

10 20 30 40 50 60 70
CCGCGGCAGCCATATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGCGGATCCGAATTCATGCCCAACAG
Top
ProArgGlnProTyrGly . HisAspTrpTrpThrAlaAsnGlySerArgIleArgIleHisAlaGlnGln
ArgGlySerHisMetAlaSerMetThrGlyGlyGlnGlnMetGlyArgGlySerGluPheMetProAsnSer
AlaAlaAlaIleTrpLeuAla . LeuValAspSerLysTrpValAlaAspProAsnSerCysProThrVal
pET-28a_WRS(1-65)-1-T7ter.seq(1>1203) ← CCGCGGCAGCCATATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGCGGATCCGAATTCATGCCCAACAG
pET-28a_WRS(1-65)-1-T7.seq(1>1214) → TGGACAGCAAATGGGTCGCGGATCCGAATTCATGCCCAACAG
WRS(1-65).seq(1>195) → EcoR atgcccaacag

80 90 100 110 120 130 140
TGAGCCCGCATCTCTGCTGGAGCTGTTCAACAGCATCGCCACACAAGGGGAGCTCGTAAGGTCCTCAAAGC
Top
. AlaArgIleSerAlaGlyAlaValGlnGlnHisArgHisThrArgGlyAlaArgLysValProGlnSer
GluProAlaSerLeuLeuGluLeuPheAsnSerIleAlaThrGlnGlyGluLeuValArgSerLeuLysAla
SerProHisLeuCysTrpSerCysSerThrAlaSerProHisLysGlySerSer . GlyProSerLysArg
pET-28a_WRS(1-65)-1-T7ter.seq(1>1203) ← TGAGCCCGCATCTCTGCTGGAGCTGTTCAACAGCATCGCCACACAAGGGGAGCTCGTAAGGTCCTCAAAGC
pET-28a_WRS(1-65)-1-T7.seq(1>1214) → TGAGCCCGCATCTCTGCTGGAGCTGTTCAACAGCATCGCCACACAAGGGGAGCTCGTAAGGTCCTCAAAGC
WRS(1-65).seq(1>195) → tgagcccgcatctctgctggagctgttcaacagcatcgccacacaaggggagctcgtaaggtccctcaaagc

150 160 170 180 190 200 210
GGGAAATGCGTCAAAGGATGAAATTGATTCTGCAGTAAAGATGTTGGTGTTCATTAATAATGAGCTACAAAGC
Top
GlyLysCysValLysGly . Asn . PheCysSerLysAspValGlyValIleLysAsnGluLeuGlnSer
GlyAsnAlaSerLysAspGluIleAspSerAlaValLysMetLeuValSerLeuLysMetSerTyrLysAla
GluMetArgGlnArgMetLysLeuIleLeuGln . ArgCysTrpCysHis . Lys . AlaThrLysLeu
pET-28a_WRS(1-65)-1-T7ter.seq(1>1203) ← GGGAAATGCGTCAAAGGATGAAATTGATTCTGCAGTAAAGATGTTGGTGTTCATTAATAATGAGCTACAAAGC
pET-28a_WRS(1-65)-1-T7.seq(1>1214) → GGGAAATGCGTCAAAGGATGAAATTGATTCTGCAGTAAAGATGTTGGTGTTCATTAATAATGAGCTACAAAGC
WRS(1-65).seq(1>195) → gggaaatgcgtaaaggatgaaattgattctgcagtaaagatgttgggtgtcattataatgagctacaaagc

220 230 240 250 260 270 280
TGCCGCGGGGGAGGATTACAAGGCTGACTGTCCTCCAGGGTAGCTCGAGCACCACCACCACCACCTGAGA
Top
CysArgGlyGlyGlyLeuGlnGly . LeuSerSerArgValAlaArgAlaProProProProProLeuArg
AlaAlaGlyGluAspTyrLysAlaAspCysProProGly . LeuGluHisHisHisHisHisHis . Asp
ProArgGlyArgIleThrArgLeuThrValLeuGlnGlySerSerSerThrThrThrThrThrThrGluIle
pET-28a_WRS(1-65)-1-T7ter.seq(1>1203) ← TGCCGCGGGGGAGGATTACAAGGCTGACTGTCCTCCAGGGTAGCTCGAGCACCACCACCACCACCTGAGA
pET-28a_WRS(1-65)-1-T7.seq(1>1214) → TGCCGCGGGGGAGGATTACAAGGCTGACTGTCCTCCAGGGTAGCTCGAGCACCACCACCACCACCTGAGA
WRS(1-65).seq(1>195) → tgccgcgggggaggattacaaggctgactgtcctccaggg Xho

290 300 310 320 330 340
TCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGC

Top

SerGlyCys . GlnSerProLysGlySer . ValGlyCysCysHisArg .
ProAlaAlaAsnLysAlaArgLysGluAlaGluLeuAlaAlaAlaThrAlaGlu
ArgLeuLeuThrLysProGluArgLysLeuSerTrpLeuLeuProProLeuSer

pET-28a_WRS(1-65)-1-T7ter.seq(1>1203)
pET-28a_WRS(1-65)-1-T7.seq(1>1214)



TCCGGCTGC
TCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGC