



GACTCTACTAGAGGATCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGGATAACATGGCCATCATCAAGGA
 CTGAGATGATCTCCTAGATGGCCAGCGGTGGTACCACCTCGTTCGCTCCTCCTATTGTACCGGTAGTAGTTCTT

1 Met Val Ser Lys Gly Glu Glu Asp Asn Met Ala Ile Ile Lys Glu
 mCherry

GTTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTTCGAGATCGAGGGCGAGGGCGAGGG
 CAAGTACGCGAAGTTCACGTTGACCTCCCGAGGCACCTTGCCGGTGCTCAAGCTCTAGCTCCCGCTCCCGCTCCC

20 Phe Met Arg Phe Lys Val His Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly
 mCherry

CCGCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCAAGGGTGCCCCCTGCCCTTCGCCTGGGACAT
 GGCAGGGATGCTCCCGTGGGTCTGGCGGTTGACTTCCACTGGTCCCACCGGGGGACGGGAAGCGGACCCCTGTA

45 Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile
 mCherry

CCTGTCCCCTCAGTTCATGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCCGACTACTTGAAGCT
 GGACAGGGGAGTCAAGTACATGCCGAGGTTCCGGATGCACTTCGTGGGGCGGCTGTAGGGGCTGATGAACCTTCGA

70 Leu Ser Pro Gln Phe Met Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu
 mCherry

GTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGGCGTGGTGACCGTGACCCAGGA
 CAGGAAGGGGCTCCCGAAGTTCACCCTCGCGCACTACTTGAAGCTCCTGCCGCGCACCCTGGCACTGGGTCTCT

95 Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp
 mCherry

CTCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGCACCAACTTCCCCTCCGACGGCCCCGT 3225
 GAGGAGGGGACGTCTCTGCCGCTCAAGTAGATGTTCCACTTCGACGCGCCGTGGTTGAAGGGGAGGCTGCCGGGGCA
 Ser Ser Leu Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro Val
 mCherry

AATGCAGAAGAAGACCATGGGCTGGGAGGCCCTCTCCGAGCGGATGTACCCCGAGGACGGCGCCCTGAAGGGCGA 3300
 TTACGTCTTCTTCTGGTACCCGACCCCTCCGGAGGAGGCTCGCCTACATGGGGCTCTGCCGCGGGACTTCCCCT
 Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Ser Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu
 mCherry

GATCAAGCAGAGGCTGAAGCTGAAGGACGGCGGCCACTACGACGCTGAGGTCAAGACCACCTACAAGGCCAAGAA 3375
 CTAGTTCGTCTCCGACTTCGACTTCTGCGCCGGTGATGCTGCGACTCCAGTTCTGGTGGATGTTCCGGTTCTT
 Ile Lys Gln Arg Leu Lys Leu Lys Asp Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Lys Ala Lys Lys
 mCherry

GCCCGTGCAGCTGCCCGGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAGGACTACACCAT 3450
 CGGGCACGTGACGGGCGCGGATGTTGCAGTTGTAGTTCAACCTGTAGTGGAGGGTGTGCTCCTGATGTGGTA
 Pro Val Gln Leu Pro Gly Ala Tyr Asn Val Asn Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile
 mCherry

CGTGGAACAGTACGAACGCGCCGAGGGCCGCACTCCACCGGCGGCATGGACGAGCTGTACAAGTCCGGACTCAG 3525
 GCACCTTGTTCATGCTTGCAGCGGCTCCCGCGGTTGAGGTGGCCGCGGTACCTGCTCGACATGTTTCAGGCCTGAGTC
 Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Gly Met Asp Glu Leu Tyr Lys Ser Gly Leu Arg
 mCherry

MCS

XhoI EcoRI ApaI SmaI BamHI
 ATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACC GCGGGCCGGGATCCACCGGATCTAGATAACTGAT 3600
 TAGAGCTCGAGTTTCAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCTAGATCTATTGACTA
 Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly Ser Thr Gly Ser Arg *
 (in frame with mCherry)

MCS