

Supplementary information

Supplementary Table 1. Pseudomonas-like toxins (PLTs) examined in these studies.

Bacterial species	Accession#	Abbr.	%GC	MW (Da)	pI
<i>Pseudomonas aeruginosa</i>	AKG00567.1	PE	68	66,755	5.28
<i>Vibrio cholera</i>	QKU75906.1	Chx	43	70,704	5.12
<i>Aeromonas hydrophila</i>	APJ14853.1	Ahx	64	66,596	5.15
<i>Acinetobacter baumannii</i>	SCY08530.1	Abx	66	68,969	5.36
<i>Collimonas fungivorans</i>	PFH04378.1	Cfx	58	71,413	6.77
<i>Chromobacterium haemolyticum</i>	OQS34021.1	Hmx	62	68,085	6.05
<i>Janthinobacterium lividum</i>	AMC33769.1	Jlx	57	73,057	6.01
<i>Serratia fonticola</i>	QIP94533.1	Sfx	45	69,451	5.17
<i>Shewanella putrefaciens</i>	WP_152829160.1	Spx	49	71,042	5.00

Accession# identifiers were obtained from GenBank. Abbr. = three-letter abbreviation used to define each PLT. %GC = Relative guanine-cytosine content. MW (molecular weight in Daltons) and pI (isoelectric point) were calculated using https://web.expasy.org/compute_pi/.

Supplementary Figure 1. Comparison of amino acid homology of Pseudomonas-like toxins (PLTs) for a) the overall protein, b) domain I, c) domain II, and d) domain III. Toxin amino acid sequences were aligned in pairs with identities of each pair obtained and gathered using DNAMAN. Mean homology scores for overall protein, domain I, domain II, and domain III were 47.9%, 42.7%, 47.4%, and 54.9%, respectively.

Overall Homology

	PE	Chx	Alx	Abx	Cfx	Hmx	Jlx	Sfx	Spx
PE	100.00	33.22	63.88	98.14	48.44	39.12	39.25	58.39	58.29
Chx	33.22	100.00	34.67	32.19	37.85	38.08	38.04	32.55	35.29
Alx	63.88	34.67	100.00	63.73	50.65	41.41	42.06	52.30	63.22
Abx	98.14	32.19	63.73	100.00	47.29	38.30	38.78	57.63	57.67
Cfx	48.44	37.85	50.65	47.29	100.00	48.59	49.25	42.48	49.75
Hmx	39.12	38.08	41.41	38.30	48.59	100.00	84.39	37.41	41.62
Jlx	39.25	38.04	42.06	38.78	49.25	84.39	100.00	38.23	43.46
Sfx	58.39	32.55	52.30	57.63	42.48	37.41	38.23	100.00	50.33
Spx	58.29	35.29	63.22	57.67	49.75	41.62	43.46	50.33	100.00

Domain I Homology

	PE	Chx	Alx	Abx	Cfx	Hmx	Jlx	Sfx	Spx
PE	100.00	28.28	59.04	100.00	40.73	33.74	33.20	47.58	51.60
Chx	28.28	100.00	32.11	27.82	35.20	37.07	36.54	26.45	33.06
Alx	59.04	32.11	100.00	58.57	43.60	36.73	35.77	43.09	60.56
Abx	100.00	27.82	58.57	100.00	40.08	33.20	32.66	47.01	51.18
Cfx	40.73	35.20	43.60	40.08	100.00	41.6	41.43	35.37	42.06
Hmx	33.74	37.07	36.73	33.20	41.60	100.00	91.15	32.78	35.63
Jlx	33.20	36.54	35.77	32.66	41.43	91.15	100.00	33.06	35.89
Sfx	47.58	26.45	43.09	47.01	35.37	32.78	33.06	100.00	42.74
Spx	51.60	33.06	60.56	51.18	42.06	35.63	35.89	42.74	100.00

Domain II Homology

	PE	Chx	Alx	Abx	Cfx	Hmx	Jlx	Sfx	Spx
PE	100.00	30.99	60.84	98.61	40.14	40.14	40.14	62.94	57.34
Chx	30.99	100.00	33.11	30.07	36.30	39.46	37.41	34.27	32.87
Alx	60.84	33.11	100.00	60.42	43.24	42.95	43.62	53.47	60.42
Abx	98.61	30.07	60.42	100.00	39.86	39.86	39.86	61.81	56.94
Cfx	40.14	36.30	43.24	39.86	100.00	55.33	56.67	36.36	46.15
Hmx	40.14	39.46	42.95	39.86	55.33	100.00	86.84	36.36	43.36
Jlx	40.14	37.41	43.62	39.86	56.67	86.84	100.00	35.66	45.45
Sfx	62.94	34.27	53.47	61.81	36.36	36.36	35.66	100.00	48.61
Spx	57.34	32.87	60.42	56.94	46.15	43.36	45.45	48.61	100.00

Domain III Homology

	PE	Chx	Alx	Abx	Cfx	Hmx	Jlx	Sfx	Spx
PE	100.00	40.87	71.96	95.38	62.67	45.50	46.70	69.01	66.82
Chx	40.87	100.00	39.71	39.47	42.51	38.27	40.41	38.54	39.22
Alx	71.96	39.71	100.00	72.31	64.02	46.00	48.22	63.38	68.22
Abx	95.38	39.47	72.31	100.00	62.05	44.09	46.45	68.21	66.67
Cfx	62.67	42.51	64.02	62.05	100.00	52.50	53.81	55.87	62.15
Hmx	45.50	38.27	46.00	44.09	52.50	100.00	73.89	43.50	48.00
Jlx	46.70	40.41	48.22	46.45	53.81	73.89	100.00	46.70	51.27
Sfx	69.01	38.54	63.38	68.21	55.87	43.50	46.70	100.00	61.03
Spx	66.82	39.22	68.22	66.67	62.15	48.00	51.27	61.03	100.00



Supplementary Table 2. PLTs sequence and structure alignments performed with Clustal and TM-align with comparison to *Pseudomonas aeruginosa* exotoxin A (PE) and Cholix (Chx), for the full-length toxin (a) and domain I (b).

a

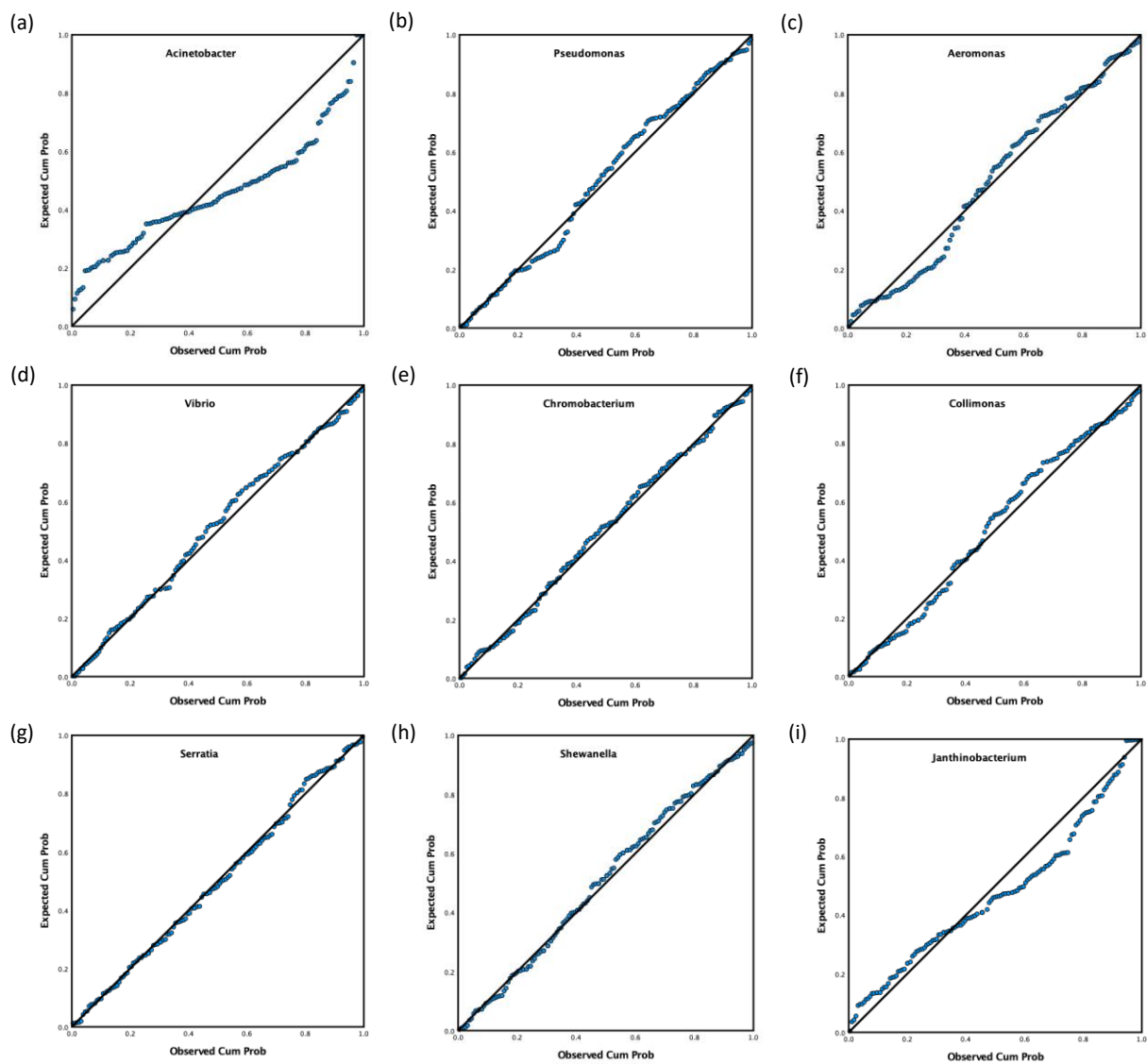
	PE		Cholix	
	% ID	rmsd (Å) [Cα] ¹	% ID	rmsd (Å) [Cα] ¹
PE	-	-	33.2	3.2 [561]
Chx	33.2	3.2 [561]	-	-
Ahx	63.9	2.5 [593]	34.7	2.9 [575]
Hmx	39.1	2.7 [581]	38.1	2.9 [583]
Jlx	39.3	2.7 [577]	38.0	2.4 [579]
ShE	58.3	2.3 [593]	35.3	2.8 [571]
Cfx	48.4	2.6 [589]	37.9	2.9 [572]

b

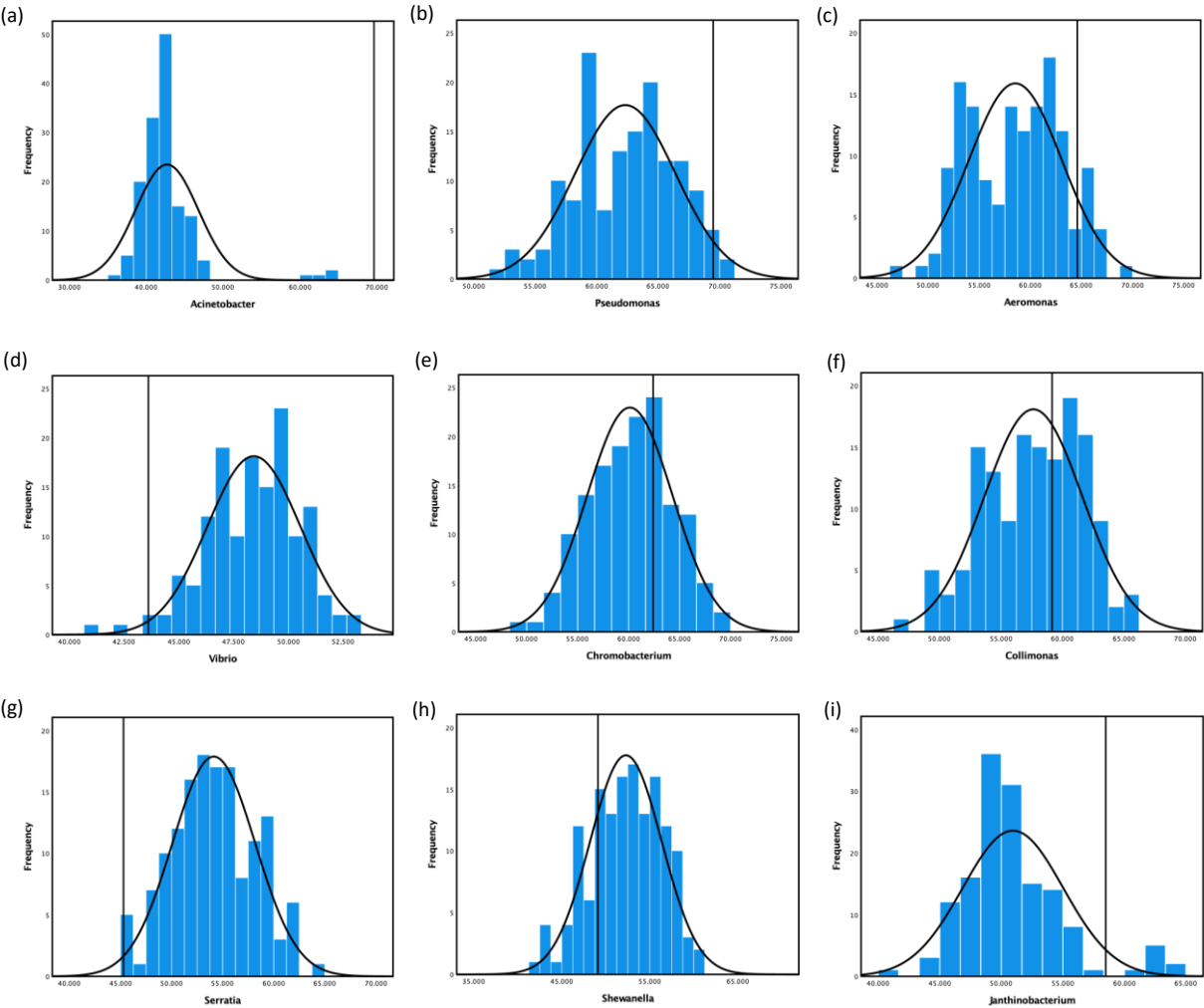
	PE		Cholix	
	% ID	rmsd (Å) [Cα] ¹	% ID	rmsd (Å) [Cα] ¹
PE	-	-	28.3	2.6 [219]
Chx	28.3	2.6 [219]	-	-
Ahx	59.0	2.0 [240]	32.1	2.3 [225]
Hmx	33.7	2.4 [238]	37.1	2.0 [237]
Jlx	33.2	2.5 [238]	36.5	2.0 [237]
ShE	51.6	2.0 [238]	33.1	2.3 [224]
Cfx	40.7	2.1 [236]	35.2	2.0 [223]

¹ Number of aligned Cα atoms.

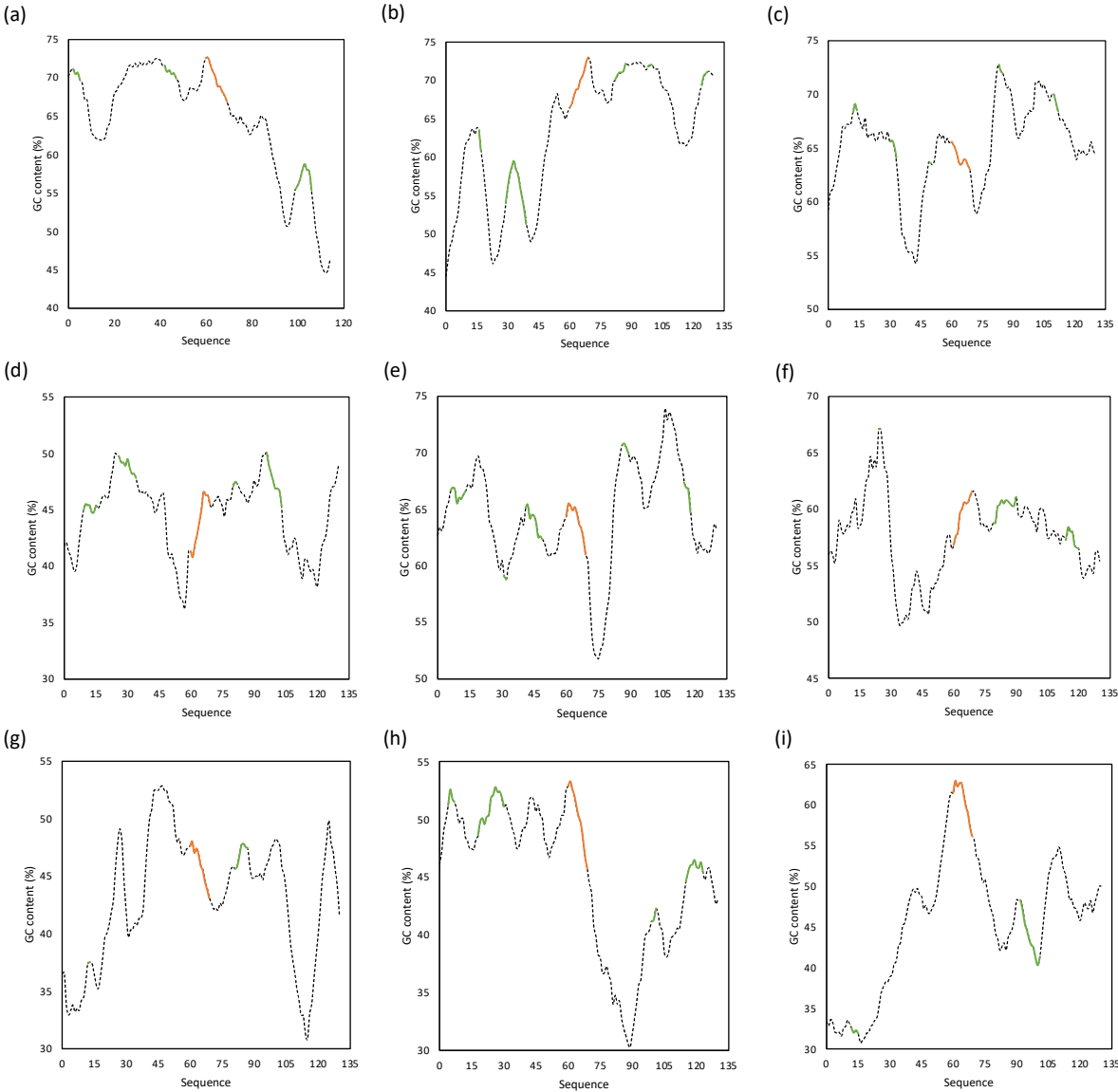
Supplementary Figure 2. P-P (probability–probability) plots of guanine-cytosine (GC) content in 145 core genes shown individually for (a) *Acinetobacter baumannii*, (b) *Pseudomonas aeruginosa*, (c) *Aeromonas hydrophila*, (d) *Vibrio cholerae*, (e) *Chromobacterium haemolyticum*, (f) *Collimonas fungivorans*, (g) *Serratia fonticola*, (h) *Shewanella putrefaciens*, and (i) *Janthinobacterium lividum*. Diagonal lines describe the normal distribution when GC expected and observed GC content are equivalent.



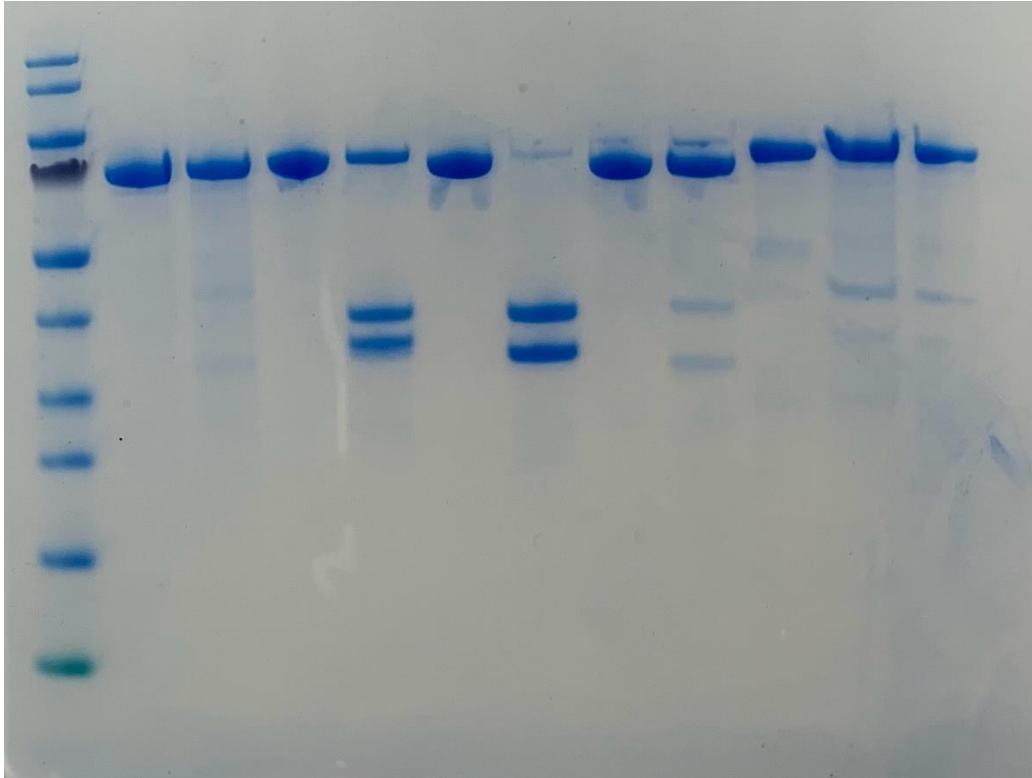
Supplementary Figure 3. Comparison of toxin gene and core gene guanine-cytosine (GC) content. GC content observed in 145 core genes plotted as histograms with fitted normal distribution trendlines and where the straight line represents CG content for the corresponding PLT (a) *Acinetobacter baumannii*, (b) *Pseudomonas aeruginosa*, (c) *Aeromonas hydrophila*, (d) *Vibrio cholerae*, (e) *Chromobacterium haemolyticum*, (f) *Collimonas fungivorans*, (g) *Serratia fonticola*, (h) *Shewanella putrefaciens*, and (i) *Janthinobacterium lividum*.



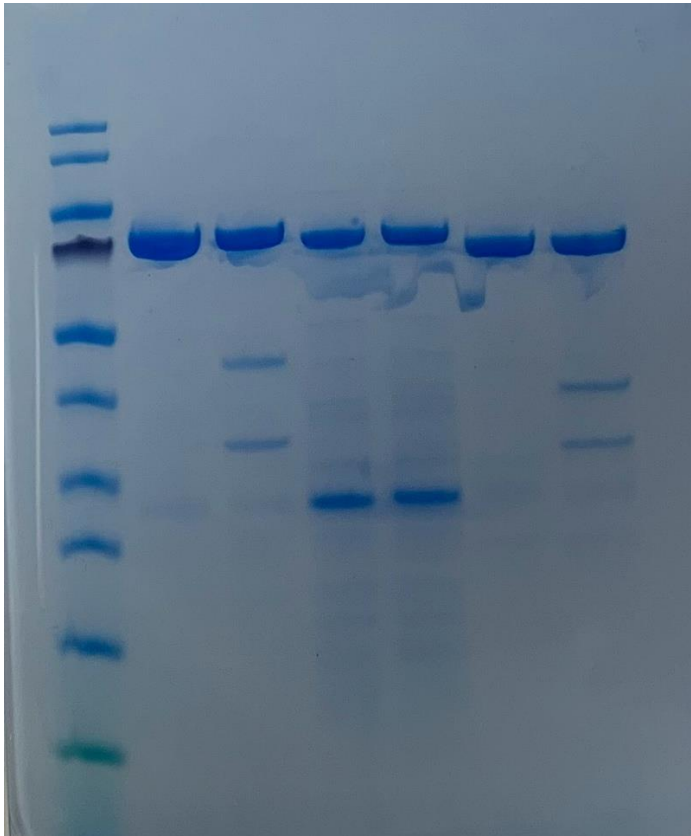
Supplementary Figure 4. Base composition analysis of toxin gene neighbourhood. It was a sliding window analysis that included calculation of GC content of toxin gene and the regions around (4400 – 6000 bp away from either side). The length of every tested sequence is 1000 bp and the interval between the start positions of every two consecutive sequences is 100 bp. (a-i) It was clearly shown separately that the trends of GC contents of mARTs gene in *Acinetobacter*, *Pseudomonas*, *Aeromonas*, *Vibrio*, *Chromobacterium*, *Collimonas*, *Serratia*, *Shewanella*, and *Janthinobacterium*. The data from toxin gene were highlighted in orange and those from other coding genes within the tested region were marked in green.



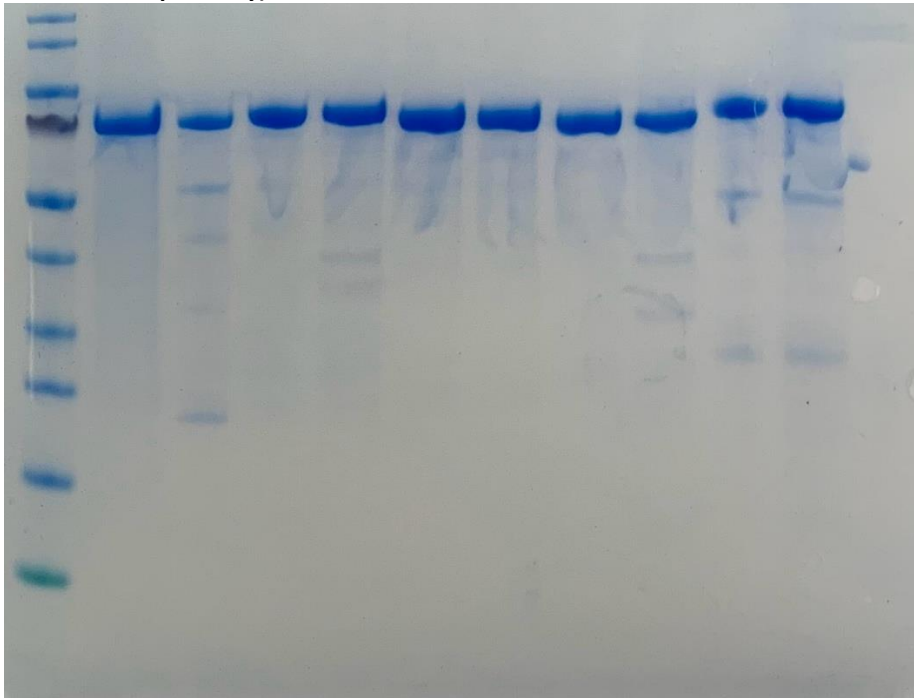
Supplementary Figure5. Original SDS PAGE pictures from the furin cleavage assay (Figure 4)
(a) Furin cleavage of PLTs at pH 5.5 (#1):
MW Marker, *Shewanella*, *Janthinobacterium*, *Chromobacterium*, *Collimonas* and *Vibrio* exotoxins (without or with furin, respectively)



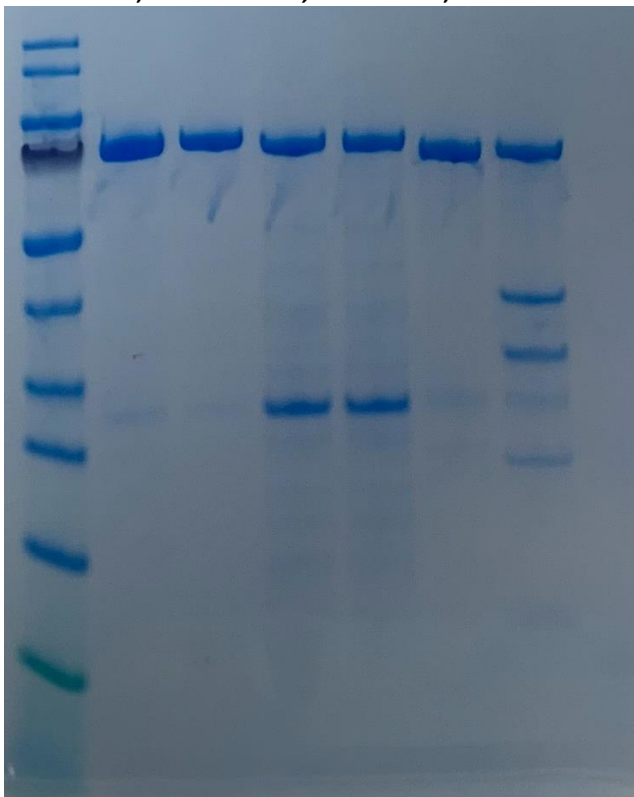
(b) Furin cleavage of PLTs at pH 5.5 (#2):
MW Marker, *Pseudomonas*, *Aeromonas*, and *Serratia* exotoxins (without or with furin, respectively)



59 (c) Furin cleavage of PLTs at pH 7.0 (#1):
60 MW Marker, *Shewanella*, *Janthinobacterium*, *Chromobacterium*, *Collimonas* and *Vibrio* exotoxins (without or
61 with furin, respectively)



62
63
64 (d) Furin cleavage of PLTs at pH 7.0 (#2):
65 MW Marker, *Pseudomonas*, *Aeromonas*, and *Serratia* exotoxins (without or with furin, respectively)



66

67 **Protein sequences from database.** The predicted signal peptide is highlighted in grey.

68 **> *Pseudomonas aeruginosa* exotoxin A (PE)**

69 MHLTPHWIPLVASLGLLAGGSFASAAEEAFDLWNECAKACVLDLKDGVSRSSMSVDPAPAIADTNGQGV LHYSMVLEGGNDALKLAI
70 DNALSITSDGLTIRLEGGVEPNKPVRYSTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLAR
71 DATFFVRAHESNEMQPTLAISHAGVSVMMAQAQPRREKRWSEWASGKVLCLLDPLDGVVNYLAQQRCNLDDTWEGKIYRVLAG
72 NPAKHDLDIKPTVISHRLHFPEGGSAAALTAHQACHLPLETFTRRHQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNAL
73 ASPGSGGDLGEAIREQPEQARLALTAAAESERFVRQGTGNDEAGAASADVSLTCPVAAGECAGPADSGDALLERNYPTGAEFLG
74 DGGDISFSTRGTQNWTVRLLQHRQLEERGYVFGYHGTFLAAQSVIFGGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEP
75 DARGRIRNGALLRVVYPRSSLPGFYRTGLTAAPEAAGEVERLIGHPLPLRLDAITGPEEEGGRLETILGWPLAERTVVIPSAIPTDPRN
76 VGGDLDPSSIPDKEQAISALPDYASQPGKPPREDLK

77 **> *Vibrio cholerae* Cholix (Chx)**

78 MYLTFYLEKVMKKMLLIAGATVISSMAHPTFAVEDELNIFDECRSPCSLTPEPGKPIQSKLSIPSDVVLDEGVLYYSMTINDEQNDIKD
79 EDKGESIITIGEFATVRATRHYVNQDAPFGVIHLDTTENGTKTYSYNRKEGEFAINWLVPIGEDSPASIKISVDELDDQQRNIIIEVPKLYSI
80 DLDNQTLQWKTQGNVSFSVTRPEHNIAISWPSVSYKAAQKEGSRHKRWAWHTGLALCWLVPMDAIYNYITQQNCTLGDNW
81 FGGSYETVAGTPKVITVKQGIEQKPVQRIHFSKGNAMSALAAHRVCGVPLETLARSRKPRDLTDDLSCAYQAQNIIVSLFVATRILFS
82 HLDVSFTLNLDEQEPEVAERLSDLRRINENNPGMVTQVLTVARQIYNDYVTHHPGLTPEQTSAGAQAADILSLFCPDADKSCVASN
83 NDQANINIESRSGRSYLPENRAVITPQGVTNWTYQELEATHQALTREGYVFGYHGTNHVAAQTIVNRIAPVPRGNNTENEKKGW
84 GLYVATHAEVAHGYARIKEGTGEYGLPTRAERDARGVMRLRVYIPRASLERFYRTNTPLENAEEHITQVIGHSLPLRNEAFTGPESAGG
85 EDETIVIGWDMAIHAVAIPSTIPGNAYEELAIDEEAFAKEQSISTKPPYKERKDELK

86 **> *Aeromonas hydrophila* exotoxin A (Ahx)**

87 MAMLGGAISPVMMADESFNLWQECATRCTLDLAQGVASQLDVASLLGGQTD SGVLHYSMVLEEGGDSLKLALGNALTLRTDGT
88 ITLTSATAGKGPRTYSYTRQGRGNWSLHWLVPVGDDAPASIKVFFHELDAGSEVSHISPIYSIEVSDDLRTMASNSTLFRHVENNE
89 INRSLTSAAGVGFAAPTQHSRQKRWSEWHTGKVLCLLDPLDAVYNYLSQRTCNLGD TWEGKVYRVLAGAPASHDTHIVPTAISH
90 RLHFAKGDGLAALTTHQVCAIPLESARSRQPRGWEELSQC GYPVHNLTLYLLTRLPWSQLDVTITQALANTTPEDGSTPRGQLAQ
91 AIRENPAQARLALSMAAAQSDAFSHQQAGNSQEQAASADVNLTC PAADLNCLAPADSADALQERDYPNGDSFLGDGDEVSFST
92 AGTRNWSVTRLEQVHRQLLARGYLFVGYHGTFLAAHSIVFEGVHERDQSSIAPWQGFYVAGDPALAYGYAQDQEQADARGRIRN
93 GVLLRVYVPRAALPRLYATQQTADPGAVDEVGRILGHPLPLQLEAITGPEEEGGRLETILGWRLAEQAVVIPSTIPTDPRNVGGNLD
94 PASVPQEESAISLDPDYTTQPREDLK

95 **> *Chromobacterium haemolyticum* exotoxin A (Hmx)**

96 MRLYKSLAAGLIPLLSACETDEASPFAAGTAQTASFKAASSVIKTDFEIFKQCADNCILSPAEPGKFISTSLPLQITPSPDEGVLYYS
97 MFVQDRFAAAANNSATIKIDEFAKVRINDGQGTGHAPGTLTIELATPDGKVKKFTHKRRTEWFTLNWVVPIGKDAPTSIKLFIMDM
98 DSNKKIVDHSPLYSDLDAAALARWPDKAKLAFSSANPRNDIILSWPGVGYTAAPTQHNRQKRWSEWHS GILLCWLDPDAIYNY
99 VTQNRCLNKTWEGKLYQVAGKPQINEFKPLAKAPIQHRVHFSKENALGALSAHRVCGIPLESARSRQPRGWEELSACGYRVES
100 IVGLYIATRLSFDRFRQVDDLIHSRPVSGAQDPEALEQLGTAVRETPGLAREGLAEAEALLD TYLDYHPGASADDAQRADVLSLTC
101 ADSEPCAAANADGAHVNLEYHPGSSFFAPGELVEFLSNGTTSNWSQERLLATHQRLLDQGYVFAGYHGGSTIAARSIVTGGITPRT
102 QELPIIWKGFIYIAGNPEVAYGYALDNDNPRSRGIMMRIYVPTALPQLFRTSQPLSDEAAALREMSRLFGRNVTL DSTLGYESITGP
103 QAPGEADETVLGWLMARHSVAIPSMIQGNGNNAKGIDVPDYEEKISALPDYVTKR

104 **> *Collimonas fungivorans* exotoxin A (Cfx)**

105 MSKFMSQRWIYLFGLWFLLLGTGSTRANTIIEGNFRLWDDCSSYCLVYAAPHKIYQTPLATQAVPDSPGKEGV LHYSMVMMKDYVGN
106 GQVLALRLDDFATVFVEQESLRLSLLGSDGKPRNFQYARQGAKHWSLNLVLPVGDDAPTSIKVFFKNLDGQNNILSISPLYSVEVD
107 DKTLARWPALATFSVTQENV TQGQGLLIRAGVSYYAAPVNHDRHKRWSEWHS GKLLCLLDPAIYNYVSQNRCSLGETWEG
108 AIYQTLAGRPVDKYAPPASKPVISQRIHFAGKNALEALTSHRVCGIPLESARRRKPRGWEEWSSCGNPAANFVALYIATRLPFDQFR

109 QVIHNLVHGQAVAAPDPVPLDALRTAVIEQPELARQSIAQAADIFRNYQAANPGASAAAAQQADVLAVTCPADARPCGSGASSGV
110 LVQRENPTGAHFLNDGELPSFTVQGTQNWNLNRLQAAHLRLQVQGYVFAGYHGTSLEGAQSIVFGGIHNRQQDLEEIWRGLYVA
111 GDPALAYGYAQDAEGDERGRIRNGTMLRVVYVPRSALPRLFATSLPLDHPGASQEVARLIGHPLPLLYESITGPEAAGGNRLETILGW
112 QLAEQAVAIPSMIPTNSRTVGNPLDPATVTLEEKQISSLPGYATKPAKDDKTEL

113 > *Shewanella putrefaciens* exotoxin A (Spx)

114 MIKTRYLCLSVAISSFLAITSVNATDLRGLEPQITSAAQVNEAFDLWQECATHCQLDLSQGIRSSSELDLTLFETSNEEGILHYSMLLG
115 EGNGLKLALDNLTLHTTHSTINFSETAESGPRSYIRKGENNWSLNWLVPVGDDAPASIKIFFLEQDAVGLNRYISPIYSIEVSNN
116 LLNSLAHKSTFYIRAFDNNQTLSMVNISAGVSYAAPQQHHRQKRWSEWHTGKLLCFDPDAFYNYVTQHTCNPDDTWEGQI
117 YRVLAGNPATLDTTAPSTTPAVISHRIHFDRGNSLASLTAHQVCGIPLESARTRHPRGWHEELNNGYPVRNLVSLFILARLSWDRVE
118 QVIHNALTNPTPGNALDDAIREAPERARVTLTAAQVNQFDNQAAGNTPAQASADVSLSCSAGALHCSAPADSANALLEREH
119 PNGANFLGAGEAVSFTRGTRNWSSARLNHAHQQLIARGYVFVGYHGSSLEGAQSIVFGGIRTRTQALDDVWQGLYISGDPNAVY
120 GYAQDQEPDSRGRIRNGTMLRVVYVPGTATAYLYETPLTLADPEAVDAVGHLIGHPLPLQTEAITGPEEAGGRPETILGWELAEQAVAI
121 PSTIPTDPSNIGGDLDPSSIPDEESDISALPDNVTKPHHDEL

122 > *Janthinobacterium lividum* exotoxin A (Jlx)

123 MMRLYKGFAIAAGLIPLLSGCVTEEVRSATEEVRSNTVAAAGFQQAAASSIIKTDFEIKQCADSCILSPSEPGKFISTSLPVQITPSPD
124 EGVLYYSMFVQDRFASAANNSATIKIDDFAKIRINDGYDTGSAPGSLTIELATPDGQVKKFTHKRRTEWFTLNWAVPIGKDAPTSIKL
125 FIMDIDSNNKIVDHSPLYSDLDAAALARWPAKAKLAFSSANAMNDIILSWPGVGYTAAPTQHSRQKRWSEWHSGILLCWLDPLD
126 AIYNYVTQNRCLKNTWEGSLYKVVAGNPQINEFKPVAKAPIQHRVHFSKENALGALSAHRVCGIPLESARSQPRGWEELSACG
127 FRVENIVGLYIATRLSFDRFRQVVEDLIHSRPVSGAQDPVALEQLGSSVVRETPELAREGLAEAEARLNAYRANHPGSSADDAQRADV
128 LSLTCPADSAPCNAPDAAGAHVNREYHPGTDYFAPGEPVEFLPNGTTRNWSQDRLLATHQRLLDLGYVFAGYHGGSSIAARSIVTG
129 GITRRSQDLQPIWRGLYIASDPEVAYGYALDNNTGATGTMVRVYVPGTALSRLFRTNQALSDEAAALREIGRLLGRNITLADTLGYE
130 SITGPQDPGDPDETILGWDLAEHAVVIPSIRGNNGSQLNVPDYEEKISPLPNYVTKR

131 > *Serratia fonticola* exotoxin A (Sfx)

132 MSNKAKLRTAAIAILASYSLPAPAFANDKFDLWTQCADSCSLDLNQRWSSPMDLSLFGQTSEQGVLHFSMVLGENNDSVRIGIDN
133 AFSLINENSIQFKGVSDITKPVKNFYTRQDKGNISVNWLVPIGGGTPEIKVFIHEVNSANQITSMSPYITIPVSEVLSTLEKKSTIYIR
134 GTNSNSLSYELIVKNAGVSIASSTQSGPTRKRRWTHWDSGKTLCFIDPLNAIYNYLSQNTCQLDDTWEGKVYLTLYGSPATHDIEMPA
135 SPISTRTHFSEGGSLAALTAHRVCAIPFETFRHRQPRGWEDLEKCGYPVHSLIAFYIAARHSWSQVDQVIQNALDNQESDSDLRA
136 IRESPQQSRLALTTAAQTSAVFVSQSSNTEASAANADILTLCPLSGLNCMPADGNEAHQERIYPTGAIFLGDGDDISFTTRGTQN
137 WTTDRLIAAHQQLTSQGYVFVGYHGTFLEAAHSIVFEGVRARSQSLDNAWHGFYIAGDPAVSYGALDQDPDPNTGRIRNGVML
138 RVYVRQESLPNFYQTNVALSSPDAVNAVSSLIGHTLPLQLDSITGQEDEEGRLETIIGWPLAEQLLVIPSTISTDPRNPGGVLDPSIPE
139 AEKAISVLPNYSTSPTNTH

140 > *Acinetobacter baumannii* exotoxin A (Abx)

141 MHLTPHWIPLVASLGLLAGLSASAAEEAFDLWNECAKACVLDLKDGVRSRMSVDPADTNGQGVLHYSMVLEGGNDALKLAI
142 DNALSITSDGLTIRLEGGVEPNKPVRYSTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLAR
143 DATFFVRAHESNEMQPTLAISHAGVSVMMAQAQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRVLAG
144 NPAKHDLDIKPTVISHRLHFPEGGSAAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNAL
145 ASPGSGGDLGEAIREQPEQARLALTAAAESEFVRQGTGNDEASADVSLTCPVAAGECAGPADSGDALLERNYPTGAFLGDG
146 GDVSFSTRGTQNWTVRLLQAHRQLEERGYVFVGYHGTFLEAAQSIVFGGVRARSQDLDAIWRGFYVAGDPALAYGYAQDQEPD
147 ARGRIRNGALLRVYVPRSSLPGFYRTGLTAAPEAAGEVERLIGHPLPLRLDAITGPEEEGGRLETILGWPLAERTVVIPSAIPTDPRNV
148 GGDLPSSIPDQEQAISALPDYASQPGKPSREDLK

149

150 Sequences of produced inactive proteins

151 TEV-cleavable N-terminal poly-Histidine tag highlighted in grey, with catalytic mutation E>A highlighted in yellow

152 > *Pseudomonas aeruginosa* exotoxin A (PE)

153 MHHHHHHHENLYFQGAEEAFDLWNECAKACVLDLKDGVSRSSMSVDPADTNGQGVLHYSMVLEGGNDALKLAIDNALSITSD
154 GLTIRLEGGVEPNKPVRSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAH
155 ESNEMQPTLAISHAGVSVMMAQAQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCLDDTWEGKIYRVLAGNPAKHDLDI
156 KPTVISHRLHFPEGGSAAALTAHQACHLPLETFRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNALASPGSGGD
157 LGEAIREQPEQARLALTLAAAESERFVRQGTGNDEAGAASADVSLTCPVAAGECAGPADSGDALLERNYPTGAEFLDGGDISFST
158 RGTQNWTVRLLQAHRLQLEERGVYFVGHYHGTFLAAQSVIFGGVRARSQDLDAIWGRGYIAGDPALAYGYAQDQEPDARGIRN
159 GALLRVYVPRSSLPGFYRTGLTLAAPEAAEVERLIGHPLRLDAITGPEEEGGR^AATILGWPLAERTVVIPSAIPTDPRNVGGDLDP
160 SSIPDKEQAISALPDYASQPGKPPREDLK

161 > *Vibrio cholerae* Cholix (Chx)

162 MHHHHHHHENLYFQGVDELNIFDECRSPCSLTPEPGKPIQSKLSIPSDVVLDEGVLYYSMTINDEQNDIKDEDKGESITIGEFATVRA
163 TRHYVNQDAPFGVIHLDITTENGTKTYSYNRKEGEFAINWLVPIGEDSPASIKISVDELDQQRNIIIVPKLYSIDLDNQTLQWKTQG
164 NVSFSVTRPEHNIAISWPSVSYKAAQKEGSRHKRWAWHTGLALCWLPMDAIYNYITQQNCTLGDNWFGGSYETVAGTPKVIT
165 VKQGIEQKPVEQRIHFSKGNAMSALAAHRVCGVPLETLARSRKPRDLTDDLSCAYQAQNVSLFVATRILFSHLDSVFTLNLDQEPE
166 VAERLSDLRRINENNPGMVTQVLTVARQIYNDYVTHHPGLTPEQTSAGAQAADILSLFCPDADKSCVASNNQDANINIESRSGRSYL
167 PENRAVITPQGVTNWTYQELEATHQALTREGYVFGYHGTNHVAAQTIVNRIAPVPRGNNTENEKWWGGLYVATHAEVAHGYARI
168 KEGTGEYGLPTRAERDARGVMLRVYIPRASLERFYRTNTPLENAEEHITQVIGHSLPLRNEAFTGPESAGGED^ATVIGWDMAIHAV
169 AIPSTIPGNAYEELAIDEEAFAKEQSISTKPPYKERKDELK

170 > *Aeromonas hydrophila* exotoxin A (Ahx)

171 MHHHHHHHENLYFQGADESFNLWQECATRCTLDAQGVVASQLDVASLLGGQTDGVLHYSMVLEEGGDSLKLALGNALTRLTD
172 GTTITLTSATAGKGPRTYSYTRQGRGNWSLHWLVPVGDDAPASIKVFFHELDAGSEVSHISPIYSIEVSDDLRTMASNSTLFVRHVE
173 NNEINRSLTSAAGVGFAAPTQHSRQKRWSEWHTGKVLCLLDPLDAVYNYLSQRTCNLGDTWEGKVYRVLAGAPASHDTHIVPT
174 AISHRLHFAGKDGLAALTTHQVCAIPLESLSRQPRGWEELSQCYPVHNLTLYLLTRLPWSQLDVTITQALANTTPEDGSTPRG
175 QLAQAIRENPAQARLALSMAAAQSDAFSHQQAGNSQEQAASADVNLTPAADLNCLAPADSADALQERDYPNGDSFLGDGDE
176 VSFSTAGTRNWSVTRLEQVHRQLLARGYLFVGYHGTFLAAHSIVFEGVHERDQSSIAPWQGFYVAGDPALAYGYAQDQEADARG
177 RIRNGVLLRVYVPRAALPRLYATQQTLADPGAVDEVGRIGHPLPLQLEAITGPEEEGGR^AATILGWRLAEQAVVIPSTIPTDPRNVG
178 GNLDPASVPQEESAISLDPDYTTQPPREDLK

179 > *Chromobacterium haemolyticum* exotoxin A (Hmx)

180 MHHHHHHHENLYFQKTDIFEIKQCADNCILSPAEPGKFISTSLPLQITPSPDEGVLYYSMFVQDRFAAAANNSATIKIDEFAKVRIND
181 GQGTGHAPGTLTIELATPDGKVKKFTHKRTEWFTLNWVVPIGKDAPTSIKLFIMDMDSNKKIVDHSPLYSVLDLDAALARWPDK
182 AKLAFSSANPRNDIILSWPGVGYYTAAPTQHNRQKRWSEWHSIGILLCWLDPLDAIYNYVTQNRCLNKTWEGKLYQVVAGKPQIN
183 EFKPLAKAPIQHRVHFSKENALGALSAHRVCGIPLESLSRQPRGWEELSACGYRVESIVGLYIATRLSFDRFRQVVDLIHSRPVSG
184 AQDPEALEQLGTAVRETPLAREGLAEAEALLDTYLDYHPGASADDAQRADVLSLTPADSEPCAAANADGAHVNLLEYHPGSSFFA
185 PGELVEFLSNGTTSNWSQERLLATHQRLLDQGYVFAGYHGGSTIAARSIVTGGITPRTQELPPIWKGFYIAGNPEVAYGYALDNDNP
186 RSRGIMMRIYVPTALPQLFRTSQPLSDEAAALREMSRLFGRNVTLDSLGYESITGPQAPGEAD^ATVLGWL MARHSAIPSMIQQ
187 NGNNAGKIDVPDYEKKISALPDYVTKR

188 > *Collimonas fungivorans* exotoxin A (Cfx)

189 MHHHHHHHENLYFQGIENFRLWDDCSSYCLVYAAPHKIYQTPLATQAVPDSPGKEGVHYSMVMDKYVNGNQVLALRLDDFATV
190 FVEQESLRLSLLGSDGKPRNFQYARQGAKHWSLNWLVPVGDDAPTSIKVFFKNLDGQNNILSISPLYSVEVDDKTARWPALATFSV
191 TQENVTQGGQLLGIRRAGVSYVAAPVNHDRHKRWSEWHSIGILLCLLDPLDAIYNYVSQNRCSLGETWEGAIYQTLAGRVPDKYA

192 PPASKPVISQRIHFAKGNALALTSHRVCIPLESARRRKPRGWEEWSSCGNPAANFVALYIATRLPFDQFRQVIHNLVHGQAVAA
193 PDPVPLDALRTAVIEQPQLARQSIQAADIFRNYQAANPGASAAAQADVLAVTCPADARPCGSGASSGVLVQRENPTGAHFLN
194 DGELPSFTVQGTQNWNLNRLQAAHLRLQVQGYVFAGYHGTSLEGAQSIVFGGIHNRQQDLEEIWRLVYAGDPALAYGYAQDAE
195 GDERGRIRNGTMLRVYVPRSALPRLFATSLPLDHPGASQEVARLIGHPLPLLYESITGPEAAGGNRLATILGWQLAEQAVAIPSMIPT
196 NSRTVGNPDPATVTLEEKQISSLPGYATKPAKDDKTEL

197 > *Shewanella putrefaciens* exotoxin A (Spx)

198 MHHHHHHHENLYFQGVNEAFDLWQECATHCQLDLSQGISSSELDLTPLFETSNEEGILHYSMLLGEGNEGLKLAI DNALTHTTHSTI
199 NFTSETAESGPRSYIRKGENNWSLNLVLPVGDDAPASIKIFFLEQDAVGLNRYISPIYSIEVSNNLLNSLAHKSTFYIRAFDNNQTLS
200 MVNISSAGVSYAAPQQHHRQKRWSEWHTGKLLCFLDPFADFYNVYTQHTCNPDWTWEGQIYRVLAGNPATLDTTAPSTTPAVI
201 SHRIHFDGRNSLASLTAHQVCGIPLESARTRHPRGWEE LNCCGYPVRNLVSLFILARLSWDRVEQVIHNA LTNPTPGNALDDAIRE
202 APERARVTLTAAQVNQFDNQAAGNTPEQAQSADVVSLSCSAGALHCSAPADSANALLEREHPNGANFLGAGEAVSFTRGTR
203 NWSSARLNHAHQQLIARGYVFVGYHGSSLEGAQSIVFGGIRTRTQALDDVWQGLYISGDPVAVGYAQDQEPDSRGRIRNGTML
204 RVYVPGTATAYLETPLTADPEAVDAVGH LIGHPLPLQTEAITGPEEAGGRPATILGWELAEQAVAIPTIPTDPSNIGGDLPSSIPD
205 EESDISALPDNVTKPHHDEL

206 > *Janthinobacterium lividum* exotoxin A (Jlx)

207 MHHHHHHHENLYFQGIKTDFEIFKQCADSCILSPSEPGKFISTSLPVQITPSPDEGVLYYSMFVQDRFASAANNSATIKIDDFAKIRIND
208 GYDTGSAPGSLTIELATPDGQVKKFTHKRRTWFTLNWAVPIGKDAPTSIKLFIMDIDSNKKIVDHSPLYSVDLDDAALARWPAKAK
209 LAFSSANAMNDIILSWPGVGYTAAPTQHSRQKRWSEWHS GILLCWLDPLDAIYNVYTQNRCLKNTWEGSLYKVVAGNPQINEF
210 KPVAKAPIQHRVHFSKENALGALSAHRVCIPLESARSRQPRGWEE LSACGFRVENIVGLYIATRLSFDRFRQVVEDLIHSRPVSGA
211 QDPVALEQLGSVVRETPELAREGLAEAEARLNAYRANHPGSSADDAQRADVLSLTCPADSAPCNAPDAAGAHVNREYHPGTDYFA
212 PGEPVEFLPNGTTRNWSQDRLLATHQRLLDLGYVFAGYHGGSIAAARSIVTGGITRRSQDLQPIWRGLYASDPEVAYGYALDNNNG
213 ATGTMMRVYVPGTALSRLFRTNQALSDEAAALREIGRLLGRNITLADTLGYESITGPQDPGDPDATILGWDLAEHAVVIPS MIRGN
214 NGSQNLNVPDYEEKISPLPNYVTKR

215 > *Serratia fonticola* exotoxin A (Sfx)

216 MHHHHHHHENLYFQGANDKFDLWTQCADSCSLDLSNQRIWSSPMDLSLFGQTSEQVLHFSMV LGENND SVRIGIDNAFSLLINE
217 NSIQFKGVSDITKPVKFNYTRQDKGNISVNLVPIGGGTPSEIKVFIHEVNSANQITSMSPYITIPVSNEVLSTLEKKSTIYIRGTNSNSL
218 SYELIVKNAGVSIAS TQSGPTRKRRWTHWDSGKTLCFIDPLNAIYNYSQNTCQLDDTWEGKVYLTLYGSPATHDIEMPASPISTRTH
219 FSEGGSLAALTAHRVCAIPFETFTRHRQPRGWEDLEKCGYPVHSLIAFYIARHSWSQVDQVIQNALDNQESDSDL DRAIRESQQ
220 SRLALTAAQTSAVFVSQSSNTEASAANADILTLCPLSGLNCMVPADGNEAHQERITYPTGAIFLGDGDDISFTTRGTQNWTTDRL
221 IAAHQQLTSQGYVFVGYHGTFLAAHSIVFEGVRARSQSLD NAWHGFYIAGDPAVSYGYALDQDPDPNTGRIRNGVMRLRVYVRQ
222 ESLPNFYQTNVALSSPDVNAVSSLIGHTLPLQLDSITGQEDEEGRLATIIGWPLAEQLVVIPSTISTDPRNPGGVLD PSSIEAEKAISV
223 LPNYSTSPTNTH

224 > *Acinetobacter baumannii* exotoxin A (Abx)

225 MHHHHHHHENLYFQGAEEAFDLWNECAKACVLDLKDGVRRSRMSVDP AIADTNGQGV LHYSMVLEGGNDALKLAIDNALSITSD
226 GLTIRLEGGVEPNKPVRYSYTRQARGSWSLNLVPIGHEKPSNIKVFIHEL NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAH
227 ESNEMQPTLAISHAGVSVMQAQPRREKRWSEWASGKVLCLDPLDGVYNYLAQQRCNLDDTWEGKIYRVLAGNPAKHDLDI
228 KPTVISHRLHFPEGGS LAALTAHQACHLPLETFTRHRQPRGWELQCGYPVQRLVALYLAARLSWNQVDQVIRNALASPGSGGD
229 LGEAIREQPEQARLALTAAAESERFVRQGTGNDEASADVVS LTCPVAAGECAGPADSGDALLERNYPTGAEFLGDGDDVSFSTRG
230 TQNWTVERLLQAHRLQEERGVYVFVGYHGTFLAAQSIVFGGVRARSQDLDAIWRGFYVAGDPALAYGYAQDQEPDARGRIRNGA
231 LLRVYVPRSSLPGFYRTGLTAAPEAAGEVERLIGHPLPLRLDAITGPEEEGGRLATILGWPLAERTVVIPSAIPTDPRNVGGDLAPSSI
232 PDQEQAISALPDYASQPGKPSREDLK

233

234 **DNA sequences**

235 **>ENA|AAB59097|AAB59097.1 *Pseudomonas aeruginosa* exotoxin type A**

236 ATGCACCTGATACCCATTGGATCCCCCTGGTCGCCAGCCTCGGCCTGCTCGCCGGCGGCTCGTCCGCTCCGCCGCCGAGGA
237 AGCCTTCGACCTCTGGAACGAATGCGCCAAAGCCTGCGTGCTCGACCTCAAGGACGGCGTGCGTTCCAGCCGCATGAGCGTC
238 GACCCGGCCATCGCCGACACCAACGGCCAGGGCGTGCTGCTACTTCCATGGTCTGGAGGGCGGCAACGACGCGCTCAAGC
239 TGGCCATCGACAACGCCCTCAGCATCACCAGCGACGGCCTGACCATCCGCCTCGAAGGCGGCGTCGAGCCGAACAAGCCGGT
240 GCGCTACAGCTACACGCGCCAGGCGCGCGGCAGTTGGTCGCTGAACTGGCTGGTACCGATCGGCCACGAGAAGCCCTCGAAC
241 ATCAAGGTGTTTCATCCACGAACCTGAACGCCGGCAACCAGCTCAGCCACATGTGCGCCGATCTACACCATCGAGATGGGCGACGA
242 GTTGCTGGCGAAGCTGGCGCGCGATGCCACCTTCTTCGTGAGGGCGCACGAGAGCAACGAGATGCAGCCGACGCTCGCCATC
243 AGCCATGCCGGGGTCAGCGTGGTCATGGCCCAGACCCAGCCGCGCGGGGAAAAGCGCTGGAGCGAATGGGCCAGCGGCAA
244 GGTGTTGTGCTGCTCGACCCGCTGGACGGGGTCTACAACCTCGCCAGCAACGCTGCAACCTCGACGATACCTGGGAAG
245 GCAAGATCTACCGGGTGCTCGCCGGCAACCCGGCGAAGCATGACCTGGACATCAAACCCACGGTCATCAGTCATGCCTGCAC
246 TTTCCCGAGGGCGGCGAGCCTGGCCGCGCTGACCGCGCACCAGGCTTGCCACCTGCCGCTGGAGACTTTACCCGTCATCGCC
247 AGCCGCGCGGCTGGGAACAACCTGGAGCAGTGCGGCTATCCGGTGACGCGCTGGTTCGCCCTTACCTGGCGGCGCGGCTGTC
248 GTGGAACCAAGTCGACCAGGTGATCCGCAACGCCCTGGCCAGCCCCGGCAGCGGCGGCGACCTGGGCGAAGCGATCCGCGA
249 GCAGCCGGAGCAGGCCGCTGCGCCCTGACCTGGCCGCGCGGAGAGCGAGCGCTTCGTCCGGCAGGGCACCGGCAACGA
250 CGAGGCCGGCGCGGCCAACGCCGACGTGGTGAGCCTGACCTGCCCGGTGCGCGCGGTGAATGCGCGGGCCCGGCGGACA
251 GCGGCGACGCCCTGCTGGAGCGCAACTATCCACTGGCGCGGAGTTCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCG
252 CGGCACGCAGAACTGGACGGTGGAGCGGCTGCTCCAGGCGCACCGCCAACTGGAGGAGCGCGGCTATGTGTTCTGTCGGCTA
253 CCACGGCACCTTCTCGAAGCGGCGCAAAGCATGCTCTTCGGCGGGGTGCGCGCGCGCAGCCAGGACCTCGACGCGATCTGG
254 CGCGGTTTCTATATCGCCGCGATCCGGCGCTGGCCTACGGCTACGCCAGGACCAGGAACCCGACGCACGCGGCCGGATCC
255 GCAACGGTGCCCTGCTGCGGGTCTATGTGCCGCGCTCGAGCCTGCCGGGCTTACCGCACAGCCTGACCTGGCCGCGCCG
256 GAGGCGGCGGGCGAGGTGCAACGGCTGATCGGCCATCCGCTGCCGCTGCGCCTGGACGCCATACCCGGCCCCGAGGAGGAA
257 GGCGGGCGCCTGGAGACCATTCTCGGCTGGCCGCTGGCCGAGCGCACCGTGGTGATTCCCTCGGCGATCCCCACCGACCCGC
258 GCAACGTGCGGCGGCGACCTCGACCCGTCCAGCATCCCCGACAAGGAACAGGCGATCAGCGCCCTGCCGGACTACGCCAGCCA
259 GCCCGGCAAAACCGCCGCGGAGGACCTGAAGTAA

260

261 **>ENA|AAW80252|AAW80252.1 *Vibrio cholerae* hypothetical exotoxin A**

262 CTGTACTTGACATTTTATTTGGAGAAAGTAATGAAGAAGATGTTATTGATAGCAGGGGCTACGGTGATATCCAGTATGGCTCATC
263 CCACATTTGCAGTCGAAGATGAGTTAAACATATTTGATGAATGCCGTTCCGATGTTCTGTTACCCCGGAACCGGGTAAGCCGA
264 TTCAATCAAAATTGTCTATCCCTAGTGATGTTGTTTAGATGAAGGTGTTCTGTATTACTCGATGACGATTAATGATGAGCAGAAT
265 GATATTAAGGATGAGGACAAAGGAGAGTCCATTATTACTATTGGTGAATTTGCCACAGTAAGAGCGACTAGACATTATGTTAATC
266 AAGATGCGCCTTTTGGTGTCATTCAATTTAGATATTACGACAGAAAATGGTACAAAAACGTACTCTTATAACCGAAAAGAGGGTG
267 AATTTGCAATTAATTGGTTAGTGCTATTGGTGAAGATTCTCTGCAAGCATTAAATTTCCGTTGATGAGCTCGATCAGCAAAG
268 AAATATCATCGAGGTGCCTAACTATATAGTATTGATCTCGATAACCAAACGTTAGAGCAGTGGAACCAAGGTAATGTTTCTT
269 TTTCGGTAACGCGACCTGAACATAATATTGCTATTTCTTGCCAAGCGTGAGTTACAAAGCAGCGCAGAAAGAGGGTTACACGC
270 CATAAGCGTTGGGCTCATTGGCATAACAGGATTAGCACTATGTTGGCTTGTCGAATGGATGCTATTATAACTATATCACCCAGCA
271 AAATTGTACTTTAGGGGATAATTGGTTTGGTGGATCTTATGAGACTGTTGCAGGAACTCCGAAGGTGATTACGGTTAAGCAAGG
272 GATTGAACAAAAGCCAGTTGAGCAGCGCATCCATTTCTCAAGGGGAATGCGATGAGCGCACTTGCTGCTCATCGAGTCTGTG
273 GTGTGCCATTAGAACTTTGGCGCGCAGTCGGAAACCTAGGGATTAAACGGATGATTTATCATGTGCCTATCAAGCGCAGAATA
274 TTGTGAGTTTATTTGTGCGACGAGAATTTTATTCTCTCATCTAGATAGCGTATTTACTCTGAATCTTGACGAACAAGAACCAGAG
275 GTGGCTGAAAGGCTAAGTGATCTTAGACGAATTAATGAAAATAACCCGGCATGGTTACACAGGTTTAAACGTTGCTCGACAG
276 ATCTATAACGATTATGTCACTCACCATCCCGGATTAACCTGAGCAAACAGTGCGGGTGACAAAGCTGCCGATATCCTCTCTTT
277 ATTTTGCCAGATGCTGATAAGTCTTGTGTGGCTTCAAACAACGATCAAGCCAATATTAACATTGAGTCTCGTTCTGGCCGTTTCAT
278 ATTTGCCTGAAAACCGTGCGGTAATCAACCCCTCAAGGAGTCACAAATTGGACTTACCAGGAACTCGAAGCAACACATCAAGCT

279 CTGACTCGAGAGGGTTATGTGTTCTGTTGGGTTACCATGGTACGAATCATGTCGCTGCGCAAACCATAGTGAATAGAATTGCCCT
280 GTTCCGAGAGGCAACAACACTGAAAACGAGGAAAAGTGGGGCGGGTTATATGTTGCAACTCACGCTGAAGTTGCCCATGGTT
281 ATGCTCGGATCAAAGAAGGGACAGGGGAGTATGGACTTCGACCCGTGCTGAGCGGGACGCTCGTGGGGTAATGCTAAGAGT
282 GTATATCCCTCGTGCTTCATTAGAACGTTTTATCGAACGAATACACCTTTGAAAATGCTGAGGAGCATATAACGCAAGTGATT
283 GGTCAATCTTTGCCATTACGAAATGAAGCATTTACTGGTCCAGAAAAGTGCGGGAGGGGAAGACGAAACTGTCATTGGCTGGG
284 ATATGGCGATTGATGCAGTTGCGATTCTTCGACTATTCCAGGGAACGCTTACGAAGAATTGGCGATTGATGAGGAGGCTGTTG
285 CAAAAGAGCAATCGATTAGCACAAAACCACCTTATAAAGAGCGAAAAGATGAACTGAAATAA

286

287 **>ENA|AXV34983|AXV34983.1 *Aeromonas hydrophila* exotoxin**

288 TTGGCCATGCTAGGCGGTGCCATCTACCGGTGATGGCCGACGAGTCATTCAACCTGTGGCAGGAGTGCGCCACCCGTTGCAC
289 TCTGGATCTGGCCAGGGGGTGCAGCGCCAGCAGCTCGATGTCGCCGGCCTGCTGGGTGAACAAGCCGGATCCGGGGTACTG
290 CACTACTCCATGGTATTGGAGGAAGGAGGAGACAGCCTCAAGCTGGCCCTCGGCAATGCGCTGACCCTGCGCACGGATGGCA
291 CCACCATCACCTGACCAGCGCCACCGCGGGCAAGGGCCGCGCACCTACAGCTATACCCGCCAGGGACACGGCAACTGGTC
292 GCTGCATTGGCTGGTTCCTCGTGGCGACGATGCGCCCGCAGCATCAAGGTCTTCTCCACGAGCTGGATGCGAGGATCCGAGG
293 TGAGCCATATCTCCCCATCTACAGCATCGAAGTGAGCGACGACCTGCTGCGCAGCATGGCCAGCAACTCGACACTCTTCGTCA
294 GGCACGTGAAAAACAATCAGATCAATCGCAGCCTCACCTCAGTGCGGCCGGTGTGCGCTTCGTGGCGGCGCCACCCAGCA
295 CAGCCGTCAGAAGCGCTGGAGCGAGTGGCACAGCGGCAAGGTGTTGTGCTGCTGGATCCGCTGGATGCGGTCTACAACACTAC
296 CTGTCGCAGCGCACCTGCAACCTGGGTGATACCTGGGAAGGCAAGGTCTACCGGGTATTGGCCGGCGCACCCGCCTCTCACG
297 ATACCCATATCGTGCCGACCGCCATCAGTCATCGTCTGCACTTTGCCAAGGGAGACGGTCTGGCGGCCCTCACCCTCATCAGG
298 TTTGCGCCATACCGCTTGAATCCCTGGCCAGAAGCCGTCAACCCAGAGGCTGGGAAGAGCTCAGCCAGTGCGTTATCCGGTC
299 CACAATCTCATCACCTCTATCTACTGACCCGCCTGCCATGGTCACAGCTTGATACCGTGATACCCAGGCGCTGGCCAACACCA
300 CGCCAGAGGATGGTTCAACGCCACGAGGGCAGCTGGCACAAGCCATTGCGGAGAACCCGGCCAGGCACGGCTGGCCCTGA
301 GCATGGCGGCCGCCAGAGCGACGCCTTCAGCCACCAACAGGCGGGCAATAGCCAAGAAGAGGCCGCCAGCGCCGACGTGG
302 TCAATCTCACCTGCCCTGCCGCCGATCTCAACTGCCTGGCGCCGGCCGACAGCGCCGATGCCCTGCAGGAGCGGGACTATCCG
303 AACGGTGCCAGCTTCTGGGTGACGGGGACGAGGTGAGCTTCAGCACGGCCGGTACTCGCAACTGGTGGTGACCCGCCTG
304 GAGCAAGCCCATCGCCAGTTGCTGGCGCGCGGTTATCTCTTCGTCGGTTATCACGGCACCTTCTCGAAGCCGCCACAGCATA
305 GTGTTTGAAGGGGTGCATGAACGGGATCAATCCTCCATCGTCTTGGCAAGGCTTCTATGTCGCTGGCGATCCGGCCCTCGCC
306 TACGGTTACGCCAGGATCAGGAAGCGGATGCCCCTGGCCGATCCGCAATGGCGTGCTGCTGCGGGTGATGTGCCGCGCG
307 CCGCGCTGCCTACCTCTACGCGACCCAGCAGACCTGGCCGATCCCGCGCGCTCGATGAGGTGCGCCGCTGATTGGTCAC
308 CCCCTGCCGCTGCAGCTGGAGGCCATCACAGGACCGGAAGAGGAAGGTGGACGCCTGGAACCATTTCTGGGTGGCGGCTG
309 GCGGAGCAGGCGGTGGTGATCCCCTCCACCATACCGACGGATCCGCGCAATGTCGGCGGCGATCTTGACCTTGCCAGCGTGCC
310 GCAGGAAGAGAGCTCCATCAGCGCCTTGCTGATTACACCACCCAGCCCCGGAAGACCTCTGA

311

312 **>MUKV01000035.1:37277-39136 *Chromobacterium haemolyticum* strain H5244 35, whole genome shotgun**
313 **sequence [GM note: Reverse complement]**

314 ATGCGATTGTATAAAGCCTTGCCCTTGCCGCGGGCCTGATTCCCTTATTGTCCGCTGCGAAACCGACGAAGCCAGCCCCTTT
315 GCCGCCGAACGGCACAAACAGCCAGTTTCAAACAAGCCGCCAGTTCCGTCATCAAAACCGATTTCGAAATCTTCAAACAATG
316 CGTGGACAACCTGCATTCTCTCCCGCGGGAACCGGGTAAATTCATCAGCACCTATTGCCGCTACAAATACCCCGTCGCCGGA
317 CGAAGGCGTGCTGTATTACTCGATGTTCTGTGCAAGACCGTTTACCACCGCCGCCAATAACAGCGCCACCATCAAGATCGACGA
318 TTTGCCAAGGTCCGGATCAACGACGGCCAGGGCACCGGTACGCGCCGGGCACCTTGACCATTGAACTGGCCACCCCGGAC
319 GGCAAGGTCAAGAAATTCACGCATAAGCGCCGCACTGAATGGTTACGCTGAATTGGGCGGTGCCCATCGGCAAAGACGCGC
320 CCACCAAGCATCAAGCTGTTTCATCATGGACATGGACAGCAATAAGAAGATCGTCGATCACTGCCACTGTACAGCGTGGACCTGG
321 ACGACACCGCGCTGGCGCGCTGGCCGACAAGGCCAAGCTGGCGTTACGCTCCGCCAATCCGAGGAATGACATCATCTGTC
322 TTGGCCGGGCGTGGGCTACACCGCCGCGCCAGCGCAGCACAACCGCCAAAAGCGCTGGAGCGAATGGCATAGCGGCGTCCT
323 GCTGTGCTGGCTGGACCCGCTGGACGCCATCTACAACACGTACCCAAAACCGCTGCCAGTTGAACAAGACCTGGGAAGGC

324 GCGCTGTACAAGGTGGTGGCCGCAAGCCGAGATCAATGAATTCAAGCCGCTGGCCAAAGCGCCCATCCAGCACCGGGTG
325 ACTTCAGCAAGGAAAACGCACTGGGCGCGCTGTCCGCCACCGCGTCTGCGGCATCCCGCTGGAGTCGCTGGCCCGAGCCG
326 CCAGCCCAGGGGCTGGGAAGAGCTGTCCGCTTTCGGGTGAAAACATCGTCGGGCTATACATCGCCACCCGGCTG
327 TCCTTCGACCGTTTCCGCCAGGTGGTCGATGACTTGATCCATCCCCGCCGGTCAGCGGCGCGCAAGACCCGGTGCGCTGGA
328 GCAATTGGGCACCGCGGTGCGCGAAACGCCGGGACTCGCCCGCAAGGCCTGGCCGAGGCGGAGGCCCTTCTGGACACCTA
329 CCTCGACTATCATCTGGCGCCAGCGCCGATGACGCGCAAAGAGCGGACGTGCTGTCGCTGACGTGCCCGGCCGACAGCGAG
330 CCTTGCGCCGCCGCAACGCCGACGGCGCCACGTCAACCTCGAGTACCACCCGGCTCAAGCTTCTTCGCGCCGGGCGAGC
331 CGGTGGAATTCTCGCCAACGGCACCACCCGCAACTGGAGCCAGGAGCGCCTGCTGGCCACCCATCAGCGGTGCTGGACCA
332 GGGCTATGTCTTCGCCGGCTATCACGGCGGCTCAACCATCGCAGCGAGAAGCATCGTCACCGGCGGCATCACGCCCCGCACCC
333 AGGAGCTACCACCGATCTGGAAGGGCTTCTACATCGCCGGCAATCCGGAAGTCGCTTACGGCTACGCGCTGGACAACGACAAC
334 CCCCCTCTCGCGGCATCATGATGCGCATCTACGTGCCTAGAACCGCTCTACCCCAATTGTTCCGCACCAGCCAGCCGCTCAGCG
335 ACGAGGCCGCGGCGCTCAGGGAGATGAGCCGCCTGTTTGCCGCAACGTCACTGGATAGTACCTTAGGATATGAATCCATC
336 ACCGGGCCACAAGCTCCCAGAGGCGGATGAAACCGTCCTGGGTTGGCTTATGGCGGACATTAGTGCGGATTCCGTCGA
337 TGATTAGGGCAACGGCAACAACGCCGGGAAGATCGACGTGCCGGACTACGAGAAGAAGATCAGCGCTCTGCCCGACTACGT
338 CACTAAGCGCTG

339

340 >NZ_VOQB01000003.1:c67414-65456 *Shewanella* sp. YLB-07 NODE_3_length_628018_cov_39.817077, whole
341 genome shotgun sequence

342 ATGATAAAACACGATATCTCTGCTTGAGTGTTGCGATTAGCTCACTGTTTCTCGCAATAACTAGCGTAAATGCAACGGATCTGC
343 GTGGCTTAGAACCACAGATAAAGCTCAGCAGCTCAAGTCAATGAAGCATTGATCTATGGCAAGATGTGCTACTCACTGCCAAC
344 TCGATTTAAGCCAAGGTATTAGATCAAGTGAATTGGATCTGACTCCCTTATTTGAAACCAGTAATGAAGAAGGCATACTGCACTA
345 CTCTATGTTACTGGGAGAAGGTAATGAGGGGCTCAAACCTTGCTATCGATAATGCTCTGACACTACATACTACTCATTCAACGATTA
346 ATTTTACCAGTGAGACGGCGGAATCCGGTCTCGCAGTTACTCATATATTCGTAAGGGAGAAAAATAATTGGTCTCTAAACTGGCT
347 TGTTCCTGTTGGTGATGATGCTCCAGCCAGCATTAAAATATTCTTCCTTGAACAGGACGCCGTAGGCCTGAACAGATATATCTCTC
348 CCATCTACAGTATAGAGGTGAGTAACAACCTGTTAAATAGTTTGCGCATAAATCCACGTTTTATATTAGGGCTTTGACAATAAC
349 CAAACATTGTCAATGGTCAATATCAGCAGTGCCGGAGTGAGCTATGTGGCAGCGCCGAGCAGCACCATCGACAGAAACGCTG
350 GAGTGAATGGCACACAGGTAAATTACTCTGCTTCTTGACCCCTTCGATGCGTTCTACAATTACGTGACTCAACACACCTGTAAT
351 CCTGATGACACGTGGGAAGGGCAAATTTATCGCGTGTTGGCAGGTAATCCAGCGACCCTGGATAACAACCGTCCCTCAACGAC
352 ACCGGCCGTTATCAGTCATCGAATCCATTTCGATAGAGGTAACAGCCTAGCATCCTTAAGTCCCATCAGGTATGCGGTATTCCTC
353 TTGAATCTCTAGCTCGTACCCGCCATCCAGAGGTTGGGAAGAACTCAATAATTGTGGTTATCCGGTACGTAACCTTGTCAGCCT
354 CTTTATATTGGCCGACTATCATGGGACAGGGTAGAGCAAGTGATCCACAATGCTTTGACCAACCCGACTCCTGGTAATGCGCT
355 GGATGATGCTATTCGAGAAGCACCAGAGAGAGCTAGGGTGACCCTGACCCTGGCAGCTGCGCAGGTCAATCAATTTGATAATC
356 AGGCCGCTGGCAATACGCCTGAACAAGCCCAAAGTGCTGACGTGGTGAGCCTATCCTGCTCTGCAGGTGCGCTTCATTGTAGT
357 GCGCCAGCCGACAGTGCCAACGCGTTACTCGAACGAGAACACCCCAATGGTGCAAACCTTTAGGAGCGGGGGAGGCGGTA
358 AGCTTTACCAGAGGGGAACCAGAACTGGTCTTCAGCACGCTTGAATCATGCACATCAGCAACTGATCGCGCGAGGGTATGT
359 TTTTGTGGGCTATCACGGCAGCTCTTTGGAAGGTGCTCAAAGCATTGTTTTCGGGGGGATCAGAACCAGAACACAGGCACTG
360 GATGATGTATGGCAAGGCTTGATATATCAGGTGACCCTGCCGTGCGCTATGGATATGCGCAAGATCAAGAGCCTGACTCGCGTG
361 GCCGGATCCGCAATGGCACTATGTTGAGAGTCTATGTACCAGGCACTGCCACAGCATACCTCTATGAAACGCCTCTGACTCTGGC
362 CGATCCTGAAGCTGTCGATGCTGTAGGTACCTGATTGGCCACCCACTTCCGTTACAAACGGAAGCCATCACTGGCCCCGAAGA
363 AGCAGGCGGGGCGCCCGGAAACATTCTCGGCTGGGAACTGGCTGAACAGGCTGTAGCAATCCCTCCACGATACCGACAGAT
364 CCGAGTAATATCGGCGGTGATCTCGACCATCGAGTATTCCTGATGAGGAAAGTGATATCAGTGCATTACCAGACAATGTCTACTA
365 AACCTCATCACGACGAATTATAG

366

367 >PDBX01000002.1:22019-23977 *Collimonas* sp. PA-H2 Ga0114272_12, whole genome shotgun sequence

368 ATGTCCAAATTCATGTCGCAACGCTGGATCTATCTGTTGGATGGCTTTTCTGCTCGGAACCGGCAGCACCAGGGCGAATACG
369 ATAGAGGGAAACTTCAGGCTTTGGGACGATTGCAGCAGCTACTGCCTGGTTTACGCCGCCCCCATAAAATCTATCAGACCCCT
370 TTGGCCACGCAGGCTGTGCCGATTCTCCCGCAAGGAAGGCGTACTGCATTACTCCATGGTGATGAAAGACTATGTCGGCAA
371 CGGCCAGGTTCTGGCCTTGCGCCTTGACGATTTGCCACCGTCTTGTGCGAGCAAGAAAGCCTGAGACTGAGCCTGCTTGGCT
372 CTGACGGCAAGCCCAGGAATTTCCAGTATGCTCGCCAAGGCGCGAAACATTGGTCGCTTAACTGGCTGGTGCCCGTTGGCGAT
373 GACGCTCCCAACAGCATCAAGGTCTTCTTCAAGAACCTCGACGGCCAGAATAATATTCTCTCCATCTCGCCTCTTTACAGTGTGG
374 AGGTAGACGACAAGACTCGCGCGCTGCCCCGCACTGCCACCTTCTCTGTCAACCAGGAGAATGTCACTCAGGGCCAAGG
375 CCTGCTTGGGATACGACGTGCAGGCGTCAGTTACGTGCGCGCTCCCGTGAACCATGACCGTCACAAACGCTGGAGCGAGTGG
376 CACAGCGGCAAGCTGCTCTGCCTGCTCGACCCTTTGGATGCCATTTACAACCTACGTGAGCCAGAACCGCTGCAGTCTGGGCGA
377 AACCTGGGAAGGCGCAATTTATCAAACCTGGCAGGCCGCGCTGTGACAAATACGCCACCGGCAAGCAAGCCAGTTATTA
378 GCCAACGCATCCATTTTGCCAAGGGCAACGCTCTGGAAGCGCTAACCCAGTCACCGGGTATGCGGCATACCTCTTGAGTCCTTG
379 GCACGCAGACGCAAGCCGAGAGGATGGGAAGAATGGTCTTCGTGTGGCAATCCCGCGGCCAATTTCTAGCCCTTTACATCGC
380 CACCCGCTTGCCGTTGACCAATTCGTCAGGTGATTATAACCTGGTTACAGGGCAAGCAGTTGCAGCGCCTGATCCGGTGCC
381 TCTGGATGCCCTGAGAACGGCCGTCATTGAGCAACCGGAACTGGCAGCTCAAAGCATCGCCAGGCAGCCGACATCTTCAGG
382 AACTACCAGGCAGCCAATCCTGGCGCCAGTGCCGCCGCCGACACAGGCCGATGTGCTGGCCGTACCTGTCCGGCTGACG
383 CGCGCCCGTGCGGCTCCGGCGCAAGCAGCGGCGTGCTGGTCCAGCGTGAAGAAATCCACCGGAGCGCACTTTCTGAATGACGG
384 AGAGCTGCCAAGCTTACCGTACAAGGCACGCAAACTGGAACCTGAACCGCCTGCAGGCTGCTACCTGCGCCTGCAGGTG
385 CAGGGATACGTTTTTGCGGGTTATCACGGCACATCGCTGGAGGGCGCACAGAGTATCGTGTTTGGCGGCATCCATAACGCCCA
386 GCAGGATCTTGAGGAAATCTGAGAGGCGCTGTACGTTGCCGAGATCCCGCTTGCCTACGGCTATGCGCAAGATGCGGAAG
387 GAGATGAGCGCGGCCGCATCCGCAACGGCACGATGTTGCGCGTCTATGTCCCGCGCAGCGCTCTCCCGCGACTCTTTGCCACC
388 AGCCTGCCTCTGGACCATCCAGGCGCCTCGCAAGAAGTTGCGCGTTTGATCGGCCACCGCTGCCCTTGCTTTATGAATCGATC
389 ACCGGTCCGGAAGCAGCAGGCGGCAATCGCTTGAGACGATCCTGGGCTGGCAGCTCGCGGAGCAGGCAGTCGCGATTCCC
390 TCGATGATCCCGACCAATAGCCGCACTGTGCGAAATCCCCTCGATCCCGCCACCGTCACGCTTGAAGAAAAGCAGATCAGCAG
391 CTTGCCGGGCTACGCCACAAAACCTGCGAAAGACGACAAGACGGAACCTATGA

392

393 >CP014222.1:847765-849768 *Janthinobacterium* sp. B9-8, complete genome

394 GCGCTTGGTGACGTAGTTGGGCACTGGGCTGATCTTTTTCTCGTAGTCCGGGCACATTGAGTTGTGAGCCGTTATTGCCCCGAAT
395 CATTGACGGAATTACCACCGCATGTTCCGCCAGATCCCAACCAAGATGGTTTCATCCGGGTCGCCGGGATCTTGCGGCCCGGT
396 GATCGATTATATCCCAAGGTATCTGCAAGCGTAATATTTGCGCCGAGCAAGCGACCAATTTCTCTGAGCGCTGCGGCCTCGTCG
397 CTCAGTGCCTGGTTGGTGCGGAATAACCGGGAGAGAGCGGTGCCGGGTACATAGACGCGCATCATGGTGCCCGTTGCGCCGG
398 TATTGTTATCCAGGGCGTAGCCGTAGGCGACTTCCGGATCGCTGGCGATGTAGAGGCCGCGCCAGATTGGCTGCAGGTCCTGA
399 GACCGGCGAGTGATGCCGCCGGTCACAATGCTTCTGGCGGCAGCGATCGAACCGCCGTGATAGCCGGCGAAGACATAGCCCA
400 GATCCAATAGCCGCTGATGGGTGGCCAGCAGGCGGTCTGGCTCCAGTTGCGGGTGGTGCCATTAGGGAGGAATTCCACTGG
401 CTCGCCCCGGTGCAAAATAGTCTGTGCCGGGGTGGTACTCGCGGTTGACGTGCGCGCCGGCGGCATCGGGTGCGTTGCAAGGT
402 GCGCTGTGCGCCGGGCAAGTTAAGGACAGCACGTCCGCTCTTTGCGCGTATCGGCACTGCTGCCCCGGGTGGTTGGCGCGGT
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404 AGCGCCACGGGGTCTTGAGCACCGCTGACTGGGCGGGAATGGATCAAATCCTCGACCACCTGGCGGAAGCGATCGAAAGAC
405 AGCCGGGTAGCAATGTACAGGCCGACGATGTTTTCCACCGGGAAGCCGAGGCAGATAGCTTCTCCAACCCCTGGGTTGGCG
406 ACTGCGGGCTAGCGATTCCAGCGGGATGCCGAGACACGGTGCGCGGATAGCGCGCCGAGTGCGTTTTCTTGCTGAAGTGC
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411 ACGCTGTATAGCGGCGAGTGATCGACAATCTTTTTATTGCTGTGATGTCCATGATAAATAACTGATGCTGGTGGGCGCGTCTT
412 TGCCAATCGGCACGGCCCAATTCAGGGTGAACCATTCGGTGCGGCGTTTATGAGTAAATTTTTGACCTGGCCATCGGGTGTG
413 GCTAATTCGATGGTTAACTGCCCCGCGCGGAGCCGGTGTCGTAACCATCGTTGATCCGAATCTTGCGGAAGTCGTCAATTTTG
414 ATGGTGGCGCTATTATTGGCGGCGGAGGCGAAACGGTCTTGTACAAACATCGAATAATATAAAACGCCCTCATCCGGTGATGGG

415 GTGATTTGCACCGGTAGCGAGGTGCTGATGAACTTGCCGGGTTTCGGAGGGGAGAGTATGCAGCTGTCGGCGCATTGCTTGA
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417 CGGTTGCAGATGGACGGACCTCCTCGGTTACGCATCCGGACAATAATGGAATGAGCCCCGAGCAATGGCAAACCTTTATAA
418 AGTCTCATCAT

419

420 **>CP050172.1:c68807-66903 Serratia fonticola strain CPSE11 plasmid plas1, complete sequence**

421 ATGTCAAATAAAGCCAAATTAAGGACTGCTGCGATAGCGATTATTCTCGCATCATATTTATCCCTCCCTGCTTTTGCCAACGACAA
422 GTTTGATTTGTGGACCCAGTGTGCAGATTCTTGCTCACTTGATCTAAGTAACCAAAGAATCTGGTCAAGCCCGATGGACTTATCA
423 TTATTTGGCCAGACGTCCGAACAAGGTGTACTTCATTCTCCATGGTACTTGGTGAGAACAATGACTCTGTGCGGATAGGAATA
424 GACAATGCATTTTCTTCTGATAAACGAAAACAGCATTCAAGGTGTCTCTGATATAACTAAACCGGTAAAATTTAATTA
425 CACCAGACAAGACAAGGGCAATATCTCAGTAACTGGCTAGTACCCATAGGAGGAGGTACTCCCTCAGAGATAAAAGTTTTCAT
426 TCATGAGGTCAACTCAGCTAACCAAATCACCTCAATGTCCCCATATACACAATCCCCGTCTCAAATGAAGTACTCAGCACACTTG
427 AAAAAAATCGACTATATACATTAGAGGGACTAACAGCAACAGCCTATCGTATGAACTTATAGTAAAGAATGCCGGCGTAAGCAT
428 TGCGAGCACCCAAAGTGGACCTACACGAAAAAGACGCTGGACACACTGGGACAGTGGAAGAACTCTTTGCTTCATTGACCCG
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433 TCTCGATAACCAAGAAAGCGATAGCGATCTAGACCGCGCTATTCGAGAGAGTCCGCAACAATCGGACTAGCTTTGACTACGGC
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435 CTGCCCCACTGTGGGTTTGAATTGTATGGTGCCCGCAGATGGCAACGAGGCTCACCAAGAAAGAATCTACCAACGGGGGCTA
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437 AGCAACTGACTTCACAGGGGTATGTCTTTGTTGGATATCATGGAACTTTTTAGAAGCCGCCCATAGCATCGTATTGGAAGGAGT
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439 ATCAAGATCCTGACCCCAATACTGGCCGATTTCGTAATGGAGTTATGCTCCGTGTCTACGTTAGACAAGAATCACTGCCTAACTTT
440 TACCAAATAACGTGCGACTATCTCCCCGGATGCGGTAAATGCTGTATCTAGTTTGATAGGACATACTTTACCGCTTCAACTTGA
441 TTCTATTACAGGTCAGGAGGACGAGGAAGGACGGTTGGAAACAATCATCGGCTGGCCATTGGCAGAGCAACTTGTAGTAATCC
442 CATCGACAATCTCTACTGACCTCGTAACCTGGGGGAGTTTTAGACCCATCCTCTATCCCTGAAGCAGAGAAGGCGATTAGCG
443 TTTTGCCAACTACTCAACGTCACCTACGAATACCCACTAA

444

445 **>FMVV01000003.1:c239527-237620 Acinetobacter baumannii isolate AB32_M genome assembly, contig:**
446 **gnlProkkacontig000003, whole genome shotgun sequence**

447 ATGCACCTGACACCCATTGGATCCCCCTGGTCGCCAGCCTCGGCCTGCTCGCCGGCGGCTTGTCCGCTCCGCCGCCGAGG
448 AAGCCTTCGACCTCTGGAACGAATGCGCCAAGGCCTGCGTGCTCGACCTCAAGGACGGCGTGCGTTCCAGCCGCATGAGCG
449 TCGACCCGGCCATCGCCGACCAACGGCCAGGGCGTGCTGCACTACTCCATGGTCTGAGGGCGGCAACGACGCGCTCA
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461 GGGCACCGGCAACGACGAGGCCAGCGCCGACGTGGTGAGCCTGACCTGCCCGGTCGCCGCCGGTGAATGCGCGGGCCCCGG
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470 GGACTIONGCCAGCCAGCCCGGCAAACCGTCGCGCGAGGACCTGAAGTAG

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