Supplementary Material to "The AidB Component of the *Escherichia coli* Adaptive Response to Alkylating Agents is a Flavin-Containing, DNA-Binding Protein" by Mukta S. Rohankhedkar, Scott B. Mulrooney, William J. Wedemeyer, and Robert P. Hausinger.

Figure S1. Consensus of secondary-structure predictions from the PsiPred (3, 6), SAM-T2K (4), SABLE2 (1), and PROFsec (7) servers, the four best-validated methods (5). Results are shown for only the C-terminal domain (residues 441-541) of AidB; red and blue indicate high and low probability, respectively, while the magenta bars at the bottom of each section indicate every tenth residues. These predictions are consistent with the hypothesis that the C-terminal domain adopts a four-helix bundle similar to that seen in the 1IS2 structure.

Figure S2. Alignment of 34 non-redundant, full-length homologs of AidB. Absolutely conserved residues are indicated in red, whereas conserved residues are indicated in yellow. The residue numbering at the top is taken from AidB. This Figure was produced with the ESPript server (2).

- 1. Adamczak, R., A. Porollo, and J. Meller. 2005. Combining prediction of secondary structure and solvent accessibility in proteins. Proteins: Structure, Function, and Genetics **59**:467-475.
- 2. **Gouet, P., E. Courcelle, D. I. Stuart, and F. Metoz.** 1999. ESPrint: Multiple sequence alignments in PostScript. Bioinformatics **15**:305-308.
- 3. **Jones, D. T.** 1999. Protein secondary structure prediction based on positionspecific scoring matrices. Journal of Molecular Biology **292:**195-202.
- 4. Karplus, K., R. Karchin, C. Barrett, S. Tu, M. Cline, M. Diekhans, L. Grate, J. Casper, and R. Hughey. 2001. What is the value added by human intervention in protein structure prediction? Suppl. 5.
- Koh, I. Y. Y., V. A. Eyrich, M. A. Marti-Renom, D. Przybylski, M. S. Madhusudhan, N. Eswar, O. Grana, F. Pazos, A. Valencia, A. Sali, and B. Rost. 2003. EVA: evaluation of protein structure prediction servers. Nucleic Acids Research 31:3311-3315.
- 6. **McGuffin, L. J., K. Bryson, and D. T. Jones.** 2000. The PSIPRED protein structure prediction server. Bioinformatics **16:**404-405.
- 7. **Rost, B.** 2001. Review: Protein secondary structure prediction continues to rise. Journal of Structural Biology **134**:204-218.

Figure S1

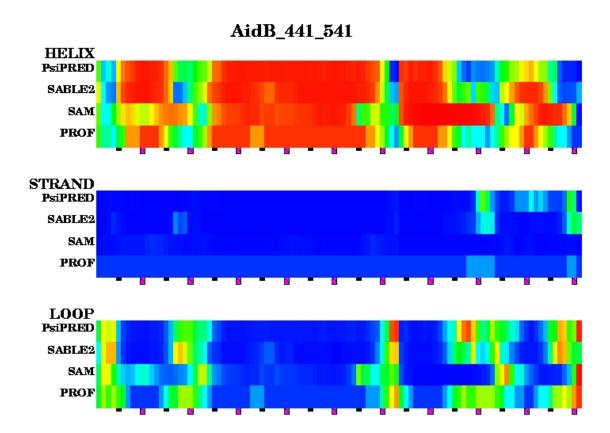


Figure S2

		i	10	20	зò	40
AidB E coli		MEWQTE	VENOPIPLNN	SNLYLSDGAL	CEAVIREGA	GWDSD
Salmonella_enterica		MSWQTH	VFNOPAPLNN	SNLFLSDGAI	CEAVSREGA	GWDSD
Yersinia_pestis	MNIGFQGSPEM	GKGMDWQTHI	VFNOPEPLSN	SNLFLSDLAI	REAVVREHA	GWDGE
Idiomarina_loihiensis	MTHKYPR					
Acinetobacter_ADP1						
Pseudomonas_aeruginosa	M	NLHQYAETHE	VTNOVPSLDG	ANLYRIDLPI	OEWVRRYQG	GWAEE
Pseudomonas_fluorescens	M	NLHQFAETH	V TNOPPSLDG	TNLYRIDLPI	QEWSRRFGA	GWAES
Pseudomonas_putida						
Pseudomonas_syringae		NLNQFAETHE	V TNOPPPLDG	ANLYRIDVPI	QEWSSRFGA	.GWAQP
Azotobacter_vinelandii	M	DLHQYAETHE	V TNQVPPLDG	ANLYRIDRPI	QEWLRRYDG	GWAER
Chromohalobacter_salexigens	MPDH					
Chromobacterium_violaceum						
Burkholderia_cenocepacia						
Burkholderia_fungorum	M					
Burkholderia_pseudomallei_1		QQDLMT <mark>AT</mark> H F	VTNQAPPLSD	YNAFETDAAI	VEAVRRYGA	SWRQT
Burkholderia_pseudomallei_2						
Ralstonia_solanacearum						
Ralstonia_eutropha						
Ralstonia_metallidurans_1						
Ralstonia_metallidurans_2	MDATSF					
Azoarcus_EbN1						
Bordetella_parapertussis						
Rhodopseuodomonas_palustris	MLNAAI					
Brucella_suis	MNQA					
Agrobacterium_tumefaciens	MT	QNSRTE ET L	ELNOPSLWSG	INAYRSDPLJ	VDLTSGLSR	.NLRD
Mesorhizobium_loti		MRQGQS <mark>VT</mark> DI	VINCPPPLIG	GNAWRGDPLI	IQLAERFSD	.PVRK
Mesorhizobium_BNC1						
Bradyrhizobium_japonicum						
Sinorhizobium_meliloti	MN	OWNELE OR P	ELNOPKPWSG	VNAFRSDPL	VDITSSMPK	.TRD
Mycobacterium_tuberculosis		MSDTH	VINQVPPLEN	YNP.ASSPVI	TEALIQEGG	QWGLD
Nocardia_farcinica		MQTHE	VENOVPNIVP	EDV.SRNPAI	LEGLHREGA	GWAEA
Streptomyces_coelicolor_1						
Steptomyces_coelicolor_2	MTTLAQEPPYESYEPSEEPW					
Streptomyces_avermitilis		MAA <mark>ST</mark> H <mark>I</mark>	TNO A 5 5 10 A G	IDVFAADRAI	VEAVERHLD	FALLDEART

	5 0	60	7 Q	8 <u>0</u>	ەد	100	
AidB_E_coli	FLASIGQUEGTAESI	ELGRIAN	NPPELLRYDAQ	RRLDDVR	FHPAWHLLMQ	ALCINR <mark>V</mark> HNLAW.	EE.
Salmonella_enterica	LLASI GQQLGTAESI						
Yersinia_pestis	NLSLI <mark>GL</mark> QLGSLESI						
Idiomarina_loihiensis	DLIAF <mark>GE</mark> LAGKADSI	EQGEQANE	YQPELRTHDRY	HRIDLID	FHPTYHOLMS	TAIEHG <mark>L</mark> H <mark>A</mark> SPW,	SE.
Acinetobacter_ADP1	Q <mark>L</mark> TTP <mark>GE</mark> ILGHQRS)						
Pseudomonas_aeruginosa	.RLQRY <mark>GE</mark> LAG.GPLN						
Pseudomonas_fluorescens	R <mark>I</mark> DAY <mark>GA</mark> LAG.GPLN	4 BAGFLANC	NK PVF A S H D RY	HRIDLVE	FHPAYHELMR	TAIEHG <mark>L</mark> T <mark>S</mark> LPW./	AH.
Pseudomonas_putida	R <mark>I</mark> DAY <mark>GA</mark> LAG.GPLN						
Pseudomonas_syringae	R <mark>I</mark> DAY <mark>GA</mark> LAG.GPLN	AAGFLAN	HRPEFASHDRY	HRIDLVE	FHPAYHQLMS	TAIAHG <mark>I</mark> P <mark>S</mark> LPW.1	ΤE.
Azotobacter_vinelandii	R <mark>L</mark> DDY <mark>GA</mark> LAG.GPLI						
Chromohalobacter_salexigens	R <mark>L</mark> APL <mark>AC</mark> NAGRESW(
Chromobacterium_violaceum	W <mark>L</mark> AEY <mark>GE</mark> RLGRAETE						
Burkholderia_cenocepacia	Q <mark>L</mark> DAY <mark>GA</mark> RLGSADT <i>I</i>						
Burkholderia_fungorum	ALLRHGAALTTPETI						
Burkholderia_pseudomallei_1	ALSHDGAALTTPDVI						
Burkholderia_pseudomallei_2	RLDAF <mark>GA</mark> RLGTRDI <i>I</i>						
Ralstonia_solanacearum	ALRAF <mark>GE</mark> TLGSPRTI						
Ralstonia_eutropha	D <mark>L</mark> MAY <mark>GA</mark> RLGEPEVI						
Ralstonia_metallidurans_1	E <mark>LTAYGARLGSAETI</mark>						
Ralstonia_metallidurans_2	T <mark>l</mark> aaf <mark>ga</mark> rlgdpev(AWAADAN	FTPELHTHSRT	GERIDQ V E	FHPSWHNLLA	LLRSQQ <mark>L</mark> Q <mark>A</mark> MPF.J	AQ.
Azoarcus_EbN1	A <mark>l</mark> hgq <mark>ge</mark> vlgsadt(RLAQLADE	HVPELVAYDRC	RRVDDVD	FHPAWSCLLA	LLYADG <mark>V</mark> H <mark>S</mark> SAW.I	FE.
Bordetella_parapertussis	E <mark>l</mark> reh ga wlgraqti	EAAAE	NSPRLLAYDP T	HRQDKVA	FHPAWNALMT	GIVARG <mark>L</mark> H S RAW.	AQ.
Rhodopseuodomonas_palustris	D <mark>I</mark> ADF <mark>GA</mark> RIGTAEYI	ELGALANI	RHLPEPDTHDRY	RRTDLVR	FHPAYHRLMQ	ISIENGLHSSPW.	TD.
Brucella_suis	E <mark>l</mark> eça <mark>gr</mark> fvlsaea(2DLARLAN	ELPKLRTHDRO	RRIDLVE	YHPAYHALMR	RSVAQG <mark>L</mark> HSSIW.1	EDN
Agrobacterium_tumefaciens	E <mark>Y</mark> DQL <mark>GR</mark> YVTSHEA(
Mesorhizobium_loti	DGLGRFVLTQEA(
Mesorhizobium_BNC1	DVEQLGRFVRTQEA(
Bradyrhizobium_japonicum	ELSEF GK HWGSAAMA						
Sinorhizobium_meliloti	EFDGLGRYVTSPEA(
Mycobacterium_tuberculosis	EVNEVGAISASCOA(
Nocardia_farcinica	EVREL <mark>GA</mark> LAGGERA(ELSGL GR SCGSWOT(
Streptomyces_coelicolor_1							
Steptomyces_coelicolor_2	GLRRLGRRAGSAQA(A.D .
Streptomyces_avermitilis	E <mark>l</mark> sgl gl sagsaqv(APWGALANI	NE EKTRUBUKW	NKIDEVE	F HE SWHRLLG	NGVSAG <mark>H</mark> I <mark>M</mark> .AW.	

	110	120	130	140	150	160
					•	
AidB_E_coli						.PFQDWTTPLLSDRYDSHL
Salmonella_enterica						.TFHDWLAPLRSDRYDSHL
Yersinia_pestis				CPITMTEGAIPL		. LFQNWLSPLLSDRYDPHL
Idiomarina_loihiensis				CPITMTEASIPA		LFKEWGPKITARQYDPRN
Acinetobacter_ADP1				CPSAMTLGSIPL		. LWQTLGKKLLSCDYDERD
Pseudomonas_aeruginosa				CPLTMT YASVPA		. LAEKWLPKILSREYDPRN
Pseudomonas_fluorescens				CPLTMT FASVPA		LAEHWLPKILATEYDPRN
Pseudomonas_putida				CPLTMT FAAVPA		. LAEYWLPKILACEYDPRN
Pseudomonas_syringae				CPLTMT FASVPA		.LAEIWLPK <mark>V</mark> LSTEYDPRN
Azotobacter_vinelandii				CPLTMTFASVAA		.IAESW1PRV1AGEYDPRN
Chromohalobacter_salexigens				CPITMTHAAYPV		.VLATWGPRLLAHDYDPRA
Chromobacterium_violaceum				CP <mark>AT</mark> MT <mark>QAAI</mark> PL		.LWAQLGDK <mark>L</mark> L <mark>S</mark> REH <mark>D</mark> ARD
Burkholderia_cenocepacia				CPATMT QAAI PV		LWDLLRDK <mark>L</mark> Y <mark>S</mark> DDY <mark>D</mark> PRD
Burkholderia_fungorum				CPLTMTFASIPV		. LFARLEDKLYAREHDPED
Burkholderia_pseudomallei_1				CPLTMT FASIPV		.LFATLRDKLYAREHDARD
Burkholderia_pseudomallei_2				CPATMTQASIPV		. LWAQLKDKLYSDTHDPRD
Ralstonia_solanacearum				CPATMT FASIPV		. LFADLAPRLYAREHDARD
Ralstonia_eutropha						. LFADLEPRLYAKNHDARD
Ralstonia_metallidurans_1						. LFAALAPKLYSRTYDARD
Ralstonia_metallidurans_2						.LFCDLEPRLYATEHDARD
Azoarcus_EbN1						LFGALADK F R S RDY D GRD
Bordetella_parapertussis						DYGRDWLDV <mark>L</mark> YSREF D ASD
Rhodopseuodomonas_palustris						.VAKVWLPKVLARSYDARN
Brucella_suis	PLESG.RR	I <mark>QARAA</mark> RFY <mark>L</mark> I	AQLEAGHL	CPLTMT SASLAA	L.MASPE	.VYKQWSPAVLSRKYDFSQ
Agrobacterium_tumefaciens						.VOKEWMPKILSRKYDSAO
Mesorhizobium_loti	DAEIG.RR	QVRAARFYLI	AELETGHL	CPITMT SASLAA	L.MASPK	LFREWAPRVTTRKYDQSQ
Mesorhizobium_BNC1						LFRAWAPRVI A RKYDNAN
Bradyrhizobium_japonicum	GKPAGDAA	E VIRAA KEY I A	SQVETGHL	CPITMT RASVAA	L.ATQPD	LLARVMPVLATKSYDPTF
Sinorhizobium_meliloti	PDERG.RS	KVRAIRFYL 1	AQLECCHL	CPLTMT SASVAA	I.TASPA	.VQKEWAPKILSRKYDSSN
Mycobacterium_tuberculosis	DRP.GA	I VVRAA KTS <mark>V</mark> W	IT.VEPGHI	CPISMTYAVVPA	L.RYNSE	LAAVYEPLLTSREYDPEL
Nocardia farcinica	ERP.GA	VARAAKFYT	IG AAD AGHM	CPISMTYAAVPA	L.RHNPE	. LAAKYEPLLGSRVYDFGL
Streptomyces_coelicolor_1						LAAEWEPRLTSRVYDREL
Steptomyces_coelicolor_2						.LAEVYEPLLTSREYEPGL
Streptomyces_avermitilis						LAAEWEPRLTSMVYDOGM
			Colorado - Las - Col			

*
AidB_E_coli
Salmonella_enterica
Yersinia_pestis
Idiomarina_loihiensis
Acinetobacter_ADP1
Pseudomonas_aeruginosa
Pseudomonas_fluorescens
Pseudomonas_putida
Pseudomonas_syringae
Azotobacter_vinelandii
Chromohalobacter_salexigens
Chromobacterium_violaceum
Burkholderia_cenocepacia
Burkholderia_fungorum
Burkholderia_pseudomallei_1
Burkholderia_pseudomallei_2
Ralstonia_solanacearum
Ralstonia_eutropha
Ralstonia_metallidurans_1
Ralstonia_metallidurans_2
Azoarcus_EbN1
Bordetella_parapertussis
Rhodopseuodomonas_palustris
Brucella_suis
Agrobacterium_tumefaciens
Mesorhizobium_loti
Mesorhizobium_BNC1
Bradyrhizobium_japonicum
Sinorhizobium_meliloti
Mycobacterium_tuberculosis
Nocardia_farcinica
Streptomyces_coelicolor_1
Steptomyces_coelicolor_2
Streptomyces_avermitilis

3	170	1	80	190	200	2	10	220
	E P (G G Q <mark>K R</mark> G I	LIGI	G <mark>m</mark> tekqgg <mark>s</mark> d	MSNTTRA B	ER <mark>L</mark> EDG <mark>SY</mark>	RLVGHKWF	SVPQSDAHLVLA
						ER <mark>L</mark> ADD <mark>SY</mark> EP L SIRGOGE VY		
						YPIGKEGSGOAY		
						KP <mark>V</mark> GISGRGE e ¥		
						YP <mark>V</mark> GIPGPGQ <mark>AY</mark>		
s						YP <mark>V</mark> GASGPGQ <mark>AY</mark>		
						YP <mark>V</mark> GAPGPGQ <mark>AY</mark> FS V GAGGPGO AY		SAPMCDAFLTLA
						WPWGAAGPGOAY		SAPMSDAFLTLA
igens	L P	ÍGD <mark>KR</mark> A <mark>A</mark>	TFGI	AMTEKQGGSD	RSNTTRA I	TPNADG <mark>SV</mark>	RLTGHKWFC	
eum						TP <mark>T</mark> GAGGRGG <mark>BY</mark>		
ia						TP <mark>V</mark> GAGGRGG <mark>EY</mark> YA T AGSGRGA AY		
lei_1						YPLGAGGRGOAY		
lei_2	AP	IGAKOSI	MIGI	GMTEKQGGSD	VRANTTLA	VP <mark>V</mark> GAGGRGG <mark>EH</mark>	LLRGHKWFF	SAPMCDAHLVVA
						VP <mark>l</mark> ggkdggegrga <mark>ty</mark>		
						HP <mark>V</mark> RGEGRGA <mark>EY</mark> BP L RGEGRGG EY		
s_1 s_2						SPERGEGRGG <mark>E</mark> I LP <mark>V</mark> RGDGRGA E I		
a_e						RPLAAGSRDH		
is	AP:	ÍGR <mark>KR</mark> G				EP <mark>V</mark> GAPGRGQ <mark>AY</mark>		
stris		A E Q <mark>K Q</mark> G I				IP <mark>I</mark> GAGGPGG <mark>by</mark>		
ens						EP <mark>A</mark> IGG <mark>AW</mark> ER V GEG IY		SAPMSDAPLTLA
ens						ERAGSGFY		
						EPAGBGLY		
um						VR <mark>D</mark> GD.AY		
4 -	RPI					ER <mark>V</mark> GEG <mark>IY</mark>		
osis	K P J					TP <mark>N</mark> A.DG <mark>SY</mark> TP O P.DG TY		
r_1	RP					RPLAEDGTY		
2	RT	? TD <mark>KR</mark> G <mark>I</mark>	LAGI	GMTEKQGGSD	RTNAT	TA <mark>T</mark> AEPG <mark>VY</mark>	TLRGHKWFT	SAPMCDVFLVLA
is	RP.	A A Q <mark>KA</mark> G <mark>A</mark>	EFGI	GMTEKQGGSD	VRANTTAA B	RP <mark>l</mark> aedG ty	ELTGHKWFC	SAPMSDGFLVLA

AidB_E_coli Salmonella_enterica Yersinia_pestis Idiomarina_lohiensis Acinetobacter_ADP1 Pseudomonas_fluorescens Pseudomonas_putida Pseudomonas_putida Pseudomonas_putida Pseudomonas_putida Chromohalobacter_salexigens Chromohalobacter_salexigens Chromohalobacter_salexigens Chromohalobacter_salexigens Chromohalobacter_salexigens Chromohalobacter_salexigens Burkholderia_cenocepacia Burkholderia_fungorum Burkholderia_fungorum Burkholderia_pseudomallei_2 Ralstonia_solanacearum Ralstonia_metallidurans_1 Ralstonia_metallidurans_1 Ralstonia_metallidurans_2 Azoarcus_EbN1 Bordetella_parapertussis Brucella_suis Agrobacterium_tumefaciens Mesorhizobium_loti Bradyrhizobium_japonicum Sinorhizobium_meliloti Mycobacterium_tuberculosis Nocardia_farcinica Streptomyces_coelicolor_1 Steptomyces_avermitilis

ò	24	iò		23	5 <u>0</u>			26	ò	2	70		28	ò.	
Ó	TA	VPR	FLP	DGOF	NA	İR	ERL	KD	KLGNE	SNAS	CEVE	O DA	tGW	LLG	LE
õ	AKGGLSCF	VPR	FLP	DGQE	NS.	VRI	ERL	KD	KLGNF	SNAS	AEVER	ODT	/GW	RLG	EE
õ	AEGGL <mark>SCF</mark> E					IR	ERL	KE	KLGNC	SNAS	SEVE	DNA:	CAW.	LLG	EÉ
õ	TASGLSCFI	VPR	WRP	DGSB	NP	101	LOOL	KO	K <mark>M</mark> GN/	ANAS	SETEI	RGAI	LGW	MVG	EE
õ	TSCEELACF	VPR	WLS	NGSE	N R	IE	LOOL	KN	K <mark>V</mark> GNK	SNSS	SEVE	RDAI	LGI	MIG	EE
¥	TD	LPR	H R P	DGSF	NO				KLGN			RGAI	UA.W	MVG	EE
Q	TDKGLSCFI	LPR	HRP1	DDTF	NÖ	FY	ORL	ΚN	KLGNC	SNAS	SEVE	RGA1	LAW	MVG	EE
õ				DDNF	υNÖ				KLGNS						EE
õ	TDKGLSCFI								KLGN						EE
W	SD								KLGN						
R	DEAGI <mark>G</mark> CFI														
Q	LRDGGP <mark>SCF</mark>)														
R	TEAGSP <mark>SCE</mark> N														
	TDDHEGL <mark>SCF</mark> E														
Ŕ	TABQAGISCEY														
	TEAGGPSCF														
	MGAEDGPL <mark>SCF</mark> É														
R	MGAEDGPL <mark>SCF</mark> E														
R	TES.GPACE	VPR	YRPI	DGTH	NA				K <mark>V</mark> GNF				/ G R	MIG	E E
R	MGAADGPL <mark>SCF</mark> E			DGSB					KLGNF					LIG	
H									KLGNF						
R	TDEGL <mark>GCF</mark> E														
Q	APGGL <mark>SCF</mark> I													MIG	
Q	TKEGL <mark>SCF</mark> I														
Q	MGDGM <mark>GCF</mark> I														
Q	APEGL <mark>SCF</mark> I														
Q	AEEGL <mark>SCF</mark> I								K <mark>l</mark> gnF						
Q	ADEGL <mark>TCF</mark> E														
Q	TREGL <mark>GCF</mark> I													LLG	
	AP,DGL <mark>S</mark> CFI		V L P	DGTR					K <mark>l</mark> gnH						ΕE
Q		LPR	VL₽	DGTE					KLGNK						ΡE
R	APGGTARAEGNGGGL <mark>TCF</mark> I								K <mark>l</mark> g n F						ΑE
	AAGGL <mark>SCF</mark> I								KLGNF						
Q	AASATDĠĠĠĿ <mark>tcf</mark> i	VPR	VLE	DGTF	NV	FR	ORL	KD	KLGNF	SNAS	SEVEI	DGT	1A.R	RVG	D E 🛛

Nà de la coltá
AidB_E_coli
Salmonella_enterica
Yersinia_pestis
Idiomarina_loihiensis
Acinetobacter_ADP1
Pseudomonas_aeruginosa
Pseudomonas_fluorescens
Pseudomonas_putida
Pseudomonas_syringae
Azotobacter_vinelandii
Chromohalobacter_salexigens
Chromobacterium_violaceum
Burkholderia cenocepacia
Burkholderia_fungorum
Burkholderia_pseudomallei_1
Burkholderia pseudomallei 2
Ralstonia_solanacearum
Ralstonia_eutropha
Ralstonia_metallidurans_1
Ralstonia_metallidurans_2
Azoarcus EbN1
Bordetella_parapertussis
Rhodopseuodomonas_palustris
Brucella suis
Agrobacterium_tumefaciens
Mesorhizobium_loti
Mesorhizobium BNC1
Bradyrhizobium_japonicum
Sinorhizobium meliloti
Mycobacterium_tuberculosis
Nocardia farcinica
Streptomyces_coelicolor_1
Steptomyces_coelicolor_2
Streptomyces avermitilis

	2	9 ç)			30	ò			3	10				2	32	ō.			3	330	2			34	ò			3	50			
	I	R	IL	MG	GM	TR	FDC	AL	GS	HA	MM	RR	AF	SI	A	ΪY	H A	HO	H	F	GNP	LI	ୁହ	PL	RH	VL.	SRI	AL	0 L	EG	QT/	A 🚺 I	5
	I	R	IL	KМG	GΜ	TR	LDC	AL	GS	H G	LM	RR	A F	s١	A.	ΙY	Y A	HQ.	0	AFC	GKP	LI	E Q	PLM	RQ	TL	SRI	AL	C L	EG	QT 7	A L I	i.
	1	RIC	ILI	KMC	CΥ	TR	FDC	AL	GS	HG	L.M	RR	AF	S1	/AI	LY.	H A	LO	100	JFO	3 K A		E O	PLM	RO	VL	SRI	IAL	RL	EG	HT/Z	A 💶 I	1
	V	R	III	EMV	ΑT	ΤR	YDC	MI	GS	S S	GM	RQ	Α <mark>V</mark>	VS	2A	Π	H.A.	SH	E	AFO	g t K	(IS	EQ	PLM	QN	LL	ADI	LAI	ΞS	EA	AM)	T <mark>Y</mark> N	
	I	P	III	- MIA	ΤY	ΤR	LTC	sv	GS	TΑ	IL	RQ	A L	vç	2C :	ΙA	ΥT	RQ	R	AFO	GR	LA	ÐQ	PLN	QA	VL.	TDI	IAL	ΕT	EA	AL	H 🗖 S	
			III																														
			III																														
			III																			LN											
			III																														
			IL																														
-	I	A	ILI																							VI.	ADI	LAL	ΞT	EA	SL7	A L (i.
m	1	P 7					LSC																			VL.	ADI	LAL	ES	EA	AL	214	4
2	I		III																											EA	ALS	S L /	
	V	P	III	MA	ΝY	ΤR	LDC	IVI	GS.	AΑ	LM	R.	ΛĽ	vç	2A.	H	HA	RH	ss	AFC	GR	LA	DQ.	PLN	RN	VL.	ADI	LAL	ES	EA	AT	VLE	f.
ei_1	Y		III																											EA	AT		2
≥i_2	I		III																													AL7	4
	Ξ		ILI																													(L)	
	Ξ		III																													LLN	
_1			III																														
_2			III																													L. <mark>M</mark> I	
			IME																														
			LLI																														
			III																														
			IMI																														
			IMI																														
			IMI																														
			III																														
			ILI																														
sis			III																													I VZ	
			III																													TV	
1			III																													TL	
2			TIT																													_	
6	Č.		III																			Ťv											i .
,		n (100	nn	1.15	100	- V L	00.	0	1.0		110	~		122	0.4	-1-1	12	121	330		UR.		N.N	V L1		JAL	20	DA	A 1 .	1 1 1 1	1

AidB_E_coli Salmonella_enterica Yersinia_pestis Idiomarina_loihiensis Acinetobacter_ADP1 Pseudomonas_fluorescens Pseudomonas_fluorescens. Pseudomonas_putida Pseudomonas_putida Pseudomonas_putida Chromobacter_vinelandii Burkholderia_pseudomallei_1 Burkholderia_pseudomallei_2 Ralstonia_solanacearum Ralstonia_metallidurans_1 Ralstonia_metallidurans_1 Ralstonia_metallidurans_2 Azoarcus_EbN1 Bordetella_parapertussis Brucella_suis Agrobacterium_tumefaciens Mesorhizobium_loti Mesorhizobium_loti Bradyrhizobium_ploicum Sinorhizobium_meliloti Mycobacterium_tuberculosis Nocardia_farcinica Streptomyces_coelicolor_1 Steptomyces_avermitilis

360	37 Q	380	390	400	410
FRLARAWDRR	ADAKEALWARL	TPAAKEVI	CKRGMPFVAEAM	EVIGGIGYC	EESELPRLYREM
FRLARAWEQR				EVL <mark>GGMGY</mark> C	
LRLARAWEAS			C <mark>GQ</mark> GSÀF <mark>V</mark> A <mark>EAM</mark>		
MRIARAMDNQ		TPIGKYWI			
MHLAACYQR	DDDI <mark>SQ</mark> AW <mark>VRL</mark> I				ETGI <mark>m</mark> srl fkea
L <mark>RMG</mark> H <mark>A</mark> LDRA			C <mark>KR</mark> APAM <mark>I</mark> N <mark>EAS</mark>		BÉTI <mark>l</mark> PRL yrea
L <mark>RMG</mark> K <mark>A</mark> LDHL			C KR APAM <mark>I</mark> N <mark>EAA</mark>		
L <mark>RMGQA</mark> LEQL		TA <mark>V</mark> G <mark>KYWI</mark>			EDSILPRE <mark>YREA</mark>
L <mark>RVG</mark> R <mark>A</mark> LDHL	· · · · · · · · · · · · · · · · · · ·		C <mark>KR</mark> APAM <mark>IN<mark>EAA</mark></mark>		
L <mark>rla</mark> r <mark>a</mark> ldha	EDES <mark>ER</mark> SL <mark>ARL</mark> I				EESILPRL <mark>yrea</mark>
L <mark>RTA</mark> R <mark>A</mark> FDGAP	HDDH <mark>ER</mark> AL <mark>ARL</mark> I				EEAPLARLYREA
ARLAEGFEND					DDGPMARLEREA DDGPTARLEREA
MRLADAFERD MRLARAFEESADA	AASTSLAERAWRRIN				DDGP <mark>IARLFREA</mark> Etgemarf yrea
MRLARAFEESAUA	AASISLAERAWRRIN AARSPO AR GWRRIN	TPAAKEWV			ETGPMARETREA ETGPMAREYREA
MRLAGAFERG		APAAKEWV	CKRAVEAAGEVM		DDGPTARLEREA
MALGDAFERA	PADDVAAAWKRTI	TPAAKEWV	CKRAIEATGEAM		EEGPMARLYREA
MELAHAFEHA	ETOPLAAAWKBU	TPAAKEWT	CKRTIEATGEAM	EVWGGNGYV	EDGPMARLYREA
MRLTEAFALA	DEDELORAVERT		AKRSVELSGEAM		DEGEMGRLYRET
MALAHAFEHA	DODPLAAAWRDUN		CKRALEATCETM	EVWGGNGYV	EDGPMARLYREA
MRLAKAVES	DDDPLERAWRET	TPAAKFWI	CKRATAFVARCM		BOGPMARLYREA
LRLARAVDER	ADPVARALVRV	TPAAKLWV	CKRAIAALGECM		EEAPLARLYREA
MRIARALDHR.	TDEREARLIRI	SAICKYWI	CKRTPGLTAEAM	ECIGGSGVM	EDGPMPRHERES
MRLARAFDMAA	SDRA <mark>EA</mark> AF <mark>ARS</mark> N	TPVVKYWV	C KI APALLY EAM	ECLGGNGYI	EDGNLARAYREA
FRLATAFDAAR	NNPA EA AY <mark>ARV</mark> M	TPIVKYWC	CKIAPALIYEAM	ECLGGNGY	EERPIARHYREA
FRLARSFDEAA		TPVVXYWV	CKIAPPLLYEAM		E E A P L A R Y Y REA
FRLARSFDEAA		TPVTKYWV			EEAPLARYYREA
MRLCRAFDRIP		TPAIKYWT			EDGILARHYRES
	SSAE <mark>da</mark> ay <mark>ari</mark>)				EERALARH YREA
		LAAAKYWV		ECL <mark>GGN</mark> GYV	
M <mark>rla</mark> g <mark>a</mark> t d raa		LAVT <mark>KYWV</mark>			EESC <mark>M</mark> PRL YRES
L <mark>rla</mark> a <mark>a</mark> c <mark>d</mark> aaa		VPAA <mark>kywv</mark>		ECL <mark>GGN</mark> GYV	
L <mark>rla</mark> g <mark>a</mark> adrav			T <mark>KR</mark> GPAF TA<mark>EAL</mark>		
L <mark>RLA</mark> A <mark>A</mark> Y D DG	GEQ <mark>er</mark> af <mark>lrl</mark> 7	VPVA <mark>kywv</mark>	T KR C TP V <mark>A</mark> A <mark>EAL</mark>	ECL <mark>GGNGY</mark> V	BEFGLARLLRES

AidB_E_coli
Salmonella_enterica
Yersinia_pestis
Idiomarina_loihiensis
Acinetobacter ADP1
Pseudomonas_aeruginosa
Pseudomonas_fluorescens
Pseudomonas putida
Pseudomonas_syringae
Azotobacter_vinelandii
Chromohalobacter_salexigens
Chromobacterium violaceum
Burkholderia_cenocepacia
Burkholderia_fungorum
Burkholderia_pseudomallei_1
Burkholderia_pseudomallei_2
Ralstonia_solanacearum
Ralstonia_eutropha
Ralstonia_metallidurans_1
Ralstonia_metallidurans_2
Azoarcus EbN1
Bordetella_parapertussis
Rhodopseuodomonas_palustris
Brucella_suis
Agrobacterium_tumefaciens
Mesorhizobium_loti
Mesorhizobium_BNC1
Bradyrhizobium_japonicum
Sinorhizobium_meliloti
Mycobacterium tuberculosis
Nocardia_farcinica
Streptomyces_coelicolor_1
Steptomyces_coelicolor_2
Streptomyces_avermitilis

	42	. <u>o</u>	43	o 4	40		45	o 4	eò	470	480
								SEAFVEVK.G			
								SEAFAEVK.G			
								QQEFYPVR.G			
								FAELQRAQ.G			
								FĎSFGDVÍ.A FAELGDGH.G			
								FSELGDGH.G			
								FVELGDGH.G			
								FDELGDGH.G			
	P	VNSIWEGS	GN	VQCLDVLRV	LG	EPEALE	VL	FDELDGGH.G	.DARLKAR	IEWLR	KA <mark>L</mark> ÄDRT.EI <mark>H</mark> YC <mark>A</mark>
ŝ								RQÉLALAR.G			
								QQELAALA.G			
								FDELADLG.A			
-											AFNGPAEHREASA
1								FDEWRDAA.R IDELHALG.G			
×.											MLHOSGDIOEASA
											MLREPABOLEAHA
											GLRTOGEATEWLA
	P	VNSIWEGS	GN	IMCLDVLRA	LOI	DPGDGA	RI	LQDLARLS.N	GDAAVRAE	LASLQ	AM <mark>L</mark> RGPAEQL <mark>E</mark> TS <mark>A</mark>
								WRELSQAL.A			
											LL <mark>V</mark> AQPDSVP Q AL <mark>A</mark>
s	P							FAEVEQAK.G			DOMRDPS.DFEERA
	2							LDWISGQL.G			
								FQTLERDL.G LAGIDRDL.G			
								LOGMAADL.G			
								LOSLAAETKG			
		VNAIWEGS						FATIGRDL.G			
	₽	LMGIWEGS	GN					FDELARSA.G			
								FDEVNKSR.G			(E <mark>L</mark> ADLS.DI <mark>E</mark> YR <mark>A</mark>
								LTEVGAAR.G			FE <mark>L</mark> ADLA.AA <mark>E</mark> GR <mark>A</mark>
								FGELSLAR.G			IGLTEASETGA
	P	LNSIWEG	GN	VQALUVLRA	LQI	EPQALN	ΑY	LQEVGRAR.G	ADHRLDGA	IKGLL	TE <mark>L</mark> ADLE.GI E GR <mark>A</mark>

AidB_E_coli
Salmonella_enterica
Yersinia_pestis
Idiomarina_loihiensis
Acinetobacter_ADP1
Pseudomonas_aeruginosa
Pseudomonas_fluorescens
Pseudomonas_putida
Pseudomonas_syringae
Azotobacter_vinelandii
Chromohalobacter_salexigens
Chromobacterium_violaceum
Burkholderia_cenocepacia
Burkholderia_fungorum
Burkholderia_pseudomallei_1
Burkholderia_pseudomallei_2
Ralstonia_solanacearum
Ralstonia_eutropha
Ralstonia_metallidurans_1
Ralstonia_metallidurans_2
Azoarcus_EbN1
Bordetella_parapertussis
Rhodopseuodomonas_palustris
Brucella_suis
Agrobacterium_tumefaciens
Mesorhizobium_loti
Mesorhizobium_BNC1
Bradyrhizobium_japonicum
Sinorhizobium_meliloti
Mycobacterium_tuberculosis
Nocardia_farcinica
Streptomyces_coelicolor_1
Steptomyces_coelicolor_2
Streptomyces_avermitilis

	490	500 510	520	530 540	
				QNDLLLRATGGVCV	
				/QND <mark>LL</mark> L <mark>RA</mark> TGGLR.	
				/CAR <mark>ll</mark> e ra tgah	
				. IGLNC. AA <mark>IV</mark> E RA SPANAQ	
			QSRYGTWHGRVTGIL		
				P.RGVEV.EALLARATPHLT.	
				RGLDV.EAIVARSTPOGF.	
				P.RGVNV.MA LV T RA TPAWPL P.TGVDV.ET LLORS SPOVA.	
				.RGLDV.AGLLARSAPOPG.	
ens				AOAPL.AAILARINP	
m				ARAAGADYLLERALPAA	
				. PHAIDVAALLORAYPA	
	RRIAQOVVLIAO	ATILLEHAPAE <mark>VA</mark> EAFI	ATRLADGCGESGRVY <mark>G</mark> TL	ATFDH.AAIVERAFPA	
i_1				P.ATIDH.AA <mark>LV</mark> E RA FPA	
i_2).ARRVDAAA <mark>LL</mark> Q RA YAA	
				.GNAQELGA <mark>AL</mark> Q <mark>RA</mark> WPA	
				.MEPEVLKR <mark>VF</mark> ERGWTA	
1				P. DGVAHAA <mark>IL</mark> D RA WTQ	
2	REFACELVLTAC	AALMIAHGNAESAALFV	ASRLGRQHGRVFGIL).ADASTLAR <mark>IA</mark> A <mark>RA</mark> WPA IKP.DATT <mark>LI</mark> D RA WPG	
				P.ID. DPAPILARAWPG	
ris				KGVNF.AAIIDRARPR	
				ARHNA.MRIIDOLYPAS	
s				SREDP.NYIIDLLYPPAS.	
-				.SRHDA.RMIIDTLYPPVN.	
	RILTEOLALAAA	AAELKRLGAGO <mark>VA</mark> DAFI	etrl agQwrgty <mark>g</mark> m <mark>l</mark> d	.ARYDA.VAILDMLYPEAM.	
	RLAVEKLALLAA	AAALNGVSP.RHAELFA	ATRLATTHASMY <mark>G</mark> A <mark>V</mark> E	LESGDV.RALLERALP	
				SRFDS.AY <mark>VL</mark> D <mark>LL</mark> YPAAT.	
i,s				AGLDL.AP <mark>IL</mark> E <mark>RA</mark> LVKG	
_				P.IGVDI.ES <mark>II</mark> E <mark>RA</mark> FVE	
1				PTLDL.AA <mark>VV</mark> E RA RPVV	
				P.DTADL.DG <mark>ILTRA</mark> LPGEG.	
	RVVERLALVLO	GALLVRYAPPE <mark>VA</mark> D AF C	ASRL GGDWGTAF <mark>G</mark> T <mark>L</mark> P	P.HSLDL.AT <mark>VV</mark> E RA RPVA	