Supporting Information for

Archaic and alternative chaperones preserve pilin folding energy by providing incomplete structural information

Natalia Pakharukova, Sophie McKenna, Minna Tuittila, Sari Paavilainen, Henri Malmi, Yingqi Xu, Olena Parilova, Steve Matthews, and Anton V. Zavialov

Supplementary Tables S1-S3

Supplementary Figures S1-S10

Supplementary references

Crystal parameters	CsuC-CsuA/B	CsuC-CsuA/B	CsuA/Bsc			
			Native dataset	Se-Met SAD dataset		
Space group	P6 ₅ 22	НЗ	P21212	P21212		
Cell dimensions, (Å, °)	a=94.379,	<i>a</i> =111.419,	<i>a</i> =49.21, <i>b</i> =92.02,	a=48.913, b=92.486,		
	<i>b</i> =94.379,	<i>b</i> =111.419,	$c=34.11, \alpha=90.00,$	$c=34.113, \alpha=90.00,$		
	c=390.745,	<i>c</i> =167.745,	β=90.00, γ=90.00	β=90.00, γ=90.00		
	α=90.00,	α=90.00, β=90.00,				
	β=90.00,	γ=120.00				
	$\gamma = 120.00$					
Number of molecules	2	2	1	1		
per asymmetric unit						
Data collection						
Beamline	ID23-1	ID23-1	ID23-1	ID29		
Wavelength (Å)	0.8731	0.968	0.8725	0.979		
Resolution (Å)	47.19-2.85	55.71-2.50 (2.64-	49.21-1.47 (1.52-	49.31-1.60 (1.66-1.60)		
	(3.00-2.85)	2.50)	1.47)	· · · · · ·		
Unique observations	24880 (3546)	24003 (3555)	27069 (2591)	19295 (1889)		
R _{merge}	0.157 (0.866)	0.041 (0.245)	0.055 (0.637)	0.051 (0.689)		
R _{sym}	0.157	0.041	0.054	0.058		
<i>/\sigmaI</i>	11.3 (2.0)	20.2 (5.0)	12.1 (1.8)	12.7 (1.8)		
Completeness (%)	99.2 (99.5)	89.3 (90.2)	99.7 (99.5)	92.4 (93.4)		
Redundancy	7.9 (6.4)	3.3 (3.1)	4.3 (4.09)	3.8 (3.78)		
Overall <i>B</i> factor from	47.5	39.5	14.67	16.64		
Wilson plot (Å)						
Refinement						
$R_{\rm work}/R_{\rm free}$ (%)	20.97/25.68	17.17/22.64	19.67/21.91			
Number of protein	718	668	157			
residues						
Number of ligands/ions	-	-	-			
rmsd stereochemistry						
Bond lengths (Å)	0.003	0.008	0.011			
Bond angles (°)	0.661	1.161	1.370			
Ramachandran analysi	is [*]					
Residues in outlier	1.59	0.47	0			
regions (%)						
Residues in favored	94.93	96.06	97.39			
regions (%)						
Residues in allowed	98.41	99.53	100			
regions (%)						
PDB code	6FQA	6FQ0	6FM5			

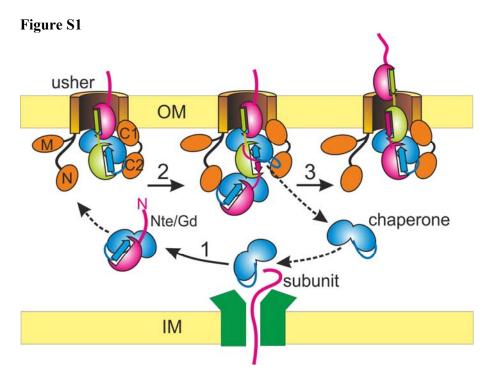
 Table S1. Diffraction data and refinement statistics

Structure	PDB	Number of	RMSD	Z-score	% of
	code	Ca atoms			identity
CfaE, pilin domain, CFA/I fimbriae	2HB0	133	2.7	11.7	8
LpfD, adhesin domain, LPF	5AFO	130	3.1	10.6	19
CssB, CS6 colonization factor	4B9G	120	2.7	10.0	13
PsaA, pH6 antigen	4F8N	120	2.6	10.0	10
FimG, type 1 pili	5IQM	115	2.4	9.7	16
CsuA/B in complex with CsuC	5D6H	93	3.3	9.5	84
chaperone					
CooA, CS1 colonization factor	4HJI	127	3.0	9.5	10
FimA, type 1 pili	2JTY	127	2.9	9.3	15
CfaB, CFA/I fimbriae	3F83	126	3.2	9.2	10
EcpA, Ecp	3QS3	125	3.0	8.8	13
FimH, lectin domain, type 1 pili	4ATT	126	3.0	7.4	9.0
Caf1, F1-antigen	1Z9S	103	2.6	6.6	14.0

 Table S2. Structural homologues of CsuA/B

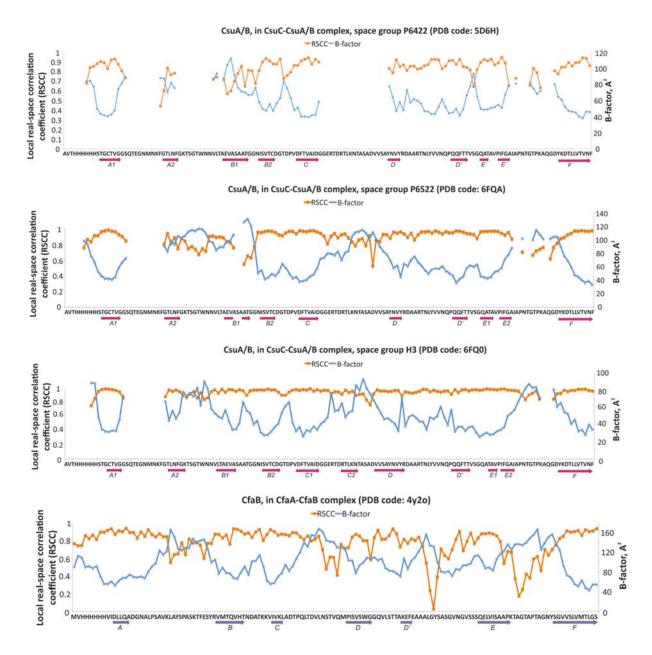
 Table S3. Oligonucleotides

Name	Sequ	ence ((5'→3	')							
CsuAB_F-GR	ССТ	TGT	TCA	TAT	TTC	CTT	CAG	TTT	GAC		
CsuAB_F-GF	GTG	GTA	CTT	TAA	ATT	TTG	GTA	AAA	CTT	CC	
CsuAB_V-GR	CTT	CAG	CTG	TTA	ATA	CGT	TGT	TCC	AAG		
CsuAB_V-GF	GTG	CTT	CAG	CAG	CAA	CAG	GTG				
CsuC_LN-R	TTA	AAG	AAG	CAT	CTT	GCT	CGT	TGC	С		
CsuC_IN-R	TTA	TAG	AAG	CAT	CTT	GCT	CGT	TGC	С		
CsuC_NI-F	ATA	TAA	AAG	TAA	GTT	TCC	AAA	TGC	GTT	ACT	С
CsuC_NL-F	ATT	TAA	AAG	TAA	GTT	TCC	AAA	TGC	GTT	ACT	С
CsuAB_F-GR	ССТ	TGT	TCA	TAT	TTC	CTT	CAG	TTT	GAC		
CsuAB_F-GF	GTG	GTA	CTT	TAA	ATT	TTG	GTA	AAA	CTT	CC	
CsuAB_V-GR	CTT	CAG	CTG	TTA	ATA	CGT	TGT	TCC	AAG		
CsuAB_V-GF	GTG	CTT	CAG	CAG	CAA	CAG	GTG				



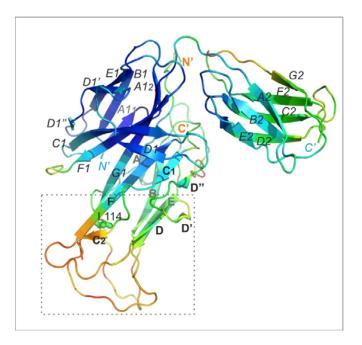
Schematic illustration of pilus assembly via the classical chaperone-usher pathway. Step 1: Periplasmic chaperones (blue) bind to pilus subunits (red or green) to form pre-assembly complexes. Step 2: The pre-assembly complex binds to the N-terminal domain of the usher (N) and the N-terminal extension (Nte or donor strand Gd) of the subunit in the pre-assembly complex replaces the donor strand G₁ of the chaperone in the acceptor cleft of the subunit at the base of the fiber. Strand G₁ and Gd runs in opposite directions in the cleft and the donor strand exchange (DSE) occurs gradually in a zipout-zip-in fashion. Strand G_1 is shown wider than strand Gd to reflect the fact that it has larger side chains of its donor residues. Step 3: The complex becomes incorporated into the fiber, the former fiber-capping chaperone is released, the fiber dissociates from the usher N-terminal domain, binds at usher C-terminal domains (C1 and C2) and translocates to the cell surface. Some details of the assembly mechanism were omitted for clarity: (a) in addition to donor strand G_1 , β strand A_1 of the chaperone plays role in the subunit binding (1); (b) the chaperone-subunit binding causes a conformational change in the chaperone ("proline lock" opening) that enables its binding to the Nterminal domain of the usher (2); (c) DSE is initiated in pocket P5 in the subunit acceptor cleft, which is either fully or partially/transiently exposed (3,4); (d) upon DSE, subunits collapse into a more compact structure due to a movement of two β -sheets towards each other, releasing energy that drives the assembly process (1,5).





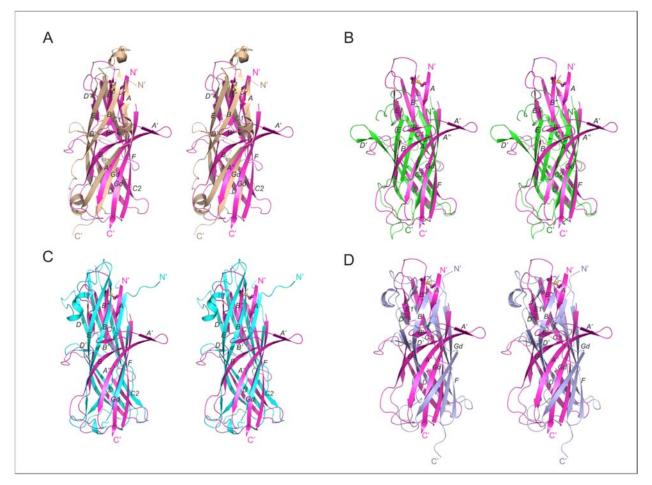
B-factors and local real-space correlation coefficients between the models and the electron density (RSCC) as a function of residue number. The protein sequence is depicted along abscissa with secondary structure elements shown bellow the sequence. B-factors and RSCC are shown in blue and orange, respectively.





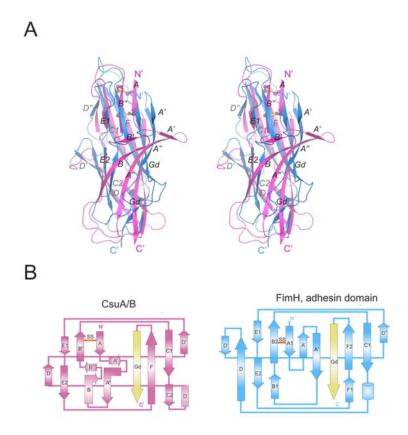
Cartoon diagram of the crystal structure of the CfaA-CfaB chaperone-subunit complex (PDB code 4Y2O). The structure is colored by B-factor of $C\alpha$ atoms with the color ranging from blue (lowest) to red (highest). High-B-factor region in CfaB is framed in a rectangle. Leucine 114 that was introduced instead of native threonine to stabilize the complex is shown as a ball-and-stick diagram. β -Strands are labeled.





Superposition of the archaic CsuA/Bsc (magenta) and representative pilin subunits from the classical FGS (PapA, PDB code 2UY6, wheat) (A) and FGL (Caf1, PDB code 1Z9S green) (B) and alternative Ecp-like (EcpA, PDB code 3QS3, cyan) (C) and Cfa-like (CfaB, PDB code 3F83, lilac) (D) CUPs (cartoon representations, stereo views). β -strands, N and C termini are labeled.

Figure S5

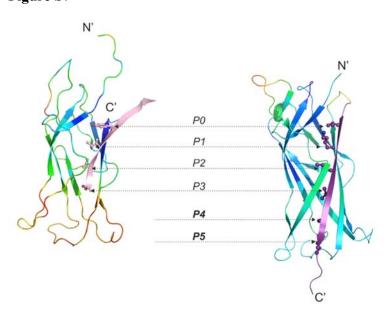


Comparison of CsuA/Bsc with the lectin domain of FimH adhesin subunit. (A) Structural superposition of CsuA/Bsc (magenta) and the lectin domain of the FimH adhesin subunit (blue, PDB code 4ATT) from the classical type 1 fimbriae (cartoon representation, stereo view). Note the presence of the A-A' hairpin in the structure of the lectin domain of FimH. β -strands and N and C termini are labeled. (B) Topology diagrams of CsuA/Bsc and FimH. Donor strand Gd in CsuA/B and strand G in FimH are shown in yellow.

Figure S6

I Igui e So					_	-		-
	Gd	A	A'	A"	В	B	<i>B''</i>	C1
	10	*	20	20 40	50		*	70 80
Psefu 0840/1-154	AGTVTGQLGIQLV	TDOOT	1 NONA	G - GT FGT I DFGSVAA - I T -		cheese		
PSetu_0840/1-154 PA14_61500/1-159				- GGINQWGTLDFGSHSD-LT-				
YPK_1778/1-161				GSLSNLGTINFGSVVA-LS-				
Pecwa 1449/1-156				GTTWGTIDFGSHSN-LM-				
YPC 2119/1-161				-GSLSNLGTINFGSVVA-LS-				
YpAngola_A2668/1-148				- GSTSFGTLDFGSTVA-LT-				
MDS_2707/1-156				- G S S N T F G S I S F <mark>G</mark> N Y N D - L A -				
M495_10245/1-156	AGT IQ <mark>G</mark> NLGVTLT	I G A G C V V G	GGNSA -	- G S A N D F G A <mark>I</mark> S F <mark>G</mark> T Y S S - L S -	NI-IDASATGS-	GGAGT	L S L T <mark>C</mark> T T G - '	T A Y T <mark>V</mark> A L NN <mark>G</mark> L H V G A
PADK2_24695/1-159	AGTL <mark> G</mark> QVGVQMV	I G A G C T I I	NGSVS -	- GG INQ <mark>W</mark> GTLDF <mark>G</mark> SHSD - LT -	NV-VDAQTVG	– T S G N	IQ QCSTG-I	L T <mark>P S L T V</mark> NA <mark>G</mark> L HASG
PAM18 4745/1-159				- GG I NQ <mark>W</mark> GT L DF <mark>G</mark> S H S D - L T -				
PSPA7_5297/1-159				- GGINQWGTLDF <mark>G</mark> SHSD-LT-				
KOX_23780/1-157				- GENNRWGN INF <mark>G</mark> SYGD - LA - GTTWGT IDFGSHSN - LM -				
W5S_1333/1-156 EbC_38170/1-166				- TTGVNFGTLDFGSHSN-LM-				
PAJ_2575/1-166								Q TENVQVTSSNAAPG TV
ROD 19381/1-166								DYT VQV TGNTNSSAPGSV
A3UG 14090/1-166								SYTVAITGNTNSTAPGTV
M634_16995/1-156				TASGIGFGLLDF <mark>G</mark> DVPA-IF-				
PP1Y_Mpl9658/1-152				- TSNVD <mark>F</mark> GSLDF <mark>G</mark> SVST - FF -				
PSEEN3400/1-154				- AGAQA <mark>L</mark> GR <mark>I</mark> DL <mark>G</mark> SAAR - LD -				
Pput 3338/1-154				- AGAQALGR I DL <mark>G</mark> VTAR - L D -				
BP1026B /1999/1-158				- G DL G RL DF <mark>G</mark> A Q G P - L W -				
Ent638_2462/1-166								SYTVAITGNTNSTAPGTV
BBK_77/1-158				-GDLGRLDFGAQGP-LW-				T AFSITIDGGRNGDQ AFSITIDSGTHAGQ - GAG
Acav_4528/1-164 PP2357/1-154				- AGAQALGR IDL <mark>G</mark> ATAR - LD -				
X969 07655/1-155				- AGAQALGRIDLGATAR-LD-				
ABBFA_001232/1-155				- GNMNKFGTLDFGKTSG - TW-				
Ab_CsuA/B/1-155				-GNMNKFGTLNFGKTSG-TW-				
ABK1_1269/1-155	AVT <mark>G</mark> QVDVKLN	IST <mark>GC</mark> TVG	GSQTE -	- GNMNK <mark>F</mark> GT <mark>LDFG</mark> KTSG - TW -	NNVLTAEVASA-	A T <mark>G</mark> G N	ISVTCDGT-I	DPVDFTVAIDGGERTD
BTH_10867/1-144	ATATATFTVSLT	VQAN <mark>C</mark> T IS	A	NA <mark>L</mark> S <mark>F G</mark> T NG V - L A -	T A - V N -	-QQTT	LSVS <mark>C</mark> SNT - "	T SYN <mark>VGL</mark> DA <mark>G</mark> SVSGS T -
Bphyt 1270/1-149	A V Y S NG T A V T F T V T L T I	NANCSIS	A	NPL NF <mark>G</mark> TNGV - LA -	T A - I N -	-QQTT	VAVT <mark>C</mark> TNT-	T PYN <mark>VGL</mark> DA <mark>G</mark> TVTGS T -
BP1026B_12529/1-144				NALSF <mark>G</mark> TNGV-LA-				
VAPA_1c20590/1-147				SNIDFGAVDS-SA-				
Smlt1513/1-152				TNVDFGTAAS-TT-				
XCR_1648/1-152				T D <mark>V D F G</mark> S V L S - T S - T D V D F G S V L S - T S -				
XOO1873/1-152 XAC29 07205/1-152				TDVDFGSVL3-T3-				
XC 2857/1-152				TDVDFGSVLS-TS-				
MYSTI 01789/1-150	ATATANLTVTAT	SAACSIN	S	GTLNFGNYDP-VV-	IN-SSAGID-L-	LASGS	LTVQCTLL -:	STAVVTLGQGSHPDT-GST
HNE_0086/1-134	ATANGTLDVQAT	VNTCVVL	ТАР	<mark>v</mark> v f a s v	GL-D-EV-	TANGS	ITVNCTNT-	S A F T VAL DGG DSG D I
CFU_2414/1-146	TATMTNTVT	ISNN <mark>C</mark> SIS	Τ	<mark>L G F T</mark> T T Y D P I V -	T NATTNQD -	- ITAS	VTTTCTIG-/	A SPVITLGQGANANT - GST
Lferr_0006/1-138				T N L A F <mark>G</mark> T Y T G - A V -				
AFE_0005/1-138	STATATETVTAT	AATCTIS	A	T N L A F <mark>G</mark> T Y T G - A V -	T N -	- ANST	VTVTCTNT-	T - PYN <mark>V</mark> GLNA <mark>G</mark> TATAA - T -
	Co		D	- -	N'	E.	Fa	F
	C2	_	D	E)'	E1	E2	F
	C2	-		D)'		E2	F
		90	D		2'		E2	F
Psefu 0840/1-154		90 - NG T D T L A		110	120	E1		
Psefu_0840/1-154 PA14_61500/1-159				10 A <mark>G</mark> RTTPWGD <mark>G</mark> SNGGD-T	120 LTTTGT-GTTQE			- EVPSV <mark>G</mark> T <mark>Y</mark> TDTVQVTVAW
Psefu_0840/1-154 PA14_61500/1-159 YPK 1778/1-161	GQ <mark>R</mark> YMQNT ⁻	TTTSSTIA PTTFEYVN	Y N I Y S D Y N L F K D	110 AGRTTPWGDGSNGGD-T AARSAL IQANT-PVD SSYNQPWNATP-TTG-V	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP	PL \ PL T \	Y <mark>G</mark> RVVPTGQS YAQVP-I	- EVPSVGTYTDTVQVTVAW STPTPTAGTYTDTLLVTIAW QTTPSV <u>S</u> TYIDTVIVTVTW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156	GQ <mark>R</mark> YMQNT ⁻ GQRRL RGGAAAI NSL <mark>RRL</mark> TPS	TTTSSTIA PTTFEYVN - T <mark>G</mark> TYNV <mark>P</mark>	Y N I Y S D Y N L F K D Y R L Y S D	110 AGRTTPWGDGSNGGD-T AARSALIQANTPVD SSYNOPWNATP-TTG-V STRSTEIPLID-ATG	120 LTTTGT - GTTQE ISSVST - GTAVN QSGTGT - GTAVN IATPAT - GNPQL	<mark>PL</mark> PLT <mark>P</mark>	Y <mark>G</mark> RVVPTGQ8 YAQVP - YAR APADQ1	EVPSVGTYTDTVQVTVAW STPTPTAGTYTDTLLVTIAW - QTTPSVSTYIDTVIVTVTW - VMSPAAGAYTDTITATIEW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161	GQ <mark>R</mark> YMQNT GQRRL RGGAAAA NSL RRL TPS GQ <mark>R</mark> RL RGGAAAA	TTTSSTIA PTTFEYVN - T <mark>G</mark> TYNVP PTTFEYVN	Y N I Y S D Y N L F K D Y R L Y S D Y N L F K D	110 AGRTTPWGDGSNGGD-T AARSALIQANT-PVD SSYNOPWNATP-TTG-V STRSTEIPLID-ATG-V SYNOPWNATP-TTG-V	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP	PL` PL T ` P ` PL T `	Y <mark>G</mark> RVVPTGQS YAQVP - I YAR I APADQ1 YAQVP - I	EVPSVGTYTDTVQVTVAW STPTPTAGTYTDTLLVTIAW - QTTPSVSTYIDTVIVTVTW - VMSPAAGAYTDTITATIEW - QTTPSVSTYIDTVIVTVTW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148	GQRYMQNT GQRRLRGGAAAI NSLRRLTPS -GQRRLRGGAAAI NNRYLSGG	TTTSSTIA PTTFEYVN - T <mark>G</mark> TYNVP PTTFEYVN - PSAQQVS	Y N I Y S D Y NL F K D Y RL Y S D Y NL F K D Y NL Y T N	10 AGRTTPWGDGSNGGD-T AARSALIQANT-PVD SSYNQPWNATP-TTG-V SSYNQPWNATP-TTG-V SSYNQPWNATP-TTG-V TYSVIWDVVG	120 LTTIGT-GTIQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP VSQVAT-GQVVT	PL \ PL T \ P \ PL T \ P \	Y <mark>G</mark> RVVPTGQS YAQVP - YAR I APADQT YAQVP - YGL VPAQ	EVPSVGTYTDTVQVTVAW STPTPTAGTYTDTLLVTIAW - QTTPSVSTYIDTVIVTVTW - VMSPAAGAYTDTITATIEW - QTTPSVSTYIDTVIVTVTW STPAVGTYTDTVQVTVSW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148 MDS_2707/1-156		TTSSTIA PTTFEYVN - TGTYNVP PTTFEYVN - PSAQQVS - AGAYVA	Y N I Y S D Y NL F K D Y RL Y S D Y NL F K D Y NL F K D Y NL Y Q N	10 AGRTT FWGDGSNG GD - T AARSAL IQANT - P VD - SSYNOPWNAT P - T TG - V STRSTE IP ID - A TG - V TTSVI WDDV G - V TTSVI WDDV G TGSV	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP VSQVAT-GQVVT LSGTGT-GNNEE		Y <mark>G</mark> RVVPTGQS YAQVP - I YAR I APADQT YAQVP - I YGL VPAQ YGRVPS - Q - 1	- EVPSVGTYTDTVQVTVAW STPTPTAGTYTDTLLVTIAW -QTTPSVSTYIDTLLVTIAW -QTTPSVSTYIDTVIVTVW -VMSPAAGAYTDTITATIEW -QTTPSVSTYIDTVIVTVW - STPAVGTYTDTVQVTVSW - STPAVGTYTDTVQVTIAW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148 MDS_2707/1-156 M495 10245/1-156		TTSSTIA PTTFEYVN - TGTYNVP PTTFEYVN - PSAQQVS - AGAYVA - TAGALIK	YNIYSD YNLFKD YRLYSD YNLFKD YNLYTN YNLYQN YNLYQD	10 AGRTTPWGDGSNGGD-T AARSALIQANT-PVD SYNOPWNATP-TTG-V STRSTEIPLDO-ATG-V STRSTEIPLDO-ATG-V TYSVIWDDVVG GRSLPWGDGG-ATGSV SARATAWSGAN-A	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP VSQVAT-GQVVT LSGTGT-GNNEE LTGTGT-GAAVP	PL \ PL T \ P \ PL T \ P \ V V \ L V \	Y <mark>G</mark> RVVPTGQS YAQVP-I YARIAPADQ1 YAQVP-I YGLVPAQ YGRVPS-Q-1 YGRVPS-Q-1	EVPSVETYTDTVQVTVAW STPIPTAETYTDTLLVTIAW OTTPSVSTVIDTVIVTVW VMSPAAGAYTDTITATIEW GTTPSVSTVIDTVIVTVV - STPAVETYTDTVQVTVSW TPSPETYTDTVQVTIAW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148 MDS_2707/1-156 M495 10245/1-156 PADK2_24695/1-159		TTTSSTIA PTTFEYVN -TGTYNVP PTTFEYVN -PSAQQVS -AGAYVA -TAGALIK TTSSTIA	YNIYSD YNLFKD YRLYSD YNLFKD YNLYTN YNLYQN YNLYQD YNLYSD	10 AGRTTPWGDGSNGGD-T AARSAL IQANT-PVD SYNOPWNATP-TTG-V STRSTEIPLD-AT-G-V STRSTEIPLDVG GRSLPWGDG-ATGSV SARATAWSGAN-A AARSAL IQANT-PVD VD-V	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GAVP LSGTGT-GAVP LSGTGT-GAAVP LSGTGT-GAAVP LSSVST-GTAVN	- PL' PLT - P PLT - PV - V V L V PL	Y GRVVPTGQS Y AQVP - 1 Y AR I APADQT Y AQVP - 1 Y GRVPA Y GRVPS - Q - T Y GRVPA - AA Y GRVVPTGQS	EVPSVG TYTDTVQVTVAW STPTPTAG TYTDTLLVTIAW OTTPSVSTYIDTVIVTVW VMSPAGAYTDTITATIEW GTTPSVSTYIDTVIVTVV - STPAVGTYTDTVQVTVSW TPSPGTYTDTVQVTIAW STPTPTAGTYTDTLLVTIAW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148 MDS_2707/1-156 M495 10245/1-156		TTTSSTIA PTTFEYVN -TGTYNVP PTTFEYVN -PSAQQVS -AGAYVA -TAGALIK TTSSTIA	YNIYSD YNLFKD YRLYSD YNLFKD YNLYTN YNLYQN YNLYQD YNLYSD	10 AGRTTPWGDGSNGGD-T AARSAL IQANT-PVD SYNOPWNATP-TTG-V STRSTEIPLD-AT-G-V STRSTEIPLDVG GRSLPWGDG-ATGSV SARATAWSGAN-A AARSAL IQANT-PVD VD-V	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GAVP LSGTGT-GAVP LSGTGT-GAAVP LSGTGT-GAAVP LSSVST-GTAVN	- PL' PLT - P PLT - PV - V V L V PL	Y GRVVPTGQS Y AQVP - 1 Y AR I APADQT Y AQVP - 1 Y GRVPA Y GRVPS - Q - T Y GRVPA - AA Y GRVVPTGQS	EVPSVG TYTDTVQVTVAW STPTPTAG TYTDTLLVTIAW OTTPSVSTYIDTVIVTVW VMSPAGAYTDTITATIEW GTTPSVSTYIDTVIVTVV - STPAVGTYTDTVQVTVSW TPSPGTYTDTVQVTIAW STPTPTAGTYTDTLLVTIAW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YDAnq0ba A268/1-148 MDS_2707/1-156 M495 10245/1-156 PADK2_24695/1-159 PAM18_4745/1-159 PSPA7 5297/1-159 KOX_23760/1-157		TTTSSTIA PTTFEYVN -TGTYNVP PTTFEYVN -PSAQQVS -AGAYVA -TAGALIK TTSSTIA	YNIYSD YNLFKD YRLYSD YNLFKD YNLYTN YNLYQN YNLYQD YNLYSD	10 AGRTTPWGDGSNGGD-T AARSAL IQANT-PVD SYNOPWNATP-TTG-V STRSTEIPLD-AT-G-V STRSTEIPLDVG GRSLPWGDG-ATGSV SARATAWSGAN-A AARSAL IQANT-PVD VD-V	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GAVP LSGTGT-GAVP LSGTGT-GAAVP LSGTGT-GAAVP LSSVST-GTAVN	- PL' PLT - P PLT - PV - V V L V PL	Y GRVVPTGQS Y AQVP - 1 Y AR I APADQT Y AQVP - 1 Y GRVPA Y GRVPS - Q - T Y GRVPA - AA Y GRVVPTGQS	EVPSVG TYTDTVQVTVAW STPTPTAG TYTDTLLVTIAW OTTPSVSTYIDTVIVTVW VMSPAGAYTDTITATIEW GTTPSVSTYIDTVIVTVV - STPAVGTYTDTVQVTVSW TPSPGTYTDTVQVTIAW STPTPTAGTYTDTLLVTIAW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148 MDS_2707/1-156 PADK2_24695/1-159 PAM16_4745/1-159 PSPA7 5297/1-159 KOX_23780/1-157 W55_1332/1-156		TTTSSTIA TTFEYVN TTFEYVN PTTFEYVN PSAQVS - AGAYVA TAGALIK TTSSTIA TTSSTIA GGTQQIA - GTYNVP	Y N I Y S D Y NL F K D Y NL F K D Y NL Y T N Y NL Y Q N Y NL Y Q D Y NI Y S D Y NI Y S D Y NI Y S D Y RL Y S D Y RL Y S D	10 AG RTT PWG DG SNG GD - T AARSAL I QANT - P VD SSYNOPWNAT P -T TG - V STRSTE I PL D - A T G G SSYNOPWNAT P -T TG - V TYSV I WDDVV G GRSL PWG DG G - A TG SV SARAT AWSGA N A AARSAL I QANT - P VD AARSAL I QANT - P VD AARSAL I QANT - P VD AARSAL I QANT - P MD AARSAL I QANT - P MD AARSAL I QANT - P MD AARNE I L PG G T G	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP VSQVAT-GQVVT LSGTGT-GAAVP ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN IPIIGT-GNPQL IAIPAT-GNPQL	- PL PL T - P PL T - PV - PV - PV - PL - PL - PL - PV - PV	Y G RVVPTGQS Y AQVP - I Y AR I AP ADQT Y AQVP - I Y G L VP AQ Y G RVPS - Q - T Y G RVPS - Q - T Y G RVVPTGQS Y G RVVPTGQS Y G RVVPTGQS Y G RVVPTGQS Y AR I AP ADQT	- EVPSVETYTDTVQVTVAW STPPFAETYTDTVQVTVAW OTTPSVSYIDTVIVTVW OTTPSVSYIDTVIVTVW - STPAVETYIDTVIVTVV - STPAVETYTDTVQVTVSW TPSPETYTDTVQVTVAW STPPFAETYTDTVQVTVAW STPPFAETYTDTLVTIAW STPPFAETYTDTLVTIAW SVNPFAEQYTDILVTIAW SVNPFAEQYTDILVTIAW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YDAnqola A268/1-168 M495 10245/1-156 PADK2_24695/1-159 PADK2_24695/1-159 PAM18_4745/1-157 KOX_23780/1-157 W55_1333/1-156 EbC_38170/1-166		TTTSSTIA PTTFEYVN PTTFEYVN PSAQQVS AGAYVA TAGALIK TTSSTIA TTSSTIA GGTQQIA TGTYNV SDATQQIA	Y N I Y S D Y NL F K D Y NL F K D Y NL Y K D Y NL Y Q D Y NL Y Q D Y NI Y S D Y NI Y S D Y RL Y S D Y RL Y S D Y RL Y S D	10 AGRTTPWGDGSNGGD-T AARSALIQANT-PVD SSYNOPWNATP-T	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP LSGTGT-GNPQL LTGTGT-GNPQL LTGTGT-GNPQL ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN IPIIGT-GNPQA IAIPAT-GNPQL	- PL PL T - P PL T - PV - V V PV - PL - PL - PL - PV - PV - PV	Y G RV V P T G Q S Y A Q V P - I Y A R I A P A D Q T Y G R V P A Q Y G R V P A Q A - Y G R V P T G Q S Y G R V V P T G Q S Y G R V V P T G Q S Y G R V V P T G Q S Y G R V V P T G Q S Y G R I T G G G F I Y G R I T G G G F I	- EVPSVSTYTDTVQVTVAW STPIPTASTYTDTLLVTIAW QTTPSVSTYIDTVIVTVW VMSPAGAYTDTITATIEW - STPAVGAYTDTVQVTVVW - TPSPSTYTDTVQVTIAW STPIPTASTYTDTVQVTIAW STPIPTASTYTDTLLVTIAW STPIPTASTYTDTLLVTIAW SVNAPTADYTDTLLVTIAW SVNAPTADYTDTLLVTIAW SVNAPTADYTDTLLVTIAW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148 MDS_2707/1-156 M495 10245/1-156 PADK2_24695/1-159 PADK2_4695/1-159 PSPA7 5297/1-159 KOX_23780/1-157 W5S_1333/1-156 EbC_38170/1-166 PAJ_2575/1-166		TTTSSTIA TTFEYVN TGTYNVP TFFEYVN PSAQQVS - AGAYVA TAGALIK TTSSTIA TTSSTIA TTSSTIA - GGTQQIA ADNTQGIA	YNIYSD YNLFKD YRLYSD YNLFKD YNLYQD YNLYQD YNIYSD YNIYSD YRLYSD YRLYSD YLYSD	110 AGRTTPWGDGSNGGD-T AARSALIQANT-PVD STRSTEIPLID-AT-G-V STRSTEIPLD-AT-G-V ATYSVIWDDVVG GRSLPWGDGG-ATGSV AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARNEILPGGTG TRSTEIPLID-ATG TSYTTPIANST-NL-T	120 LTTTGT-GTTQE ISSVST-GTAVN GGTGT-GIATP VSQVAT-GOVVT LSGTGT-GNAVP USSVST-GTAVN ISSVST-GTAVN	P L Y P L Y P L Y P V P V P L 	Y GRVVPTGQS Y AQ VP - I Y AQ VP - I Y GLVPAQ Y GRVPS - Q - I Y GRVPS - Q - I Y GRVVPTGQS Y AR I APADQ Y AR I APADQ Y AR I APADQ Y GR I TGGGFF Y GRVVGGFF	- EVPSVOTT TDTVQVTVAW STPTPTAG TY TDTVQVTVAW OTTPSVSY IDTVIVTVW VMSPAAGAY TDTIITATIEW - STPAVGTY IDTVIVTVW - STPAVGTY IDTVIVTVW - TPSPOTY TDTVQVTIAW - TPSPOTY TDTVQVTIAW STPTPTAG TY TDTLLVTIAW STPTPTAG TY TDTLLVTIAW STPAPTAG TY TDTLLVTIAW VMSPAAGAY TDTIITATIEW - AAIPAG TY TDTIINVANY
PA14_61500/1-159 YPK 1778/1-161 Pocwa_1449/1-156 YPC_2119/1-161 YPAnqola A2668/1-164 MD5 10245/1-156 PADK2_24695/1-159 PADK2_24695/1-159 PADK2_24695/1-159 PSPA7 5297/1-157 WSS_1333/1-156 EbC_38170/1-166 PAJ_2575/1-166 ROD_1931/1-166		TTTSSTIA TTFEYVN -TGTYNVP -PSAQQVS -AGAYVA TTSSTIA TTSSTIA GGTQQIA -GGTQQIA -GTYNVP SDATQGIA ANTTQGVA	YNIYSD YNLFKD YNLFKD YNLYCN YNLYQN YNIYSD YNIYSD YNIYSD YRLYSD YRLYSD YRLYSD YRLYSD YLYSD	10 AG RTTP WG DG SNG GD - T AARSAL I QANT - P VD STRSTE I PL I D - A T G SYNOPWNATP - T TG - V STRSTE I PU D V G GRSL PWG DG G- A TG - V SARATAWSG A N A AARSAL I QANT - P VD AARSAL I QANT - P VD STRSTE I PL I D -A T G TSYTTP I ANST -N L -T SG FSN V ANNT - P L -P	LTTTGT-GTTQE USSTGT-GTAVD QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP IAIPAT-GNPQL USGVGT-GAVT LSGTGT-GAVT LSGTGT-GAVT ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN IPIIGT-GNPQL NIGTTDPVNGDN PSGTTDPTLGTN RA-STT-AGVDN	P L Y P L T I Y P I Y P L T I Y P V P L Y P L Y Y A I Y	Y GRV VPT GQS	- EVPSVETYTDTVQVTVAW STPIPAETYTDTVQVTVAW OTTPSVSTYIDTVIVTW VMSPAAGAYTDTIATIEW - STPAVETYTDTVQVTVW - STPAVETYTDTVQVTVSW TPSPETYTDTVQVTIAW STPIPAETYTDTLLVTIAW STPIPAETYTDTLLVTIAW STPIPAETYTDTLLVTIAW SVNAPTADVYDDIVTATLAW VMSPAAGAYTDTIATIEW - AAIPASTYTDTINVAVNY - PVIPAETYTDTINVAVNY - PVIPAETYTDTINVAVNY
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YpAngola A2668/1-148 MDS_2707/1-156 M495 10245/1-156 PADK2_24695/1-159 PADK2_4695/1-159 PSPA7 5297/1-159 KOX_23780/1-157 W5S_1333/1-156 EbC_38170/1-166 PAJ_2575/1-166		TT SSTIA TT FEYVN TT FEYVN PAQQVS - AGAYVA TAGAL IK TTSSTIA TTSSTIA - GGTQQIA - TGTYNV SDATQGIA ANT TQGVA	YNIYSD YNLFKD YNLFKD YNLYN YNLYQN YNLYQD YNIYSD YNIYSD YRLYSD YRLYSD YTLYGT YTLYSD YSLYSD YSLYSD	110 AGRTTPWGDGSNGGD-T AARSAL IQANT-PVD STRSTEIPLID-AT-G-V STRSTEIPLID-AT-G-V ATYSVIWDDVVG GRSLPWGDGGATGSV AARSAL IQANT-PVD AARSAL IQANT-PVD AARSAL IQANT-PVD AARSAL IQANT-PVD STRSTEIPLID-AT-G STRSTEIPLID-AT-G STSYTTPIANST-NL-T STSTSTANN-N	120 LTTTGT-GTTQE ISSVST-GTAVN GSGTGT-GIATP IAIPAT-GNPGL QSGTGT-GAVP USQVAT-GQVVT LSGTGT-GAAVP ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN NTGTTDPVNGDN PSGTTDPTLGTN KA-STT-AGVDS	- PL' PLT ' PV' PV' PV' PL' PL' PL' PV' PV' PV' PI' YPI' YTL'	Y GRVPTGQ YAQVP-I YARIAPADQ YAQVP-I YGRVPS-Q YGRVPS-Q YGRVPTGQ YGRVVPTGQ YGRVVPTGQ YARIAPADQ YARIAPADQ YGRITGGGFY YGRVGGGFM YGRITGGGSN YGRIGGGSN YGRIGGGSN	
PA14_61500/1-159 YPK 1778/1-161 Pecws_1449/1-156 YPC_2119/1-161 YDAngola A2668/1-168 MDS_2707/1-156 M495 10245/1-156 PADK2_24695/1-159 PADK2_24695/1-159 PSPA7 5297/1-159 KOX_23760/1-156 EbC_3817/1-156 PAJ_2575/1-166 ROD_19381/1-166 ROD_19381/1-166		TT F SYTIA TG T YNV P TF F E YVN P TF AQQVS TG T YNV P TT SYTIA TT SYTIA GG T QQIA TT SYTIA GG T QQIA TG T YNV P SD AT QG I A AD T T QG VA NT AQGVA SNG SY YI P NG SYY I P	YNIYSD YNLFKD YRLYSD YNLFKD YNLYN YNLYQN YNIYSD YNIYSD YNIYSD YRLYSD YRLYSD YTLYSD YSLYSD YSLYSD YSLYSD YKLFTD YKLFTD	10 AGRTTPWGDGSNGGD-T AARSALIQANT-PVD SYNQPWNATP-TTG-V STRSTEIPLID-ATG SGRSLPWGDGG-ATGSV SGRATAWSSGANA AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AARSALIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-PVD AGRSLIQANT-P AGRSLIQANT-P AGRSLIQANT-P AGRSLIQANT-P	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GTAPPQL QSGTGT-GIATP IAIPAT-GNPQL USGVGT-GANVP LSGTGT-GANVP LSGTGT-GANVP ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN IPIIGT-GNPQA IAIPAT-GPQA IAIPAT-GPQA IAIPAT-GAVDS LTGTTDPTLGTN KA-STT-AGVDS LTEFTT-ATAQT	PL PLT \ PV PV PV PV PL PV PV - PV PV PV PV PV PV - PV PV PV - PV PV - PV PV -	Y GR VVPTGQ YAQVP - I	- EVPSVOT TO TVQVTVAW STPIPAG TY TDTL VT LVT IAW OTTPSVST IDTV IVTVW VMSPAAGAY TDT IAT IEW OTTPSVST VIDTV IVTVW - STPAVOTY IDTV IVTVW - TTPDPDTY NDTVTVTW STPIPAG TY TDTL VT IAW STPIPAG TY TDTL VT IAW - AI PAGTY TDTL VT IAW - AI PAGTY TDTL VX VIY - AI PAGTY TDTL VX VIY - VVVPG TY TDT INVXVIY - VTVVPG TY TDT INVXVIY - TSSTAGSY SDT IS VTLSW
PA14_61500/1-159 YPK 1778/1-161 Pacwa_1449/1-156 YPC_2119/1-161 YDAngola A2668/1-148 MDS_2707/1-156 PADK2_24695/1-156 PADK2_24695/1-159 PAM18_4745/1-159 PSPA7_5297/1-157 WSS_1337/1-156 EbC_38170/1-166 ROD_19381/1-166 A3UG_14090/1-166		TTSSTIA TGTYNVP TTFEYVNV PTTFEYVNV PTTFEYVNV PSAQAYVA - FAGAYVA TTSSTIA TTSSTIA TTSSTIA GGTQQIA - GGTQQIA - GGTYNVP SDATQGIA ADNTQGIA ADNTQGIA SDATTGIA SDAT	YNIYSD YNLFKD YRLYSD YNLFKD YNLFKD YNLYCD YNLYCD YNIYSD YNIYSD YRLYSD YRLYSD YFLYSD YSLYSD YSLYSD YKLFTD YDIYSD YRLYSD	10 AG RTTPWGDG SNGGD -T AARSAL IQANT -PVD STRSTE IPL ID -ATG -V STRSTE IPL ID -AT	120 LITTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP VSQVAT-GQVVT LSGTGT-GNNEE LIGTGT-GAAVP ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN NGTTDPVNCON LAIPAT-GNPQL NTGTTDPVNCON KA-STT-AGVON IA-STT-AGVON LTEFTT-ATAQT LSVTGD-GTEQT LSVTGD-GTEQT	- PL PLT ' PV PV PV PV PL PL PL PL PL PL YTL YTL YTL VTL EL VE	Y GR VVPTGQ2 YAQ VP - I YAR I AP ADQ T YAQ VP - I YAR VP - YAQ YGR VPTGQ2 YGR VVPTGQ2 YGR VVPTGQ2 YGR VVPTGQ2 AR I AP ADQ T YGR VGGGF Y YGR VGG Y YGR VG Y YGR VG Y YGR VG Y YGR VG Y YGR VG Y YGR YG Y YG YG YG Y YG YG YG Y YG YG YG YG YG YG YG YG YG YG YG YG YG	
PA14_61500/1-159 YPK 1778/1-161 Pocws_1449/1-156 YPC_2119/1-161 YPAncola A2668/1-164 M495 10245/1-155 PADK2_24695/1-159 PADK2_24695/1-157 WSS_133/1-156 EbC_38170/1-166 PAJ_2575/1-166 ROD_1938/1-156 PP1Y_M0)9658/1-152 PSER340/1-154 PpuL_3338/1-154		TTTSST A PTTFEVVN TTFEVVN PTTFEVVN PSAQQVS - AGAVVA TTGSTIA TTSSTIA TTSSTIA GGTQQIA TGTVNP BDATQGIA ADNTQQIA NTTQQVA SNGSEY IE -NGSVYIP SSNARP IP SSNARP IP	YNIYSD YNLFKD YNLFKD YNLYTN YNLYTN YNLYGN YNIYSD YNIYSD YRLYSD YRLYSD YRLYSD YSLYSD YSLYSD YSLYSD YSLYSD YLYTU YDIYSD YRLYRD YRLYRD	10 AGRTTPWGDGSNGGD-T AARSAL QANT-PVD STRSTEIPLID-ATG SSYNOPWNATP-TTG-V STRSTEIPLID-ATG YTSVIWDVVG GRSLPWGDGG-ATGSV SARATAWSSGAN-A AARSAL QANT-PVD AARSAL QANT-PVD AARSAL QANT-PVD STRSTEIPLIQANT-PVD STRSTEIPLIQANT-PVD STRSTEIPLIQANT-PVD STRSTEIPLIQANT-PU-T STRSTEIPLIANST-NL-T SGFSNVIANNT-PL-P SGFSNVVANNA-AL-P SDRNTQIVQNGL-T AAWROPLAVDV-AQS	LTTTGT-GTTQE USSTGT-GTAVE USSTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP IAIPAT-GNPQL USGTGT-GAVP ISSVST-GTAVN ISS	P L T Y P L T Y P V I V P V V P L Y P L Y P L Y P L Y Y P L Y Y P I Y Y T L Y Y E L F V P I Y L P L Y	Y GR VV PT GQ YAQ VP - I	- EVPSVGTYTDTVQVTVAW STPIPAGTYTDTLLVTIAW GTTPSVSTYIDTVIVTVTW VMSPAGAYTDTIATIEW GTTPSVSTYIDTVIVTW - STPAVGTYTDTVQVTVSW TPSPGTYTDTVQVTIAW STPIPAGTYTDTLLVTIAW STPIPAGTYTDTLLVTIAW STPIPAGAYTDTLLVTIAW SVNAPTADYDDIVTATLAW - AAIPAGTYTDTLIVTIAW - AVPAGTYTDTINVAVNY - PVIPAGTYTDTINVAVNY - VTVVPGTYTDTINVSVIY - VTVVPGTYTDTINVSVIY - SSTASSYSTISVILSW - AGLSPGTYDTISVILTF - WVPNAGTYADLLKVTVW
PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YDAnc00a A2668/1-148 MDS_2707/1-156 M495 10245/1-156 PADK2_24695/1-159 PADK2_24695/1-159 KOX_23780/1-157 KOS_217/1-156 PAL_2575/1-166 ROD_1938/1-166 A3UG_14090/1-166 M634_16995/1-156 PP1Y_M9680/1-152 PSEEN3400/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B9680/1-154 PpUZ_B998/1-154 PpUZ_B988/1-154 PpU		TTTSST A PTTFEYVN PTTFEVN PTTFEVN PSAQQVS AGAYVA AGAYVA AGAYVA AGAYVA AGAYVA AGAYVA AGAYVA AGAYVA 	YNIYSD YNLYSD YNLYNY YNLYN YNLYN YNLYN YNLYQD YNIYSD YNIYSD YNIYSD YRLYSD YRLYSD YTLYSD YSLYSD YSLYSD YSLYSD YSLYSD YSLYSD YSLYSD YSLYSD YRLYRD YRLYRD	110 AG RT T P WG DG SNG GD - T AARSAL I QANT - P VD ST NSTE I PL ID -A T G SS YN OP WNAT P -T TG - V AT YS V I WDD V TG - V AT YS V I WDD V TG - V ARSAL I QANT - P VD AARSAL I QANT - P VD AARSV NA - AA L - P SORNTOI VONG T A GF ST VL NNG S T AWROPL AVOV - A QS AAWROPL AVOV - A QS	120 LTTTGT - GTTQE ISSVST - GTAVN GGTGT - GIATP IAIPAT - GNPQL USGTGT - GNAVP USQVAT - GQVVT LSGTGT - GAAVP ISSVST - GTAVN ISSVST - G		Y GRVVPTGQ2 YAQVP-I YARIAPADD1 YAQVP-I YGRVPS-Q YGRVPS-Q YGRVVPTGQ2 YGRVVPTGQ2 YGRVVPTGQ2 YGRVVPTGQ2 YGRVVPTGQ2 YGRVVPTGQ2 YGRVVPTGQ2 GRUTGGGFI YGRVGGFF YGRVGGGFA ZAKAY-G ZARIDSLA YARIDSLA YARIDSLA YARIDSLA	- EVPSVOT TO TVQVTVAW STPIPTAG TY TDTL VTT AW OTTPSVSY IDTV IVTVW VMSPAGAY TDT IVTVW - STPAVGTY IDTV IVTVW - STPAVGTY IDTV IVTVW - TPSPOTY IDTV IVTVW - TPSPOTY TDTVQVT IAW - TPSPOTY TDTL VTI AW STPIPTAG TY TDTL VTI AW STPIPTAG TY TDTL VTI AW STAPTAVY DD I VTATL AW VMSPAAGAY TDT I TAT I EW - AA IPAG TY TDT IVAVNY - VTVVPGTY TDTI NVXNY - STSTAGSY SDT I SVTLF - WSPAGAY ADLL KVTVTW - AGLSPOTY DD I VTATLSW - WSPAGAY ADLL KVTVTW - WSPAGE VADL KVTVTW - WSPAGE VADL KVTVTW - WSPAGE VADL KVTVTW
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PA14_61500/1-159 YPK 1778/1-161 Pecwa_1449/1-156 YPC_2119/1-161 YDAnqola A2681/1-158 M495 10245/1-158 PADK2_24695/1-159 PADK2_24695/1-159 PADK2_24695/1-159 PSPA7 5297/1-159 KOX_23780/1-156 EbC_38170/1-166 PAJ_2575/1-166 ROD_13981/1-166 M634_16995/1-152 PSPEX_341/1-54 PPIU_288_11999/1-158 Ent038_2462/1-166 BBK_77/1-158		TTTSST A PTTFEYVN PTTFEVVN PTTFEVVN PTTFEVVN PSAQQVS - AGAYYA TAGAL IK TTTSST IA TTTSST IA TTTSST IA TTTSST IA AGGTQQ IA AGTQVA NGSVY IE NGSVY IE NGSVY IE NGSVY IE DSNARP IP DSNARP IP DRAGQVA SNAGQVA SNAGQVA SNAGQVA SNAGQVA SNAGQVA SNAGQVA	YNIYSD YNLYSD YNLYTN YNLYTN YNLYTN YNLYQD YNIYSD YNIYSD YNIYSD YRLYSD YSLYSD YSLYSD YSLYSD YSLYSD YSLYSD YRLYRD YRLYRD YRLYRD YRLYRD YRLYRD YRLYRD YRLYRD YRLYRD YRLYRD	110 AG RT T P WG DG SNG GD - T AARSAL I QANT -P VD ST NOL WNAT P -T TG - V ST RSTE I PL I D - A T - G SS VI D WD DV V TG - V AT Y SV I WD DV V TG - V AT Y SV I WD DV V TG - V AT Y SV I WD DV V TG - V ARSAL I QANT -P VD AARSAL I QANT -P VD ST RSTE I PL I D -A T ST RSTE I PL NST -N L - T ST RST ANN - N L - T SG FNN V ANN - A L - T AWROPL A VD V -A QS AAWROPL A VD V -A QS GG FNN I ANNA -P I - P SG RSV V PL M -P QS	120 LTTTGT-GTTQE ISSVST-GTAVN QSGTGT-GIATP IAIPAT-GNPGL QSGTGT-GAVP ISSVST-GTAVN	P L Y P L T Y - P T Y P Y L V Y P L Y Y P I Y Y P I Y L P L Y L P L Y L P L Y	Y GRVVPTGQ YAQVP - I	- EVPSVOT TO TVQVTVAW STPIPTAG TY TDTL VTU V VMSPAAGAY TDTL VTU VTW VMSPAAGAY TDTL IXT IEW OTTPSVST IDTV IVTVW - STPAVGTY IDTV IVTVW - STPAVGTY TDTVQVT IAW - TTPPDTV NDTV TMTV TW STPIPTAG TY TDTL VTI IAW STPIPTAG TY TDTL VTI IAW STPIPTAG TY TDTL VTI IAW - AA IPAG TY TDTL VTI IAW - AA IPAG TY TDTL VTI IAW - AA IPAG TY TDTL VVI VI - VVVPGTY TDTI NVA VNY - VTVVPGTY TDTI NVA VNY - TSSTAGS S SDT I SVTUSW - WVPAG I ADLL KVT VTW - WVPAG I ADLL KVT VTW - WVPAG TY TDTI NVSVTY - WVPAG TY TDTI NVSVTY - WVPAG TY DDL VTVTW - WVPAG TY DDL VTVTW - WVPAG TY DDL VTVTW - WVPAG TY TDTI NVSVTY - WVPAG TY TDTI NVSVTY
PA14_61500/1-159 YPK_1778/1-161 Pacwa_1449/1-156 YPC_2119/1-161 YDAngola A2668/1-164 MJS_2707/1-156 PADK2_24695/1-156 PADK2_24695/1-159 PSAT_527/1-159 PSAT_527/1-157 WS_133/1-166 PA1_2573/1-166 ROD_19381/1-166 A3UG_14090/1-166 MG34_16995/1-156 PP1Y_MpJ8588/1-152 PSEEN340/1-154 BP10268_11999/1-158 Ent638_2462/1-168 Aaau_1528/1-164		TTTSST A PTTFEVVN PTTFEVVN PTTFEVVN PTTFEVVN TTFEVVN TTFEVVN TTTSST A GGTQIA GGTQIA GGTQIA GGTQIA GGTQIA GGTQIA GGTQIA CGTVV DDA GGTQIA CGTV DDA GGTQIA CGT CGT CGT CGT CGT CGT CGT CGT	Y N 1 YSD Y N 1 FKD Y N 1 FKD Y N 1 FKT Y N 1 YQD Y N 1 YQD Y N 1 YSD Y R 1 YSD Y K 1 YSD Y K 1 YSD Y K 1 YSD Y K 1 YSD Y S 1 YSD Y N 1 YSD Y S 1 YSD Y N 1 YSD Y N 1 YSD Y S 1 YSD Y N 1 YSD Y S 1 YSD Y N 1 YSD Y S 1 YSD Y N 1 YSD Y N 1 YSD Y N 1 YSD Y S 1 YSD Y N 1 YSD Y Y 1 Y YSD Y Y 1 Y Y Y 1 YSD Y Y 1 Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y	10 AG RT T P WG DG S NG GD - T AAR SAL I Q ANT - P VD ST NG P MA T P -T TG - V ST RSTE I PL D - A T G O ST NO PWNAT P -T TG - V TTS VI WD DV V G G RSL P WG DG G - A TG - V AR SAL I Q ANT - P VD AAR SAL I Q ANT - P VD G F SN V ANN - P VD AWR PL AV QV - A QS AAWR PL AV QV - A QS AAR SAL Y P V PL M - P QS AAR SAL Y P V V - M - P QS AAR SAL Y V V - M V GS	LTTTGT-GTTQE USSTGT-GTAVE QSGTGT-GIATP IAIPAT-GNPQL QSGTGT-GIATP VSQVAT-GQVVT LSGTGT-GAAVP ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN ISSVST-GTAVN IAIPAT-GNPQL NTGTTDPVNCDN KA-STT-AGVDN IA-STA-GGVDS LSTTGD-GTSQT ARVPDS-G-SVE ARVPGS-G-SVE ARVPGS-G-SVE ARVPGS-G-SVE FLVDGG-RDDVT IAV-STT-GGIDS FLVDGG-RDPVT	P L P L T Y - P T Y - P Y P Y P L Y Y T L Y V P L Y L P L Y 	Y GRVPTGQ YAQ VP - I	- EVPSVG TYTDTVQVTVAW STPTPTAG TYTDTVQVTVAW OTTPSVST IDTVIVTVTV VMSPAGA YTDTIVATVTVW - STPAVG TYTDTVQVTVSW TPSPG TYTDTVQVTVSW TPSPG TYTDTVQVTVAW STPTPTAG TYTDTLVTIAW STPTPTAG TYTDTLVTIAW STPTPTAG TYTDTLVTIAW STPTPTAG TYTDTLVTIAW STPTPTAG TYTDTLVTIAW STPTTAG TYTDTLVTIAW STPTTAG TYTDTLVTIAW STPTTAG TYTDTLVTIAW STPTTAG TYTDTLVTIAW STPTTAG TYTDTLVTV - NASAG SVDTISVTISW - STVVPG TYTDTIVXVY - WVPRAG YADLLKVTVW - WVPRAG YADLLKVTVW - RAV-PSG TYEDLG ITLDW
PA14_61500/1-159 YPK 1778/1-161 Pecws_1449/1-156 YPC_2119/1-161 YPAnqola A2668/1-159 PADK2_24695/1-159 PADK2_24695/1-159 PADK2_24695/1-156 KOX_23780/1-157 WSS_133/1-156 EbC_38170/1-166 PA1_2575/1-166 ROD_1333/1-154 PP1Y_MD/9858/1-152 PSEEN3400/1-154 PP1Y_MD/9858/1-154 PP1Z268_11999/1-156 Eb1333/1-154 PP1Z268_11999/1-156 BBK_77/1-156		TTTSST A PTTFEYVN TTFEYVN PTTFEVN PSAQQVS - AGAYA - TAGAL K TTSST A TTSST A - TGTYNVP SDATQG A - TGTYNVP SDATQG A NTTGVA SNGSEY I E SNAGKI P SNAGKI P	YN I YSD YNL FKD YNL FKD YNL FKD YNL YKD YNL YQN YNL YQD YNL YSD YNI YSD YNI YSD YRL YSD YRL YSD YRL YSD YSL YSD YSL YSD YRL YRD YRL YRD YRL YRD YNVYRD YNVYRD YNVYRD YNVYRD YNVYRD	110 AGRTTPWGDGSNGGD-T AARSALIQANT-PVD SYNOPWNATP-TTG-V STRSTEIPLID-A	LTTTGT - GTTQE USSTGT - GTAVN GSGTGT - GIATP IAIPAT - GNPQL QSGTGT - GIATP IAIPAT - GNPQL USGTGT - GAVP ISSVST - GTAVN ISSVST - GGVDS LTEFTT - ATAQTD IAVPGS - GSVE FLVDGG - RDDVT IAVPSA - GSVE GSVGC - SVE	P L P L T Y P V P V P V P L - P	Y GRVPTGQ2 YAQVP-I YAQVP-I YGVPA-AA YGVPS-Q YGVPA-AA YGVPTGQ2 YAQVP	- EVPSVOT TO TVQVTVAW STPIPAGIN TO TVQVTVAW CTTPSVSTIDTV IVTVW VMSPAAGAY TO TI IATIEW OTTPSVSTIDTV IVTVW - STPAVOTY DIV VIVTVW - TTPOPDTY NDTVTVTW - TTPOPDTY NDTVTMVTW STPIPAGINT TDTL VTIAW STPIPAGINT TDTL VTIAW STPIPAGINT TDTL VTIAW STPIPAGINT TDTL VTIAW - TVYVPGTY TDTINVAVNY - AAIPAGINT TDTINVAVNY - AVPVAGINT TDTINVAVNY - AVVPGTY TDTINVAVNY - TSSTAGS STISTLSF - WVPAGINT DI INVAVNY - WVPAGINT TTINVAVNY - WVPAGINT TTINVAVNY - AGLSPGTY TDTINVAVNY - AGLSGTY TDTINVAVNY - AGLSGTY TDTINVAVNY - TSSTAGS STISTLSF - WVPAGINT TDTINVAVNY - TVVVPGTY TDTINVAVNY - TSSTAGS STISTLSF - WVPAGINT TDTINVAVNY - VTVVPGTY TDTINVAVNY - TSSTAGS STISTLSF - WVPAGINT TDTINVAVNY - VTVVPGTY TDTINVAVNY - VTVVPGTY TDTINVAVNY - TSSTAGS STISTLSF - WVPAGINT TDTINVAVNY - TSSTAGS STAGING - TVVPGTY TDTINVAVNY - VTVVPGTY TDTINVAVNY - VTVVPGTY TDTINVAVNY - VTVVPGTY TDTINVAVNY - VTVVPGTY TDTINVAVNY - VTVPGTY TD
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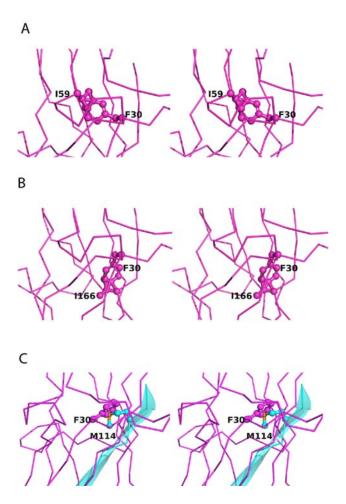
Alignment of sequences of single-domain subunits from the archaic pathway. Single-domain major subunit dataset derived from $\sigma 1$, $\sigma 2$, $\sigma 2/3$ and $\sigma 3$ family clusters is indicated in red, violet, orange and green, respectively. The sequences of single-domain subunits were analyzed with SignalP 4.1 to exclude secretion signal peptides. Structural-based sequence alignment was produced with the program *EXPRESSO* [http://tcoffee.crg.cat/apps/tcoffee/do:expresso]. The CsuA/Bsc structure was assigned as a template for the sequence dataset. The aligned sequences were annotated using the package JalView (6). Completely invariant residues are indicated with an asterisk, highly conserved regions are marked with a colon and residues essential for semi-conservation are dotted. Color-coding scheme of amino acid residues has been incorporated above conservation threshold according to their chemical properties: blue — hydrophobic, green — hydrophilic, red — basic and magenta — acidic. Conserved cysteine residues are colored in pink. Glycine residues are shaded in orange, proline in yellow, and aromatic residues in cyan. The secondary structure of CsuA/B is shown above the amino acid sequences. β -Strands and α -helices are depicted by arrows and bars, respectively, above the alignment table.



CfaA chaperone from the alternative pathway provides only partial information of the CfaB subunit folding. Cartoon representation of the chaperone-bound CfaB (left, PDB code 4Y2O) and CfaBsc (right, PDB code 3F83). Subunits are colored by B-factors. The chaperone G_1 and subunit Gd donor strands are colored in magenta and orange, respectively. The donor residues are shown as balls-and-sticks. The acceptor pockets P0-P5 are indicated and β -strands and N and C termini are labeled.

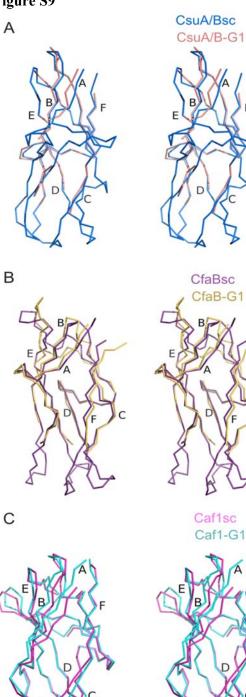
Figure S7





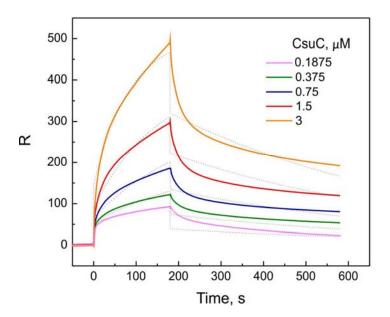
If the double-hairpin were ordered in the CsuC-CsuA/B complex, side chain of Phe30 would form steric clashes with residues of either CsuA/B or CsuC in any of its possible rotamer conformation. Fragments of the CsuA/Bsc structure (A and B) and the CsuA/Bsc and CsuC-CsuA/B superposition as in Fig. 4C, but with only CsuA/Bsc and donor strand G₁ shown for clarity (C) (ribbon representation, stereo view). Phe30 in three possible rotamer conformations: t30 with 33% probability (A), p90 rotamer with 13% probability (B), and m30 rotamer with 9% probability (C) and residues with which it collides (labeled) are shown as balls and sticks.





Superpositions of the chaperone-bound and self-complemented pilin subunits (ribbon diagrams, stereo views). A. Archaic system. The chaperone-bound and self-complemented CsuA/B are shown in pink and blue, respectively. B. Alternative system. The chaperone-bound and self-complemented CfaB are colored yellow and purple, respectively. C. Classical system. The chaperone-bound and self-complemented caf1 are colored cyan and magenta, respectively.





Association and dissociation kinetics of CsuC and CsuA/B. A Biacore X100 system (Biacore, GE Healthcare, Uppsala, Sweden) was used for biosensor experiments. The purified CsuC:CsuA/B complex carrying a His-tag on CsuA/B (0.075 μ M) was loaded on an NTA sensor chip. CsuC was removed from the chip by continuous washing of the chip with loading buffer. To minimize the time for CsuA/B aggregation on the chip, we immediately performed binding experiments. Resonance signals were plotted as a function of time for several concentrations (0.138 – 3 μ M) of CsuC. The association phase was followed through 180 s after which time infusion of the soluble CsuC was stopped, and the dissociation phase in continuous buffer flow was monitored for an additional 400 s. The chip was regenerated at each cycle of the experiment. The software supplied with the device was used to determine the *k-on* and *k-off* rate constants assuming a 1:1 binding model. The model accounted for the balk effect observed in the data.

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