

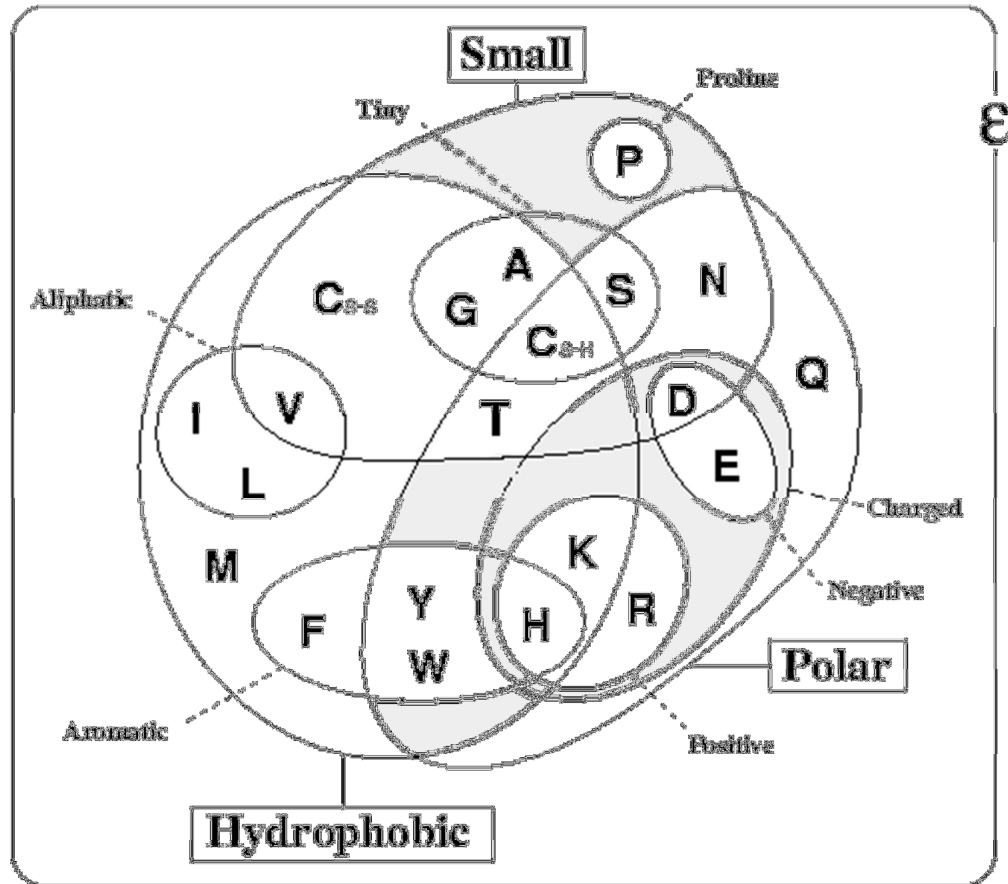
APPENDICES

Appendix A

A-1: Table of Standard Amino Acid

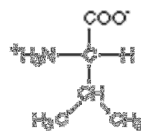
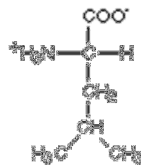
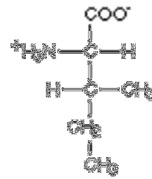
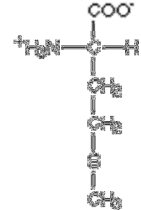
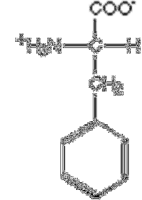
Name	One-letter code	Three-letter-code
Alanine	A	Ala
Cysteine	C	Cys
Aspartic Acid	D	Asp
Glutamic Acid	E	Glu
Phenylalanine	F	Phe
Glycine	G	Gly
Histidine	H	His
Isoleucine	I	Ile
Lysine	K	Lys
Leucine	L	Leu
Methionine	M	Met
Asparagine	N	Asn
Proline	P	Pro
Glutamine	Q	Gln
Arginine	R	Arg
Serine	S	Ser
Threonine	T	Thr
Valine	V	Val
Tryptophan	W	Trp
Tyrosine	Y	Tyr

A-2: Amino Acid Properties

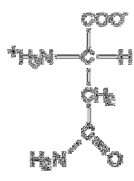
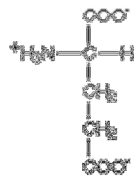
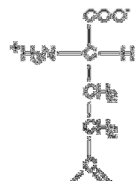
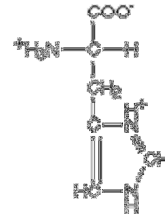
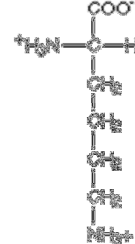
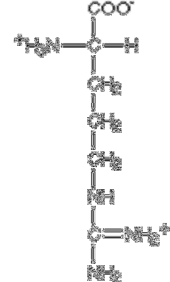
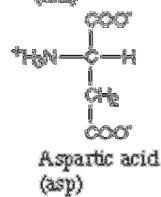


A-3: Amino Acid Side Groups Structural Formula

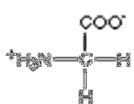
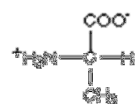
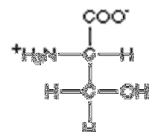
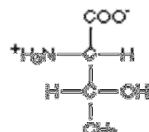
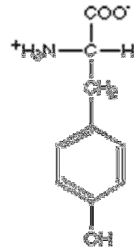
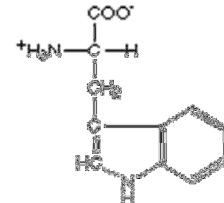
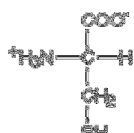
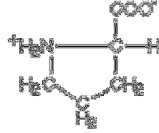
Amino acids with hydrophobic side groups

Valine
(val)Leucine
(leu)Isoleucine
(ile)Methionine
(met)Phenylalanine
(phe)

Amino acids with hydrophilic side groups

Asparagine
(asn)Glutamic acid
(glu)Glutamine
(gln)Histidine
(his)Lysine
(lys)Arginine
(arg)Aspartic acid
(asp)

Amino acids that are in between

Glycine
(gly)Alanine
(ala)Serine
(ser)Threonine
(thr)Tyrosine
(tyr)Tryptophan
(trp)Cysteine
(cys)Proline
(pro)

A-4: Results of Multiple Sequences Alignment of 50 Sequences

Marinomonas_posidonica	-----MKCKAAVAVWGPQQ	13
Marinomonas_mediterranea	-----MKCKAAVAVWGPQQ	13
Marinobacterium_stanieri	-----MKSRAAVAVWAKAGD	13
Bdellovibrio_bacteriovorus	-----MKIKAAVAVWKAGA	13
Mus_musculus_Chain_A	-----GTQGGVIKCKAAIAWKTGS	19
Mus_musculus_Chain_B	-----GTQGGVIKCKAAIAWKTGS	19
Laribacter_hongkongensis	-----MTIKSRAAVAFAGQ	15
Synechococcus_sp.	-----MIRSRAAVAWAAGQ	14
Methylomicrobium_album	-----MIKSRAAIAWGSGR	14
Pantoea_ananatis	-----MNMIKTRAAVWAAGE	16
Pantoea_stewartii	-----MNMIKTRAAVWAAGE	16
Pantoea_vagans	-----MNMIKTRAAVWAAGE	16
Erwinia_amylovora	-----MQMIKTRAAVWAAGE	16
Erwinia_pyrifoliae	-----MQMIKTRAAVWAAGE	16
Erwinia_tasmaniensis	-----MQMIKTRAAVWAAGE	16
Commensalibacter_intestini	-----MDFIKTRAAVWGPQK	16
Glaciecola_sp.	-----MQS IKTRAAVWAAGE	16
Pseudoalteromonas_atlantica	-----MQS IKTRAAVWAAGE	16
Tolumonas_auensis	-----MNMIKTRAAVWEAGK	16
Actinobacillus_ureae	-----MEF IKTRAAVAVAPNE	16
Actinobacillus_pleuropneumonia	-----MEF IKTRAAVAVAPNE	16
Simonsiella_muelleri	-----MTQF IKTRAAVAYAPNQ	17
Moraxella_catarrhalis	-----MDF IKTRAAVWAANE	16
Alishewanella_jeotgali	-----MQMIKTRAAVWGPQQ	16
Photobacterium_profundum	-----MSDQF IKSKAAIAWGPQK	18
Vibrio_coralliilyticus	-----MALDIQPGQTSIKSKAMVAWAAGE	24
Oceanobacter_sp.	-----MSDTF IKSKAAIAWGPQQ	18
Marinobacter_aquaeolei	-----MAEIIKSKAAIAWGPQQ	17
Marinobacter_hydrocarbonoclast	-----MAEMIKSKAAIAWGPQQ	17
Marinobacter_algicola	-----MIKSRAAIAWGPQQ	14
Marinobacter_manganoxydans	-----MTQTIKSKAAIAWGPQK	17
Oceanospirillum_sp.	-----MSEQMIKSRAAIAWGNPQ	18
Pseudoalteromonas_haloplanktis	-----MSDKF IKSKAAIAWGPQK	18
Psychromonas_ingrahamii	-----MTEKY IKSKAAIAWGNPQ	18
Saccharophagus_degradans	-----MTDTF IKSRAAVWAAGE	18
Reinekea_sp.	-----MTAETLTCRAAVWAAGE	18
Ferrimonas_balearica	-----MTTPQTIKSKAAVAVWGPQK	19
Shewanella_halifaxensis	-----MMTAKTIKSKAAVAVAVGE	19
Shewanella_pealeana	-----MTAKTIKSKAAVAVAVGE	18
Shewanella_woodyi	-----MTAQT IKSKAAVAVAVGE	18
Shewanella_sediminis	-----MTAQT IKSKAAVAVAVGE	18
Shewanella_piezotolerans	-----MTAQT IKSKAAVAVAVGE	18
Shewanella_oneidensis	-----MTAQLKSKAAVAVAVGE	18
Chromobacterium_violaceum	-----MSHDI IRCQAAVWAAGQ	18
Alteromonas_sp.	-----MSAEPITCKAAVAVWKAGE	18
Aeromonas_caviae	-----MAQVQSIKCKAAIAWGPQQ	19
Aeromonas_salmonicida	-----MAQVQSIKCKAAIAWGPQQ	19
Aeromonas_hydrophila	-----MAQVQSIKCKAAIAWGPQQ	19
Aeromonas_veronii	-----MAQVQSIKCKAAIAWGPQQ	19
Kangiella_koreensis	-----MSNEVIKCKAAVAVWEAGK	18
P	-----A--A-----	
	: * * :	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGEDPEGIFPAILGHE	63
Marinomonas_mediterranea	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGDDPEGIFPAILGHE	63
Marinobacterium_stanieri	PLTIEEVDVQGPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Bdellovibrio_bacteriovorus	PLSIEEVDLEGGKAGEVLIRVVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Mus_musculus_Chain_A	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKKKALFPVVLGHE	68
Mus_musculus_Chain_B	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKKKALFPVVLGHE	68
Laribacter_hongkongensis	PLEIVEVDVAPPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	65
Synechococcus_sp.	PLEITEIEVAPPAAGEVLLRVVASGVCHTDAFTLSGQDPEGVFPAILGHE	64
Methylomicrobium_album	PLEVTEVNVAPPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	64
Pantoea_ananatis	PLKIEEVDLMPPQKAGEVLVRIVATGVCHTDAFTLSGSDPEGVFPAILGHE	66
Pantoea_stewartii	PLKIEEVDLMPPQKAGEVLVRIVATGVCHTDAFTLSGSDPEGVFPAILGHE	66
Pantoea_vagans	PLKIEEVDLMPPQKAGEVLVRIVATGVCHTDAFTLSGTDPEGVFPAILGHE	66
Erwinia_amylovora	PLKIEEVDLMPPQKAGEVLVRIVATGVCHTDAFTLSGKDPEGVFPAILGHE	66
Erwinia_pyrifoliae	PLKIEEVDLMPPQKAGEVLVRIVATGVCHTDAFTLSGKDPEGVFPAILGHE	66
Erwinia_tasmaniensis	PLKIEEVDLMPPQKAGEVLVRIVATGVCHTDAFTLSGKDPEGVFPAILGHE	66
Commensalibacter_intestini	PLTIEEVDLMPPQKAGEVLIRIVATGVCHTDAFTLSGADPEGIFPAILGHE	66
Glaciecola_sp.	PLTIEEVDLMPPQKAGEVLIRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	66
Pseudoalteromonas_atlantica	PLSIEEVDLMPPQKAGEVLIRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	66
Tolumonas_auensis	PLSIEEVDLMPPQKAGEVLVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	66
Actinobacillus_ureae	PLKIEEVDLMPPQKAGEVLRLVATGVCHTDAFTLSGQDSEGVFPAILGHE	66
Actinobacillus_pleurpneumonia	PLKIEEVDLMPPQKAGEVLRLVATGVCHTDAFTLSGQDSEGVFPAILGHE	66
Simonsiella_muelleri	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGQDSEGVFPAILGHE	67
Moraxella_catarrhalis	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	66
Alishewanella_jeotgali	PLSIEEVDLMPPQKAGEVLVRIVASGVCHTDAFTLSGEDPEGIFPAILGHE	66
Photobacterium_profundum	PLSIEEIDVMLPRAGEVLVRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Vibrio_coralliilyticus	PLKMEEVDVQLPKAGEVLVRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	74
Oceanobacter_sp.	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGVFPAILGHE	68
Marinobacter_aquaeolei	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGVFPAILGHE	67
Marinobacter_hydrocarbonoclast	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGVFPAILGHE	67
Marinobacter_algicola	PLSIEEVDVMPKAGEVLVKI IASGVCHTDAFTLSGEDPEGVFPAILGHE	64
Marinobacter_manganoxydans	PLSIEEVDVMPKAGEVLVRIVASGVCHTDAFTLSGEDPEGIFPAILGHE	67
Oceanospirillum_sp.	PLSIEEVDVMPKAGEVLVRIVATGVCHTDAFTLSGEDPEGIFPAILGHE	68
Pseudoalteromonas_haloplanktis	PLSIEEIDVMLPRKAGEVLVKI IASGVCHTDAFTLSGDDPEGIFPAILGHE	68
Psychromonas_ingrahamii	PLSIEEIDVMLPKKAGEVLVKI IASGVCHTDAFTLSGEDPEGVFPAILGHE	68
Saccharophagus_degradans	PLSIEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGIFPAILGHE	68
Reinekea_sp.	PLKVEIVQVAPPKAGEVRIKVVASGVCHTDAFTLSGDDPEGIFPAILGHE	68
Ferrimonas_balearica	PLSIEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGDDPEGVFPAILGHE	69
Shewanella_halifaxensis	PLTMEIVDVMPKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	69
Shewanella_pealeana	PLTMEIVDVMPKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_woodyi	PLSMEIVDVMPKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_sediminis	PLSMEIVDVMPKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_piezotolerans	PLTMEIVDVMPKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_oneidensis	PLSIEIVDVMPKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Chromobacterium_violaceum	PLSIEEIEVHPPKAGEVVRVIVATGVCHTDAFTLSGADPEGVFPAILGHE	68
Alteromonas_sp.	PLSIEEIVVAPPKAGEVRIKMIATGVCHTDAFTLSGADPEGVFPAILGHE	68
Aeromonas_caviae	PLSIEEVEVMPKAGEVVRIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Aeromonas_salmonicida	PLSIEEVEVMPKAGEVVRIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Aeromonas_hydrophila	PLSIEEVEVMPKAGEVVRIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Aeromonas_veronii	PLSIEEVEVMPKAGEVVRIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Kangiella_koreensis	PLSIEEVEVMPKAGEVVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	68
P	PL-----P---EV-----A--VC-TD-----FP--LGHE	
	** : : : * ** : : : : ** ** : . . . ** :****	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	GAGVVEAVGEGVTTLKP GDHVIPLYTAECGECKFCQSGKTNLCQAVR---	110
Marinomonas_mediterranea	GAGVVEAVGEGVTTLKP GDHVIPLYTAECGECKFCCKSGKTNLCQAVR---	110
Marinobacterium_stanieri	GAGVVEAVGEGVTTLKP GDHVIPLYTAECGECKFCCKSGKTNLCQAVR---	110
Bdellovibrio_bacteriovorus	GGGIVEEVGEGVTTLKKGDHVIPLYTPECKECKFCLSGKTNLCQAVR---	110
Mus_musculus_Chain_A	CAGIVESVGPVGNFPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRNFK	118
Mus_musculus_Chain_B	CAGIVESVGPVGNFPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRNFK	118
Laribacter_hongkongensis	GGGIVEAVGEGVTSVAVGDHVIPLYTAECRECKFCCKSGKTNLCQAVR---	112
Synechococcus_sp.	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRCACSFCLSGKTNLCQAVR---	111
Methylomicrobium_album	GGGIVEAVGEGVTSVAVGDHVIPLYTPECCKCKFCLSGKTNLCQAVR---	111
Pantoea_ananatis	GGGIVEAVGEGVTSVEVGDHVIPLYTPECQCKFCCKSGKTNLCQAVR---	113
Pantoea_stewartii	GGGIVEAVGEGVTSVEVGDHVIPLYTPECQCKFCCKSGKTNLCQAVR---	113
Pantoea_vagans	GGGIVEAVGEGVTSVEVGDHVIPLYTPECQCKFCCKSGKTNLCQAVR---	113
Erwinia_amylovora	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRCQCKFCCKSGKTNLCQAVR---	113
Erwinia_pyrifoliae	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRCQCKFCCKSGKTNLCQAVR---	113
Erwinia_tasmaniensis	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRCQCKFCCKSGKTNLCQAVR---	113
Commensalibacter_intestini	GAGIVEAVGEGVTSISVGDYVIPLYTPECCKCYCLSGKTNLCQAVR---	113
Glaciecola_sp.	GAGIVEAIGEGVTSVEVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	113
Pseudoalteromonas_atlantica	GAGIVEAIGEGVTSVEVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	113
Tolumonas_auensis	GAGIVEAIGEGVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	113
Actinobacillus_ureae	GAGIVEAVGEGVTDKVGVDHVIPLYTAECRCCKFCCKSGKTNLCQAVR---	113
Actinobacillus_pleuropneumonia	GAGIVEAVGEGVTDKVGVDHVIPLYTAECRCCKFCCKSGKTNLCQAVR---	113
Simonsiella_muelleri	GAGIVEAVGEGVTDFAVGDHVIPLYTAECQCKFCCKSGKTNLCQAVR---	114
Moraxella_catarrhalis	GAGIVEAVGEGVTDFAVGDHVIPLYTAECQCKFCCKSGKTNLCQAVR---	113
Alishewanella_jeotgali	GGGIVEAVGEGVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	113
Photobacterium_profundum	GGGIVEQIGEGVTSVQVGDHVIPLYTAECCKFCCKSGKTNLCQAVR---	115
Vibrio_coralliilyticus	GGGIVEMVGEVTSVEVGDHVIPLYTAECCKFCCKSGKTNLCQAVR---	121
Oceanobacter_sp.	GGGIVEAVGEGVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Marinobacter_aquaeolei	GGGIVEAVGEGVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	114
Marinobacter_hydrocarbonoclast	GGGIVEAIGEGVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	114
Marinobacter_algicola	GGGIVEAVGEGVTSVEIGDHIPLYTPECCKFCCKSGKTNLCQAVR---	111
Marinobacter_manganoxydans	GGGIVEAVGEGVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	114
Oceanospirillum_sp.	GGGIVEAVGEGVTSVQVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Pseudoalteromonas_haloplanktis	GGGIVEQVGEVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Psychromonas_ingrahamii	GGGIVEQVGEVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Saccharophagus_degradans	GGGIVEALGEGVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Reinekea_sp.	GGGIVEAIGEGVTSVSVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Ferrimonas_balearica	GGGIVESIGEGVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	116
Shewanella_halifaxensis	GGGIVESIGEGVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	116
Shewanella_pealeana	GGGIVESIGEGVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Shewanella_woodyi	GGGIVESIGEGVTSVQVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Shewanella_sediminis	GGGIVESIGEGVTSVQVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Shewanella_piezotolerans	GGGIVESIGEGVTSVQVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Shewanella_oneidensis	GGGIVESIGEGVTSVQVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Chromobacterium_violaceum	GGGVVESVGPVTSVAVGDHVIPLYTPECRECKFCCKSGKTNLCQAVR---	115
Alteromonas_sp.	GGGVVESVGEVTSVAVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
Aeromonas_caviae	GGGIVESVGEVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	116
Aeromonas_salmonicida	GGGIVESIGEGVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	116
Aeromonas_hydrophila	GGGIVESVGEVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	116
Aeromonas_veronii	GGGIVESVGEVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	116
Kangiella_koreensis	GGGIVESVGEVTSVKVGDHVIPLYTPECCKFCCKSGKTNLCQAVR---	115
P	---VE--G--VT---GD--VIP-----C--C--S--TNLC---R---	
	..: ** : * . * * . * * * * : : : * * . * * * * * : *	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	-ETQGKGLMPDGTSRFSINGEPIFHYMGTSTFSEYSVVPEISLAKIHVDA	159
Marinomonas_mediterranea	-ETQGKGLMPDGTSRFSINGEPIFHYMGTSTFSEYSVVPEISLAKIHVDA	159
Marinobacterium_stanieri	-ATQGGQLMPDGTSRFSLNGETLYHYMGTSTFSEYTVVPEISLAKIHVDA	159
Bdellovibrio_bacteriovorus	-ATQGKGLMPDGTSRFSKDGKMIHHYMGCSFSAEYTVVPEIALAKVNPAA	159
Mus_musculus_Chain_A	YPTIDQELMEDRTSRFTCKGRS IYHFMGVSSFSQYTVVSEANLARVDDEA	168
Mus_musculus_Chain_B	YPTIDQELMEDRTSRFTCKGRS IYHFMGVSSFSQYTVVSEANLARVDDEA	168
Laribacter_hongkongensis	-ATQGKGLMPDGTTRFSYKGGPIYHYMGTSTFSEYTVVPEISLAKIPKDA	161
Synechococcus_sp.	-GTQGRGLMPDGTSRFSSAGRLIHHYMGTSFSEYTVVPEIAVARISKEA	160
Methylomicrobium_album	-ATQGKGLMPDGTSRFSKDGKPIFHYMGTSTFSEYTVLPEIAVARINKEA	160
Pantoea_ananatis	-TTQGKGLMPDGTTRFFKDGKPIFHYMGTSTFSEYTVVPEISLAKISKEA	162
Pantoea_stewartii	-TTQGKGLMPDGTTRFFKDGKPIFHYMGTSTFSEYTVVPEISLAKISKEA	162
Pantoea_vagans	-TTQGKGLMPDGTTRFFKDGKPIFHYMGTSTFSEYTVIPEISLAKISKEA	162
Erwinia_amylovora	-TTQGKGLMPDGTTRFFKDGQPVYHYMGTSTFSEYTVVPEISLAKISKEA	162
Erwinia_pyrifoliae	-TTQGKGLMPDGTTRFFKDGQPIYHYMGTSTFSEYTVVPEISLAKISKEA	162
Erwinia_tasmaniensis	-TTQGKGLMPDGTTRFFKDGQPIYHYMGTSTFSEYTVVPEISLAKISKEA	162
Commensalibacter_intestini	-VTQGKGLMPDGTTRFFKDGKPIFHYMGTSTFSEYTVVPEISVAKISKEA	162
Glaciecola_sp.	-TTQGGQLMPDGTTRFSKNGKPIYHYMGTSTFAEHTVVPEIALAKIPKEA	162
Pseudoalteromonas_atlantica	-ATQGKGLMPDGTTRFSKNGKPIYHYMGTSTFAEHTVVPEIALAKIPKEA	162
Tolumonas_auensis	-ATQGKGLMPDGTTRFFKDGKPIFHYMGTSTFAEHTVVPEISLAKISKDA	162
Actinobacillus_ureae	-ETQGKGLMPDGTTRFFKDGQPIFHYMGTSTFSEYTVVSEYSLAKIQENA	162
Actinobacillus_pleuropneumonia	-ETQGKGLMPDGTTRFFKDGQPIFHYMGTSTFSEYTVVSEYSLAKIQENA	162
Simonsiella_muelleri	-ATQGKGLMPDGTTRFYKDGKPIYHYMGTSTFSEYTVVSVQYSLAKIQDDA	163
Moraxella_catarrhalis	-ETQGGKGLMPDGTTRFFKDGKPIYHYMGTSTFSEYTVVSVQYSLAKIQKDA	162
Alishewanella_jeotgali	-ATQGKGLMPDGTTRFSKDGKPIYHYMGTSTFSEYTVLPEISLAKVNKEA	162
Photobacterium_profundum	-ETQGGKGLMPDGTTRFYKDGQPLFHYMGCSFSEFTVLPEISLAKVNKEA	164
Vibrio_coralliilyticus	-ETQGGKGLMPDGTTRFSINGETIYHYMGCSFSEYTVLPEISLAKVNKEA	170
Oceanobacter_sp.	-ETQGGKGLMPDGTTRFYKDGKPIYHYMGTSTFSEYTVLPDISLAKVNKSA	164
Marinobacter_aquaeolei	-ETQGGKGLMPDGTTRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Marinobacter_hydrocarbonoclast	-ETQGGKGLMPDGTTRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Marinobacter_algicola	-ETQGGKGLMPDGTTRFYKDGQPIHHYMGCSFSEYTVLPEISLAKVNKDA	160
Marinobacter_manganoxydans	-ETQGGKGLMPDGTTRFSLNGEPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Oceanospirillum_sp.	-ETQGGKGLMPDGTTRFYKDGKPIYHYMGCSFSEYTVLPEISLAKVNKEA	164
Pseudoalteromonas_haloplanktis	-ETQGGKGLMPDGTTRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKSA	164
Psychromonas_ingrahamii	-ETQGGKGLMPDGTTRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKAA	164
Saccharophagus_degradans	-ATQGGKGLMPDGTTRFYKDGQPIYHYMGTSTFSEYTVLPEISLAKVNQKA	164
Reinekea_sp.	-TTQGGQLMPDGTSRFSIDGQPIFHYMGCSFSEYTVLPEISLAKVNPQA	164
Ferrimonas_balearica	-ETQGGKGLMPDGTTRFSKDGKPIYHYMGCSFSEYTVLPEISLAKVNPAA	165
Shewanella_halifaxensis	-ETQGGKGLMPDGTTRFSKDGVEIFHYMGTSTFSEYTVLPEISLAKVNPDA	165
Shewanella_pealeana	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGTSTFSEYTVLPEISLAKVNPDA	164
Shewanella_woodyi	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGTSTFSEYTVLPEISLAKVNPDA	164
Shewanella_sediminis	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGTSTFSEYTVLPEISLAKVNPDA	164
Shewanella_piezotolerans	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGTSTFSEYTVLPEISLAKVNPDA	164
Shewanella_oneidensis	-ETQGGKGLMPDGTTRFSKDGQIIYHYMGTSTFSEYTVLPEISLAKVNPDA	164
Chromobacterium_violaceum	-ATQGGKGLMPDGTTRFSKDGKPIYHYMGTSTFSEYTVLPEISLAKVNKAA	164
Alteromonas_sp.	-ATQGGKGLMPDGTTRFTVNGKPVFHYMGTSTFSEYTVLPEISVAKVNKNA	164
Aeromonas_caviae	-ATQGGKGLMPDGTTRFSKDGQPIYHYMGTSTFSEYTVLPEISIAKVDPA	165
Aeromonas_salmonicida	-ATQGGKGLMPDGTTRFSKDGQPIYHYMGTSTFSEYTVLPEISIAKVDPA	165
Aeromonas_hydrophila	-ATQGGKGLMPDGTTRFSKDGQPIYHYMGTSTFSEYTVLPEISIAKVDPA	165
Aeromonas_veronii	-ATQGGKGLMPDGTTRFSKDGQPIYHYMGTSTFSEYTVLPEISIAKVDPA	165
Kangiella_koreensis	-ETQGGKGLMPDGTTRFSINGKPIYHYMGTSTFSEYTVLPEISLAKVNPKA	164
P	--T-----LM-D-T-RF---G---H-MG-S-F-----V-----A-----A	
	* .: * * * * * * .: * * * * * * .: * * * * * * .: * * * * * *	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	PLEKVLLGCGITTTGIGAVLNTAKVEEGATIAVFGGLGGIGLSVIQGARMA	209
Marinomonas_mediterranea	PLEKVLLGCGITTTGIGAVLNTAKVEEGATVAVFGGLGGIGLSVIQGARMA	209
Marinobacterium_stanieri	PLEKVLLGCGITTTGIGAVLNTAKVEPGSTVAIFGMGGIGLSVIQGARMA	209
Bdellovibrio_bacteriovorus	PLDKVLLGCGVTTGIGAVLNTAKVEKATVAVFGGLGGIGLSVIQGAKMA	209
Mus_musculus_Chain_A	NLERVCLIGCGFSSSGYAAINTAKVTPGSTCAVFGLCVGLSAIIGCKIA	218
Mus_musculus_Chain_B	NLERVCLIGCGFSSSGYAAINTAKVTPGSTCAVFGLCVGLSAIIGCKIA	218
Laribacter_hongkongensis	PLEKVLLGCGVTTGIGAVLNTAKVTAGSTVAVFGGLGGIGLAAIIGASMA	211
Synechococcus_sp.	PLEKVLLGCGVTTGIGAVLNTAKVEPGSTVAVFGGLGGIGLAVIIGAVMA	210
Methylomicrobium_album	PLEKVLLGCGVTTGIGAVMNTAKVEEGATVAVFGGLGGIGLSAIIGAVMA	210
Pantoea_ananatis	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Pantoea_stewartii	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Pantoea_vagans	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAVIIGAKMA	212
Erwinia_amylovora	PLEEVLLGCGVTTGMGAVINTANVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Erwinia_pyrifoliae	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Erwinia_tasmaniensis	PLEEVLLGCGVTTGMGAVLNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Commensalibacter_intestini	PLEKVLLGCGITTTGMGAVNTAKVQPGDSVAVFGGLGGIGLSVINGAKAA	212
Glaciecola_sp.	PLEKVLLGCGVTTGMGAVNTAKVKEGDTVAVFGGLGGIGLSVLIIGAKMA	212
Pseudoalteromonas_atlantica	PLEEVLLGCGVTTGMGAVNTAKVQEGDTVAVFGGLGGIGLSVLIIGAKMA	212
Tolumonas_auensis	PLEKVLLGCGVTTGMGAVMNTAKVQPGDTVAVFGGLGGIGLSVLIIGAVMA	212
Actinobacillus_ureae	PLDEVLLGCGVTTGIGAVTRTAKVKQGDVAVFGGLGGIGLAAIIGARMA	212
Actinobacillus_pleuropneumonia	PLDEVLLGCGVTTGIGAVTRTAKVKKGDVAVFGGLGGIGLAAIIGARMA	212
Simonsiella_muelleri	PLEEVLLGCGVTTGIGAVTKTAKVKAGDTVAVFGGLGGIGLAAIIGARMS	213
Moraxella_catarrhalis	PLEEVLLGCGVTTGMGAVLTKAKVKPGDTVAIFGLGGIGLAAVIGAKMA	212
Alishewanella_jeotgali	PLEEVLLGCGVTTGMGAVFNTAKVKPGDTVAIFGLGGIGLSAVIASVMA	212
Photobacterium_profundum	PLEEVLLGCGVTTGMGAVLNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	214
Vibrio_coralliilyticus	PLEEVLLGCGVTTGMGAVLNTAKVKEGDTVAIFGLGGIGLSAIIGARMA	220
Oceanobacter_sp.	PLEEVLLGCGVTTGMGAVMNTAKVQAGDSVAIFGLGGIGLSAIIGATMA	214
Marinobacter_aquaeolei	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGGLGGIGLSAIIGATMA	213
Marinobacter_hydrocarbonoclast	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGGLGGIGLSAIIGATMA	213
Marinobacter_algicola	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGGLGGIGLSAIIGATMA	210
Marinobacter_manganoxydans	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAIIGATMA	213
Oceanospirillum_sp.	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGGLGGIGLSAVIGATMA	214
Pseudoalteromonas_haloplanktis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGGLGGIGLSAVIGATMA	214
Psychromonas_ingrahamii	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGGLGGIGLSAVIGATMA	214
Saccharophagus_degradans	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAVIGATMA	214
Reinekea_sp.	PLEEVLLGCGVTTGMGAVMNTAKVQSSDTVAIFGLGGIGLSAIIGATMA	214
Ferrimonas_balearica	PLEEVLLGCGVTTGMGAVNTANVQPGDTVAVFGGLGGIGLSAIIGAAMA	215
Shewanella_halifaxensis	PLEEVLLGCGVTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAIIGAVMA	215
Shewanella_pealeana	PLEEVLLGCGVTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAIIGAVMA	214
Shewanella_woodyi	PLEEVLLGCGVTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAVIGATMA	214
Shewanella_sediminis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAVIGATMA	214
Shewanella_piezotolerans	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAVIGAQMA	214
Shewanella_oneidensis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAVIGATMA	214
Chromobacterium_violaceum	PLEEVLLGCGVTTGMGAVNTAKVKAGDNVAVFGGLGGIGLSAIIGARMA	214
Alteromonas_sp.	PLEEICLLGCGVTTGMGAVANTAKVEEGASVAVFGGLGGIGLATIOGARLA	214
Aeromonas_caviae	PLEEVLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAIIGARLA	215
Aeromonas_salmonicida	PLEEVLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAVIGARLA	215
Aeromonas_hydrophila	PLEEVLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAVIGARLA	215
Aeromonas_veronii	PLEEVLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAVIGARLA	215
Kangiella_koreensis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGGLGGIGLSAVIGAVMA	214
P	-L---CL-GCG---G-GA---TA-V-----A-FG-G--GL-----	
	*.:**:*:*:*.:* ** .**:* . . *:*:* *:*:* : . . :	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	GASKI I A I D I N E S K F E M A T Q F G A T D C V N P K N F D A P I Q Q V I V D M T D G G V D Y	259
Marinomonas_mediterranea	GASKI I A I D I N E S K F E M A T Q F G A T D C V N P K N F D A P I Q Q V I V D M T D G G V D Y	259
Marinobacterium_stanieri	GAERI I A I D I N E E K F E M A R Q F G A T D C V N P K D F S D P I Q Q V I V D M T D G G V D Y	259
Bdellovibrio_bacteriovorus	GASRI I A I D I N D A K W E M A Q K F G A T D F V N P K K H D K P I Q Q V I V E M T E W G V D Y	259
Mus_musculus_Chain_A	GASRI I A I D I N G E K F P K A K A L G A T D C L N P R E L D K P V Q D V I T E L T A G G V D Y	268
Mus_musculus_Chain_B	GASRI I A I D I N G E K F P K A K A L G A T D C L N P R E L D K P V Q D V I T E L T A G G V D Y	268
Laribacter_hongkongensis	KAGRI I A I D I N P D K F A K A R E L G A T D C I N P N D Y D K P I Q D V I V E L T D G G V D Y	261
Synechococcus_sp.	GASRI I G I D T N P E K F A I A R Q L G A S D C L D P G A F D A P I Q E V V I D L T D G G V D Y	260
Methylomicrobium_album	KASRI V A V D I N P A K F E I A Q Q L G A T D C L N P L D Y D R P I Q E V I V D L T D G G V D Y	260
Pantoea_ananatis	KAGRI I G I D I N T S K F D L A R K L G A T D L I N P K D Y D K P I Q D V I V E L T D G G V D Y	262
Pantoea_stewartii	KAGRI I G I D I N T S K F D L A R K L G A T D L I N P K D Y D K P I Q D V I V E L T D G G V D F	262
Pantoea_vagans	KAGRI I A I D L N T S K F D L A R K L G A T D L I N P K D Y D K P I Q D V I V E L T D G G V D F	262
Erwinia_amylovora	KAGRI I G I D I N S S K Y D L A R K L G A T D L I N P K D F D K P I Q D V I V E M T D G G V D F	262
Erwinia_pyrifoliae	KAGRI I G I D I N T S K Y D L A R K L G A T D L I T P K D F D K P I Q D V I V E M T D G G V D F	262
Erwinia_tasmaniensis	KAGRI I G I D I N T S K Y D L A R K L G A T D L I N P K D F D K P I Q D V I V E M T D G G V D F	262
Commensalibacter_intestini	KAERI I A I D I N T D K F D L A K K L G A T D C I N P K D Y Q K S I Q D V I V E L T N G G V D F	262
Glaciecola_sp.	NAGRI I A I D V N E D K F K I A K Q L G A T D V V N P K D F D K S I Q E V I V E M T D G G V D Y	262
Pseudoalteromonas_atlantica	NAGRI I A I D V N E D K F K I A K Q L G A T D V V N P K D F D K S I Q E V I V E M T D G G V D Y	262
Tolumonas_auensis	KASRI I A I D I N E D K F D I A K K L G A T D V V N P K N F D K P I Q D V I V E M T D G G V D F	262
Actinobacillus_ureae	GAGRI I A I D I N P A K F E K A K E L G A T D C I N P K D Y D K P I Q N V I I E M T D G G V D F	262
Actinobacillus_pleuropneumonia	GAGRI I A I D I N P A K F E K A K E L G A T D C I N P K D Y D K P I Q N V I I E M T D G G V D F	262
Simonsiella_muelleri	KASRI I A V D I N P D K F A K A K E L G A T D F V N P K D Y D K P I Q D V I I E M T D G G V D F	263
Moraxella_catarrhalis	GAGRI I V D I N E D K F A K A Q E L G A T D C V N P K N F D K P I Q Q V I I E M T D G G V D F	262
Alishewanella_jeotgali	KAGRI I A I D I N E D K F D I A K K L G A T D V V N P K K Y D K P I Q E V I V E M T D G G V D F	262
Photobacterium_profundum	GASRI I G V D I N E T K Y E L A K K L G A T D C I N P T K F D K P I Q D V I V E M T D G G V D Y	264
Vibrio_coralliilyticus	GASRI I G I D I N E S K F D L A K Q L G A T D C I N P Q K F D K P I Q E V I V E M T D G G V D Y	270
Oceanobacter_sp.	GASRI I G I D I N E S K F E L A K Q L G A T D C I N P N D Y D K P I Q E V I V E L T D G G V D F	264
Marinobacter_aquaeolei	KASRI I G I D I N S K F D L A R Q L G A T D C I N P K D Y D K P I Q E V I V E L T D G G V D F	263
Marinobacter_hydrocarbonoclast	KASRI I V I D I N N S K F D L A R Q L G A T D C I N P N D Y D K P I Q E V I V E L T D G G V D Y	263
Marinobacter_algicola	KASRI I A I D I N E S K F D L A R Q L G A T D C I N P K D Y E K P I Q E V I V E L T D G G V D Y	260
Marinobacter_manganoxydans	KASRI I A I D I N E S K F E L A R Q L G A T D C I N P K D Y D K P I Q E V I V E L T D G G V D Y	263
Oceanospirillum_sp.	KASRI I A I D I N S K F E L A K Q L G A T D C I N P K E F D K P I Q E V I V E M T D G G V D Y	264
Pseudoalteromonas_haloplanktis	KASRI I A I D I N E S K F E L A K K L G A T D F I N P K D Y D K P I Q D V I V E L T D G G V D Y	264
Psychromonas_ingrahamii	KASRI I A I D I N E S K F E L A K K L G A T D C I N P K D F D K A I Q D V I V E M T D G G V D Y	264
Saccharophagus_degradans	KASRI I A I D I N E S K F E L A K K L G A T D C I N P K L Y D K P I Q D V I V E L T D G G V D F	264
Reinekea_sp.	GASRI I A I D I N E S K F D L A K Q L G A T D C I N P K D Y D Q P I Q E V I V E L T D G G V D Y	264
Ferrimonas_balearica	KAGRI I A I D I N E S K F E L A R K L G A T D C I N P K D Y D K P I Q E V I V E M T D G G V D F	265
Shewanella_halifaxensis	KASRI I A I D I N E S K F E L A R K L G A T D C I N P K D Y D K P I Q E V I I E L T D G G V D Y	265
Shewanella_pealeana	KASRI I A I D I N E S K F E L A R K L G A T D C I N P K D Y D K P I Q E V I I E L T D G G V D Y	264
Shewanella_woodyi	KAARI I V I D I N E S K F E L A R K L G A T D C I N P K D Y D K P I Q D V I V E L T D G G V D Y	264
Shewanella_sediminis	KASRI I V I D I N E S K F E L A R K L G A T D F I N P K D Y D K P I Q D V I V E L T D G G V D Y	264
Shewanella_piezotolerans	KASRI I A I D I N E S K F E L A R Q L G A T D C I N P K D Y D K P I Q D V I V E L T D G G V D Y	264
Shewanella_oneidensis	KASRI I V I D I N E S K F E L A G K L G A T D F I N P K D Y D K P I Q D V I V E L T D G G V D Y	264
Chromobacterium_violaceum	GAGRI I G I D I N E G K F E L A K K L G A T D C V N P N G F D K P I Q D V I V E M T D G G V D F	264
Alteromonas_sp.	KAGRI I A I D I N E G K F E L A K K L G A T D C I N P K S F D K P I Q D V I V E L T D G G V D Y	264
Aeromonas_caviae	KAGRI I A I D I N E S K F E L A R K L G A T D C I N P N T F D K P I Q E V I V E M T D G G V D F	265
Aeromonas_salmonicida	KAGRI I A I D I N E S K F E L A R K L G A T D C I N P N D F D K P I Q E V I V E M T D G G V D F	265
Aeromonas_hydrophila	KAGRI I A I D I N E S K F E L A R K L G A T D C I N P N D Y D K P I Q E V I V E L T D G G V D F	265
Aeromonas_veronii	KAGRI I A I D I N E S K F E L A R K L G A T D C I N P N D Y D K P I Q E V I V E L T D G G V D F	265
Kangiella_koreensis	KASRI I A I D I N E S K F E L A K K L G A T D C V N P K D Y D K P I Q E V I V E M T D G G V D Y	264
P	-A--I---D-N--K---A---GA--D---P-----Q-V----T--GVD-	
	* : * : * * * * : * : * * * : * : * . . : * : * : * * * :	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	309
Marinomonas_mediterranea	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	309
Marinobacterium_stanieri	SFECIGNVQVMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	309
Bdellovibrio_bacteriovorus	SFECVGNLQMLRAALECAHRGWGQSVIGVAGAGQEI STRPFQLVTGRVW	309
Mus_musculus_Chain_A	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
Mus_musculus_Chain_B	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
Laribacter_hongkongensis	SFECVGNVLMRAALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	311
Synechococcus_sp.	SFECIGNVQVMRAALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	310
Methylomicrobium_album	SIECIGNVKVMRSALECCHKGWQSVIIGVAGAGQEI STRPFQLVTGRVW	310
Pantoea_ananatis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Pantoea_stewartii	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Pantoea_vagans	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Erwinia_amylovora	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Erwinia_pyrifoliae	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Erwinia_tasmaniensis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Commensalibacter_intestini	SFECIGNVKVMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Glaciecola_sp.	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Pseudoalteromonas_atlantica	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Tolumonas_auensis	SFECIGNVKVMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	312
Actinobacillus_ureae	SFECVGNADLMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTGRVW	312
Actinobacillus_pleuropneumonia	SFECVGNVDMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTGRVW	312
Simonsiella_muelleri	SFECVGNVDMRAALECCHKGWGESVIGVAPAGAEIKTRPFQLVTGRVW	313
Moraxella_catarrhalis	SFECIGNVDMRAALECCHKGWGESVIGVAPAGAEI STRPFQLVTGRVW	312
Alishewanella_jeotgali	SFECIGNVNMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	312
Photobacterium_profundum	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Vibrio_coralliilyticus	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	320
Oceanobacter_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Marinobacter_aquaeolei	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	313
Marinobacter_hydrocarbonoclast	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	313
Marinobacter_algicola	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	310
Marinobacter_manganoxydans	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	313
Oceanospirillum_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Pseudoalteromonas_haloplanktis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Psychromonas_ingrahamii	SFECIGNVDMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	314
Saccharophagus_degradans	SFECIGNVNMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTGRVW	314
Reinekea_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Ferrimonas_balearica	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	315
Shewanella_halifaxensis	SFECIGNIHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	315
Shewanella_pealeana	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Shewanella_woodyi	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Shewanella_sediminis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Shewanella_piezotolerans	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Shewanella_oneidensis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Chromobacterium_violaceum	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Alteromonas_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
Aeromonas_caviae	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	315
Aeromonas_salmonicida	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	315
Aeromonas_hydrophila	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	315
Aeromonas_veronii	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	315
Kangiella_koreensis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTGRVW	314
P	S--C-G-----A-----GWG-----G-----E-----GR--	
	: * . . : : * : . * * * . . : : * . * : . . : : *	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHTMPLEQINEAFDLMHE	359
Marinomonas_mediterranea	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHTMSLEKINDAFDLMHE	359
Marinobacterium_stanieri	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHTMGLEDINKAFDLMHE	359
Bdellovibrio_bacteriovorus	KGSAGGGVKGSRTELPYVEQYMSGEINIDDMVFTMPLEDINKAFDYMHE	359
Mus_musculus_Chain_A	NGTFFGGWKSVDSPNLSVDYKNNKFDLLLVTHALPFESINDAIDLKME	366
Mus_musculus_Chain_B	NGTFFGGWKSVDSPNLSVDYKNNKFDLLLVTHALPFESINDAIDLKME	366
Laribacter_hongkongensis	RGSAGGGVGRTELPAYVEKAQKGEIPLDTFVTHHTLPLEEINQAFELMH	361
Synechococcus_sp.	RGSAGGGVGRTELPYVERFQSGEIPLDTFVTHHTLPLEEINRAFELMHA	360
Methylomicrobium_album	RGSAGGGVHGRSELPYVERAQRGEIPLDVFVTHHTLPLEEINQAFELMH	360
Pantoea_ananatis	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFVTHHTMPLLEINDAFDLMHE	362
Pantoea_stewartii	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFVTHHTMPLAEINDAFDLMHE	362
Pantoea_vagans	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFVTHHTMPLLEINDAFDLMHE	362
Erwinia_amylovora	RGSAGGGVKGRTQLPGIVERVMNGEFQLNDFVTHHTMPLLEINDAFELMH	362
Erwinia_pyrifoliae	RGSAGGGVKGRTQLPGIVERVMNGEFRLNDFVTHHTMPLLEINDAFELMH	362
Erwinia_tasmaniensis	RGSAGGGVKGRTQLPGLVERYMNGEFQLNDFVTHHTMPLLEINDAFELMH	362
Commensalibacter_intestini	RGSAGGGVKGSRQLPNVNDYLDGKFQDDFVTHEMPLDQINKAFDLMHD	362
Glaciecola_sp.	RGSAGGGVKGSRQLPDYVQRYMDGEFELDTFVTHHTMGLLEDINTAFDLMHE	362
Pseudoalteromonas_atlantica	RGSAGGGVKGSRQLPDYVQRYMDGEFELDTFVTHHTMPLLEDINTAFDLMHE	362
Tolumonas_auensis	KGSAGGGVKGSRQLPGIVEQYMNNGEFELDTFVTHHTMGLDDINHAFLDLMHE	362
Actinobacillus_ureae	RGSAGGGVKGSRTELPGIDQFMKGEFKLRDFVTHHTMPLLEDINKAFDLMHQ	362
Actinobacillus_pleurpneumonia	RGSAGGGVKGSRTELPGIDQFMKGEFKLRDFVTHHTMPLLEDINKAFDLMHE	362
Simonsiella_muelleri	RGSAGGGVKGSRTELPDIDQYQHGEFKLSDFVTHHTMPLLEDINNAFLDLMHE	363
Moraxella_catarrhalis	RGSAGGGVKGSRTELPGIVSQYMQGDFALSDFVTHHTMPLDQINAAFLDLMHE	362
Alishewanella_jeotgali	RGTAFGGVKGSRSELPYVDRYLNNGEFELDTFVTHHTMPLLEDINKAFDLMHE	362
Photobacterium_profundum	RGSAGGGVKGSRSELPIVERVMAGEFALDDFVTHHTMGLLEDINTAFDLMHE	364
Vibrio_coralliilyticus	RGSAGGGVKGSRSELPIVERVMAGEFGLQEFVTHHTMGLDVAINDAFDLMHE	370
Oceanobacter_sp.	RGSAGGGVKGSRSELPIVEKYLAGEFKLNDFVTHHTMGLLEDINEAFDLMHE	364
Marinobacter_aquaeolei	RGSAGGGVKGSRSELPIVERYLQGEFKLNDFVTHHTMGLDDINEAFELMH	363
Marinobacter_hydrocarbonoclast	RGSAGGGVKGSRSELPIVERYLQGEFKLNDFVTHHTMGLDDINEAFELMH	363
Marinobacter_algicola	KGSAGGGVKGSRSELPIVERYLQGEFKLNDFVTHHTMGLDDINEAFELMH	360
Marinobacter_manganoxydans	KGSAGGGVKGSRSELPIVERVMQGEFKLNDFVTHHTMGLLEDINKAFDLMHE	363
Oceanospirillum_sp.	RGTAFGGVKGSRSELPIVERVMAGEFALDDFVTHHTMGLDKINEAFDLMHE	364
Pseudoalteromonas_haloplanktis	RGSAGGGVKGSRSELPDYVERYLAGEFKLSDFVTHHTMGLLEDINESFLDLMRR	364
Psychromonas_ingrahamii	KGSAGGGVKGSRTELPDYVERYLQGEFKLSDFVTHHTMPLLEDVNEAFELMHK	364
Saccharophagus_degradans	RGTAFGGVKGSRSELPIVEQYLAGDFKLDDFVTHHTMGLLEDINTAFDLMHH	364
Reinekea_sp.	RGTAFGGVKGSRSELPYVERYLDGEFKLSDFVTHHTMPLLEDINEAFDLMHE	364
Ferrimonas_balearica	RGSAGGGVKGSRSELPQYVERYLAGEFKLDDFVTHHTMGLDKINDAFDLMHQ	365
Shewanella_halifaxensis	KGSAGGGVKGSRSELPYVERYMAGEFKLDDFVTHHTMGLLEDQVNDAFDLMHE	365
Shewanella_pealeana	KGSAGGGVKGSRSELPYVERYMAGEFKLDDFVTHHTMGLLEDQVNDAFDLMHE	364
Shewanella_woodyi	KGSAGGGVKGSRSELPYVERYMAGEFKLNDFVTHHTMGLLEDQVNEAFDLMHE	364
Shewanella_sediminis	KGSAGGGVKGSRSELPYVERYMAGEFKLNDFVTHHTMGLLEDQVNDAFDLMHE	364
Shewanella_piezotolerans	KGSAGGGVKGSRSELPYVERYMAGEFKLNDFVTHHTMGLDQVNEAFDLMHE	364
Shewanella_oneidensis	KGSAGGGVKGSRSELPYVERYLAGEFKLSDFVTHHTMGLLEDQVNDAFDLMHQ	364
Chromobacterium_violaceum	RGSAGGGVGRTELPYVERYLAGEFKLDDFVTHHTMPLLEDVNEAFDLMHE	364
Alteromonas_sp.	RGTAFGGVKGSRQLPDYVERYLAGEFKLDDFVTHHTMPLLEDINKAFDLMHE	364
Aeromonas_caviae	RGSAGGGVGRSELPYVQRYMQGEFKLDDFVTHHTMPLLEDINKAFDLMHE	365
Aeromonas_salmonicida	RGSAGGGVGRSELPYVQRYMQGEFKLDDFVTHHTMPLLEDINKAFELMH	365
Aeromonas_hydrophila	RGSAGGGVGRSELPYVQRYMQGEFKLDDFVTHHTMGLLEDINKAFDLMHE	365
Aeromonas_veronii	RGSAGGGVGRSELPYVQRYMQGEFKLDDFVTHHTMGLLEDINKAFELMHQ	365
Kangiella_koreensis	KGTAFGGVKGSRSELPDYVERYLAGEFKLDDFVTHHTMPLLEDINKAFDLMHE	364
P	-G--FG-----P-----T-----N-----M--	
	.*: *. :. :.* :. :. : : :.* : : : * : : *	

A-4: Results of Multiple Sequences Alignment of 50 Sequences (cont)

Marinomonas_posidonica	GKSIRTVILFDQ-----	371
Marinomonas_mediterranea	GKSIRTVILFDQ-----	371
Marinobacterium_stanieri	GKSIRSVILFDQ-----	371
Bdellovibrio_bacteriovorus	GKSIRSVIKM-----	369
Mus_musculus_Chain_A	GKSIRTILTF-----	376
Mus_musculus_Chain_B	GKSIRTILTF-----	376
Laribacter_hongkongensis	GKSIRTVIHF-----	371
Synechococcus_sp.	GQSIRSVIHFNR-----	372
Methylomicrobium_album	GKSIRTVIHFNH-----	372
Pantoea_ananatis	GKSIRSVVHFNK-----	374
Pantoea_stewartii	GKSIRSVVHFNK-----	374
Pantoea_vagans	GKSIRSVVHFNK-----	374
Erwinia_amylovora	GKSIRTVVHFTKS-----	375
Erwinia_pyrifoliae	GKSIRTVVHFVAKS-----	375
Erwinia_tasmaniensis	GKSIRTVVHFVSKA-----	375
Commensalibacter_intestini	GKSIRTVIIRY-----	372
Glaciecola_sp.	GKSIRSVVHY-----	372
Pseudoalteromonas_atlantica	GKSIRSVVHY-----	372
Tolumonas_auensis	GKSIRTVILFDK-----	374
Actinobacillus_ureae	GKSIRTVIHF-----	372
Actinobacillus_pleuropneumonia	GKSIRTVIHF-----	372
Simonsiella_muelleri	GKSIRTVIHF-----	373
Moraxella_catarrhalis	GKSIRSVIHF-----	372
Alishewanella_jeotgali	GKSIRTVIHF-----	372
Photobacterium_profundum	GKSIRSVIHFDK-----	376
Vibrio_coralliilyticus	GKSIRTVIHMDQ-----	382
Oceanobacter_sp.	GKSIRSVIHYNK-----	376
Marinobacter_aquaeolei	GKSIRSVIHFDK-----	375
Marinobacter_hydrocarbonoclast	GKSIRSVIHFDK-----	375
Marinobacter_algicola	GKSIRSVIHFDK-----	372
Marinobacter_manganoxydans	GKSIRTVIHYDK-----	375
Oceanospirillum_sp.	GKSIRSVIHYDR-----	376
Pseudoalteromonas_haloplanktis	GESIRTVIHFVK-----	376
Psychromonas_ingrahamii	GESIRSVIHFAK-----	376
Saccharophagus_degradans	GKSIRSVIHFNK-----	376
Reinekea_sp.	GKSIRSVVHF-----	374
Ferrimonas_balearica	GKSIRSVIHFDQ-----	377
Shewanella_halifaxensis	GKSIRTVLHFGK-----	377
Shewanella_pealeana	GKSIRTVLHFDK-----	376
Shewanella_woodyi	GKSIRTVIHFVK-----	376
Shewanella_sediminis	GKSIRTVIHFVK-----	376
Shewanella_piezotolerans	GKSIRTVIHFVK-----	376
Shewanella_oneidensis	GKSIRTVIHFVK-----	376
Chromobacterium_violaceum	GKSIRSVIHYAAEPA-----	379
Alteromonas_sp.	GKSIRSVIHYA-----	375
Aeromonas_caviae	GKSIRTVIHY-----	375
Aeromonas_salmonicida	GKSIRTVIHY-----	375
Aeromonas_hydrophila	GKSIRSVIHY-----	375
Aeromonas_veronii	GKSIRTVIHY-----	375
Kangiella_koreensis	GKSIRSVIHY-----	374
P	G-SIR-----	
	*:***:~::~	

A-5: Results of Multiple Sequences Alignment of Partition P0

Marinomonas_posidonica	-----MKCKAAVAVWGPQG	13
Marinomonas_mediterranea	-----MKCKAAVAVWGPQG	13
Marinobacterium_stanieri	-----MKSRAAVAVWAGKD	13
Bdellovibrio_bacteriovorus	-----MKIKAAVAVWKAGA	13
Mus_musculus_Chain_A	-----GTQGKVIKCKAAIAWKTGS	19
Mus_musculus_Chain_B	-----GTQGKVIKCKAAIAWKTGS	19
Laribacter_hongkongensis	-----MTIKSRAAVAFAGQ	15
Synechococcus_sp.	-----MIRSRAAVAWAAGQ	14
Methylobacterium_album	-----MIKSRAAIAWGSGR	14
Pantoea_ananatis	-----MNMIKTRAAVWAAGE	16
Pantoea_stewartii	-----MNMIKTRAAVWAAGE	16
Pantoea_vagans	-----MNMIKTRAAVWAAGE	16
Erwinia_amylovora	-----MQMIKTRAAVWAAGE	16
Erwinia_pyrifoliae	-----MQMIKTRAAVWAAGE	16
Erwinia_tasmaniensis	-----MQMIKTRAAVWAAGE	16
Commensalibacter_intestini	-----MDFIKTRAAVWGPQK	16
Glaciecola_sp.	-----MQS IKTRAAVWAAGE	16
Pseudoalteromonas_atlantica	-----MQS IKTRAAVWAAGE	16
Tolumonas_auensis	-----MNMIKTRAAVWAAGE	16
Actinobacillus_ureae	-----MEF IKTRAAVWAPNE	16
Actinobacillus_pleuropneumonia	-----MEF IKTRAAVWAPNE	16
Simonsiella_muelleri	-----MTQF IKTRAAVAYAPNQ	17
Moraxella_catarrhalis	-----MDF IKTRAAVWAANE	16
Alishewanella_jeotgali	-----MQMIKTRAAVWGPQG	16
Photobacterium_profundum	-----MSDQF IKSKAAIAWGPQK	18
Vibrio_coralliilyticus	-----MALDIQPGQTSIKSKAMVAWAAGE	24
Oceanobacter_sp.	-----MSDTF IKSKAAIAWGPQG	18
Marinobacter_aquaeolei	-----MAEIIKSKAAIAWGPQG	17
Marinobacter_hydrocarbonoclast	-----MAEMIKSKAAIAWGPQG	17
Marinobacter_algicola	-----MIKSRAAIAWGPQG	14
Marinobacter_manganoxydans	-----MTQTIKSKAAIAWGPQK	17
Oceanospirillum_sp.	-----MSEQMIKSRAAIAWGPNQ	18
Pseudoalteromonas_haloplanktis	-----MSDKF IKSKAAIAWGPQK	18
Psychromonas_ingrahamii	-----MTEKY IKSKAAIAWGPNQ	18
Saccharophagus_degradans	-----MTDTF IKSRAAVWAAGE	18
Group 1	-----A--A-----	
	:: : * : * : .	
Reinekea_sp.	-----MTAETILTCAAVWAAGE	18
Ferrimonas_balearica	-----MTTPQTIKSKAAVAVWGPQK	19
Shewanella_halifaxensis	-----MMTAKTIKSKAAVAVAVGE	19
Shewanella_pealeana	-----MTAKTIKSKAAVAVAVGE	18
Shewanella_woodyi	-----MTAQT IKSKAAVAVAVGE	18
Shewanella_sediminis	-----MTAQT IKSKAAVAVAVGE	18
Shewanella_piezotolerans	-----MTAQT IKSKAAVAVAVGE	18
Shewanella_oneidensis	-----MTAQILKSKAAVAVAVGE	18
Chromobacterium_violaceum	-----MSHDI IRCQAAVWAAGQ	18
Alteromonas_sp.	-----MSAEPITCKAAVAVWAKAGE	18
Aeromonas_caviae	-----MAQVQSIKCKAAIAWGPQG	19
Aeromonas_salmonicida	-----MAQVQSIKCKAAIAWGPQG	19
Aeromonas_hydrophila	-----MAQVQSIKCKAAIAWGPQG	19
Aeromonas_veronii	-----MAQVQSIKCKAAIAWGPQG	19
Kangiella_koreensis	-----MSNEVIKCKAAVAVWAEAGK	18
Group 2	-----AA-AW--G-	
	. : . : * * * * *	
P0	-----A--A-----	
	: : * : * :	

A-5: Results of Multiple Sequences Alignment of Partition P0 (cont.)

Marinomonas_posidonica	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGEDPEGIFPAILGHE	63
Marinomonas_mediterranea	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGDDPEGIFPAILGHE	63
Marinobacterium_stanieri	PLTIEEVDVQGPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Bdellovibrio_bacteriovorus	PLSIEEVDLEGGKGEVLIRVVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Mus_musculus_Chain_A	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKKKALFPVVLGHE	68
Mus_musculus_Chain_B	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKKKALFPVVLGHE	68
Laribacter_hongkongensis	PLEIVEVDVAPPQKGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	65
Synechococcus_sp.	PLEITEIEVAPPAAGEVLLRVVASGVCHTDAFTLSGQDPEGVFPAILGHE	64
Methylomicrobium_album	PLEVTEVNVAPPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	64
Pantoea_ananatis	PLKIEEVDLMPQKGEVLVRIVATGVCHTDAFTLSGSDPEGVFPAILGHE	66
Pantoea_stewartii	PLKIEEVDLMPQKGEVLVRIVATGVCHTDAFTLSGSDPEGVFPAILGHE	66
Pantoea_vagans	PLKIEEVDLMPQKGEVLVRIVATGVCHTDAFTLSGTDPEGVFPAILGHE	66
Erwinia_amylovora	PLKIEEVDLMPQKGEVLVRIVATGVCHTDAFTLSGKDPEGVFPAILGHE	66
Erwinia_pyrifoliae	PLKIEEVDLMPQKGEVLVRIVATGVCHTDAFTLSGKDPEGVFPAILGHE	66
Erwinia_tasmaniensis	PLKIEEVDLMPQKGEVLVRIVATGVCHTDAFTLSGKDPEGVFPAILGHE	66
Commensalibacter_intestini	PLTIEEVDLMPQKGEVLIRIVATGVCHTDAFTLSGADPEGIFPAILGHE	66
Glaciecola_sp.	PLTIEEVDLMPQKGEVLIRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	66
Pseudoalteromonas_atlantica	PLSIEEVDLMPQKGEVLIRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	66
Tolumonas_auensis	PLSIEEVDLMPQKGEVLVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	66
Actinobacillus_ureae	PLKIEEVDLMPQKGEVLRLVATGVCHTDAFTLSGQDSEGVFPAILGHE	66
Actinobacillus_pleurpneumonia	PLKIEEVDLMPQKGEVLRLVATGVCHTDAFTLSGQDSEGVFPAILGHE	66
Simonsiella_muelleri	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGQDSEGVFPAILGHE	67
Moraxella_catarrhalis	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	66
Alishewanella_jeotgali	PLSIEEVDLMPQKGEVLVRIVASGVCHTDAFTLSGEDPEGIFPAILGHE	66
Photobacterium_profundum	PLSIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Vibrio_coralliilyticus	PLKMEEVDVQLPKAGEVLVRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	74
Oceanobacter_sp.	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGVFPAILGHE	68
Marinobacter_aquaeolei	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGVFPAILGHE	67
Marinobacter_hydrocarbonoclast	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGVFPAILGHE	67
Marinobacter_algicola	PLSIEEVDVMPKAGEVLVKI IASGVCHTDAFTLSGEDPEGVFPAILGHE	64
Marinobacter_manganoxydans	PLSIEEVDVMPQAGEVLVRIVASGVCHTDAFTLSGEDPEGIFPAILGHE	67
Oceanospirillum_sp.	PLSIEEVDVMPQAGEVLVRIVATGVCHTDAFTLSGEDPEGIFPAILGHE	68
Pseudoalteromonas_haloplanktis	PLSIEEIDLMPKAGEVLVKI IASGVCHTDAFTLSGDDPEGIFPAILGHE	68
Psychromonas_ingrahamii	PLSIEEIDLMPKAGEVLVKI IASGVCHTDAFTLSGEDPEGVFPAILGHE	68
Saccharophagus_degradans	PLSIEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGIFPAILGHE	68
P0 Group 1	PL---E-----P---EV-----A--VC-TD-----FP--LGHE	
	** : *::: * ** :::: ** ** :. . :. ** :****	
Reinekea_sp.	PLKIVTVQVAPPKAGEVRIKVVASGVCHTDAFTLSGDDPEGIFPAILGHE	68
Ferrimonas_balearica	PLSIEEVDVAPPKAGEVRIK IATGVCHTDAFTLSGDDPEGVFPAILGHE	69
Shewanella_halifaxensis	PLTMEIVDVMPQKGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	69
Shewanella_pealeana	PLTMEIVDVMPQKGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_woodyi	PLSMEIVDVMPQKGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_sediminis	PLSMEIVDVMPQKGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_piezotolerans	PLTMEIVDVMPQKGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_oneidensis	PLSIEIVDVMPQKGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Chromobacterium_violaceum	PLSIEEIEVHPPKAGEVVRVIVATGVCHTDAFTLSGADPEGVFPAILGHE	68
Alteromonas_sp.	PLSIEEIVVAPPKAGEVRIK IATGVCHTDAFTLSGADPEGVFPAILGHE	68
Aeromonas_caviae	PLSIEEIVVAPPKAGEVVRVIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Aeromonas_salmonicida	PLSIEEIVVAPPKAGEVVRVIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Aeromonas_hydrophila	PLSIEEIVVAPPKAGEVVRVIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Aeromonas_veronii	PLSIEEIVVAPPKAGEVVRVIVATGVCHTDAFTLSGEDPEGVFPAILGHE	69
Kangiella_koreensis	PLSIEEIVVAPPKAGEVVRVIVATGVCHTDAFTLSGDDPEGVFPAILGHE	68
P0 Group 2	PL--E---V-PP--GEVR---A--GVCHTDAFTLSG--DPEG--FP--ILGHE	
	.:* : * ** : **: : : :***** ***:** :****	
P0	PL-----P---EV-----A--VC-TD-----FP--LGHE	
	** : : : * ** :::: ** ** :. . :. ** :****	

A-5: Results of Multiple Sequences Alignment of Partition P0 (cont.)

Marinomonas_posidonica	GAGVVEAVGEGVTTLKP GDHVIPLYTAECGECKFCQSGKTNLCQAVR---	110
Marinomonas_mediterranea	GAGVVEAVGEGVTTLKP GDHVIPLYTAECGECKFCKSGKTNLCQAVR---	110
Marinobacterium_stanieri	GAGVVEAVGEGVTTLKP GDHVIPLYTAECGECKFCKSGKTNLCQAVR---	110
Bdellovibrio_bacteriovorus	GGGIVEEVGEGVTTLKG GDHVIPLYTPECKECKFCLSGKTNLCVRI---	110
Mus_musculus_Chain_A	CAGIVESVGPVGNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRNFK	118
Mus_musculus_Chain_B	CAGIVESVGPVGNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRNFK	118
Laribacter_hongkongensis	GGGIVEAVGEGVTSVAVGDHVIPLYTAECRECKFCKSGKTNLCQAVR---	112
Synechococcus_sp.	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRACSFCLSGKTNLCQAVR---	111
Methylomicrobium_album	GGGIVEAVGEGVTSVAVGDHVIPLYTPECGKCKFCLSGKTNLCQAVR---	111
Pantoea_ananatis	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGKCKFCLSGKTNLCQAVR---	113
Pantoea_stewartii	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGKCKFCLSGKTNLCQAVR---	113
Pantoea_vagans	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGKCKYCLSGKTNLCQAVR---	113
Erwinia_amylovora	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAVR---	113
Erwinia_pyrifoliae	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAVR---	113
Erwinia_tasmaniensis	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAVR---	113
Commensalibacter_intestini	GAGIVEAVGEGVTSISVGDYVIPLYTPECGKCKYCLSGKTNLCQAVR---	113
Glaciecola_sp.	GAGIVEAIGEGVTSVEVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	113
Pseudoalteromonas_atlantica	GAGIVEAIGEGVTSVEVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	113
Tolumonas_auensis	GAGIVEAIGEGVTSVAVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	113
Actinobacillus_ureae	GAGIVEAVGEGVTDKVG GDHVIPLYTAECRCKKFCLSGKTNLCQAVR---	113
Actinobacillus_pleuropneumonia	GAGIVEAVGEGVTDKVG GDHVIPLYTAECRCKKFCLSGKTNLCQAVR---	113
Simonsiella_muelleri	GAGIVEAVGEGVTDFAVGDHVIPLYTAECKQCKFCTSGKTNLCQAVR---	114
Moraxella_catarrhalis	GAGIVEAVGEGVTDFAVGDHVIPLYTAECGQCKMCLSNKTNLCQAVR---	113
Alishewanella_jeotgali	GGGIVEAVGEGVTSVAVGDHVIPLYTPECGKCKFCLSGKTNLCQAVR---	113
Photobacterium_profundum	GGGIVEQIGEGVTSVQVGDHVIPLYTAECGECKFCKSGKTNLCQAVR---	115
Vibrio_coralliilyticus	GGGIVEMVGEVTSVEVGDHVIPLYTAECGECKFCTSGKTNLCQAVR---	121
Oceanobacter_sp.	GGGIVEAVGEGVTSVAVGDHVIPLYTPECGECKFCTSGKTNLCQAVR---	115
Marinobacter_aquaeolei	GGGIVEAIGEGVTSVAVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	114
Marinobacter_hydrocarbonoclast	GGGIVEAIGEGVTSVAVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	114
Marinobacter_algicola	GGGIVEAVGEGVTSVEIGD HVIPLYTPECGECKFCLSGKTNLCQAVR---	111
Marinobacter_manganoxydans	GGGIVEAVGEGVTSVKVGDHVIPLYTPECGECKFCTSGKTNLCQAVR---	114
Oceanospirillum_sp.	GGGIVEAVGEGVTSVQVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	115
Pseudoalteromonas_haloplanktis	GGGIVEQVGEVTSVKVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	115
Psychromonas_ingrahamii	GGGIVEQIGEGVTSVKVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	115
Saccharophagus_degradans	GGGIVEALGEGVTSVAVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	115
Group 1	----VE--G--VT----GD-VIP-----C--C--C-S--TNLC---R---	
	..:*. * . * * . * * * * : : : * * . * * * * * : *	
Reinekea_sp.	GGGIVEAIGEGVTSVAVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	115
Ferrimonas_balearica	GGGIVESIGEGVTSVAVGDHVIPLYTPECGECKFCRSKTNLCQAVR---	116
Shewanella_halifaxensis	GGGIVESIGEGVTSVKVGDHVIPLYTPECGECKYCKSGKTNLCQAVR---	116
Shewanella_pealeana	GGGIVESIGEGVTSVKVGDHVIPLYTPECGECKYCKSGKTNLCQAVR---	115
Shewanella_woodyi	GGGIVESIGEGVTSVQVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	115
Shewanella_sediminis	GGGIVESIGEGVTSVQVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	115
Shewanella_piezotolerans	GGGIVESIGEGVTSVQVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	115
Shewanella_oneidensis	GGGIVESIGEGVTSVQVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	115
Chromobacterium_violaceum	GGGVVESVGPVTSVAVGDHVIPLYTPECRECKFCLSGKTNLCQAVR---	115
Alteromonas_sp.	GGGVVESVGEVTSVAVGDHVIPLYTPECGECKFCLSGKTNLCQAVR---	115
Aeromonas_caviae	GGGIVESVGEVTSVKVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	116
Aeromonas_salmonicida	GGGIVESIGEGVTSVKVGDHVIPLYTPECGECKFCRSKTNLCQAVR---	116
Aeromonas_hydrophila	GGGIVESVGEVTSVKVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	116
Aeromonas_veronii	GGGIVESVGEVTSVKVGDHVIPLYTPECGECKFCKSGKTNLCQAVR---	116
Kangiella_koreensis	GGGIVESVGEVTSVKVGDHVIPLYTPECGDCKFCLSGKTNLCQAVR---	115
Group 2	GGG--VE--G--VTSV--GDHVIPLYTPEC--CK--C--SGKTNLCQ--IR---	
	***:*. * : *	
P0	----VE--G--VT----GD-VIP-----C--C--C-S--TNLC---R---	
	..:*. * . * * . * * * * : : : * * . * * * * * : *	

A-5: Results of Multiple Sequences Alignment of Partition P0 (cont.)

Marinomonas_posidonica	-ETQKGKGLMPDGTSRFSINGEPIFHYMGTSFSEYSVVPEISLAKIHVDA	159
Marinomonas_mediterranea	-ETQKGKGLMPDGTSRFSINGEPIFHYMGTSFSEYSVVPEISLAKIHVDA	159
Marinobacterium_stanieri	-ATQGGQLMPDGTSRFSLNGETLYHYMGTSFSEYTVVPEISLAKIHVDA	159
Bdellovibrio_bacteriovorus	-ATQKGKGLMPDGTSRFSKDGKMIHHYMGCSFSAEYTVVPEIALAKVNPAA	159
Mus_musculus_Chain_A	YPTIDQELMEDRTSRFTCKGRS IYHFMGVSSFSQYTVVSEANLARVDDEA	168
Mus_musculus_Chain_B	YPTIDQELMEDRTSRFTCKGRS IYHFMGVSSFSQYTVVSEANLARVDDEA	168
Laribacter_hongkongensis	-ATQKGKGLMPDGTTRFSYKGGQPIYHYMGTSFSEYTVVPEISLAKIPKDA	161
Synechococcus_sp.	-GTQGRGLMPDGTSRFSSAGRLIHHYMGTSFSEYTVVPEIAVARISKEA	160
Methylomicrobium_album	-ATQKGKGLMPDGTSRFSKDGKPIFHYMGTSFSEYTVLPEIAVARINKEA	160
Pantoea_ananatis	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISLAKISKEA	162
Pantoea_stewartii	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISLAKISKEA	162
Pantoea_vagans	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVIPEISLAKISKEA	162
Erwinia_amylovora	-TTQKGKGLMPDGTTRFFKDGQPVYHYMGTSFSEYTVVPEISLAKISKEA	162
Erwinia_pyrifoliae	-TTQKGKGLMPDGTTRFFKDGQPIYHYMGTSFSEYTVVPEISLAKISKEA	162
Erwinia_tasmaniensis	-TTQKGKGLMPDGTTRFFKDGQPIYHYMGTSFSEYTVVPEISLAKISKEA	162
Commensalibacter_intestini	-VTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISVAKISKEA	162
Glaciecola_sp.	-TTQGGQLMPDGTTRFSKNGKPIYHYMGTSFSAEHTVVPEIALAKIPKEA	162
Pseudoalteromonas_atlantica	-ATQKGKGLMPDGTTRFSKNGKPIYHYMGTSFSAEHTVVPEIALAKIPKEA	162
Tolumonas_auensis	-ATQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSAEHTVVPEISLAKISKDA	162
Actinobacillus_ureae	-ETQKGKGLMPDGTTRFFKDGQPIFHYMGTSFSEYTVVSEYSLAKIQENA	162
Actinobacillus_pleuropneumonia	-ETQKGKGLMPDGTTRFFKDGQPIFHYMGTSFSEYTVVSEYSLAKIQENA	162
Simonsiella_muelleri	-ATQKGKGLMPDGTTRFYKDGKPIYHYMGTSFSEYTVVVSQYSLAKIQDDA	163
Moraxella_catarrhalis	-ETQKGKGLMPDGTTRFFKEGEP IYHYMGTSFSEYTVVVSQYSLAKIQKDA	162
Alishewanella_jeotgali	-ATQKGKGLMPDGTSRFSKDGKPIYHYMGTSFSEYTVLPEISLAKINKEA	162
Photobacterium_profundum	-ETQKGKGLMPDGTTRFYKDGQPLFHYMGCSFSEFTVLPEISLAKVNKEA	164
Vibrio_coralliilyticus	-ETQKGKGLMPDGTSRFSINGET IYHYMGCSFSEYTVLPEISLAKVNKEA	170
Oceanobacter_sp.	-ETQKGKGLMPDGTSRFYKDGKPIYHYMGTSFSEYTVLPDISLAKVNKSA	164
Marinobacter_aquaeolei	-ETQKGKGLMPDGTTRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Marinobacter_hydrocarbonoclast	-ETQKGKGLMPDGTSRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Marinobacter_algicola	-ETQKGKGLMPDGTTRFYKDGQPIHHYMGCSFSEYTVLPEISLAKVNKDA	160
Marinobacter_manganoxydans	-ETQKGKGLMPDGTTRFSLNGEPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Oceanospirillum_sp.	-ETQKGKGLMPDGTTRFYKDGEP IYHYMGCSFSEYTVLPEISLARVNKEA	164
Pseudoalteromonas_haloplanktis	-ETQKGKGLMPDGTTRFYKDGQPIFHYMGCSFSEYTVLPEISLAKVNKSA	164
Psychromonas_ingrahamii	-ETQKGKGLMPDGTTRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKAA	164
Saccharophagus_degradans	-ATQKGKGLMPDGTTRFYKDGQPIYHYMGTSFSEYTVLPEISLAKVNQKA	164
Group 1	--T---LM-D-T-RF---G---H-MG-S-F---V-----A-----A * .: ** * * * * * .: * : ** * : * : * : * : * : * : * : *	
Reinekea_sp.	-TTQGGQLMPDGTSRFSIDGQPIFHYMGCSFSEYTVLPEISLAKVNPQA	164
Ferrimonas_balearica	-ETQKGKGLMPDGTTRFSKDGEP IYHYMGCSFSEYTVLPEISLAKVNPAA	165
Shewanella_halifaxensis	-ETQKGKGLMPDGTTRFSKDGVEIFHYMGTSFSEYTVLPEISLAKVNPDA	165
Shewanella_pealeana	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGTSFSEYTVLPEISLAKVNPDA	164
Shewanella_woodyi	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGTSFSEYTVLPEISLAKVNPEA	164
Shewanella_sediminis	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGTSFSEYTVLPEISLAKVNPEA	164
Shewanella_piezotolerans	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGTSFSEYTVLPEISLAKVNPEA	164
Shewanella_oneidensis	-ETQKGKGLMPDGTSRFSKDGQIIYHYMGTSFSEYTVLPEISLAKVNPDA	164
Chromobacterium_violaceum	-ATQKGKGLMPDGTTRFSKDGKPIYHYMGTSFSEYTVLPEISLAKVNKAA	164
Alteromonas_sp.	-ATQKGKGLMPDGTSRFTVNGKPVFHYMGTSFSEYTVLPEISVAKVNKNA	164
Aeromonas_caviae	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGTSFSEYTVLPEISIAKVDPA	165
Aeromonas_salmonicida	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGTSFSEYTVLPEISIAKVDPA	165
Aeromonas_hydrophila	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGTSFSEYTVLPEISIAKVDPA	165
Aeromonas_veronii	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGTSFSEYTVLPEISIAKVDPA	165
Kangiella_koreensis	-ETQKGKGLMPDGTTRFSINGKPIYHYMGTSFSEYTVLPEISLAKVNPKA	164
Group 2	--TQ-G-LMPDGT-RF---G---HYMG-SFSEYTVLPEIS-AKV---A ***:*****:*. : * : : * * * * * : * * * * * : * * * * *	
P0	--T---LM-D-T-RF---G---H-MG-S-F---V-----A-----A * .: ** * * * * * .: * : ** * : * : * : * : * : * : * : *	

A-7: Results of Multiple Sequences Alignment of Partition P0 (cont.)

Marinomonas_posidonica	PLEKVLLGCGITTTGIGAVLNTAKVEEGATIAVFLGGIGLSVIQGARMA	209
Marinomonas_mediterranea	PLEKVLLGCGITTTGIGAVLNTAKVEEGATVAVFGLGGIGLSVIQGARMA	209
Marinobacterium_stanieri	PLEKVLLGCGITTTGIGAVLNTAKVEPGSTVAIFGMGGIGLSVIQGARMA	209
Bdellovibrio_bacteriovorus	PLDKVLLGCGVTTGIGAVLNTAKVEKGTAVAVFGLGGIGLSVIQGAKMA	209
Mus_musculus_Chain_A	NLERVCLIGCGFSSSGYAAINTAKVTPGSTCAVFLGCVGLSAIIGCKIA	218
Mus_musculus_Chain_B	NLERVCLIGCGFSSSGYAAINTAKVTPGSTCAVFLGCVGLSAIIGCKIA	218
Laribacter_hongkongensis	PLEKVLLGCGVTTGIGAVLNTAKVTAGSTVAVFGLGGIGLAAIIGASMA	211
Synechococcus_sp.	PLEKVLLGCGVTTGIGAVLNTAKVEPGSTVAVFGLGGIGLAVIIGAVMA	210
Methylomicrobium_album	PLEKVLLGCGVTTGIGAVMNTAKVEEGATVAVFGLGGIGLSAIIGAVMA	210
Pantoea_ananatis	PLEEVLLGCGVTTGMGAVMNTAKVEKGDVAIFGLGGIGLSAIIGAKMA	212
Pantoea_stewartii	PLEEVLLGCGVTTGMGAVMNTAKVEKGDVAIFGLGGIGLSAIIGAKMA	212
Pantoea_vagans	PLEEVLLGCGVTTGMGAVMNTAKVEKGDVAIFGLGGIGLSAVIIGAKMA	212
Erwinia_amylovora	PLEEVLLGCGVTTGMGAVINTANVKEKGDVAIFGLGGIGLSAIIGAKMA	212
Erwinia_pyrifoliae	PLEEVLLGCGVTTGMGAVMNTAKVEKGDVAIFGLGGIGLSAIIGAKMA	212
Erwinia_tasmaniensis	PLEEVLLGCGVTTGMGAVLNTAKVEKGDVAIFGLGGIGLSAIIGAKMA	212
Commensalibacter_intestini	PLEKVLLGCGITTTGMGAVNTAKVQPGDSVAVFGLGGIGLSVIMGAKAA	212
Glaciecola_sp.	PLEKVLLGCGVTTGMGAVNTAKVEKGDVAVFGLGGIGLSVLIIGAKMA	212
Pseudoalteromonas_atlantica	PLEKVLLGCGVTTGMGAVNTAKVQEGDVAIFGLGGIGLSVLIIGAKMA	212
Tolumonas_auensis	PLEKVLLGCGVTTGMGAVMNTAKVQPGDVAIFGLGGIGLSVLIIGAVMA	212
Actinobacillus_ureae	PLDEVLLGCGVTTGIGAVTRTAKVKQGDVAIFGLGGIGLAAIIGARMA	212
Actinobacillus_pleuropneumonia	PLDEVLLGCGVTTGIGAVTRTAKVKKGDVAIFGLGGIGLAAIIGARMA	212
Simonsiella_muelleri	PLEEVLLGCGVTTGIGAVTKTAKVKAGDVAIFGLGGIGLAAIIGARMS	213
Moraxella_catarrhalis	PLEEVLLGCGVTTGMGAVLTKAKVKPGDVAIFGLGGIGLAAVIGARMA	212
Alishewanella_jeotgali	PLEKVLLGCGVTTGMGAVFNTAKVKPGDVAIFGLGGIGLSAVIASVMA	212
Photobacterium_profundum	PLEEVLLGCGVTTGMGAVLNTAKVEKGDVAIFGLGGIGLSAIIGAKMA	214
Vibrio_coralliilyticus	PLEEVLLGCGVTTGMGAVLNTAKVEKGDVAIFGLGGIGLSAIIGARMA	220
Oceanobacter_sp.	PLEEVLLGCGVTTGMGAVMNTAKVQAGDSVAIFGLGGIGLSAIIGATMA	214
Marinobacter_aquaeolei	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGLGGIGLSAIIGATMA	213
Marinobacter_hydrocarbonoclast	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGLGGIGLSAIIGATMA	213
Marinobacter_algicola	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGLGGIGLSAIIGATMA	210
Marinobacter_manganoxydans	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGMGGIGLSAVIGATMA	213
Oceanospirillum_sp.	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGLGGIGLSAVIGATMA	214
Pseudoalteromonas_haloplanktis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGLGGIGLSAVIGATMA	214
Psychromonas_ingrahamii	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGLGGIGLSAVIGATMA	214
Saccharophagus_degradans	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAVIGATMA	214
Group 1	-L--VCL-GCG---G-GA---TA-V--G---A-FG-G--GL----- *:.***:***.:** ** .**:* * :*:** * **: : . . :	
Reinekea_sp.	PLEEVLLGCGVTTGMGAVMNTAKVQSSDTVAIFGLGGIGLSAIIGATMA	214
Ferrimonas_balearica	PLEEVLLGCGVTTGMGAVNTANVQPGDVAIFGLGGIGLSAIIGAAMA	215
Shewanella_halifaxensis	PLEEVLLGCGVTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAIIGAVMA	215
Shewanella_pealeana	PLEEVLLGCGVTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAIIGAVMA	214
Shewanella_woodyi	PLEEVLLGCGVTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAVIGATMA	214
Shewanella_sediminis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGMGGIGLSAVIGATMA	214
Shewanella_piezotolerans	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAVIGAQMA	214
Shewanella_oneidensis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGMGGIGLSAVIGATMA	214
Chromobacterium_violaceum	PLEEVLLGCGVTTGMGAVNTAKVKAGDNVAVFGLGGIGLSAIIGARMA	214
Alteromonas_sp.	PLEEICLLGCGVTTGMGAVANTAKVEEGASVAVFGLGGIGLTIIGARLA	214
Aeromonas_caviae	PLEEVLLGCGVTTGIGAVMNTAKVEGESVAIFGLGGIGLSAIIGARLA	215
Aeromonas_salmonicida	PLEEVLLGCGVTTGIGAVMNTAKVEGESVAIFGLGGIGLSAVIGARLA	215
Aeromonas_hydrophila	PLEEVLLGCGVTTGIGAVMNTAKVEGESVAIFGLGGIGLSAVIGARLA	215
Aeromonas_veronii	PLEEVLLGCGVTTGIGAVMNTAKVEGESVAIFGLGGIGLSAVIGARLA	215
Kangiella_koreensis	PLEEVLLGCGVTTGMGAVMNTAKVEEGATVAIFGLGGIGLSAVIGAVMA	214
Group 2	PLEE-CLLGCGVTTG-GAV-NTA-V-----VA-FG-GGIGL---IGA--A ****:*****:*** ***: * . . **:**:*****:*** :*	
P0	-L---CL-GCG---G-GA---TA-V-----A-FG-G--GL----- *:.**:***.:** ** .**:* . . **:** * **: : . . :	

A-5: Results of Multiple Sequences Alignment of Partition P0 (cont.)

Marinomonas_posidonica	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHTMPLEQINEAFDLMHE	359
Marinomonas_mediterranea	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHTMPLEKINDAFDLMHE	359
Marinobacterium_stanieri	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHTMPLEKINDAFDLMHE	359
Bdellovibrio_bacteriovorus	KGSAGGGVKGSRTELPGYVEQYMSGEINIDDMVFTMPLEKINDAFDYMHE	359
Mus_musculus_Chain_A	NGTFFGGWKSVDSPVNLVSDYKNNKFDLLLVTHALPFESINDAIDLKME	366
Mus_musculus_Chain_B	NGTFFGGWKSVDSPVNLVSDYKNNKFDLLLVTHALPFESINDAIDLKME	366
Laribacter_hongkongensis	RGSAGGGVGRTELPGYVERFQSGEIPLDTFIHTMPLEEINRAFELMHA	360
Synechococcus_sp.	RGSAGGGVGRSELPGYVERAQRGEIPLDVFITHTLGLEDINQAFDLMHE	360
Methylomicrobium_album	RGSAGGGVGRSELPGYVERAQRGEIPLDVFITHTLGLEDINQAFDLMHE	360
Pantoea_ananatis	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFIHTMPLEEINDAFDLMHE	362
Pantoea_stewartii	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFIHTMPLEAEINDAFDLMHE	362
Pantoea_vagans	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFIHTMPLEEINDAFDLMHE	362
Erwinia_amylovora	RGSAGGGVKGRTQLPGIVERYMNGEFQLNDFIHTNPLLEEINDAFELMHE	362
Erwinia_pyrifoliae	RGSAGGGVKGRTQLPGIVERYMNGEFRLNDFIHTNPLLEEINDAFELMHE	362
Erwinia_tasmaniensis	RGSAGGGVKGRTQLPGLVERYMNGEFQLNDFIHTNPLLEEINDAFDLMHE	362
Commensalibacter_intestini	RGSAGGGVKGSRQLPNVNDYLDGKFLDQDFIHTEMPLDQINKAFDLMHD	362
Glaciecola_sp.	RGSAGGGVKGSRQLPDYVQRYMDGEFELDTFIHTMQLLEDINTAFDLMHE	362
Pseudoalteromonas_atlantica	RGSAGGGVKGSRQLPDYVQRYMDGEFELDTFIHTMPLEKINDAFDLMHE	362
Tolumonas_auensis	KGSAGGGVKGSRQLPGIVEQYMNNGEFELDTFIHTMGLDDINAFDLMHE	362
Actinobacillus_ureae	RGSAGGGVKGRTLPGIIDQFMKGEFKLRDFIHTMPLEKINDAFDLMHQ	362
Actinobacillus_pleuropneumonia	RGSAGGGVKGRTLPGIIDQFMKGEFKLRDFIHTMPLEKINDAFDLMHE	362
Simonsiella_muelleri	RGSAGGGVKGSRSELPLDIDQYQHGEFKLSDFIHTMPLEKINDAFDLMHE	363
Moraxella_catarrhalis	RGSAGGGVKGSRSELPGIVSQYMQGDFALSDFIHTMPLEKINDAFDLMHE	362
Alishewanella_jeotgali	RGTAFGGVKGSRSELPGYVDRYLDGKFLDQDFIHTMPLEKINDAFDLMHE	362
Photobacterium_profundum	RGSAGGGVKGSRSELPEIVERYMAGEFALDDFIHTMGLDQINDAFDLMHE	364
Vibrio_coralliilyticus	RGSAGGGVKGSRSELPEIVERYMAGEFGLQDFIHTMGLDQINDAFDLMHE	370
Oceanobacter_sp.	RGSAGGGVKGSRSELPGIVEKYLAGEFKLNDFIHTMGLDQINDAFDLMHE	364
Marinobacter_aquaeolei	RGSAGGGVKGSRSELPGIVERYLQGEFKLNDFIHTMGLDDINEAFELMHE	363
Marinobacter_hydrocarbonoclast	RGSAGGGVKGSRSELPGIVERYLQGEFKLNDFIHTMGLDDINEAFELMHE	363
Marinobacter_algicola	KGSAGGGVKGSRSELPGIVERYLQGEFKLNDFIHTMGLDDINEAFELMHE	360
Marinobacter_manganoxydans	KGSAGGGVKGSRSELPGIVERYMAGEFKLNDFIHTMGLDQINDAFDLMHE	363
Oceanospirillum_sp.	RGTAFGGVKGSRSELPEIVERYMAGEFKLNDFIHTMGLDQINDAFDLMHE	364
Pseudoalteromonas_haloplanktis	RGSAGGGVKGSRSELPDYVERYLAGEFKLSDFIHTMGLDQINDAFDLMRR	364
Psychromonas_ingrahamii	KGSAGGGVKGRTLPGYVERYLQGEFKLSDFIHTMPLEKINDAFELMHK	364
Saccharophagus_degradans	RGTAFGGVKGSRSELPGIVEQYLAGDFKLDQDFIHTMGLDQINDAFDLMHH	364
Group 1	-G--FG-----P-----T-----N----M-- .*: ** .: .:* .: .: : :*. : : * : : *	
Reinekea_sp.	RGTAFGGVKGSRSELPSYVERYLAGEFKLSDFIHTMPLEKINDAFDLMHE	364
Ferrimonas_balearica	RGSAGGGVKGSRSELPGYVERYLAGEFKLDDFIHTMGLDQINDAFDLMHQ	365
Shewanella_halifaxensis	KGSAGGGVKGSRSELPEYVERYMAGEFKLDDFIHTMGLDQINDAFDLMHE	365
Shewanella_pealeana	KGSAGGGVKGSRSELPEYVERYMAGEFKLDDFIHTMGLDQINDAFDLMHE	364
Shewanella_woodyi	KGSAGGGVKGSRSELPEYVERYMAGEFKLNDFIHTMGLDQINDAFDLMHE	364
Shewanella_sediminis	KGSAGGGVKGSRSELPEYVERYMAGEFKLNDFIHTMGLDQINDAFDLMHE	364
Shewanella_piezotolerans	KGSAGGGVKGSRSELPEYVERYMAGEFKLNDFIHTMGLDQINDAFDLMHE	364
Shewanella_oneidensis	KGSAGGGVKGSRSELPEYVERYLAGEFKLSDFIHTMGLDQINDAFDLMHQ	364
Chromobacterium_violaceum	RGSAGGGVGRTELPEYVERYLKGEFRLDDFIHTMPLEKINDAFDLMHE	364
Alteromonas_sp.	RGTAFGGVKGSRQLPDYVERYLAGEFKLDDFIHTMPLEKINDAFDLMHE	364
Aeromonas_caviae	RGSAGGGVGRSELPSYVQRYMQGEFKLDDFIHTMPLEQINEAFDLMHE	365
Aeromonas_salmonicida	RGSAGGGVGRSELPSYVQRYMQGEFKLDDFIHTMPLEQINEAFELMHE	365
Aeromonas_hydrophila	RGSAGGGVGRSELPSYVQRYMQGEFKLDDFIHTMGLDQINDAFDLMHE	365
Aeromonas_veronii	RGSAGGGVGRSELPSYVQRYMQGEFRLDDFIHTMGLDQINDAFELMHQ	365
Kangiella_koreensis	KGTAFGGVKGSRSELPDYVERYLAGEFKLDDFIHTMPLEKINDAFDLMHE	364
Group 2	-G-AFGGV-GR--LP-YV-RY--GEF-L-DFIHTM-L---N-AF-LMH- *:*****:***:***:***:***:*****:***:***:***:***:***:	
P0	-G--FG-----P-----T-----N----M-- .*: ** .: .:* .: .: : :*. : : * : : *	

A-5: Results of Multiple Sequences Alignment of Partition P0 (cont.)

Marinomonas_posidonica	GKSIRTVILFDQ-----	371
Marinomonas_mediterranea	GKSIRTVILFDQ-----	371
Marinobacterium_stanieri	GKSIRSVILFDQ-----	371
Bdellovibrio_bacteriovorus	GKSIRSVIKM-----	369
Mus_musculus_Chain_A	GKSIRTILTF-----	376
Mus_musculus_Chain_B	GKSIRTILTF-----	376
Laribacter_hongkongensis	GKSIRTVIHF-----	371
Synechococcus_sp.	GQSIRSVIHFNR-----	372
Methylomicrobium_album	GKSIRTVIHFNH-----	372
Pantoea_ananatis	GKSIRSVVHFNK-----	374
Pantoea_stewartii	GKSIRSVVHFNK-----	374
Pantoea_vagans	GKSIRSVVHFNK-----	374
Erwinia_amylovora	GKSIRTVVHFTKS-----	375
Erwinia_pyrifoliae	GKSIRTVVHFVAKS-----	375
Erwinia_tasmaniensis	GKSIRTVVHFVSKA-----	375
Commensalibacter_intestini	GKSIRTVIRY-----	372
Glaciecola_sp.	GKSIRSVVHY-----	372
Pseudoalteromonas_atlantica	GKSIRSVVHY-----	372
Tolumonas_auensis	GKSIRTVILFDK-----	374
Actinobacillus_ureae	GKSIRTVIHF-----	372
Actinobacillus_pleuropneumonia	GKSIRTVIHF-----	372
Simonsiella_muelleri	GKSIRTVIHF-----	373
Moraxella_catarrhalis	GKSIRSVIHF-----	372
Alishewanella_jeotgali	GKSIRTVIHF-----	372
Photobacterium_profundum	GKSIRSVIHFDK-----	376
Vibrio_coralliilyticus	GKSIRTVIHMDQ-----	382
Oceanobacter_sp.	GKSIRSVIHYNK-----	376
Marinobacter_aquaeolei	GKSIRSVIHFDK-----	375
Marinobacter_hydrocarbonoclast	GKSIRSVIHFDK-----	375
Marinobacter_algicola	GKSIRSVIHFDK-----	372
Marinobacter_manganoxydans	GKSIRTVIHFDK-----	375
Oceanospirillum_sp.	GKSIRSVIHVDR-----	376
Pseudoalteromonas_haloplanktis	GKSIRTVIHFDK-----	376
Psychromonas_ingrahamii	GKSIRSVIHFAK-----	376
Saccharophagus_degradans	GKSIRSVIHFNK-----	376
Group 1	G-SIR-----	
	*:***:::	
Reinekea_sp.	GKSIRSVVHF-----	374
Ferrimonas_balearica	GKSIRSVIHFDQ-----	377
Shewanella_halifaxensis	GKSIRTVLHFGK-----	377
Shewanella_pealeana	GKSIRTVLHFDK-----	376
Shewanella_woodyi	GKSIRTVIHFDK-----	376
Shewanella_sediminis	GKSIRTVIHFDK-----	376
Shewanella_piezotolerans	GKSIRTVIHFDK-----	376
Shewanella_oneidensis	GKSIRTVIHFDK-----	376
Chromobacterium_violaceum	GKSIRSVIHAAEPA-----	379
Alteromonas_sp.	GKSIRSVIHYA-----	375
Aeromonas_caviae	GKSIRTVIHV-----	375
Aeromonas_salmonicida	GKSIRTVIHV-----	375
Aeromonas_hydrophila	GKSIRSVIHV-----	375
Aeromonas_veronii	GKSIRTVIHV-----	375
Kangiella_koreensis	GKSIRSVIHV-----	374
Group 2	GKSIR-V-H-----	
	*****:*:*:	
P0	G-SIR-----	
	*:***:::	

A-6: Results of Multiple Sequences Alignment of Partition P1 (cont.)

Marinomonas_posidonica	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGEDPEGIFPAILGHE	63
Marinomonas_mediterranea	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGDDPEGIFPAILGHE	63
Marinobacterium_stanieri	PLTIEEVDVQGPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Bdellovibrio_bacteriovorus	PLSIEEVDLEGGKAGEVLIRVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Mus_musculus_Chain_A	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKKKALFPVVLGHE	68
Mus_musculus_Chain_B	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKKKALFPVVLGHE	68
Laribacter_hongkongensis	PLEIVEVDVAPPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	65
Synechococcus_sp.	PLEITEIEVAPPAAGEVLLRVVAVSGVCHTDAFTLSGDDPEGVFPAILGHE	64
Methylomicrobium_album	PLEVTEVNVAPPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	64
Pantoea_ananatis	PLKIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Pantoea_stewartii	PLKIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Pantoea_vagans	PLKIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Erwinia_amylovora	PLKIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Erwinia_pyrifoliae	PLKIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Erwinia_tasmaniensis	PLKIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Commensalibacter_intestini	PLTIEEVDLMPQKAGEVLIRIVATGVCHTDAFTLSGADPEGIFPAILGHE	66
Glaciecola_sp.	PLTIEEVDLMPQKAGEVLIRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	66
Pseudoalteromonas_atlantica	PLSIEEVDLMPQKAGEVLIRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	66
Tolumonas_auensis	PLSIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	66
Actinobacillus_ureae	PLKIEEVDLMPQKAGEVLRLVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Actinobacillus_pleuropneumonia	PLKIEEVDLMPQKAGEVLRLVATGVCHTDAFTLSGDDPEGVFPAILGHE	66
Simonsiella_muelleri	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	67
Moraxella_catarrhalis	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	66
Alishewanella_jeotgali	PLSIEEVDLMPQKAGEVLVRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	66
Photobacterium_profundum	PLSIEEIDLMPQAGEVLVRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Vibrio_coralliilyticus	PLKMEEVDVQPKAGEVLVRIVATGVCHTDAFTLSGDDPEGIFPAILGHE	74
P1 Group 1	PL---E-----P---EV-----A--VC-TD-----FP--LGHE ** : *::: * ** :::: * ** * :. . : : ** :****	
Oceanobacter_sp.	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGNFPAILGHE	68
Marinobacter_aquaeolei	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGNFPAILGHE	67
Marinobacter_hydrocarbonoclast	PLSVEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGNFPAILGHE	67
Marinobacter_algicola	PLSIEEVDVMPKAGEVLVKI IASGVCHTDAFTLSGEDPEGNFPAILGHE	64
Marinobacter_manganoxydans	PLSIEEVDVMPQAGEVRI RIVASGVCHTDAFTLSGEDPEGIFPAILGHE	67
Oceanospirillum_sp.	PLSIEEVDVMPQAGEVLRIVATGVCHTDAFTLSGEDPEGIFPAILGHE	68
Pseudoalteromonas_haloplanktis	PLSIEEIDLMPKAGEVLVKI IASGVCHTDAFTLSGDDPEGIFPAILGHE	68
Psychromonas_ingrahamii	PLSIEEIDLMPKAGEVLVKI IASGVCHTDAFTLSGEDPEGIFPAILGHE	68
Saccharophagus_degradans	PLSIEEVDVMPKAGEVLVKI IATGVCHTDAFTLSGEDPEGIFPAILGHE	68
P1 Group 2	PL--EE-DVM-P---EV-----A-GVCHTDAFTLSG--DPEG-FP--LGHE ***:*:* ** * : ** ::::*****:***** ** :****	
Reinekea_sp.	PLKIVTVQVAPPKAGEVRIKIVASGVCHTDAFTLSGDDPEGIFPAILGHE	68
Ferrimonas_balearica	PLSIEEVDVAPPKAGEVRIKI IATGVCHTDAFTLSGDDPEGVFPAILGHE	69
Shewanella_halifaxensis	PLTMEIVDVMPQKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	69
Shewanella_pealeana	PLTMEIVDVMPQKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_woodyi	PLSMEIVDVMPQKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_sediminis	PLSMEIVDVMPQKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_piezotolerans	PLTMEIVDVMPQKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
Shewanella_oneidensis	PLSIEIVDVMPQKAGEVRIKMIATGVCHTDAFTLSGDDPEGIFPAILGHE	68
P1 Group 3	PL--E-V-V-PP--GEVR-K--A-GVCHTDAFTLSG--DPEG-FP--ILGHE *.: * * * ** : ** :*:::*****:***** ** :****	
Chromobacterium_violaceum	PLSIEEIEVHPPKAGEVVRKVMATGVCHTDAFTLSGADPEGVFPAILGHE	68
Alteromonas_sp.	PLSIEEIVVAPPKAGEVRI RLLATGVCHTDAFTLSGADPEGVFPAILGHE	68
Aeromonas_caviae	PLSIEEIVVAPPKAGEVVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	69
Aeromonas_salmonicida	PLSIEEIVVAPPKAGEVVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	69
Aeromonas_hydrophila	PLSIEEIVVAPPKAGEVVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	69
Aeromonas_veronii	PLSIEEIVVAPPKAGEVVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	69
Kangiella_koreensis	PLSIEEIVVAPPKAGEVVRIVATGVCHTDAFTLSGADPEGVFPAILGHE	68
P1 Group 4	PLSIEE--V-PP--GEVR---ATGVCHTDAFTLSG--DPEGVFP--ILGHE *****: * ** : ** :*:::*****:***** ** :****	

A-6: Results of Multiple Sequences Alignment of Partition P1 (cont.)

Marinomonas_posidonica	-ETQKGKGLMPDGTSRFSINGEPIFHYMGSTSFSEYSVVPEISLAKIHVDA	159
Marinomonas_mediterranea	-ETQKGKGLMPDGTSRFSINGEPIFHYMGSTSFSEYSVVPEISLAKIHVDA	159
Marinobacterium_stanieri	-ATQGGQLMPDGTSRFSLNGETLYHYMGSTSFSEYTVVPEISLAKIHVDA	159
Bdellovibrio_bacteriovorus	-ATQKGKGLMPDGTSRFSKDGKMIHHYMGCSFSAEYTVVPEIALAKVNPAA	159
Mus_musculus_Chain_A	YPTIDQELMEDRTSRFTCKGRS IYHFMGVSSFSQYTVVSEANLARVDDEA	168
Mus_musculus_Chain_B	YPTIDQELMEDRTSRFTCKGRS IYHFMGVSSFSQYTVVSEANLARVDDEA	168
Laribacter_hongkongensis	-ATQKGKGLMPDGTTRFSYKGGQPIYHYMGSTSFSEYTVVPEISLAKIPKDA	161
Synechococcus_sp.	-GTQGRGLMPDGTSRFSSAGRLIHHYMGSTSFSEYTVVPEIAVARISKEA	160
Methylomicrobium_album	-ATQKGKGLMPDGTSRFSKDGKPIFHYMGSTSFSEYTVLPEIAVARINKEA	160
Pantoea_ananatis	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGSTSFSEYTVVPEISLAKISKEA	162
Pantoea_stewartii	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGSTSFSEYTVVPEISLAKISKEA	162
Pantoea_vagans	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGSTSFSEYTVIPEISLAKISKEA	162
Erwinia_amylovora	-TTQKGKGLMPDGTTRFFKDGQPVYHYMGSTSFSEYTVVPEISLAKISKEA	162
Erwinia_pyrifoliae	-TTQKGKGLMPDGTTRFFKDGQPIYHYMGSTSFSEYTVVPEISLAKISKEA	162
Erwinia_tasmaniensis	-TTQKGKGLMPDGTTRFFKDGQPIYHYMGSTSFSEYTVVPEISLAKISKEA	162
Commensalibacter_intestini	-VTQKGKGLMPDGTTRFFKDGKPIFHYMGSTSFSEYTVVPEISVAKISKEA	162
Glaciecola_sp.	-TTQGGQLMPDGTTRFSKNGKPIYHYMGSTSFSAEHTVVPEIALAKIPKEA	162
Pseudoalteromonas_atlantica	-ATQKGKGLMPDGTTRFSKNGKPIYHYMGSTSFSAEHTVVPEIALAKIPKEA	162
Tolumonas_auensis	-ATQKGKGLMPDGTTRFFKDGKPIFHYMGSTSFSAEHTVVPEISLAKISKDA	162
Actinobacillus_ureae	-ETQKGKGLMPDGTTRFFKDGQPIFHYMGSTSFSEYTVVSEYSLAKIQENA	162
Actinobacillus_pleuropneumonia	-ETQKGKGLMPDGTTRFFKDGQPIFHYMGSTSFSEYTVVSEYSLAKIQENA	162
Simonsiella_muelleri	-ATQKGKGLMPDGTTRFYKDGKPIYHYMGSTSFSEYTVVSVQYSLAKIQDDA	163
Moraxella_catarrhalis	-ETQKGKGLMPDGTTRFFKEGEP IYHYMGSTSFSEYTVVSVQYSLAKIQKDA	162
Alishewanella_jeotgali	-ATQKGKGLMPDGTSRFSKDGKPIYHYMGSTSFSEYTVLPEISLAKINKEA	162
Photobacterium_profundum	-ETQKGKGLMPDGTTRFYKDGQPLFHYMGCSFSEFTVLPEISLAKVNKEA	164
Vibrio_coralliilyticus	-ETQKGKGLMPDGTSRFSINGETIFHYMGCSFSEYTVLPEISLAKVNKEA	170
P1 Group 1	--T-----LM-D-T-RF---G----H-MG-S-F----V-----A-----A * . : * * * * * * * . : * : * * * * : * : : * : : * * : *	
Oceanobacter_sp.	-ETQKGKGLMPDGTSRFYKDGKPIYHYMGSTSFSEYTVLPDISLAKVNKSA	164
Marinobacter_aquaeolei	-ETQKGKGLMPDGTSRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Marinobacter_hydrocarbonoclast	-ETQKGKGLMPDGTSRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Marinobacter_algicola	-ETQKGKGLMPDGTSRFYKDGQPIHHYMGCSFSEYTVLPEISLAKVNKDA	160
Marinobacter_manganoxydans	-ETQKGKGLMPDGTTRFSLNGEPIYHYMGCSFSEYTVLPEISLAKVNKEA	163
Oceanospirillum_sp.	-ETQKGKGLMPDGTTRFYKDGEP IYHYMGCSFSEYTVLPEISLAKVNKEA	164
Pseudoalteromonas_haloplanktis	-ETQKGKGLMPDGTTRFYKDGQPIFHYMGCSFSEYTVLPEISLAKVNKSA	164
Psychromonas_ingrahamii	-ETQKGKGLMPDGTTRFYKDGQPIYHYMGCSFSEYTVLPEISLAKVNKAA	164
Saccharophagus_degradans	-ATQKGKGLMPDGTTRFYKDGQPIYHYMGSTSFSEYTVLPEISLAKVNQKA	164
P1 Group 2	--TQKGKGLMPDGT-RF---G--PI-HYMG-STFSEYTVLP-I-SLA-VN--A *****: * * : * : * * * * * : * * * * * : * * * * * : *	
Reinekea_sp.	-TTQGGQLMPDGTSRFSDGQPIFHYMGCSFSEYTVLPEISLAKVNPQA	164
Ferrimonas_balearica	-ETQKGKGLMPDGTTRFSKDGEP IYHYMGCSFSEYTVLPEISLAKVNPAA	165
Shewanella_halifaxensis	-ETQKGKGLMPDGTTRFSKDGVEIFHYMGSTSFSEYTVLPEISLAKVNPDA	165
Shewanella_pealeana	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPDA	164
Shewanella_woodyi	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPEA	164
Shewanella_sediminis	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPEA	164
Shewanella_piezotolerans	-ETQKGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPEA	164
Shewanella_oneidensis	-ETQKGKGLMPDGTTRFSKDGQIIYHYMGSTSFSEYTVLPEISLAKVNPDA	164
P1 Group 3	--TQG-GLMPDGT-RF--DG--I-HYMG-STFSEYTVLPEISLAKVNP-A * * : * * * * * : * * * * * : * * * * * : * * * * * : *	
Chromobacterium_violaceum	-ATQKGKGLMPDGTSRFSKDGKPIYHYMGSTSFSEYTVLPEISLAKVNKAA	164
Alteromonas_sp.	-ATQKGKGLMPDGTSRFTVNGKPVFHYMGSTSFSEYTVLPEISVAKVNKNA	164
Aeromonas_caviae	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA	165
Aeromonas_salmonicida	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA	165
Aeromonas_hydrophila	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA	165
Aeromonas_veronii	-ATQKGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA	165
Kangielia_koreensis	-ETQKGKGLMPDGTTRFSINGKPIYHYMGSTSFSEYTVLPEISLAKVNPKA	164
P1 Group 4	--TQKGKGLMPDGT-RF---G-P--HYMGSTSFSEYTVLPEIS-AKV---A *****: * * : * : * * * * * : * * * * * : * * * * * : *	

A-6: Results of Multiple Sequences Alignment of Partition P1 (cont.)

Marinomonas_posidonica	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	309
Marinomonas_mediterranea	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	309
Marinobacterium_stanieri	SFECIGNVQVMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	309
Bdellovibrio_bacteriovorus	SFECVGNLQMLRAALECAHRGWGQSVIGVAGAGQEI STRPFQLVTRVW	309
Mus_musculus_Chain_A	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
Mus_musculus_Chain_B	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
Laribacter_hongkongensis	SFECVGNVLMRAALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	311
Synechococcus_sp.	SFECIGNVQVMRAALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	310
Methylomicrobium_album	SIECIGNVKVMRSALECCHKGWQSVIIGVAGAGQEI STRPFQLVTRVW	310
Pantoea_ananatis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Pantoea_stewartii	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Pantoea_vagans	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Erwinia_amylovora	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Erwinia_pyrifoliae	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Erwinia_tasmaniensis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Commensalibacter_intestini	SFECIGNVKVMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Glaciecola_sp.	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Pseudoalteromonas_atlantica	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Tolumonas_auensis	SFECIGNVKVMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	312
Actinobacillus_ureae	SFECVGNADLMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTRVW	312
Actinobacillus_pleuropneumonia	SFECVGNVDMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTRVW	312
Simonsiella_muelleri	SFECVGNVDMRAALECCHKGWGESVIGVAPAGAEIKTRPFQLVTRVW	313
Moraxella_catarrhalis	SFECIGNVDVMRAALECCHKGWGESVIGVAPAGAEIRTRPFQLVTRVW	312
Alishewanella_jeotgali	SFECIGNVNMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	312
Photobacterium_profundum	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Vibrio_coralliilyticus	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	320
P1 Group 1	S--C-G-----A-----GWG-----G-----E-----GR-- *:* * . . . : : * : . * * . . : * . * : : : * *	
Oceanobacter_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Marinobacter_aquaeolei	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	313
Marinobacter_hydrocarbonoclast	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	313
Marinobacter_algicola	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	310
Marinobacter_manganoxydans	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	313
Oceanospirillum_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Pseudoalteromonas_haloplanktis	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Psychromonas_ingrahamii	SFECIGNVDMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	314
Saccharophagus_degradans	SFECIGNVNMRSALECCHKGWGESIIIGVAGAGQEI STRPFQLVTRVW	314
P1 Group 2	SFECIGNV--MRSALECCHKGWGES--IGVAGAG--EISTRPFQLVTRVW *****:*****:*****:*****	
Reinekea_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Ferrimonas_balearica	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	315
Shewanella_halifaxensis	SFECIGNIHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	315
Shewanella_pealeana	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Shewanella_woodyi	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Shewanella_sediminis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Shewanella_piezotolerans	SFECIGNVHMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Shewanella_oneidensis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
P1 Group 3	SFECIGN--VMR--ALECCHKGWGESV--GVAGAGQEI STRPFQLVTRVW *****:*****:*****:*****	
Chromobacterium_violaceum	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Alteromonas_sp.	SFECIGNVDMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
Aeromonas_caviae	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	315
Aeromonas_salmonicida	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	315
Aeromonas_hydrophila	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	315
Aeromonas_veronii	SFECIGNVKVMRAALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	315
Kangiella_koreensis	SFECIGNVNMRSALECCHKGWGESVIGVAGAGQEI STRPFQLVTRVW	314
P1 Group 4	SFECIGNV--VMR--ALECCHKGWGESVIGVAGAG--EISTRPFQLVTRVW *****:*****:*****:*****	

A-6: Results of Multiple Sequences Alignment of Partition P1 (cont.)

Marinomonas_posidonica	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHTMPLEQINEAFDLMHE	359
Marinomonas_mediterranea	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHMTSLEKINDAFDLMHE	359
Marinobacterium_stanieri	KGSAGGGVKGSRQLPGYVEDYMNGKIEIDPFVTHMTGLEDINKAFDLMHE	359
Bdellovibrio_bacteriovorus	KGSAGGGVKGSRTELPYVEQYMSGEINIDDMVFTMPLEDINKAFDYMHE	359
Mus_musculus_Chain_A	NGTFFGGWKSVDSPNLSVDYKNNKFDLLLVTHALPFESINDAIDLKME	366
Mus_musculus_Chain_B	NGTFFGGWKSVDSPNLSVDYKNNKFDLLLVTHALPFESINDAIDLKME	366
Laribacter_hongkongensis	RGSAGGGVGRTELPAYVEKAQKGEIPLDTFIHTTLPLEEINQAFELMHE	361
Synechococcus_sp.	RGSAGGGVGRTELPYVERFQSGEIPLDTFIHTTLPLEEINRAFELMHA	360
Methylomicrobium_album	RGSAGGGVHGRSELPYVERAQRGEIPLDVFITHTLGLEDINQAFDLMHE	360
Pantoea_ananatis	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFIHTTLPLEEINDAFDLMHE	362
Pantoea_stewartii	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFIHTTLPLEEINDAFDLMHE	362
Pantoea_vagans	RGSAGGGVKGSRQLPGIVQDYLDGKFALNDFIHTTLPLEEINDAFDLMHE	362
Erwinia_amylovora	RGSAGGGVKGRTQLPGIVERYMNGEFQLNDFIHTNLPLEEINDAFELMHE	362
Erwinia_pyrifoliae	RGSAGGGVKGRTQLPGIVERYMNGEFRLNDFIHTNLPLEEINDAFELMHE	362
Erwinia_tasmaniensis	RGSAGGGVKGRTQLPGLVERYMNGEFQLNDFIHTNLPLEEINDAFELMHE	362
Commensalibacter_intestini	RGSAGGGVKGSRQLPNVNDYLDGKFQDDFIHTEMPLDQINKAFDLMHD	362
Glaciecola_sp.	RGSAGGGVKGSRQLPDYVQRYMDGEFELDTFIHTMQLDINTAFDLMHE	362
Pseudoalteromonas_atlantica	RGSAGGGVKGSRQLPDYVQRYMDGEFELDTFIHTMQLDINTAFDLMHE	362
Tolomonas_auensis	KGSAGGGVKGSRQLPGIVEQYMNNGEFELDTFIHTMGLDDINAFDLMHE	362
Actinobacillus_ureae	RGSAGGGVKGRTELPGIIDQFMKGEFKLRDFIHTMPLDINKAFDLMHQ	362
Actinobacillus_pleuropneumonia	RGSAGGGVKGRTELPGIIDQFMKGEFKLRDFIHTMPLDINKAFDLMHE	362
Simonsiella_muelleri	RGSAGGGVKGSRSELPDLIDQYQHGEFKLSDFIHTMPLDINNAFDLMHE	363
Moraxella_catarrhalis	RGSAGGGVKGSRSELPDQYVQYMDGDFALSDFIHTMPLDQINNAFDLMHE	362
Alishewanella_jeotgali	RGTAFGGVKGSRSELPYVDRYLNDFELDTFIHTMPLDINKAFDLMHE	362
Photobacterium_profundum	RGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMPLDINKAFDLMHE	364
Vibrio_coralliilyticus	RGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMPLDINKAFDLMHE	370
P1 Group 1	-G--FG-----P-----T-----N-A--M-- .*: ** . . .:* . . . : : :* . : : * * : *	
Oceanobacter_sp.	RGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMPLDINKAFDLMHE	364
Marinobacter_aquaeolei	RGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	363
Marinobacter_hydrocarbonoclast	RGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	363
Marinobacter_algicola	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	360
Marinobacter_manganoxydans	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	363
Oceanospirillum_sp.	RGTAFGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	364
Pseudoalteromonas_haloplanktis	RGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	364
Psychromonas_ingrahamii	KGSAGGGVKGRTELPDYVDRYLNDFELDTFIHTMPLDINKAFDLMHQ	364
Saccharophagus_degradans	RGTAFGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	364
P1 Group 2	-G-AFGGVKGR-ELP--VE-Y--G-FKL-DFIHTM-L--N--F-LM-- *:*****:* **:* :*.*.***** *:.* :*:*:	
Reinekea_sp.	RGTAFGGVKGSRSELPYVDRYLNDFELDTFIHTMPLDINKAFDLMHE	364
Ferrimonas_balearica	RGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDDINEAFELMHE	365
Shewanella_halifaxensis	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDQVNAFDLMHE	365
Shewanella_pealeana	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDQVNAFDLMHE	364
Shewanella_woodyi	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDQVNAFDLMHE	364
Shewanella_sediminis	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDQVNAFDLMHE	364
Shewanella_piezotolerans	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDQVNAFDLMHE	364
Shewanella_oneidensis	KGSAGGGVKGSRSELPYVDRYLNDFELDTFIHTMGLDQVNAFDLMHQ	364
P1 Group 3	-G-AFGGVKGRSELP-YVERY--GEFKL-DFIHTM-L--N-AFDLMH- *:*****.*****: *****.***** *:.*:*****:	
Chromobacterium_violaceum	RGSAGGGVGRTELPYVDRYLNDFELDTFIHTMPLERVNEAFDLMHE	364
Alteromonas_sp.	RGTAFGGVKGSRQLPDYVDRYLNDFELDTFIHTMPLERVNEAFDLMHE	364
Aeromonas_caviae	RGSAGGGVGRSELPYVDRYLNDFELDTFIHTMPLERVNEAFDLMHE	365
Aeromonas_salmonicida	RGSAGGGVGRSELPYVDRYLNDFELDTFIHTMPLERVNEAFDLMHE	365
Aeromonas_hydrophila	RGSAGGGVGRSELPYVDRYLNDFELDTFIHTMPLERVNEAFDLMHE	365
Aeromonas_veronii	RGSAGGGVGRSELPYVDRYLNDFELDTFIHTMPLERVNEAFDLMHQ	365
Kangiella_koreensis	KGTAFGGVKGSRSELPYVDRYLNDFELDTFIHTMPLERVNEAFDLMHE	364
P1 Group 4	-G-AFGGV-GR--LP-YV-RY--GEF-LDDFIHTM-LE--N-AF-LMH- *:*****:.*:***.***: *****.***** *:.*:***:	

A-6: Results of Multiple Sequences Alignment of Partition P1 (cont.)

Marinomonas_posidonica	GKSIRTVILFDQ-----	371
Marinomonas_mediterranea	GKSIRTVILFDQ-----	371
Marinobacterium_stanieri	GKSIRSVILFDQ-----	371
Bdellovibrio_bacteriovorus	GKSIRSVIKM-----	369
Mus_musculus_Chain_A	GKSIRTILTF-----	376
Mus_musculus_Chain_B	GKSIRTILTF-----	376
Laribacter_hongkongensis	GKSIRTVIHF-----	371
Synechococcus_sp.	GQSIRSVIHFNR-----	372
Methylomicrobium_album	GKSIRTVIHFNH-----	372
Pantoea_ananatis	GKSIRSVVHFNK-----	374
Pantoea_stewartii	GKSIRSVVHFNK-----	374
Pantoea_vagans	GKSIRSVVHFNK-----	374
Erwinia_amylovora	GKSIRTVVHFTKS-----	375
Erwinia_pyrifoliae	GKSIRTVVHFAKS-----	375
Erwinia_tasmaniensis	GKSIRTVVHFSKA-----	375
Commensalibacter_intestini	GKSIRTVIRY-----	372
Glaciecola_sp.	GKSIRSVVHY-----	372
Pseudoalteromonas_atlantica	GKSIRSVVHY-----	372
Tolumonas_auensis	GKSIRTVILFDK-----	374
Actinobacillus_ureae	GKSIRTVIHF-----	372
Actinobacillus_pleuropneumonia	GKSIRTVIHF-----	372
Simonsiella_muelleri	GKSIRTVIHF-----	373
Moraxella_catarrhalis	GKSIRSVIHF-----	372
Alishewanella_jeotgali	GKSIRTVIHF-----	372
Photobacterium_profundum	GKSIRSVIHFDK-----	376
Vibrio_coralliilyticus	GKSIRTVIHMDQ-----	382
P1 Group 1	G-SIR-----	
	*:***:::	
Oceanobacter_sp.	GKSIRSVIHYNK-----	376
Marinobacter_aquaeolei	GKSIRSVIHFDK-----	375
Marinobacter_hydrocarbonoclast	GKSIRSVIHFDK-----	375
Marinobacter_algicola	GKSIRSVIHFDK-----	372
Marinobacter_manganoxydans	GKSIRTVIHFDK-----	375
Oceanospirillum_sp.	GKSIRSVIHFDK-----	376
Pseudoalteromonas_haloplanktis	GKSIRTVIHFDK-----	376
Psychromonas_ingrahamii	GKSIRSVIHFAK-----	376
Saccharophagus_degradans	GKSIRSVIHFNK-----	376
P1 Group 2	G-SIR-VIH-----	
	*:***:***: :	
Reinekea_sp.	GKSIRSVVHF-----	374
Ferrimonas_balearica	GKSIRSVIHFDQ-----	377
Shewanella_halifaxensis	GKSIRTVLHFGK-----	377
Shewanella_pealeana	GKSIRTVLHFDK-----	376
Shewanella_woodyi	GKSIRTVIHFDK-----	376
Shewanella_sediminis	GKSIRTVIHFDK-----	376
Shewanella_piezotolerans	GKSIRTVIHFDK-----	376
Shewanella_oneidensis	GKSIRTVIHFDK-----	376
P1 Group 3	GKSIR-V-HF-----	
	*****:***	
Chromobacterium_violaceum	GKSIRSVIHAAEPA-----	379
Alteromonas_sp.	GKSIRSVIHYA-----	375
Aeromonas_caviae	GKSIRTVIHY-----	375
Aeromonas_salmonicida	GKSIRTVIH-----	375
Aeromonas_hydrophila	GKSIRSVIH-----	375
Aeromonas_veronii	GKSIRTVIH-----	375
Kangiella_koreensis	GKSIRSVIH-----	374
P1 Group 4	GKSIR-VIH-----	
	*****:***	

A-7: Results of Multiple Sequences Alignment of Partition P2

Marinomonas_posidonica	-----MKCKAAVAWGPQ	13
Marinomonas_mediterranea	-----MKCKAAVAWGPQ	13
Marinobacterium_stanieri	-----MKSRAAVAWKAGD	13
Bdellovibrio_bacteriovorus	-----MKIKAAVAWKAGA	13
Glaciecola_sp.	-----MQSIKTRAAVAWAAGE	16
Pseudoalteromonas_atlantica	-----MQSIKTRAAVAWAAGE	16
Tolumonas_auensensis	-----MNMIKTRAAVAWEAGK	16
Alishewanella_jeotgali	-----MQMIKTRAAVAWGPQ	16
Pantoea_ananatis	-----MNMIKTRAAVAWAAGE	16
Pantoea_stewartii	-----MNMIKTRAAVAWAAGE	16
Pantoea_vagans	-----MNMIKTRAAVAWAAGE	16
Erwinia_amylovora	-----MQMIKTRAAVAWAAGE	16
Erwinia_pyrifoliae	-----MQMIKTRAAVAWAAGE	16
Erwinia_tasmaniensis	-----MQMIKTRAAVAWAAGE	16
Commensalibacter_intestini	-----MDFIKTRAAVAWGPQ	16
Actinobacillus_ureae	-----MEFIKTRAAVAWAPNE	16
Actinobacillus_pleuropneumonia	-----MEFIKTRAAVAWAPNE	16
Simonsiella_muelleri	-----MTQFIKTRAAVAYAPNQ	17
Moraxella_catarrhalis	-----MDFIKTRAAVAWAANE	16
Synechococcus_sp.	-----MIRSRAAVAWAAGQ	14
Methylomicrobium_album	-----MIKSRAAIWAGSGR	14
Laribacter_hongkongensis	-----MTIKSRAAVAFAGQ	15
Mus_musculus_Chain_A	-----GTQGVKICKAAIAWKTGS	19
Mus_musculus_Chain_B	-----GTQGVKICKAAIAWKTGS	19
	:: : ** : * : .	
P2 Group 1	-----AA-A-----	
Photobacterium_profundum	-----MSDQFIKSKAAIAWGPQ	18
Vibrio_coralliilyticus	-----MALDIQPGQTSIKSKAMVAWAAGE	24
	:: : **** : * : .	
P2 Group 2	-----IKSKA--AW-----	
Marinobacter_aquaeolei	-----MAEIIKSKAAIAWGPQ	17
Marinobacter_hydrocarbonoclast	-----MAEMIKSKAAIAWGPQ	17
Marinobacter_algicola	-----MIKSKAAIAWGPQ	14
Oceanobacter_sp.	-----MSDTFIKSKAAIAWGPQ	18
Marinobacter_manganoxydans	-----MTQTIKSKAAIAWGPQ	17
Oceanospirillum_sp.	-----MSEQMIKSRAAIWGPQ	18
Pseudoalteromonas_haloplanktis	-----MSDKFIKSKAAIAWGPQ	18
Psychromonas_ingrahamii	-----MTEKYIKSKAAIAWGPQ	18
	*** : ***** *	
P2 Group 3	-----IKS-AAIAWGP-Q	
Reinekea_sp.	-----MTAETLTCRAAVAWAAGE	28
Ferrimonas_balearica	-----MTTPQTIKSKAAVAWGPQ	29
	* : * : . : * : * : . : *	
P2 Group 4	-----T--T---AAVAW--G-	
Shewanella_halifaxensis	-----MMTAKTIKSKAAVAWAVGE	19
Shewanella_pealeana	-----MTAKTIKSKAAVAWAVGE	18
Shewanella_piezotolerans	-----MTAQTIKSKAAVAWAVGE	18
Shewanella_woodyi	-----MTAQTIKSKAAVAWAVGE	18
Shewanella_sediminis	-----MTAQTIKSKAAVAWAVGE	18
Shewanella_oneidensis	-----MTAQILKSKAAVAWAVGE	18
	*** : *****	
P2 Group 5	-----MTA--KSKAAVAWAVGE	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	-----	MAQVQSIKCKAAIAWGPGQ	19
Aeromonas_veronii	-----	MAQVQSIKCKAAIAWGPGQ	19
Aeromonas_salmonicida	-----	MAQVQSIKCKAAIAWGPGQ	19
Aeromonas_caviae	-----	MAQVQSIKCKAAIAWGPGQ	19
Chromobacterium_violaceum	-----	MSHDIIRCQAAVAWAAGQ	18
Alteromonas_sp.	-----	MSAEPITCKAAVAWKAGE	18
		. : * **:*:* .*:	
P2 Group 6	-----	-I-C-AA-AW--G-	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	PLSIEEVEVMPPQAGEVVRIVATGVCHTDAFTLSGEDPEGVFFPCILGHE	69
Aeromonas_veronii	PLSIEEVEVMPPQAGEVVRIVATGVCHTDAFTLSGEDPEGVFFPCILGHE	69
Aeromonas_salmonicida	PLSIEEVEVMPPQAGEVVRIVATGVCHTDAFTLSGEDPEGVFFPCILGHE	69
Aeromonas_caviae	PLSIEEVEVMPPQAGEVVRIVATGVCHTDAFTLSGEDPEGVFFPCILGHE	69
Chromobacterium_violaceum	PLSIEEIEVHPPKAGEVRVKMVAITGVCHTDAFTLSGADPEGVFFPCILGHE	68
Alteromonas_sp.	PLSIEEVEVMPPQAGEVVRIRLLATGVCHTDAFTLSGADPEGVFFPCILGHE	68
	*****: * *:*****:::***** ***** .*****	
P2 Group 6	PLSIEE--V-PP-AGEVR---ATGVCHTDAFTLSG-DPEGVFP-ILGHE	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Marinomonas_posidonica	GAGVVEAVGEGVTTLLKPGDHVIPLYTAECGECKFCQSGKTNLCQAVR--- 110
Marinomonas_mediterranea	GAGVVEAVGEGVTTLLKPGDHVIPLYTAECGECKFCCKSGKTNLCQAVR--- 110
Marinobacterium_stanieri	GAGVVEAVGEGVTTLLKPGDHVIPLYTAECGKCKFCCLSGKTNLCQAVR--- 110
Bdellovibrio_bacteriovorus	GGGIVEEVGEGVTTLLKGDHVIPLYTPECKECKFCLSGKTNLCVRI--- 110
Glaciecola_sp.	GAGIVEAIGEGVTSVEVGDHVIPLYTPECKECKFCLSGKTNLCQAIR--- 113
Pseudoalteromonas_atlantica	GAGIVEAIGEGVTSVEVGDHVIPLYTPECKECKFCLSGKTNLCQAIR--- 113
Tolomonas_auensis	GAGIVEAIGEGVTSVAVDHVIPLYTPECKECKFCCKSGKTNLCQAIR--- 113
Alishewanella_jeotgali	GGGIVEAVGEGVTSVAVDHVIPLYTPECKKFCCLSGKTNLCQAIR--- 113
Pantoea_ananatis	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGQCKFCLSGKTNLCQAIR--- 113
Pantoea_stewartii	GGGIVEAVGEGVTSVEVGDHVIPLYTPECKKFCCLSGKTNLCQAIR--- 113
Pantoea_vagens	GGGIVEAVGEGVTSVEVGDHVIPLYTPECKKCYCLSGKTNLCQAIR--- 113
Erwinia_amylovora	GGGIVEAVGEGVTSVAVDHVIPLYTPECRQCKFCLSGKTNLCQAIR--- 113
Erwinia_pyrifoliae	GGGIVEAVGEGVTSVAVDHVIPLYTPECRQCKFCLSGKTNLCQAIR--- 113
Erwinia_tasmaniensis	GGGIVEAVGEGVTSVAVDHVIPLYTPECRQCKFCLSGKTNLCQAIR--- 113
Commensalibacter_intestini	GAGIVEAVGEGVTSISVGDYVIPLYTPECKCEYCLSGKTNLCQAIR--- 113
Actinobacillus_ureae	GAGIVEAVGEGVTDKVDHVIPLYTAECRCKFCCLSGKTNLCSAVR--- 113
Actinobacillus_pleuropneumonia	GAGIVEAVGEGVTDKVDHVIPLYTAECRCKFCCLSGKTNLCSAVR--- 113
Simonsiella_muelleri	GAGIVEAVGEGVTDFAVDHVIPLYTAECKQCKFCLSGKTNLCSAVR--- 114
Moraxella_catarrhalis	GAGIVEAVGEGVTDFAVDHVIPLYTAECGQCKMCLSNKTNLCSAVR--- 113
Synechococcus_sp.	GGAVEEVGADVTSVAVDHVIPLYTPECRACSFCLSGKTNLCQAIR--- 111
Methylomicrobium_album	GGGIVEAVGEGVTSVAVDHVIPLYTPECKKFCCLSGKTNLCQAIR--- 111
Laribacter_hongkongensis	GGGIVEAVGEGVTSVAVDHVIPLYTAECRECKFCCKSGKTNLCQAVR--- 112
Mus_musculus_Chain_A	GAGIVESVGPVTFNFKPGDKVIFPFAPQCKRCKLCLSPNLNLCGKLRNFK 118
Mus_musculus_Chain_B	CAGIVESVGPVTFNFKPGDKVIFPFAPQCKRCKLCLSPNLNLCGKLRNFK 118
	..:*** :* .** . ** ***::::!* . * * * ** * :*
P2 Group 1	----VE--G--VT---GD--VIP-----C--C--C--S--TNLC---R---
Photobacterium_profundum	GGGIVEQIGEGVTSVQVGDHVIPLYTAECGECKFCCKSGKTNLCQAVR--- 115
Vibrio_corallilyticus	GGGIVEMVGEVTSVEVGDHVIPLYTAECGECKFCTSGKTNLCQAVR--- 121
	***** :*****:***** *****
P2 Group 2	GGGIVE--GEGVTSV--VGDHVIPLYTAECGECKFC--SGKTNLCQAVR---
Marinobacter_aquaeolei	GGGIVEAIGEGVTSVAVDHVIPLYTPECKECKFCLSGKTNLCGKIR--- 114
Marinobacter_hydrocarbonoclast	GGGIVEAIGEGVTSVAVDHVIPLYTPECKECKFCLSGKTNLCGKIR--- 114
Marinobacter_algicola	GGGIVEAVGEGVTSVEIGDHVIPLYTPECKECKFCLSGKTNLCGKIR--- 111
Oceanobacter_sp.	GGGIVEAVGEGVTSVAVDHVIPLYTPECKECKFCTSGKTNLCQKIR--- 115
Marinobacter_manganoxydans	GGGIVESVGEVTSLSKVDHVIPLYTPECKECKFCTSGKTNLCGKIR--- 114
Oceanospirillum_sp.	GGGIVEAVGEGVTSLSQVDHVIPLYTPECKECKFCCKSGKTNLCQKIR--- 115
Pseudoalteromonas_haloplanktis	GGGIVEQVGEVTSVKVDHVIPLYTPECKECKFCLSGKTNLCQKIR--- 115
Psychromonas_ingrahamii	GGGIVEQIGEGVTSVKLGDHVIPLYTPECKECKFCLSGKTNLCQKIR--- 115
	:** :** :***** ***** **
P2 Group 3	GGG-VE--GEGVTS---GDHVIPLYTPECKECKFC--SGKTNLC--KIR---
Reinekea_sp.	GGGIVEAIGEGVTSVSGDHVIPLYTPECKECKFCLSGKTNLCQKIR--- 144
Ferrimonas_balearica	GGGIVESIGEGVTSVAVDHVIPLYTPECKECKFCRSKTNLCQKIR--- 145
	*****:*****:***** *****
P2 Group 4	GGGIVE--IGEGVTSV--VGDHVIPLYTPECKECKFC--SGKTNLCQKIR---
Shewanella_halifaxensis	GGGIVESIGEGVTSVKVDHVIPLYTPECKECKYCKSGKTNLCQKIR--- 116
Shewanella_pealeana	GGGIVESIGEGVTSVKVDHVIPLYTPECKECKYCKSGKTNLCQKIR--- 115
Shewanella_piezotolerans	GGGIVESIGEGVTSVQVGDHVIPLYTPECKECKFCCKSGKTNLCQKIR--- 115
Shewanella_woodyi	GGGIVESIGEGVTSVQVGDHVIPLYTPECKECKFCCKSGKTNLCQKIR--- 115
Shewanella_sediminis	GGGIVESIGEGVTSVQVGDHVIPLYTPECKECKFCCKSGKTNLCQKIR--- 115
Shewanella_oneidensis	GGGIVESIGEGVTSVQVGDHVIPLYTPECKECKFCCKSGKTNLCQKIR--- 115
	*****:*****:***** ***** **
P2 Group 5	GGGIVESIGEGVTSV--VGDHVIPLYTPECKECK--CKSGKTNLCQ--IR---

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	GGGIVESVGEVTSVKVGDHVIPLYTPECGECKFCKSGKTNLCQKIR--- 116
Aeromonas_veronii	GGGIVESVGEVTSVKVGDHVIPLYTPECGECKFCKSGKTNLCQKIR--- 116
Aeromonas_salmonicida	GGGIVESIGEGVTSVKVGDHVIPLYTPECGECKFCRSKTNLCQKIR--- 116
Aeromonas_caviae	GGGIVESVGEVTSVKVGDHVIPLYTPECGECKFCKSGKTNLCQKIR--- 116
Chromobacterium_violaceum	GGGVVESVGPVTSVAVGDHVIPLYTPECRECKFCLSGKTNLCQKIR--- 115
Alteromonas_sp.	GGGVVESVGEVTSVAVGDHVIPLYTPECGECKFCLSGKTNLCQKIR--- 115
	::* ***** ***** ***** ***** *****
P2 Group 6	GGG-VES-G-GVTSV-VGDHVIPLYTPEC-ECKFC-SGKTNLCQKIR---

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Marinomonas_posidonica	-ETQGGKGLMPDGTSRFSINGEPIFYHYMGSTSFSEYSVVPEISLAKIHVDA	159
Marinomonas_mediterranea	-ETQGGKGLMPDGTSRFSINGEPIFYHYMGSTSFSEYSVVPEISLAKIHVDA	159
Marinobacterium_stanieri	-ATQGGKGLMPDGTSRFSLNGETLYHYMGSTSFSEYTVVPEISLAKIHVDA	159
Bdellovibrio_bacteriovorus	-ATQGGKGLMPDGTSRFSKDGKMIHHYMGSTFAEYTVVPEIALAKVNPAA	159
Glaciecola_sp.	-TTQGGKGLMPDGTTRFSKNGKPIYHYMGSTFAEHTVVPEIALAKIPKEA	162
Pseudoalteromonas_atlantica	-ATQGGKGLMPDGTTRFSKNGKPIYHYMGSTFAEHTVVPEIALAKIPKEA	162
Tolomonas_auensis	-ATQGGKGLMPDGTTRFFKDGKPIFYHYMGSTFAEHTVVPEISLAKISKDA	162
Alishewanella_jeotgali	-ATQGGKGLMPDGTSRFSKDGKPIYHYMGSTSFSEYTVLPEISLAKINKEA	162
Pantoea_ananatis	-TTQGGKGLMPDGTTRFFKDGKPIFYHYMGSTSFSEYTVVPEISLAKISKEA	162
Pantoea_stewartii	-TTQGGKGLMPDGTTRFFKDGKPIFYHYMGSTSFSEYTVVPEISLAKISKEA	162
Pantoea_vagans	-TTQGGKGLMPDGTTRFFKDGKPIFYHYMGSTSFSEYTVVPEISLAKISKEA	162
Erwinia_amylovora	-TTQGGKGLMPDGTTRFFKDGQPVYHYMGSTSFSEYTVVPEISLAKISKEA	162
Erwinia_pyrifoliae	-TTQGGKGLMPDGTTRFFKDGQPIYHYMGSTSFSEYTVVPEISLAKISKEA	162
Erwinia_tasmaniensis	-TTQGGKGLMPDGTTRFFKDGQPIYHYMGSTSFSEYTVVPEISLAKISKEA	162
Commensalibacter_intestini	-VTQGGKGLMPDGTTRFFKDGKPIFYHYMGSTSFSEYTVVPEISVAKISKEA	162
Actinobacillus_ureae	-ETQGGKGLMPDGTTRFFKDGQPIFYHYMGSTSFSEYTVVSEYSLAKIQENA	162
Actinobacillus_pleuropneumonia	-ETQGGKGLMPDGTTRFFKDGQPIFYHYMGSTSFSEYTVVSEYSLAKIQENA	162
Simonsiella_muelleri	-ATQGGKGLMPDGTTRFYKDGKPIYHYMGSTSFSEYTVVVSQYSLAKIQDDA	163
Moraxella_catarrhalis	-ETQGGKGLMPDGTTRFFKDGQPIFYHYMGSTSFSEYTVVVSQYSLAKIQDDA	162
Synechococcus_sp.	-GTQGGKGLMPDGTSRFSSAGRLIHHYMGSTSFSEYTVVPEIAVARISKEA	160
Methylomicrobium_album	-ATQGGKGLMPDGTSRFSKDGKPIFYHYMGSTSFSEYTVLPEIAVARINKEA	160
Laribacter_hongkongensis	-ATQGGKGLMPDGTTRFSYKQPIYHYMGSTSFSEYTVVPEISLAKIPKDA	161
Mus_musculus_Chain_A	YPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEA	168
Mus_musculus_Chain_B	YPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEA	168
	* .: ** * * * * * .: .: *	
P2 Group 1	--T----LM-D-T-RF---G----H-MG-S-F----V-----A-----A	
Photobacterium_profundum	-ETQGGKGLMPDGTTRFYKDGQPLFYHYMGSTSEFTVLPEISLAKVNKEA	164
Vibrio_corallilyticus	-ETQGGKGLMPDGTSRFSINGEPIFYHYMGSTSFSEYTVLPEISLAKVNKEA	170
	*****: * * .: .: *****: *****	
P2 Group 2	-ETQGGKGLMPDGT-RF---G---FHYMGSTFSE-TVLPEISLAKVNKEA	
Marinobacter_aquaeolei	-ETQGGKGLMPDGTSRFYKDGQPIYHYMGSTSFSEYTVLPEISLAKVNKEA	163
Marinobacter_hydrocarbonoclast	-ETQGGKGLMPDGTSRFYKDGQPIYHYMGSTSFSEYTVLPEISLAKVNKEA	163
Marinobacter_algicola	-ETQGGKGLMPDGTSRFYKDGQPIHHYMGSTSFSEYTVLPEISLAKVNKDA	160
Oceanobacter_sp.	-ETQGGKGLMPDGTSRFYKDGKPIYHYMGSTSFSEYTVLPDISLAKVNKSA	164
Marinobacter_manganoxydans	-ETQGGKGLMPDGTTRFSLNGETLYHYMGSTSFSEYTVLPEISLAKVNKEA	163
Oceanospirillum_sp.	-ETQGGKGLMPDGTTRFYKDGQPIYHYMGSTSFSEYTVLPEISLAKVNKEA	164
Pseudoalteromonas_haloplanktis	-ETQGGKGLMPDGTTRFYKDGQPIFYHYMGSTSFSEYTVLPEISLAKVNKSA	164
Psychromonas_ingrahamii	-ETQGGKGLMPDGTTRFYKDGQPIYHYMGSTSFSEYTVLPEISLAKVNKAA	164
	*****: * * .: * * . *	
P2 Group 3	-ETQGGKGLMPDGT-RF---G-P-I-HYMG-STFSEYTVLP-ISLA-VNK-A	
Reinekea_sp.	-TTQGGKGLMPDGTSRFSIDGQPIFYHYMGSTSFSEYTVLPEISLAKVNPQA	
Ferrimonas_balearica	-ETQGGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISLAKVNPAA	
	* * * : * * * * * : * * * * * : * * * * * : * * * * * * * * * * * * * * * * *	
P2 Group 4	--TQG-GLMPDGT-RFS-DG-PI-HYMGSTFSEYTVLPEISLAKVNP-A	
Shewanella_halifaxensis	-ETQGGKGLMPDGTTRFSKDGVEIFHYMGSTSFSEYTVLPEISLAKVNPDA	165
Shewanella_pealeana	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPDA	164
Shewanella_piezotolerans	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPEA	164
Shewanella_woodyi	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPEA	164
Shewanella_sediminis	-ETQGGKGLMPDGTTRFSKDGVDIFHYMGSTSFSEYTVLPEISLAKVNPEA	164
Shewanella_oneidensis	-ETQGGKGLMPDGTSRFSKDGQPIYHYMGSTSFSEYTVLPEISLAKVNPDA	164
	*****: *	
P2 Group 5	-ETQGGKGLMPDGT-RFSKDG--I-HYMGSTFSEYTVLPEISLAKVNP-A	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	-ATQGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA 165
Aeromonas_veronii	-ATQGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA 165
Aeromonas_salmonicida	-ATQGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA 165
Aeromonas_caviae	-ATQGKGLMPDGTTRFSKDGQPIYHYMGSTSFSEYTVLPEISIAKVDPA 165
Chromobacterium_violaceum	-ATQGKGLMPDGTSRFSKDGKPIYHYMGSTSFSEYTVLPEISLAKVNKA 164
Alteromonas_sp.	-ATQGKGLMPDGTSRFTVNGKPVFHYMGSTSFSEYTVLPEISVAKVNKA 164
	*****:*: :*:::*****:***: *
P2 Group 6	-ATQGKGLMPDGT-RF--G-P--HYMGSTSFSEYTVLPEID-AKV--A

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Marinomonas_posidonica	PLEKVCLLGCGETTTGIGAVLNTAKVEEGATIAVFLGGIGLSVIQGARMA	209
Marinomonas_mediterranea	PLEKVCLLGCGETTTGIGAVLNTAKVEEGATVAVFLGGIGLSVIQGARMA	209
Marinobacterium_stanieri	PLEKVCLLGCGETTTGIGAVLNTAKVEPGSTVAIFGMGGIGLSCIQGARMA	209
Bdellovibrio_bacteriovorus	PLDKVCLLGCGETTTGIGAVLNTAKVEKGTAVAVFLGGIGLSVIQGARMA	209
Glaciecola_sp.	PLEKVCLLGCGETTTGMGAVTNTAKVKEGDTVAVFLGGIGLSVLIQAKMA	212
Pseudoalteromonas_atlantica	PLEKVCLLGCGETTTGMGAVTNTAKVQEGDTVAVFLGGIGLSVLIQAKMA	212
Tolomonas_auensis	PLEKVCLLGCGETTTGMGAVLNTAKVQPGDTVAVFLGGIGLSVIQAKMA	212
Alishewanella_jeotgali	PLEKVCLLGCGETTTGMGAVFNTAKVKPGDTVAIFLGGIGLSAVIASVMA	212
Pantoea_ananatis	PLEEVCLLGCGETTTGMGAVMNTAKVKEGDTVAIFLGGIGLSAIQAKMA	212
Pantoea_stewartii	PLEEVCLLGCGETTTGMGAVMNTAKVKEGDTVAIFLGGIGLSAIQAKMA	212
Pantoea_vagans	PLEEVCLLGCGETTTGMGAVMNTAKVKEGDTVAIFLGGIGLSAVIQAKMA	212
Erwinia_amylovora	PLEEVCLLGCGETTTGMGAVINTANVKEGDTVAIFLGGIGLSAIQAKMA	212
Erwinia_pyrifoliae	PLEEVCLLGCGETTTGMGAVMNTAKVKEGDTVAIFLGGIGLSAIQAKMA	212
Erwinia_tasmaniensis	PLEEVCLLGCGETTTGMGAVLNTAKVKEGDTVAIFLGGIGLSAIQAKMA	212
Commensalibacter_intestini	PLEKVCLLGCGETTTGMGAVTNTAKVQPGDSVAVFLGGIGLSVIMGAKAA	212
Actinobacillus_ureae	PLEEVCLLGCGETTTGIGAVTRTAKVKQGDVAIFLGGIGLAAIQAKMA	212
Actinobacillus_pleuropneumonia	PLDEVCLLGCGETTTGIGAVTRTAKVKKGDTVAIFLGGIGLAAIQAKMA	212
Simonsiella_muelleri	PLEEVCLLGCGETTTGIGAVTKTAKVKAGDTVAIFLGGIGLSAVIQAKMA	213
Moraxella_catarrhalis	PLEEVCLLGCGETTTGMGAVLKTAKVKPGDTVAIFLGGIGLAAVIQAKMA	212
Synechococcus_sp.	PLEKVCLLGCGETTTGIGAVLNTAKVEPGSTVAVFLGGIGLAVIQAKMA	210
Methylomicrobium_album	PLEKVCLLGCGETTTGIGAVMNTAKVEEGATVAVFLGGIGLSAIQAKMA	210
Laribacter_hongkongensis	PLEKVCLLGCGETTTGIGAVLNTAKVTAGSTVAVFLGGIGLAAIQAKMA	211
Mus_musculus_Chain_A	NLERVCLIGCGFSSGYGAAINTAKVTPGSTCAVFLGCVGLSAIQCKIA	218
Mus_musculus_Chain_B	NLERVCLIGCGFSSGYGAAINTAKVTPGSTCAVFLGCVGLSAIQCKIA	218
	*.:***:***.:* ** . **:* * :*:***:***: : .. :	
P2 Group 1	-L--VCL-GCG---GYGA---TA-V--G---A-FG-G--GL-----	
Photobacterium_profundum	PLEEVCLLGCGETTTGMGAVLNTAKVEKGTVAIFLGGIGLSAIQAKMA	214
Vibrio_corallilyticus	PLEEVCLLGCGETTTGMGAVLNTAKVEKGTVAIFLGGIGLSAIQAKMA	220

P2 Group 2	PLEEVCLLGCGETTTGMGAVLNTAKVEKGTVAIFLGGIGLSAIQAKMA	
Marinobacter_aquaeolei	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAIFLGGIGLSAIQAKMA	213
Marinobacter_hydrocarbonoclast	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAIFLGGIGLSAIQAKMA	213
Marinobacter_algicola	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAIFLGGIGLSAIQAKMA	210
Oceanobacter_sp.	PLEEVCLLGCGETTTGMGAVMNTAKVQAGDSVAIFLGGIGLSAIQAKMA	214
Marinobacter_manganoxydans	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAIFGMGGIGLSAVIQAKMA	213
Oceanospirillum_sp.	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAIFLGGIGLSAVIQAKMA	214
Pseudoalteromonas_haloplanktis	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAIFLGGIGLSAVIQAKMA	214
Psychromonas_ingrahamii	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAIFLGGIGLSAVIQAKMA	214
	*****: * :*****:*****:*****	
P2 Group 3	PLEEVCLLGCGETTTGMGAVMNTAKV--G--VAIFG--GGIGLSA--IQAKMA	
Reinekea_sp.	PLEEVCLLGCGETTTGMGAVMNTAKVQSSDTVAIFLGGIGLSAIQAKMA	
Ferrimonas_balearica	PLEEVCLLGCGETTTGMGAVINTANVQPGDTVAVFLGGIGLSAIQAKMA	
	***** **:*..****:*****:*****:*****	
P2 Group 4	PLEEVCLLGCGETTTGMGAV--NTA--VQ--DTVA--FGLGGIGLSAIQAKMA	
Shewanella_halifaxensis	PLEEVCLLGCGETTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAIQAKMA	215
Shewanella_pealeana	PLEEVCLLGCGETTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAIQAKMA	214
Shewanella_piezotolerans	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAVIQAKMA	214
Shewanella_woodyi	PLEEVCLLGCGETTTGMGAVMNTAKVEEGSTVAVFGMGGIGLSAVIQAKMA	214
Shewanella_sediminis	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAVIQAKMA	214
Shewanella_oneidensis	PLEEVCLLGCGETTTGMGAVMNTAKVEEGATVAVFGMGGIGLSAVIQAKMA	214
	*****:***:*****:*****:*****:*** **	
P2 Group 5	PLEEVCLLGCGETTTGMGAVMNTAKVEEG--TVA--FGMGGIGLSA--IQAKMA	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	PLEEVCLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAVIGARLA	215
Aeromonas_veronii	PLEEVCLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAVIGARLA	215
Aeromonas_salmonicida	PLEEVCLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAVIGARLA	215
Aeromonas_caviae	PLEEVCLLGCGVTTGIGAVMNTAKVKEGESVAIFGLGGIGLSAIIIGARLA	215
Chromobacterium_violaceum	PLEEVCLLGCGVTTGMGAVNTAKVKAGDNVAVFGLGGIGLSAIIIGARMA	214
Alteromonas_sp.	PLEEICLLGCGVTTGMGAVNTAKVEEGASVAVFGLGGIGLATIIGARLA	214
	****:*****:*** *****: * .*:*****::****:*	
P2 Group 6	PLEE-CLLGCGVTTG-GAV-NTAKV--G--VA-FGLGGIGL---IGAR-A	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Marinomonas_posidonica	GASKIIAIDINESKFEMATQFGATDCVNPKNFDAPIQQVIVDMTDGGVDY	259
Marinomonas_mediterranea	GASKIIAIDINESKFEMATQFGATDCVNPKNFDAPIQQVIVDMTDGGVDY	259
Marinobacterium_stanieri	GAERIIAIDINEKFEEMARQFGATDCVNPKDFSDPIQQVIVDMTDGGVDY	259
Bdellovibrio_bacteriovorus	GASRIIAIDINDAKWEMAQKFGATDFVNPKKHDKPIQQVIVEMTEWGVY	259
Glaciecola_sp.	NAGRIIAIDVNEKFKIAKQLGATDVVNPKDFDKSIQEIVIVEMTDGGVDY	262
Pseudoalteromonas_atlantica	NAGRIIAIDVNEKFKIAKQLGATDVVNPKDFDKSIQEIVIVEMTDGGVDY	262
Tolomonas_auensis	KASRIIAIDINEDKFDIAKKLGATDVVNPKNFDKPIQDVIVEMTDGGVDF	262
Alishewanella_jeotgali	KAGRIIAIDINEDKFDIAKKLGATDVVNPKKYDKPIQEIVIVEMTDGGVDF	262
Pantoea_ananatis	KAGRIIGIDINTSKFDLARKLGATDLINPKDYDKPIQDVIVELTDGGVDY	262
Pantoea_stewartii	KAGRIIGIDINTSKFDLARKLGATDLINPKDYDKPIQDVIVELTDGGVDF	262
Pantoea_vagans	KAGRIIAIDLNTSKFDLARKLGATDLINPKDYDKPIQDVIVELTDGGVDF	262
Erwinia_amylovora	KAGRIIGIDINSKDYDLARKLGATDLINPKDFDKPIQDVIVEMTDGGVDF	262
Erwinia_pyrifoliae	KAGRIIGIDINTSKYDLARKLGATDLITPKDFDKPIQDVIVEMTDGGVDF	262
Erwinia_tasmaniensis	KASRIIVAVDINPAKFEIAQQLGATDCLNPLDYDRPIQEIVIVDLTDGGVDY	260
Commensalibacter_intestini	KAERIIAIDINTDKFDLAKKLGATDCINPKDYQKSIQDVIVELTNGGVDF	262
Actinobacillus_ureae	GAGRIIAIDINPAKFEKAKELGATDCINPKDYDKPIQNVIIEMTDGGVDF	262
Actinobacillus_pleuropneumonia	GAGRIIAIDINPAKFEKAKELGATDCINPKDYDKPIQNVIIEMTDGGVDF	262
Simonsiella_muelleri	KASRIIAVDINPKFAKAKELGATDFVNPKYDKPIQDVIIEMTDGGVDF	263
Moraxella_catarrhalis	GAGRIIVVDINEDKFAKAQELGATDCVNPKNFDKPIQQVIEIEMTDGGVDF	262
Synechococcus_sp.	GASRIIGIDTNPKEFAIARQLGASDCLDPGAFDAPIQEVVIDLTDGGVDY	260
Methylomicrobium_album	KASRIIVAVDINPAKFEIAQQLGATDCLNPLDYDRPIQEIVIVDLTDGGVDY	260
Laribacter_hongkongensis	KAGRIIAIDINPKFAKARELGATDCINPNDYDKPIQDVIVELTDGGVDY	261
Mus_musculus_Chain_A	GASRIIAIDINGEKFPKAKALGATDCLNPRELDKPVQDVITELTAGGVY	268
Mus_musculus_Chain_B	GASRIIAIDINGEKFPKAKALGATDCLNPRELDKPVQDVITELTAGGVY	268
	*:	
P2 Group 1	-A--I---D-N--K---A---GA-D---P-----Q-V----T---GVD-	
Photobacterium_profundum	GASRIIGVDINETKYELAKKLGATDCINPTKFDKPIQDVIVEMTDGGVDY	264
Vibrio_corallilyticus	GASRIIGIDINESKFDLAKQLGATDCINPKDYDKPIQEIVIVEMTDGGVDY	270
	*****:	
P2 Group 2	GASRIIG-DINE-K--LAK-LGATDCINP-KFDKPIQ-VIVEMTDGGVDY	
Marinobacter_aquaeolei	KASRIIGIDINDSKFDLARQLGATDCINPKDYDKPIQEIVIVELTDGGVDY	263
Marinobacter_hydrocarbonoclast	KASRIIVIDINNSKFDLARQLGATDCINPNDYDKPIQEIVIVELTDGGVDY	263
Marinobacter_algicola	KASRIIAIDINESKFDLARQLGATDCINPKDYDKPIQEIVIVELTDGGVDY	260
Oceanobacter_sp.	GASRIIGIDINESKFEKALQGLGATDCINPNDYDKPIQEIVIVELTDGGVDF	264
Marinobacter_manganoxydans	KASRIIAIDINESKFEKALQGLGATDCINPKDYDKPIQEIVIVELTDGGVDY	263
Oceanospirillum_sp.	KASRIIAIDINDSKFELAKQLGATDCINPKDYDKPIQEIVIVEMTDGGVDY	264
Pseudoalteromonas_haloplanktis	KASRIIAIDINESKFEKALQGLGATDFINPKDYDKPIQDVIVELTDGGVDY	264
Psychromonas_ingrahamii	KASRIIAIDINESKFEKALQGLGATDCINPKDFDKAIQDVIVEMTDGGVDY	264
	****:****:	
P2 Group 3	-ASRI--IDIN-SKF-LA--LGATD-INP----K-IQ-VIVE-TDGGVD-	
Reinekea_sp.	GASRIIAIDINESKFDLAKQLGATDCINPKDYDQPIQEIVIVELTDGGVDY	264
Ferrimonas_balearica	KAGRIIAIDINESKFEKALQGLGATDCINPKDYDKPIQEIVIVEMTDGGVDF	265
	*.*****:	
P2 Group 4	-A-RIIAIDINESKF-LA--LGATDCINPKDYD-PIQEIVIVE-TDGGVD-	
Shewanella_halifaxensis	KASRIIAIDINESKFEKALQGLGATDCINPKDYDKPIQEVIIVELTDGGVDY	265
Shewanella_pealeana	KASRIIAIDINESKFEKALQGLGATDCINPKDYDKPIQEVIIVELTDGGVDY	264
Shewanella_piezotolerans	KASRIIAIDINESKFEKALQGLGATDCINPKDYDKPIQDVIVELTDGGVDY	264
Shewanella_woodyi	KAARIIVIDINESKFEKALQGLGATDCINPKDYDKPIQDVIVELTDGGVDY	264
Shewanella_sediminis	KASRIIVIDINESKFEKALQGLGATDFINPKDYDKPIQDVIVELTDGGVDY	264
Shewanella_oneidensis	KASRIIVIDINESKFEKALQGLGATDFINPKDYDKPIQDVIVELTDGGVDY	264
	*:	
P2 Group 5	KA-RII-IDINESKFELA--LGATD-INPKDYDKPIQ-VI-ELTDGGVDY	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	KAGRIIAIDINESKFELARKLGATDCINPNNDYDKPIQEVIVELTDGGVDF	265
Aeromonas_veronii	KAGRIIAIDINESKFELARKLGATDCINPNNDYDKPIQEVIVELTDGGVDF	265
Aeromonas_salmonicida	KAGRIIAIDINESKFELARKLGATDCINPNDFDKPIQEVIVEMTDGGVDF	265
Aeromonas_caviae	KAGRIIAIDINESKFELARKLGATDCINPNTFDKPIQEVIVEMTDGGVDF	265
Chromobacterium_violaceum	GAGRIIGIDINEGKFELAKKLGATDCVNPNGFDKPIQDVIVEMTDGGVDF	264
Alteromonas_sp.	KAGRIIAIDINEGKFELAKKLGATDCINPKSFDKPIQDVIVELTDGGVDY	264
	****.****.****:*****:**:****:****:*****:	
P2 Group 6	-AGRII-IDINE-KFELA-KLGATDC-NP---DKPIQDVIVE-TDGGVD-	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Marinomonas_posidonica	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEISTRPFQVLTGRVW	309
Marinomonas_mediterranea	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEISTRPFQVLTGRVW	309
Marinobacterium_stanieri	SFECIGNVQVMRSALECCHKGWGESIIIGVAGAGQEISTRPFQVLTGRVW	309
Bdellovibrio_bacteriovorus	SFECVGNQLMRAALECAHRGWQSIVIGVAGAGQEISTRPFQVLTGRVW	309
Glaciecola_sp.	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Pseudoalteromonas_atlantica	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Tolumonas_auensis	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Alishewanella_jeotgali	SFECIGNVNVMSALECCHKGWGESIIIGVAGAGQEISTRPFQVLTGRVW	312
Pantoea_ananatis	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Pantoea_stewartii	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Pantoea_vagens	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Erwinia_amylovora	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Erwinia_pyrifoliae	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Erwinia_tasmaniensis	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Commensalibacter_intestini	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	312
Actinobacillus_ureae	SFECVGNADLMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQVLTGRVW	312
Actinobacillus_pleuropneumonia	SFECVGNVDLMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQVLTGRVW	312
Simonsiella_muelleri	SFECIGNVNDLMRSALECCHKGWGESVIIIGVAPAGAEIKTRPFQVLTGRVW	313
Moraxella_catarrhalis	SFECIGNVDVMRAALECCHKGWGESVIIIGVAPAGAEISTRPFQVLTGRVW	312
Synechococcus_sp.	SFECIGNVQVMRAALECCHKGWGESIIIGVAGAGQEISTRPFQVLTGRVW	310
Methylomicrobium_album	SIECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	310
Laribacter_hongkongensis	SFECVGNVLMRSALECCHKGWGESIIIGVAGAGQEISTRPFQVLTGRVW	311
Mus_musculus_Chain_A	SLDCAGTAQTLKAAVDCTVLGWSCTVVGAK--VDEMTIPTVDVILGRSI	316
Mus_musculus_Chain_B	SLDCAGTAQTLKAAVDCTVLGWSCTVVGAK--VDEMTIPTVDVILGRSI	316
	: *... :*: **.. :*: *: ..: **	
P2 Group 1	S--C-G-----A-----GWG-----G-----E-----GR--	
Photobacterium_profundum	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Vibrio_corallilyticus	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	320
	*****.*****	
P2 Group 2	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	
Marinobacter_aquaeolei	SFECIGNVDVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	313
Marinobacter_hydrocarbonoclast	SFECIGNVDVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	313
Marinobacter_algicola	SFECIGNVDVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	310
Oceanobacter_sp.	SFECIGNVDVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Marinobacter_manganoxydans	SFECIGNVDVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	313
Oceanospirillum_sp.	SFECIGNVDVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Pseudoalteromonas_haloplanktis	SFECIGNVNLMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Psychromonas_ingrahamii	SFECIGNVDVMSALECCHKGWGESIIIGVAGAGQEISTRPFQVLTGRVW	314
	*****.:*****.:*****.:*****	
P2 Group 3	SFECIGNV--MRSALECCHKGWGES--IGVAGAG-EISTRPFQVLTGRVW	
Reinekea_sp.	SFECIGNVDVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	
Ferrimonas_balearica	SFECIGNVHVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	
	*****.*****.:*****.:*****	
P2 Group 4	SFECIGNV--VMRSALECCHKGWGESVI--GVAGAGQEISTRPFQVLTGRVW	
Shewanella_halifaxensis	SFECIGNIHVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	315
Shewanella_pealeana	SFECIGNVHVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Shewanella_piezotolerans	SFECIGNVHVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Shewanella_woodyi	SFECIGNVHVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Shewanella_sediminis	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
Shewanella_oneidensis	SFECIGNVNVMSALECCHKGWGESVIIIGVAGAGQEISTRPFQVLTGRVW	314
	*****.:*****.:*****.:*****	
P2 Group 5	SFECIGN--VMRSALECCHKGWGESV-IGVAGAGQEISTRPFQVLTGRVW	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	SFECIGNVKVMRAALECCHKGWGESVIIGVAGAGQEISTRPFQLVTGRVW	315
Aeromonas_veronii	SFECIGNVKVMRAALECCHKGWGESVIIGVAGAGQEISTRPFQLVTGRVW	315
Aeromonas_salmonicida	SFECIGNVKVMRAALECCHKGWGESVIIGVAGAGQEISTRPFQLVTGRVW	315
Aeromonas_caviae	SFECIGNVKVMRAALECCHKGWGESVIIGVAGAGQEISTRPFQLVTGRVW	315
Chromobacterium_violaceum	SFECIGNVKVMRAALECCHKGWGESVIIGVAGAGQEISTRPFQLVTGRVW	314
Alteromonas_sp.	SFECIGNVDVMRSALECCHKGWGESVIIGVAGAGKEICTRPFQLVTGRVW	314
	*****.*:**:*****:*****:*.*****	
P2 Group 6	SFECIGNV-VMR-ALECCHKGWGESVIIGVAGAG-EI-TRPFQLVTGRVW	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	RGSFAGGVGRSELPSYVQRYMQGEFKLDDFIHTMGLEQINEAFDLMHE	365
Aeromonas_veronii	RGSFAGGVGRSELPSYVQRYMQGEFKLDDFIHTMGLEQINEAFELMHQ	365
Aeromonas_salmonicida	RGSFAGGVGRSELPSYVQRYMQGEFKLDDFIHTMPLEQINEAFELMHE	365
Aeromonas_caviae	RGSFAGGVGRSELPSYVQRYMQGEFKLDDFIHTMPLEQINEAFDLMHE	365
Chromobacterium_violaceum	RGSFAGGVGRTELPYVERYLKGFEKLLDDFIHTMPLEKINEAFDLMHE	364
Alteromonas_sp.	RGTAFGGVKGRSQLPDYVERYLKGFEKLLDDFIHTMPLEKINEAFDLMHE	364
P2 Group 6	RG-AFGGV-GR--LP-YV-RY--GEF-LDDFIHTM-LE--NEAF-LMH-	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Marinomonas_posidonica	GKSIRTVILFDQ-----	371
Marinomonas_mediterranea	GKSIRTVILFDQ-----	371
Marinobacterium_stanieri	GKSIRSVILFDQ-----	371
Bdellovibrio_bacteriovorus	GKSIRSVIKM-----	369
Glaciecola_sp.	GKSIRSVVHY-----	372
Pseudoalteromonas_atlantica	GKSIRSVVHY-----	372
Tolomonas_auensis	GKSIRTVILFDK-----	374
Alishewanella_jeotgali	GKSIRTVIHF-----	372
Pantoea_ananatis	GKSIRSVVHFNK-----	374
Pantoea_stewartii	GKSIRSVVHFNK-----	374
Pantoea_vagans	GKSIRSVVHFNK-----	374
Erwinia_amylovora	GKSIRTVVHFTKS-----	375
Erwinia_pyrifoliae	GKSIRTVVHFAKS-----	375
Erwinia_tasmaniensis	GKSIRTVVHFSKA-----	375
Commensalibacter_intestini	GKSIRTVIRY-----	372
Actinobacillus_ureae	GKSIRTVIHF-----	372
Actinobacillus_pleuropneumonia	GKSIRTVIHF-----	372
Simonsiella_muelleri	GKSIRTVIHF-----	373
Moraxella_catarrhalis	GKSIRSVIHF-----	372
Synechococcus_sp.	GQSIRSVIHFNR-----	372
Methylobacterium_album	GKSIRTVIHFNH-----	372
Laribacter_hongkongensis	GKSIRTVIHF-----	371
Mus_musculus_Chain_A	GKSIRTILTF-----	376
Mus_musculus_Chain_B	GKSIRTILTF-----	376
	*:***:!!:	
P2 Group 1	G-SIR-----	
Photobacterium_profundum	GKSIRSVIHFDK-----	376
Vibrio_corallilyticus	GKSIRTVIHMDQ-----	382
	*****:***:*	
P2 Group 2	GKSIR-VIH-D-----	
Marinobacter_aquaeolei	GKSIRSVIHFDK-----	375
Marinobacter_hydrocarbonoclast	GKSIRSVIHFDK-----	375
Marinobacter_algicola	GKSIRSVIHFDK-----	372
Oceanobacter_sp.	GKSIRSVIHYNK-----	376
Marinobacter_manganoxydans	GKSIRTVIHYDK-----	375
Oceanospirillum_sp.	GKSIRSVIHYDR-----	376
Pseudoalteromonas_haloplanktis	GESIRTVIHFDK-----	376
Psychromonas_ingrahamii	GESIRSVIHFAK-----	376
	*:***:***: :	
P2 Group 3	G-SIR-VIH-----	
Reinekea_sp.	GKSIRSVVHF-----	
Ferrimonas_balearica	GKSIRSVIHFDQ-----	
	*****:***	
P2 Group 4	GKSIRSV-HF-----	
Shewanella_halifaxensis	GKSIRTVLHFGK-----	377
Shewanella_pealeana	GKSIRTVLHFDK-----	376
Shewanella_piezotolerans	GKSIRTVIHFDK-----	376
Shewanella_woodyi	GKSIRTVIHFDK-----	376
Shewanella_sediminis	GKSIRTVIHFDK-----	376
Shewanella_oneidensis	GKSIRTVIHFDK-----	376
	*****:***,*	
P2 Group 5	GKSIRTV-HF-K-----	

A-7: Results of Multiple Sequences Alignment of Partition P2 (cont.)

Aeromonas_hydrophila	GKSIRSVIHY-----	375
Aeromonas_veronii	GKSIRTVIHY-----	375
Aeromonas_salmonicida	GKSIRTVIHY-----	375
Aeromonas_caviae	GKSIRTVIHY-----	375
Chromobacterium_violaceum	GKSIRSVIHYAAEPA-----	379
Alteromonas_sp.	GKSIRSVIHYA-----	375
	*****:****	
P2 Group 6	GKSIR-VIHY-----	

A-8: Results of Multiple Sequences Alignment of Partition P3 (cont.)

Marinomonas_posidonica	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGEDPEGIFPAILGHE	63
Marinomonas_mediterranea	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGDDPEGIFPAILGHE	63
Marinobacterium_stanieri	PLTIEEVDVQGPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Bdellovibrio_bacteriovorus	PLSIEEVDLEGGKGEVLIRVVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Mus_musculus_Chain_A	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKPKALFPVVLGHE	68
Mus_musculus_Chain_B	PLCIEEIEVSPPKACEVRIQVIATVCVPTDIN-ATDPKPKALFPVVLGHE	68
Laribacter_hongkongensis	PLEIVEVDVAPPQKGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	65
Synechococcus_sp.	PLEITEIEVAPPAAGEVLLRVVASGVCHTDAFTLSGQDPEGVFPAILGHE	64
Methylomicrobium_album	PLEVTEVNVAPPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	64
P3 Group 1	PL---E-----P---EV-----A--VC-TD-----FP--LGHE	
	** : *::: * ** ::::: ** ** . . . : ** :****	
Pantoea_ananatis	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGSDPEGVFPAILGHE	66
Pantoea_stewartii	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGSDPEGVFPAILGHE	66
Pantoea_vagans	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGTDPEGVFPAILGHE	66
Erwinia_amylovora	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGKDPEGVFPAILGHE	66
Erwinia_pyrifoliae	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGKDPEGVFPAILGHE	66
Erwinia_tasmaniensis	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGKDPEGVFPAILGHE	66
Commensalibacter_intestini	PLIIEEVDLMPPQKGEVLIRIVATGVCHTDAYTLSGADPEGIFPAILGHE	66
Glaciecola_sp.	PLTIEEVDLMPPQKGEVLIRVVATGVCHTDAYTLSGDDPEGIFPAILGHE	66
Pseudoalteromonas_atlantica	PLSIEEVDLMPPQKGEVLIRVVATGVCHTDAYTLSGDDPEGIFPAILGHE	66
Tolomonas_aeuensis	PLSIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGADPEGVFPAILGHE	66
Actinobacillus_ureae	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGQDSEGVFPAILGHE	66
Actinobacillus_pleuropneumonia	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGQDSEGVFPAILGHE	66
Simonsiella_muelleri	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAYTLSGQDSEGVFPAILGHE	67
Moraxella_catarrhalis	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAYTLSGADPEGIFPAILGHE	66
Alishewanella_jeotgali	PLSIEEVDLMPPQKGEVLVRIVASGVCHTDAFTLSGEDPEGIFPAILGHE	66
P3 Group 2	PL-IEE-DLMPQ-GEVL---A-GVCHTDA-TLSG-D-EG-FP--LGHE	
	** ***:***** ***::::*,*****:***** *.*.*.* :****	

A-8: Results of Multiple Sequences Alignment of Partition P3 (cont.)

Marinomonas_posidonica	GAGVVEAVGEGVTTLKPGDHVIPLYTAECGECKFCQSGKTNLCQAVR---	110
Marinomonas_mediterranea	GAGVVEAVGEGVTTLKPGDHVIPLYTAECGECKFCKSGKTNLCQAVR---	110
Marinobacterium_stanieri	GAGVVEAVGEGVTTLKPGDHVIPLYTAECGECKFCKSGKTNLCQAVR---	110
Bdellovibrio_bacteriovorus	GGGIVEEVGEGVTTLKGDHVIPLYTPECKECKFCLSGKTNLCVRI---	110
Mus_musculus_Chain_A	CAGIVESVGPVGNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGLRNFK	118
Mus_musculus_Chain_B	CAGIVESVGPVGNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGLRNFK	118
Laribacter_hongkongensis	GGGIVEAVGEGVTSVAVGDHVIPLYTAECRECKFCKSGKTNLCQAVR---	112
Synechococcus_sp.	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRACSFCLSGKTNLCQAIR---	111
Methylomicrobium_album	GGGIVEAVGEGVTSVAVGDHVIPLYTPECGKCKFCLSGKTNLCQAIR---	111
P3 Group 1	----VE-VG--VT----GD-VIP----C--C--C--S--TNLC---R---	
	..:* * * . * * . . * * : * * * * : : * * : * * * * * * * : *	
Pantoea_ananatis	GGGVVEAVGEGVTSVEVGDHVIPLYTPECGQCKFCLSGKTNLCQAIR---	113
Pantoea_stewartii	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGKCKFCLSGKTNLCQAIR---	113
Pantoea_vagans	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGKCKYCLSGKTNLCQAIR---	113
Erwinia_amylovora	GGGVVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAIR---	113
Erwinia_pyrifoliae	GGGVVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAIR---	113
Erwinia_tasmaniensis	GGGIVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAIR---	113
Commensalibacter_intestini	GAGIVEAVGEGVTSISVGDYVIPLYTPECGKCEYCLSGKTNLCQAIR---	113
Glaciecola_sp.	GAGIVEAIGEGVTSVEVGDHVIPLYTPECGECKFCLSGKTNLCQAIR---	113
Pseudoalteromonas_atlantica	GAGIVEAIGEGVTSVEVGDHVIPLYTPECGECKFCLSGKTNLCQAIR---	113
Tolomonas_auensis	GAGIVEAIGEGVTSVAVGDHVIPLYTPECGECKFCKSGKTNLCQAIR---	113
Actinobacillus_ureae	GAGIVEAVGEGVTDFKVGDHVIPLYTAECRCKCKFCLSGKTNLCQAVR---	113
Actinobacillus_pleuropneumonia	GAGIVEAVGEGVTDFKVGDHVIPLYTAECRCKCKFCLSGKTNLCQAVR---	113
Simonsiella_muelleri	GAGIVEAVGEGVTDFAVGDHVIPLYTAECKQCKFCTSGKTNLCSSVR---	114
Moraxella_catarrhalis	GAGIVEAVGEGVTDFAVGDHVIPLYTAECGQCKMCLSNKTNLCQAVR---	113
Alishewanella_jeotgali	GGGIVEAVGEGVTSVAVGDHVIPLYTPECGKCKFCLSGKTNLCQAIR---	113
P3 Group 2	G-G-VEA-GEGVT---VGD-VIPLYT-EC--C--C-S-KTNLC---R---	
	.:*:*:*:*:*.*.*.*:*:*:*:*.*.*:*:*.*.*:*:*:*:*:*:*:*:	

A-8: Results of Multiple Sequences Alignment of Partition P3 (cont.)

Marinomonas_posidonica	-ETQGKGLMPDGTSRFSINGEPIFHYMGTSFSEYSVVPEISLAKIHVDA	159
Marinomonas_mediterranea	-ETQGKGLMPDGTSRFSINGEPIFHYMGTSFSEYSVVPEISLAKIHVDA	159
Marinobacterium_stanieri	-ATQGQGLMPDGTSRFSLNGETLYHYMGTSFSEYTVVPEISLAKIHVDA	159
Bdellovibrio_bacteriovorus	-ATQGKGLMPDGTSRFSKDGKMIHHYMGCSFPAEYTVVPEIALAKVNPAA	159
Mus_musculus_Chain_A	YPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEA	168
Mus_musculus_Chain_B	YPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEA	168
Laribacter_hongkongensis	-ATQGKGLMPDGTTRFSYKQPIYHYMGTSFSEYTVVPEISLAKIPKA	161
Synechococcus_sp.	-GTQGRGLMPDGTSRFSSAGRLIHHYMGTSFSEYTVVPEIAVARISKEA	160
Methylomicrobium_album	-ATQGKGLMPDGTSRFSKDGKPIFHYMGTSFSEYTVLPEIAVARINKEA	160
P3 Group 1	--T-----LM-D-T-RF---G---H-MG-S-F--Y-V--E---A-----A	
	* .: ** * *: **: * . :*:** *:***:*. * :*: *	
Pantoea_ananatis	-TTQGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISLAKISKEA	162
Pantoea_stewartii	-TTQGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISLAKISKEA	162
Pantoea_vagans	-TTQGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVIPEISLAKISKEA	162
Erwinia_amylovora	-TTQGKGLMPDGTTRFFKDGQPVYHYMGTSFSEYTVVPEISLAKISKEA	162
Erwinia_pyrifoliae	-TTQGKGLMPDGTTRFFKDGQPIYHYMGTSFSEYTVVPEISLAKISKEA	162
Erwinia_tasmaniensis	-TTQGKGLMPDGTTRFFKDGQPIYHYMGTSFSEYTVVPEISLAKISKEA	162
Commensalibacter_intestini	-VTQGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISVAKISKEA	162
Glaciecola_sp.	-TTQGQGLMPDGTTRFSKNGKPIYHYMGTSFAEHTVVPEIALAKIPKEA	162
Pseudoalteromonas_atlantica	-ATQGKGLMPDGTTRFSKNGKPIYHYMGTSFAEHTVVPEIALAKIPKEA	162
Tolomonas_auensis	-ATQGKGLMPDGTTRFFKDGKPIFHYMGTSFAEHTVVPEISLAKISKDA	162
Actinobacillus_ureae	-ETQGKGLMPDGTVRFFKDGQPIFHYMGTSFSEYTVVSEYSLAKIQENA	162
Actinobacillus_pleuropneumonia	-ETQGKGLMPDGTVRFFKDGQPIFHYMGTSFSEYTVVSEYSLAKIQENA	162
Simonsiella_muelleri	-ATQGKGLMPDGTTRFYKDGKPIYHYMGTSFSEYTVVVSQYSLAKIQDDA	163
Moraxella_catarrhalis	-ETQGKGLMPDGTVRFFKEGEPYHYMGTSFSEYTVVVSQYSLAKIQKDA	162
Alishewanella_jeotgali	-ATQGKGLMPDGTSRFSKDGKPIYHYMGTSFSEYTVLPEISLAKINKEA	162
P3 Group 2	--TQG-GLMPDGT-RF-K-G-P--HYMGTSF-E-TV-----AKI---A	
	:** ** *:***:*****:***:.. :**** .:*	

A-8: Results of Multiple Sequences Alignment of Partition P3 (cont.)

Marinomonas_posidonica	PLEKVLLGCGITTTGIGAVLNTAKVEEGATIAVFLGGIGLSVIQGARMA	209
Marinomonas_mediterranea	PLEKVLLGCGITTTGIGAVLNTAKVEEGATVAVFGLGGIGLSVIQGARMA	209
Marinobacterium_stanieri	PLEKVLLGCGITTTGIGAVLNTAKVEPGSTVAIFGMGGIGLSCIQGARMA	209
Bdellovibrio_bacteriovorus	PLDKVLLGCGVTTGIGAVLNTAKVEKATVAVFGLGGIGLSVIQGAKMA	209
Mus_musculus_Chain_A	NLERVCLIGCGFSSGYGAAINTAKVTPGSTCAVFLGCVGLSAIIGCKIA	218
Mus_musculus_Chain_B	NLERVCLIGCGFSSGYGAAINTAKVTPGSTCAVFLGCVGLSAIIGCKIA	218
Laribacter_hongkongensis	PLEKVLLGCGVTTGIGAVLNTAKVTAGSTVAVFGLGGIGLAAIIGASMA	211
Synechococcus_sp.	PLEKVLLGCGVTTGIGAVLNTAKVEPGSTVAVFGLGGIGLAVIIGAVMA	210
Methylomicrobium_album	PLEKVLLGCGVTTGIGAVMNTAKVEEGATVAVFGLGGIGLSAIIGAVMA	210
P3 Group 1	-L--VCL-GCG--G-GA--NTA-V--G-T-A-FG-G--GL--I-G---A *::***:***:::* **:****** *.* **:* *::* * * . :*	
Pantoea_ananatis	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Pantoea_stewartii	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Pantoea_vagans	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIVIGAKMA	212
Erwinia_amylovora	PLEEVLLGCGVTTGMGAVINTANVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Erwinia_pyrifoliae	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Erwinia_tasmaniensis	PLEEVLLGCGVTTGMGAVLNTAKVKEGDTVAIFGLGGIGLSAIIGAKMA	212
Commensalibacter_intestini	PLEKVLLGCGITTTGMGAVNTAKVQPGDSVAVFGLGGIGLSVIMGAKAA	212
Glaciecola_sp.	PLEKVLLGCGVTTGMGAVNTAKVKEGDTVAVFGLGGIGLSVLIIGAKMA	212
Pseudoalteromonas_atlantica	PLEKVLLGCGVTTGMGAVNTAKVQEGDTVAVFGLGGIGLSVLIIGAKMA	212
Tolomonas_auensis	PLEKVLLGCGVTTGMGAVKNTAKVQPGDTVAVFGLGGIGLSVIIGAVMA	212
Actinobacillus_ureae	PLDEVLLGCGVTTGIGAVTRTAKVKQGDVAIFGLGGIGLAAIIGARMA	212
Actinobacillus_pleuropneumonia	PLDEVLLGCGVTTGIGAVTRTAKVKKGDVAIFGLGGIGLAAIIGARMA	212
Simonsiella_muelleri	PLEEVLLGCGVTTGIGAVTKTAKVKAGDTVAVFGLGGIGLAAIIGARMS	213
Moraxella_catarrhalis	PLEEVLLGCGVTTGMGAVLKTAKVKPGDTVAIFGLGGIGLAAVIGARMA	212
Alishewanella_jeotgali	PLEKVLLGCGVTTGMGAVFNTAKVKPGDTVAIFGLGGIGLSAVIASVMA	212
P3 Group 2	PL--VCLLGGC-TTG-GAV--TA-V--GD-VA-FGLGGIGL----- **:*:*****:***:*** .**:*: **:*:*****:..: : :	

A-8: Results of Multiple Sequences Alignment of Partition P3 (cont.)

Marinomonas_posidonica	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEISTRPFQLVTGRVW	309
Marinomonas_mediterranea	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEISTRPFQLVTGRVW	309
Marinobacterium_stanieri	SFECIGNVQVMRSALECCHKGWGESIIIGVAGAGEEISTRPFQLVTGRVW	309
Bdellovibrio_bacteriovorus	SFECVGNQLMRAALECAHRGWGQSIIVGVAGAGQEISTRPFQLVTGRVW	309
Mus_musculus_Chain_A	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
Mus_musculus_Chain_B	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
Laribacter_hongkongensis	SFECVGNVLMRAALECCHKGWGESIIIGVAGAGQEISTRPFQLVTGRVW	311
Synechococcus_sp.	SFECIGNVQVMRAALECCHKGWGESIIIGVAGAGQEIATRPFQLVTGRVW	310
Methylomicrobium_album	SIECIGNVKVMRSALECCHKGWGQSVIIIGVAGAGEEICTRPFQLVTGRVW	310
P3 Group 1	S--C-G-----A-----GWG-----G-----E-----GR--	
	: *..: :: *::. ***.. :*: .*: .:..: **	
Pantoea_ananatis	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Pantoea_stewartii	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Pantoea_vagans	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEISTRPFQLVTGRVW	312
Erwinia_amylovora	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEIATRPFQLVTGRVW	312
Erwinia_pyrifoliae	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEIATRPFQLVTGRVW	312
Erwinia_tasmaniensis	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEIATRPFQLVTGRVW	312
Commensalibacter_intestini	SFECIGNVKMRSALECCHKGWGESVIIIGVAGAGEEISTRPFQLVTGRVW	312
Glaciecola_sp.	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Pseudoalteromonas_atlantica	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Tolumonas_auensis	SFECIGNVKMRSALECCHKGWGESVIIIGVAAAGQEISTRPFQLVTGRIW	312
Actinobacillus_ureae	SFECVGNADLMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTGRVW	312
Actinobacillus_pleuropneumonia	SFECVGNVDLMRAALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTGRVW	312
Simonsiella_muelleri	SFECVGNVDLMRAALECCHKGWGESVIIIGVAPAGAEIKTRPFQLVTGRVW	313
Moraxella_catarrhalis	SFECIGNVDMRAALECCHKGWGESVIIIGVAPAGAEISTRPFQLVTGRVW	312
Alishewanella_jeotgali	SFECIGNVNMRSALECCHKGWGESIIIGVAGAGQEISTRPFQLVTGRVW	312
P3 Group 2	SFEC-GN---MR-ALECCHKGWGES-IIGVA-AG-EI-TRPFQLVTGR-W	
	****:*..: **:******:***** ** * *****:*	

A-8: Results of Multiple Sequences Alignment of Partition P3 (cont.)

Marinomonas_posidonica	KGSAGGGVKGRSQLPGYVEDYMNGKIEIDPFVTHTMPLEQINEAFDLMHE	359
Marinomonas_mediterranea	KGSAGGGVKGRSQLPGYVEDYMNGKIEIDPFVTHMTSLEKINDAFDLMHE	359
Marinobacterium_stanieri	KGSAGGGVKGRSQLPGYVEDYMNGKIEIDPFVTHMTGLEDINKAFDLMHE	359
Bdellovibrio_bacteriovorus	KGSAGGGVKGRTELPYVEQYMSGEINIDDMVFTMPLEDINKAFDYMHE	359
Mus_musculus_Chain_A	NGTFFGGWKSVDSPNLVSDYKNNKFDLLLVTHALPFESINDAIDLME	366
Mus_musculus_Chain_B	NGTFFGGWKSVDSPNLVSDYKNNKFDLLLVTHALPFESINDAIDLME	366
Laribacter_hongkongensis	RGSAGGGVGRTELPAYVEKAQKGEIPLDTFITHTLPLEEINQAFELMHE	361
Synechococcus_sp.	RGSAGGGVGRTELPYVERFQSGEIPLDTFITHTMPLEEINRAFELMHA	360
Methylomicrobium_album	RGSAGGGVHGRSELPYVERAQRGEIPLDVFITHTLGLEDINQAFDLMHE	360
P3 Group 1	-G--FGG-----P--V-----D---T----E-IN-A---M--	
	.*: *** :. :.* *. : : * : : * : : * : * : * :	
Pantoea_ananatis	RGSAGGGVKGRSQLPGIVQDYLDGKFALNDFITHTMPLEEINDAFDLMHE	362
Pantoea_stewartii	RGSAGGGVKGRSQLPGIVQDYLDGKFALNDFITHTMPLAEINDAFDLMHE	362
Pantoea_vagans	RGSAGGGVKGRSQLPGIVQDYLDGKFALNDFITHTMPLEEINDAFDLMHE	362
Erwinia_amylovora	RGSAGGGVKGRTELPGIVERYMNGEFQLNDFITHNLPLEEINDAFELMHE	362
Erwinia_pyrifoliae	RGSAGGGVKGRTELPGIVERYMNGEFRLNDFITHNLPLEEINDAFELMHE	362
Erwinia_tasmaniensis	RGSAGGGVKGRTELPGLVERYMNGEFQLNDFITHNLPLEQINDAFDLMHE	362
Commensalibacter_intestini	RGSAGGGVKGRSQLPNIVNDYLQKGFQLDDFITHEMPLDQINKAFDLMHD	362
Glaciecola_sp.	RGSAGGGVKGRSQLPDYVQRYMDGEFELDTFITHTMQLEDINTAFDLMHE	362
Pseudoalteromonas_atlantica	RGSAGGGVKGRSQLPDYVQRYMDGEFELDTFITHTMPLDINTAFDLMHE	362
Tolomonas_auensis	KGSAGGGVKGRSQLPGIVEQYMNNGEFELDTFITHTMGLDDINHAFDLMHE	362
Actinobacillus_ureae	RGSAGGGVKGRTELPGIIDQFMKGEFKLRDFITHTMPLDINKAFDLMHQ	362
Actinobacillus_pleuropneumonia	RGSAGGGVKGRTELPGIIDQFMKGEFKLRDFITHTMPLDINKAFDLMHE	362
Simonsiella_muelleri	RGSAGGGYKGRSELPDLIDQYQHGEFKLSDFITHTMPLDINNAFDLMHE	363
Moraxella_catarrhalis	RGSAGGDVKGRSELPGIVSQYMGDFALSDFITHTMPLDQINAAFDLMHE	362
Alishewanella_jeotgali	RGTAFGGVKGRSELPYVDRYLNGEFELDTFITHTMPLDINKAFDLMHE	362
P3 Group 2	-G-AFG--KGR--LP-----G-F-L--FITH---L--IN-AF-LMH-	
	:*:***. ***: :*. :. : *.* * **** : * : ** ** : ** :	

A-8: Results of Multiple Sequences Alignment of Partition P3 (cont.)

Marinomonas_posidonica	GKSIRTVILFDQ-----	371
Marinomonas_mediterranea	GKSIRTVILFDQ-----	371
Marinobacterium_stanieri	GKSIRSVILFDQ-----	371
Bdellovibrio_bacteriovorus	GKSIRSVIKM-----	369
Mus_musculus_Chain_A	GKSIRTILTF-----	376
Mus_musculus_Chain_B	GKSIRTILTF-----	376
Laribacter_hongkongensis	GKSIRTVIHF-----	371
Synechococcus_sp.	GQSIRSVIHFN-----	372
Methylomicrobium_album	GKSIRTVIHFNH-----	372
P3 Group 1	G-SIR-----	
	*:***::: :	
Pantoea_ananatis	GKSIRSVVHFNK-----	374
Pantoea_stewartii	GKSIRSVVHFNK-----	374
Pantoea_vagans	GKSIRSVVHFNK-----	374
Erwinia_amylovora	GKSIRTVVHFTKS-----	375
Erwinia_pyrifoliae	GKSIRTVVHFKA-----	375
Erwinia_tasmaniensis	GKSIRTVVHFKA-----	375
Commensalibacter_intestini	GKSIRTVIRY-----	372
Glaciecola_sp.	GKSIRSVVHY-----	372
Pseudoalteromonas_atlantica	GKSIRSVVHY-----	372
Tolomonas_auensis	GKSIRTVILFDK-----	374
Actinobacillus_ureae	GKSIRTVIHF-----	372
Actinobacillus_pleuropneumonia	GKSIRTVIHF-----	372
Simonsiella_muelleri	GKSIRTVIHF-----	373
Moraxella_catarrhalis	GKSIRSVIHF-----	372
Alishewanella_jeotgali	GKSIRTVIHF-----	372
P3 Group 2	GKSIR-V-----	
	*****:*: :	

A-9: Results of Multiple Sequences Alignment of Partition P4

Marinomonas_posidonica	-----MKCKAAVAVWGPQ	13
Marinomonas_mediterranea	-----MKCKAAVAVWGPQ	13
Marinobacterium_stanieri	-----MKSRAAVAVWAGD	13
Bdellovibrio_bacteriovorus	-----MKIKAAVAVWKAGA	13
Mus_musculus_Chain_A	-----GTQGKVIKCKAAIAWKTGS	19
Mus_musculus_Chain_B	-----GTQGKVIKCKAAIAWKTGS	19
P4 Group 1	-----K--AA-AW--G-	
	:* :*:** .*	
Laribacter_hongkongensis	-----MTIKSRAAVAFAGQ	15
Synechococcus_sp.	-----MIRSRAAVAWAAGQ	14
Methylomicrobium_album	-----MIKSRAAIAWGSGR	14
P4 Group 2	-----I-SRAA-A--G-	
	*:*****:*:*:	
Pantoea_ananatis	-----MNMIKTRAAVWAAGE	16
Pantoea_stewartii	-----MNMIKTRAAVWAAGE	16
Pantoea_vagans	-----MNMIKTRAAVWAAGE	16
Erwinia_amylovora	-----MQMIKTRAAVWAAGE	16
Erwinia_pyrifoliae	-----MQMIKTRAAVWAAGE	16
Erwinia_tasmaniensis	-----MQMIKTRAAVWAAGE	16
Commensalibacter_intestini	-----MDFIKTRAAVWGPQ	16
Glaciecola_sp.	-----MQS IKTRAAVWAAGE	16
Pseudoalteromonas_atlantica	-----MQS IKTRAAVWAAGE	16
Tolumonas_auensis	-----MNMIKTRAAVWAAGE	16
Actinobacillus_ureae	-----MEF IKTRAAVWAPNE	16
Actinobacillus_pleuropneumonia	-----MEF IKTRAAVWAPNE	16
Simonsiella_muelleri	-----MTQF IKTRAAVYAPNQ	17
Moraxella_catarrhalis	-----MDF IKTRAAVWAANE	16
P4 Group 3	-----IKTRAAVA-----	
	: *****: . :	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGEDPEGIFPAILGHE	63
Marinomonas_mediterranea	PLKIEEVDVQDPQAGEVLVRMVATGVCHTDAFTLSGDDPEGIFPAILGHE	63
Marinobacterium_stanieri	PLTIEEVDVQGPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	63
Bdellovibrio_bacteriovorus	PLSIEEVDLEGGKGEVLIRVVATGVCHTDAFTLSGADPEGLFPVILGHE	63
Mus_musculus_Chain_A	PLCIEEIEVSPPKACEVRIQVIATCVCPDIN-ATDPKPKALFPVVLGHE	68
Mus_musculus_Chain_B	PLCIEEIEVSPPKACEVRIQVIATCVCPDIN-ATDPKPKALFPVVLGHE	68
P4 Group 1	PL-IEE----P---EV-----AT-VC-TD-----FP--LGHE ** **::: * : ** ::::** ** ** :. . :::** :****	
Laribacter_hongkongensis	PLEIVEVDVAPPQKGEVLVRIVATGVCHTDAFTLSGDDPEGVFPAILGHE	65
Synechococcus_sp.	PLEITEIEVAPPAAGEVLLRVVAVSGVCHTDAFTLSGDDPEGLFPVILGHE	64
Methylomicrobium_album	PLEVTEVNVAPPKAGEVLVRIVATGVCHTDAFTLSGADPEGIFPAILGHE	64
P4 Group 2	PLE--E--VAPP--GEVL-R-VA-GVCHTDA-TLSG-DPEG-FPA-LGHE ***: .:::**** **::*:**:*:*****:**** **::**:*:****	
Pantoea_ananatis	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGSDPEGVFPAILGHE	66
Pantoea_stewartii	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGSDPEGVFPAILGHE	66
Pantoea_vagans	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGDPEGVFPAILGHE	66
Erwinia_amylovora	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGDPEGVFPAILGHE	66
Erwinia_pyrifoliae	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGDPEGVFPAILGHE	66
Erwinia_tasmaniensis	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGDPEGVFPAILGHE	66
Commensalibacter_intestini	PLIIEEVDLMPPQKGEVLIRIVATGVCHTDAYTLSGADPEGIFPAILGHE	66
Glaciecola_sp.	PLTIEEVDLMPPQKGEVLIRIVATGVCHTDAYTLSGDDPEGIFPAILGHE	66
Pseudoalteromonas_atlantica	PLSIEEVDLMPPQKGEVLIRIVATGVCHTDAYTLSGEDPEGIFPAILGHE	66
Tolumonas_auensis	PLSIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGADPEGVFPAILGHE	66
Actinobacillus_ureae	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGDSEGVPFCVLGHE	66
Actinobacillus_pleuropneumonia	PLKIEEVDLMPPQKGEVLVRIVATGVCHTDAYTLSGDSEGVPFCVLGHE	66
Simonsiella_muelleri	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAYTLSGDSEGVPFCVLGHE	67
Moraxella_catarrhalis	PLVIEEIDLMPQAGEVLVRIVATGVCHTDAYTLSGADPEGIFPAILGHE	66
P4 Group 3	PL-IEE-DLMPQ-GEVL---ATGVCHTDA-TLSG-D-EG-FP--LGHE ** **:::**** **::*:**:*:*****:**** **::**:*:****	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	GAGVVEAVGEGVTTLKPGDHVIPLYTAECGECKFCQSGKTNLCQAVR---	110
Marinomonas_mediterranea	GAGVVEAVGEGVTTLKPGDHVIPLYTAECGECKFCKSGKTNLCQAVR---	110
Marinobacterium_stanieri	GAGVVEAVGEGVTTLKPGDHVIPLYTAECGECKFCKSGKTNLCQAVR---	110
Bdellovibrio_bacteriovorus	GGGIVEEVGEGVTTLKGDHVIPLYTPECKECKFCLSGKTNLCVRI---	110
Mus_musculus_Chain_A	CAGIVESVPGVTNFKPGDKVIPFFAPQCKRCKLCLSPNLNCGKLRNFK	118
Mus_musculus_Chain_B	CAGIVESVPGVTNFKPGDKVIPFFAPQCKRCKLCLSPNLNCGKLRNFK	118
P4 Group 1	--G-VE-VG-GVT--K-GD-VIP-----C--C--C-S--TNLC---R--- .*:** ** **.* **:*:**:.* **.* ** * ** ** *	
Laribacter_hongkongensis	GGGIVEAVGEGVTSVAVGDHVIPLYTAECRECKFCKSGKTNLCQAVR---	112
Synechococcus_sp.	GGGIVEAVGADVTSVAVGDHVIPLYTPECRACSFCLSGKTNLCQAIR---	111
Methylomicrobium_album	GGGIVEAVGEGVTSVAVGDHVIPLYTPECGKCKFCLSGKTNLCQAIR---	111
P4 Group 2	GG-IVE-VG--VTSVAVGDHVIPLYT-EC--C-FC-SGKTNLCQA-R--- **.* ** * .***** ** * ** *****:*	
Pantoea_ananatis	GGGVEAVGEGVTSVEVGDHVIPLYTPECGQCKFCLSGKTNLCQAIR---	113
Pantoea_stewartii	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGKCKFCLSGKTNLCQAIR---	113
Pantoea_vagans	GGGIVEAVGEGVTSVEVGDHVIPLYTPECGKCKYCLSGKTNLCQAIR---	113
Erwinia_amylovora	GGGVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAIR---	113
Erwinia_pyrifoliae	GGGVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAIR---	113
Erwinia_tasmaniensis	GGGVEAVGEGVTSVAVGDHVIPLYTPECRQCKFCLSGKTNLCQAIR---	113
Commensalibacter_intestini	GAGIVEAVGEGVTSISVGDYVIPLYTPECGKCEYCLSGKTNLCQAIR---	113
Glaciecola_sp.	GAGIVEAIGEGVTSVEVGDHVIPLYTPECGECKFCLSGKTNLCQAIR---	113
Pseudoalteromonas_atlantica	GAGIVEAIGEGVTSVEVGDHVIPLYTPECGECKFCLSGKTNLCQAIR---	113
Tolumonas_auensis	GAGIVEAIGEGVTSVAVGDHVIPLYTPECGECKFCKSGKTNLCQAIR---	113
Actinobacillus_ureae	GAGIVEAVGEGVTDKVGVDHVIPLYTAECRCKCKFCLSGKTNLCQAVR---	113
Actinobacillus_pleuropneumonia	GAGIVEAVGEGVTDKVGVDHVIPLYTAECRCKCKFCLSGKTNLCQAVR---	113
Simonsiella_muelleri	GAGIVEAVGEGVTDFAVGDHVIPLYTAECKQCKFCTSGKTNLCSSVR---	114
Moraxella_catarrhalis	GAGIVEAVGEGVTDFAVGDHVIPLYTAECGQCKMCLSNKTNLCQAVR---	113
P4 Group 3	G-G-VEA-GEGVT---VGD-VIPLYT-EC--C--C-S-KTNLC---R--- *.*:**:**.* **.*:**:**.* **.* ** * ** ** *	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	-ETQKGKGLMPDGTSRFSINGEPIFHYMGTSFSEYSVVPEISLAKIHVDA	159
Marinomonas_mediterranea	-ETQKGKGLMPDGTSRFSINGEPIFHYMGTSFSEYSVVPEISLAKIHVDA	159
Marinobacterium_stanieri	-ATQGGKGLMPDGTSRFSLNGETLYHYMGTSFSEYTVVPEISLAKIHVDA	159
Bdellovibrio_bacteriovorus	-ATQKGKGLMPDGTSRFSKDGKMIHHYMGCSFPAEYTVVPEIALAKVNPAA	159
Mus_musculus_Chain_A	YPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEA	168
Mus_musculus_Chain_B	YPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEA	168
P4 Group 1	--T---LM-D-TSRF---G---H-MG-S-F--Y-VV-E--LA-----A * .: ** * ****: .* .:*.** *:.**:*.* **:. *	
Laribacter_hongkongensis	-ATQKGKGLMPDGTTRFSYKGPFIHYMGTSFSEYTVVPEISLAKIPKDA	161
Synechococcus_sp.	-GTQGRGLMPDGTSRFSSAGRLIHHYMGTSFSEYTVVPEIAVARISKEA	160
Methylomicrobium_album	-ATQKGKGLMPDGTSRFSKDGKPIFHYMGTSFSEYTVLPEIAVARINKEA	160
P4 Group 2	--TQG-GLMPDGT-RFS--G--I-HYMGTSFSEYTV-PEI--A-I-K-A .***:*****:*** *: *.******:***:***:*** **	
Pantoea_ananatis	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISLAKISKEA	162
Pantoea_stewartii	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISLAKISKEA	162
Pantoea_vagans	-TTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVIPEISLAKISKEA	162
Erwinia_amylovora	-TTQKGKGLMPDGTTRFFKDGQPVYHYMGTSFSEYTVVPEISLAKISKEA	162
Erwinia_pyrifoliae	-TTQKGKGLMPDGTTRFFKDGQPIYHYMGTSFSEYTVVPEISLAKISKEA	162
Erwinia_tasmaniensis	-TTQKGKGLMPDGTTRFFKDGQPIYHYMGTSFSEYTVVPEISLAKISKEA	162
Commensalibacter_intestini	-VTQKGKGLMPDGTTRFFKDGKPIFHYMGTSFSEYTVVPEISVAKISKEA	162
Glaciecola_sp.	-TTQGGKGLMPDGTTRFSKNGKPIYHYMGTSFAEHTVVPEIALAKIPKEA	162
Pseudoalteromonas_atlantica	-ATQKGKGLMPDGTTRFSKNGKPIYHYMGTSFAEHTVVPEIALAKIPKEA	162
Tolumonas_auensis	-ATQKGKGLMPDGTTRFFKDGKPIFHYMGTSFAEHTVVPEISLAKISKDA	162
Actinobacillus_ureae	-ETQKGKGLMPDGTVRFFKDGQPIFHYMGTSFSEYTVVSEYSLAKIQENA	162
Actinobacillus_pleuropneumonia	-ETQKGKGLMPDGTVRFFKDGQPIFHYMGTSFSEYTVVSEYSLAKIQENA	162
Simonsiella_muelleri	-ATQKGKGLMPDGTTRFYKDGKPIYHYMGTSFSEYTVVVSQYSLAKIQDDA	163
Moraxella_catarrhalis	-ETQKGKGLMPDGTVRFFKEGEPYHYMGTSFSEYTVVVSQYSLAKIQKDA	162
P4 Group 3	--TQG-GLMPDGT-RF-K-G-P--HYMGTSF-E-TV-----AKI---A ***:*****.* ** *:.**:*.******:***:***:*** .:*** .:*	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	PLEKVLLGCGITTTGIGAVLNTAKVEEGATIAVFGGLGGIGLSVIQGARMA	209
Marinomonas_mediterranea	PLEKVLLGCGITTTGIGAVLNTAKVEEGATVAVFGLGGIGLSVIQGARMA	209
Marinobacterium_stanieri	PLEKVLLGCGITTTGIGAVLNTAKVEPGSTVAIFGMGGIGLSCIQARMA	209
Bdellovibrio_bacteriovorus	PLDKVLLGCGVTTGIGAVLNTAKVEKATVAVFGLGGIGLSVIQAKMA	209
Mus_musculus_Chain_A	NLERVCLIGCGFSSGYGAAINTAKVTPGSTCAVFGLCVGLSAIIIGCKIA	218
Mus_musculus_Chain_B	NLERVCLIGCGFSSGYGAAINTAKVTPGSTCAVFGLCVGLSAIIIGCKIA	218
P4 Group 1	-L--VCL-GCG--G-GA--NTAKV--G-T-A-FG-G--GLS-I-G---A *::***:***.::* **.:***** *:* *::**:* :*** * *::**	
Laribacter_hongkongensis	PLEKVLLGCGVTTGIGAVLNTAKVTAGSTVAVFGLGGIGLAAIIGASMA	211
Synechococcus_sp.	PLEKVLLGCGVTTGIGAVLNTAKVEPGSTVAVFGLGGIGLAVIIGAVMA	210
Methylomicrobium_album	PLEKVLLGCGVTTGIGAVMNTAKVEEGATVAVFGLGGIGLSAIIIGAVMA	210
P4 Group 2	PLEKVLLGCGVTTGIGAV-NTAKV--G-TVAVFGLGGIGL--IIGA-MA *****:*****:***** *.:*****:***** **	
Pantoea_ananatis	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIIGAKMA	212
Pantoea_stewartii	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIIGAKMA	212
Pantoea_vagans	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIIGAKMA	212
Erwinia_amylovora	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIIGAKMA	212
Erwinia_pyrifoliae	PLEEVLLGCGVTTGMGAVMNTAKVKEGDTVAIFGLGGIGLSAIIIGAKMA	212
Erwinia_tasmaniensis	PLEEVLLGCGVTTGMGAVLNTAKVKEGDTVAIFGLGGIGLSAIIIGAKMA	212
Commensalibacter_intestini	PLEKVLLGCGITTTGMGAVTNTAKVQPGDSVAVFGLGGIGLSVIMGAKAA	212
Glaciecola_sp.	PLEKVLLGCGVTTGMGAVTNTAKVKEGDTVAVFGLGGIGLSVLIIGAKMA	212
Pseudoalteromonas_atlantica	PLEKVLLGCGVTTGMGAVTNTAKVQEGDTVAVFGLGGIGLSVLIIGAKMA	212
Tolumonas_auensis	PLEKVLLGCGVTTGMGAVKNTAKVQPGDTVAVFGLGGIGLSVLIIGAVMA	212
Actinobacillus_ureae	PLDEVLLGCGVTTGIGAVTRTAKVKQGDVAIFGLGGIGLAAIIGARMA	212
Actinobacillus_pleuropneumonia	PLDEVLLGCGVTTGIGAVTRTAKVKKGDVAIFGLGGIGLAAIIGARMA	212
Simonsiella_muelleri	PLEEVLLGCGVTTGIGAVTKTAKVKAGDTVAVFGLGGIGLAAIIGARMS	213
Moraxella_catarrhalis	PLEEVLLGCGVTTGMGAVLKTAKVKPGDTVAIFGLGGIGLAAVIGARMA	212
P4 Group 3	PL--VCLLGGC-TTG-GAV--TA-V--GD-VA-FGLGGIGL----GA--- **.:*****:***:*** .**:*: **:*:*****:..** :	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	GASKIIAIDINESKFEMATQFGATDCVNPKNFDAPIQQVIVDMTDGGVDY	259
Marinomonas_mediterranea	GASKIIAIDINESKFEMATQFGATDCVNPKNFDAPIQQVIVDMTDGGVDY	259
Marinobacterium_stanieri	GAERIIAIDINEEKFEMARQFGATDCVNPKNFSDPIQQVIVDMTDGGVDY	259
Bdellovibrio_bacteriovorus	GASRIIAIDINDAKWEMAQKFGATDFVNPKKHKPIQQVIVEMTEWGVY	259
Mus_musculus_Chain_A	GASRIIAIDINGEKFPKAKALGATDCLNPRELDKPVQDVITELTAGGVY	268
Mus_musculus_Chain_B	GASRIIAIDINGEKFPKAKALGATDCLNPRELDKPVQDVITELTAGGVY	268
P4 Group 1	GA--IIAIDIN--K---A---GATD--NP-----P-Q-VI---T--GVDY *.:***** *: * :**** :*:. . *:*:**.:* ****	
Laribacter_hongkongensis	KAGRIIAIDINPKFAKARELGATDCINPNYDKPIQDVIVELTDGGVDY	261
Synechococcus_sp.	GASRIIGIDTNPKEFAIARQLGASDCLDPGAFDAPIQEVVIDLTDGGVDY	260
Methylomicrobium_album	KASRIIVAVDINPAKFEIAQQLGATDCLNPLDYDRPIQEVIVDLTDGGVDY	260
P4 Group 2	-A-RI---D-NP-KF--A--LGA-DC--P---D-PIQ-V---LTDGGVDY *.:*.:* ** ** *:*:***:*:* * :* ***:*****	
Pantoea_ananatis	KAGRIIGIDINTSKFDLARKLGATDLINPKDYDKPIQDVIVELTDGGVDY	262
Pantoea_stewartii	KAGRIIGIDINTSKFDLARKLGATDLINPKDYDKPIQDVIVELTDGGVDF	262
Pantoea_vagans	KAGRIIAIDLNTSKFDLARKLGATDLINPKDYDKPIQDVIVELTDGGVDF	262
Erwinia_amylovora	KAGRIIGIDINSSKYDLARKLGATDLINPKDFDKPIQDVIVEMTDGGVDF	262
Erwinia_pyrifoliae	KAGRIIGIDINTSKYDLARKLGATDLITPKDFDKPIQDVIVEMTDGGVDF	262
Erwinia_tasmaniensis	KAGRIIGIDINTSKYDLARKLGATDLINPKDFDKPIQDVIVEMTDGGVDF	262
Commensalibacter_intestini	KAERIIAIDINTDKFDLAKKLGATDCINPKDYQKSIQDVIVELTNGGVDF	262
Glaciecola_sp.	NAGRIIAIDVNEKFKIAKQLGATDVVNPKNFDKSIQEVIVEMTDGGVDY	262
Pseudoalteromonas_atlantica	NAGRIIAIDVNEKFKIAKQLGATDVVNPKNFDKSIQEVIVDMTDGGVDY	262
Tolumonas_auensis	KASRIIAIDINEDKFDIAKKGATDVVNPKNFDKPIQDVIVEMTDGGVDF	262
Actinobacillus_ureae	GAGRIIAIDINPAKFEKAKELGATDCINPKDYDKPIQNVIIEMTDGGVDF	262
Actinobacillus_pleuropneumonia	GAGRIIAIDINPAKFEKAKELGATDCINPKDYDKPIQNVIIEMTDGGVDF	262
Simonsiella_muelleri	KASRIIAVDINPKFAKAKELGATDFVNPKNFDKPIQDVIIEMTDGGVDF	263
Moraxella_catarrhalis	GAGRIIVVDINEDKFAKQELGATDCVNPKNFDKPIQQVIEEMTDGGVDF	262
Alishewanella_jeotgali	KAGRIIAIDINEDKFDIAKKGATDVVNPKNFDKPIQEVIVEMTDGGVDF	262
P4 Group 3	-A-RII--D-N--K---A--LGATD---P-----K-IQ-VI---T-GGVD- * ** * :*: * : * :*:***** :*.:*.:* ***:*****:	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEISTRPFQLVTGRVW	309
Marinomonas_mediterranea	SFECIGNVQIMRQALECCHKGWGESIIIGVAGAGQEISTRPFQLVTGRVW	309
Marinobacterium_stanieri	SFECIGNVQVMRSALECCHKGWGESIIIGVAGAGEEISTRPFQLVTGRVW	309
Bdellovibrio_bacteriovorus	SFECVGNQLMRAALECAHRGWGQSIIVGVAGAGQEISTRPFQLVTGRVW	309
Mus_musculus_Chain_A	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
Mus_musculus_Chain_B	SLDCAGTAQTLKAAVDCTVLGWGSCVVGAK--VDEMTIPTVDVILGRSI	316
P4 Group 1	S--C-G--Q----A--C---GWG-----G-----E-----GR-- *:* *.* *::*:* * **.. :*: . :*: . :*: . :*: *	
Laribacter_hongkongensis	SFECVGNVKLMRAALECCHKGWGESTIIIGVAGAGQEISTRPFQLVTGRVW	311
Synechococcus_sp.	SFECIGNVQVMRAALECCHKGWGESTIIIGVAGAGQEIATRPFQLVTGRVW	310
Methylomicrobium_album	SIECIGNVKVMRSALECCHKGWGQSVIIIGVAGAGEEICTRPFQLVTGRVW	310
P4 Group 2	S-EC-GNV--MR-ALE-CHKGWG-S-IIGVAGAG-EI-TRPFQLVTGRVW *:*	
Pantoea_ananatis	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Pantoea_stewartii	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Pantoea_vagans	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEISTRPFQLVTGRVW	312
Erwinia_amylovora	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEIATRPFQLVTGRVW	312
Erwinia_pyrifoliae	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEIATRPFQLVTGRVW	312
Erwinia_tasmaniensis	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGEEIATRPFQLVTGRVW	312
Commensalibacter_intestini	SFECIGNVKMRSALECCHKGWGESVIIIGVAGAGEEISTRPFQLVTGRVW	312
Glaciecola_sp.	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Pseudoalteromonas_atlantica	SFECIGNVNMRSALECCHKGWGESVIIIGVAGAGQEISTRPFQLVTGRVW	312
Tolumonas_auensis	SFECIGNVKMRSALECCHKGWGESVIIIGVAAAGQEISTRPFQLVTGRVW	312
Actinobacillus_ureae	SFECVGNADLMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTGRVW	312
Actinobacillus_pleuropneumonia	SFECVGNVDMRSALECCHKGWGESIIIGVAPAGAEIRTRPFQLVTGRVW	312
Simonsiella_muelleri	SFECVGNVDMRAALECCHKGWGESVIIIGVAPAGAEIKTRPFQLVTGRVW	313
Moraxella_catarrhalis	SFECIGNVDVMRAALECCHKGWGESVIIIGVAPAGAEISTRPFQLVTGRVW	312
P4 Group 3	SFEC-GN--MR-ALECCHKGWGES-IIGVA-AG-EI-TRPFQLVTGR-W ***:*.*.*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	KGSAGGGVKGRSQLPGYVEDYMNGKIEIDPFVTHTMPLEQINEAFDLMHE	359
Marinomonas_mediterranea	KGSAGGGVKGRSQLPGYVEDYMNGKIEIDPFVTHMTSLEKINDAFDLMHE	359
Marinobacterium_stanieri	KGSAGGGVKGRSQLPGYVEDYMNGKIEIDPFITHMTGLEDINKAFDLMHE	359
Bdellovibrio_bacteriovorus	KGSAGGGVKGRTELPYVEQYMSGEINIDDMVFTMPLEDINKAFDYMHE	359
Mus_musculus_Chain_A	NGTFFGGWKSVDSPNLVSDYKNNKFDLLLVTHALPFESINDAIDLME	366
Mus_musculus_Chain_B	NGTFFGGWKSVDSPNLVSDYKNNKFDLLLVTHALPFESINDAIDLME	366
P4 Group 1	-G--FGG-K-----P--V--Y-----D---T-----E-IN-A-D-M-E :*: *** * . :*: *:* . :*: * :*: :*: *:*:* *:*	
Laribacter_hongkongensis	RGSAGGGVGRTELPAYVEKAQKGEIPLDTFITHTLPLEEINQAFELMHE	361
Synechococcus_sp.	RGSAGGGVGRTELPYVERFQSGEIPLDTFITHTMPLEEINRAFELMHA	360
Methylomicrobium_album	RGSAGGGVHGRSELPYVERAQRGEIPLDVFITHTLGLEDINQAFDLMHE	360
P4 Group 2	RGSAGGGV-GR-ELP-YVE--Q-GEIPLD-FITH--LE-IN-AF-LMHE *****:*:*:*:*:*: * *****.*****: **:*:*:*:**	
Pantoea_ananatis	RGSAGGGVKGRSQLPGIVQDYLDGKFALNDFITHTMPLEEINDAFDLMHE	362
Pantoea_stewartii	RGSAGGGVKGRSQLPGIVQDYLDGKFALNDFITHTMPLAEINDAFDLMHE	362
Pantoea_vagans	RGSAGGGVKGRSQLPGIVQDYLDGKFALNDFITHTMPLEEINDAFDLMHE	362
Erwinia_amylovora	RGSAGGGVKGRTELPYVERYMNGEFQLNDFITHNLPLEEINDAFELMHE	362
Erwinia_pyrifoliae	RGSAGGGVKGRTELPYVERYMNGEFRLNDFITHNLPLEEINDAFELMHE	362
Erwinia_tasmaniensis	RGSAGGGVKGRTELPYVERYMNGEFQLNDFITHNLPLEEINDAFDLMHE	362
Commensalibacter_intestini	RGSAGGGVKGRSQLPNIVNDYLDGKFALNDFITHMPLDQINKAFDLMHD	362
Glaciecola_sp.	RGSAGGGVKGRSQLPDYVQRYMDGEFELDTFITHTMQLEDINTAFDLMHE	362
Pseudoalteromonas_atlantica	RGSAGGGVKGRSQLPDYVQRYMDGEFELDTFITHTMPLDQINKAFDLMHE	362
Tolumonas_auensis	KGSAGGGVKGRSQLPGIVEQYMNGEFELDTFITHTMGLDDINHAFDLMHE	362
Actinobacillus_ureae	RGSAGGGVGRTELPYVERYMNGEFKLRDFITHTMPLDQINKAFDLMHQ	362
Actinobacillus_pleuropneumonia	RGSAGGGVGRTELPYVERYMNGEFKLRDFITHTMPLDQINKAFDLMHE	362
Simonsiella_muelleri	RGSAGGGYGRSELPDLIDQYQHGEFKLSDFITHTMPLDQINKAFDLMHE	363
Moraxella_catarrhalis	RGSAGGDVGRSELPYVERYMNGEFKLSDFITHTMPLDQINKAFDLMHE	362
P4 Group 3	-GSAGG--KGR--LP-----G-F-L--FITH---L--IN-AF-LMH- :*****.***:*:*:. . : * * * * * : * : * * * * * :	

A-9: Results of Multiple Sequences Alignment of Partition P4 (cont.)

Marinomonas_posidonica	GKSIRTVILFDQ-----	371
Marinomonas_mediterranea	GKSIRTVILFDQ-----	371
Marinobacterium_stanieri	GKSIRSVILFDQ-----	371
Bdellovibrio_bacteriovorus	GKSIRSVIKM-----	369
Mus_musculus_Chain_A	GKSIRTILTF-----	376
Mus_musculus_Chain_B	GKSIRTILTF-----	376
P4 Group 1	GKSIR-----	
	*****::: :	
Laribacter_hongkongensis	GKSIRTVIHF-----	371
Synechococcus_sp.	GQSIRSVIHFN-----	372
Methylomicrobium_album	GKSIRTVIHFNH-----	372
P4 Group 2	G-SIR-VIHF-----	
	*:***:****	
Pantoea_ananatis	GKSIRSVVHFNK-----	374
Pantoea_stewartii	GKSIRSVVHFNK-----	374
Pantoea_vagans	GKSIRSVVHFNK-----	374
Erwinia_amylovora	GKSIRTVVHFTKS-----	375
Erwinia_pyrifoliae	GKSIRTVVHFVAKS-----	375
Erwinia_tasmaniensis	GKSIRTVVHFVSKA-----	375
Commensalibacter_intestini	GKSIRTVIRY-----	372
Glaciecola_sp.	GKSIRSVVHY-----	372
Pseudoalteromonas_atlantica	GKSIRSVVHY-----	372
Tolumonas_auensis	GKSIRTVILFDK-----	374
Actinobacillus_ureae	GKSIRTVIHF-----	372
Actinobacillus_pleuropneumonia	GKSIRTVIHF-----	372
Simonsiella_muelleri	GKSIRTVIHF-----	373
Moraxella_catarrhalis	GKSIRSVIHF-----	372
P4 Group 3	GKSIR-V-----	
	*****:*: :	

A-10: Trace Residues of Partition P0

P0	-----A--A-----
P0	PL-----P--EV-----A--VC-TD-----FP--LGHE
P0	---VE--G--VT---GD-VIP---C--C--C-S--TNLC--R---
P0	--T---LM-D-T-RF---G---H-MG-S-F---V-----A-----A
P0	-L---CL-GCG---G-GA---TA-V-----A-FG-G--GL-----
P0	-A--I---D-N--K---A---GA-D---P-----Q-V---T--GVD-
P0	S--C-G-----A-----GWG-----G--E-----GR--
P0	-G--FG-----P-----T-----N---M--
P0	G-SIR-----

A-11: Trace Residues of Partition P1

P1	-----A--A-----
P1	PL-----P--EV-----A-VC-TD-----FP--LGHE
P1	---VE--G--VT---GD-VIP---C--C--C-S--TNLC--R---
P1	--T---LM-D-T-RF---G---H-MG-S-F---V-----A-----A
P1	-L---CL-GCG---G-GA---TA-V-----A-FG-G--GL-----
P1	-A--I---D-N--K---A---GA-D---P-----Q-V---T--GVD-
P1	S--C-G-----A-----GWG-----G-----E-----GR--
P1	-G--FG-----P-----T-----N---M--
P1	G-SIR-----

A-12: Trace Residues of Partition P2

P2	-----P-----EV-----A--VC-TD-----FP--LGHE
P2	PL-----P-----EV-----A--VC-TD-----FP--LGHE
P2	---VE--G--VT---GD-VIP---C--C--C-S--TNLC--R---
P2	--T---LM-D-T-RF---G---H-MG-S-F---V---A---A
P2	-L--VCL-GCG--GYGA--TA-V--G--A-FG-G--GL-----
P2	-A--I---D-N--K--A--GA-D--P-----Q-V---T--GVD-
P2	S--C-G-----A-----GWG-----G-----E-----GR--
P2	-G--FG-----P-----T-----N---M--
P2	G-SIR-----

A-13: Trace Residues of Partition P3

P3	-----AA-A-----
P3	PL-----P--EV-----A-VC-TD-----FP--LGHE
P3	---VE--G--VT---GD-VIP---C--C--C-S--TNLC--R---
P3	--T---LM-D-T-RF---G---H-MG-S-F---V--E---A-----A
P3	-L--VCL-GCG---G-GA---TA-V--G---A-FG-G--GL-----
P3	-A--I---D-N--K---A---GA-D---P-----Q-V---T--GVD-
P3	S--C-G-----A-----GWG-----G--E-----GR--
P3	-G--FG-----P-----T-----N-A--M--
P3	G-SIR-----

A-14: Trace Residues of Partition P4

P4	-----AA-A-----
P4	PL---E---P---EV---A--VC-TD-----FP--LGHE
P4	---VE--G--VT---GD-VIP-----C--C--C-S--TNLC---R---
P4	--T---LM-D-T-RF---G---H-MG-S-F---V-----A-----A
P4	-L--VCL-GCG---G-GA---TA-V--G---A-FG-G--GL----G----
P4	-A--I---D-N--K---A---GA-D---P-----Q-V---T--GVD-
P4	S--C-G-----A-----GWG---G-----E-----GR--
P4	-G--FG-----P-----T-----IN-A--M--
P4	G-SIR-----

