

M. capsulatus mmoX sequence

```
10          30          50
.           .           .
ATGGCACTTAGCACCGCAACCAAGGCCGCGACGGACGCGCTGGCTGCCAATCGGGCACCC
MetAlaLeuSerThrAlaThrLysAlaAlaThrAspAlaLeuAlaAlaAsnArgAlaPro
1

70          90          110
.           .           .
ACCAGCGTGAATGCACAGGAAGTGCACCGTTGGCTCCAGAGCTTCAACTGGGATTTCAAG
ThrSerValAsnAlaGlnGluValHisArgTrpLeuGlnSerPheAsnTrpAspPheLys
21

130         150         170
.           .           .
AACCAACCGGACCAAGTACGCCACCAAGTACAAGATGGCGAACGAGACCAAGGAACAGTTC
AsnAsnArgThrLysTyrAlaThrLysTyrLysMetAlaAsnGluThrLysGluGlnPhe
41

190         210         230
.           .           .
AAGCTGATCGCCAAGGAATATGCGCGCATGGAGGCAGTCAAGGACGAAAGGCAGTTCGGT
LysLeuIleAlaLysGluTyrAlaArgMetGluAlaValLysAspGluArgGlnPheGly
61

250         270         290
.           .           .
AGCCTGCAGGATGCGCTGACCCGCCTCAACGCCGGTGTTCGCGTTCATCCGAAGTGGAAAC
SerLeuGlnAspAlaLeuThrArgLeuAsnAlaGlyValArgValHisProLysTrpAsn
81

310         330         350
.           .           .
GAGACCATGAAAGTGGTTTCGAACTTCCTGGAAGTGGGCGAATACAACGCCATCGCCGCT
GluThrMetLysValValSerAsnPheLeuGluValGlyGluTyrAsnAlaIleAlaAla
101

370         390         410
.           .           .
ACCGGGATGCTGTGGGATTCGCCCCAGGCGGGAACAGAAGAACGGCTATCTGGCCCAG
ThrGlyMetLeuTrpAspSerAlaGlnAlaAlaGluGlnLysAsnGlyTyrLeuAlaGln
121

430         450         470
.           .           .
GTGTTGGATGAAATCCGCCACACCCACCAGTGTGCCTACGTCAACTACTACTTCGCGAAG
ValLeuAspGluIleArgHisThrHisGlnCysAlaTyrValAsnTyrTyrPheAlaLys
141
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Figure 1-5

1450 1470 1490
GTGATCGCCGAACTGCACGGGCTGCGCAGTGATGGCAAGACCCTGATCGCCAGCCGCAT
ValIleAlaGluLeuHisGlyLeuArgSerAspGlyLysThrLeuIleAlaGlnProHis
481

1510 1530 1550
GTCCGTGGCGACAAGCTGTGGACGTTGGACGATATCAAACGCCTGAACTGCGTCTTCAAG
ValArgGlyAspLysLeuTrpThrLeuAspAspIleLysArgLeuAsnCysValPheLys
501

1570
AACCCGGTGAAGGCATTCAATTGA
AsnProValLysAlaPheAsnEnd
521

Figure 1-5

M. capsulatus mmoY sequence

```
10          30          50
.           .           .
ATGAGCATGTTAGGAGAAAAGACGCCGCGGTCTGACCGATCCGGAAATGGCGGCCGTCATT
MetSerMetLeuGlyGluArgArgArgGlyLeuThrAspProGluMetAlaAlaValIle
1

70          90          110
.           .           .
TTGAAGGCGCTTCCTGAAGCTCCGCTGGACGGCAACAACAAGATGGGTTATTTTCGTCACC
LeuLysAlaLeuProGluAlaProLeuAspGlyAsnAsnLysMetGlyTyrPheValThr
21

130         150         170
.           .           .
CCCCGCTGGAAACGCTTGACGGAATATGAAGCCCTGACCGTTTATGCGCAGCCCAACGCC
ProArgTrpLysArgLeuThrGluTyrGluAlaLeuThrValTyrAlaGlnProAsnAla
41

190         210         230
.           .           .
GACTGGATCGCCGGCGGCCTGGACTGGGGCGACTGGACCCAGAAATTCCACGGCGGCCGC
AspTrpIleAlaGlyGlyLeuAspTrpGlyAspTrpThrGlnLysPheHisGlyGlyArg
61

250         270         290
.           .           .
CCTTCCTGGGGCAACGAGACCACGGAGCTGCGCACCGTCGACTGGTTCAAGCACCGTGAC
ProSerTrpGlyAsnGluThrThrGluLeuArgThrValAspTrpPheLysHisArgAsp
81

310         330         350
.           .           .
CCGCTCCGCCGTTGGCATGCGCCGTACGTCAAGGACAAGGCCGAGGAATGGCGCTACACC
ProLeuArgArgTrpHisAlaProTyrValLysAspLysAlaGluGluTrpArgTyrThr
101

370         390         410
.           .           .
GACCGCTTCCTGCAGGGTTACTCCGCCGACGGTCAGATCCGGGCGATGAACCCGACCTGG
AspArgPheLeuGlnGlyTyrSerAlaAspGlyGlnIleArgAlaMetAsnProThrTrp
121

430         450         470
.           .           .
CGGGACGAGTTCATCAACCGGTATTGGGGCGCCTTCTGTTCACGAATACGGATTGTTC
ArgAspGluPheIleAsnArgTyrTrpGlyAlaPheLeuPheAsnGluTyrGlyLeuPhe
141
```

Figure 1-5

M. capsulatus mmoB sequence

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      10              30              50
      .             .             .
ATGAGCGTAAACAGCAACGCATACGACGCCGGCATCATGGGCCTGAAAGGCAAGGACTTC
MetSerValAsnSerAsnAlaTyrAspAlaGlyIleMetGlyLeuLysGlyLysAspPhe
  1

      70              90              110
      .             .             .
GCCGATCAGTTCTTTGCCGACGAAAACCAAGTGGTCCATGAAAGCGACACGGTCGTTCTG
AlaAspGlnPhePheAlaAspGluAsnGlnValValHisGluSerAspThrValValLeu
  21

     130              150              170
      .             .             .
GTCCTCAAGAAGTCGGACGAGATCAATACCTTTATCGAGGAGATCCTTCTGACGGACTAC
ValLeuLysLysSerAspGluIleAsnThrPheIleGluGluIleLeuLeuThrAspTyr
  41

     190              210              230
      .             .             .
AAGAAGAACGTCAATCCGACGGTAAACGTGGAAGACCGCGGGTTACTGGTGGATCAAG
LysLysAsnValAsnProThrValAsnValGluAspArgAlaGlyTyrTrpTrpIleLys
  61

     250              270              290
      .             .             .
GCCAACGGCAAGATCGAGGTCGATTGCGACGAGATTTCCGAGCTGTTGGGGCGGCAGTTC
AlaAsnGlyLysIleGluValAspCysAspGluIleSerGluLeuLeuGlyArgGlnPhe
  81

     310              330              350
      .             .             .
AACGTCTACGACTTCCTCGTCGACGTTTCTCCACCATCGGCCGGGCCTATACCCTGGGC
AsnValTyrAspPheLeuValAspValSerSerThrIleGlyArgAlaTyrThrLeuGly
 101

     370              390              410
      .             .             .
AACAAGTTCACCATTACCAGTGAGCTGATGGGCCTGGACCGCAAGCTCGAAGACTATCAC
AsnLysPheThrIleThrSerGluLeuMetGlyLeuAspArgLysLeuGluAspTyrHis
 121

GCTTAA
AlaEnd
141
```

Figure 1-5

M. capsulatus mmoZ sequence

```
10          30          50
.           .           .
ATGGCGAAACTGGGTATACACAGCAACGACACCCGCGACGCCTGGGTGAACAAGATCGCG
MetAlaLysLeuGlyIleHisSerAsnAspThrArgAspAlaTrpValAsnLysIleAla
1

70          90          110
.           .           .
CAGCTCAACACCCTGGAAAAAGCGGCCGAGATGCTGAAGCAGTTCCGGATGGACCACACC
GlnLeuAsnThrLeuGluLysAlaAlaGluMetLeuLysGlnPheArgMetAspHisThr
21

130         150         170
.           .           .
ACGCCGTTCCGCAACAGCTACGAACTGGACAACGACTACCTCTGGATCGAGGCCAAGCTC
ThrProPheArgAsnSerTyrGluLeuAspAsnAspTyrLeuTrpIleGluAlaLysLeu
41

190         210         230
.           .           .
GAAGAGAAGGTGCGCGTCCCTCAAGGCACGCGCCTTCAACGAGGTGGACTTCCGTCATAAG
GluGluLysValAlaValLeuLysAlaArgAlaPheAsnGluValAspPheArgHisLys
61

250         270         290
.           .           .
ACCGCTTTCGCGCAGGATGCCAAGTCCGTTCTGGACGGCACCGTCGCGAAGATGAACGCG
ThrAlaPheGlyGluAspAlaLysSerValLeuAspGlyThrValAlaLysMetAsnAla
81

310         330         350
.           .           .
GCCAAGGACAAGTGGGAGGCGGAGAAGATCCATATCGGTTTCCGCCAGGCCTACAAGCCG
AlaLysAspLysTrpGluAlaGluLysIleHisIleGlyPheArgGlnAlaTyrLysPro
101

370         390         410
.           .           .
CCGATCATGCCGGTGAACTATTTCTGGACGGCGAGCGTCAGTTGGGGACCCGGCTGATG
ProIleMetProValAsnTyrPheLeuAspGlyGluArgGlnLeuGlyThrArgLeuMet
121

430         450         470
.           .           .
GAACTGCGCAACCTCAACTACTACGACACGCCGCTGGAAGAACTGCGCAAACAGCGCGGT
GluLeuArgAsnLeuAsnTyrTyrAspThrProLeuGluGluLeuArgLysGlnArgGly
141
```

Figure 1-5

M. capsulatus orfY sequence

```

      10              30              50
      .              .              .
ATGGTCGAATCGGCATTTTCAGCCATTTTCGGGCGACGCAGACGAATGGTTCGAGGAACCA
MetValGluSerAlaPheGlnProPheSerGlyAspAlaAspGluTrpPheGluGluPro
1

      70              90              110
      .              .              .
CGGCCCCAGGCCGGTTTCTCCCTTCCGCGGACTGGCATCTGCTCAAACGGGACGAGACC
ArgProGlnAlaGlyPhePheProSerAlaAspTrpHisLeuLeuLysArgAspGluThr
21

     130              150              170
      .              .              .
TACGCAGCCTATGCCAAGGATCTCGATTTTCATGTGGCGGTGGGTTCATCGTCCGGAAGAA
TyrAlaAlaTyrAlaLysAspLeuAspPheMetTrpArgTrpValIleValArgGluGlu
41

     190              210              230
      .              .              .
AGGATCGTCCAGGAGGGTTGCTCGATCAGCCTGGAGTCGTTCGATCCGCGCCGTGACGCAC
ArgIleValGlnGluGlyCysSerIleSerLeuGluSerSerIleArgAlaValThrHis
61

     250              270              290
      .              .              .
GTACTGAATTATTTTGGTATGACCGAACAAACGCGCCCCGGCAGAGGACCGGACCGGCGGA
ValLeuAsnTyrPheGlyMetThrGluGlnArgAlaProAlaGluAspArgThrGlyGly
81

     310
      .
GTTCAACATTGA
ValGlnHisEnd
101
```

Figure 1-5

M. capsulatus mmoC sequence

```
      10              30              50
      .             .             .
ATGCAGCGAGTTCACACTATCACGGCGGTGACGGAGGATGGCGAATCGCTCCGCTTCGAA
MetGlnArgValHisThrIleThrAlaValThrGluAspGlyGluSerLeuArgPheGlu
      1

      70              90              110
      .             .             .
TGCCGTTCCGGACGAGGACGTCATCACCGCCGCCCTGCGCCAGAACATCTTTCTGATGTGC
CysArgSerAspGluAspValIleThrAlaAlaLeuArgGlnAsnIlePheLeuMetSer
      21

     130              150              170
      .             .             .
TCCTGCCGGGAGGGCGGCTGTGCGACCTGCAAGGCCTTGTGCGAGCGAAGGGGACTACGAC
SerCysArgGluGlyGlyCysAlaThrCysLysAlaLeuCysSerGluGlyAspTyrAsp
      41

     190              210              230
      .             .             .
CTCAAGGGCTGCAGCGTTCAGGCGCTGCCGCCGAAGAGGAGGAGGAAGGGTTGGTGTTG
LeuLysGlyCysSerValGlnAlaLeuProProGluGluGluGluGluGlyLeuValLeu
      61

     250              270              290
      .             .             .
TTGTGCCGGACCTACCCGAAGACCGACCTGGAAATCGAACTGCCCTATACCCATTGCCGC
LeuCysArgThrTyrProLysThrAspLeuGluIleGluLeuProTyrThrHisCysArg
      81

     310              330              350
      .             .             .
ATCAGTTTTGGTGAGGTTCGGCAGTTTCGAGGCGGAGGTCGTCGGCCTCAACTGGGTTTCG
IleSerPheGlyGluValGlySerPheGluAlaGluValValGlyLeuAsnTrpValSer
     101

     370              390              410
      .             .             .
AGCAACACCGTCCAGTTTCTTTGCAGAAGCGGCCCGACGAGTGCGGCAACCGTGGCGTG
SerAsnThrValGlnPheLeuLeuGlnLysArgProAspGluCysGlyAsnArgGlyVal
     121

     430              450              470
      .             .             .
AAATTCGAACCCGGTCAGTTCATGGACCTGACCATCCCCGGCACCGATGTCTCCCGCTCC
LysPheGluProGlyGlnPheMetAspLeuThrIleProGlyThrAspValSerArgSer
     141
```

Figure 1-5

970 990 1010
GATGCCGCCTGCGAGCTGGTACGCAGCCGCGGTATCCCCGGCGAACAGGTCTTCTTCGAA
AspAlaAlaCysGluLeuValArgSerArgGlyIleProGlyGluGlnValPhePheGlu
321

1030
AAATTCCTGCCGTCCGGGGCGGCCTGA
LysPheLeuProSerGlyAlaAlaEnd
341

Figure 1-5