P (left) and a structural model of *N. meningitidis* EF-P (right) built by the Phyre2 server (57), using *P. aeruginosa* EF-P (PDB code: 3OYY) as the template, and visualized by the PyMOL viewer (<https://www.pymol.org/>). The Lys34 residue in EF-P(*Ec*) and the corresponding residue (Arg32) in EF-P(*Nm*) are shown as stick models. Secondary structure assignments (α -helices, 3_{10} -helices, and β -sheets) in EF-P(*Ec*) are represented as α , η , and β , respectively. The α -helices, 3_{10} -helices, and β -sheets are colored deep purple, dark olive, and green, respectively.