Supplementary Information

Supplementary Table S1. Properties of the characterized cluster A-I solute binding proteins.

Protein	Organism	Ligand	PDB codes	UniProtKB code	References	ко	Sites	Kd	Binding site 1 st coordination sphere	Flexible loop	Gra m
ZnuA	Acinetobacter baumannii	Zn ²⁺	Not found	B0VNJ6	[1,2]	Zn[2]	nd	nd	nd	nd	-
ZnuA (YcdH)	Bacillus subtilis	Mn ⁺²	201E	O34966	Unpublished [3]	Zn[4]	nd	nd	His2(His51 and His128)/ Glu1(Glu267)	Length: 16 a.a 5 histidines	+
ZnuA	Brucella abortus biovar 1	Zn ²⁺	Not found	Q576K1	[5]	Zn[5]	nd	nd	nd	nd	-
ZnuA2	Candidatus Liberibacter asiaticus str. psy62	Mn ⁺² Mn ⁺² (mut) Cd ⁺² Zn ⁺² Apo Apo (mut)	4UDO, 4CL2 5ZHA, 5Z2K 6IXI 5AFS 4UDN 5Z35, 5Z2J	C6XF58	[6-9]	nd	1	Zn:430uM Mn:370uM [10]	His2(His39, His106) Asp:(Asp247) Glu:(172) H-bond: asp and arginine	No loop.	-
ZnuA	Campylobacter jejuni	Zn ²⁺	Not found	Q0PBZ4	[11]	Zn[11]	nd	nd	nd	Length: 14 a.a. 8 histidines	-
YtgA	Chlamydia trachomatis	Fe*3	6NSI	Q9S529	[12]	nd	1	nd	His3(His75, His141, His207) Asp1(299)	No major loop structure The loop connecting alpha 9 and B6 on the surface of the C- terminal domain dwells directly above the Fe(III)	-
ZnuA	Escherichia coli	Zn ⁺² Co ⁺² Apo	2OSV, 2OGW, 2PS0 2PRS 2PS9 2PS3	P39172	[13] [14] [15]	Zn[16]	2	Zn: < 20 nM [15]	His ³ (His78, His161, His225) Glu:(Glu77).	Length: 21a.a 6 histidines	-
ZnuA (PZP1)	Haemophilus influenzae Rd KW20 (serotype d)	Zn ²⁺	Not found	P44526	[17]	Zn[17]	nd	nd	nd	Length: 50 a.a. 25 hisitidines[18]	-
Lmo1671	Listeria monocytogenes EGD-e	unknown	Not found	Q8Y6L3	none	nd	nd	nd	nd	Loop with histidines[19]	+
MntA	Listeria monocytogenes EGD-e	Cd ⁺² Mn ⁺² Apo	5JPD 5I4K 5HX7	Q8Y653	Unpublished[20]	nd	nd	nd	His ₂ (His67, His140) Glu1(206) Asp1(281)	No loop	+
ZinA	Listeria monocytogenes	Zn ²⁺	Not found	Q8YAH3	[21]	Zn[21]	nd	nd	nd	nd	+
MntC	Neisseria gonorrhoeae	Zn ²⁺ Mn ²⁺	Not found	B4RIV9	[22]	Zn, Mn[22]	1	Zn ²⁺ : 104 ±5 nM Mn ²⁺ : 100±8 nM[22]	nd	Histidine rich loop[22]	-
AztC	Paracoccus denitrificans	Zn ⁺² Zn ⁺² (mut) Apo	5W57 5KZJ 5W56	A1B2F3	[23]	Zn[24]	1	Zn: 0.3 ± 0.1 nM[24]	His3(His61, His138, His204) Asp1(279)	Length: 15 a.a 3 histidines	-
ZnuA	Paracoccus denitrificans	Zn ²⁺	Not found	A1B9L0	[24]	Zn[24]	5	Main binding site Zn: 1nM [24]	nd	Length: 38 a.a. 15 Histidines	-
ZnuA	P. aeuroginosa PAO1: PA5498	Zn ²⁺	Not found	Q9HT75	[18]	nd	2	Zn: 22.6±6.4 nM[18]	His3(His60, His140 and His204)	Length: 15 a.a. 5 Histidines	-

									Water molecule Based on homology[18]		
ZnuA	Salmonella enterica subsp. enterica serovar Typhimurium	Zn ⁺² Zn ⁺² /PH Apo (mut)	2XQV, 2XY4 4BBP 2XH8	Q8ZNV8	[25,26]	Zn[27]	2	1 st site: <20nM 2 nd site: uM range[28]	His3(His140, His147, His211) Glu ₁ (Glu59)	Length: 21a.a 3 histidines	-
SitA	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2	Аро	5JG7	Q7CPX8	Unpublished[29]	nd	nd	nd	nd	Length: 11 a.a No histidines	-
MntC	Staphylococcus aureus	Fe ³ /co structure with mAB 305-78-7 Zn ⁺² Mn ⁺² Apo/anta gonistic fab fragment	5HDQ 4NNO 4K3V 4NNP	A0A0H3JT S7	[30-32]	Mn[33]	1	Mn*2:~4 nM[32]	Mn ⁺² /Fe ⁺³ His2(His50, His123) Asp ₁ (Asp264) Glu ₁ (Glu189) Zn⁺²: His2(His67, His140) Asp ₁ (Asp281) Glu ₁ (Glu206)	No major loop structure Peptides 28-51 and 37-51 include a flexible loop with one of the four Mn+2 coordinating residues :H50 residues covered by peptides 111- 125 and 111-126. They include another flexible loop and another Mn2+ -coordinating residue, H123	+
SitA	Staphylococcus pseudintermedius	Zn ⁺² Mn ⁺²	4OXQ 4OXR	NCBI WP_014614 644.1	[34]	nd	1	Mn ⁺² and Zn ⁺² : Low nM range.[34]	His2(His64, His137) Glu1(Glu203) Asp1(Asp278)	No Loop	+
SitA	Sinorhizobium meliloti	Mn ²⁺ Fe ²⁺	Not found	F7XAF4	[35]	Mn, Fe(II)[35]	nd	nd	nd	nd	-
Lmb	Streptococcus agalactiae NGBS572	Zn ⁺² Zn ⁺² (mut)	3HJT 4H0F	Q9ZHG8	[36],[37]	Zn[38]	nd	nd	His ³ (His66, His142 and His206). Glu ₁ (Glu281).	Length: 12a.a No histidines Residue range: 124-135	+
AdcA	Streptococcus agalactiae A909 serotype Ia	Zn ²⁺	Not found	Q8E128	[38]	Zn[38]	nd	nd	3 Histidines 1 Glutamate Predicted from sequence homology. [39]	Length: 11 a.a. 6 Histidines	+
PsaA	Streptococcus pneumoniae	Apo Mn ⁺² Zn ⁺² Cd ⁺²	3ZK8 3ZK7 3ZK9 3ZKA 3ZTT 1PSZ 4UTO 4UTP	P0A4G2	[39-41]	Mn[42]	nd	231 nM Zn, 3.3 nM Mn[43]	His2(His67, His139) Glu205 Asp280	7 a.a No histidines Residue range: 129-135	+
AdcA	Streptococcus pneumoniae	Zn ²⁺	Not found	Q8CWN2	[44,45]	Zn[45]	2	Zn ⁺² : High Affinity site: 4±0.1 nM Low Affinity Site: 228±88 nM[46]	His ₃ (His63, His140, His204) Glu ₁ (Glu279) Based on homology.[46]	Histidine Rich Loop is present.	+
AdcAII (Lmb)	Streptococcus pneumoniae	Zn+2	3CX3	Q8DQ09	[19]	Zn [45]	nd	nd	His ³ (His71, His147, His211) Glu ₁ (Glu286)	Length: 13 a.a No histidines Residue range: 129-142	+
MtsA	Streptococcus pyogenes	Fe ⁺³	3HH8	P0A4G4	[46]	Mn, Fe[47,48]	1	4.3 μM Fe(II)	His2(His68, His140)	No loop	+

								50 µM Mn	Glu1(Glu206)		
									Asp1(Asp281)		
Lmb (Lbp)	Streptococcus pyogenes Serotype M1	Zn ⁺²	3GI1	Q99XV3	[49]	Zn[50],[51]	1	nd	His3(His66, His142, His206) Glu1(Glu281)	Length: 15 a.a. No histidine Residue range: 123-137	+
TroA	Streptococcus suis	Zn+2	3MFQ	A4VY63	[52]	Mn[53]	1	434nM Zn 254nM Mn[53]	His3(His76, His139, His205) Asp1(Asp289)	Length: 4a.a Residue range: 126-129	+
ZnuA	Synechocystis sp. PCC 6803 substr. Kazusa	Zn ⁺² Zn ⁺² (mut) Apo (mut)	1PQ4 2OV3 2OV1	P73085	[54,55]	nd	4	7 nM, 9 μM Zn[55]	His3(His83, His179, His243) Water molecule	Length: 34 a.a 8 histidines	-
MntC	Synechocystis sp. PCC 6803	Mn ⁺² Mn ⁺² (mut) Zn ⁺² , Mn ⁺²	1XVL 4IRM 3UJP	Q79EF9	[56,57]	Mn[58]	nd	nd	His2(His89, His154) Glu1(Glu220) Asp1(Asp295)	No loop	-
TroA	Treponema pallidum	Zn ⁺² Apo	1TOA 1K0F	P96116	[59,60]	nd	1	23nM Zn 7.1nM Mn[61],[62]	His3(His68, His133, His 199) Asp1(Asp279)	4a.a No histidines	-
VC_2081 (ZnuA)	Vibrio cholerae	Zn ²⁺	Not found	Q9KQB9	[63]	Zn[63]	nd	nd	nd	nd	-
VC_2552 (ZrgA)	Vibrio cholerae	Zn ²⁺	Not found	Q9KP27	[63]	Zn[63]	nd	nd	nd	nd	-
YfeA	Yersinia pestis	Zn ⁺² Fe ⁺³ Mn ⁺² Apo	5UXS 5UXU 5UY0 6Q1D 5UYG 5UYD 5UYA 5UYW 5UYV 5UY4 5UYV 5UY4 5UYE 5UYB 5UY5 5UYH 5UYF 5UYC 6Q1C	Q56952	[64-65]	Fe[66]	2	17.8 nM Mn, 6.6 nM Zn[67] Iron nd	His2(His76, His141) Glu(207(holo), Glu256(apo)) Asp1(Asp282)	Length: 21 a.a. Residue range: 119-140	-
ZnuA	Yesinia pestis	Zn ²⁺	Not found	Q8ZEU2	[67,68]	Zn[67]	nd	nd	Hiss(His62, His153, His217) Water molecule Based on homology modeling.[69]	Histidine Rich loop present.	-

Strain/plasmid	Genotype/ description	Source
PD1222	<i>P. denitrificans</i> Wild-type, Rm ^r	A gift from Dr. Stephen Sprio UT Dallas
	PD1222 mutant, $\Delta aztC$, Rif ^r	[24]
	PD1222 mutant, ΔznuA, Rif ^r	[24]
	PD1222 mutant, $\Delta aztC$, $\Delta znuA$ Rif ^r	[24]
	PD1222 mutant, ΔD -loop <i>aztC</i> , $\Delta znuA$, Rif ^r	This work
	PD1222 mutant, ΔZ -loop <i>aztC</i> , $\Delta znuA$, Rif ^r	This work
	PD1222 mutant, ΔD -loop <i>znuA</i> , $\Delta aztC$, Rif ^r	This work
	PD1222 mutant, $\Delta aztC \Delta znuBC$, Rif ^r	This work
	PD1222 mutant, $\Delta znuA \Delta aztBA$, Rif ^r	This work
S17-1	<i>E. coli,</i> with derivative RP4 plasmid integrated, for incorporation of plasmid constructs into <i>P. denitrificans.</i>	A gift from Dr. Stephen Sprio UT Dallas
PRK2013	<i>E. coli</i> with pRK2013 plasmid, which contains transfer system RK2 for mobilization of non-self-transmissible plasmids	A gift from Dr. Stephen Sprio UT Dallas
Plasmids		·
pK18mobsacB	Gene replacement vector, sacB, Km ^r	
	pK18mobsacB, with upstream and downstream 600bp flanking sequences of <i>D-loop</i> from <i>aztC</i> , Km ^r	This work
	pK18mobsacB, with upstream and downstream 600bp flanking sequences of <i>Z</i> -loop from <i>aztC</i> , Km ^r	This work
	pK18mobsacB, with upstream and downstream 600bp flanking sequences of <i>loop</i> from <i>znuA</i> , Km ^r	This work
	pK18mobsacB, with upstream and downstream 600bp flanking sequences of <i>znuBC</i> , Km ^r	This work
	pK18mobsacB, with upstream and downstream 600bp flanking sequences of <i>aztBA</i> , Km ^r	This work

Supplementary Table S2. Strains used in this study.

Primer	Primer sequence 5' to 3'
UP600aztAB_FWD	gaaacagctatgacatgattacgaacctcgggtcggatccgg
UP600aztAB_REV	cgatgcggaagagccagtctttcatcactggatagcggactc
DWN600aztAB_FWD	caaaatatcgagtccgctatccagtgatgaaagactggctcttc
DWN600aztAB_REV	gaggatccccgggtaccgagctcgaacacggtgcggcggtcttg
UP600znuBC_FWD	cagctatgacatgattacggggttatatcaccatccagacgctgc
UP600znuBC_REV	caccgaggccggcctgtgacctacgtatcggagcgggcgg
DWN600znuBC_FWD	tttccgcccgctccgatacgtaggtcacaggccggcctcggtg
DWN600znuBC _REV	atccccgggtaccgagctcgacgacgggaatatcggtcacc
UP600Loop_znuA_FWD	ctatgacatgattacggcccatggcgcgatgcgatt
UP600Loop_znuA_REV	catgaggatcggtgccggcatagtcccggcgatgcg
DWN600Loop_znuA_FWD	catcgccgggactatgccggcaccgatcctcatgcct
DWN600Loop_znuA_REV	ccgggtaccgagctcgtgaaagcgaaaaggcgggc
UP600D-Loop_aztC_FWD	gctatgacatgattacgcggcgcggttctgggtgaacg
UP600D-Loop_aztC_REV	tggggatcatgcgcgccgccgccgccgcccgctcc
DWN600D-Loop_aztC_FWD	gagccgggcggcggcgcgcgcatgatccccatgcc
DWN600D-Loop_aztC_REV	ccgggtaccgagctcggtctccttgatggggttcggggg
UP600Z-Loop_aztC_FWD	ctatgacatgattacgcaggcggaaccgctggacg
UP600 Z-Loop_aztC_REV	cacatcggccgcagcggcctgcggcgacaggaaatgcac
DWN600Z-Loop_aztC_FWD	tttcctgtcgccgcaggccgctgcggccgatgtg
DWN600Z-Loop_aztC_REV	cgggtaccgagctcgacgagatgccgctgcggatgaact
znuA_RT-PCR_FWD	actatcatatgatccgaccttcttccctt
znuA_RT-PCR_REV	actatggtaccctagtcagccccaagg
znuB_RT-PCR_FWD	ttatttcctgcaaaccact
znuB_RT-PCR_REV	atgcttgacgatttcctga
znuC_RT-PCR_FWD	tcaatgcggatgggcgca
znuC_RT-PCR_REV	gtgacgccgctgatttgc
aztA_RT-PCR_FWD	atgcccagaaccgatccga
aztA_RT-PCR_REV	tcacgccacccctctgac
aztB_RT-PCR_FWD	atggtcgacggggtcgt
aztB_RT-PCR_REV	tcaggccgtccgatgat
aztC_RT-PCR_FWD	atgaaagactggctcttccgc
aztC_RT-PCR_REV	gaaatctggtcagcgggc

Supplementary Table S3. Primers used in this study.



850 bp 650 bp

Supplementary Figure S1. RT-PCR of full-length ABC transporter genes from WT and hybrid transporter strains.

znuC: 765 bp

znuB: 783 bp

aztC: 939 bp

V.cholerae VC2552/25-242
C.jejuni_ZnuA/29-296
Synechocystis ZnuA/46-334
L.monocytogenes_Lmo1671/33-315
S.agalactiae_AdcA/29-311
S.pneumoniae_AdcA/26-307
B.subtilis_ZnuA/34-315
L.monocytogenes_ZnuA/32-312
S.pneumoniae_AcdAII/35-310
S.agalactiae_Lmb/30-305
S.pyogenes_Lmb/30-305
S.aureus_MntC/30-308
L.monocytogenes_MntA/30-308
S.pyogenes_MtsA/31-308
S.pneumoniae_PsaA/30-307
Ca.L.asiaticus_ZnuA2/21-293
Synechocystis_MntC/52-322
Y.pestis_YfeA/39-309
S.enterica_SitA/27-297
S.meliloti_SitA/29-299
Rhizobium/Agrobacterium_TroA/24-294
N.gonorrhoeae_MntC/19-302
P.denitrificans_AztC/24-306
Rhizobium/Agrobacterium_ZnuA/26-324
C.trachomatis_YtgA/38-320
S.suis_TroA/40-316
T.pallidum_TroA/32-306
A.baumannii_ZnuA/17-274
P.denitrificans_ZnuA/22-323
B.abortus_ZnuA/24-332
P.aeruginosa_ZnuA/23-304
V.cholerae_VC2081/21-294
H.influenzae_ZnuA/20-335
1.pestis_znuA/25-317
E. col1_ZnuA/23-307
S.enterica_ZnuA/42-330

	1 10 2	0 30	40	50
	SDHQHRQHEAHVHGQVELN	IAQDGHDLLLEI	TAPGADVVGFEHAPODDA.	
	TSSNLVSVSIAPQAFFIKK ADAMDITVSIPPOOYFLEK	IAANTLDVNVIL IGGDLVRVSVLV	. PPNSNEHNFEFKPSTMKK . PGNNDPHTYEPKPOOLAA	LEKSDIYFTIGLEFEKVF LSEAEAYVLIGLGFEOPW
15	SDOLTVYTTVYPLOYLTEO	IGGKYVDVHSIY	. PPGSDAHSFEPTOKOMMK	IADSDLFFYIGLGMEGF
	DGKLNIVTTFYPVYEFTKQ	VAGDTANVELLI	. GAGTEPHEYEPSIKNIAA	IQDADTFVYENENMETW
	GDKLHVVTTFYPMYEFTKQ KDKLKVVTTFYPMYDETKN	IVKDKGDVDLLI	. PSSVEPHDWEPTPKDIAN	IQDADLFVYNSEYMETW TEAADVEVYNSEDME
	GKGMKIVTSFYPIYAMVKE	VSGDLNDVRM.I	.QSSSGIHSFEPSANDIAA	IYDADVFVYHSHTLESW
	TQGMSVVTSFYPMYAMTKE TOGMSVVTSFYPMYAMTKE	VSGDLNDVRM.I VSGDLNDVRM.I	. QSGAGIHSFEPSVNDVAA . OSGAGIHSFEPSVNDVAA	IYDADLFVYHSHTLEAW IYDADLFVYHSHTLEAW
	NĞKLKVVTTNSILYDMAKN	VGGDNVDIHSIV	. PVGQDPHEYEVKPKDIKK	LTDADVILYNGLNLETG.NGW
	SDKLKVVATNSIIADMTKA	IAGDKIDLHSIV	. PIGQDPHEYEPLPEDVEK	TSNADVIFYNGINLEDGGQAW
	GOKLKVVATNSIIADITKN TOKKVVISSESIIGDITON	IAGDKIDLHSIV	. PIGODPHEYEPLPEDVKK	TSEADLIFYNGINLETGGNAW
	EĚKKKVLTTFTVLADMVŎN	VAGDKLVVESIT	. RIGAEIHGYĚPTPSDIVK	AQDADLILYNGMNLERW
	KEKFKVITTFTVIADMAKN	VAGDVAVVESIT	. KPGAEIHDYQPTPRDIVK . KPGAEIHEYOPTPGDIKR	AQSADLILWNGMNLERW
124 204	AEKLKAVTTFTVIADMAQN	VAGDAAVVESIT	. KPGAEIHNYQPTPRDILK	AĤDADLILWNGLNLELW
/24-294	AAPLPVVTSFSILGDVAKQ	IGGERVAVQSLV.	. GANQDTHAYHMTSGDIKK	IRSAKLVLLNGLGLEAA
/26-324	AEPLDVVATFSIIGDFAAK	VGGDRIRLNVLV	. GPD SD THVYEP RPADAIA	LAGADVVLTNGLEFEGF
, 20 524	DESIYVLSMNRMICDCVSR	ITGDRVKNIVLI	. DGAIDPHSYEMVKGDEDR	MAMSQLIFCNGLGLEHS AS
	G. KPLVVTTIGMIADAVKN	IAGDEVERDLLI IAOGDVHLKGLM	. GPGVDPHLYVAKSSDLSK	LOKADLVLYHGLHFEGK LGNADLILYNGLHLETK
	GWSQGLVVSTHPIYLIAKE	ITRGVEEPQLLL.	.Q. GQSGHDVQLTPAHRKA	INDASLVIWLGKAHEAP
	GEREGVVVSIKPLHSIVSA	VMQGVGKPKLIV	.QGAGSEHVYSLKPSDAEA	IEHAKVIFWAGPSMETF
	RAEVSVLTSIKPLQLVAAA ASAIEVLTSIKPTOMITYE	IQDGVGQPDVLL	. PPGASPHQYALRPSDVRR PSGASPHDYALRPSDVKR	LREVQLFYWIGPDLENF
	MANADVLASVKPLĞFIVSS	IADGVTGTQVLV	. PAGASPHDYNLKLSDIQK	VKŠADLVVWIGEDIDSF
	AADAAVVASLKPVGFIASA	IADGVLPIEVLL	. PDGASEHDYSLRPSDVQR	LONADLVVWVGPEMEAF
	AADAAVVASLKPLGFIASA	IADGVTDTQVLL.	. PDGASEHDYSLRPSDVKR	LQGADLVVWVGPEMEAF
	60 LRKALRTTHHPRKIM	70, 80, AUSDKAOCEKREVI	90 100	110 EEHEHOHGEGEHDHKAHD
	60 LEKALETLHHPEKLF TDKFKQNFS.KLQVV	70 80 ALSDKAQCEKREVI NMOKNIALIQTH	90 100 .IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSHE
15	60 LERALETTHHPEKLF TDKFKQNFS.KLQVV LEKLKAANA.NMKLT VDKAKKTLANEV	70 80 ALSDKAQCEKREVI NMQKNIALIQTH DSAQGITPLEME TFVPTAEKLDLP	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSH.E. KHDHSHGEEG KDPDAAE
15	60 LERALETTHHPEKLF TDNFF(ONFS.KLQVV LEKLKAANA.NMKLT VDKAKTLANEHV VPKVAKSVKSKV VPKVANSVKSKV	70 80 ALSDKAQCEKREVI NMQKNIALIQTH DSAQGITPLEME TFVFTAEKLDLP TTIKGTGDMLLT KTIVATEDMLLT.	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSH.E. KHDHSHGEEEG KOPDAAE KGVEEGG
15	50 LEKALETLHHPEKLF TDKFRONFS.KLQVV LEKLKANA.NM.KLT VDKAKKTLANEHV VPKVARSVKSKKV VPKULDTLDKKKV VPSARKSMGQGHA	70 80 ALSDKAQCEKREVI DSAQCITPLEME. TFVPTAEKLDLP. TTIKGTGDMLLT. KTIKATGDMLLL.	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD ,DTHEHSH.E. ,K.HDHSHGEEEG ,KDPD,AAE ,KQVEEEG ,PGGEEEH
15	50 LERALETIHHPEKLF TDKFKQNFS.KLQVV LEKLKAANA.NM.KLT VDKAKTLANEHV VPKVAKSVKSKKV VPKULDTLDKKKV VPSAEKSMGQGHA VPSVLKSLDSKKL	70 80 ALSDKAQCEKREVI NMQKNIALIQTH. DSAQGITPLEME. TFVPTAEKLDLP. TTIKGTGDMLLL. KTIKATGDMLLL. VFVNASKGIDLM. TVIDASKGIDLU.	90 100 .IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD , DTHEHSHE. , K.HDHSHGEEEG , KDPD, AAE , KGVE, EEG , PGGE, EEH , EGTE, EEH , EGTE, EEH , EGTE, EEH
15	60 LERALETIHHPEKLF TDKFFKONFS.KLQVV LEKLKAANA.NM.KLT VDKAKTIANEHV VPKVAKSVKSKK.VV VPKULDTIDKKK.VV VPSAEKSMGQGH.AA VPSVLKSIDSKK.VV ACSLDDNIKKSK.VV ARDIDDNIKKSK.VV	70 BQ A[]SDKAQCEK[REVI NMOKNIALIQTH- DIAQGITPLEME. TFUTKGTGDMLLT. KTIKATCDMLLT. KTIKATCDMLLT. TVIVASKGIELV. TVILEASEGMTLE. DIVEASKDIELD.	90 100 .IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSH.E .K.HDHSHGEEG .KDPD.AAE .KGVE.EEG .PGGE.EEG .EGSE.EEH .EGTE.EEH .RVFG.LED .RVFG.LED
15	60 LEKALETIHHPEKLF TDK/FKONFS.KLQVV LEKLKANAN.MM.KLI VDKAKTLANEHV VPKVAKSVKSKK.VV VPKVAKSVKSKK.VV VPSAEKSMGQGH.A VPSVLKSLDSKK.LL AGSLDPNLKKSK.VV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV	70 BC BC BC BC BC BC BC BC BC BC	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSHE K.HDHSHGEEG KDPD KGVEEG PGGEEEE EGSEEEH EGTEED RVVGLED RVKGLED GVKGLED
15	60 LEKALETIHHPEKLF TDKFFKONFS.KIQVV LEKLKANA.MM.KI VDKVAKSVKSKKV VPKLLDTLDKKKV VPKLLDTLDKKKV VPSLKSLDSKKL AGSLDPNLKKSKV ARDLDPNLKKSKV ARDLDPNLKKSKV FCKALEOAGKSLKD.KKVI FDRMLETADKSFEDKNOVV	70 ALSDKAQCEKREVI NMOKNIALIQTH. TPVPTAEKLDLP. TPVPTAEKLDLP. TPVPTAEKLDLP. TPVTAEKLDLP. TPVTAEKLDLP. TVTTAEKEDKLL. VPVNASGIDLM. VFVNASGIDLM. VFVNASGIDLM. NVLEASEMTLE. DVFEASENTILD. DVFEASKPITLD. DVFEASKPITLD. NSSDKIPVIL.	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSHE. K.HDHSHGEEG KDPDAAE KGVEEEG FGEEEE EGSEEEH RVPGLED RVKGLED RVKGLED RVKGLED EGS
15	59 LEKALETIHHPEKLF TDKFKQNFS.KL.QVV UKAKATLANA.NM.KLT VDKAAKATLANBH.VV VPKVAKSVKSKK.VV VPKULDTLDKKK.VV VPSAEKSMGQGH.A VPSVLKSLDSKK.LL ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV FEKALEQAGKSLKD.KVV FEKLALEQAGKSLKD.KVV FTKLVNNAQKYKN.KDYF TKLVNAQKYKN.KDYF	70 80 ALD SDKAQCEK (REVI NMQKNIALIQHME. TFVPTAEKLDLP TFVPTAEKLDLP TFVPTAEKLDLP TVTAEKGENLLT TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELV TVTDASKGIELS SGKYKPKILT AVSDGUVVIILE	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSHE K.V.HDHSHGEEEG KDPDAAE KGVEEEE EGSEEEE EGSEEEE RVPGLED RVKGLED RVKGLED GEEG. EKK.G GA.S. GQ.N
15	EQ LERALETLHHPEKLF TDKFFKONFS.KLQVV LEKLKANA.NM.KLT VDKAKKTLANEHV VPKVARSVKSKKV VPKULDTLDKKKV VPSAEKSMGQGH.AA VPSVLSLDSKL AGSLDPNLKKSKV ARDLDPNLKKSKV ARDLDPNLKKSKV FEKALEQAGKSLKD.KKVI FTKLVKNAQKTKN.KDYF YMKVFTNLKKGTKIT FMLFTNLKKGTKIT FMCFTNLKKGTKIT	70 80 ALSDKAQCEKREVI NMQKNIALIQTHA TFVPTAEKLDLP TFVPTAEKLDLP TFVPTAEKLDLP TFVFTAEKLDLP TFVTAEKCDLM TVIDASKGIELV TVIDASKGIELV NVFASKPITLD AVSKOVKPITLN AVSKOVKPITLN AVSGUVVITLE LSKGVKPKILT AVSDGUVTILE	90 100 .IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSH.E. K.HDHSHGEEEG KDPD.AAE C.KCVE.EEG PGGE.EEE EGSE.EEH EGTE.EEH RVKG.LED RVKG.LED RVKG.LED GEEG GA.S. GQ.N EDTS. DGP.
15	50 LE RALET LHHPE KLF TDKFF (NFS .KL QVV LEKLKAANA .NM .KLT VDKAKKTLANEH V VPKVAKSVKSKK V VPKULDT LDKKK V VPSAEKSMGQGH A VPSVLKSLDTKK V AGSLDPNLKKSK V ARDLDPNLKKSK V ARDLDPNLKKSK V FEKALEQAGKSLKD.KKVT FTKLVKNAQKTKN .KDYF TKLVKNAQKTKN .KDYF YMKYFTNLKKGT KIT FEQFLCWK.DV PSV FEKFFSIK.DV PSV FEKFFSIK.DV PSV	70 80 ALS DKAQCE KREVI NMG KNIALIQTH. TFT LEME. TFT LKGT GDM LLT. TFT LKGT GDM LLT. TFT LKGT GDM LLT. TFT DAS KGT ELV. TFT DAS KGT ELV. TFT DAS KGT ELV. DVF EAS KPT TLD. AVS KDV KPT YLN. AVS GC DV TY LLE. TFT DG LNPIGVS. TFT TFT DE LS. TFT DE LS CAS KPT TLD. AVS GC DV TY LLE.	90 100 .IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD , DTHEHSH.E , K.HDHSHGEEEG , KDPD, AAE , KGVE, EEG , PGGE, EEG , CGE, EEH , EGTE, EEH , RVKG, LED , RVKG, LED , CGA.S, , GA.S, , GQ.N, , EGP, , EGP, , EGP, , EGP,, , CGP,, , CGP,, , CGP,, , CGP,, , CGP,, , CGP,, , CGP,, , CGP,, , CGP,, , CGP,,, , CGP,,,, , CGP,,,,,,,
15	50 LE KALETIHHPEKLF TDKFK (NFS.KLQVV LEKLKAANA.MM.KLI VDKAKTIANEHV VPKVAKSVKSKKV VPKULDTIDKKKV VPSLLDTIDKKKV VPSLLDTIDKKSV AGSLDPNLKKSKV ARDLDNLKKSKV ARDLDNLKKSKV FEKLEADKSELKONVV FTKLVKNAQKTEN.KDYF FTKLVKNAQKTEN.KDYF FTKLVKNAQKTEN.KDYF FTKLVKNAQKTEN.KDYF FTKLVKNACKTEN.KDYF FTKLVKNACKTEN.KDYF FTKLVKNACKTEN.KDYF FTKLVKNACKTEN.V.PSA FARFYCHLS.GV.PCV	70 BO ALSDKAQCEKREVI NMOKNIALIQTHA TFTPIKEKLDLP TFTPIKEKLDLP TFTFKGTGDMLLT KITKATGDMLLT TKITASGENLUT TKITASKGTELV TKITASKG	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSH.E .K.HDHSHGEEEG .KDPD.AAE .KGVEEEG .PGGEEEE .EGSEEEH .EGTEEE .RVKG.LED .RVKG.LED .RVKG.LED .GEEGEEG .GA.S .GQ.N .EDTS .DGP .EGP .EGP .EGP
15 /24-294	60 LE KALETIHHPEKLF TDKFKQNFS.KLQVV LEKLKAANA.MM.KLI VDKAKTIANEHV VPKVAKSVKSKKV VPKULDTIDKKKV VPSLLDTIDKKKV VPSLKSLDKKV ACSLDDNIKKSK.V ARDLDPNIKKSK.V ARDLDNIKKSK.V ARDLDNIKKSK.V ARDLDNIKKSK.V FDRMLDTADKSREDKNQVV FEKALDQAGKSLKD.KKVI FDRMLDTADKSREDKNQVV FTKLVNAQKTKN.KDYF FTKLVNAQKTKN.KDYF FTKLVNAQKTKN.KDYF FTKLVNAQKTKN.KDYF FTKLVNAQKTKN.FYF FTKLVNAQKTV.PSA FARFYGHLS.GV.PGV FEKFFBJ.KVQSKV.SYA	70 ALS DKAQCE KREVI NMQ KNIALIQTHA DSAQGITPLEME TTT KGT GDM LLT KTIKAT GDM LLT KTIKAT GDM LLT KTIKAT GDM LLT TKILEASEG MTLE LAS KOVENT LAS K	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHERSHE KHDHSHGEEG KDPDAAE KOVEEEG FGEEEG FGEEEH FGEEEH FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FVKGLED FCF
15 /24-294 /26-324	EQ LERALETIHHPEKLF TDKFFCNFS.KL.QVV UDKAKKTLANF.KLT VDKAKKTLANFHV VPKVAKSVKSKK.VV VPKVLDTLDKKK.VV VPSLLDTLDKKK.VV VPSLLDTLDKKK.V ARDLDNIKKSK.VV ARDLDNIKKSK.VV ARDLDNIKKSK.VV FEKALQGGSLKDKVV FTKVVAKKKEN.KVV FTKVVAKKKEN.KVV FTKVVAKKKEN.KVV FTKVVFLSTKVV FTKVVFLSTKVV FTKVVSVVV FTKVVSVV FTKVVSVV FTKVVSVV FTKVVSVVV FTKVVSVVV FTKVVSVVV FTKVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV	70 80 ALL SDKAQCEKREVI NOGKAQCEKREVI NOGKAQCIP ALE TFVPTAEKLDLP TFVPTAEKLDLP TFVPTAEKLDLP NOGKOTON TVTDAEKDLT NOTASKGELV NOTASKGELV TVTDASKGELV NOFFASKPTLD AVSEVTE SUBJECT TVTDGIP AVSEVTE SUBJECT TVTDGIP AVSEVTE SUBJECT TVTDGIP SUBJECT TVTDGIP SUBJECT SUBJE	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSHE. K.HDHSHGEEG KOVEEEG FGEEEEE EGTEEED RVKGLED RVKGLED RVKGLED GQ.N EGPEGP EGP
15 /24-294 /26-324	50 LERALETIHHPEKLF TDKFFKONFS.KLQVV LEKLKANA.NM.KLT VDKAKKTLANEN.KLT VDKVAKSVKSKK.VV VPKVLKSVKSKK.VV VPKULDTLDKKK.VV VPSAEKSMGQGH.A VPSVLKSLDSKK.LL AGLDPNLKKSK.VV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV FKLVNAQKKKN.KDYF FKLVNAQKKKN.KDYF FKLVNAQKKKN.KDYF FKLVNAQKKKN.KDYF FKLVSVK.VV.PSV FFKFLSVK.VV.PSV FFKFLSVK.VV.PSV FEKFLALS.CV.PSV FEKFFASIK.VV.PSV FEKFFASIK.VV.SYA LTRLIASGTDA.VV.SYA LKRLIDTSGTKA.PVV	70 80 ALLSDKAQCEKREVI NNQKNIALIQTHA TFVPTAEKLDLP TFVPTAEKLDLP TFVPTAEKLDLP VFVNASKGDLM TVIDASKGTELV VFVNASKGDLM TVIDASKGTELV VFVNASKGDLM TVIDASKGTELV VFVNASKGDLM TVIDASKGTELV VFVNASKGTLM VFVNASKGTLM VFVASKKKT NJSGCVDVILLE SKGVKPKIT NJSGCFPTPIA VVTAGTPPIA VVTAGTPPIA VVTAGTPPIA VVSEGKVMGTT VVSEGKVMGTT VVSEGKVMGTT VVSEGKVMGTT	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSH.E KHDHSHGEEG KDPD.AAE CKOYP.AAE EGSE.EEH EGSE.EEH EGSE.EEH RVKG.LED RVKG.LED CEEG GA.S. CQ.N EGP EGP EGP EGP CGA E CA EGA EGP EGP CGA E C CGA E C CGA E C CGA E C CGA E C CGA E C CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CGA CE CC CC CC CC CC CC CC CC CC
15 /24-294 /26-324	50 LERALETLHHPEKLF TDKFFKONFS.KLQVV UEKLKANA.NM.KLT VDKAKKTLANEHV VPKVARSVKSKKV VPKULDTLDKKKV VPSLLDTLDKKKV VPSLKSLDSKL AGLDPNLKKSKV ARDLDPNLKKSKV ARDLDPNLKKSKV ARDLDNLKKSKV FEKALEQAGKSLKDLKKVT FTKLVKNAQKTKN.KDYF TKLVKNAQKTKN.KDYF YMKYFTNLKKGTKIT FEQFLGVK.DV.PSV FEKFLANGKKEN.VPSV FEKFLANGKSV.SYA LKRLISGV.SV.SYA LKRLISGV.VV.SYA KVKQSKV.SYA LKRLISGV.VV.SV VVERLSGV.VV.SYA LKRLISGV.VV.VV	70 80 ALS DKAQCE KREVI NMQKNIALIQTHA TFVPTAEKLDLP TFVPTAEKLDLP TFVPTAEKLDLP TFVTAEKLDLP TFVTAEKLDLP TFVTAEKLDLP TVTAEKCOLM TVIDASKGIELV VVTASKGIELV NVFASKTLT DVFEASKPITLD AVSEVTPTLA AVSDUVFTYLN AVSDUVFTYLN TVTDGINFIGVS VVTAGITPLPIR TVTDGINFIGVS VVTAGITPLPIR TVSGUPMGIT TVSGUPMGIT TVSGUPMGIT TVSGUPMGIT TVSGUPMGIT TSGUPMGIT AVSEVTPL AVSEVTPL TTDQVETKE TVSGUPMGIT TVSSGUPMGIT	90 100 .IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD DTHEHSH.E. K.HDHSHGEEEG KDPD.AAE C.KOVE.EEG PGGE.EEE EGSE.EEH EGTE.EED RVKG.LED RVKG.LED RVKG.LED RVKG.LED GEEG GA.S. GQ.N EDTS. DGP EGP EGP EGP EGA ECP EGA ECP EGA EC EGA EC EC EC EC EC EC EC EC EC EC
15 /24-294 /26-324	50 LE RALET LHHPEKLF TDKFF KONFS.KLQVV LEKLKANA.NM.KLT VDKAKKTLANEHV VPKVARSVKSKK.VV VPKULDTLDKKK.VV VPSLLDTLDKKK.VV VPSLLSTLDKKK.VV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV FKLVLNAQKTKN.KDYF TKLVLNAQKTKN.KDYF TKLVLNAQKTKN.KDYF TKLVKNAQKTKN.KDYF TKLVKNAQKTKN.KDYF TKLVKNAQKTKN.KDYF TKLVKNAQKTKN.KDYF TKLVKNAQKTKN.KDYF TKLVKNAQKTKN.KDYF TKLVKNAQKTN.KV FEKFLANSGTNA.VA KRLIDTSGTKA.VV VEKHLSGV.V.VV VELEKTGV.V.VV NKLLSNKK.KAN	70 80 ALS DKAQCE KREVI NMG KNI A LI QTH. TFT LKGT GDN LLT. TFT LKGT GDN LLT. TFT LKGT GDN LLT. TFT LKGT GDN LLT. TFT DA SKG TE LLV. TFT DA SKG TE LLV. TFT DA SKG TE LLV. TFT DA SKG TE LLV. TFT DA SKG TE LLV. DVF EA SKP TILD. AVS LGV TY LLE. LS GK VKP TILD. AVS LGV TY LLE. TTT DG LNP I GVS. TVT SG LF PP I RA. TTT DG LNF I GVS. TTT DG LNF LEV. TTT DG LUC. TTT DG LUC. TT	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD , DTHEHSH.E , KHDHSHGEEG , KDPD, AAE , KQYE, EEG , PGGE, EEG , PGGE, EEH , EGTE, EEH , RVKG, LED , RVKG, LED , RVKG, LED , RVKG, LED , CA.S, GA.S, , GQ.N, , CGP, EGP, , EGP, EGP, , EGP, EGP, , CGA, , PGG, , DEPAGHAHPEAEEEA , KN, FURTHER, PS.
15 /24-294 /26-324	50 LE RALETLHHPEKLF TDKFF (NFS.KLQVV LEKLKAANA.NM.KLI VDKAKKTLANEHV VPKVAKSVKSKKV VPKVLDTLDKKKV VPSLLDTLDKKKV VPSLLDTLDKKSV AGSLDPNIKKSKV ARDLDPNIKKSKV ARDLDPNIKKSKV ARDLDPNIKKSKV ARDLDPNIKKSKV FKLVKNAQKTKN.KDYF FKLVKNAQKTKN.KDYF FKLVKNAQKTKN.KDYF FKLVKNAQKTKN.KDYF FKLVKNAQKTKN.KDYF FKLVKNACKTKN.KDYF FKLVKNACKTKN.KDYF FKLVKNACKTKN.VPSV FEOFLCWK.DV.PSV FEOFLCWK.DV.PSV FEKFESIK.DV.PSV FEKFESIK.DV.PSV FEKFESIK.DV.PSV FEKFESIK.DV.PSV FKLVKNACKTN.KNYF VKVSKCV.SVA LTRLIASGTDA.VVV LKRLIDTSGTKA.VVV MGEVFSKLRGSR.LVV MEVFSKLRGSR.LVV	70 BO ALSDKAQCEKREVI NOSAQCIPLEME. TFTPIKENDLME. TFTPIKGTOMULT. TFTIKGTOMULT. TFTIKGTOMULT. TVIDASKGIELU. VIVASKGIELU. NOFEASKPITLD. DOFEASKPITLD. DOFEASKPITLD. NOFEASKPITLD. NOFEASKPITLD. VIVAGIPLIC. VIVAGIPLI	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD , DTHEHSHE , KHDHSHGEEGG , KDPDAAE , CYEEEG , PGGEEEH , EGE , EGE , EGE , EGE , EGE , C, LED , VKGLED , VKGLED , LED , CGA, EGP , CGA, EGP , CGA, EGP , CGA, EGP , CGA, EGP , DGP , CGA, EGP , EHEHEHEHEH, EHEH , CGA, EHEHEHEHEH, EHEH , CGA,
15 /24-294 /26-324	EQ LERALETIHPPEKLF TDKFFKONFS.KLQVV UDKAKKTLANDEV UDKAKKTLANDEV VDKVAKSVKSKK.V VPKVLASVKSKK.V VPKVLASVKSKK.V VPSLESTLDKKK.V VPSLESTLDKKK.V PSLESTLSK.V PSLESTLSK.V PSLESTLSK.V PSLESTLKDV	70 BC ALSDKAQCEKREVI NMQKNIALIQTHA NMQKNIALIQTHA TFTPIKGIGDMLLT NTILKGIGDMLLT NTILKGIGDMLLT NTILASKGIELV NTVIDASKGIELV NTVIDASKGIELV NTVIDASKGIELV NTVIDASKGIELV NTVIDASKGIELV NTVIDGINVILL NTVIDGINVILL NTVIDGINVILL NTVIDGIPVILL NTVID NTV	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQHGEGEHDHKAHD
15 /24-294 /26-324	50 LEKALETIHHPEKLF TDKFFKONFS.KLQVV UPKVARSVKSK.K.VV VPKVARSVKSK.VV VPKVARSVKSK.VV VPKVLDTLDKKK.VV VPSLLDTLDKKK.VV VPSAEKSMGQGH.A VPSVLKSLDSKK.LV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV ARDLDPNLKKSK.VV FKLVANAQKKKN.KDYF FKLVANAQKKKN.KDYF FKLVANAQKKKN.KDYF FKLVANAQKKN.KDYF FKFLADKSEDKNQVV FTKLVANAQKKN.KV FEKFLANSK.VV FEKFLANSSTAN FEKFLANSSTAN FEKFLANSSTAN VPSKLLDSCKV.SYA LKRLIDTSGTKA.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VV VVAAFAKTGV.VVV VVAAFAKTGV.VVVV VVAAFAKTGV.VVVVVAVVVVVVAVVVVVVVVVVVVVVVVVVVVVVV	70 80 ALLSDKAQCEKREVI NMQKNIALIQHKEVI DSAQCITPICHME TPUPTAEKLDLP TPUPTAEKLDLP NMQKNIALIGUN TPUPTAEKLDLP NMULT TIKGTOMLIT NMK TVIDASKGIELV NMULT TVIDASKGIELV NMULA TVIDASKGIELV NMULA TVIDFASKVIT NMK AVSKVKPITLD NMSGUDVILE TVTDGINPIGVS NMK NVSEGUPVILE TVTBGIPPIA TVSEGUPMAIN NSKGUPPIA NSKGUPPIA NSKGUPPIA NSKGUPPIA NSKGUPIA NSSGUPUII NSGUPIA NSSGUPUII NSGUPIA NSSGUPUII NSGUPIA NSSGUPUII NSGUPIALIA NSSGUPUII NSGUPIALIA NSSGUPUII NSGUPIALIA NSGUPUII NSGUPIALIA NSGUPUII NSGUPIALIA NSGUPUII NSGUPIALIA NSGUPUII NSGUPIALIA NSGUPUII NSGUPUII NSGUPUII NSGUPUII <	90 100 IKHTLGGEEYQHSHAYGED	110 EEHEHQ HGEGEHDHKAHD , DTHEHSH.E , KHDHSHGEEG , KDPD, AAE , CVEEEG , PGGEEEH , EGE , EGE , EGE , CLED , CVE , EGE , CA , CA
15 /24-294 /26-324	50 LERALETIHHPEKLF TDKFFKONFS.KLQVV UEKLKANA.NM.KLT VDKAKKTLANENVV VPKVARSVKSKKVV VPKVLSLDTLDKKKVV VPSAEKSMGQGH.A VPSVLKSLDSKKL AGSLDPNLKKSKV ARDLDPNLKKSKV REKLDPNLKKSKV FEKALEOAGKSLKD.KKVT FEKFLATADKSREDKNOVV FTKLVKNAQKTKN.KDYF TKLVKNAQKTKN.KDYF TKLVKNAKKT.K.KIT FEOFLCNVK.DV.PSV FEKFLANSGTDA.VPSV FEKFLANSGTDA.VA LKRLIDTSGTKAVV NGEVFSKLRGSR.LVV LNKLSNNK.KAT LKRH.LEGNT.SLAGS.EML LKKH.LEGNT.SLAGS.EML LDKPIDTLGEGAKVT DSKLLEGRTSL	70 80 ALLSDKAQCEKREVI NMQKNIALIQTHA DAGGITPLME. TFVPTAEKLDLP TFVPTAEKLDLP TFVPTAEKLDLP TFVPTAEKLDLP TVIDASKGIELV VIVASKGIDLM TVIDASKGIELV VIVASKGIDLM TVIDASKGIELV VIVASKGIDVITLE DVFEASKPITLD AVSKOVKPITLN AVSKOVKPITLN AVSKOVKPITLN VITAGITPLPIR TVTDGINFIGVS VITAGITPLPIR TVSSGVEPMGIA TVSSGVEPMGIA TVSSGVEPMGIA TVSSGVEPMGIA TVSSGVEPMGIA AVSETIPV AVSKTVPL AVSKOVKPILL AVSETIVV AVSETIVV AVSETIVV AUSETIVV AUSETIVV AUSETIVV AUSETIVV AUSETIVV AUSETIVV AUSETIVV AUSETIVV AUSETIVV	90 100 IKHTLGGEEYQHSHAYGED 	110 EEHEHQHGEGEHDHKAHD HD HD

V. cholerae_VC2552/25-242 C. jejuni_ZmuA/29-296 Synechocystis_ZmuA/26-334 L.monocytogenes_Lmolf71/33-31 S.agalactiae_AdcA/26-307 B.subtlis_ZnuA/34-315 L.monocytogenes_ZnuA/32-312 S.pneumoniae_AdcAI/155-310 S.gaglactiae_Lmb/30-305 S.aureus_MhtC/30-308 L.monocytogenes_MtA/30-308 S.pneumoniae_PsaA/30-307 Ca.L.asiaticus_ZnuA/30-307 Ca.L.asiaticus_ZnuA/21-293 Synechocystis_MhtC/25-322 Y.pestis_YfeA/39-309 S.enterica_SitA/27-297 S.melloti_SitA/29-299 Hhirobium/Agrobacterium_TroA/ N.gonorrhoeae_MhtC/19-302 S.etaricas_ItA/29-230 S.isig_TroA/40-316 T.pallidum_TroA/32-306 Abaumannii_ZnuA/17-274 J.entificams_AtuA/22-332 B.abortus_ZnuA/25-317 S.enterica_ZnuA/25-317 S.enterica_ZnuA/42-330

1	120	130	140	150	160	170	180	190
V.cholerae_VC2552/25-242	HKDHDHK	GHDHAADEH	ADHDHKEHD	HKGHEHEGI	HDHDEHQHGSFTA	QYQFHCEAVDQI	KQIDTQ	WFQYFPST
C. jejuni_ZnuA/29-296 Swnechocystis_ZnuA/46-334	HDDHSHD	GHD		HOSESE	KEKAKCALMVADP	HTWLDPILVQTM	ALNIYDT	LIQKYPQN
L.monocytogenes_Lmo1671/33-315	EHDHES.				EEEHEHGDINP	HVWLNPVYMEQN	ATVVKDK	LIKEMPNQ
S.agalactiae_AdcA/29-311	EEHEGH.				GHEGHHHELDP	HVWLSPERAISV	VENIRNK	FVKAYPKD
B. subtilis_ZnuA/34-315	E.EHDH.				GEHEHSHAMDP	HVWLSPVLAQKE	VKNITAQ	IVKQDPDN
L.monocytogenes_ZnuA/32-312	H.DHEH.				EE. GHHHEHDP	HVWLSPVLAEQE	VTNIQNG	LTKADKTN
S.agalactiae_Lmb/30-305	M.EVTQ.				GI.DPATLYDP	HTWTDPVLAGEE	AVNIAKE	LGRLDPKH
S.pyogenes_Lmb/30-305	M.EVTQ.				GI.DPATLYDP	HTWTDPVLAGEE	AVNIAKE	LGRLDPKH
L.monocytogenes MntA/30-308					KTSETDP	HAWLDLHNGIIY	TENVRDA	LVKADPDN
S.pyogenes_MtsA/31-308					EKGKEDP	HAWLNLENGIIY	SKNIAKO	LIAKDPKN
Ca.L.asiaticus ZnuA2/21-293					VDSEPNP	HAWMSLTNAMIY	IENIRKA	LTALDPSN
Synechocystis_MntC/52-322					YTDKPNP	HAWMSPRNALVY	VENIRQA	FVELDPDN
S.enterica SitA/27-297					YNGKPNP	HAWMSPSNALII HAWMSAENALIY	VDNIRDA	LVEHDPAH
S.meliloti_SitA/29-299					YTGKPNP	HAWMSPSAALIY	VDNIRDA	FVQHDPPN
Rhizobium/Agrobacterium_TroA/24-294 N.gonorrhoeae MntC/19-302	GHHHDH			DHD	HEGHHHDHGEYDP	HAWMSPDNALII HVWNDPVLMSDY	AONVAEA	LAGIDPAH
P.denitrificans_AztC/24-306	GHYHYI.				DGKAVFHAGAHDP	HAWQAVPNAKVY	VÕNIAAA	FCAADAEG
Rhizobium/Agrobacterium ZnuA/26-324 C.trachomatis YtgA/38-320	GHDHKA.			EEA.H	HDHEGHNHGEFDP.	HAWQSIKNAEIY HIWTDMRVWGAA	VKNIAGA	FCEVDKAG
S.suis_TroA/40-316				1	NTMDEDGEEIVDP	HFWFSIPLYKSA	VAVASEE	LQKLLPAK
T.pallidum_TroA/32-306					SQRLSLEEAEFDP	HVWFDVKLWSYS	VKAVYES	LCKLLPGK
P.denitrificans_ZnuA/22-323	EHEHEH.	E		HGHAEEQA	AHHDHD.HSGTDP	HAWLDPANGQAW	LAGIAET	LSRHDPDN
B. abortus_ZnuA/24-332	EHD		AHGSGDH	DHAAEVAE	EGHEHHHHGEYDL	HFWLDPONGKII	AADIAKT	LGESDPEH
V.cholerae_VC2081/21-294				EEEQI	HEHDGHHHGHYDP	HFWLGIGPVGQV	ASAITAK	LIELDADQ
H.influenzae_ZnuA/20-335	KHDHKH.	DH	. DHDHDHKH	EHKHDHEH	HDHDHHEGLTTNW	HVWYSPAISKIV	AQKVADK	LTAQFPDK
E.coli ZnuA/23-307				EKS	SDEDHHH.GDFNM	HLWLSPEIARAT	AVAIHGK	LVELMPOS
S.enterica_ZnuA/42-330				DEEKO	GDVHHHH.GEYNM	HLWLSPEIARAT	AVAIHEK	LVELMPQS
		200						
V.cholerae_VC2552/25-242	E.KIQAN ENLYKEN	VLTE	SUNLOTASK	LEK LEN	REVVYHDSWTVE	AKDYNT	· · · · · · · · · · · · · · · · · · ·	OT PVFTT.
Synechocystis_ZnuA/46-334	RDQYEAN	LAAFLAELE	RLNQELGQI	LQPLPQ	RKFIVFHPSWAYF	ARDYNL	v	QIPIEVE.
L.monocytogenes_Lmo1671/33-315 S.agalactize_AdcA/29-311	KETFEKN	YQAVEEKLK	NLDQDFRTV	TSEAKQ	KDFVTAHAAYSYW KSEVTOHAAECYM	ETEYGL	H	QIPIAGVS
S.pneumoniae_AdcA/26-307	KETFEKN	AAAYIEKLQ	SLDKAYAEG	LSQ. AKQ	SFVTQHAAFNYL	ALDYGL		QVAISGLS
B. subtilis_ZnuA/34-315	KEYYEKN	SKEYIAKLQ	DLDKLYRTT	AKK. AEK	KEFITQHTAFGYL.	AKEYGL	K	QVPIAGLS
S.pneumoniae_AcdAII/35-310	KETYQKN	AQAFIKKAQ	ELTKKFQPK	FEK.ATQ	KTFVTQHTAFSYL.	AKRFGL		QLGIAGIS
S.agalactiae_Lmb/30-305	KDSYTKK	AKAFKKEAE	QLTEEYTOK	FKKVRS	KTFVTQHTAFSYL.	AKRFGL	K	QLGISGIS
S.aureus_MntC/30-308	KADYEKQ	GNKYIAQLE	KLNNDSKDK	FNDIPKEQ	RAMITSEGAFKYF	SKQYGI	T	PGYIWEIN
L.monocytogenes_MntA/30-308 S.pyogenes_MtsA/31-308	ADFYKEN	AKKYIDKLA	TLDKEAKOK	FADLPENO	KTLVTSEGAFKYF.	AARYGL	K	AAYIWEIN
S.pneumoniae_PsaA/30-307	KEFYEKN	LKEYTDKLD	KLDKESKDK	FNKIPAEK	LIVTSEGAFKYF	SKAYGV	P	SAYIWEIN
Ca.L.asiaticus ZnuA2/21-293 Synechocystis MntC/52-322	AKKYELN	AREYSEKIR	NSILPLKTR	IEKVDPEK LEOVPANO	RWFVTSEGCLVYL. RFLVSCEGAFSYL	AEDFGF	K	SLYLWPIN
Y.pestis_YfeA/39-309	AETYNRN	AQAYAEKIK	ALDAPLRER	LSRIPAEQ	RWLVTSEGAFSYL	AKDYGF	K	EVYLWPIN
S.enterica_SitA/27-297 S.meliloti_SitA/29-299	ACIYKON	AERYKAKIR	MADPLRAE	LEKIPADO	RWLVTSEGAFSYL. RWLVSSEGAFSYL	ARDNDM	· · · · · · K	ELYLWPIN
Rhizobium/Agrobacterium_TroA/24-294	AEIYAAN	AKAYSDKIR	ATVQPIRDE	LSALPENK	RWLVTSEGAFSYL	ARDFGL	K	ELFLWPVN
N.gonorrhoeae_MntC/19-302 D.denitrificans ArtC/24-306	CAAYOAN	LGNYQMQLK	KLHSDAQAA ALDTEIDAA	FNAVPAAK	RKVLTGHDAFSYM	GNRYNI	S	FIAPQGVS
Rhizobium/Agrobacterium_ZnuA/26-324	CATYTAN	SQAYIAKLA	ALNEKVKTE	IAAIPPEK	RNIITSHDAFGYF	EHAYGL	E	FLAPEGIS
C.trachomatis_YtgA/38-320 S.suis_TroA/40-316	EEDFQKN	ADQILSEME	ELDRWAARS DLHAWVEFF	LSTIPEKN	RYLVTGHNAFSYF RYLVTDHDAPNVP	TRRYLSSDAERV	SGEWRSR	CISPEGLS
T.pallidum_TroA/32-306	TREFTOR	YQAYQQQLD	KLDAYVRRK	AQSLPAER	RVLVTAHDAFGYF	SRAYGE	E	VKGLQGVS
A.baumannii_ZnuA/17-274	KAKYWNN	ANTFARNML	AAQAY	DSSSNG	PYWSYHDAY QYL	ERSLNL	· · · · · · · K	FAGALTDD
B.abortus_ZnuA/24-332	AAQYEKN	AKAYGEKLD	ALTREVAAE	LKPVKD	KPFIVFHDAYQYF	ENRFGM		AAGSITVS
P.aeruginosa_ZnuA/23-304	AGRYRAN	LKAFDERLG	GLDGKLRER	LGK LAG	PFFVFHEAFDYF	EEAYGL	R	HTGVFAVS
H.influenzae_ZnuA/20-335	KALIAON	LSDFNRTLA	EOSEKITAO	LANVKD	KGFYVFHDAYGYF	NDAYGL	N	OTGYFTIN
Y.pestis_ZnuA/25-317	KDKLDAN	LRRFEYQLA	ONEKNIVTM	LKPVQG	GYFVFHDAYGYF	ENHFGL	s	PLGHFTVN
S.enterica ZnuA/42-330	RAKLDAN	LKDFEAGLA.	ATDKOVGNE	LAPLKG	G I F V F H D A Y G Y F G Y F V F H D A Y G Y Y	EKQFGL		PLGHFTVN

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V.cholerae_VC2552/25-242 C.jejuni_ZnuA/29-296	. KOOSALOINAKOTLIKL
L.monocytogenes Lmo1671/33-315	ISDEPS OKKIKSIVERIE AEKIPYIMLE ONTNSKIADVIQOEINIKKITLHNLETLTOKDIE
S.agalactiae_AdcA/29-311	PDAEPSSKRLIGELIAKYLIKKYNINYLYFEENASNKVAKTLADEV GVKTAVLSPLEGLSKKEMA
S.pneumoniae_AdcA/26-30/ B.subtilis_ZnuA/34-315	PDQEPSAAKLAKLIKTYAKEHNVKVIYFELASSKVADTLASEIGAKTEVLNTLEGLSKEEQD
L.monocytogenes_ZnuA/32-312	PDÖEPSPARLAELOKYVKENNISTIYFEEVASPKVAETLANETGAKLEVLSPIEGITDKEÖK
S.pneumoniae_AcdAII/35-310 S.agalactiae_Lmb/30-305	PEOEPSPROLITEIQEFVKTYKVKTIFTESNASSKVAETLVKSTGMGLKTLNPLESDPQN PEOEPSPROLITEIQEFVKTYKVKTIFAEDNVNPKTAHAAIAKSTGMVK.TLSPLEAAPSG
S.pyogenes_Lmb/30-305	PEČEPSPRČIKE I ODFVKE VNVKTI PAEDNVNPKIAHAJAKSTGAKVKTLSPLEAAPSG
L.monocytogenes MntA/30-308	TESOGTPDOMKOIVGIVEKEKVPNLFVETSVDPRSMESVSKETGVPT.AKTDSTGKE.GI
S.pyogenes_MtsA/31-308	TEERGTPDOILSSLIEKIKVIKPSALFVESSVDRRPMETVSKDSGIPIYSEIFTDSIAKK.GK
S.pneumoniae_PsaA/30-30/ Ca.L.asiaticus ZnuA2/21-293	IDEEGIPEGIRIJVENLKUINVESLIVESSVDDRPMAIVSQDINJEII.AUIFIDSIAEQ.GK SDSERSPSMMRHAINOMRSHKIKFIPSDSITNSDOPAKOVAYEINASVG.GVLVVDSLSKP.DG
Synechocystis_MntC/52-322	AEQ QET PK QVQ TVI E EVKTNNVPTI FCESTV SDŘGQK QVAQATGARFGGNLY VD SLSTE.EG
S.enterica SitA/27-297	ADOOGTPKOVRKVIDTIIKENAIPVVISESIIISDAPAAQVSAEIGAQIGGVLIVDSLSGE.KG
S.meliloti_SitA/29-299	ADÇÇĞİCTPQÇİVRKİVID VVRANRIPVV FSESTISPDPAEÇVAR.ETÇAKYG.GVLYVDSLSEA.DG
N.gonorrhoeae MntC/19-302	ADS GGIP QOVRGVID AMREHNIQ VITSESIV SADPAROVAREIGAATGGILIVDSLSEA.DG SEAEVS AKOVA AIIR OIKREGIKAV FTENIKDTRWVDRIAKETGVN VSGKLYSDALGNA
P.denitrificans_AztC/24-306	TESEAAAADVAGLIREIRARNASAIFAENISDTRLLEOIAR EAGLPLA GTLYSDALSGP.DG
C.trachomatis YtqA/38-320	TDS BASAA DVA KLVDO IKHDKASAI TVENIITDKR LMDOIAKEIGLVG. GTLISDALSIA.DG PEAQISIRDIMRVVEYISAN DVEVVELEDTLNODALIKKIVSCSKSGOKIRLLK.SPLYSDN
S.suis_TroA/40-316	TDSEVANSDMIETVNLIIDHNIKAIFTESTTNPERMKKLQEAVKAKGGQVEVVTGEGKELFSDSLAPE.GE
A.baumannii ZnuA/17-274	IAS EASAHDMOELAAFILAQKALPAIFIESSIPHANVEALKDAVQAKGHVVQIGGELFSDAMGDA.GI PHVAPTAAOIKYLNDSR.PKAOMCLIAESFTTK.VGOYQKLGSIFTFOPUDESMN.
P.denitrificans_ZnuA/22-323	DASTPSAARURAIRDEIAEEGAVCAPPSANHDPKLIIAAVIEGSEIROGA.ALDPEGIGATP
P.aeruginosa_ZnuA/23-304	AEVQPGARHVAAMRAQLIKAAGPACIISEPPLEPRLAADTUSEGLPVRLAELDDLGVNVSV
V.cholerae_VC2081/21-294	PERKPGAKTLIAIIKKTUNDOLAKCVFSEPOFEPAIIETVVRGISAKIGVLDPLGISIEL
Y.pestis_ZnuA/25-317	PEIQPGAQRIHQIRTQUVEHKAVCVFAEPQFRPAVINAVAKGTNVRSGTLDPLGSGIVL
E.coli_ZnuA/23-307	PEIOPGAORIHEIRTOLVEOKATCVEARPAVVESWARGTSWRMGTLDPLGTNIKL
V.cholerae_VC2552/25-242 C.jejuni_ZnuA/29-296 Synechocystis_ZnuA/46-334 L.monocytogenes_Lmol671/33-315 S.agalactiae_AdcA/26-307 B.subtilis_ZnuA/34-315 L.monocytogenes_ZnuA/32-312 S.pneumoniae_AdcA/26-307 S.agalactiae_Imb/30-305 S.aureus_MntC/30-305 S.aureus_MntC/30-308 L.monocytogenes_MntA/30-308 S.ppegnes_MntA/31-308 S.ppegnes_MntA/31-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.ppegnes_MntA/30-308 S.pneinciae_PsaA/30-307 Ca.L.ssiaticus_ZnuA2/21-293 S.enterica_SitA/72-297 S.meliloti_SitA/29-299 Phirobium/Agrobacterium_TroA/24-294 N.gonorrhoese_MntC/19-302	YDWENELLKTNDAFSHNL ADWSSNLKAVAQKIANAN QKRDYFSSNLKAVAQKIANAN QKRDYFSSNLKAVAQKIANAN AGENYISVMENLKALKKCI KGLQYIDIMKQNLDALKOSI KGMDYIAYMEQNLAQLQKTI NKTYLENLEANLEVIYQQL NKTYLENLEANLEVIYQQL NKTYLENLANLEVIYQL NKTYLENLANLEVIYQL NKTYL
<pre>knizoplum/Agrobacterlum_ZnuA/26-324 C.trachomatis_YtgA/38-320 S.suis_TroA/40-316 T.pallidum_TroA/32-306 A.baumannii_ZnuA/17-274 D.denitrificane_ZnuA/22-323</pre>	YAALILUMYMNILLILAAV VCDNYESTEQHINVELTEEL SCDTFLDMYKENVELTEEL SCGTYCMYTHNIDTIVAAL SECTYCMYTHNIDTIVAAL SCGTYCHILDGMCOULAACT
B. abortus_ZnuA/24-332	GPDL YPQL IRN LANS LKDCL
P.aeruginosa_ZnuA/23-304 V.cholerae_VC2081/21-294	DANGYEN LIUNN LAGEFAG CL DAGSYFA FUNS LAF SWYA CL
H.influenzae_ZnuA/20-335	ĞKN <mark>S</mark> YATFLQSTADSYMECL
Y.pestis_ZnuA/25-317 E.coli ZnuA/23-307	D K DIS 17 V N FLIS Q LISN Q1 V S CL G K TIS 15 S FLIS O LANOYA S CL
S.enterica_ZnuA/42-330	GKT <mark>SY</mark> SAFILSÕLANÕYASČI

Supplementary Figure S2. Multiple sequence alignment of SBPs from Supplementary Table S1.



Supplementary Figure S3. Genome neighborhood network where the hub node represents each group indicated in Figure 5. The gray spoke nodes indicate the prevalence of Pfam [69] protein family genes within 10 genes of *zrgA* in at least 20% of genomes.

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