Concentration of Ca2+(mg/L)
 0
 40
 80
 120
 160
 200

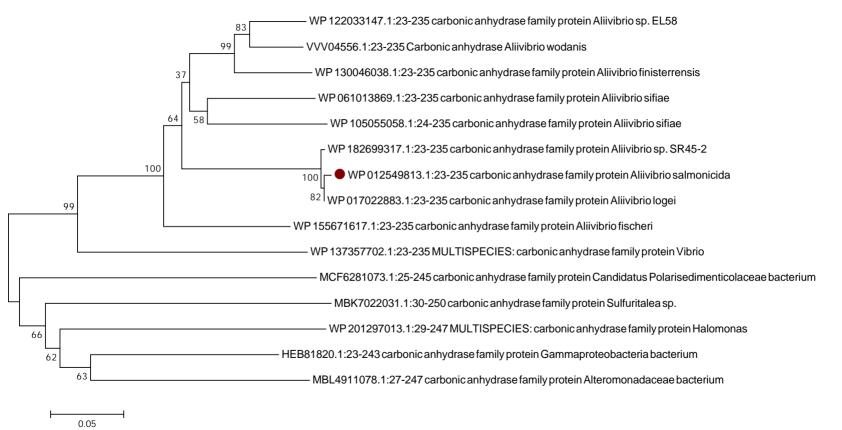
 OD630
 0.152
 0.158
 0.162
 0.149
 0.189
 0.144

 110
 120
 130
 140
 150

 0.126
 0.086
 0.065
 0.05
 0.085

bacterial strains 0 1 2 3 4 5 OD348(3min)-OD348(0min) 0.043 0.098 0.281 0.085 0.087 0.068

6 7 8 9 10 11 0.072 0.03 0.033 0.05 0.057 0.037



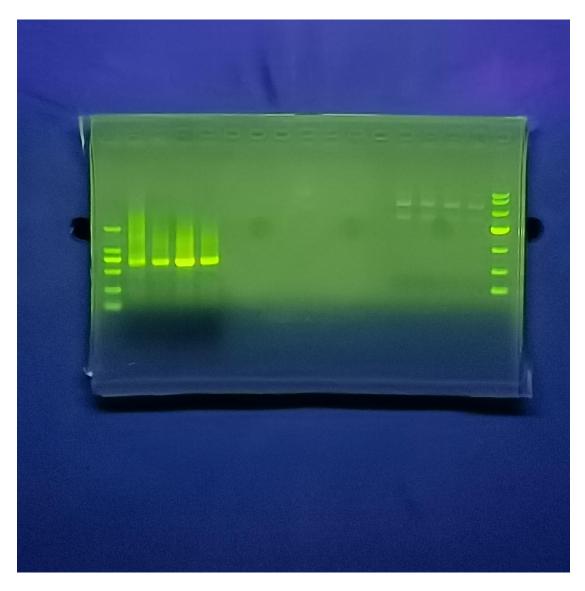


Fig. 2.3.1b Product electrophoresis results (35 circles)

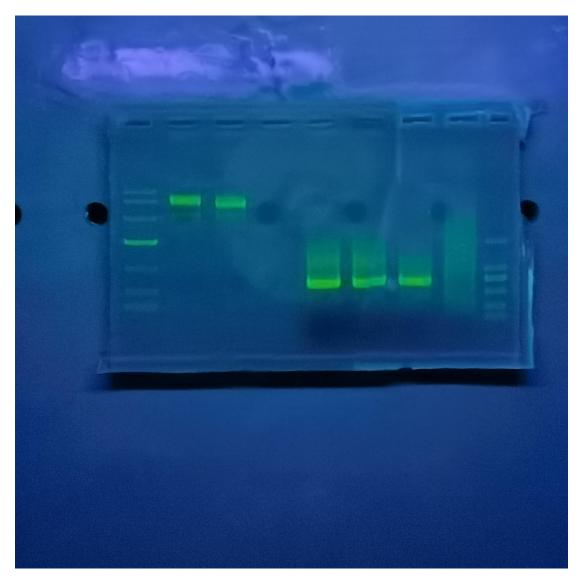


Fig. 2.3.1a Product electrophoresis results (45 circles)

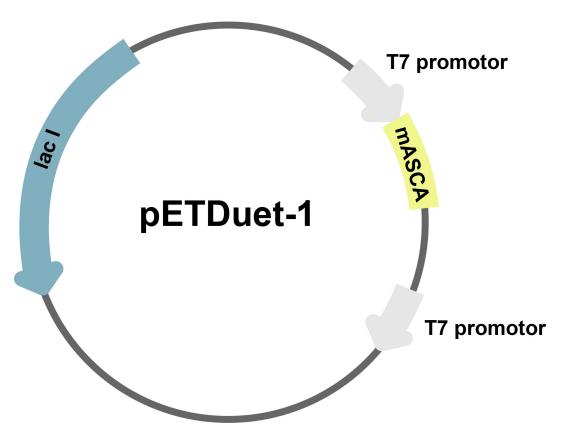


Fig.2.1.4 pETD-mASCA

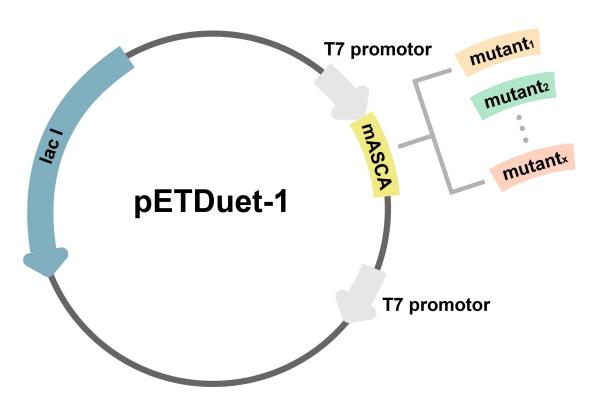


Fig. 2.3.1c Plasmids for mutant constructs

>mASCA

>WP_012549813.1:23-235 carbonic anhydrase family protein [Aliivibrio salmonicida] SEWSYSGETAPTNWHGTCQSGVNQSPIDITHAIESTLDPIIFNYSKAGKNVVNNGHTVQVN FDAKQSIQIEGKTFTLLQL

HFHAPSENLIEGHSFPLEMHLVHADKDGNLAVIGVMLKEGKPNSELTKIWAKMPQSGQVD LENQLDLTKLLPRDQAYYRF

NGSLTTPPCSEGVTWLVMKNPIEISSEQLAQFTALYNGNNCPTQAINARPILK

>WP_017022883.1:23-235 carbonic anhydrase family protein [Aliivibrio logei]

SEWSYSGETAPTNWHGTCQSGVNQSPIDITHAIESTLDPIIFNYSKAGKNVVNNGHTVQVN FDAKQSIQIEGKTFTLLQL

HFHAPSENLIEGHSFPLEMHLVHADKDGNLAVIGVMLKEGKPNSELTKIWAKMPQSGQVD LENQLDLTKLLPRDQAYYRF

NGSLTTPPCSEGVTWLVMKNPIEISSEQLAQFTALYNGNNRPTQAINARPILK

>WP_182699317.1:23-235 carbonic anhydrase family protein [Aliivibrio sp. SR45-2]

SEWSYSGETAPTNWHGTCQSGVNQSPIDITHAIESTLDPIIFNYSKAGKNVVNNGHTVQVNFDVKQSIQIEGKTFTLLQL

HFHAPSENLIEGHSFPLEMHLVHADKDGNLAVIGVMLKEGKPNSELTKIWAKMPQSGQVD LENQLDLTKLLPRDQAYYRF

NGSLTTPPCSEGVTWLVMKNPIEISSEQLAQFTALYNGNNRPTQAINARPILK

>WP_122033147.1:23-235 carbonic anhydrase family protein [Aliivibrio sp. EL58]

SEWSYAGETAPANWHGNCQTGVNQSPIDITNAIESTLDPITFNYAQAGKNIVNNGHTVQVNFDGKQSIQVEGKTFSLLQL

HFHAPSENLIAGHSYPLEMHLVHANKDGNLAVIGVMFKEGKENTELAKVWAQMPKSGDV KLDSKLTLTKLLPGDQAYYRF

NGSLTTPPCTEGVTWLVMKNPITISAEQLTQFESLYQGNNRPVQAINARPVLK

>WP 061013869.1:23-235 carbonic anhydrase family protein [Aliivibrio sifiae]

SEWSYSGETAPAHWHGTCQSGVNQSPIDITGAVESELKPITFNYTQAGKNIVNNGHTVQVN FDGKQSIKIEGKTFNLLQL

HFHAPSENLIAGHSFPLEMHLVHSDKEGNLAVIGVMFKEGKANTELAKVWKEMPKSGEVD LTNKLDLVNLLPADQAYYRF

NGSLTTPPCSEGVTWFVMKNPISISSQQLTQFKALYDGNNRPTQAINARPVLQ

>VVV04556.1:23-235 Carbonic anhydrase [Aliivibrio wodanis]

SEWSYAGETAPANWHGTCQTGVNQSPIDITNAIESTLEPITFNYAQAGKNIVNNGHTVQVNFDGKQSIQVEGTTFNLLQL

HFHAPSENLIAGHSYPLEMHLVHADKDGNLAVIGVMFKEGKTNTELAKIWAQMPKSGDVN LDSKLMLTRLLPSNQAYYRF

NGSLTTPPCTEGVTWFVMKNPITISAEQLIQFKSLYQGNNRPVQAINARPILK

>WP_130046038.1:23-235 carbonic anhydrase family protein [Aliivibrio finisterrensis] SEWSYAGETAPANWHGTCQSGLNQSPIDITNAIESTLKPITFNYAQAGKNIVNNGHTVQVN FDGKQSIQVEGKTFNLLQL

HFHAPSENLIAGHSYPLEMHLVHADKDGNLAVVGVMFKEGKANPELAKIWAQMPKSGDV KLDNKLRLIDLLPSDQAYYRF

NGSLTTPPCTEGVTWLVMKKPITISTEQLTQFRTLYKGNNRPVQSINARPVLK

>WP_105055058.1:24-235 carbonic anhydrase family protein [Aliivibrio sifiae]

EWSYSGKTAPEHWHGTCQTGVNQSPIDITGAIESTLSPIVFNYAQAGKNIVNNGHTVQVNF

DGKQSIEIEGKIFNLLQLH

FHTPSENLIAGHSFPLEMHLVHSDKNGNLAVVGVMFKEGKTNLELAKIWSKMPKSGEVDL DSKINLTNLLPKEQAYYRFN

GSLTTPPCTEGVTWFVMKNPITISSQQLAQFKSLYEGNNRPVQTINARPVLK

>WP 155671617.1:23-235 carbonic anhydrase family protein [Aliivibrio fischeri]

SEWGYTGDTGPNHWHGVCQTGVNQSPIDITNAIESELEPITFNYGQAGKNIVNNGHTVQVN IKSPQSIQIEGKTFSLLQL

HFHAPSENLIAGHSYPLEMHLVHADKDGNLAVVGVMFKEGKANPELAKIWSQMPESGEIT LDKKLTLTNLLPNDQAYYRF

NGSLTTPPCSEGVTWLVMKNPIEISSEQLSQFKELYNGNNRPTQAINARPILK

>WP_137357702.1:23-235 MULTISPECIES: carbonic anhydrase family protein [Vibrio] SEWGYSGKQGPEHWHGICQTGKNQSPIDISKGIESELEPIKFNYDVSGENVVNNGHTIQVN FNGDQSIEVEGKSYSLLQF

HFHAPSENLIKGHSYPLEVHLVHADENKNLAVVGVMFEEGATNPELEKVWDVMPANKGQ QDLQHSINLTGLLPKQSDYFR

FNGSLTTPPCSEGVTWLVMKNPITISKAQLEKFRTLYSGNNRPTQDVNARPVL

>HEB81820.1:23-243 carbonic anhydrase family protein [Gammaproteobacteria bacterium]

SHWGYSGHEGPENWAKLSADNFACAGRNQSPINLTGFIEAELSPINFNYQPGGREILNNG HTVQINYQPGSSMTIDGKVF

KLLQFHFHAPSENNINGKSFPLEAHLVHADKDGNLAVVAVMFEEGKANSGLSKAWQKMP EHEGDKNALQTTVSVDDILPA

DRDYYRFNGSLTTPPCTEGVRWLVMKQPVSASAEQLAKFRHALHGPNNRPLQAVNARPV LK

>MBL4911078.1:27-247 carbonic anhydrase family protein [Alteromonadaceae bacterium]

ADWGYSGHQGPENWAKLSGDNLSCDGKNQSPINLTGFIEADLTPLIFDYQQGGEQVINNG HTVQVNYQQGSSITIDGKHF

NLLQFHFHAPSENHINGHSYPLEAHLVHADKNGNLAVVAVMFKEGKSNALLAKAWQSMP KHAGEQHKLTSKVNVDKLLPK

NRDYYRFNGSLTTPPCSEGVRWLVMKDAVSASKTQIENFESALHEANNRPIQPLNARSVM Q

>MBK7022031.1:30-250 carbonic anhydrase family protein [Sulfuritalea sp.]

AHWGYSGDVGPDRWVKLKPEFSACAGKNQSPIDVSGLIEAQLPPVKFDYKQGGSEVVNN GHAIQVNYDAGSGIEVDGTRF

DLKQFHFHSPSENRINGKSFPLEAHLVHADKDGNLAVVSVMFDEGKENSAVGAAWGQMP KSAGGKNALPNKVAATGILPA

DRDYYRYNGSLTTPPCSEGVRWIVMKKPLTVSKQQIETFQKTLGFANNRPLQAVNARPILK >MCF6281073.1:25-245 carbonic anhydrase family protein [Candidatus Polarisedimenticolaceae bacterium]

AHWGYSGSTGPDKWGKIAPSYKICGTGRNQSPIDITTGIRAALEPITFNYEAGTTAILNNGH TIQVNYEAGNSIVLNGHE

YELKQFHFHAPSENHIDGKSYPLEAHFVHADKDGHLAVVGVMLAESGSNAVIGKLWEHMP ANAGDKNELPWKIDGELLLP

NDRSYYRFNGSLTTPPCSEGVTWLVMKTPVAISSAQLEAFTTVMGEDNNRPLQAINARPIL >WP_201297013.1:29-247 MULTISPECIES: carbonic anhydrase family protein [Halomonas]

WSYSGETGPENWAQLTPEYGACAGSNQSPIDLTGFIDAELEPIDFHYENGGAEILNNGHTV QINVHPGDTITVDGIEFEL

KQFHFHVPSENLIHGESFPMEGHLVHADEDGNLAVVAVMVTEGEANEALARAWAQMPEE GETLALTSDISPLGILPADRD

YYRFNGSLTTPPCTEGVRWLVLKQPITASQEQIDQFLAAIDDHHNNRPVQPVNARPVLQ