

Supplemental Material

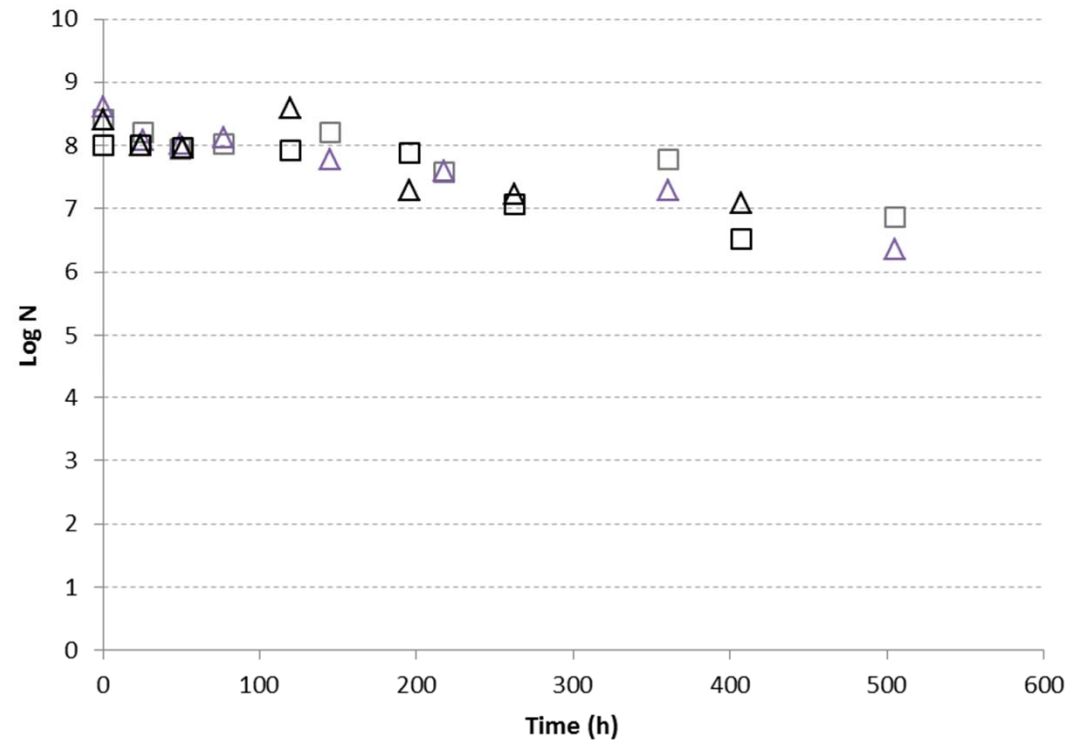
Table S1. Growth of WT and Δ BC_2216-17 mutant in various stressful conditions

Stress tested	Stress condition	Growth condition	Time to reach stationary phase for both strains	Conclusion for the 2 strains
high temperature	42°C	microplate	OD>1 in 3.5h	similar growth
	45°C	microplate	OD>1 in 4.5h	similar growth
acid (HCl supplementation)	pH 5.5	microplate	OD>1 in 7h	similar growth
	pH 5.0	microplate	OD>1 in 12h	similar growth
	pH 4.7	microplate	OD>1 in 32h	similar growth
basic (NaOH supplementation)	pH 8.5	microplate	OD>1 in 12h	similar growth
	pH 8.6	microplate	OD>1 in 13h	similar growth
Oxydative agent	100µM paraquat	microplate	OD>1.5 in 16h	similar growth
	150µM paraquat	microplate	OD>1.3 in 14h	similar growth
	AAPH 100mM	microplate	OD>1.2 in 12h	similar growth
	AAPH 150mM	microplate	OD>1.0 in 12h	similar growth
	0.020% H ₂ O ₂	microplate	OD>1 in 12h	similar growth
	0.025% H ₂ O ₂	microplate	OD>1 in 12h	similar growth
high osmolarity	4 % NaCl	microplate	OD>1 in 18h	similar growth
	6 % NaCl	microplate	OD>0.8 in 36h	similar growth
low osmolarity	0 % NaCl	flask	OD>1 in 4h	similar growth
Ethanol	4%	flask	OD>1 in 3h	similar growth
	6%	flask	OD>0.1 in 9h	similar growth
Ions chelators	EDTA 0.1mM	flask	OD>1 in 7h	similar growth
	EGTA 0.1mM	flask	OD>0.5 in 8h	similar growth
	2,2'-bipyridyl 100µM	flask	OD>0.2 in 5h	similar growth
	2,2'-bipyridyl 500µM	flask	OD>0.1 in 5h	similar growth

Growth in Erlenmeyer flasks was performed in 50ml LB at 37°C with shaking at 200rpm, after inoculation to an OD₆₀₀ of 0.01 by an overnight grown culture. OD₆₀₀ was measured in microcuvettes. Growth in microplates was performed in 250 µl LB at 37°C with shaking, after inoculation by 10µl of an overnight grown culture in an automatic turbidimeter (see material & methods section). OD₆₀₀ was measured every 15 min.

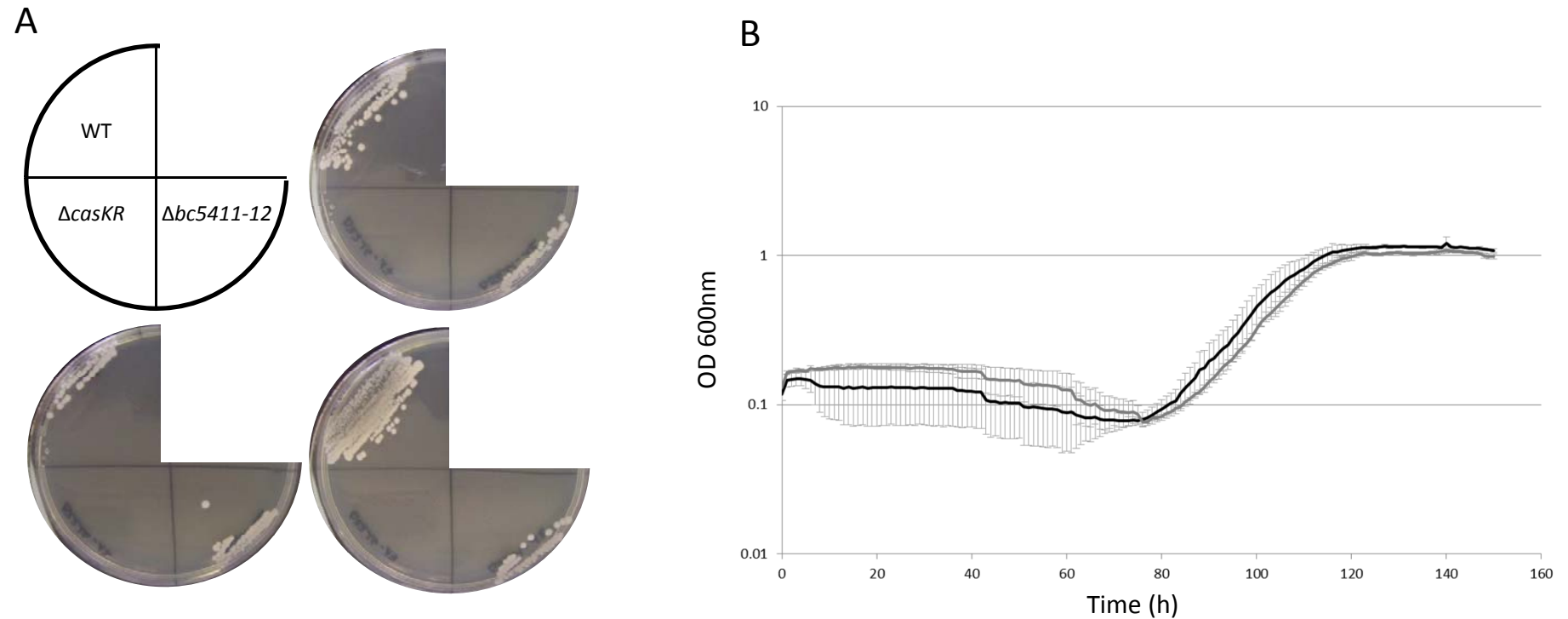
Temperature was set at 37°C, pH at 7.0, and NaCl concentration at 1%, unless stated differently.

Fig. S2 Survival of *B. cereus* WT and $\Delta casKR$ strains at 37°C



Bc WT (squares) and $\Delta casKR$ (triangles) bacterial suspension were incubated in LB at 37°C. Cfu numeration was performed regularly over time. Black and grey represent data from replicates 1 and 2, respectively.

Fig. S3. The $\Delta BC_5411-12$ mutant can grow at low temperature

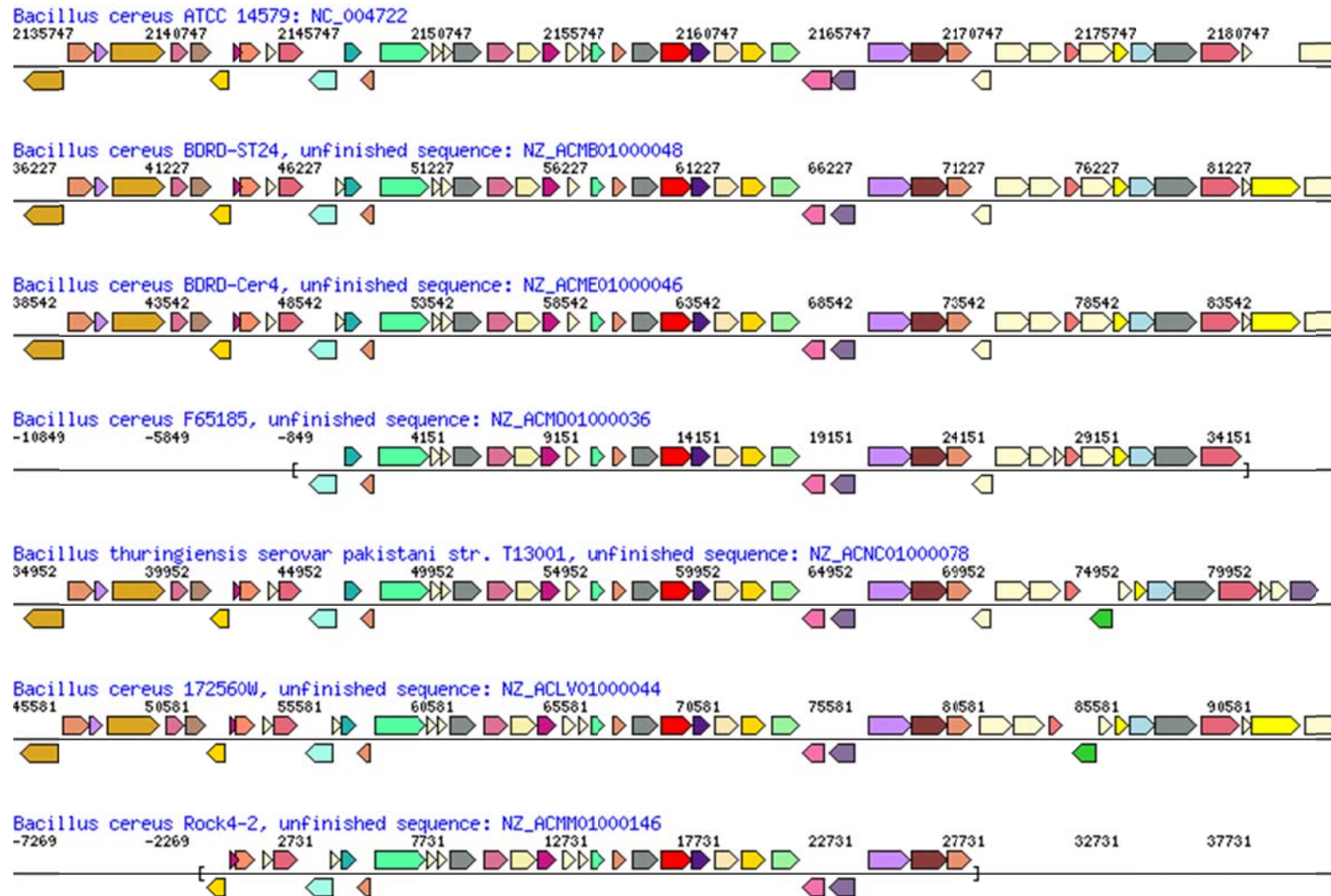


A. The $\Delta BC_5411-12$ mutant can grow at T_{min} . One colony of overnight grown culture of *B. cereus* WT, $\Delta BC_5411-12$ and $\Delta casKR$ was struck on LB agar and incubated at 10°C for 14 days. Three independent replicates are shown.

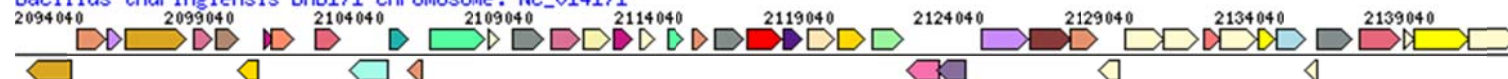
B. The $\Delta BC_5411-12$ mutant can grow at 12°C , similarly as the WT strain. Growth of WT (black) and $\Delta BC_5411-12$ (grey) strains was performed in an automated turbidimeter with shaking at 12°C . Mean values \pm SD of three biological replicates are shown.

Fig. S4. Graphic display of *casKR* Orthologs and Neighborhood genes in the *B. cereus* Group (*sensu lato*).

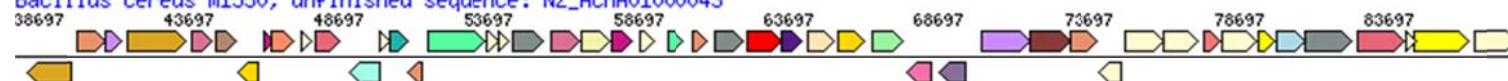
Orthologs of *casKR* genes (*bc2216-17*) and their neighborhoods in all available genomes are shown below, using Conserved Neighborhood Viewer of Integrated Microbial Genomes (Markowitz *et al.*, 2012). Genes of the same color (except light yellow) are from the same cluster of orthologous gene (COG). Light yellow: no COG assignment; Red/Blue: *casKR* orthologs.



Bacillus thuringiensis BMB171 chromosome: NC_014171



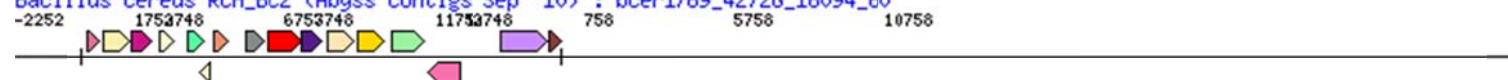
Bacillus cereus m1550, unfinished sequence: NZ_ACMA01000043



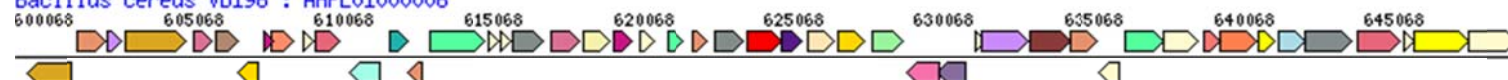
Bacillus thuringiensis serovar kurstaki str. T03a001, unfinished sequence: NZ_ACND01000061



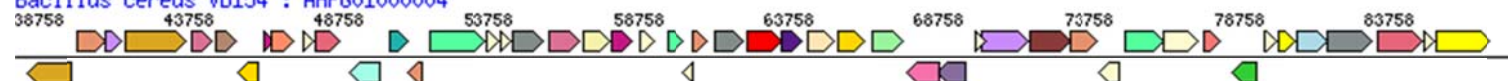
Bacillus cereus RCH_BC2 (Abyss contigs Sep '10) : bcer1769_4272G_16094_60



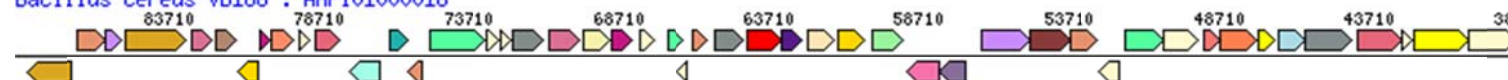
Bacillus cereus VD196 : AHFL01000006



Bacillus cereus VD154 : AHFG01000004



Bacillus cereus VD166 : AHFI01000016



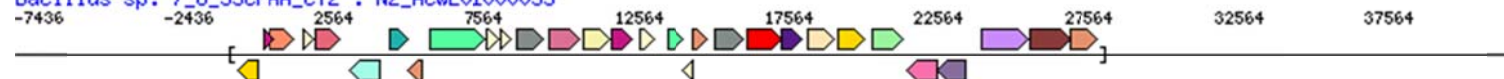
Bacillus cereus B4264: NC_011725



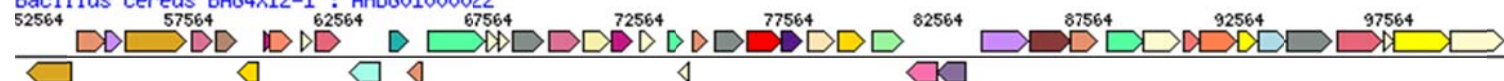
Bacillus cereus AH676, unfinished sequence: NZ_ACMQ01000078



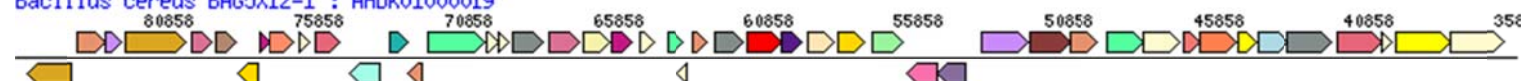
Bacillus sp. 7_6_55CFAA_CT2 : NZ_ACWE01000035



Bacillus cereus BAG4X12-1 : AHDG01000022



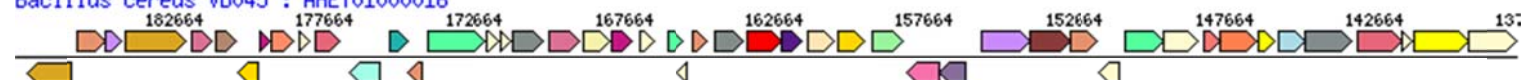
Bacillus cereus BAG5X12-1 : AHDK01000019



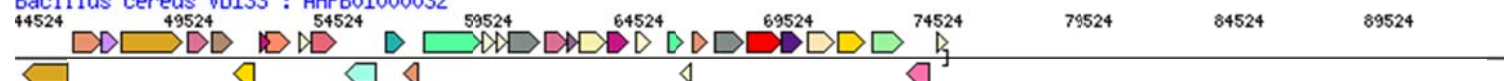
Bacillus cereus ATCC 10876, unfinished sequence: NZ_ACLT01000051



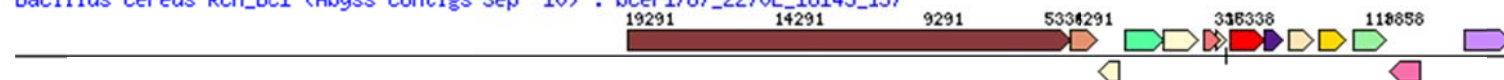
Bacillus cereus VD045 : AHET01000016



Bacillus cereus VD133 : AHFB01000032



Bacillus cereus RCH_BC1 (Abyss contigs Sep '10) : bcer1767_2270L_16145_157



Bacillus thuringiensis serovar berliner ATCC 10792, unfinished sequence: NZ_ACNF01000056



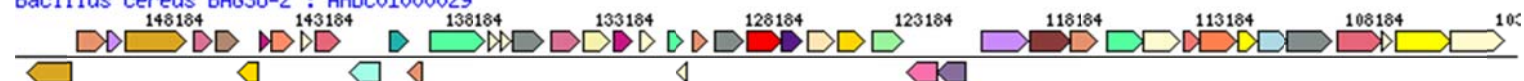
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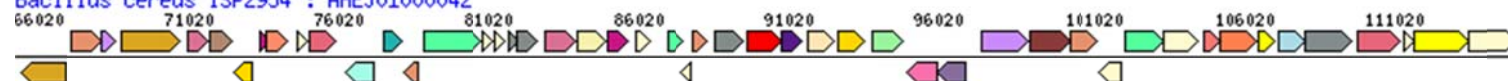
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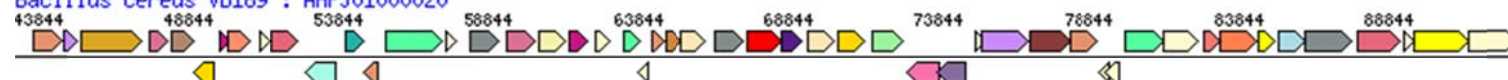
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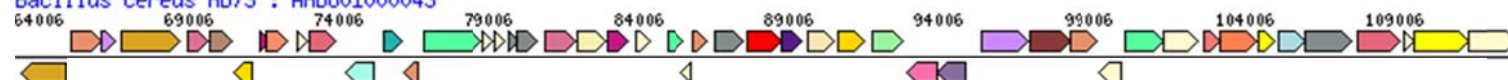
Bacillus cereus ISP2954 : AHEJ01000042



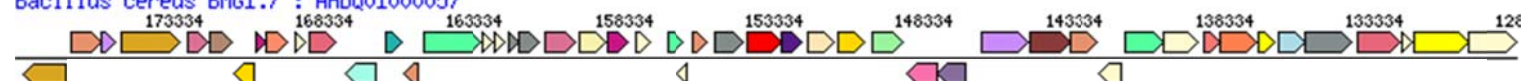
Bacillus cereus VD169 : AHFJ01000020



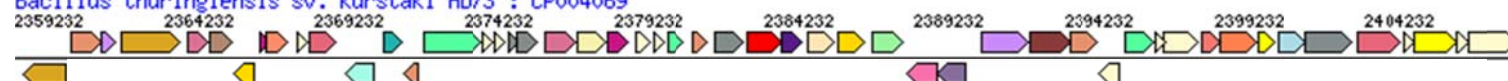
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Bacillus cereus BMG1.7 : AHDQ01000057



Bacillus thuringiensis sv. *kurstaki* HD73 : CP004069



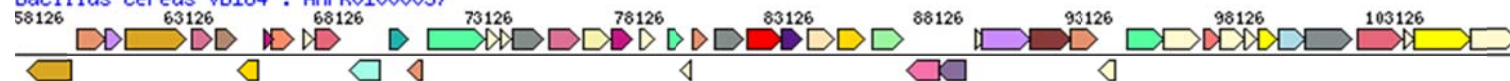
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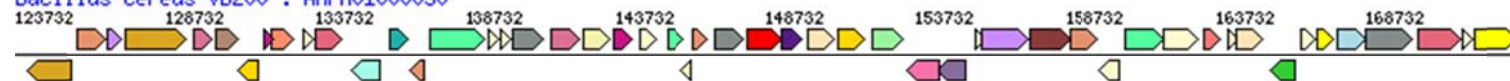
Bacillus cereus Rock1-15, unfinished sequence: NZ_ACMH01000053



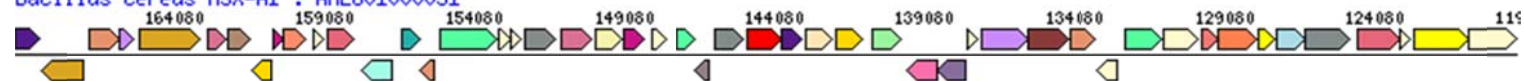
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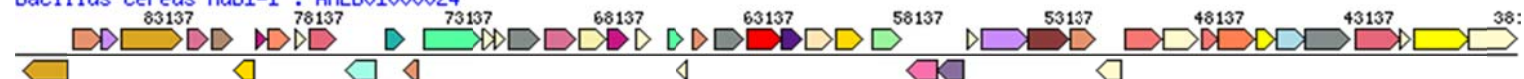
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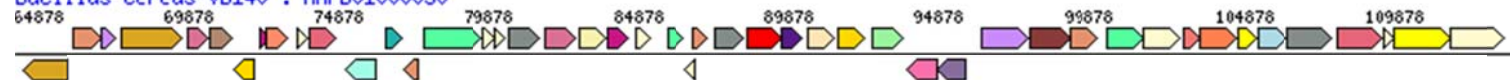
Bacillus cereus MSX-A1 : AHE001000031



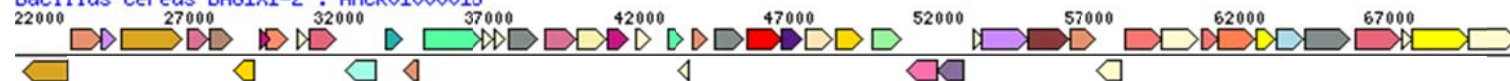
Bacillus cereus HuB1-1 : AHEB01000024



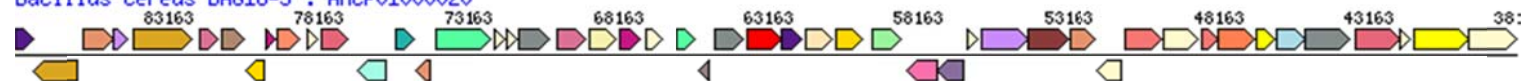
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Bacillus cereus BAG1X1-2 : AHCR01000018



Bacillus cereus BAG10-3 : AHCP01000020



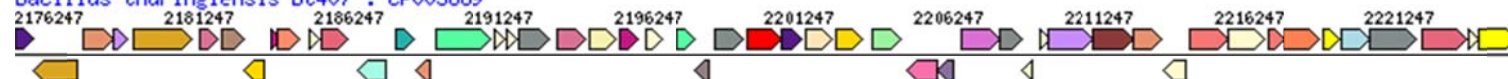
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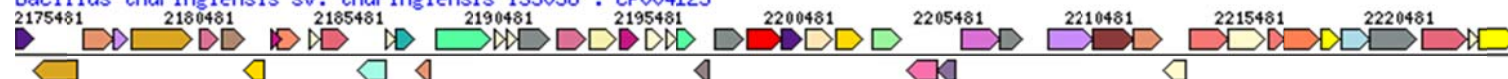
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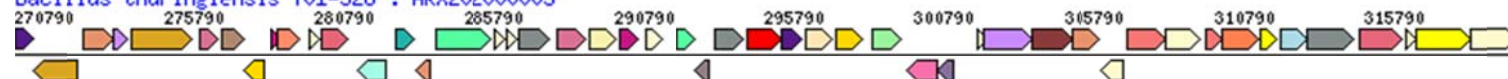
Bacillus thuringiensis Bt407 : CP003889



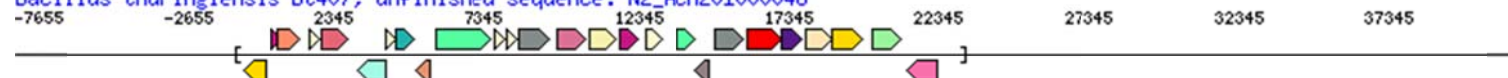
Bacillus thuringiensis sv. *thuringiensis* IS5056 : CP004123



Bacillus thuringiensis T01-328 : ARXZ02000003



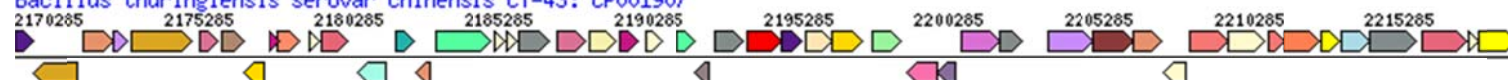
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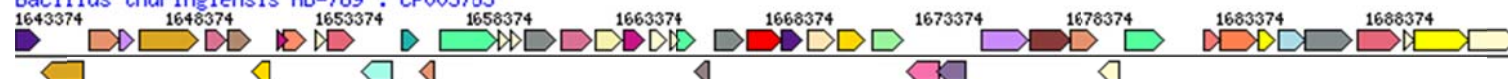
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Bacillus thuringiensis serovar *chinensis* CT-43: CP001907



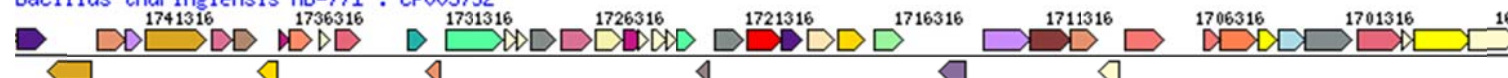
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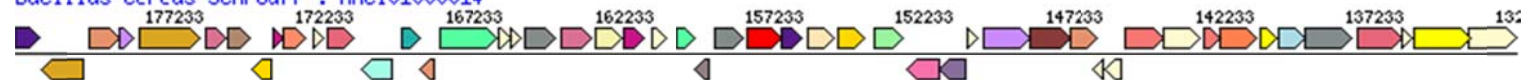
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Bacillus thuringiensis HD-771 : CP003752



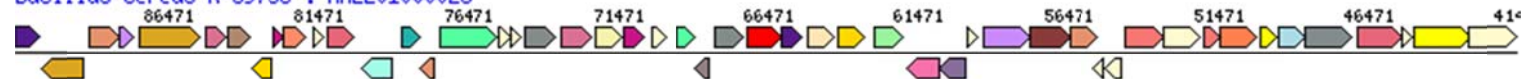
Bacillus cereus Schrouff : AHCI01000014



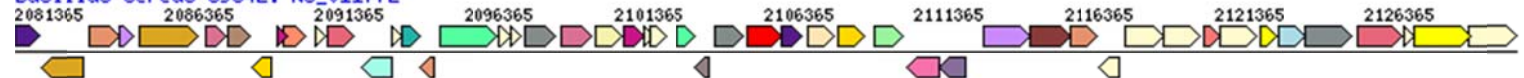
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Bacillus cereus K-5975c : AHEL01000026



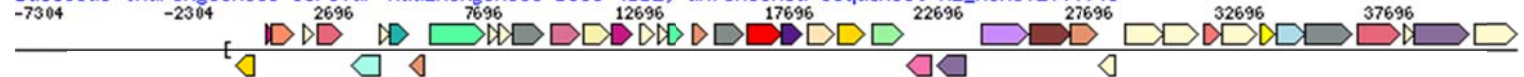
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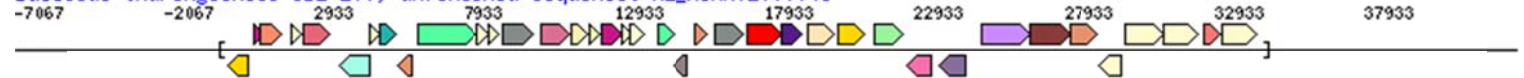
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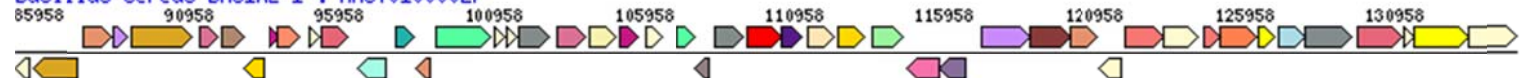
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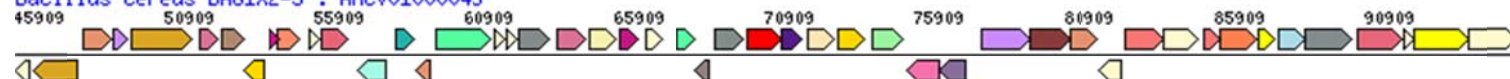
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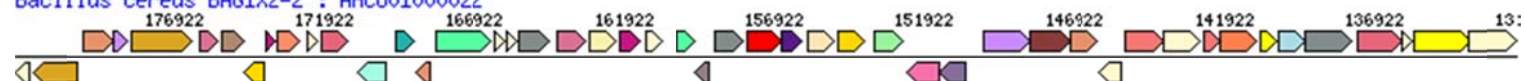
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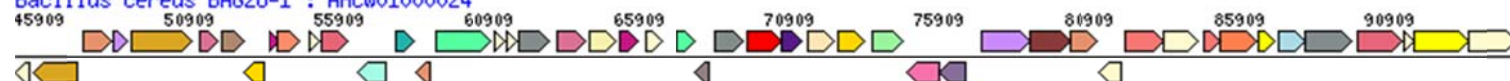
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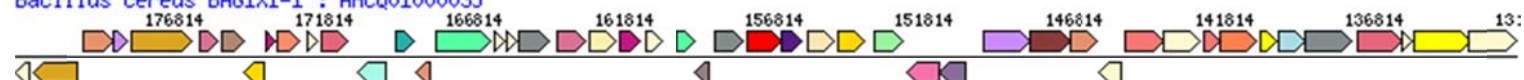
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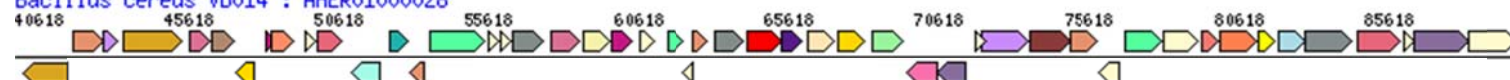
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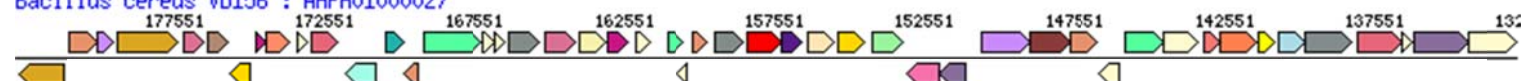
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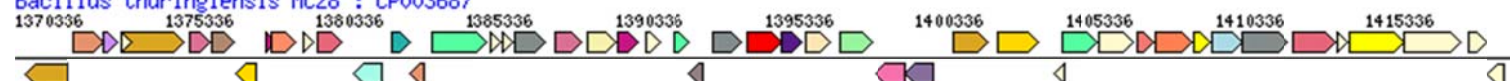
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Bacillus cereus VD156 : AHFH01000027



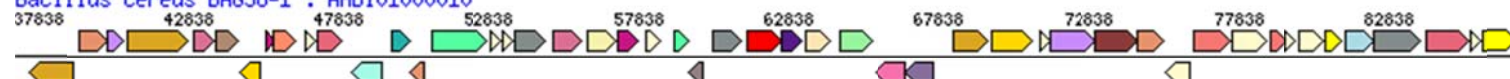
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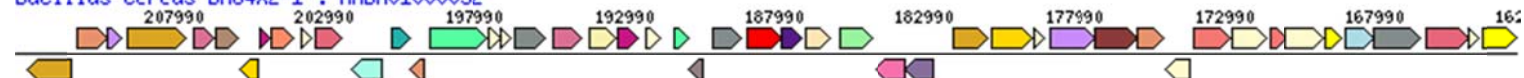
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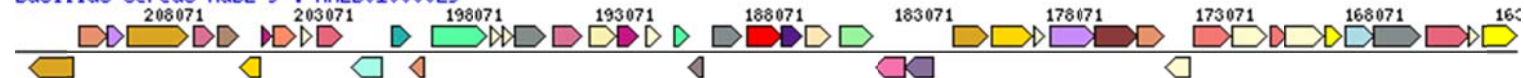
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Bacillus cereus BAG4X2-1 : AHDH01000032



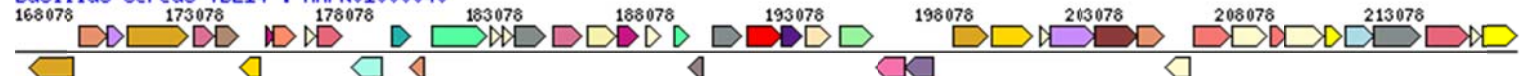
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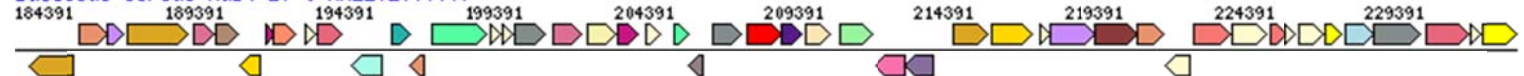
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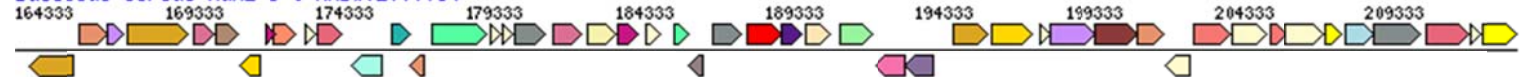
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Bacillus cereus HuB4-10 : AHEE01000007



Bacillus cereus HuA2-3 : AHDW01000034



Bacillus cereus VD148 : AHFF01000025



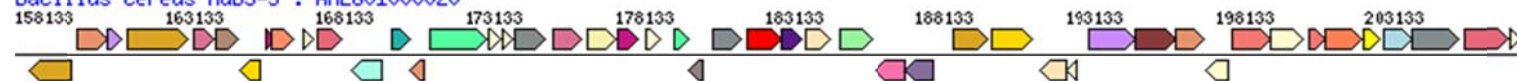
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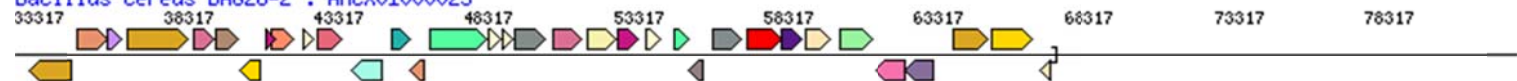
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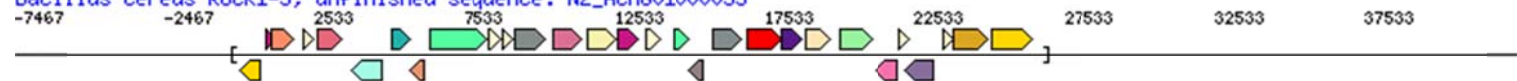
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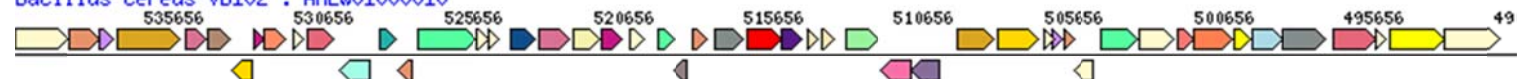
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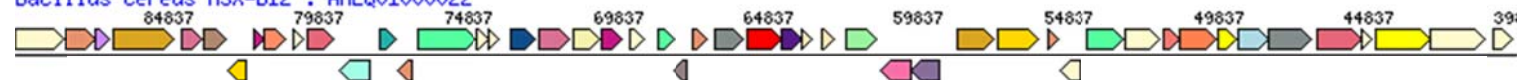
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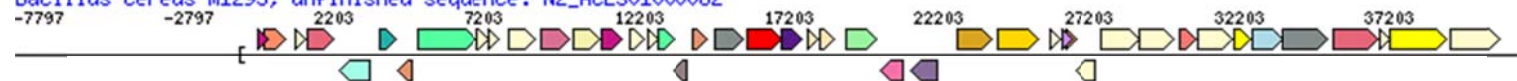
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Bacillus cereus MSX-D12 : AHEQ01000022



Bacillus cereus m1293, unfinished sequence: NZ_ACLS01000062



Bacillus cereus AND1407 : AHCM01000013



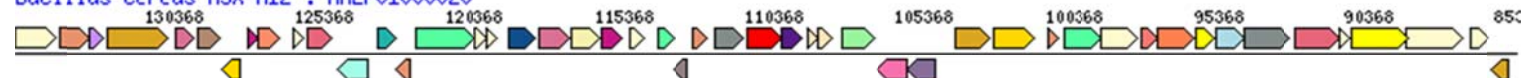
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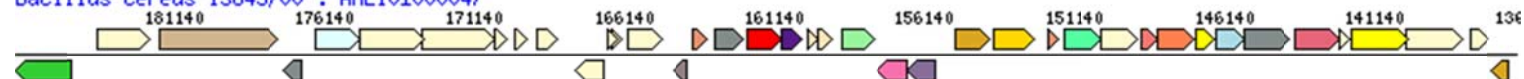
Bacillus thuringiensis serovar tochiensis BGSC 4Y1, unfinished sequence: NZ_ACMY01000057



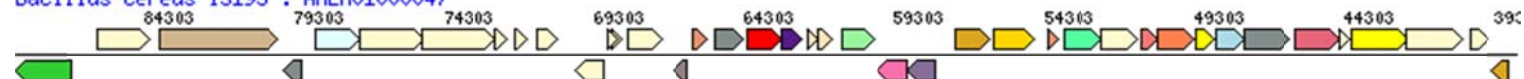
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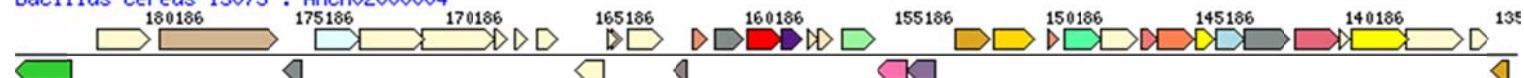
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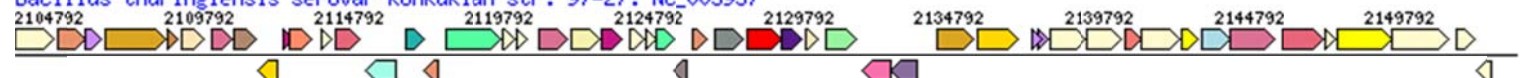
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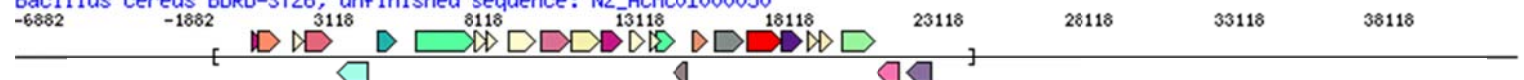
Bacillus cereus IS075 : AHCH02000004



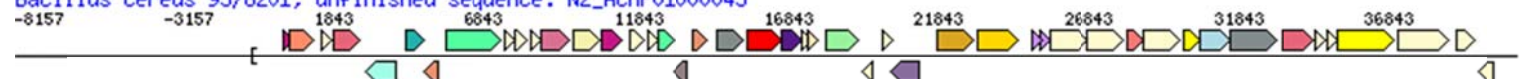
Bacillus thuringiensis serovar konkukian str. 97-27: NC_005957



Bacillus cereus BDRD-ST26, unfinished sequence: NZ_ACMC01000050



Bacillus cereus 95/8201, unfinished sequence: NZ_ACMF01000045



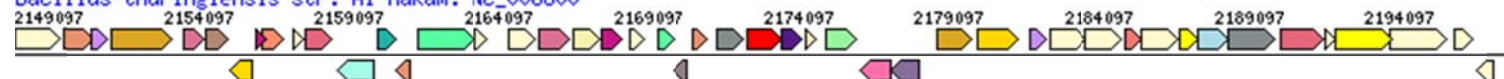
Bacillus thuringiensis serovar monterrey BGSC 4AJ1, unfinished sequence: NZ_ACNE01000046



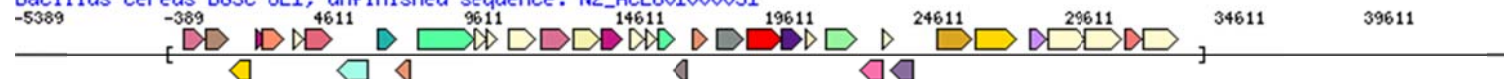
Bacillus cereus ISP3191 : AHEK01000015



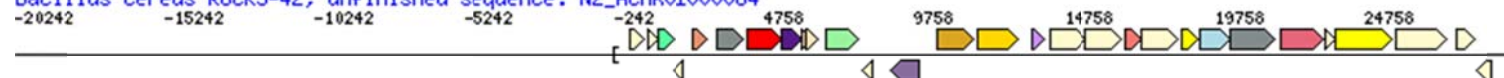
Bacillus thuringiensis str. Al Hakam: NC_008600



Bacillus cereus BGSC 6E1, unfinished sequence: NZ_ACLU01000051



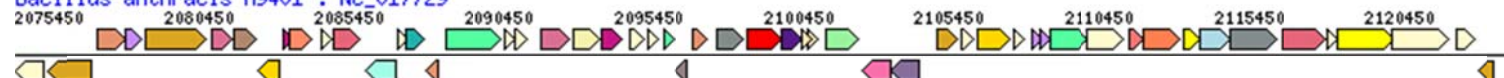
Bacillus cereus Rock3-42, unfinished sequence: NZ_ACMK01000064



Bacillus thuringiensis serovar pulsiensis BGSC 4CC1, unfinished sequence: NZ_ACNJ01000044



Bacillus anthracis H9401 : NC_017729



Bacillus anthracis str. A2012, unfinished sequence: NZ_AAAC02000001



Bacillus thuringiensis serovar andalousiensis BGSC 4AW1, unfinished sequence: NZ_ACNG01000061

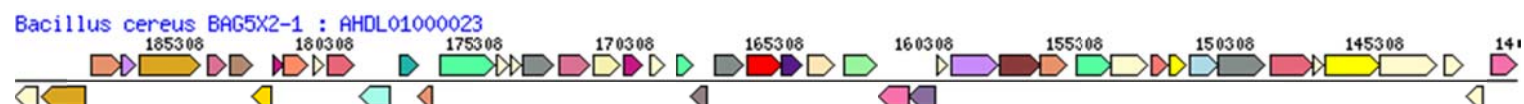


Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1, unfinished sequence: NZ_ACNH01000040



Bacillus cereus RCH_BC3 (Abyss contigs Sep '10) : bcer1768_2129C_15225_56

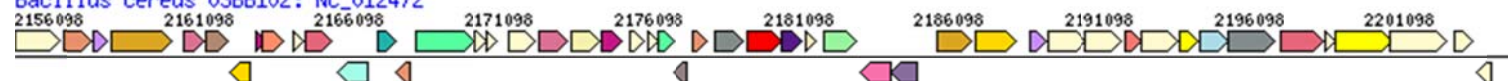




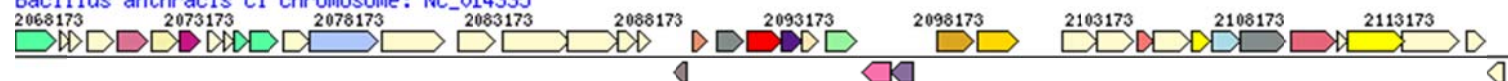
Bacillus cereus 03BB108, unfinished sequence: NZ_ABDM01000021



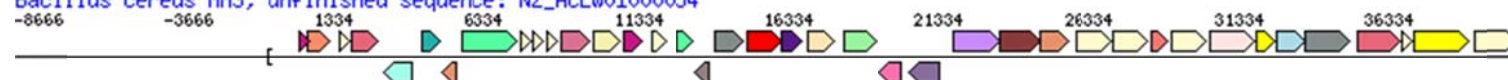
Bacillus cereus 03BB102: NC_012472



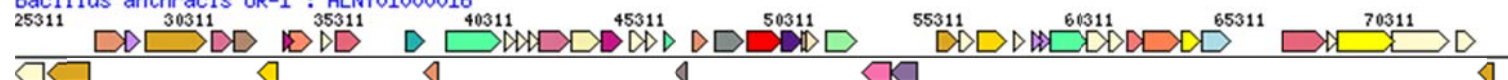
Bacillus anthracis CI chromosome: NC_014335



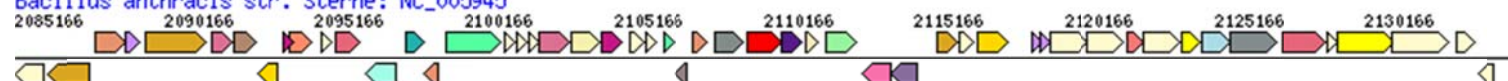
Bacillus cereus MM3, unfinished sequence: NZ_ACLW01000054



Bacillus anthracis UR-1 : ALNY01000016



Bacillus anthracis str. Sterne: NC_005945



Bacillus anthracis Tsiankovskii-I, unfinished sequence: NZ_ABDN01000002

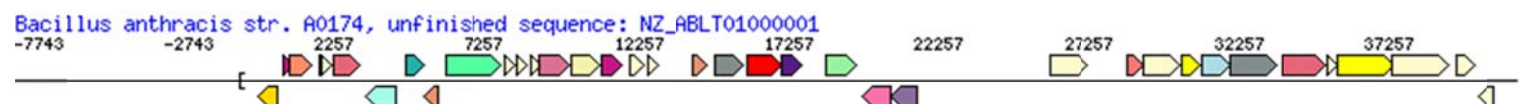


Bacillus anthracis str. A0193, unfinished sequence: NZ_ABKF01000011

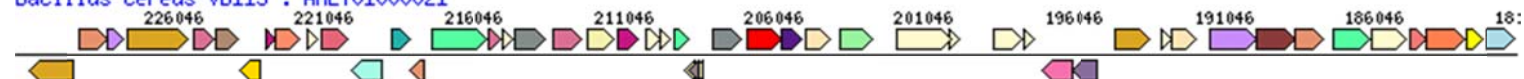


Bacillus anthracis str. A0442, unfinished sequence: NZ_ABKG01000002

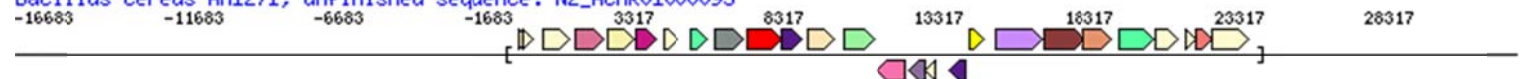




Bacillus cereus VD115 : AHEY01000021



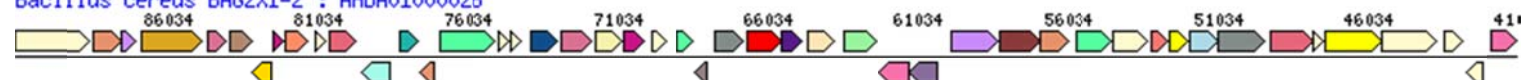
Bacillus cereus AH1271, unfinished sequence: NZ_ACMR01000093



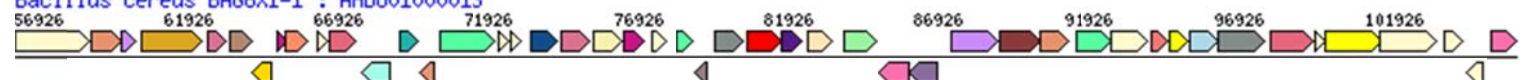
Bacillus cereus R309803, unfinished sequence: NZ_ACLY01000040



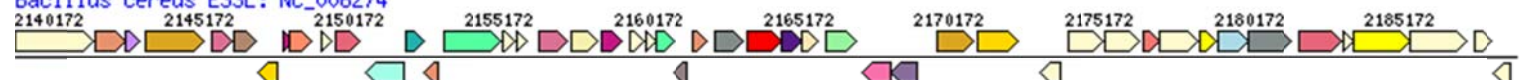
Bacillus cereus BAG2X1-2 : AHDA01000026



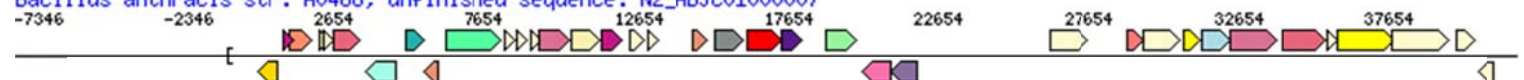
Bacillus cereus BAG6X1-1 : AHDO01000013



Bacillus cereus E33L: NC_006274



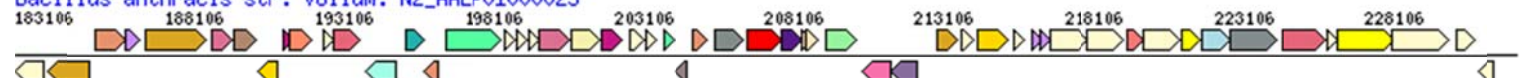
Bacillus anthracis str. A0488, unfinished sequence: NZ_ABJC01000007



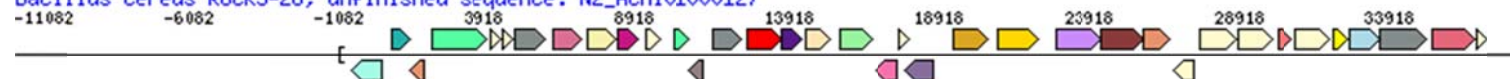
Bacillus anthracis str. CDC 684: NC_012581



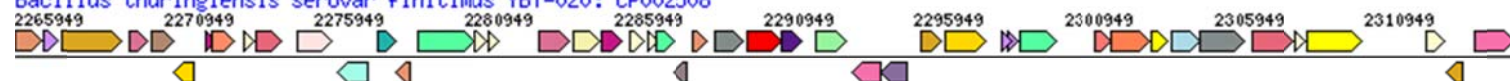
Bacillus anthracis str. Vollum: NZ_AAEP01000025



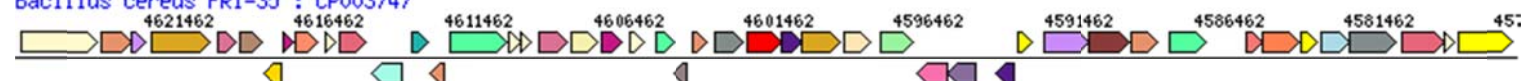
Bacillus cereus Rock3-28, unfinished sequence: NZ_ACMI01000127



Bacillus thuringiensis serovar finitimus YBT-020: CP002508



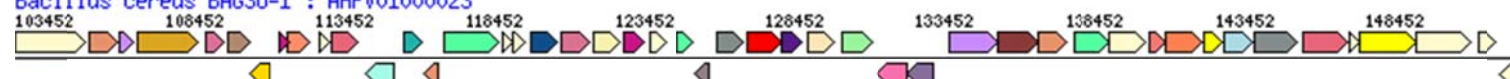
Bacillus cereus FRI-35 : CP003747



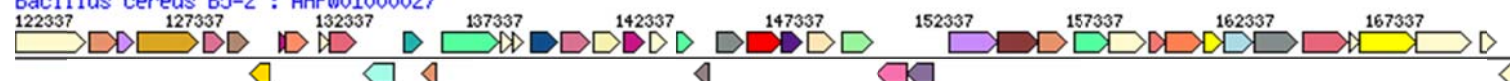
Bacillus cereus BAG20-3 : AHFY01000026



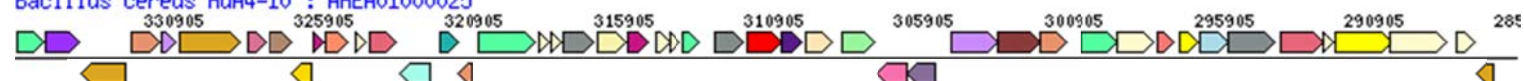
Bacillus cereus BAG30-1 : AHFV01000023



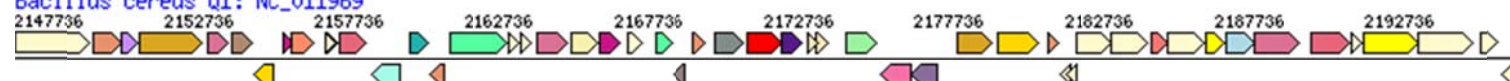
Bacillus cereus B5-2 : AHFW01000027



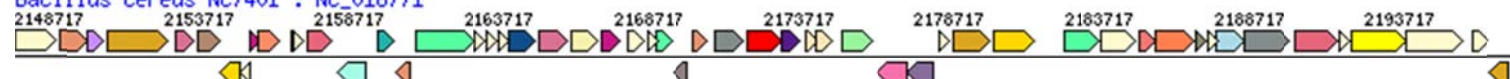
Bacillus cereus HuA4-10 : AHEA01000025



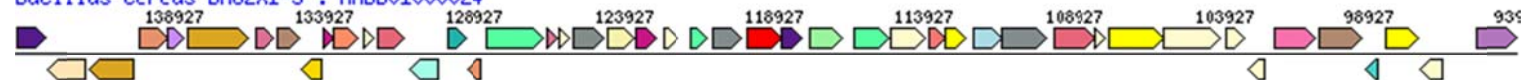
Bacillus cereus Q1: NC_011969



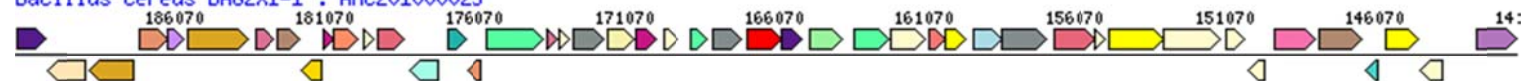
Bacillus cereus NC7401 : NC_016771



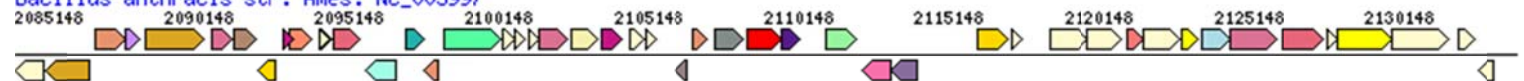
Bacillus cereus BAG2X1-3 : AHDB01000024



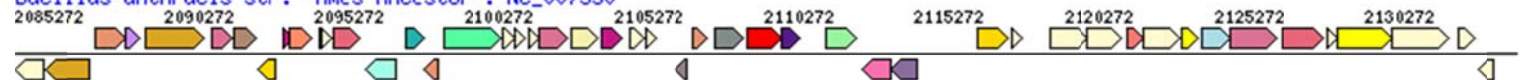
Bacillus cereus BAG2X1-1 : AHCZ01000025



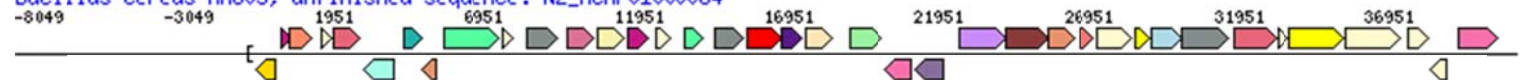
Bacillus anthracis str. Ames: NC_003997



Bacillus anthracis str. 'Ames Ancestor': NC_007530



Bacillus cereus AH603, unfinished sequence: NZ_ACMP01000064



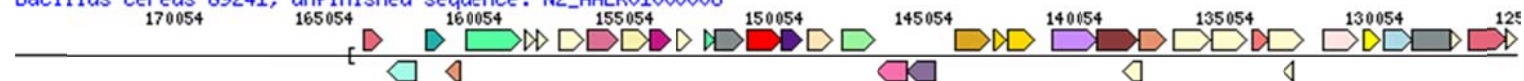
Bacillus cereus BAG6X1-2 : AHDP01000020



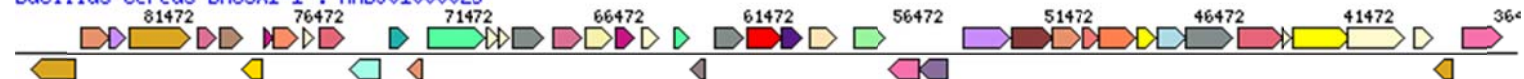
Bacillus cereus VD107 : AHGX01000014



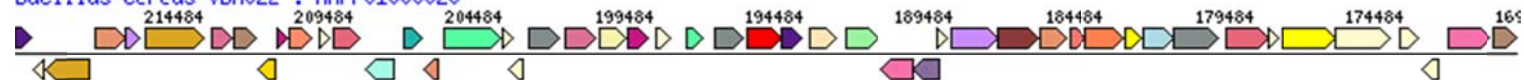
Bacillus cereus G9241, unfinished sequence: NZ_AAEK01000006



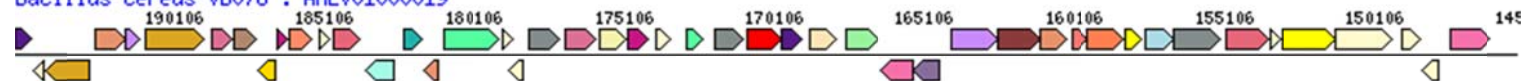
Bacillus cereus BAG5X1-1 : AHDJ01000028



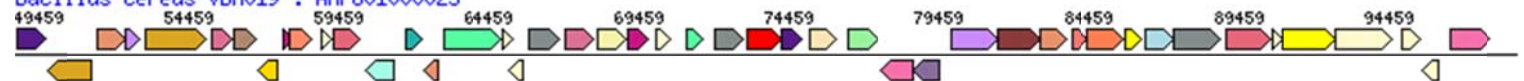
Bacillus cereus VDM022 : AHFP01000020



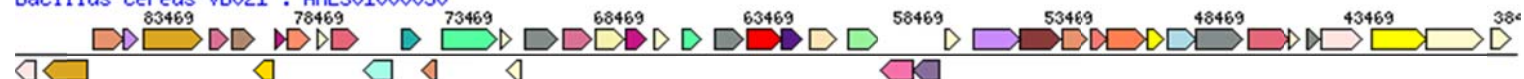
Bacillus cereus VDM078 : AHEV01000019



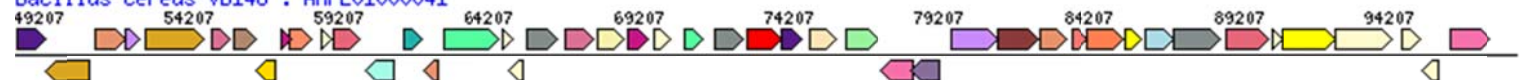
Bacillus cereus VDM019 : AHF001000023



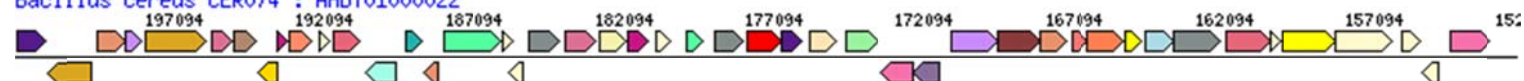
Bacillus cereus VDM021 : AHES01000030



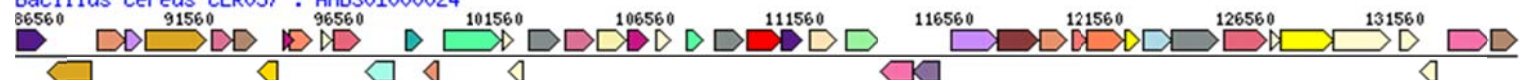
Bacillus cereus VDM146 : AHFE01000041



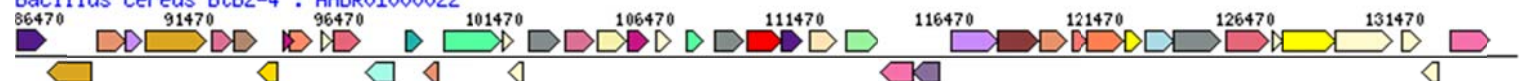
Bacillus cereus CER074 : AHDT01000022



Bacillus cereus CER057 : AHDS01000024



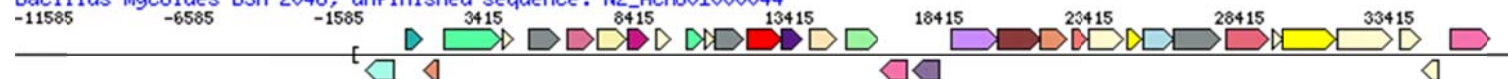
Bacillus cereus BtB2-4 : AHDR01000022



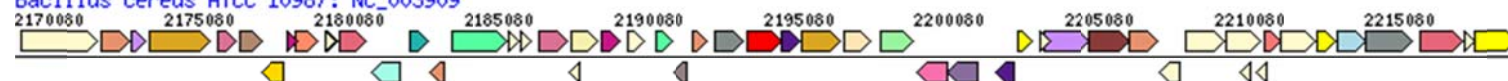
Bacillus cereus BDRD-ST196, unfinished sequence: NZ_ACMD01000078



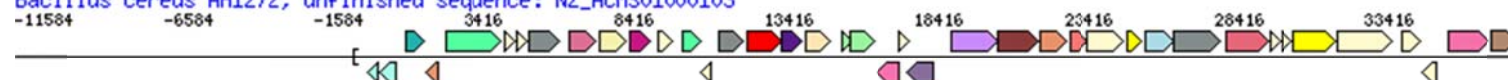
Bacillus mycoides DSM 2048, unfinished sequence: NZ_ACMU01000044



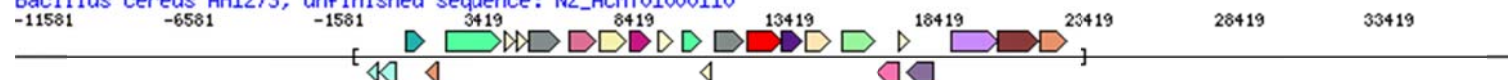
Bacillus cereus ATCC 10987: NC_003909



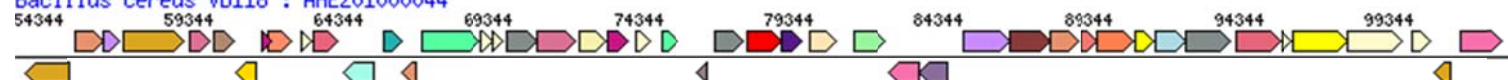
Bacillus cereus AH1272, unfinished sequence: NZ_ACMS01000103



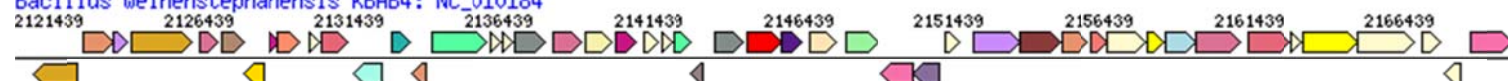
Bacillus cereus AH1273, unfinished sequence: NZ_ACMT01000110



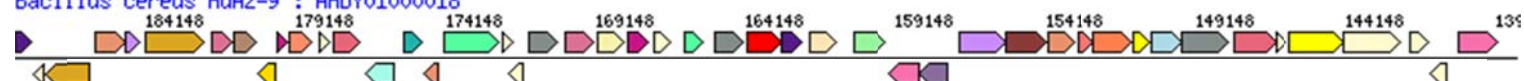
Bacillus cereus VD118 : AHEZ01000044



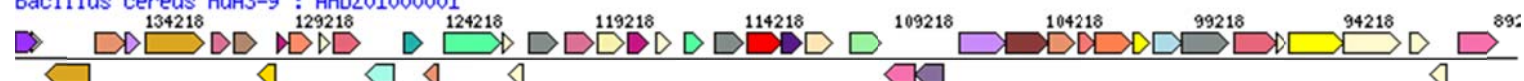
Bacillus weihenstephanensis KBAB4: NC_010184



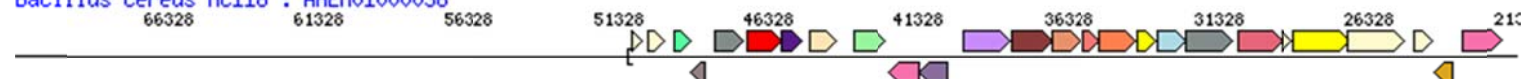
Bacillus cereus HuA2-9 : AHDY01000018

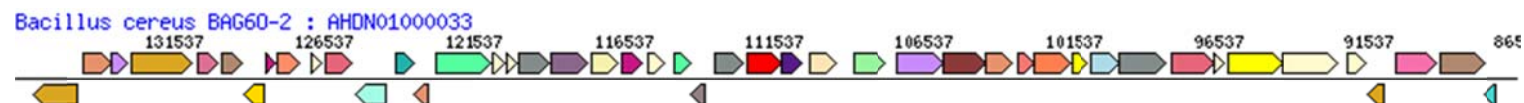


Bacillus cereus HuA3-9 : AHDZ01000001

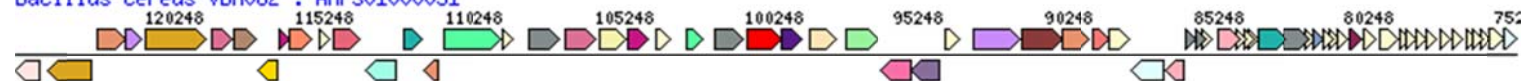


Bacillus cereus MC118 : AHEM01000036

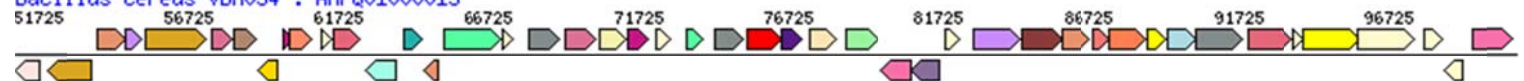




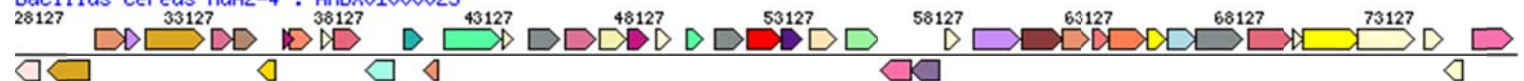
Bacillus cereus VDM062 : AHFS01000031



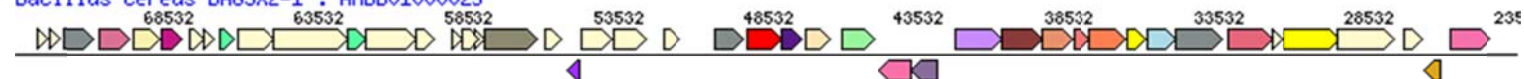
Bacillus cereus VDM034 : AHFQ01000013



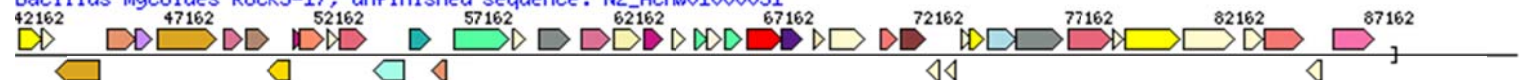
Bacillus cereus HuA2-4 : AHDX01000025



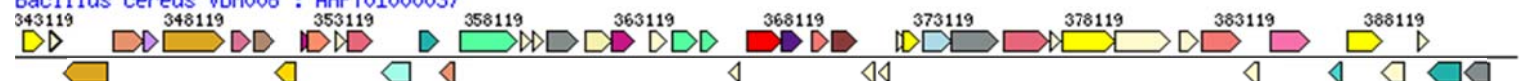
Bacillus cereus BAG3X2-1 : AHDD01000023



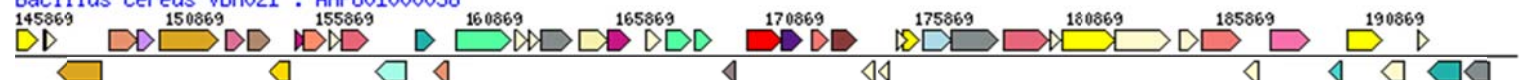
Bacillus mycoides Rock3-17, unfinished sequence: NZ_ACMW01000051



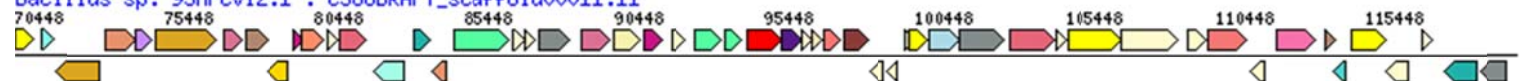
Bacillus cereus VDM006 : AHFT01000037



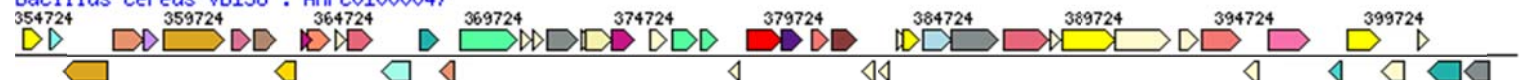
Bacillus cereus VDM021 : AHFU01000038



Bacillus sp. 95MFCvi2.1 : C568DRAFT_scaffold00011.11



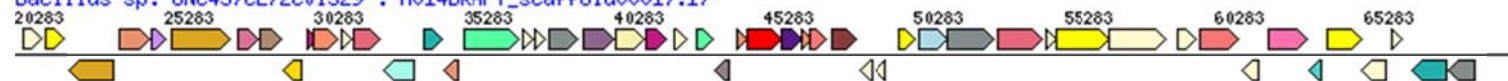
Bacillus cereus VD136 : AHFC01000047



Bacillus pseudomycoloides DSM 12442, unfinished sequence: NZ_ACMX01000036



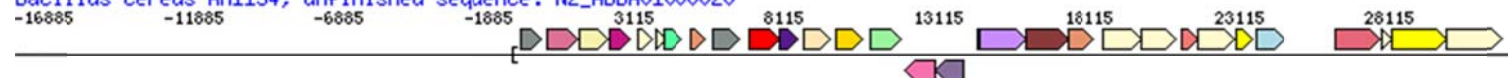
Bacillus sp. UNC437CL72CviS29 : M014DRAFT_scaffold00017.17



Bacillus cereus Rock3-44, unfinished sequence: NZ_ACML01000120



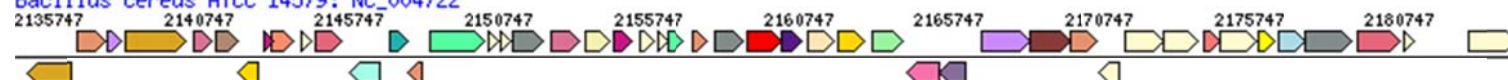
Bacillus cereus AH1134, unfinished sequence: NZ_ABD01000020



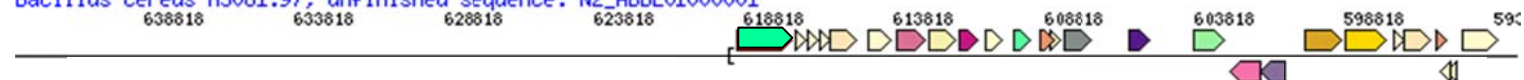
Bacillus mycoloides Rock1-4, unfinished sequence: NZ_ACMV01000133



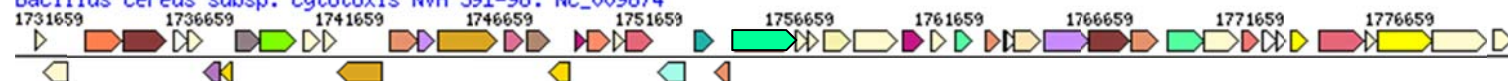
Bacillus cereus ATCC 14579: NC_004722



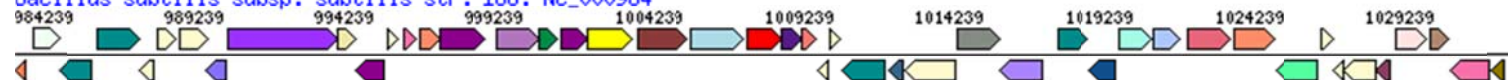
Bacillus cereus H3081.97, unfinished sequence: NZ_ABDL01000001



Bacillus cereus subsp. *cytotoxicus* NVH 391-98: NC_009674



Bacillus subtilis subsp. *subtilis* str. 168: NC_000964



Bacillus cereus VD107	VI	AHEX01000014	145386bp	D	IIM_01397	hypothetical protein	90.30%	372aa	1.9e-193	681
Bacillus cereus BAG5X1-1	VI	AHDJ01000028	167843bp	D	IEE_03023	hypothetical protein	91.10%	372aa	2.5e-193	680
Bacillus cereus VD118	VI	AHEZ01000044	257274bp	D	IIQ_01180	two-component sensor protein yhcY	90.90%	372aa	1.2e-192	678
Bacillus cereus MC118	VI	AHEM01000036	50635bp	D	I11_03385	two-component sensor protein yhcY	90.60%	372aa	2.0e-192	677
Bacillus cereus BAG6O-2	VI	AHDN01000033	230347bp	D	IEM_03141	hypothetical protein	90.90%	372aa	2.0e-192	677
Bacillus cereus MC67	VI	AHEN01000003	229617bp	D	I13_00196	hypothetical protein	90.60%	372aa	2.0e-192	677
Bacillus cereus BAG1X1-3	VI	AHCS01000023	1262248bp	D	ICG_03309	hypothetical protein	90.60%	372aa	2.8e-192	677
Bacillus cereus VDM053	VI	AHFR01000039	621715bp	D	IKQ_01731	two-component sensor protein yhcY	90.60%	372aa	2.6e-192	677
Bacillus cereus BAG10-1	VI	AHCN01000021	162560bp	D	IC7_01508	two-component sensor protein yhcY	90.60%	372aa	2.6e-192	677
Bacillus cereus BAG3X2-1	VI	AHDD01000023	113935bp	D	IJE3_03212	hypothetical protein	90.10%	372aa	1.4e-191	674
Bacillus mycoides Rock3-17	I	NZ_ACMW01000051	87918bp	D	bmyco0003_19320	Two-component sensor protein yhcY	84.80%	374aa	6.3e-184	649
Bacillus cereus VDM006	I	AHFT01000037	802420bp	D	KOW_00626	two-component sensor protein yhcY	84.70%	372aa	2.9e-183	647
Bacillus cereus VDM021	I	AHFU01000038	209010bp	D	KOY_03298	two-component sensor protein yhcY	84.70%	372aa	2.9e-183	647
Bacillus cereus VD136	I	AHFC01000047	594013bp	D	I1W_01264	two-component sensor protein yhcY	84.40%	372aa	8.3e-183	645
Bacillus pseudomycoides DSM 12442	I	NZ_ACMX01000036	125315bp	D	bpmyx0001_20100	Two-component sensor protein yhcY	84.40%	372aa	2.0e-182	644
Bacillus cereus Rock3-44	I	NZ_ACMLO1000120	22469bp	D	bcere0022_18280	Two-component sensor protein yhcY	83.60%	372aa	6.5e-181	639
Bacillus mycoides Rock1-4	I	NZ_ACMV01000133	85498bp	D	bmyco0002_19200	Two-component sensor protein yhcY	84.30%	313aa	4.8e-152	543

All data, except data from the second column, came from Integrated Microbial Genomes data base (Markowitz et al., 2012); homologs for *casKR* genes were first determined through BLASTp hits between *casKR* genes from ATCC14579 genome (bc2216-17) and genes in all other genomes, and orthologs were computed as bidirectional best hits between genomes; percent identity, length of sequence, E-value and bit score are displayed for each ortholog. The C2S was absent on NVH391-98 genome (phylogenetic group VII)

⁽¹⁾ affiliation to phylogenetic groups using *panC* gene sequence, as previously described (Guinebretiere et al., 2010); ⁽²⁾ Genome completion, D : draft, F : finished; ⁽³⁾ percent identity for translated proteins; ⁽⁴⁾ NA : not applicable

Bacillus cereus VD107	VI	AHEX01000014	145386bp	D	IIM_01398	hypothetical protein	91.90%	211aa	3.1e-103	380
Bacillus cereus BAG5X1-1	VI	AHDJ01000028	167843bp	D	IEE_03022	hypothetical protein	92.40%	211aa	1.6e-104	384
Bacillus cereus VD118	VI	AHEZ01000044	257274bp	D	IIQ_01181	two-component system response regulator yhcZ	91.90%	211aa	1.5e-104	384
Bacillus cereus MC118	VI	AHEM01000036	50635bp	D	I11_03384	two-component system response regulator yhcZ	93.40%	211aa	8.0e-106	389
Bacillus cereus BAG6O-2	VI	AHDN01000033	230347bp	D	IEM_03140	hypothetical protein	91.90%	211aa	1.5e-104	384
Bacillus cereus MC67	VI	AHEN01000003	229617bp	D	I13_00195	hypothetical protein	93.40%	211aa	8.0e-106	389
Bacillus cereus BAG1X1-3	VI	AHCS01000023	1262248bp	D	ICG_03308	hypothetical protein	92.90%	211aa	8.6e-106	389
Bacillus cereus VDM053	VI	AHFR01000039	621715bp	D	IKQ_01732	two-component system response regulator yhcZ	91.90%	211aa	8.8e-105	385
Bacillus cereus BAG1O-1	VI	AHCN01000021	162560bp	D	IC7_01509	two-component system response regulator yhcZ	92.90%	211aa	8.0e-106	389
Bacillus cereus BAG3X2-1	VI	AHDD01000023	113935bp	D	IE3_03211	hypothetical protein	92.90%	211aa	6.6e-106	389
Bacillus mycoides Rock3-17	I	NZ_ACMW01000051	87918bp	D	bmyco0003_19330	DNA-binding response regulator	90.40%	211aa	6.5e-101	372
Bacillus cereus VDM006	I	AHFT01000037	802420bp	D	KOW_00627	two-component system response regulator yhcZ	89.90%	211aa	4.2e-99	366
Bacillus cereus VDM021	I	AHFU01000038	209010bp	D	KOY_03299	two-component system response regulator yhcZ	89.90%	211aa	4.2e-99	366
Bacillus cereus VD136	I	AHFC01000047	594013bp	D	I1W_01265	two-component system response regulator yhcZ	89.90%	211aa	4.2e-99	366
Bacillus pseudomycolides DSM 12442	I	NZ_ACMX01000036	125315bp	D	bpmyx0001_20110	DNA-binding response regulator	90.40%	211aa	6.5e-101	372
Bacillus cereus Rock3-44	I	NZ_ACMLO1000120	22469bp	D	bcere0022_18290	DNA-binding response regulator	89.50%	211aa	1.3e-98	365
Bacillus mycoides Rock1-4	I	NZ_ACMV01000133	85498bp	D	bmyco0002_19210	DNA-binding response regulator	90.40%	211aa	6.5e-101	372

All data, except data from the second column, came from Integrated Microbial Genomes data base (Markowitz et al., 2012); homologs for *casKR* genes were first determined through BLASTp hits between *casKR* genes from ATCC14579 genome (bc2216-17) and genes in all other genomes, and orthologs were computed as bidirectional best hits between genomes; percent identity, length of sequence, E-value and bit score are displayed for each ortholog. The C2S was absent on NVH391-98 genome (phylogenetic group VII)

⁽¹⁾ affiliation to phylogenetic groups using *panC* gene sequence, as previously described (Guinebreiere et al., 2010); ⁽²⁾ Genome completion, D : draft, F : finished; ⁽³⁾ percent identity for translated proteins; ⁽⁴⁾ NA : not applicable