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Nano

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(54) **VACCINES COMPRISING HEAT-SENSITIVE TRANSGENES**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

This patent is subject to a terminal disclaimer.

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(2), (4) Date: **Apr. 12, 2012**

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PCT Pub. Date: **Apr. 14, 2011**

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Related U.S. Application Data

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(51) **Int. Cl.**

C12N 15/74 (2006.01)

C12N 1/20 (2006.01)

C07H 21/02 (2006.01)

C07K 1/00 (2006.01)

(52) **U.S. Cl.**

USPC **435/471**; 435/476; 435/488; 435/320.1;
435/252.3; 435/252.33; 536/23.1; 530/350;
424/93.2

(58) **Field of Classification Search**

None

See application file for complete search history.

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(74) Attorney, Agent, or Firm — Klarquist Sparkman, LLP

(57) **ABSTRACT**

The present disclosure provides temperature sensitive essential nucleic acid molecules from a psychrophilic bacterium, proteins encoded by the nucleic acid molecules, as well as recombinant cells into which have been introduced such nucleic acid molecules. The disclosed recombinant cells containing one or more essential nucleic acid molecules from a psychrophilic bacterium are thereby made temperature sensitive, and can be administered to a mammal to induce an immune response in the mammal.

13 Claims, 21 Drawing Sheets

FIG. 1

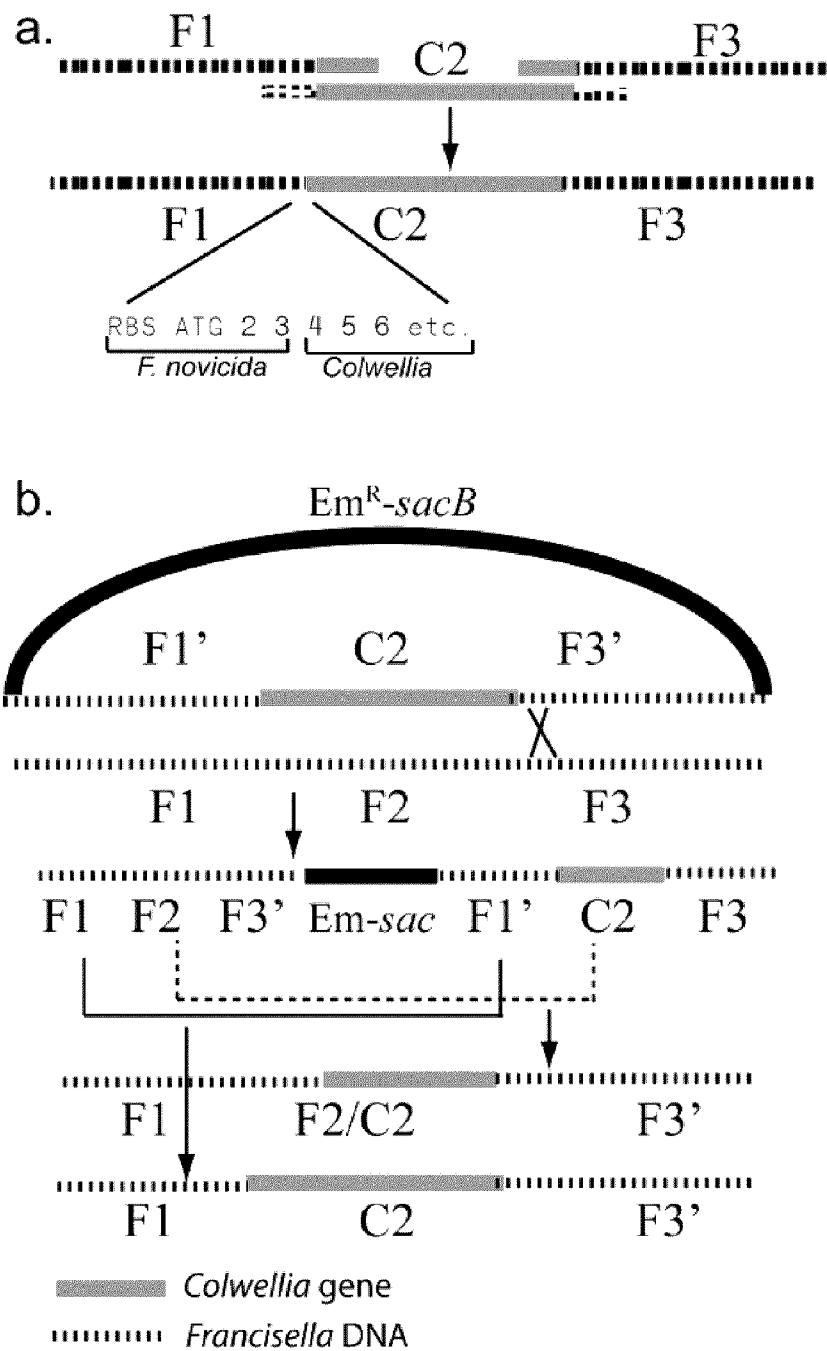


FIG. 2

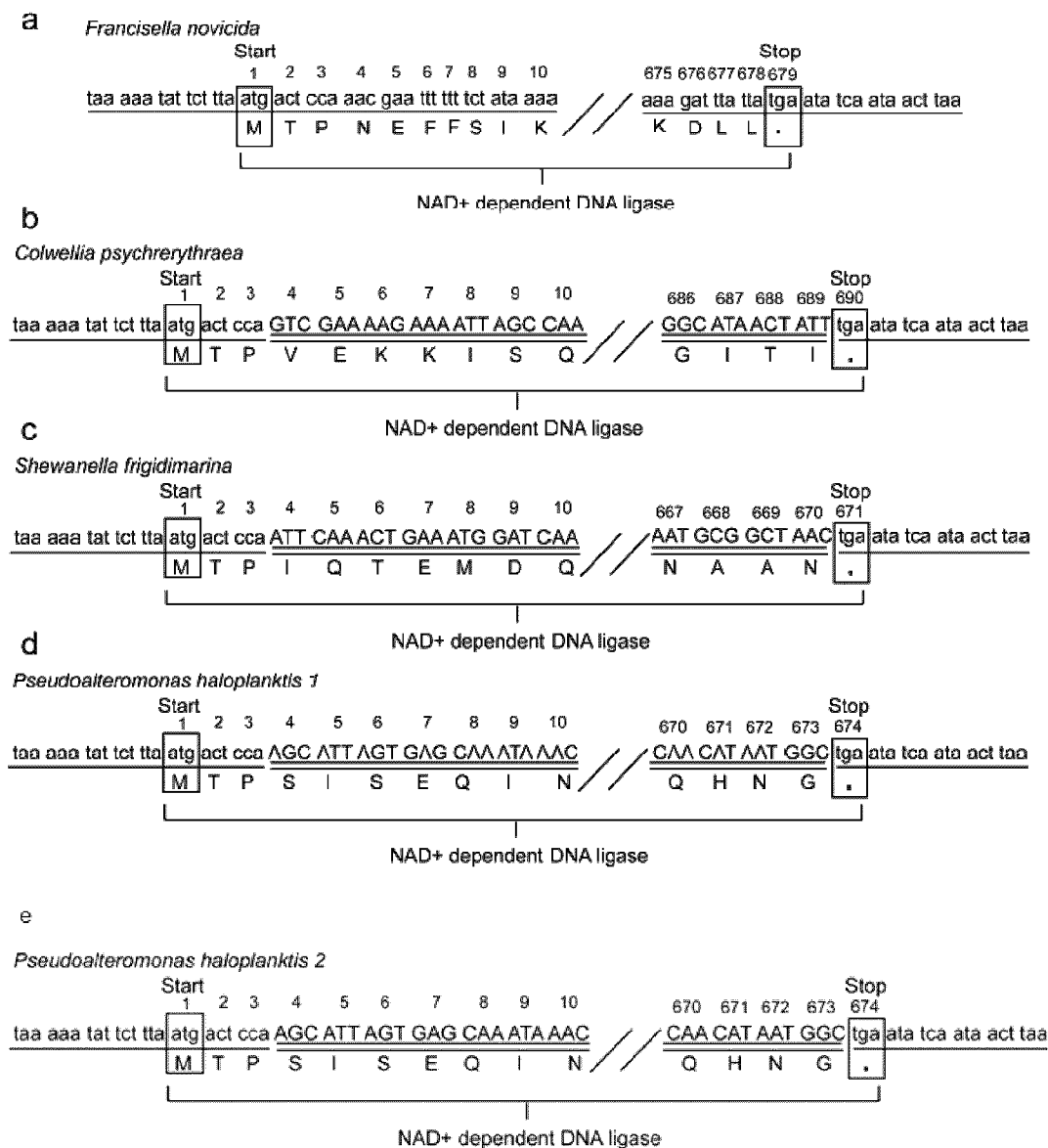


FIG. 3

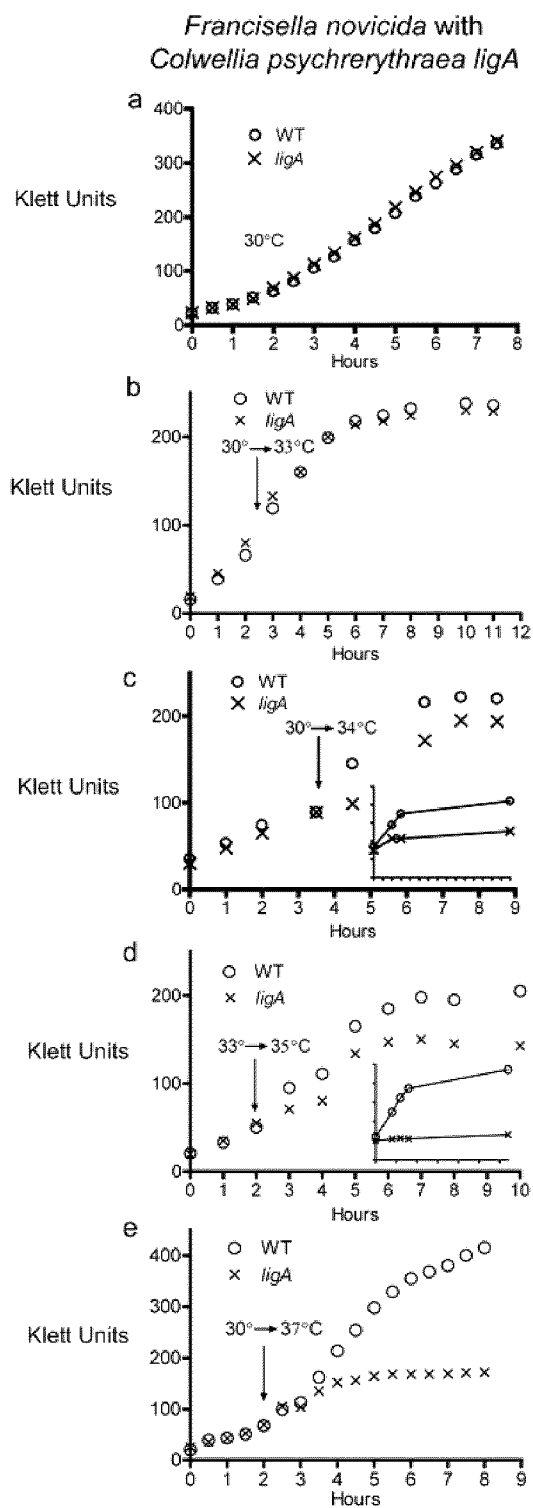


FIG. 4

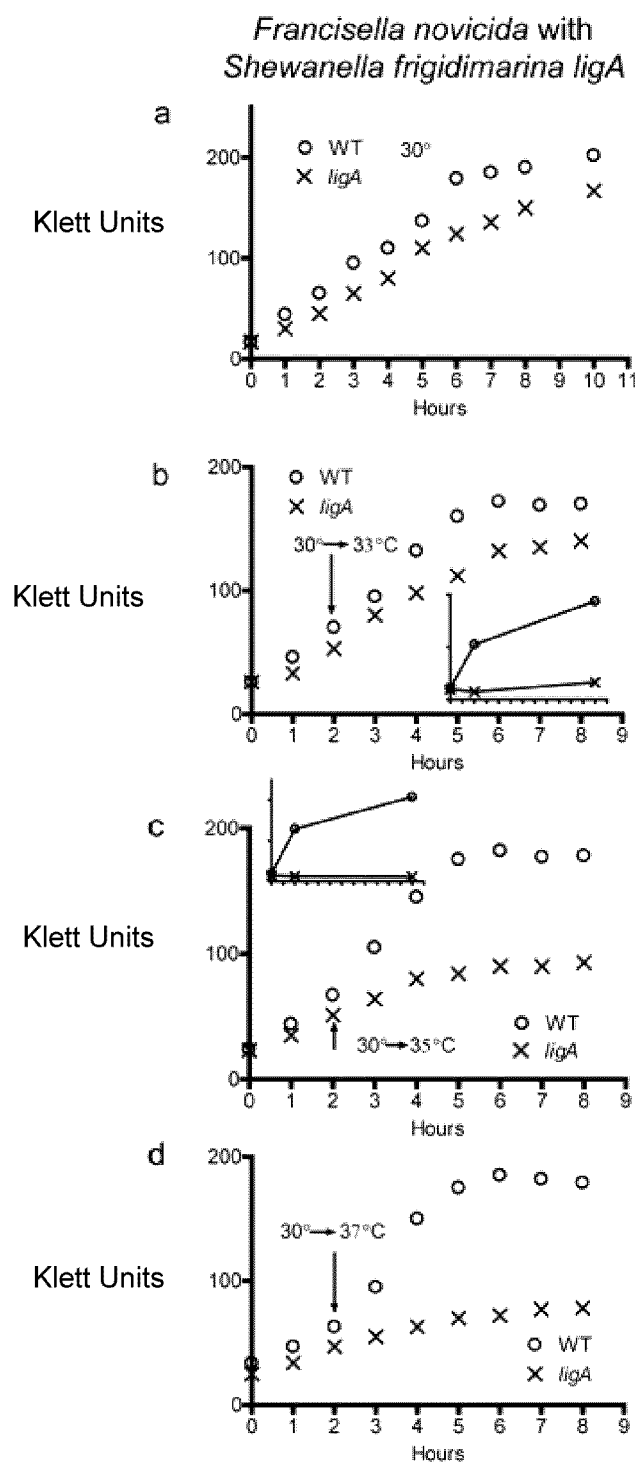


FIG. 5

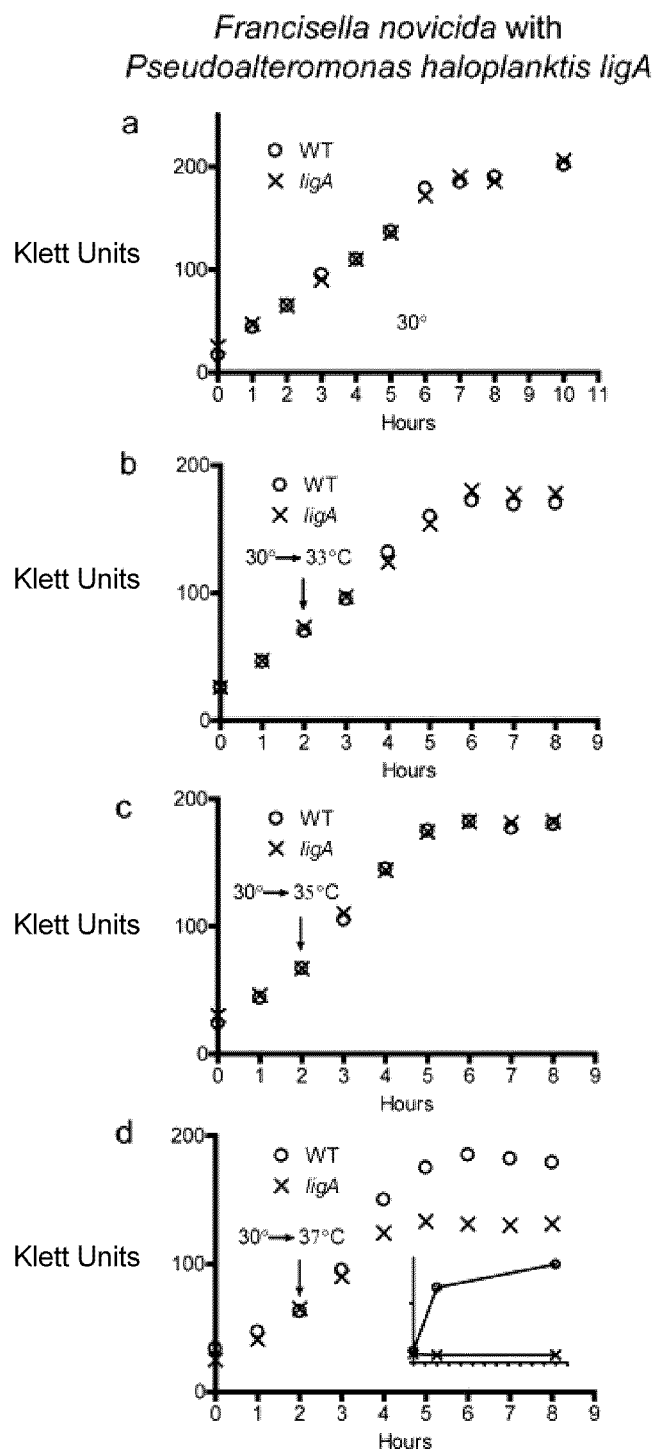


FIG. 6

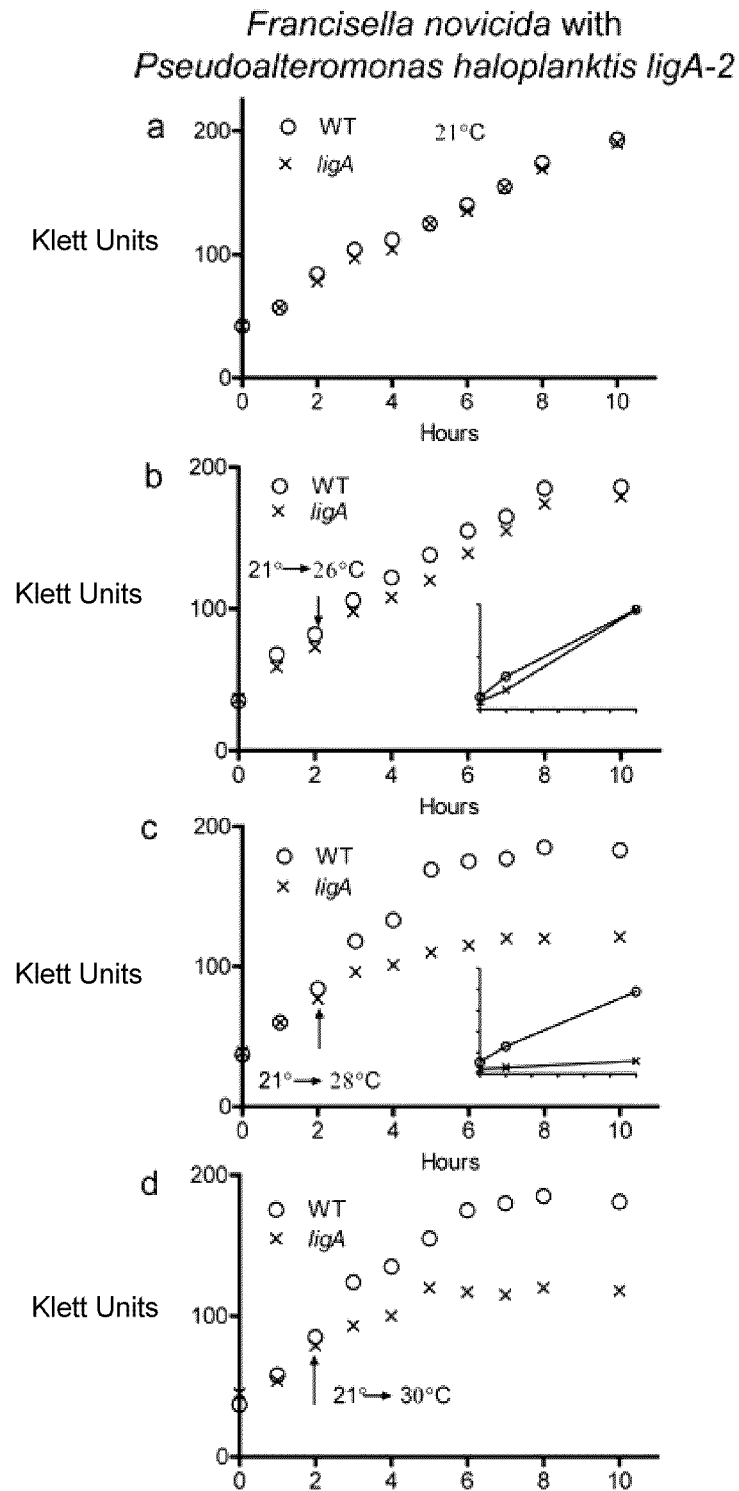


FIG. 7

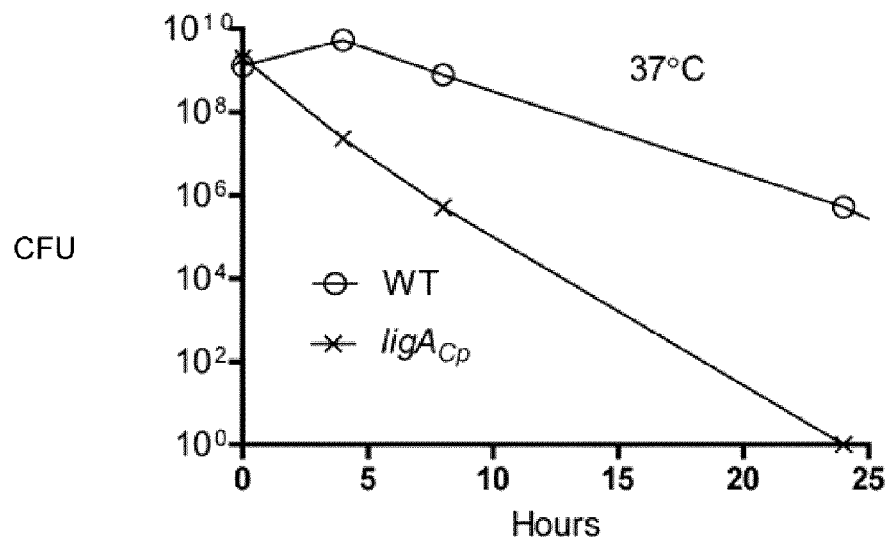


FIG. 8

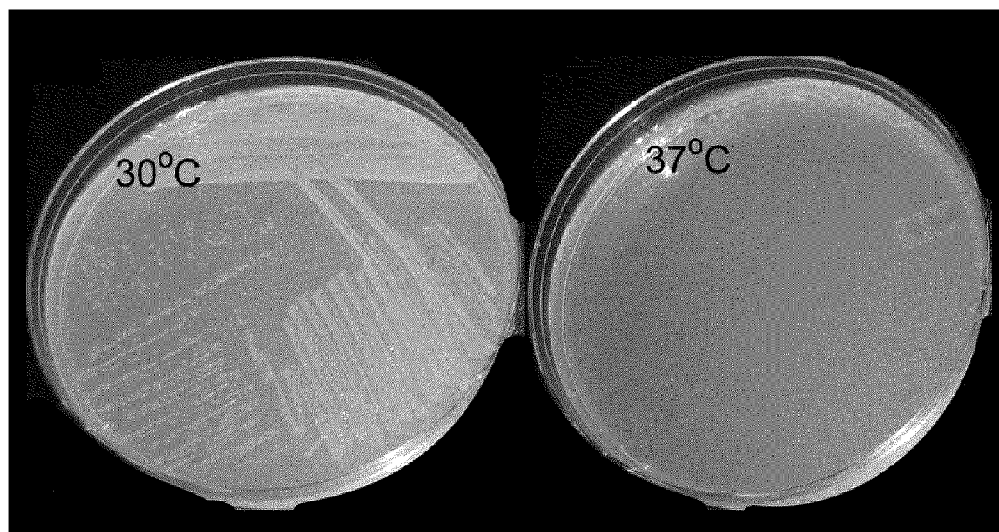


FIG. 9

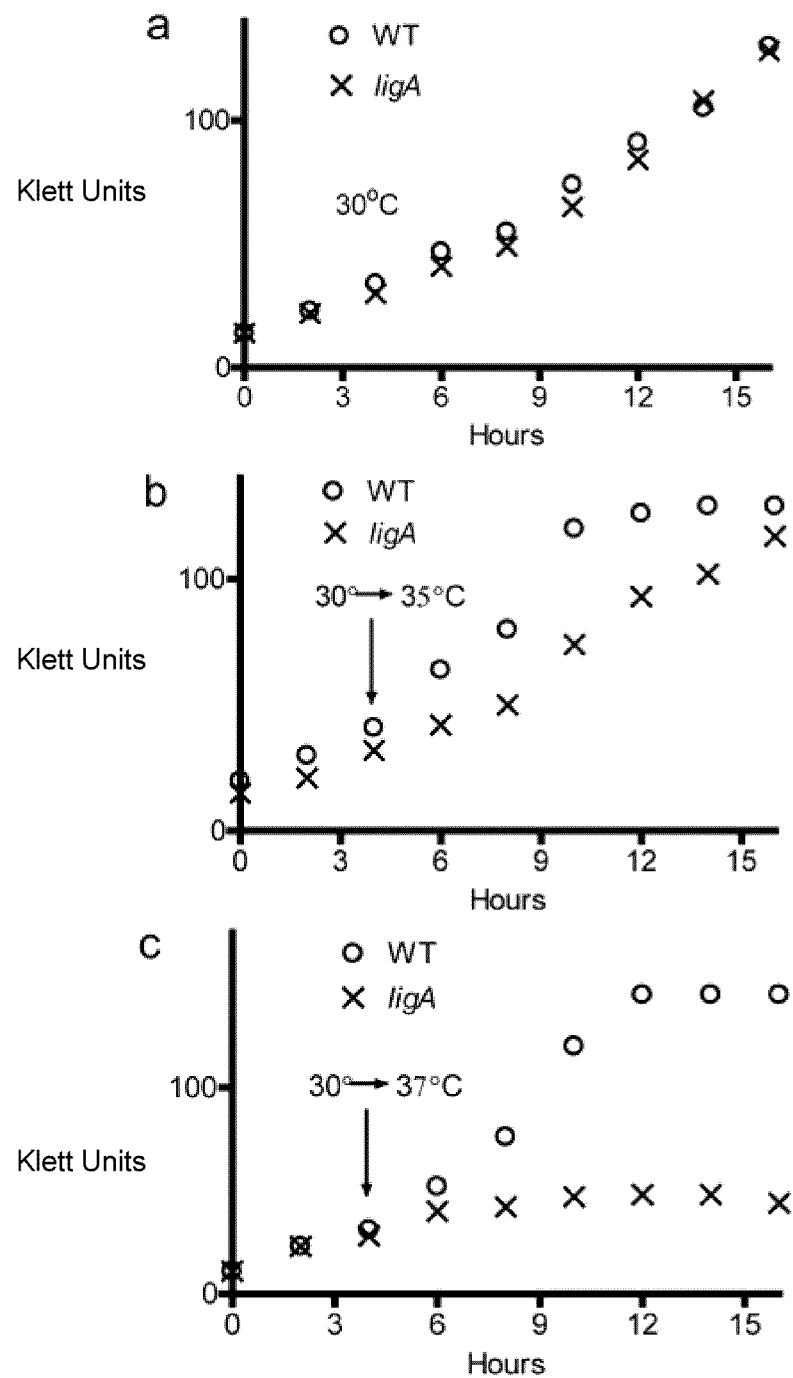


FIG. 10

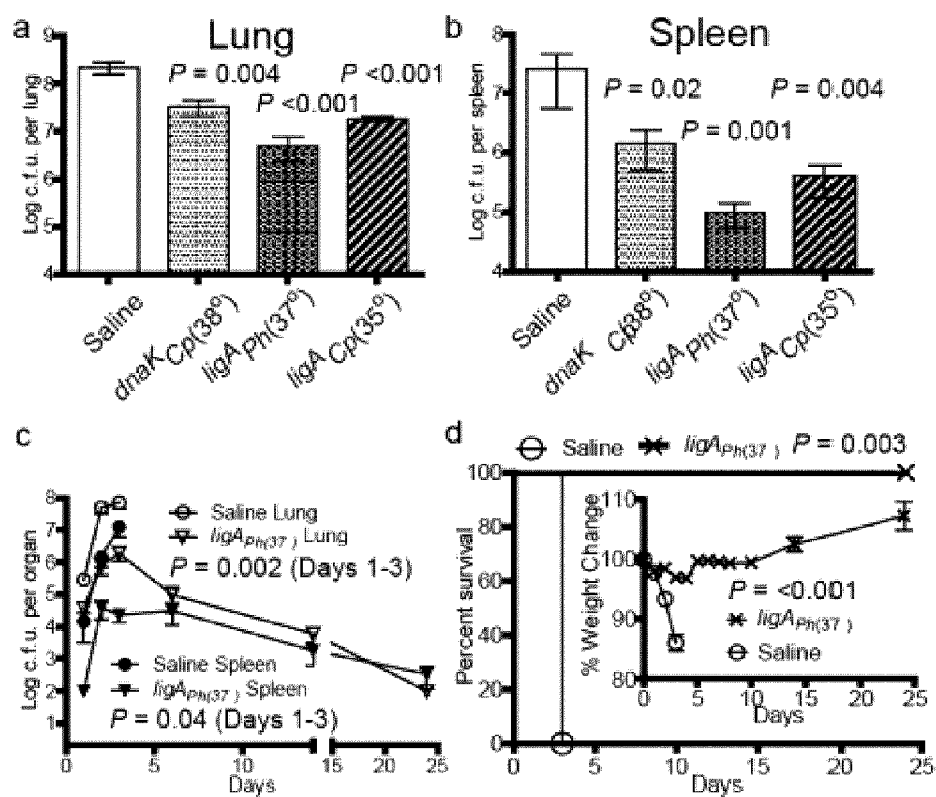


FIG. 11A

SEQ ID NO: 1

ATGACTCCAGTCGAAAAGAAAATTAGCCAACTGCAACAGCAGCTTAATCAATATAATCATGAATATTA
TGTATTAGACCAACCTAGTGTGCCTGATGCAGAATATGACCGATTAATGACAGCATTAAATCGATTTAG
AAAAGACTAATCCTGAGCTTAAGACTATTGACTCACCTAGCCAAAAAGTTGGCGGTCAGGCATTAAAA
TCTTTCACCTCAAGTAACTCATCAGCTGCCGATGCTTTCTCTTGATAATGTTTTTCTTTAGATGATTT
TCACGCATTTGTAAACGCGTAAAAGATAGGTTAAATGACAATCAAGCGATAGTCTTTTGTGCCGAGC
CTAAATTAGACGGTTTAGCAGTGAGTTTACGTTATGAGCACGGGCAGTTAATAACAAGCGGCTACACGT
GGCGATGGTAGTGTAGGGGAGAATATTACGACTAACATTCTGACAAATAAAATCTATTCCGCTTAAGTT
AATGGGCACACCAGGTAAAGATTTTCTGATATCGTTGAAGTCCGCGGTGAAGTTTTATGCCTAAGG
CAAGTTTTGACGCATTAAATACATKGGCTAAAAAACGTGGCGAGAAAGGTTTTGCAAATCCACGTAAT
GCAGCGGCGGGAAGTTTACGACAACTTGATTCTAAAATCACCGCTAAACGTAATTTAGCTTTTTACGC
TTATAGCCTTGGATTTGTAGGGAACTGTCTGATGGAGGCGCTGAAAGTACCGATTTAACCAATGACT
TTTTTGCTAACTCTCATCATGAAAGACTATGTCAGCTTAAAGGTTGGGTTTGCCATGTGTCCAGAA
GTACGCTTACTTGAAAGTGAGCAAGCCTGTGATGCGTTTTATCAAGATATCTTAGCAAAGCGTAGTGC
CTTGAGTTATGAAATTGATGGCACTGTATTAAGTTGATGAAATCTCTTGCAGAAACGTTTAGGGT
TTGTGCGACGTGCCCCACGTTGGGCTATTGCTTATAAATCCCTGCGGAAGAAGAATTAACCTGTGTT
GAAGATGTCGAGTTTCAAGTAGGGCGTACCGGCGCGATTACTCCCGTAGCACGTTTGAAACCGGTATT
TGTTGGTGGCGTAACAGTTTCTAATGCCACATTACATAACCAAGATGAAATAACCCGATTAGGGCTGA
AAGTGAATGATTTTCGTGGTTATCCGCGGTGCCGGTGAIGTTATTCCTCAAATTGTTAGCGTAGTACTT
GATAAACGACCAGATAATGCCGTGATATAGTCTTTCTACCAGTTGCCCTGTTTGTGACTCTGCAGT
GGCTAAACCTGAAGGTGAAGCCGTACTGAGATGTACCGCCGGACTTTTCTGTGCGGCGCAAAGAAAAG
AAGCTATTAAACATTTTGCTTCTCGAAAAGCACATGATGTTGATGGTTTAGGTGACAACTAGTAGAG
CAACTGTAGATGAAAAGTTAATTAATACGCYCGCTGATTTATTCAAATTAACCGAAATACAAGTTAG
TACTATAGATCGTATGGGTAAAAAATCAGCGACCAATTTAATTAATGGACTTGAGCAGGCTAAAAAGTA
CCACACTAGCAAAATTTATTTATGGTCTGGGCATACGCGAAGTCGGTGAAGCAACTGCTGCTAATCTA
GCAAAATCATTTTTATACCTTAGCGGCAATTGAAAGTGCTTCTCTTGAAGACTTACAAAATGTTTCAGA
TGTTGGCGAAGTCGTTGCCAAAAATATTATTAATTTCTTTAAAGAAGAGCATAACTTAGCGATCGTTT
CTGACTAAGTGAAGTAATGCACTGGCCAACTATTGAAATAAAGTCAGCTGAGGAGTTACCGCTTGCA
GAGCAGATATTTGTTTTAACAGGCACATTAACCCAAATGGGAAGAACTGAAGCTAAACAGCCTTACA
GTCCCTGGGAGCTAAAGTATCAGGTAGTGTCTCGAAGAATACACACTTCGTTGTTGCAGGTGATAAAG
CGGGATCTAAACTGACTAAGGCTCAGGATTTAGGTATCTCAGTGCTTACCGAAGATGGGTTAGTAGCG
TTACTTGCCGAACATGGCATAACTATTTGA

SEQ ID NO: 2

MTPVEKKISQLQQQLNQYNHEYVLDQPSVPDAEYDRLMTALIDLEKTNPELKTIDSPSQKVGQALK
SFTQVTHQLPMLSLDNVFSLDDFHAFVVRKVKDRINDNQATVFCAPKLDGLAVSLRYEHGQLTQAATR
GDGSGVENITTNIRTIKSIPLKLMGTPGKDFPDIVEVRGEVFMKASFDALNTXAKKRGEKGFANPRN
AAAGSLRQLDSKITAKRNLAFYAYSLGFVVGKLSDGGAESTDLTNDFFANSIIHERLCQLKRLGLPMCPE
VRLLESEQACDAFYQDILAKRSALSYEIDGTVLKVDEISLQKRLGFVARAPRWAIAYKFPAEEELTCV
EDVEFQVGRTGATPVARLKPVFVGGVTVSNATLIHQDEITRLGLKVNDIVVIRRAGDVIPQIVSVVL
DKRPDNAVDIVFPTSCPVCDSAVAKPEGEAVLRCTAGLFCAAQRKEAIKHFASRKAHDVDGLGDKLVE
QLVDEKLINTXADLFKLTEIQVSTIDRMGKKSATNLINGLEQAKSTTLAKFIYGLGIREVGEATAANL
ANHFYTLAAIESASLEDLQNVSDVGEVVAKNIINFFKEEHNLAIVSGLSEVMHWPTIEIKSAEELPLA
EQIFVLTGTLTQMGRTEAKTALQSLGAKVSGSVSKNTHFVVAGDKAGSKLTKAQDLGTSVLTEDGLVA
LLAEHGITI

FIG. 11B

SEQ ID NO: 3

ATGACTCCAAGCATTAGTGAGCAAATAAACCATCTTCGTAGTACGCTTGAACAGCACAGTTACAATTA
TTATGTACTTGATACCCCCAGTATTCTTGATGCTGAATACGACCGTTTATTACAACAACCTCAGCGCAC
TAGAAACTCAGCACCCAGAATTAATAACTGCCGACTCACCAACCCAAAAAGTGGGCGGTGCTGCGCTA
AGTAAATTTGAGCAAGTAGCGCACCAAGTGCCTATGTTATCGCTTGATAACGCCTTTAGCGAAGATGA
GTTTATTGCCTTTAATCGCCGTATAAAAGACCGTTTAAATGAGTACCSAAGAGCTTACTTTTTGTTGTG
AGCCAAAACCTAGATGGCTTAGCTGTGTGCGATTATTTATCGTGATGGCGTACTAGTGCAAGCCGCGACC
CGAGGTGATGGCTTGACGGGAGAAAATGIAACTCAAAACGTTAAAACAATTCTGTAATGTGCCACTTAA
ATTACGAGGTAGCGATTATCTGCTGAACTAGAAGTGCGCGGCGAAGTGTTTATGGATAATGCAGGCT
TTGAAAAGTTTAACATTGAAGCTGAAAAACGTGGTGAAAAAGTATTTGTAAACCCACGCAACGCCGCC
GCAGGTAGCCTGCGCCAGCTTGACTCTAAAATTACGGCTAAACGCCCACTGATGTTTTATGCCTACAG
CACAGGTCTTGTAGCCGACGGTAGCATTGCAGAGGATCATTATCAGCAATTAGAAAAATTGACTGATT
GGGGGTTACCACTTTGCCCTGAAACAAAATTAGTAGAAGGCCCAAGCTGCACTGGCTTATTATACT
GACATTTTAACGCGCCGTGGCGAGCTTAAATATGAAATAGATGGCGTGGAATaAAAAaTaATCAAAA
AGCCTTACAAGAGCGTTTAGGCTTTGTAGCACGCGCTCCGCGTTGGGCTATTGCTTATAAGTTCCCGG
CCCAAGAAGAAATAACCAAATTACTCGATGTAGAGTTTTAGGTGGGCGTACGGGAGCAATTACACCG
GTTGCACGCTTAGAGCCGGTATTTGTTGCTGGTGTTACTGTATCAAACGCTACCTTGACAAATGGCGA
TGAAATAGCGCGCTTAGGCGTAAAAGTGGCGACACGGTAATTATTCGCCGTGCAGGGGACGTAATTC
CACAAATAACGCAAGTAGTACTTGAGCGCCGCCCTGATGATGCCCGCGATATTGAGTTtCCGGTaACT
TGCCCAATTTGTGACTCCCATGTAGAAAAAGTAGAAGGTGAAGCCGTAGCGCGTTGTACTGGTGGTTT
AGTGTGCCCCGCGCAACGTAAACAAGCGATtAAACACTtGCATCGCCCAAAGCACTCGATATTGACC
GCCTTGGCGATAAAATTGTTGATCaACTCGTCGACAGAGAGCTGATTAAACCCCTGCAGATTGTTT
ATTTTAAAGCAAGGACATTTTGAATCGCTTGAGCGTATGGGGCCAAAGTCGGCTAAAAATTTGGTTAC
TGCGCTTCAAGACGCTAAAGCAACAACCTTTGGCTAAGTTTTTATACTCATTGGGTATTCGTGAAGCGG
GTGAGGCAACCACACAAAATTTAGCTAATCATTCTTAACCTTGAAAAAGTAATAAATGCCAGCATT
GATAGTTTAACTCAAGTAAGTGATGTGGCGCAATAGTAGCAACCCATGTACGTAGCTTTTTTGCCGA
ACAGCATAATTTAGATGTTGTAAATGCGCTGGTAGAGCAAGGTATTAATTGGCCTGAACTTACTCCAC
CTTCAGCGCAAGAGCAGCCATTAGCTGGCCTTGTTTATGTGCTTACCGGTACCTTAAACACATTAAAC
CGTAATGACGCCAAAGCACGTTTGCAACAGTTAGGTGCTAAAGTGTCGGGTAGTGTGTGGCTAAAAAC
CGATGCGTTAGTAGCAGGCGAAAAGCGCGCTCTAAACTAACTAAGGCACAAGACTTAGGTATAGATG
TACTGACAGAAGAAGATTTAATTAATTTATTAGAGCAACATAATGGCTGA

SEQ ID NO: 4

MTPSISEQINHLRSTLEQHSYNYVLDTPSIPDAEYDRLLQQLSALETQHPELITADSPTQKVGAAL
SKFEQVAHQVPMPLSLDNAFSEDEFIAFNRRIKERLMSTEELTFCCEPKLDGLAVSIIYRDGVLVQAAT
RGDGLTGENVQTQNVKTI RNVP LKL RGS DYP AELEVRGEVFM DNAGFEKFNIEAEKRGEKVFNPRNAA
AGSLRQLDSKITAKRPLMFYAYSTGLVADGSI AEDHYQQL EKLTDWGLPLCPETKLVEGPQAALAYYT
DILTRRGELKYEIDGVVIKINQKALQERLGFVARAPRWAIAYKFPAQEEITKLLDVEFQVGRGTGATP
VARLEPVFVGGVTVS NATLHNGDEIARLCVKVGD TVI IRRAGDVIPQITQVVLERRPDDARDIEFPVT
CPICDSHV EKV EGEAVARCTGGLVCPAQRKQAIKH FASRKALDIDGLGDKIVDQLVDRELKTPADLF
ILKQGHFESLERMGPKSAKNLVTALQDAKATT LAKFLYSLGIREAGEATTQNLANHFLTLENVINASI
DSL TQVSDVGEIVATHIVRSFFAEQHNL DVVNALVEQGINWP ELTPPSAQEQPLAGLVVLTGTLNLTN
RNDAKARLQQLGAKVSGSVSAKT DALVACEKAGSKLTKAQDLGIDVLTEEDLINLLEQHNH

FIG. 11C

SEQ ID NO: 5

ATGACTCCAAGCATTAGTGAGCAAATAAACCATCTTCGTAGTAGCGTTGAACAGCACAGTTACAATTA
TTATGTACTTGATACCCCCAGTATTCCCTGATGCTGAATACGACCGTTTATTACAACAACCTCAGCGCAC
TAGAAACTCAGCACCCAGAATTAATAACTGCCGACTCACCAACCCAAAAAGTGGCGGTGCTGCGCTA
AGTAAATTTGAGCAAGTAGCGCACCAAGTGCCATGTTATCGCTTGATAACCCCTTTAGCGAAGATGA
GTTTATTGCCCTTAATGCCCGTATAAAAAAGCGTTTAAATGAGTACCGAAGAGCTTACTTTTTGTTGTG
AGCCAAAACCTAGATGGCTTAGCTGTGTCCGATTATTTATCGTGATGGCGTACTAGTGCAAGCCGCGACC
CGAGGTGATGGGTGACCGGAGAAAAATGTAACCTCAAAAAGTTAAAACAATTCGTAATGTGCCACTTAA
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TTGAAAAGTTTAAACATTGAAGCTGAAAAACGTGGTGAAAAAGTATTTGTAAACCCACGCAACGCCGCC
GCAGGTAGCCTGCGCCAGCTTGACTCTAAAATTACGGCTAAACGCCCACTGATGTTTTATGCCTACAG
CACAGGTCTTGTAGCCGACGGTAGCATTTCAGAGGATCATTATCAGCAATTAGAAAAATTGACTGATT
GGGGGTTACCCTTTGCCCTGAAACAAAATTAGTAGAAGGCCACACAAGCTGCACTGGCTTATTATACT
GACATTTTAAACGCGCGTGGCGAGCTTAAATATGAAATAGATGGCGTGGTAAATAAAAATAAATCAAAA
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CCCAAGAAGAAATAACCAAAATTACTCGATTGAGCGTATGGGGCCAAAGTCCGCTAAAAATTTGGTTAC
GTTGCACGCTTAGAGCCGGTATTTGTTGGTGGTGTACTGTATCAAACGCTACCTTGCACAATGGCGA
TGAAATAGCGCGCTTAGCGCTAAAAGTGGCGACACGGTAATTATTCCCGCTGCAGGGGACCTAATTC
CACAAATAACGCAAGTAGTACTTGTAGCGCGCCCTGATGATGCCCGCGATATTGAGTTTCCGGTAACT
TGCCCAATTTGTGACTCCCATGTAGAAAAAGTAGAAGGTGAAGCCGTAGCGCGTTGTACTGGTGGTTT
AGTGTGCCCGGCGCAACGTAAACAAGCGATTAAACACTTTGCATCGCGCAAAAGCACTCGATATTGACG
GCCTTGGCGATAAAATTGTTGATCAACTCGTCGACAGAGAGCTGATTAACCCCTGCAGATTTGTTT
ATTTTAAAGCAAGGACATTTTGAATCGCTTGAGCGTATGGGGCCAAAGTCCGCTAAAAATTTGGTTAC
TGCGCTTCAAGACCGCTAAAGCAACAACTTTGGCTAAGTTTTTATACTCATTCCGTATTTCGTGAAGCGG
GTGAGGCAACCACACAAAATTTAGCTAATCATTTCTTAACCCCTGAAAACGTAATAAATGCCAGCATT
GATAGTTTTAACTCAAGTAAGTGATGTGGCGAAATAGTAGCAACCCATGTACGTAGCTTTTTTGGCGA
ACAGCATAATTTAGATGTTGTAAATGCGCTGGTAGAGCAAGGTATTAATTGGCTGAACCTTACTCCAC
CTTCAGCGCAAGAGCAGCCATTAGCTGGCCTTGTTTATGTGCTTACCGGTACCTTAAACACATTAAAC
CGTAATGACGCCAAAGCACGTTTGCAACAGTTAGGTGCTAAAGTGTCCGGTAGTGTGTCGGCTAAAAAC
CGATGCGTTTAGTAGCAGCGGAAAAGCCGCTCTAAACTAACTAAGGCACAAGACTTAGGTATAGATG
TACTGACAGAAGAAGATTTAATTAATTTATTAGAGCAACATAATGGCTGA

SEQ ID NO: 6

MTPSISEQINHLRSTLEQHSYNYVLDTPSIPDAEYDRLLQQLSALETQHPELITADSPTQKVGAAL
SKFEQVAHQVPMLSLDNAFSEDEFIAFNRRIKERLMSTEELTFCCPEKLDGLAVSIIYRDGVLVQAAT
RGDGLTGENVTQKVKTIRNVPLKLRGSDYPAELEVRGEVFMNAGFEKFNTEAEKRGEKVFNPRNAA
AGSLRQLDSKITAKRPLMFYAYSTGLVADGSIAEDHYQQLEKLTDWGLPLCPETKLVEGPQAALAYYT
DILTRRGELKYEIDGVVVIKINQKALQERLGFVARAPRWAIAYKFPAQEEITKLLDVEFQVGRITGATP
VARLEPVFVGGVTVSNA TLHNGDEIARLGVKVGDTVIIIRAGDVIPQITQVVLERRPDDARDIEFPVT
CPICDSHVEKVEGEAVARCTGGLVCPAQRKQAIKHFA SRKALDIDGLGDKIVDQLVDREL IKT PADLF
ILKQGHFESLERMGPKSAKNLVTALQDAKATTLAKFLYSLGIREAGEATTQNLANHFLTLENVINASI
DSL TQVSDVGEIVATHVRSFFAEQHNLDVVNALVEQGINWPELTTPPSAQEQPLAGLVVYVLTGTINTLN
RNDAKARLQQLGAKVSGSVSAKTDALVAGEKAGSKLTAKQDLGIDVLTEEDLINLLEQHNG

FIG. 11D

SEQ ID NO: 7

ATGACTCCAATTCAAACCTGAAATGGATCAACTTACTCACACCATTAAACCAACATAATATTCGTTATTA
CGTTGATGATGCTCCGTCAATACCCGATGCTGAATACGACAGATTAATTAAGCGCTTAAGTGAAGTAA
AACGTGACTATCCGCAATTTAAATCGGTAGATTACCCGACACAACGCGTCCGGTGGTATAGCATTACAA
AAATTTGCTCAAATTACCCACCTTAAACCGATGTTAAGTCTCGACAATGCGTTTGAACAAGCCGATT
TGCAGCATTAAATAAGCGTATAACTGATAAAGTCGATAGCGTCGATTATGTTTGCGAACCAAACTAG
ACGGATTGGCCGTGAGTATTACTTATCGTTTGGCGTCTTGAACGCGCCGCAACGCGAGGTGATGGC
AGTGTGGGCGAAGATATTACCGCTAATGTGCGTACTATTGTTCAATTCTCTTAAGTTACGCGGTGA
AGGATTTCCAGATTTAGTTGAAGTACGTGGCGAAGTGTATATGCTAAAGCGGCATTTGAGGCATTAA
ACCAGCGTCAAATCAGCAAAGGTGACAAAGTCTTTGTTAATCTCTCGCAACGCGAGCTGCCGGCAGTTG
CGCCAATTAGACAGTAAAAATTACCGCTTCAAGGGCTCTTGGGTTTATGCTTATGCATTAGGTGTAGT
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GCAACAAACACTTGGTTTTGTGGCTAAAGCTCCTCGATGGGCCATAGCCTATAAATTTCCAGCCCAGG
AAGAAATGACCTTGTAGAGTCTGTTGACTTTTCAGGTTGGCCGAACGGGTGCTGTTACCCCTGTGCT
CGCCTCAAACCGATATTTGTGGTGGCGTGACTGTGTGCAATGCGACCTTGACAATGCTGATGAAAT
TGCCCGTCTTGGGGTGAAAAATAGGCGATACAGTGATTATTCCCGCGCAGGTGACGTTATCCCGCAAA
TTGTTGCTATCGTGCCAGAAAAGCGCCCTGATGATGCACAAGATATTATCTTCCACTGCATTGTCTCT
GTGTGCCAAAGCATTGTTGAGCGTTTGAAGGTTGAAGCTGTAGCGCGTTGTAGTGGTGGACTTTTTTG
TGAAGCGCAACGTAAAGAGGCGATTAAACATTTTGCATCCCGTAAAGCATTAAATATTGATGGCATGG
GCGATAAAATCGTTGAGCAATTAATTGATAAAGAACTAGTCAAAACGCCAGCAGACTTGTTCCTT
ACCGCTTCTAGCATCAGCATGTTAGATCGCATGGCGATGAAGTCAGCCACAAATATTGTGCGCGCGAT
TAAACACGCTAAAGCCACTACATTAGCGCGTTTTTTATATAGTCTTGGGATCCGCGAAGTCGGCGAAG
CTACCGCCGCTAATTTAGCCCCAACCTTTGCCGAATTTGAGCGTATTCCGAAGTCTAGCGTTGAACAA
CTGCTCGAAGTCGCTGATGTTGGTGACATTTCTAGCAAAACACATTTCGACAATTTTTGACACAGCCACA
TAACATTGAAGTAATAGAGCAATTGCTTGAAGCGCGCATTAATTGGCCTGTTATTGAACAAGCTGACG
AATCCGAGCTTAGTCTTAAAGGGCAAACGTCGGTGTAACTCGTACGCTAACTCAACTTAATCGTAAC
GATGCCAAAGCCCAATTACAGGCTTTGGGCCCCAAAGTGGCTGGCAGTGTTCGAAAAATACTGATTG
CCTTGTGCTGGTGAACGAGCGGGTTCTAAATTAGCAAAAGCTGAAGAATTGCCGCTTAAGGTGATAG
ATGAACAAGCTCTGATGGATTTATTGAATGCGGCTAACTGA

SEQ ID NO: 8

MTPIQTEMDQLTHTINQHNIRYYVDDAPSIPDAEYDRLIKRLTELERDYPQFKSVDSPTQRVGGIALQ
KFAQITHLKPMLSLDNAFEQADFAAFNKRIIDKVDSVDYVCEPKLDGLAVSITYRFGVLERAAATRGDG
SVGEDITANVRTIIRSIPLKLRGEGFPDLVEVRGEVFMKAAFEALNQRIISKGDVVFVNPRNAAAGSL
RQLDSKITASRALGFYAYALGVVEGESQPMQTSYHGQLTQLQQWGIPIVSSEVKVTDLLEKVVYAYYADI
MARRSALEYEIDGVVIKVNDIAKQQLGFVAKAPRWAIAYKFPAQEEMTLLESVDFQVGRGTGAVTPVA
RLKPIFVGGVTVSNAHLHNADEIARLGVKIGDVIIRAGDVIPQIVAIIVPEKRPDDAQDIIFPLHCP
VCQSIVERLEGEAVARCSGGLFCEAQRKEAIKHFASRKALNIDGMGDKIVEQLIDKELVKTPADLFSL
TASSITMLDRMAMKSATNIVAAIKHAKATTLARFLYSLGIREVGEATAANLAQHFAEFERIRTASVEQ
LLEVADVGDIVAKHIRQFFAQPHNIEVIEQLLEAGITWPVIEQADESQLSLKGQTWVLTGTLTQLNLRN
DAKAQLQALGAKVAGSVSKNTDCLVAGEAAGSKLAKAEELGVKVIDEQALMDLLNAA

FIG. 11E

SEQ ID NO: 9

ATGAATTCTAACACTAAAATTATTTTCGTACAGGTGGGGTAGTATCATCACTTGGTAAGGGTGTAACT
TGCGGCATCTTTGGCTACTCTCTTAGAAAAGTCGTGGTCTTAATGTAACAATGATGAAGCTTGATCCAT
ACATCAATGTTGATCCAGGGACTATGAGTCCATTGCAACATGGTGAAGTTTTTGTAAACCGAAGATGGC
GCAGAGACTGATCTTGATTTAGGTCATTATGAGCGCTTTATCCGCAATAAGATGACTCAAGCAAATAA
CTTCACAACCGGTAAAGTATACCAGAGTGTGTTAAGAAGAGAGCGTAAGGGTGATTATCTAGGTGCTA
CTATCCAGGTGATTCACATATCATTGATGAGATCAAAAGGCGTATTTGTAGTGGTATTGCTGATGAT
GTTGATGTTGCGATTGTTGAGATTGGTGGTACTGTTGGTGATATCGAGTCACAACCATTTTTAGAAAGC
TATTCGTCAATTGGCATTAGAGGTAGGTGCTGATCGTGCATATGTTTATGCATTTGACCTTAGTGCCAT
ATTTAGCACCAGCAGCTGAAATCAAACTAAACCAACACACCACTCACTAAAAGATTTACGCTCTATC
GGTATTTTTCTGACATTTTAGTATGTCGTTGACACCGCGCTATTCCTAACGCCGAACGCGCTAAAAT
ATCTCTCTTCACTAATGTTGAAGAGAAAGCGGTTGTATCAATGCGTGATGTAGACAGTATTTATAAGA
TTCTTGCTTTATTAAGCTCAAGGTACCGATGAAATAGTTGTTAAGCGATTTGGTTAGATGTACCT
GAAGCCGACTTAACCTGAATGGGAAGAAGTCTTTACCATGAAGCAAATCCTATCGGTGAAGTGACAT
TGGTATGGTTGGTAAATFACACTGAATTACCTGATGCGTACAAATCAGTAAACGAAGCGTTAAAACATG
CAGGTCTTAAAAACCAAGTCACTGTAAATATTAATACATTGACTCGCAAGATGTAGAAGTCAAAGCT
GTTGAAATCTTAGCTAACTGGATGCTATTTAGTTTCTGTTGGTTTCGGTGAACGTGGTGTGGAAGG
TAAAATTTTAACGGCACAAATATGCGCGTGAAAACAAAGTACCTTATTTAGGTATTTGTTTAGGTATGC
AAGTAGCCTTAATTGAATTTGCTCGTAATGTTGCCGTTTAACTGATGCGCACAGTACTGAATTTAAT
AGCGAAACTCCACACCCAGTGGTTGGTTTAACTAGTGAATGGTTAGACGAAGAAGGCCAAGTTGAGTA
CCGAAATGAGCAATCAGATTTACGTGCTACTATCCGTTTACGTTTACAATTGTGCCACTTGGTGAAAG
GTACCAAGGCTTGCGACGTATATGGTAGTGAAACAATCAATGAGAGACACCGTCATCGTTTTGAGGTA
AATAATAACTACCGAGAACAAATTAAGCAAAGCAGGTTTGATTTTCTCGGGTTTATCGTCAGATAAAAG
TTTAGTTGAGGTGATTGAAATAGCGGATCATCCATGTTTATTGCGGGTCAATTCCATCCTGAGTTTA
ATTCTACTCCACGTGATGGTCACCCGTTATTCGAAAGCTTTGTTGCAGCGAGTTTAAACTGCAAAAT
AATTAG

SEQ ID NO: 10

MNSNTKLIIFVTGGVVSSLGKCVTAASLATLLESRGLNVTMMKLDPYINVDPGTMSPLQHCEVFVTEDC
AETDLDLGHYERFIRNKMTQANNFTTGKVYQSVLRERKGDYLGATIQVIPHIIDEIKRRICSGIADD
VDVAIVEIGGTVGDI~~ESQFLEAIRQL~~ALEVGRDRAMFMHLTLVPYLAAAGEIKTKPTQHSVKDLRSI
GIFPDILVCRSDRAIPNAERAKISLFTNVEEKAVVSMRDVDSIYKIPALLKAQGTDEIVVKRFGLDVP
EADLTWEFEVLYHEANPIGEVTIGMVGKYTELDPDAYKSVNEALKHAGLKNQVTVNIKYIDSQDVEVKG
VEILANLDAILVPGGFGERGVECKILTAQYARENKVPYLGICLGMQVALIEFARNVAGLTDHSTEFN
SETPHPVGLISEWLDEEGQVEYRNEQSDLGGMRLGSQLCHLVKGTKACDVYGSETINERHRHREFV
NNNYREQLSKAGLIFSGLSDDKSLVEVIEIADHPWFIAGQFHPEFNSTPRDGHPLFESFVAASF~~KLQN~~
~~N~~

FIG. 11F

SEQ ID NO: 11

ATGAAACAAACTACAGTACGAATTGCCACGCGTAAAAGCGCCCTCGCCTTATGGCAAGCAGAATATGT
TAAAGCGCAACTTGAGCATTTCATGACGGTATTAATGTTGAATTAGTGCCTATGACAACGAAAGGCG
ACATCATTTTAGACACGCCTTTAGCCAAAGTCGGCGGTAAAGGTTTATTTGTAAAGAGCTTGAAGTA
GCAATGCTTGAAGACCGTGCTGATATTGCTGTTCAATCAATGAAAGATGTTCCCTGTCGATTTTCCAGA
AGGCTTAGGATTAGAAGTCATTTGTCTCGTGAAGATCCCCGTGATGCTTTTGTCTTAATACCATCA
AATCATTAAAGTGATTTACCACAAGGCTCTATTGTTGGCACCTCAAGCTTACGCCGTCAGTGTCAATTA
AAAGCAAGCCGCCCTGATTTAGATAITTCGTGATTTACGTGGCAATGTAAATACCCGCCTAAGAAAATT
AGATGAAGGTCAGTACGACGCTATTATATTAGCCGCTGCAGGCCTAATTCGCTTAGAAATGAGCGAGC
GTATTGCACAGTTTATCGAACCAGAAGAAATGCTTCCTGCAAATGGCCAAGGCGCTGTTGGCATTGAA
TGTCGTAATGATGATGCGACAATTAAAGCCTTATTAGCACCATTAGAATGTGCTACCAACCCGATTTCG
TGTTCTTGCGAAGCTGCAATGAATAGAGCATTACAAGGCGGTTGCCAGGTTCTATCGGTAGCTATG
GTGTTATTTCTGCTGATGGTAAAAATATCCACTTACGTGGCTTAGTTGGCTCTGTCGATGGTAGTGAA
ATGATAGAAAGTGAAATCACCGGCCCTGTTGAAGAAGGTGAAGCGCTCGGCAATAAACTCGCGCAAGA
GTTACTAAGCCGAGGTGCAGATAAAATTTTACAGCAAGTTTATTTCAGAAAATGATATCAAAAGAGAGTT
AA

SEQ ID NO: 12

MKQTTVRIATRKSALALWQAEYVKAQLEHFHDGINVELVPMTTKGDIIILDTPLAKVGGKGLFVKELEV
AMLEDRADIAVHSMKDVVPDFPEGLGLEVICPREDPRDAFVSNTIKSLSDLPQGSIVGTSSLRRQCQL
KASRPDLDIRDLRGNVNTRLRKLDECQYDAIILAAAGLIRLEMSERIAQFIEPEEMPLPANGQGAVGIE
CRNDDATIKALLAPLECATTRIVLAFRAMNRAIQGGCQVPIGSYGVISADGKNTHILRGLVGSVDGSE
MIESEITGPVEEGEALGNKLAQELLSRGADKILQQVYSENDIKES

SEQ ID NO: 13

ATGAAAAAACCCTAAATATCATTTTTCAGGTAATTCGCTGCCCAACATTTAGCAGCGTT
AATTAATTCTGAACATAATATTGTCCCGTTTATTGTCCCCCTGATAAACAGCTGGCCGCGGTAAAA
AACTAACAGCTTGTGCAACAAAGTTACTCGCAATAGAGCAGCAGATTATTGTTGAGCAACCTATTAAC
TTTAAAAATGAGGAAGACCAACAACAATTAGCGAAATATAACGCTGATATCATGTTGTTGTTGCTTA
TGGTCTGCTATTACCTGAAGTCATTTTAACTCTCCACGTTTAGGCTGCATTAACGTACATGGCTCAA
TTCTACCAAAATGGCGTGGTGCAGCACCTATTCAACGTTCTCTGAAGCTGGAGATAAGAAAACCGGT
GTCACCATTATGCAATGGATAAAGCCTTAGACACGGGAGACATGATTCTATCCGCTGACTGCCAAAT
AGAAAATACAGATACCAGTGCAAGTCTTTATGAAAAACTTGCCAACTTAGGGCCAACTGCCTTAGTTA
ATACATTAATATTATGGCTGAACCTGATTATCAAGCCAGTAATCATAATATCGCTCAAGATGATGAA
TTAGCGACTTATGCCAAGAACTTGATAAAACTGAAGCAGAGCTTAAGTGGCAATTCAGTGCTGATGA
ACTACATCGAAAAATTCGTGCTTATATTCCTTGCCAGTTGCTCAATTTACCTTTACAGAATCTGAAG
GTAAGCAGCATAGGTTACGCATATGGCAAGCATCCGTGCAAGAATATCGAGGCAATGCTGATCCAGGC
ACGATAATAAAGGCAGACAAAGAAGCGATAGAAGTAGCAACAACAGTGGTTCGTTACGACTAGAAGT
CATTCAACTTCCAGGGAAAAAAGCATTAGCCGTAAGACATCCTAAATGGTTCGACGCGATTGGTTCTG
TTGTTGGCAGCACTATTAACAAGCTAGGATAA

SEQ ID NO: 14

MKKPLNIIIFAGTPEFAAQHLAALINSEHNIVAVYCPPDKPAGRGKKLTACATKLLAIEHDIIVEQPIN
FKNEEDQQQLAKYNADIMVVVAYGLLLPEVILNSPRLGCINVHGSILPKWRGAAPIQRSLEAGDKKTG
VTIMQMDKGLDTGDMILSAECEIENTDTSASLYEKLANLGPALVNTLTIMAEPDYQASNHNIAQDDE
LATYAKKLDKTEAELNWQFSADELHRKIRAYIPWPVAQFTFTESEGKQHRLRIWQASVQFEYRGNADPG
TIIKADKEGIEVATTSGSLRLEVIQLPGKKALAVKDILNGRSDWVVGSTINKLG

FIG. 11G

SEQ ID NO: 15

ATGAGTCTAAATCATGGCCAAGGTAATAAAGATTTAGCAAAAACTTTGTTAGTCATGGCTGGTGGCAC
CGGTGGACATATAATCCCTGGTATTGCGGTGCGCGATGAGCTGAAAAGCGCAAGGATGGAAAAATCCAT
GGTTGGGAAGTGGCGATCGTATGGAAGCTCAAATTGTACCTATGCATGGTTATGATATTTGTTTTATC
AATATAAGTGGTCTGCGTGGTAAAAATCTATTAACAACGCTTGTTATGCCTTTTAAATTGTTAAGGTC
GCTTTTTCAAGCGAGACGCGTGATTAAACAGTGAAACCTGATGTTGTTATAGGCATGGGTGGCTATG
CAAGTGCTCCGGTGGTTTGGCCGCTTGGCTAAGTAAAATACCGCTAATCGTTCATGAACAAAATGCT
GCTGCCGGATTAAGTAATCGCTTGTTAGCGCGTATCGCCAATAAAGTATGCTGCGCCTTTCCTAATGC
ATTTGTTAGCGGAATTGATGTTGAAGTGGTTGGTAATCCTTTACGCGCGTCAATCGGTCAGCAAGCAC
TGGTTTCAGAAAATATAGATCAAAGCCACGAAGGTAGTAAAAATATTCTAGTGGTAGGTGGTAGTTTA
GGCGCTCAAGTCTTAAATAAGGTGATGCCGATAGCTTTAAGGATTTATCAGAAAGTGATGAGAAATA
TTGTATATGGCACCAAACGGGCGACAATAACCAAGCACTAGTCACCGCATCTTATAAACAGGAATATA
TTGATACTGGAAAAGTGAGAGTTACCGAATTTATTACTGATATTGCTGCTGCATATCAGTGGGCTGAT
ATAGTGATTTGTCGTGCGGGAGCGCTAACCGTTTTCAGAATTAGCCATGGCAGCAACACCAGCCATTTT
TGTACCACTACCGCATGCAGTAGATGATCATCAAACAAAAATGCGTTGTACCTCGTAAAGCGAGATG
CAGCAAAGTTATTGCCACAGGCAGAACTAAATAATGAGAGTATCACGTCGTTAATAATCGAGCTGTTT
GATCAGCCTCAAACTTTAGCTGACATGGCTAAAGCTTCTTTGAGTGCTGCAACTAGTGATGCAAGTCA
GAAAGTAGCAAAATTGTGCCAACAGCTTTCAATATCGAATGGCGCAAACTTAGAAATAATGAAGAGA
ACAAATAA

SEQ ID NO: 16

MSLNHGQGNKDLAKTLLVMAGGTGGHIFPGIAVADELKAQGWKIHWLGTADRMEAQIVPMHGYDISFI
NISGLRGKNLLTTLVMPFKLLRSLFQARRVIKTVKPDVVIGMGYASAPGGLAAWLSKIPLIVHEQNA
AAGLSNRLLARIANKVCCAFPNAFVSGIDVEVVGNPLRASIGQQALVSENIDQSHEGSKNILVVGSL
GAQVLNKMVPDSFKDLSESEKCYCIWHQTDNNQALVTASYKQFEYIDTGKVRVTEFITDIAAAYQWAD
IVICRAGALTVSELAMAATPAIFVPLPHAVDDHQTKNALYLVKRDAKLLPQAE LN NESITSLIIELF
DQPQTLADMAKASLSAATSDASQKVAKLCQQLSISNGAKLRNNEENK

FIG. 11H

SEQ ID NO: 17

GTGAGCGAGAAGGAGAAGAAAATATCCCAGCTGCAACAGCAACTGAACCAATATAACCATGAGTACTA
TGTCCTCGACCAGCCATCGGTCCCCGATGCGGAGTACGATCGCCTGATGACCGCGTTAATCGATCTGG
AAAAGACCAACCCGGAGTTGAAGACGATCGACAGTCCGTCGCAGAAGGTGGGCGGTCAGGCCCTGAAG
AGCTTCACCCAAGTGACGCATCAGCTGCCCATGCTCTCGCTTGACAACGTCTTTTCGCTGGATGACTT
CCACGCCTTCGTCAAGAGGGTCAAAGACCGTCTCAATGACAACCAGGCGATCGTGTTCTGTGCCGAGC
CGAAGCTGGACGGCCTCGCGGTATCGCTCCGCTACGAGCATGGCCAGCTCATCCAGGCGGCCACGCGG
GGCGACGGCTCAGTCGGGGAGAATATCACCACGAACATCCGGACGATCAAGTCCATCCCCCTGAAGCT
CATGGGCACT'CCCGGCAAAGACTTTCCAGACATTG'IGGAAGTCCGGGGCGAAGTGTICATGCCGAAGG
CCTCGTTCGACGCGCTGAACACCCTGGCTAAGAAACGGGGGAGAAGGGCTTCGCTAACCCGCGGAAC
GCGGCAGCCGGCAGTCTGCGTCAGCTGGACAGCAAGATCACGGCCAAGCGCAACCTGGCGTTCTATGC
CTACAGCCTAGGTTTTCGTGGGGAAACTGAGCGACGGGGGCGCGGAAAGCACCGACTTGACGAACGACT
TTTTTCGCGAACTCGCACCATGAGCGATTGTGTCAATTGAAGCGACTGGGTTTGCCGATGTGTCCGGAG
GTGCGGCTGCTAGAAATCGGAGCAGGCTTCCGACGCGTTCTACCAGSACATCCTCGCGAAGCGCTCGGC
TCTTTTCATACGAAATCGACGGTACCGTTTTGAAGGTTGACGAGATCTCCCTCCAGAAGCGCCTGGGTT
TCGTGGCGCGGGCACCGCGCTGGGCCATCGCCTACAAGTTCCAGCAGAGGAAGAGCTGACCTGCGTG
GAGGACGTAGAATTTCAAGTGGGCCGCGACCGGTGCCATCACCCCGGTTGCCCGCCTGAAGCCTGTCTT
CGTGGGCGGTGTACCCGTGAGCAACGCTACCCCTCATAACCAGGACGAGATCACACGTCTGGGGCTGA
AGGTCAACGATTTTCGTGCTGATTCGCCGGGCGAGGCGACGTTATTCCGCAGATCGTGTGCGTGGTCTCTG
GACAAAAGGCCGGGATAACGCCGTCGATATCGTCTTCCCCACGTGCTGCCCGGTGTGCGACTCGGCCGT
GGCCAAGCCCGAAGGCGAGGCGAGTCTTCCGGTGCACAGCCGGGCTCTTCTGTGCGGCCACGCGCAAGG
AAGCCATCAAGCACTTCGCCTCCCGCAAGGCCACGACGTCGACGAGTGGGCGACAAGCTCGTTCGAG
CAGCTTGTAGACGAGAAGCTGATCAACACCCCGCGGATCTGTTCAAGCTCACCGAAATCCAGGTGAG
TACCATTGACAGAATGGGAAAGAAGTCTGCCACCAACCTGATAAATGGTCTGGAGCAGGCGAAGAGCA
CTACGCTGGCGAAGTTCATTTACGGCCTGGGGATCCGGGAAGTGGGAGAGGCCACGGCCGCGAACCTG
GCCAACCACTTCTACACCCTCGCCGCGATCGAGAGCGCCAGCTTGGAGGATCTGCAGAACGTATCCGA
CGTGGGTGAGGTGCTGGCAAAGAACATCATTAAATTTCTTCAAGGAAGAGCACAACTGGCGATCGTCA
GCGGTTTGAGCGAAGTGATGCACTGGCCCACCATCGAGATCAAGTCGGCCGAGGAGCTTCTCTGGCG
GAGCAGATCTTCGTCTCTACCGGAACTCTCACCAGATGGGCCGACGGAGGCGAAGACCGCCTTGCA
ATCCCTGGGCGCTAAGGTCTCGGGCTCCGTCTCCAAGAACACCCACTTCGTGGTTGCGGGCGACAAGG
CTGGCAGCAAGCTGACGAAGGCGCAGGACCTCGGCATCTCAGTCCTGACAGAGGATGGCCTGGTCGCC
CTGCTGGCAGAGCACGGCATCACCAT

SEQ ID NO: 18

MSEKEKKISQLOOQLNQYNHEYVLDQPSVPDAEYDRLMTALIDLEKTNPELKTIDSPSQKVGGOALK
SFTQVTHQLPMLSLDNVFLDDFHAFVKRVKDRLNDNQAIIVFCAEPKLDGLAVSLRYEHGQLIQAATR
GDGSVGENITTNIRTIKSIPLKLMGTPGKDFPDIVEVRGEVFMKASFDALNTLAKKRGEKGFANPRN
AAAGSLRQLDSKITAKRNLAFYAYSLGFVGLSDGGAESTDLTNDFFANSHHERLCQLKRLGLPMCPE
VRLLESEQACDAFYQDILAKRSALSIEDGTVLKVDEISLQKRLGFVARAPRWAIAYKFPAAEEELTCV
EDVEFQVGRGTGAIPTVARLKPVFVGGVTVSNATLHNQDEITRLGLKVNDVIVIRRAGDVIPQIVSVVL
DKRPDNAVDIVFPTSCPVCD SAVAKPEGEAVLRCTAGLFCAAQRKEAIKHFASRKAHDVDGLGDKLVE
QLVDEKLINTPADLFLKLEIQVSTIDRMGKKSATNLINGLEQAKSTTLAKFIYGLGIREVGEATAANL
ANHFTLAAIESASLEDLQNVSDVGEVVAKNIINFFKEEHNLAIVSGLSEVMHWPTIEIKSAEELPLA
EQIFVLTGTLTQMGRTEAKTALQSLGAKVSGSVSKNTHFVVAGDKAGSKLTKAQDLGISVLTEDGLVA
LLAEHGITI

FIG. 11I

SEQ ID NO: 19

ATGGGAAAAATTATTGGTATTGACCTAGGAACAACCTAACTCATGTGTTGCTGTTTTAGATGGCGACAG
TGTACGTGTTATTGAAAATGCAGAAGGCGATCGTACAACCTCCTTCTATTATTGGTTATACAGCCGAAG
GCGAAACATTAGTAGGTCAACCTGCTAAGCGTCAATCTGTAACCTAACCCAGAAAAACACTTTATATGCA
ATTAAACGCTTAATCGGTGCTGTTTTCGAAGATAAAGAAACACAACGTGACATCGATATTATGCCATT
TGGTATTGTTAAAGCGGATAACGGTGATGCTTGGGTTCAAGTAAAAGCGGAGAAAAATTGCTCCGCCAC
AAGTTTCAGCTGAAGTTCITAAGAAAAATGAAAAAGACTGCTGAAGACTTCTTAGGTGAAACCGTAACT
GAAGCTGTTATTACTGTACCTGCTTACTTTAACGATTACACAACGCCAAGCAACGAAAGATGCTGGTCG
TATTGCTGGTCTTGAAGTCAAACGTATtAlCAACGAACCTACTGCTGCTGCCCTTGCTTACGGCATGG
ACAAACAAGAASGTGACAAAGTTGTTGCAGTTTACGATTTAGGTGGTGGTACATTTCGATATTTCAATC
ATTGAAATTGATGAAATGGATGGCGAACACACTTTTGAAGTATTAGCGACTAACGGTGATACTCACTT
AGGTGGTGAAGATTTTGATAACCGTTTTAATCAACTACCTTGTAGCTGAATTCAAAAAAGACCAAGGCA
TGGACTTAACGTCTGATCCTTTAGCAATGCAGCGTTTAAAAGAAGCAGCAGAAAAAGCTAAATGTGAA
CTTTCTTCAGCACAAACAAACAGATGTAAACTTACCTTACATCACTGCTGATGGTTCAGGTCCTAAGCA
CATGAACATCAAAGTGACTCGTGCTAAGTTAGAATCACTAGTTGAAGATATGGTTAAAGCAACATTAG
AGCCGCTTAAACAAGCGCTTAAAGATGCAGACTTATCAGTAAGCAAGATtGATGatGTTATTTTAGTT
GGTGGTCAATCTCGTATGCCACTAGTTCAAAAAACTGTTACTGATTTCTTCGGTAAAGAGCCACGTAA
AGATGTTAACCCCTGATGAAGCAGTAGCTTCTGCTGCGCGATTCAAGCGGGTGTTCCTTTCTGGTGATG
TGACTGACGTTCTTTTATLAGACGTTACACCCTATCATTAGGTATCGAAACTATGGGCGGTGTGATG
ACTAAGGttAtCGaCAAAaaCaCTACTATcCCAATAAGCAATCACAACTTTCTCTACAGCTGATGA
TAACCAAGCTGCACTAACTGTTTCATGTTTGTGACGGGTGAGCGTAAGCAAGCTTCAGCAAAACAAATCTT
TAGGTCAATTTAACCTTGAAGGTATTGAACCAGCACAAACGTGGTACACCACAAATCGAAGTAACTTTT
GATATTGATGCTGATGGTATCTTGCACGTTACGGCTAAAGATAAGAACTACTGGTAAAGAGCAAAAAaT
CACTATCAAAGCCTCTTCTGGTTTATCTGATGAAGAAGTAGAGCAGATGGTACGTGATGCAGAAGCTA
ACGCTGATGCTGATGCTAAATTTGAAGAGCTACTAACTGCACGTAATCAAGCTGATGGCATGATTAC
GCGACTCGCAAGCAAGTTGAAGAAGCAGGCGAAGAGTTACCAAGCGAAGATAAAGAAAAAATTGAAGC
AGCATTAAGTGAAGCTTGAAGAAGCAGTTAAAGGTGATGATAAAGAAGTAATTGAAGCTAAACTCAAG
CACTTATGGAAGCATCAGCTAAGTTAATGGAAATTGCTCAAGCTAAAGAACAAGCTCAAAGCGCTCCT
GAAGGTGCTCAAGAAGCTCACGCAGCTCCTGCAGACGATGTTGTTGATGCTGAGTTTGAAGAAGTTAA
AGACAAAAAATAA

SEQ ID NO: 20

MGKIIGIDLGTTNSCVAVLDGDSVRVIENAEGDRTPPSIIIGYTAEGETLVGQPAKRQSVTNPENTLYA
TKRLIGRRFEDKETQRDIDIMPFGIIVKADNGDAWVQVKGKTIAPPQVSAEVLKMKKTAEDFLGETVT
EAVITVPAYFNDSQRQATKDAGRIAGLEVKRIINEPTAAALAYGMDKQEXDKVVAVYDLGGGTFDISI
IEIDEMDGEHTFEVLATNGDTHLGGEDFDNRLINYLVAEFKKDQGMDLTSDEPLAMQRLKEAAEKAKCE
LSSAQQTVDNLPYITADGSGPKHMNIKVTRAKLESLVEDMVKATLEPLKQALKDADLSVSKIDDVILV
GGQSRMPLVQKTVDFFGKEPRKEVNPDEAVASGAATQAGVLSGDVTDVLLLDVTPLSLGIETMGGVM
TKVIDKNTTIPTKQSQTFSTADDNQAATVHVHCQGERKQASANKSLGQFNLEGIEPAQRGTPQIEVTF
DIDADGILHVTAKDKNTGKEQKIKASSGLSDEEVEQMRDAEANADADAKFEELVTARNQADGMIH
ATRKQVEEAGEELPSEDKEKIEAALTELEEAVKGDDKEVIEAKTQALMEASAKLMEIAQAKEQAQSAP
EGAQEFADAAPADDVVDAEFEEVKDKK

FIG. 11J

SEQ ID NO: 21 Uppercase Coding sequence; underlined Francisella;
normal font Colwellia)

tataaatataATGTCGAGCTTTAACCAAGCATTGCGCGAACTAAAACGCGGAGCAGAAGAAATATTAG
TAGAAGAAGAATTATTAAACAAAGCTTAAGACAGGTAAGCCGCTAAAAATCAAAGCGGGTTTTGATCCT
ACTGCGCCTGACTTACATTTAGGCCACACGGTATTAATTAACAAGCTTCGTCAATTCCAACAATTAGG
TCATGAAGTTATTTTCTTGATTGGTGACTTCACCGGAATGATTGGTGATCCAACGGGTAAAAATGTGA
CGCGTAAGGCACTCACTAAAGAAGACGTATTAGCCAATGCTGAAACGTATAAAGAGCAAGTCTTTAAA
ATATTAGATCCCGCTAAAACAACCGTTGCCTTTAACTCTACTTGGATGGATAAATTAGGCGCGGCAGG
TATGTTACAACCTTGCCCTCTCGTCAAACGGTTGCGCGTATGATGGAGCGTGACGACTTTAAAAACGTT
ATGCTAACGGCCAGGCCATTGCTATTCATGAGTTTATGTACCCTTTAGTACAAGGTTGGGATTCAAGTT
GCGCTTGAGGCTGATGTTGAGCTGGGTGGTACCGACCAAAAAGTTTAATTTATTAATGGGTCTGAGTT
ACAAAAATCTGAAGGCCAGCGTCCACAAACAGTATTAATGATGCCATTACTTGAAGGCCTAGATGGCG
TTCAGAAAATGTCTAAGTCATTAGGCAACTACATTGGCATTACTGATACGCCTACCGACATGTTTGGC
AAAATAATGTCAATTTAGATGTATTAATGTGGCGTTACTACGAGTTACTTAGCTTTAAACCGCTTGA
AGAAATTGAAGGTTATAAAACCGAGATAGAAAATGGCAAAAATCCTCGTGATGTTAAAATTGATTTAG
CCAAAGAATTGATTGCTCGTTTTTCATGATGAAGCTGCTGCACAAGCTGCCCATGATGAATTCATCAAT
CGTTTCCAAAAAGGTGCGTTACCTGATGATATGCCGGAATTAACGATTACCACTGAAAATGGTGAAAT
AGCCATTGCTAACTTGCTTAAAGATGCAGGATTAGTCGGTAGTACTTCTGATGCCTTTAGAATGATCA
AACAAGGGGCGGCTAAAATTGATAGCGAAAAAGTAACTGACCGTAGCTTAGTTATTAGCGCTGGCAGC
ACGGCAGTTTATCAAGTCGGCAAACGTAAATTTGCTCGTATTACCATATAAATAAaggggttgtaa

SEQ ID NO: 22

MSSFNQAFaelKRGAEeILVEEELLTKLKTGKPLKIKAGFDPTAPDLHLGHTVLINKLRQFQQLGHEV
IFLIGDFTGMIGDPTGKNVTRKALTKEVDLANAETYKEQVFKILDPAKTTVAFNSTWMDKLGAAGMLQ
LASRQTVARMMERDDFFKKRYANGQAIaIHEfMYPLVQGWDSVALEADVELGGTDQKFNLLMGRELQKS
EGQRpQTVLMMPLLEGLDGVQKMSKSLGNYIGITDTPDmFGKIMSISDVLmWRYyELLSFKPLEEIE
GYKTEIENGKNPRDVKIDLAKELIARFHDEAAAQAAHDEFINRFQKGALPDDMPeltITTengeIaIa
NLLKDAGLVGSTSDaFRMIKQGAakIDSEKVTDRSLVISAGTTAVYQVGKRKFARITIK

SEQ ID NO: 23 (Uppercase Coding sequence; underlined Francisella;
normal font Colwellia)

aagtctagaagATGTCGAAAACTTGTACAGTTTATGCAGGAATTTGAGAATGAACAATAGCACACCA
GTTATAACCATTTGATGGCCCAAGTGGGGCTGGTAAAGGAACCGTTGCAAGGATAGTTGCGGACCAATT
AGGTTGGCACCTTCTTGACAGTGGGGCTATTTACCGCGTCTTAGCTGTTGCCATTCAACATCACCAAC
TTTCATTAGATGATGAAGAGCCTCTTATCCCTATGGCTGCACATTTAGATGTTCAATTTGAAATTAAT
AGTCAAGGTGAAGCTAAAGTTATTTTAGAAGGTGAAAATGTTACTGAAATTATTCGTACTGAAGAAGT
TGGCGGATTAGCATCGAAAGTAGCAGCATTTCACGTGTTAGAGAAGCGCTATTACGAAGACAACGTG
CATTTAGCGTTAGCCCTGGCTTAATTGCAGATGGTCGCGACATGGGAACCGTTGTTTTTCCGAAAGCT
CCAGTAAAAATATTTTTAACTGCTAGTGCTGAAGAACGAGCTGACCGAAGATTTAATCAGTTGAAAGA
AAAAGGAATTGATGTTAACATCGGGCGCCTTTTGGATGACATACGTCAACGAGATGAGCGAGATCAAA
ACCGCAAGGTAGCTCCTCTTATCCCGGCAGAAGGAGCGTTAACTATTGATTCTACTGATATTTCTATT
ACAGAAGTCGTCAATAAAATCCTTATGTTTGCCAATGGCAAATTAACGTAGatatttttagc

SEQ ID NO: 24

MNNSTPVITIDGPSGAGKGTVARIVADQLGWHLldSGAIYRVLAVAIQHhQLSLDDEEPLIPMAAHLd
VQFEINSQGEAKVILEGENVTEIIRTEEvgGLASKVAAFPPrVREALLRRQRAFSVSPGLIADGRDMGT
VVFpKAPVKIFLTASAEERADRRFNQLKEKGIDVNIGRLldDIRQDERDQNRKVAPLIPAEgALTID
STDISITEVvNKILMFANGKLt

FIG. 11K

SEQ ID NO: 25 (Uppercase Coding sequence; underlined Francisella;
normal font Colwellia)

ggagaatcaaATGGGAAAAATTATTGGTATCGATTTAGGCACAACAAACTCGTGTGTAGCAGTCCTTG
ATGGCGGCAAAAGCACGCGTAATTGAAAACGCAGAGGGTGATCGCACACCCCATCAATTATCGCTTAT
ACCGATGATGAAATTATTGTAGGCCAGCCAGCAAAGCGTCAGGCTGTAACCAACCCAACAAACACATT
CTTTGCCATCAAGCGTTTAATCGGTCCGTCGTTTTAAAGATGACGAAGTTCAACGTGATGTGAACATCA
TGCCATTCAAAATTATCGCAGCTGATAATGGTGATGCATGGGTTGAGTCACGTGGTAACAAAATGGCA
CCACCACAAGTTTCAGCTGAAATCTTGAAAAAGATGAAAAAGACTGCTGAAGACTTTTTAGGTGAAGA
AGTGACTGAAGCGGTTATTACCGTTCCTGCTTACTTTAACGATTCCACAACGTCAAGCCACTAAAGATG
CTGGTCGTATCGCAGGTCTTGATGTTAAGCGTATTATCAACGAACCTACTGCTGCTGCACTTGCATAC
GGTATCGACAAGAAACAAGGCGACAACATTGTTGCTGTATACGATTTAGGTGGTGGTACATTTCGATAT
CTCTATCATCGAAATTGACAGCAACGATGGTGACCAAAACATTTGAAGTACTAGCAACCAATGGTGATA
CTCACTTAGGTGGTGAAGACTTTGATAACCGTATGATTAACATTTAGCTGATGAATTCAAAAAGAC
CAAGGCTTAGATCTTCGTAGAGATCCTTTAGCAATGCAACGTTTGAAAGAAGCCGCTGAAAAAGCAAA
AATCGAGCTTTCAAGCACTAACCACACTGAAGTTAACTTGCCCTTACATCACTGCTGATGCATCAGGTC
CTAAGCATTTAGTGGTTAAAATTACTCGTGCTAAGTTAGAGTCATTAGTTGAAGATTTAATTC AACGT
ACTCTAGAGCCGCTTAAAGTTGCAC TAGCTGATGCTGATTTATCAATATCAGATATCAATGAAGTGAT
TCTTGTGGGTGGTCAGACTCGTATGCCATAAAGTACAAGAAGCAGTCACTAACTTCTTTGGCAAAGAGC
CTCGTAAAGATGTTAACCCTGATGAAGCGGTTGCTGTTGGTGCGCGATT CAGGCTGGCGTACTTTCT
GGTGAAGTGAAGACGTACTTCTACTTGACGTTACCCCACTATCTCTTGGTATTGAAACCATGGGCAG
TGTGATGACAAAGCTTATCGAGAAGAACCACTATCCCGACTAAAGCTCAGCAAGTATTCTCAACAG
CTGACGACAACCAAGTGCCGTGACTATTCACCTACTTCAAGGTGAACGTAAAGCAAGCGAGTGC TAAC
AAGTCATTAGGTCAATTTAACCTTGAAGGTATTGAGCCAGCACCACGTGGCCAACCACAGGTTGAAGT
GATGTTCCGACATTGATGCTGATCGGTATCTTACATGTGCTCGCAACAGACAAGAAAACAGGTAAGAAAC
AAAACATTACTATCAAAGCCTCTTCAGGTTTATCTGATGAAGAAGTTGAACAAATGGTACGTGATGCA
GAAGCTCATGCTGATGAAGATGCTAAATTTGAAGAGTTAGTTAAAGCGCGTAATCAAGCAGATGGTTT
AGCTCATTCAACTAAAAACAAGTTGAAGAAGCTGGCGATGCACTAGCTAGTGACGAAAAAGAAAAGA
TTGAAGCAGCAATCGCAACTTTAGAAACTGCCATAAAAGGCAAAGATAAAGAAGCCATTGATACAGCA
ACTCAAGCGCTAATCGAAGCGTCTGCTAAGTTAATGGAAATTGCTCAAGCTAAAGCTCAAGGTGAAGC
AGAAGGTCAAGCGCACGATGCTGGCCAAGAAAAGCCTGCTGATGATGTTGTTGATGCTGAGTTCAAG
AAGTTAAAGACGACAAAAAATAAataatctttt

SEQ ID NO: 26

MGKIIGIDLGTTNSCVAVLDGGKARVIENAEGDRTPSIIAYTDDEIIVGQPAKRQAVTNPTNTFFAI
KRLIGRRFKDDEVQRDVNIMPFKIIAADNGDAWVESRGNKMAPPQVSAEILKKMKKTAEDFLGEEVTE
AVITVPAYFNDSQRQATKDAGRIAGLDVKRIINEPTAAALAYGIDKKQGDNI VAVYDLGGGTDFDISII
EIDSNDGDQTFEVLATNGDTHLGGEDFDNRMINYL ADEFKKDQGLDLRRDPLAMQRLKEAAEKAKIEL
SSTNHTEVNL PYITADASGPKHLVVKITRAKLESLVEDLIQRTLEPLKVALADADLSISDINEVILVG
GQTRMPKVQEAVTNFFGKEPRKDVNPDEAVAVGAAIQAGVLSGEVKDVLLLDVTPLSLGIETMGSVMT
KLIEKNTTIPTKAQQVFSTADDNQSAVTIHVLQGERKQASANKSLGQFNLEGIEPAPRGQPQVEVMFD
IDADGILHVSATDKKTGKKQ NITIKASSGLSDEEVEQMVRDAEHADEDAKFEELVKARNQADGLAHS
TKKQVEEAGDALASDEKEKEEAAIATLETAIKGKDKEAIDTATQALIEASAKIMEIAQAKAQGEAEGQ
AHDAGQEKPADDVDAEFEEVKDDKK

FIG. 11L

SEQ ID NO: 27 (Uppercase Coding sequence; underlined Francisella;
normal font Colwellia)

ATGTTTGATTTTAACGATTCAATGGTTTCAAATGCCATAATTAAAGTTGTCGGTGTGGTGGCGGTGG
CGGTAATGCTGTACAACATATGTGTGAAGAAGTTTCTGATGTTGAGTTTTTTGCCCTAAATACAGATG
GTCAAGCATTATCAAAATCAAAAGTTCAAAATATATTACAAATTGGTACAAACCTAACAAAAGGTTTA
GGTGCTGGTGC GAATCCTGAAATTTGGTAAGAGAGCTGCAACTGAAGATAGAGCGAAAATCGAGCAACT
TTTAGAGGGTGCTGATATGGTTTTTCATCACTGCTGGTATGGGTGGTGGTACAGGTACAGGTGGAGCTC
CTGTAGTTGCAGAAGTTGCAAAAGAGATGGGTATACTTACAGTAGCTGTAGTTACTAAGCCTTTCCCT
TTTGAAGGACCAAGAAGAATGAAAGCAGCAGAGCAAGGTATTGAGTTTTTATCTAAAAGTGTTGATTC
ACTGATTACTATTCTAACGAAAAGTTACTGAAAGTACTTGGCCCTGGAACAAGCTTATTAGATGCCT
TTAAAGCAGCAATAACGTGCTACTTGGCGCCGTTT CAGGGTATTGCAGAATTAATTACTCGTCCTGGT
TTGATAAATGTCGATTTTGCTGATGTACGTACCGTTATGCTGAGATGGGTACTGCCATGATGGGTTT
TGGTACTGCTTCTGGCGATGATAGACACAAGAAGCTGCTGATGCTGCTATTTCAAGTCCTTTATTAG
AGGATGTGGATTTAGCTGGTGCACGCGGGATCTTAGTTAATATTACCGCAGGTATGGATATTAGTATC
GATGAGTTTGAAACTGTTGGTAATGCCGTTAAAGCTTTTCGCTTCTGAAAATGCCACTGTTGTTGTTGG
TGCTGTTATTGATATGGATATGACAGATGAGCTTCGTGTGACTGTTGTTGCTACGGGTATTGGCGCTG
AAAGTAAGCCTGATATTACGTTAGTAAATCCTATGCCAATGGCTGAAGCAAAAGTTGTCCGGTGGGGAT
TATACACCAGCTGCACCACAGGCAAAATTTAGCGACTGAAGCAATAGCTATGACTGATAGCAATGCGCA
GAAAGCAGCAGCAACCGACTTAGATACTTATTTAGATATTCCTGCTTTTTTACGTAAGCAAGCGGATT
AAtaaaaaccaaaatttaag

SEQ ID NO: 28

MFDFNDSMVSNAIIKVVGVGGGGGNAVQHEMCEEVSDVEFFALNTDQALS KSKVQNILQIGTNLTKGL
GAGANPEIGKRAATEDRAKIEQLLEGADMFVITAGMGGGTGTGGAPVVAEVAKEMGILTVAVVTKPPF
FEGPRRMKAAEQGIEFLSKSVDSLITIPNEKLLKVLGPGTSLLD AFKAANNVLLGAVQGI AELITRPG
LINVDFADVRTVMSEMG TAMMGS GTASGDDRAQEAADAAISSPLLEDV DLAGARGILVNITAGMDISI
DEFETVGNVKAFA SENATVVVGAVIDMDMTDEL RVTVVATGIGAESKPDITLVNPMMPMAEAKVVGGD
YTPAAPQANLATEAIAMTDSNAQKAAATDLD TYLDIPAF LRKQAD

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VACCINES COMPRISING HEAT-SENSITIVE TRANSGENES

CROSS REFERENCE TO RELATED APPLICATIONS

This is the U.S. National Stage of International Application No. PCT/CA2010/001561, filed Oct. 7, 2010, which was published in English under PCT Article 21(2), which in turn claims the benefit of U.S. Provisional Application No. 61/249,385 filed Oct. 7, 2009, and U.S. Provisional Application No. 61/322,634 filed on Apr. 9, 2010, both herein incorporated by reference.

FIELD

The technology relates to genes derived from psychrophilic bacteria, for use in the development of heat-sensitive vaccines. In one example, the technology relates to recombinant pathogens harboring the heat-sensitive gene *ligA* from *Colwellia psychrerythraea*, *Pseudoalteromonas haloplanktis*, and *Shewanella frigidimarina* and to genes *ligA*, *pyrG*, *hemC*, *ftsZ*, *cmk*, *murG*, *fnt*, and *dnaK* from *C. psychrerythraea*.

BACKGROUND

Vaccines against bacterial and viral diseases have played an important role in reducing infectious diseases in humans; however, there is still a need for innovative vaccines to reduce the current global burden of infectious diseases. Cold-adapted viruses have been used for decades as vaccines against human viral diseases. The best known example of such a vaccine is the Sabin polio virus vaccine. An alternate example is a cold adapted influenza vaccine called FluMist® (Medimmune LLC, Gaithersburg, Md., USA), which was introduced in the U.S. in 2003. FluMist® has been shown to be considerably more effective in certain demographic groups than influenza vaccines that practice the more common vaccination strategy of using inactivated virus to stimulate an immune response. Typically cold-adapted or “temperature-sensitive” (TS) viral strains have been developed by passing the virus repeatedly in eggs or cell culture at low temperatures and then testing the progeny for their inability to grow above about 37° C., generally thought of as the “normal” human body temperature.

The concept of a “normal” human body temperature takes into consideration anatomical sites, individual variations, gender, physiological conditions and ambient temperature. Despite the number of variables, the human body can function only in a very narrow temperature range, which is generally about 36° C.-39° C. If the human body core temperature falls to about 35° C., the body must be warmed or death will ensue. The skin temperature is always cooler than the body core regardless of the ambient temperature and clothing worn. At moderate temperatures (e.g., 21° C.), the temperature of the skin is about 32° C.-35° C.

Those skilled in these arts are of the view that bacteria generally have a set of about 100 to 150 genes, called “essential genes” that are absolutely required for maintenance of bacterial viability. Identifying essential genes is difficult due to their nature, as knockouts of these genes results in death of the organism. Essential genes encode proteins composed of amino acid sequences that are highly conserved among almost all bacterial genera and species. This conservation presumably reflects their common function and structure among the different species. A select number of essential

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genes have been shown to be competent in substituting for a homologue in another bacterial species and in some cases these substitutions were from distantly related bacterial species. The conservation of amino acid sequences is widespread among bacteria, the deduced amino acid sequences of essential genes from psychrophiles and thermophiles shows high identity with their mesophilic counterparts. Microbiologists have generally used conditional lethal mutations, such as TS mutations, to identify essential genes.

Many bacterial species play significant roles in the global burden of infectious diseases. However, the causative agent of tuberculosis is probably the most significant contributor to human morbidity and mortality caused by an infectious bacterial disease. Although the Bacille Calmette-Guérin (BCG) vaccine has been used for several decades to protect against tuberculosis, its low efficacy has failed to lower the incidence of tuberculosis to acceptable levels.

SUMMARY

The present disclosure provides methods for engineering, producing and using heat-sensitive host microbial cells. In one example, recombinant pathogens contain heat-sensitive essential genes, for example inserted using homologous recombination. “Psychrophile” is a term that is applied to organisms that function optimally at cold temperatures e.g., <20° C. Bacteria that live in cold ocean water, especially the Arctic and Antarctic oceans, are examples of psychrophilic bacteria. Enzymes and other proteins in psychrophilic bacteria function better in the cold than their homologous counterparts in mesophilic bacteria. Many of the enzymes from psychrophilic bacteria are also prone to denaturation at temperatures much lower than those that would affect their mesophilic counterpart. Presumably the pattern of temperature-sensitivity of psychrophilic enzymes extends to the products of essential genes.

Methods of identifying and manipulating psychrophilic essential genes with desired TS properties are provided. In vitro and in vivo recombinant technologies can be used. *Francisella tularensis* is the etiologic agent of the zoonotic disease, tularemia. It can infect numerous animals by a variety of routes, and typically infects and grows in monocyte-derived cells in organs of the reticuloendothelial system. A closely related bacterium, *Francisella novicida*, has many of the properties of *F. tularensis*, and, in addition, is highly amenable to many genetic manipulations, including gene substitutions. The pathophysiology and genetic properties of *F. novicida* make it ideal for studying the effects of gene substitutions on a pathogenic bacterium. *F. novicida* is a mesophile with a maximal growth temperature of about 45° C.

This disclosure also provides methods to determine maximal growth temperature of both bacterial strains and their growth properties at restrictive temperatures. The recombinant bacterial strains tested grew below the restrictive temperature but not above the restrictive temperature. When a psychrophilic essential allele encoding an essential gene is inserted into an area of a mammalian body that is colder than the human body core, e.g., the skin, the recombinant pathogenic bacteria will have the ability to thrive thereby inducing an immune response. When the pathogenic recombinant bacteria migrate to organs in the human body core where the temperature is higher, they die and are unable to harm the host.

The present disclosure provides isolated temperature-sensitive essential nucleic acid molecules from a psychrophilic bacterium comprising at least 80%, at least 90%, or at least

95% sequence identity to the nucleotide sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 22, 23, or 24. In some examples, the psychrophilic bacteria are operable at a temperature of about -10°C . to about 30°C ., but inoperable at a temperature greater than about 30°C . Vectors and recombinant host cells (such as a recombinant bacterial host cell) that include such temperature-sensitive essential nucleic acid molecules from a psychrophilic bacterium are also provided. Immunogenic compositions that include such recombinant host bacteria (such as live or killed cells) are also disclosed. The disclosure also provides isolated proteins encoded by the disclosed isolated temperature-sensitive essential nucleic acid molecules, such as proteins having at least 80%, at least 90%, or at least 95% sequence identity to the amino acid sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 26, 27, or 28.

Methods of making a temperature-sensitive microbial host cell, such as a recombinant host cell, are provided. In one example the method includes introducing (for example by inserting, substituting or replacing) a nucleic acid construct into the genome of a mesophilic bacterial strain, wherein the nucleic acid construct includes a temperature-sensitive essential nucleic acid molecule from a psychrophilic bacterial strain and one or more control sequences operably linked to the temperature-sensitive essential nucleic acid molecule, wherein the temperature-sensitive essential peptide encoded by the introduced temperature-sensitive essential nucleic acid molecule is operable (e.g., functional) at a temperature less than about 30°C . and inoperable (e.g., non-functional) at a temperature greater than about 30°C . In some examples the method also includes culturing the temperature-sensitive microbial host cell at a temperature wherein the temperature-sensitive peptide is operable, whereby said microbial host cell produces a plurality of peptides; increasing the culturing temperature to a temperature at which the temperature-sensitive peptide is inoperable; maintaining said culturing for a period of time sufficient to kill the temperature-sensitive microbial host cell; and harvesting the killed temperature-sensitive microbial host cells.

Methods for producing an immune response to a bacterium in a subject using the disclosed nucleic acid molecules, proteins, and recombinant host cells are provided. In one example the method includes administering to the subject a therapeutically effective amount of a temperature-sensitive bacterium, wherein the temperature-sensitive bacterium expresses a temperature-sensitive essential nucleic acid molecule from a psychrophilic bacterial strain, thereby inducing an immune response to the bacterium. Such methods can be used to prevent or treat a bacterial infection (such as a *M. tuberculosis*, *Salmonella* or *Francisella* infection).

The foregoing and other features of the disclosure will become more apparent from the following detailed description of a several embodiments which proceeds with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1a is a flowchart illustrating an exemplary method using polymerase chain reaction (PCR), FIG. 1b is a schematic chart illustrating an exemplary method showing DNA integration-excision events that result in a gene substitution.

FIG. 2a is a schematic illustrating the sequence of the wild type (wt) *F. novicida* ligA gene as it exists normally in a chromosome, FIG. 2b is a schematic illustrating ligA_{CP} gene substitutions into the *F. novicida* chromosome according to an exemplary method of the present disclosure, FIG. 2c is a schematic illustrating ligA_{SF} gene substitution into the *F. novi-*

cida chromosome according to an exemplary method of the present disclosure, FIG. 2d is a schematic illustrating ligA_{Ph} gene substitutions into the *F. novicida* chromosome according to an exemplary method of the present disclosure, FIG. 2e is a schematic illustrating ligA_{Ph2} gene substitutions into the *F. novicida* chromosome according to an exemplary method of the present disclosure.

FIG. 3a is a graph illustrating the growth curve of wt *F. novicida* and *F. novicida* with the *C. psychrerythraea* ligA_{CP} gene substituted for the *F. novicida* homologue at 30°C ., FIG. 3b is a graph illustrating the growth curve of *F. novicida* with the *C. psychrerythraea* ligA_{CP} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 33°C . after 2 hours, FIG. 3c is a graph illustrating the growth curve of *F. novicida* with the *C. psychrerythraea* ligA_{CP} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 34°C . after 3.5 hours, FIG. 3d is a graph illustrating the growth curve of *F. novicida* with the *C. psychrerythraea* ligA_{CP} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 35°C . after 2 hours, FIG. 3e is a graph illustrating the growth curve of *F. novicida* with the *C. psychrerythraea* ligA_{CP} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 37°C . after 2 hours.

FIG. 4a is a graph illustrating the growth curve of wt *F. novicida* and *F. novicida* with the *S. frigidimarina* ligA_{SF} gene substituted for the *F. novicida* homologue at 30°C ., FIG. 4b is a graph illustrating the growth curve of *F. novicida* with the *S. frigidimarina* ligA_{SF} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 33°C . after 2 hours, FIG. 4c is a graph illustrating the growth curve of *F. novicida* with the *S. frigidimarina* ligA_{SF} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 35°C . after 2 hours, FIG. 4d is a graph illustrating the growth curve of *F. novicida* with the *S. frigidimarina* ligA_{SF} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 37°C . after 2 hours.

FIG. 5a is a graph illustrating the growth curve of wt *F. novicida* and *F. novicida* with the *P. haloplanktis* ligA_{Ph} gene substituted for the *F. novicida* homologue at 30°C ., FIG. 5b is a graph illustrating the growth curve of *F. novicida* with the *P. haloplanktis* ligA_{Ph} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 33°C . after 2 hours, FIG. 5c is a graph illustrating the growth curve of *F. novicida* with the *P. haloplanktis* ligA_{Ph} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 35°C . after 2 hours, FIG. 5d is a graph illustrating the growth curve of *F. novicida* with the *P. haloplanktis* ligA_{Ph} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 30°C . to 37°C . after 2 hours.

FIG. 6a is a graph illustrating the growth curve of wt *F. novicida* and *F. novicida* with the *P. haloplanktis* ligA_{Ph2} gene substituted for the *F. novicida* homologue at 21°C ., FIG. 6b is a graph illustrating the growth curve of *F. novicida* with the *P. haloplanktis* ligA_{Ph2} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 21°C . to 26°C . after 2 hours, FIG. 6c is a graph illustrating the growth curve of *F. novicida* with the *P. haloplanktis* ligA_{Ph2} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 21°C . to 28°C . after 2 hours, FIG. 6d is a graph illustrating the growth curve of *F. novicida* with the *P. haloplanktis* ligA_{Ph2} gene substituted for the *F. novicida* homologue and wt *F. novicida* with a temperature shift from 21°C . to 30°C . after 2 hours.

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FIG. 7 is a graph illustrating the decline in viability of wt *F. novicida* and *F. novicida*-ligA_{CP} cultures at 37° C. after being grown to late exponential phase at 33° C.

FIG. 8 is a digital image illustrating the growth of *S. ser. Typhimurium*-ligA_{CP} at 30° C. and the lack of growth at 37° C.

FIG. 9a is a graph illustrating the growth curve of wt *Mycobacterium smegmatis* and *M. smegmatis*-ligA_{CP} at 30° C., FIG. 9b is a graph illustrating the growth curve of *M. smegmatis*-ligA_{CP} and wt *M. smegmatis* with a temperature shift from 30° C. to 35° C. after 4 hours, FIG. 9c is a graph illustrating the growth curve of *M. smegmatis*-ligA_{CP} and wt *M. smegmatis* with a temperature shift from 30° C. to 37° C. after 4 hours.

FIGS. 10a-10d are a series of graphs showing the protective immunity induced by TS *F. novicida* strains.

FIGS. 11A-11L show sequences disclosed herein, with underlined portions being *F. novicida* sequence.

SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood to be included by any reference to the displayed strand.

SEQ ID NO: 1 is a full length nucleic acid coding sequence of the ligA_{CP} hybrid gene.

SEQ ID NO: 2 is the deduced 689 amino acid sequence of LigA_{CP} hybrid protein.

SEQ ID NO: 3 is a full length nucleic acid coding sequence of the ligA_{ph} hybrid gene.

SEQ ID NO: 4 is the deduced 673 amino acid sequence of LigA_{ph} hybrid protein.

SEQ ID NO: 5 is a full length nucleic acid coding sequence of the ligA_{ph2} hybrid gene.

SEQ ID NO: 6 is the deduced 673 amino acid sequence of LigA_{ph2} hybrid protein.

SEQ ID NO: 7 is a full length nucleic acid coding sequence of the ligA_{sf} hybrid gene.

SEQ ID NO: 8 is the deduced 670 amino acid sequence of LigA_{sf} hybrid protein.

SEQ ID NO: 9 is a full length nucleic acid coding sequence of the pyrG_{CP} hybrid gene.

SEQ ID NO: 10 is the deduced 545 amino acid sequence of PyrG_{CP} hybrid protein.

SEQ ID NO: 11 is a full length nucleic acid coding sequence of the hemC_{CP} hybrid gene.

SEQ ID NO: 12 is the deduced 317 amino acid sequence of HemC_{CP} hybrid protein.

SEQ ID NO: 13 is a full length nucleic acid coding sequence of the fnt_{CP} hybrid gene.

SEQ ID NO: 14 is the deduced 327 amino acid sequence of Fnt_{CP} hybrid protein.

SEQ ID NO: 15 is a full length nucleic acid coding sequence of the murG_{CP} hybrid gene.

SEQ ID NO: 16 is the deduced 387 amino acid sequence of MurG_{CP} hybrid protein.

SEQ ID NO: 17 is a full length nucleic acid coding sequence of codon optimized ligA_{CP} optimized for *M. tuberculosis*.

SEQ ID NO: 18 is the deduced 689 amino acid coding sequence of codon optimized LigA_{CP} hybrid protein with the first four codons changed to the *M. tuberculosis* form.

SEQ ID NO: 19 is a full length nucleic acid coding sequence of the dnaK_{CP} hybrid gene.

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SEQ ID NO: 20 is the deduced 638 amino acid coding sequence of DnaK_{CP} hybrid protein.

SEQ ID NOS: 21 and 22 are a full length nucleic acid coding sequence of the essential gene tyrS from *Colwellia psychrerythraea*, and the corresponding amino acid sequence, respectively.

SEQ ID NO: 23 and 24 are a full length nucleic acid coding sequence of the essential gene cmk from *Colwellia psychrerythraea* and the corresponding amino acid sequence, respectively. As shown in FIG. 11J, *F. novicida* sequence is underlined. The underlined regions correspond to the *F. novicida* sequence in both the nucleotide and amino acid sequence. The “non-underlined” is *Colwellia psychrerythraea* sequence. In the amino acid sequence there is no underlined amino acids at the end since the *F. novicida* sequence starts at the stop codon.

SEQ ID NO: 25 and 26 are a full length nucleic acid coding sequence of the essential gene dnaKsf from *Shewanella frigidimarina* and the corresponding amino acid sequence, respectively. As shown in FIG. 11K, *Francisella novicida* sequence is underlined. The underlined regions correspond to the *F. novicida* sequence in both the nucleotide and amino acid sequence. The “non-underlined” shows the *Shewanella frigidimarina* sequence. In the amino acid sequence at the beginning (MGK) is identical between *Shewanella* and *Francisella*, so it is double underlined. The single underline at the end of the amino acid sequence corresponds to the *F. novicida* sequence.

SEQ ID NO: 27 and 28 are a full length nucleic acid coding sequence of the essential geneftsZ from *Colwellia psychrerythraea* and the corresponding amino acid sequence, respectively. As shown in FIG. 11L, *Francisella novicida* sequence is underlined. The underlined regions correspond to the *F. novicida* sequence in both the nucleotide and amino acid sequence. The “non-underlined” regions are *Colwellia psychrerythraea* sequence. There is extensive *F. novicida* region at the 5'-end (N-terminus).

DETAILED DESCRIPTION

The following explanations of terms and methods are provided to better describe the present disclosure. The singular forms “a,” “an,” and “the” refer to one or more than one, unless the context clearly dictates otherwise. For example, the term “comprising a nucleic acid molecule” includes single or plural nucleic acid molecules and is considered equivalent to the phrase “comprising at least one nucleic acid molecule.” The term “or” refers to a single element of stated alternative elements or a combination of two or more elements, unless the context clearly indicates otherwise. As used herein, “comprises” means “includes.” Thus, “comprising A or B,” means “including A, B, or A and B,” without excluding additional elements.

Suitable methods and materials for the practice and/or testing of embodiments of the disclosure are described below. Such methods and materials are illustrative only and are not intended to be limiting. Other methods and materials similar or equivalent to those described herein can be used. For example, conventional methods well known in the art to which a disclosed invention pertains are described in various general and more specific references, including, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, 1989; Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 3d ed., Cold Spring Harbor Press, 2001; Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing Associates, 1992 (and Supplements to 2000); Ausubel et al., *Short*

Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology, 4th ed., Wiley & Sons, 1999; Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, 1990; and Harlow and Lane, *Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, 1999.

The references cited herein are incorporated by reference.

In order to facilitate review of the various embodiments of the disclosure, the following explanations of specific terms are provided. Unless otherwise noted, technical terms are used according to conventional usage by those skilled in the arts

Adjuvant:

A vehicle used to enhance antigenicity, for example antigenicity of a recombinant host bacterium containing a TS essential psychrophilic bacteria sequence disclosed herein. Adjuvants include a suspension of minerals (e.g., alum, aluminum hydroxide, or phosphate) on which antigen is adsorbed; or water-in-oil emulsion in which antigen solution is emulsified in mineral oil (Freund incomplete adjuvant), sometimes with the inclusion of killed mycobacteria (Freund's complete adjuvant) to further enhance antigenicity (inhibits degradation of antigen and/or causes influx of macrophages). Immunostimulatory oligonucleotides (such as those including a CpG motif) can also be used as adjuvants (for example see U.S. Pat. No. 6,194,388; U.S. Pat. No. 6,207,646; U.S. Pat. No. 6,214,806; U.S. Pat. No. 6,218,371; U.S. Pat. No. 6,239,116; U.S. Pat. No. 6,339,068; U.S. Pat. No. 6,406,705; and U.S. Pat. No. 6,429,199). Adjuvants include biological molecules (a "biological adjuvant"), such as costimulatory molecules. Exemplary adjuvants include IL-2, RANTES, GM-CSF, TNF- α , IFN- γ , G-CSF, LFA-3, CD72, B7-1, B7-2, OX-40L and 41 BBL.

Administration:

The introduction of a composition (such as an immunogenic composition) into a subject (such as a mammal, for example a human) by a selected route. Exemplary routes of administration include, but are not limited to, topical, injection (such as subcutaneous, intramuscular, intradermal, intraperitoneal, intratumoral, and intravenous), oral, sublingual, rectal, transdermal, intranasal, vaginal and inhalation routes.

Ameliorate:

The improvement of a disease or pathological condition (such as a bacterial infection) with respect to the effect of the treatment. The beneficial effect can be evidenced, for example, by a delayed onset of clinical symptoms of the disease in a susceptible subject, a reduction in severity of some or all clinical symptoms of the disease, a slower progression of the disease, an improvement in the overall health or well-being of the subject, or by other parameters well known to those skilled in the arts specific to the particular disease.

Animal:

Living multi-cellular vertebrate organisms, a category that includes mammals and birds. The term "mammal" includes both human and non-human mammals. Similarly, the term "subject" includes both human and veterinary subjects (such as mice, rats, rabbits, dogs, cats, horses, and cattle).

Antibody:

A polypeptide ligand comprising at least a light chain or heavy chain immunoglobulin variable region which specifically recognizes and binds an epitope of an antigen. Antibodies are composed of a heavy and a light chain, each of which has a variable region, termed the variable heavy (V_H) region and the variable light (V_L) region. Together, the V_H region and the V_L region are responsible for binding the antigen recognized by the antibody.

Antibodies include intact immunoglobulins and the variants and portions of antibodies well known in the art, such as Fab fragments, Fab' fragments, F(ab')₂ fragments, single chain Fv proteins ("scFv"), and disulfide stabilized Fv proteins ("dsFv"). A scFv protein is a fusion protein in which a light chain variable region of an immunoglobulin and a heavy chain variable region of an immunoglobulin are bound by a linker, while in dsFvs, the chains have been mutated to introduce a disulfide bond to stabilize the association of the chains.

Typically, a naturally occurring immunoglobulin has heavy (H) chains and light (L) chains interconnected by disulfide bonds. There are two types of light chain, lambda (λ) and kappa (κ). There are five main heavy chain classes (or isotypes) which determine the functional activity of an antibody molecule: IgM, IgD, IgG, IgA and IgE.

"Specifically binds" refers to the ability of individual antibodies to specifically immunoreact with an antigen, such as a bacterial antigen, relative to binding to unrelated proteins, such as non-bacterial proteins. The binding is a non-random binding reaction between an antibody molecule and an antigenic determinant of the T cell surface molecule. The desired binding specificity is typically determined from the reference point of the ability of the antibody to differentially bind the T cell surface molecule and an unrelated antigen, and therefore distinguish between two different antigens, particularly where the two antigens have unique epitopes. An antibody that specifically binds to a particular epitope is referred to as a "specific antibody".

In some examples, an antibody specifically binds to a target (such as a bacterial protein) with a binding constant that is at least 10^3 M^{-1} greater, 10^4 M^{-1} greater or 10^5 M^{-1} greater than a binding constant for other molecules in a sample or subject. In some examples, an antibody or fragments thereof, has an equilibrium constant (Kd) of 1 nM or less. For example, an antibody binds to a target, such as a bacterial protein with a binding affinity of at least about $0.1 \times 10^{-8} \text{ M}$, at least about $0.3 \times 10^{-8} \text{ M}$, at least about $0.5 \times 10^{-8} \text{ M}$, at least about $0.75 \times 10^{-8} \text{ M}$, at least about $1.0 \times 10^{-8} \text{ M}$, at least about $1.3 \times 10^{-8} \text{ M}$ at least about $1.5 \times 10^{-8} \text{ M}$, or at least about $2.0 \times 10^{-8} \text{ M}$. Kd values can, for example, be determined by competitive ELISA (enzyme-linked immunosorbent assay) or using a surface-plasmon resonance device such as the Biacore T100, which is available from Biacore, Inc., Piscataway, N.J.

Antigen:

A compound, composition, or substance that can stimulate the production of antibodies or a T cell response in an animal, including compositions that are injected or absorbed into an animal. An antigen reacts with the products of specific humoral or cellular immunity, including those induced by heterologous immunogens. The term "antigen" includes all related antigenic epitopes. "Epitope" or "antigenic determinant" refers to a site on an antigen to which B and/or T cells respond. In one embodiment, T cells respond to the epitope, when the epitope is presented in conjunction with an MHC molecule. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Generally, T cells recognize epitopes of continuous amino acids. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, and more usually, at least 5, about 9, or about 8-10 amino acids in a unique spatial conformation. Methods of determining spatial conformation of epitopes include, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance.

Examples of antigens include, but are not limited to, peptides, lipids, polysaccharides, and nucleic acids containing antigenic determinants, such as those recognized by an immune cell. An antigen can be a tissue-specific antigen, or a disease-specific antigen. These terms are not exclusive, as a tissue-specific antigen can also be a disease specific antigen. A tissue-specific antigen is expressed in a limited number of tissues, such as a single tissue. A tissue specific antigen may be expressed by more than one related type of tissue, such as alveolar and bronchial tissue. A disease-specific antigen is expressed coincidentally with a disease process. Specific non-limiting examples of a disease-specific antigen are an antigen whose expression correlates with, or is predictive of, a bacterial infection, such as tuberculosis. A disease-specific antigen can be an antigen recognized by T cells or B cells.

CD4:

Cluster of differentiation factor 4, a T cell surface protein that mediates interaction with the MHC Class II molecule. CD4 also serves as the primary receptor site for HIV on T cells during HIV infection. Cells that express CD4 are often helper T cells.

CD8:

Cluster of differentiation factor 8, a T cell surface protein that mediates interaction with the MHC Class I molecule. Cells that express CD8 are often cytotoxic T cells. "CD8+ T cell mediated immunity" is an immune response implemented by presentation of antigens to CD8+ T cells.

Contacting:

The process of incubating one agent in the presence of another. Thus, when a cell is contacted with an agent (such as an immunogenic composition), the cell is incubated with the agent for a sufficient period of time for the agent and the cell to interact.

Cool Parts of the Body:

Regions of a human or other mammalian body that generally have a lower temperature than other parts of the body. The concept of natural human (or other mammal) body temperature variation due to anatomical sites, gender, physiological and ambient temperature. Despite the number of variables, the human (or other mammalian) body can function only in a very narrow temperature range, hence, for example the human body core remains at about 36° C.-39° C. Cool parts of the body include skin, mouth and rectum. Skin temperature, for example, is about 32° C.-35° C. Thus, in some examples, cool parts of the body have temperatures that are at least 1° C. less, at least 2° C. less, at least 3° C. less, at least 4° C. less, at least 4° C. less, or at least 6° C. less, such as 1° C. to 8° C. less, 1° C. to 6° C. less, 2° C. to 6° C. less, or 2° C. to 4° C. less, than other parts of the body, such as the core.

Cytokine:

Proteins made by cells that affect the behavior of other cells, such as lymphocytes. In one embodiment, a cytokine is a chemokine, a molecule that affects cellular trafficking. Specific, non-limiting examples of cytokines include the interleukins (IL-2, IL-4, IL-6, IL-10, IL-21, etc.), and IFN- γ .

Degenerate Variant:

A TS essential psychrophilic bacteria nucleic acid sequence that encodes a TS essential psychrophilic bacteria protein that includes a nucleic acid sequence that is degenerate as a result of the genetic code. There are 20 natural amino acids, most of which are specified by more than one codon. Therefore, all degenerate nucleotide sequences are included in this disclosure as long as the amino acid sequence of the TS essential psychrophilic bacteria peptide encoded by the nucleotide sequence is unchanged.

Em^R:

Erythromycin resistance.

Essential Gene:

A gene that is necessary for the growth of the organism (such as a mesophilic bacterium) under all culturing conditions.

Expression Control Sequences:

Nucleic acid sequences that regulate the expression of a heterologous nucleic acid sequence to which it is operatively linked. Expression control sequences are operatively linked to a nucleic acid sequence when the expression control sequences control and regulate the transcription and, as appropriate, translation of the nucleic acid sequence. Thus expression control sequences can include appropriate promoters, enhancers, transcription terminators, a start codon (i.e., ATG) in front of a protein-encoding gene, splicing signal for introns, maintenance of the correct reading frame of that gene to permit proper translation of mRNA, and stop codons. The term "control sequences" is intended to include, at a minimum, components whose presence can influence expression, and can also include additional components whose presence is advantageous, for example, leader sequences and fusion partner sequences. Expression control sequences can include a promoter.

A promoter is a minimal sequence sufficient to direct transcription. Also included are those promoter elements which are sufficient to render promoter-dependent gene expression controllable for cell-type specific, tissue-specific, or inducible by external signals or agents; such elements may be located in the 5' or 3' regions of the gene. Both constitutive and inducible promoters, are included (see e.g., Bitter et al., *Methods in Enzymology* 153:516-544, 1987). For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage lambda, plac, ptrp, ptac (ptrp-lac hybrid promoter) and the like may be used. In one embodiment, when cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the retrovirus long terminal repeat; the adenovirus late promoter; the vaccinia virus 7.5K promoter) can be used. Promoters produced by recombinant DNA or synthetic techniques may also be used to provide for transcription of the nucleic acid sequences. In one embodiment, the promoter is a cytomegalovirus promoter.

Heat-Sensitive:

An inability to perform an essential biological function at temperatures above about 28° C. Similarly, the term "heat-sensitive protein or polypeptide" refers to a non-functional mature protein resulting from heat-induced deactivation. An enzyme that does not catalyze its known reaction efficiently enough to support growth, development or life of the organism above about 28° C. is an example of such a protein.

Heat-Sensitive Allele:

An allele comprising a gene encoding a heat-sensitive protein. Similarly the term, "heat-sensitive gene" refers to a gene encoding a heat-sensitive protein.

Host Cells:

Cells into which a heterologous nucleic acid molecule has been introduced. For example, such cells may include a nucleic acid vector that is propagated and its DNA expressed. The cell may be prokaryotic or eukaryotic. The cell can be prokaryotic, such as a bacterial cell. The term also includes any progeny of the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. However, such progeny are included when the term "host cell" is used.

Immune Response:

A response of a cell of the immune system, such as a B cell, T cell, or monocyte, to a stimulus. In one embodiment, the response is specific for a particular antigen or a particular TS recombinant microbial cell, such as mesophilic bacteria containing a psychrophile essential nucleic acid molecule provided herein. In one embodiment, an immune response is a T cell response, such as a CD4+ response or a CD8+ response. In another embodiment, the response is a B cell response, and results in the production of specific antibodies. The development of an immune response following administration of mesophilic bacteria containing a psychrophile TS essential nucleic acid molecule can be measured using routine methods known in the art, for example by measuring cytokine production as an indication of a protective immune response.

Immunogenic Composition:

Compositions that include recombinant mesophilic bacteria containing a psychrophile TS essential nucleic acid molecule that induces a measurable CTL response against a recombinant mesophilic bacteria protein, or induces a measurable B cell response (such as production of antibodies that specifically bind a recombinant mesophilic bacteria-specific protein) against a recombinant mesophilic bacteria protein. For example, the immunogenic polypeptide or a nucleic acid encoding the immunogenic polypeptide can be present in a heat-sensitive mesophilic bacteria generated using the methods provided herein, wherein the bacteria is art of an immunogenic composition that can further include pharmaceutically acceptable carriers, and/or other therapeutic agents. An immunogenic composition can optionally include an adjuvant, a PD-1 antagonist, a co-stimulatory molecule, or a nucleic acid encoding a costimulatory molecule. An immunogenic composition can be readily tested for its ability to induce a CTL by art-recognized assays.

Immunogenic Peptide:

A peptide which comprises an allele-specific motif or other sequence such that the peptide will bind an MHC molecule and induce a cytotoxic T lymphocyte ("CTL") response, or a B cell response (e.g. antibody production) against the antigen from which the immunogenic peptide is derived. Immunogenic peptides can also be identified by measuring their binding to a specific MHC protein and by their ability to stimulate CD4 and/or CD8 when presented in the context of the MHC protein.

Generally, immunogenic polypeptides can be used to induce an immune response in a subject, such as a B cell response or a T cell response. In one example, an immunogenic polypeptide, when bound to a MHC Class I molecule, activates cytotoxic T lymphocytes (CTLs) against the polypeptide. Induction of CTLs using synthetic peptides and CTL cytotoxicity assays are known in the art, see U.S. Pat. No. 5,662,907. In one example, an immunogenic peptide includes an allele-specific motif or other sequence such that the peptide will bind an MHC molecule and induce a cytotoxic T lymphocyte ("CTL") response against the antigen from which the immunogenic peptide is derived.

Immunologically Reactive Conditions:

Conditions that allow an antibody specific for a particular epitope to bind to that epitope to a greater degree than, and/or to the substantial exclusion of, binding to substantially all other epitopes. These conditions are dependent upon the format of the antibody binding reaction and typically are those utilized in immunoassay protocols or those conditions encountered in vivo. The immunologically reactive conditions employed in the disclosed methods are "physiological conditions" which include reference to conditions (e.g., temperature, osmolarity, pH) that are typical inside a living mam-

mal or a mammalian cell. While it is recognized that some organs are subject to extreme conditions, the intra-organ and intracellular environment is generally about pH 7 (e.g., from pH 6.0 to pH 8.0, or pH 6.5 to pH 7.5, such as pH 7.2), contains water as the predominant solvent, and exists at a temperature above 0° C. and below 50° C. Osmolarity is within the range that is supportive of cell viability and proliferation. These conditions are well known to those skilled in these arts.

Interferon Gamma (IFN-γ):

IFN-γ is a dimeric protein with subunits of 146 amino acids. The protein is glycosylated at two sites, and the pI is 8.3-8.5. IFN-γ is synthesized as a precursor protein of 166 amino acids including a secretory signal sequence of 23 amino acids. Two molecular forms of the biologically active protein of 20 and 25 kDa have been described. Both of them are glycosylated at position 25. The 25 kDa form is also glycosylated at position 97. The observed differences of natural IFN-γ with respect to molecular mass and charge are due to variable glycosylation patterns. 40-60 kDa forms observed under non-denaturing conditions are dimers and tetramers of IFN-γ. The human gene has a length of approximately 6 kb. It contains four exons and maps to chromosome 12q24.1.

IFN-γ can be detected by sensitive immunoassays, such as an ELISPOT test that allows detection of individual cells producing IFN-γ. Minute amounts of IFN-γ can be detected indirectly by measuring IFN-induced proteins such as Mx protein. The induction of the synthesis of IP-10 has been used also to measure IFN-γ concentrations. In addition, bioassays can be used to detect IFN-γ, such as an assay that employs induction of indoleamine 2,3-dioxygenase activity in 2D9 cells. The production of IFN-γ can be used to assess T cell activation, such as activation of a T cell by bacterial antigen.

Isolated:

A biological component (such as a nucleic acid molecule, protein or organelle) that has been substantially separated or purified away from other biological components in the cell of the organism in which the component naturally occurs, e.g., other chromosomal and extra-chromosomal DNA and RNA, proteins and organelles. Nucleic acid molecules and proteins that have been "isolated" include nucleic acid molecules and proteins purified by standard purification methods. In another embodiment, "isolated" refers to nucleic acid molecules and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids.

ligA:

A wt allele of the gene encoding NAD-dependent DNA ligase found in mesophilic bacteria such as *F. novicida*, *M. smegmatis* or *E. coli*. Furthermore, ligA with a subscript, such as ligA_{CP}, ligA_{SP}, or ligA_{PH}, refers to a wt allele of the gene encoding NAD-dependent DNA ligase found in psychrophilic bacteria. For example ligA_{CP} refers to the wt allele of ligA found in the Arctic bacterium *C. psychrerythraea* strain 34H which has a maximal growth temperature below 18° C. The ligA sequences from psychrophilic bacteria can be introduced into mesophilic bacteria, to confer temperature sensitivity to the mesophilic bacteria.

Mesophile:

An organism naturally found in environments at temperatures between about 20° C. and 50° C. A bacterial mesophile refers to a bacterium that is normally associated with a mammal and thus is normally functioning at temperatures between about 32° C. and 45° C.

Psychrophile:

An organism naturally found in environments that are permanently below 20° C., often permanently below 10° C. and sometimes below 0° C. Such permanently cold environments

include most ocean environments, permafrost soils, Arctic and Antarctic environments. Those skilled in these arts will understand that "psychrophile" and "psychrotroph" are commonly used to describe bacteria that grow in cold environments.

Psychrophilic:

Features found in psychrophiles. For example, a "psychrophilic enzyme" is an enzyme isolated from a psychrophile.

Peptide Modifications:

Analogs (non-peptide organic molecules), derivatives (chemically functionalized peptide molecules obtained starting with the disclosed peptide sequences) and variants (homologs) of proteins that can be used in the methods and compositions provided herein. Peptides are comprised of amino acids, which may be either L- and/or D-amino acids, naturally occurring and otherwise. The peptides can be modified by a variety of chemical techniques to produce derivatives having essentially the same activity as the unmodified peptides, and optionally having other desirable properties. Modifications are well known to those skilled in these arts.

Pharmaceutically Acceptable Carriers:

The pharmaceutically acceptable carriers (vehicles) useful in this disclosure are conventional. *Remington's Pharmaceutical Sciences*, by E. W. Martin, Mack Publishing Co., Easton, Pa., 19th Edition (1995), describes compositions and formulations suitable for pharmaceutical delivery of one or more therapeutic composition, such as an immunogenic composition.

The disclosed purified active compositions can be administered alone or combined with an acceptable carrier. Preparations can contain one type of therapeutic molecule, or can be composed of a combination of several types of therapeutic molecules. The nature of the carrier will depend on the particular mode of administration being utilized.

In general, the nature of the carrier will depend on the particular mode of administration being employed. For instance, parenteral formulations usually comprise injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, glycerol or the like as a vehicle. For solid compositions (for example, powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, or magnesium stearate. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

Preventing or Treating a Disease:

"Preventing" a disease refers to inhibiting the full development of a disease, for example in a person who is known to be at risk of infection with *M. tuberculosis*, or *M. leprae*. An example of a person with a known predisposition is someone living with a person diagnosed with tuberculosis, health care professionals, or someone otherwise known to have been exposed to *M. tuberculosis*. "Treatment" refers to a therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition, such as tuberculosis, after it has begun to develop.

Purified:

The term purified does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified protein preparation is one in which the protein is more pure than the protein in its originating environment within a cell. A preparation of a protein is typically purified such that the protein represents at least 50% of the total protein content of

the preparation. However, more highly purified preparations may be required for certain applications. For example, for such applications, preparations in which the protein includes at least 75% or at least 90% of the total protein content may be employed.

Recombinant:

A nucleic acid molecule that has a sequence not naturally occurring or a sequence that is made by an artificial combination of two naturally separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or by the artificial manipulation of isolated segments of nucleic acids, by genetic engineering techniques, for example. Also refers to cells into which a non-native nucleic acid molecule has been introduced.

Resistant to Infection:

Animals (e.g., mammals) that demonstrate decreased symptoms of infection compared to non-resistant animals. Evidence of resistance to infection can appear as, for example, lower rates of mortality, increased life spans measured after exposure to the infective agent, fewer or less intense physiological symptoms, such as fewer lesions, or decreased cellular or tissue concentrations of the infective agent. In one embodiment, resistance to infection is demonstrated by a heightened immune response.

Restrictive Temperature:

The lowest temperature at which an organism is unable to grow. For example, in Table 1 "restrictive temperature" specifically refers to the lowest temperature at which the *F. novicida* strain with a psychrophilic gene integrated is unable to form an isolated colony on agar media. Due to the variation in the temperature of incubators, these temperatures are interpreted as being about $\pm 1^\circ \text{C}$.

sacB Cassette:

A modular DNA sequence encoding the enzyme levansucrase from *Bacillus subtilis*. Expression of this gene is lethal in the presence of sucrose to many bacteria and can thus be used as a counter-selection agent to help select for the loss of gene sequences.

Selective Hybridization:

Hybridization under moderately or highly stringent conditions that exclude non-related nucleotide sequences, the techniques of hybridization are known to those skilled in these arts.

Sequence Identity:

The identity/similarity between two or more nucleic acid sequences, or two or more amino acid sequences, expressed in terms of the identity or similarity between the sequences. Sequence identity can be measured in terms of percentage identity; the higher the percentage, the more identical the sequences are. Sequence similarity can be measured in terms of percentage similarity (which takes into account conservative amino acid substitutions); the higher the percentage, the more similar the sequences are.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970; Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988; Higgins & Sharp, *Gene*, 73:237-44, 1988; Higgins & Sharp, *CABIOS* 5:151-3, 1989; Corpet et al., *Nuc. Acids Res.* 16:10881-90, 1988; Huang et al., *Computer Appls. in the Biosciences* 8, 155-65, 1992; and Pearson et al., *Meth. Mol. Bio.* 24:307-31, 1994. Altschul et al., *J. Mol. Biol.* 215: 403-10, 1990, presents a detailed consideration of sequence alignment methods and homology calculations.

The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al., *J. Mol. Biol.* 215:403-10, 1990) is available

from several sources, including the National Center for Biological Information (NCBI, National Library of Medicine, Building 38A, Room 8N805, Bethesda, Md. 20894) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. Additional information can be found at the NCBI web site.

BLASTN is used to compare nucleic acid sequences, while BLASTP is used to compare amino acid sequences. If the two compared sequences share homology, then the designated output file will present those regions of homology as aligned sequences. If the two compared sequences do not share homology, then the designated output file will not present aligned sequences.

Once aligned, the number of matches is determined by counting the number of positions where an identical nucleotide or amino acid residue is presented in both sequences. The percent sequence identity is determined by dividing the number of matches either by the length of the sequence set forth in the identified sequence, or by an articulated length (such as 100 consecutive nucleotides or amino acid residues from a sequence set forth in an identified sequence), followed by multiplying the resulting value by 100. For example, a nucleic acid sequence that has 1166 matches when aligned with a test sequence having 1154 nucleotides is 75.0 percent identical to the test sequence ($1166/1154 \times 100 = 75.0$). The percent sequence identity value is rounded to the nearest tenth. For example, 75.11, 75.12, 75.13, and 75.14 are rounded down to 75.1, while 75.15, 75.16, 75.17, 75.18, and 75.19 are rounded up to 75.2. The length value will always be an integer. In another example, a target sequence containing a 15-nucleotide region that aligns with 20 consecutive nucleotides from an identified sequence as follows contains a region that shares 75 percent sequence identity to that identified sequence (that is, $15/20 \times 100 = 75$).

For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). Homologs are typically characterized by possession of at least 30% sequence identity or more counted over the full-length alignment with an amino acid sequence using the NCBI Basic Blast 2.0, gapped blastp with databases such as the nr or swissprot database. Queries searched with the blastn program are filtered with DUST (Hancock and Armstrong, 1994, *Comput. Appl. Biosci.* 10:67-70). Other programs use SEG. In addition, a manual alignment can be performed. Proteins with even greater similarity will show increasing percentage identities when assessed by this method, such as at least about 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity with a protein disclosed herein. Thus in one example, a protein that can be used in the disclosed methods and compositions has at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28 and retains the ability to confer TS (such as heat-sensitivity) to a mesophilic bacteria.

One indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions, as described above. Nucleic acid sequences that do not show a high degree of identity may nevertheless encode identical or similar (conserved) amino acid sequences, due to the degeneracy of the genetic code. Changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid molecules that all encode substantially the same protein. Such homologous nucleic acid sequences can, for example, possess at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% sequence

identity with a disclosed nucleic acid sequence as determined by this method. Thus in one example, a nucleic acid sequence that can be used in disclosed methods and compositions has at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27 and retains the ability to encode a protein that can confer TS (such as heat-sensitivity) to a mesophilic bacteria. An alternative (and not necessarily cumulative) indication that two nucleic acid sequences are substantially identical is that the peptide which the first nucleic acid encodes is immunologically cross reactive with the peptide encoded by the second nucleic acid.

Temperature-Sensitive (TS)" or "Heat-Sensitive (HS):

A bacterial component (such as a protein) or bacterium that is active up to about 30° C. and inactivated at a temperature that is normally found in the human body, e.g., above about 30° C.

Tester Strain:

A mesophilic bacterium that is amenable to gene replacement allowing the substitution of a psychrophilic essential gene for the homologue naturally found in the tester strain.

Therapeutically Effective Amount:

An amount of a composition that alone, or together with an additional therapeutic agent(s) sufficient to achieve a desired effect in a subject, or in a cell, being treated with the agent. The effective amount of the agent (such as an immunogenic composition provided herein) can be dependent on several factors, including, but not limited to the subject or cells being treated, the particular therapeutic agent, and the manner of administration of the therapeutic composition. In one example, a therapeutically effective amount or concentration is one that is sufficient to prevent advancement, delay progression, or to cause regression of a disease, or which is capable of reducing symptoms caused by the disease, such as a bacterial infection (e.g., tuberculosis).

In one example, a desired response is to reduce or inhibit one or more symptoms associated with a bacterial infection. The one or more symptoms do not have to be completely eliminated for the composition to be effective. The effective amount of an agent that includes one of the disclosed immunogenic compositions that is administered to a human or veterinary subject will vary depending upon a number of factors associated with that subject, for example the overall health of the subject. An effective amount of an agent can be determined by varying the dosage of the product and measuring the resulting therapeutic response, such as the prevention of bacterial infection. Effective amounts also can be determined through various in vitro, in vivo or in situ immunoassays. The disclosed agents can be administered in a single dose, or in several doses, as needed to obtain the desired response.

In particular examples, a therapeutically effective dose of an immunogenic composition includes at least 10^2 colony forming units (CFU), such as at least 10^3 , at least 10^4 , at least 10^5 , at least 10^6 , at least 10^7 , or at least 10^8 CFU, for example 10^2 to 10^8 CFU. In one example, 10^2 to 10^8 CFU of live bacteria are administered intradermally or intranasally. However, one skilled in the art will recognize that higher or lower dosages also could be used, for example depending on the particular immunogenic composition. In particular examples, such daily dosages are administered in one or more divided doses (such as 2, 3, or 4 doses) or in a single formulation. The disclosed immunogenic composition can be administered alone, in the presence of a pharmaceutically acceptable carrier, in the presence of other therapeutic agents.

Treatment:

A therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition after it has begun to develop. In one example, the immunogenic compositions disclosed herein following administration to a mammal achieves a reduction in one or more signs of a bacterial infection.

Vector:

A nucleic acid molecule as introduced into a host cell, thereby producing a transduced or transformed host cell, referred to herein as a recombinant cell. A vector may include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication. A vector may also include one or more selectable marker gene and other genetic elements known in the art. Vectors include plasmid vectors, including plasmids for expression in gram negative and gram positive bacterial cells. Exemplary vectors include those for expression in *E. coli* and *Salmonella*. Vectors also include viral vectors, such as, but are not limited to, retrovirus, orthopox, avipox, fowlpox, capripox, suipox, adenoviral, herpes virus, alpha virus, baculovirus, Sindbis virus, vaccinia virus and poliovirus vectors.

Temperature-Sensitive Essential Genes from Psychrophilic Bacteria

It is disclosed herein that several nucleic acid molecules, and their corresponding peptides, can be introduced into a bacteria to confer temperature sensitivity (TS), such as heat-sensitivity, to the host bacteria. The resulting bacteria can be used to induce an immune response to the temperature-sensitive bacteria, such as a T cell response. Exemplary psychrophilic essential genes with desired temperature sensitivity, and their corresponding peptides, are provided herein. For example, host mesophilic bacteria can be transformed with one or more psychrophile TS essential nucleic acid molecules, thereby conferring TS to the mesophilic bacteria. The resulting recombinant mesophilic bacteria can be formulated into an immunogenic composition, to treat or prevent infection by the mesophilic bacteria. For example, recombinant mesophilic *M. tuberculosis* bacterium containing one or more psychrophile TS essential nucleic acid molecules can be used to treat or prevent tuberculosis. The same approach can be used to make TS forms of *Bacillus anthracis*, *Brucella abortus*, *Burkholderia pseudomallei*, *Haemophilus influenzae*, *Mycobacterium bovis*, *Salmonella typhi*, *Shigella dysenteriae*, *Staphylococcus aureus*, *Streptococcus pneumoniae*, and *Yersinia pestis* which cause anthrax, brucellosis, melioidosis, meningitis, bovine tuberculosis, typhoid fever, dysentery, numerous types of nosocomial infections, pneumonia, and plague. Thus, such TS bacteria can be used to treat or prevent such conditions.

Temperature-sensitive essential proteins from a psychrophilic bacterium are provided herein, such as those from *Corvella* sp., *Pseudalteromonas* sp., or *Shewanella* sp. Exemplarily proteins include ligA, pyrG, hemC, ftsZ, cmk, murG, fnt, and dnaK. Exemplary sequences are provided in the amino acid sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, and 28. However, one skilled in the art will appreciate that variant sequences can also be used. For example, a peptide having a sequence that is at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to the amino acid sequence set forth in one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, and 28 is encompassed by the present disclosure, and can be used in the methods provided herein. Variant sequences retain the biological activity

of the native temperature-sensitive essential protein from a psychrophilic bacterium, such as conferring the ability to make a bacterium TS (such as heat sensitivity), for example operable at a temperature of -10°C . to about 30°C . (such as 0°C . to 30°C .), but inoperable at a temperature greater than about 30°C . (for example 4°C . to 30°C .), such as greater than 35°C . Exemplary sequences can be obtained using computer programs that are readily available on the internet and the amino acid sequences set forth herein. In one example, the variant peptide retains a function of the native protein, such as the ability to confer temperature sensitivity to a bacterium.

A specific, non-limiting example of a variant protein is a conservative variant of the native protein (e.g., SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, and 28). Substitutions of the amino acids sequence shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, and 28 can be made based on this table, as long as the pathogenic mesophilic bacteria are rendered TS and are able to initiate an immune response to its pathogenic antigens. For example, protein sequences can be altered without significantly altering their biological properties, for example by introducing one or more conservative amino acid substitutions. Therefore, any of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, or 28 can be modified by making 1 to 20, 1 to 15, 1 to 12, 1 to 10, or 1 to 5 conservative amino acid substitutions, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or 50 conservative amino acid substitutions, while retaining the ability to render a mesophilic bacteria temperature sensitive (TS). Examples of conservative substitutions are shown below:

Original Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln; Glu
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Minor modifications to the disclosed protein sequences can result in peptides which have substantially equivalent activity as compared to the unmodified counterpart protein described herein. Such modifications may be deliberate, as by site-directed mutagenesis, or may be spontaneous. All of the proteins produced by these modifications are included herein.

Temperature-sensitive essential proteins (and nucleic acid molecules) from a psychrophilic bacterium are disclosed herein that can be used to induce temperature sensitivity in a desired bacterial host, wherein the resulting recombinant bacteria can be used to induce an immune response (for example in a mammal). These peptides can include fragments of the full-length native protein, as long as the ability to confer temperature sensitivity in the host cell is retained. In these examples, the peptide does not include the full-length amino acid sequences set forth as 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22,

24, 26, and 28. For example no more than 10%, no more than 5%, or no more than 1% of the amino acids can be deleted, such as 1% to 5% of the amino acids.

The isolated temperature-sensitive essential proteins can be part of a fusion protein. Thus, the fusion protein can include the temperature-sensitive essential protein (see above) and a second heterologous moiety, such as a myc protein, an enzyme or a carrier (such as a hepatitis carrier protein or bovine serum albumin) covalently linked to the temperature-sensitive essential protein. In additional examples, the temperature-sensitive essential protein includes six sequential histidine residues, a β -galactosidase amino acid sequence, or an immunoglobulin amino acid sequence, for example at the C- or N-terminus of the temperature-sensitive essential protein. The temperature-sensitive essential protein can also be covalently linked to a carrier. Suitable carriers include, but are not limited to, a hepatitis B small envelope protein HBsAg.

The temperature-sensitive essential proteins disclosed herein can be chemically synthesized by standard methods, or can be produced recombinantly. An exemplary process for polypeptide production is described in Lu et al., *Federation of European Biochemical Societies Letters*. 429:31-35, 1998. Proteins can also be produced using molecular genetic techniques, such as by inserting a nucleic acid encoding a temperature-sensitive essential protein into an expression vector, introducing the expression vector into a host cell. They can also be isolated by methods including preparative chromatography and immunological separations.

Temperature-sensitive essential nucleic acid molecules from a psychrophilic bacterium are provided herein. Exemplary sequences are provided in the nucleic acid sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27. However, one skilled in the art will appreciate that variant sequences can also be used. For example, a nucleic acid molecule having a sequence that is at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to the nucleic acid sequence set forth in one of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27 (such as at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to the nucleic acid sequence set forth in nucleotides 10-2067 of SEQ ID NO: 1, nucleotides 10-2019 of SEQ ID NO: 3, nucleotides 10-2019 of SEQ ID NO: 5, nucleotides 10-2010 of SEQ ID NO: 7) is encompassed by the present disclosure, and can be used in the methods provided herein. In some examples, the codons of a nucleic acid molecule are optimized for the bacterium into which it is introduced. In some examples, such optimization does not alter the amino acid sequence encoded thereby. For example, the psychrophilic bacterium TS essential nucleic acid can be modified to optimize codon usage for the mesophilic bacterium (e.g., *M. tuberculosis* or *F. novicida*) into which the psychrophilic bacterium TS essential nucleic acid is introduced. Exemplary sequences can be obtained using computer programs that are readily available on the internet and the nucleic acid sequences set forth herein. In one example, the variant nucleic acid sequence retains the ability to encode a protein having the function of the native protein, such as the ability to confer temperature sensitivity (e.g., heat sensitivity) to a mesophilic bacterium.

The disclosed temperature-sensitive essential nucleic acid molecules from a psychrophilic bacterium include DNA, cDNA and RNA sequences which encode the temperature-sensitive essential peptide. Silent mutations in the coding sequence result from the degeneracy (i.e., redundancy) of the genetic code, whereby more than one codon can encode the

same amino acid residue. Thus, for example, leucine can be encoded by CTT, CTC, CTA, CTG, TTA, or TTG; serine can be encoded by TCT, TCC, TCA, TCG, AGT, or AGC; asparagine can be encoded by AAT or AAC; aspartic acid can be encoded by GAT or GAC; cysteine can be encoded by TGT or TGC; alanine can be encoded by GCT, GCC, GCA, or GCG; glutamine can be encoded by CAA or CAG; tyrosine can be encoded by TAT or TAC; and isoleucine can be encoded by ATT, ATC, or ATA. Tables showing the standard genetic code can be found in various sources (e.g., L. Shyer, 1988, *Biochemistry*, 3.sup.rd Edition, W.H. Freeman and Co., NY).

A nucleic acid molecule encoding a temperature-sensitive essential peptide from a psychrophilic bacterium can be cloned or amplified by in vitro methods, such as the polymerase chain reaction (PCR), the ligase chain reaction (LCR), the transcription-based amplification system (TAS), the self-sustained sequence replication system (3SR) and the Q β replicase amplification system (QB). For example, a polynucleotide encoding the protein can be isolated by polymerase chain reaction of cDNA using primers based on the DNA sequence of the molecule. A wide variety of cloning and in vitro amplification methodologies are well known to persons skilled in the art. PCR methods are described in, for example, U.S. Pat. No. 4,683,195; Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.* 51:263, 1987; and Erlich, ed., *PCR Technology*, (Stockton Press, NY, 1989). Polynucleotides also can be isolated by screening genomic or cDNA libraries with probes selected from the sequences of the desired polynucleotide under stringent hybridization conditions.

The nucleic acid molecules encoding a temperature-sensitive essential peptide from a psychrophilic bacterium include a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (such as a cDNA) independent of other sequences. The nucleic acid molecules disclosed herein can be ribonucleotides, deoxyribonucleotides, or modified forms of either nucleotide. The term includes single and double forms of DNA.

The nucleic acid molecules encoding a temperature-sensitive essential peptide from a psychrophilic bacterium can be part of a vector, such as a plasmid or viral vector. Suitable vectors include retrovirus vectors, orthopox vectors, avipox vectors, fowlpox vectors, capripox vectors, suipox vectors, adenoviral vectors, herpes virus vectors, alpha virus vectors, baculovirus vectors, Sindbis virus vectors, vaccinia virus vectors and poliovirus vectors. Specific exemplary vectors are poxvirus vectors such as vaccinia virus, fowlpox virus and a highly attenuated vaccinia virus (MVA), adenovirus, baculovirus and the like. Other viral vectors that can be used include other DNA viruses such as herpes virus and adenoviruses, and RNA viruses such as retroviruses and polio.

The nucleic acid molecules encoding a temperature-sensitive essential peptide from a psychrophilic bacterium can be operably linked to at least one expression control element. The expression control elements are inserted in the vector or plasmid to control and regulate the expression of the nucleic acid sequence. For example, an expression control sequence operatively linked to a temperature-sensitive essential peptide coding sequence is ligated such that expression of the coding sequence is achieved under conditions compatible with the expression control sequences. The expression control sequences include, but are not limited to, appropriate promoters, enhancers, transcription terminators, a start codon (i.e., ATG) in front of a protein-encoding gene, splicing signal for introns, maintenance of the correct reading frame of that

gene to permit proper translation of mRNA, and stop codons. Specific examples of expression control elements include, but are not limited to, lac system, operator and promoter regions of phage lambda, yeast promoters and promoters derived from polyoma, adenovirus, retrovirus or SV40. Additional operational elements include, but are not limited to, leader sequence, termination codons, polyadenylation signals and any other sequences necessary for the appropriate transcription and subsequent translation of the nucleic acid sequence encoding the temperature-sensitive essential peptide from a psychrophilic bacterium in the host system. The expression vector can contain additional elements necessary for the transfer and subsequent replication of the expression vector containing the nucleic acid sequence in the host system. Examples of such elements include, but are not limited to, origins of replication and selectable markers. It will further be understood by one skilled in the art that such vectors are easily constructed using conventional methods (Ausubel et al., (1987) in "Current Protocols in Molecular Biology," John Wiley and Sons, New York, N.Y.) and are commercially available.

In one example, vector introduced into a host bacterium includes one or more of the following elements: (i) a prokaryotic origin of replication, so that the vector may be amplified in a prokaryotic host; (ii) a gene encoding a marker which allows selection of prokaryotic host cells that contain the vector (e.g., a gene encoding antibiotic resistance); (iii) at least one DNA sequence encoding one or more temperature-sensitive essential peptides from a psychrophilic bacterium located adjacent to a transcriptional promoter capable of directing the expression of the sequence; and (iv) DNA sequences homologous to the region of the parent virus genome where the foreign gene(s) will be inserted, flanking the construct of element (iii).

The vector can contain an additional gene that encodes a marker that will allow identification of recombinant cells containing inserted foreign DNA. These include genes that encode antibiotic or chemical resistance (e.g., see Spyropoulos et al., 1988, *J. Virol.* 62:1046; Falkner and Moss, 1988, *J. Virol.* 62:1849; Franke et al., 1985, *Mol. Cell. Biol.* 5:1918), as well as genes such as the *E. coli* lacZ gene, that permits identification of recombinant plaques by colorimetric assay.

Methods of introducing nucleic acid molecules, such as those that encode a temperature-sensitive essential peptide from a psychrophilic bacterium, are well known to those skilled in the art. Where the host is prokaryotic, such as, a bacterium, competent cells which are capable of DNA uptake can be prepared from cells harvested after exponential growth phase and subsequently treated by the CaCl₂ method using procedures well known in the art. Alternatively, MgCl₂ or RbCl can be used. Transformation can also be performed after forming a protoplast of the host cell if desired, or by electroporation. Hosts cells can include bacterial cells, such as bacteria that cause disease. Examples of such bacteria that can be used as host cells for temperature-sensitive essential nucleic acids/peptides from a psychrophilic bacterium include without limitation any one or more of (or any combination of) *Acinetobacter baumannii*, *Actinobacillus* sp., *Actinomycetes*, *Actinomyces* sp. (such as *Actinomyces israelii* and *Actinomyces naeslundii*), *Aeromonas* sp. (such as *Aeromonas hydrophila*, *Aeromonas veronii* biovar *sobria* (*Aeromonas sobria*), and *Aeromonas caviae*), *Anaplasma phagocytophilum*, *Alcaligenes xylosoxidans*, *Acinetobacter baumannii*, *Actinobacillus actinomycetemcomitans*, *Bacillus* sp. (such as *Bacillus anthracis*, *Bacillus cereus*, *Bacillus subtilis*, *Bacillus thuringiensis*, and *Bacillus stearothermophilus*), *Bacteroides* sp. (such as *Bacteroides fragilis*), *Bar-*

tonella sp. (such as *Bartonella bacilliformis* and *Bartonella henselae*, *Bifidobacterium* sp., *Bordetella* sp. (such as *Bordetella pertussis*, *Bordetella parapertussis*, and *Bordetella bronchiseptica*), *Borrelia* sp. (such as *Borrelia recurrentis*, and *Borrelia burgdorferi*), *Brucella* sp. (such as *Brucella abortus*, *Brucella canis*, *Brucella melintensis* and *Brucella suis*), *Burkholderia* sp. (such as *Burkholderia pseudomallei* and *Burkholderia cepacia*), *Campylobacter* sp. (such as *Campylobacter jejuni*, *Campylobacter coli*, *Campylobacter lari* and *Campylobacter fetus*), *Capnocytophaga* sp., *Cardiobacterium hominis*, *Chlamydia trachomatis*, *Chlamydomphila pneumoniae*, *Chlamydomphila psittaci*, *Citrobacter* sp. *Coxiella burnetii*, *Corynebacterium* sp. (such as, *Corynebacterium diphtherias*, *Corynebacterium jeikeum* and *Corynebacterium*), *Clostridium* sp. (such as *Clostridium perfringens*, *Clostridium difficile*, *Clostridium botulinum* and *Clostridium tetani*), *Eikenella corrodens*, *Enterobacter* sp. (such as *Enterobacter aerogenes*, *Enterobacter agglomerans*, *Enterobacter cloacae* and *Escherichia coli*, including opportunistic *Escherichia coli*, such as enterotoxigenic *E. coli*, enteroinvasive *E. coli*, enteropathogenic *E. coli*, enterohemorrhagic *E. coli*, enteroaggregative *E. coli* and uropathogenic *E. coli*) *Enterococcus* sp. (such as *Enterococcus faecalis* and *Enterococcus faecium*) *Ehrlichia* sp. (such as *Ehrlichia chafeensis* and *Ehrlichia canis*), *Erysipelothrix rhusiopathiae*, *Eubacterium* sp., *Francisella tularensis*, *Fusobacterium nucleatum*, *Gardnerella vaginalis*, *Gemella morbillorum*, *Haemophilus* sp. (such as *Haemophilus influenzae*, *Haemophilus ducreyi*, *Haemophilus aegyptius*, *Haemophilus parainfluenzae*, *Haemophilus haemolyticus* and *Haemophilus parahaemolyticus*, *Helicobacter* sp. (such as *Helicobacter pylori*, *Helicobacter cinaedi* and *Helicobacter fennelliae*), *Kingella kingii*, *Klebsiella* sp. (such as *Klebsiella pneumoniae*, *Klebsiella granulomatis* and *Klebsiella oxytoca*), *Lactobacillus* sp., *Listeria monocytogenes*, *Leptospira interrogans*, *Legionella pneumophila*, *Leptospira interrogans*, *Peptostreptococcus* sp., *Moraxella catarrhalis*, *Morganella* sp., *Mobiluncus* sp., *Micrococcus* sp., *Mycobacterium* sp. (such as *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycobacterium intracellulare*, *Mycobacterium avium*, *Mycobacterium bovis*, and *Mycobacterium marinum*), *Mycoplasma* sp. (such as *Mycoplasma pneumoniae*, *Mycoplasma hominis*, and *Mycoplasma genitalium*), *Nocardia* sp. (such as *Nocardia asteroides*, *Nocardia cyriacigeorgica* and *Nocardia brasiliensis*), *Neisseria* sp. (such as *Neisseria gonorrhoeae* and *Neisseria meningitidis*), *Pasteurella multocida*, *Plesiomonas shigelloides*, *Prevotella* sp., *Polphyromonas* sp., *Prevotella melaninogenica*, *Proteus* sp. (such as *Proteus vulgaris* and *Proteus mirabilis*), *Providencia* sp. (such as *Providencia alcalifaciens*, *Providencia rettgeri* and *Providencia stuartii*), *Pseudomonas aeruginosa*, *Propionibacterium acnes*, *Rhodococcus equi*, *Rickettsia* sp. (such as *Rickettsia rickettsii*, *Rickettsia akari* and *Rickettsia prowazekii*, *Orientia tsutsugamushi* (formerly: *Rickettsia tsutsugamushi*) and *Rickettsia typhi*), *Rhodococcus* sp., *Serratia marcescens*, *Stenotrophomonas maltophilia*, *Salmonella* sp. (such as *Salmonella enterica*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella enteritidis*, *Salmonella choleraesuis* and *Salmonella typhimurium*), *Serratia* sp. (such as *Serratia marcescens* and *Serratia Shigella* sp. (such as *Shigella dysenteriae*, *Shigella flexneri*, *Shigella boydii* and *Shigella sonnei*), *Staphylococcus* sp. (such as *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus hemolyticus*, *Staphylococcus saprophyticus*), *Streptococcus* sp. (such as *Streptococcus pneumoniae* (for example chloramphenicol-resistant serotype 4 *Streptococcus pneumoniae*, spectinomycin-resistant serotype 6B *Streptococcus pneumoniae*, streptomycin-resis-

tant serotype 9V *Streptococcus pneumoniae*, erythromycin-resistant serotype 14 *Streptococcus pneumoniae*, optochin-resistant serotype 14 *Streptococcus pneumoniae*, rifampicin-resistant serotype 18C *Streptococcus pneumoniae*, tetracycline-resistant serotype 19F *Streptococcus pneumoniae*, penicillin-resistant serotype 19F *Streptococcus pneumoniae*, and trimethoprim-resistant serotype 23F *Streptococcus pneumoniae*, chloramphenicol-resistant serotype 4 *Streptococcus pneumoniae*, spectinomycin-resistant serotype 6B *Streptococcus pneumoniae*, streptomycin-resistant serotype 9V *Streptococcus pneumoniae*, optochin-resistant serotype 14 *Streptococcus pneumoniae*, rifampicin resistant serotype 18C *Streptococcus pneumoniae*, penicillin-resistant serotype 19F *Streptococcus pneumoniae*, or trimethoprim-resistant serotype 23F *Streptococcus pneumoniae*), *Streptococcus agalactiae*, *Streptococcus mutans*, *Streptococcus pyogenes*, Group A streptococci, *Streptococcus pyogenes*, Group B streptococci, *Streptococcus agalactiae*, Group C streptococci, *Streptococcus anginosus*, *Streptococcus equisimilis*, Group D streptococci, *Streptococcus bovis*, Group F streptococci, and *Streptococcus anginosus* Group G streptococci), *Spirillum minus*, *Streptobacillus moniliformis*, *Treponema* sp. (such as *Treponema carateum*, *Treponema petenue*, *Treponema pallidum* and *Treponema endemicum*, *Tropheryma whippelii*, *Ureaplasma urealyticum*, *Veillonella* sp., *Vibrio* sp. (such as *Vibrio cholerae*, *Vibrio parahemolyticus*, *Vibrio vulnificus*, *Vibrio parahaemolyticus*, *Vibrio vulnificus*, *Vibrio alginolyticus*, *Vibrio mimicus*, *Vibrio hollisae*, *Vibrio fluvialis*, *Vibrio metchnikovii*, *Vibrio damsela* and *Vibrio furnisii*), *Yersinia* sp. (such as *Yersinia enterocolitica*, *Yersinia pestis*, and *Yersinia pseudotuberculosis*) and *Xanthomonas maltophilia* among others.

Following transformation of bacterial cells, recombinant host cells can be identified by one of several techniques. For example, expression of a gene encoding a marker or indicator gene with the temperature-sensitive gene, as described above, can be used to identify recombinant progeny. One specific non-limiting example of an indicator gene is the *E. coli* lacZ gene. Recombinant bacterial cells expressing beta-galactosidase can be selected using a chromogenic substrate for the enzyme. Once a recombinant bacterium has been identified, it can be selected and amplified for use in an immunogenic composition provided herein.

Methods of Making Temperature-Sensitive Bacterial Strains

The exemplary embodiments relate to methods for generating recombinant TS bacteria for use in stimulating an immune response to the TS bacteria. In one aspect, an exemplary TS immunogenic composition is suitable for immunoprophylaxis to prevent infectious disease or alternatively immunotherapy to treat an infectious disease. Such TS bacteria are generated by the introduction of one or more TS essential genes from psychrophilic bacteria into a target bacteria (such as a mesophilic bacteria that causes a disease that one wants to treat or prevent). Thus, the disclosure provides safe immunogenic compositions based on live genetically altered bacterial microorganisms. This was accomplished by taking advantage of essential genes from psychrophilic bacteria, by creating a fusion of the psychrophilic structural genes with the transcriptional and translational control elements of the "host" genome or by making fusions between the host gene and the psychrophilic gene. The exemplary embodiments provide live vaccines and immunogenic compositions that mimic a number of cold adapted viral vaccines and are unable to grow at the normal body temperature.

According to another exemplary embodiment it is suitable for mass production purposes, specifically of antigen; due to the TS strain's non-virulent nature the aerosols produced are rendered harmless and therefore, this methods and compositions disclosed herein can significantly reduce or eliminate human risk of infection.

Another aspect, the methods and compositions provided herein has value as a research diagnostic, or as a research/educational tool because it allows for experimentation to be performed on organisms that are normally highly pathogenic in their viable state without posing threats to the researcher.

The methods and compositions provided herein can be employed to stimulate the immune system with TS organisms with the intention of prevention or treatment of a disease.

A large number of psychrophilic bacteria contain TS genes, which can be used to generate TS mesophilic bacteria of the present disclosure. For example, one or more TS essential genes from psychrophilic bacteria can be introduced into a mesophilic bacterium (for example into a chromosome of a mesophilic bacteria), thereby generating a TS strain that can be used to induce an immune response in a subject into whom it is administered. Recombinant methods for introducing a nucleic acid into bacteria are routine in the art. Appropriate TS essential genes from psychrophilic bacteria can be identified using the methods provided herein. As shown in Tables 1 and 2, nine of the twenty one essential genes from the psychrophilic *C. psychrerhraea* were introduced into *F. novicida* and substituted for an essential host gene to generate TS strains of *F. novicida* ("Group I"). Group I genes generated a range of TS phenotypes with the restrictive temperatures of about 33° C. to 44° C. Thus, the genes of Group I can be used to generate TS strains of the present disclosure. Group II in Table 1 consists of the *C. psychrerhraea* genes that either functioned poorly or not at all in the exemplary bacterial strain *F. novicida*. *F. novicida* strains carrying an integrate with the psychrophilic essential gene resolve the integrate under counter selection pressure generated by the presence of sacB and sucrose. However, the resolved strains retain copies of both the psychrophilic gene and the *F. novicida* homologue and the strains are not TS ("Group III" in Table 1); indicating that these psychrophilic essential genes do not function in the mesophilic host. Alleles of the same gene from different psychrophilic bacteria can be selected to identify those that generate hybrid strains with the same TS properties when substituted into the chromosomes of mesophilic bacteria. The ligA alleles from three different psychrophilic bacteria generated three different TS phenotypes when substituted into the mesophile *F. novicida*. The pyrG_{CP} allele from *C. psychrerhraea* created a TS strain when substituted into *F. novicida* but the pyrG_{SF} allele from *S. frigidimarina* (SF) did not. PH refers to *P. haloplanktis*.

TABLE 1

Gene symbol	Restrictive Temp. (° C.)	Product Function	Group
ligA _{PH2}	28/PH	NAD-dependent DNA ligase	I
ligA _{SF}	33/SF	NAD-dependent DNA ligase	I
ligA _{CP}	34/CP	NAD-dependent DNA ligase	I
ligA _{PH}	36.8/PH	NAD-dependent DNA ligase	I
hemC _{CP}	36.8/CP	Porphobilinogen deaminase (Hydroxymethylbilane synthase)	I
pyrG _{CP}	37.2/CP	CTP synthetase	I
dnaK _{CP}	38.2/CP	Molecular chaperone DnaK	I

TABLE 1-continued

Gene symbol	Restrictive Temp. (° C.) Source	Product Function	Group
murG _{CP}	38.2/CP	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	I
fnt _{CP}	41/CP	Methionyl-tRNA formyltransferase	I
ftsZ _{CP}	42/CP	Cell division protein	I
cmk _{CP}	43/CP	Cytidylate kinase	I
tyrS _{CP}	44/CP	Aminoacyl tRNA synthetases for Tyr	I
adk _{CP}	>44/CP	Adenylate kinase (proved resolution)	II
accD _{CP}	>44/CP	AcetylCoA carboxylase. The <i>F. novicida</i> integrate containing accD _{CP} fails to resolve.	II
murI _{CP}	>44/CP	Glutamate racemase. The CP version of MurI appears to function poorly at all temperatures in <i>F. novicida</i> .	II
pyrG _{SF}	>44/SF	CTP synthetase	III
trxA _{CP}	>44/CP	Thioredoxin	III
glmS _{CP}	>44/CP	Glucosamine-fructose-6-phosphate aminotransferase	III
argS _{CP}	>44/CP	Aminoacyl tRNA synthetases for Arg	III
cds _{CP}	>44/CP	phosphatidate cytidyltransferase	III
murG _{CP} C	>44/CP	UDP-N-acetylmuramate-alanine ligase	III
valS _{CP}	>44/CP	Aminoacyl tRNA synthetases for Val	III
proS _{CP}	>44/CP	Aminoacyl tRNA synthetases for Pro	III
metK _{CP}	≤44/CP	S-adenosylmethionine synthetase	III
ftsW _{CP}	>44/CP	Cell division protein	III

TABLE 2

Mutation rate in <i>F. novicida</i> to temperature resistance					
Gene	Restricted Temp (° C.)	Challenge Temp (° C.)	Trial #1	Trial #2	Trial #3
ligA _{SF}	33	37	4.0×10^{-6}	3.3×10^{-7}	9.7×10^{-7}
ligA _{CP}	34	37	$<1.2 \times 10^{-10}$	$<7.93 \times 10^{-11}$	$<1.1 \times 10^{-10}$
ligA _{Ph}	36.8	39	$<1.5 \times 10^{-10}$	$<7.8 \times 10^{-11}$	$<6.2 \times 10^{-11}$
dnaK _{CP}	38.2	39.5	$<3.2 \times 10^{-10}$	$<1.9 \times 10^{-10}$	$<3.2 \times 10^{-10}$
hemC _{CP}	36.8	43	$<2.5 \times 10^{-10}$	$<3.6 \times 10^{-11}$	$<3.7 \times 10^{-11}$
pyrG _{CP}	37.2	40	8.5×10^{-8}	1.0×10^{-9}	6.5×10^{-8}
murG _{CP}	38.2	43	2.6×10^{-4}	3.0×10^{-5}	8.5×10^{-5}
dnaK _{SF}	39	42	3.1×10^{-10}	8.5×10^{-10}	

To make a TS bacterial pathogen, an essential gene from an Arctic psychrophile bacterium was substituted into the genome of a mesophilic pathogenic bacterium. The Arctic bacterial essential gene ligA_{SF} rendered *F. novicida* unable to grow at a temperature of 33° C. or higher. Table 2 outlines the restrictive temperature properties imposed on *F. novicida* following the replacement of the mesophilic essential gene for its psychrophilic counterpart. Any of the genes in Table 2 may be introduced into a pathogenic bacteria strain to create live heat-sensitive vaccines. Exemplary pathogenic bacteria include but are not limited to: *Mycobacterium* sp., *Haemophilus* sp., *Vibrio* sp., *Escherichia* sp., *Salmonella* sp., *Streptococcus* sp., *Burkholderia* sp., *Campylobacter* sp., *Neisseria* sp., and *Francisella* sp.

The disclosure relates to genes derived from psychrophilic bacteria for use in the development of heat-sensitive immunogenic compositions, and methods of using these compositions to stimulate an immune response in a subject. In a specific example, the disclosure provides recombinant pathogens (such as *Mycobacterium* sp., *Haemophilus* sp., *Vibrio* sp., *Escherichia* sp., *Salmonella* sp., *Streptococcus* sp., *Burkholderia* sp., *Campylobacter* sp., *Neisseria* sp., and *Francisella* sp.) containing one or more heat-sensitive genes,

exemplified by ligA, pyrG, hemC, ftsZ, cmk, dnaK, and fnt, that can be administered to a subject to provide a prophylactic immune response against diseases caused by such bacteria.

Methods of making a recombinant temperature-sensitive (TS) bacterial cell are provided. In one example the method includes introducing into the genome of a mesophilic bacterial strain a nucleic acid construct that includes a TS essential nucleic acid molecule from a psychrophilic bacteria (such as one that encodes a peptide that is operable at a temperature of about -10° C. to about 30° C., and/or inoperable at a temperature greater than about 30° C., for example *Corwellia* sp., *Pseudomonas* sp., or *Shewanella* sp.) and one or more control sequences operably linked to the TS essential nucleic acid molecule. The temperature-sensitive essential polynucleotide renders the mesophilic bacteria operable at a temperature less than about 30° C. and inoperable at a temperature greater than about 30° C. In some examples, the temperature-sensitive essential nucleic acid molecule includes a nucleotide sequence having at least 80%, at least 90%, or at least 95% sequence identity to the nucleotide sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27. In some examples the method also includes isolating the TS essential nucleic acid molecule from the genome of the psychrophilic bacterial strain. The method can also include constructing or generating the nucleic acid construct comprising the TS essential nucleic acid molecule and one or more control sequences operably linked to the TS essential nucleic acid molecule.

In some examples, the method further includes culturing the recombinant TS bacterial host cell at a temperature wherein the temperature-sensitive peptide is operable, whereby said recombinant TS bacterial host cell produces a plurality of peptides; increasing the culturing temperature to a temperature at which the temperature-sensitive peptide is inoperable; maintaining said culturing for a period of time sufficient to kill the recombinant TS bacterial host cell; and harvesting the killed recombinant TS bacterial host cells.

Methods of making a recombinant TS bacterial host cell can also include the following. A psychrophilic microbial genome is screened for detection of a TS essential polynucleotide that encodes a peptide that is inactivated at about greater than 30° C.; isolating said TS essential polynucleotide; constructing a nucleic acid construct comprising the TS essential polynucleotide and one or more control sequences operably linked to the TS polynucleotide; inserting the nucleic acid construct into the genome of a selected mesophilic bacterial host cell (such as *Francisella novicida*) thereby functionally replacing the host cell's homologue of the TS essential polynucleotide whereby the TS peptide (and thus the bacteria in which it is expressed) is operable at a temperature less than about 30° C., and inoperable at a temperature greater than

about 30° C. and mimics the temperature sensitivity of the original designated host bacterium. The resulting recombinant mesophilic bacterial host cell comprising the TS polynucleotide is cultured or grown at a temperature less than about 30° C. to confirm the viability of the recombinant mesophilic bacterial host cell; further culturing the recombinant mesophilic bacterial host cell comprising the TS polynucleotide at a temperature greater than about 30° C. to determine if the mesophilic bacterial host cell is killed. If the mesophilic bacterial host cell is killed, the nucleic acid construct is introduced into the genome of a selected destination mesophilic bacterial host cell (such as *Salmonella* sp. or *Mycobacterium* sp.) thereby functionally replacing the host cell's homologue of the temperature-sensitive essential polynucleotide whereby the temperature-sensitive peptide (and thus the bacteria in which it is expressed) is operable at a temperature less than about 30° C., and inoperable at a temperature greater than about 30° C. and mimics the temperature sensitivity of the original tester host bacterium.

In some examples, the mesophilic bacteria is one that is operable at a temperature selected from the range of about 10° C. to about 50° C. prior to introduction of the TS essential nucleic acid molecule from a psychrophilic bacteria. Examples of such mesophilic bacteria include strains of fermentative bacteria or bioremediation bacteria. Other exemplary bacteria are provided above.

In some examples, the TS essential nucleic acid molecule expresses a peptide during a culturing of the recombinant TS bacteria, such as a peptide having at least 80%, at least 90%, or at least 95% sequence identity to an amino acid sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, or 28.

Recombinant TS bacteria generated by these methods, as well as compositions that include such bacteria, are also provided herein.

Temperature-Sensitive Bacterial Strain Compositions

Compositions are provided that include recombinant TS bacteria provided herein. In some examples, the compositions include more than one type of recombinant TS bacteria, such as 2, 3, 4 or 5 different recombinant TS bacteria. In some examples, the recombinant TS bacteria contain two or more different TS essential psychrophilic coding sequences (such as two or more of the Group I genes listed in Table 1, such as ligA and another Group I gene). In particular examples, the recombinant TS bacteria is a *Francisella* sp., *Salmonella* sp., or *Mycobacterium* sp. (other particular examples are provided above).

In some examples, such compositions are immunogenic, in that they can stimulate an immune response in a mammal. The compositions can include other components, such as pharmaceutically acceptable carriers (such as saline), adjuvants, preservatives, combinations thereof, and the like.

Methods of Stimulating an Immune Response Using Temperature-Sensitive Bacterial Strains

The TS recombinant bacteria disclosed herein can be used to generate an immune response in a subject. In some examples, the subject is infected with a bacterium, or as at risk of being infected with a bacterium (such as a health care worker), such as *Mycobacterium tuberculosis*. Thus, in several embodiments, the methods include administering to a subject a therapeutically effective amount of one or more of the TS recombinant bacteria disclosed herein in order to generate an immune response, such as, but not limited to, a

protective immune response. For example, two or more different TS recombinant bacteria (such as those expressing different TS essential peptides from psychrophilic bacteria) can be used to generate an immune response in a subject. In some examples, the recombinant bacterium used to generate an immune response in a subject expresses two or more different temperature-sensitive essential peptides from a psychrophilic bacterium or the same temperature-sensitive essential peptide from two or more different psychrophilic bacteria.

The TS recombinant bacterium administered is selected based on the bacterial infection to be prevented or treated. For example, if the bacterial infection to be prevented or treated in the subject is tuberculosis, then the TS recombinant bacteria is *Mycobacterium tuberculosis* expressing at least one TS essential peptide from a psychrophilic bacterium. In another example, if the bacterial infection to be prevented or treated in the subject is tularemia, then the TS recombinant bacteria is *F. tularensis* expressing at least one TS essential peptide from a psychrophilic bacterium.

In exemplary applications, compositions are administered to a subject having in an amount sufficient to produce an immune response to the TS recombinant bacteria. These TS recombinant bacteria are of use to prevent a bacterial infection (such as *Mycobacterium tuberculosis*) prevent progression to disease in a subject having a latent bacterial infection, or to treat a disease resulting from the bacterial infection (such as tuberculosis). In several examples, administration of a therapeutically effective amount of a composition including the TS recombinant bacteria disclosed herein induces a sufficient immune response to decrease a symptom of a disease due to bacterial infection, to prevent the development of one or more symptoms of the disease associated with the infection, or to prevent infection with the bacteria.

In some examples, the compositions are of use in preventing a future bacterial infection. Thus, a therapeutically effective amount of the composition is administered to a subject at risk of becoming infected with a bacterium, such as *Mycobacterium tuberculosis*. For example the disclosed compositions can be used to prevent the development of tuberculosis, such as latent or active tuberculosis in the subject upon subsequent exposure to *Mycobacterium tuberculosis*. In one example, the compositions are administered to a subject with a latent *Mycobacterium tuberculosis* infection, and prevent the development of symptoms of tuberculosis. Thus the compositions are of use in treating a subject with latent tuberculosis, such that the subject does not develop active tuberculosis.

Amounts effective for these uses will depend upon the severity of the disease, the general state of the patient's health, and the robustness of the patient's immune system. In one example, a therapeutically effective amount of the compound is that which provides either subjective relief of a symptom(s) or an objectively identifiable improvement as noted by the clinician or other qualified observer. In other examples, a therapeutically effective amount is an amount sufficient to prevent an infection with the bacterium in a subject upon subsequent exposure of the subject to the bacterium. In additional examples, a therapeutically effective amount is an amount sufficient to prevent development of symptom in a subject infected with a bacterium.

The TS recombinant bacteria-containing composition can be administered by any means known to one of skill in the art either locally or systemically, such as by intramuscular injection, subcutaneous injection, intraperitoneal infection, intravenous injection, oral administration, nasal administration, transdermal administration or even anal administration. In

one embodiment, administration is by oral, subcutaneous injection or intramuscular injection. To extend the time during which the TS recombinant bacteria is available to stimulate a response, the TS recombinant bacteria can be provided as an implant, an oily injection, or as a particulate system. The particulate system can be a microparticle, a microcapsule, a microsphere, a nanocapsule, or similar particle. A particulate carrier based on a synthetic polymer has been shown to act as an adjuvant to enhance the immune response, in addition to providing a controlled release. Aluminum salts can also be used as adjuvants to produce an immune response.

In one specific, non-limiting example, the TS recombinant bacteria are administered in a manner to direct the immune response to a cellular response (that is, a cytotoxic T lymphocyte (CTL) response), rather than a humoral (antibody) response.

Optionally, one or more cytokines, such as IL-2, IL-6, IL-12, RANTES, GM-CSF, TNF- α , or IFN- γ , one or more growth factors, such as GM-CSF or G-CSF; one or more costimulatory molecules, such as ICAM-1, LFA-3, CD72, B7-1, B7-2, or other B7 related molecules; one or more molecules such as OX-40L or 41 BBL, or combinations of these molecules, can be used as biological adjuvants (see, for example, Salgaller et al., 1998, *J. Surg. Oncol.* 68 (2):122-38; Lotze et al., 2000, *Cancer J Sci. Am.* 6 (Suppl 1):S61-6; Cao et al., 1998, *Stem Cells* 16 (Suppl 1):251-60; Kuiper et al., 2000, *Adv. Exp. Med. Biol.* 465:381-90). These molecules can be administered systemically (or locally) to the subject. In some examples, IL-2, RANTES, GM-CSF, TNF- α , IFN- γ , G-CSF, LFA-3, CD72, B7-1, B7-2, B7-1 B7-2, OX-40L, 41 BBL and ICAM-1 are administered. In various embodiments, the nucleic acid encoding the biological adjuvant can be cloned into same vector as the psychrophilic TS essential peptide coding sequence, or the nucleic acid can be cloned into one or more separate vectors for co-administration into the bacteria.

A pharmaceutical composition including TS recombinant bacteria is thus provided. These compositions are of use to promote an immune response to a particular bacterium. In one embodiment, TS recombinant bacteria are mixed with an adjuvant containing two or more of a stabilizing detergent, a micelle-forming agent, and an oil. Suitable stabilizing detergents, micelle-forming agents, and oils are detailed in U.S. Pat. No. 5,585,103; U.S. Pat. No. 5,709,860; U.S. Pat. No. 5,270,202; and U.S. Pat. No. 5,695,770, all of which are incorporated by reference. A stabilizing detergent is any detergent that allows the components of the emulsion to remain as a stable emulsion. Such detergents include polysorbate, 80 (TWEEN) (Sorbitan-mono-9-octadecenoate-poly (oxy-1,2-ethanediyl); manufactured by ICI Americas, Wilmington, Del.), TWEEN 40TM, TWEEN 20TM, TWEEN 60TM, ZWITTERGENTTM 3-12, TEEMOL HB7TM, and SPAN 85TM. These detergents are usually provided in an amount of approximately 0.05 to 0.5%, such as at about 0.2%. A micelle forming agent is an agent which is able to stabilize the emulsion formed with the other components such that a micelle-like structure is formed. Such agents generally cause some irritation at the site of injection in order to recruit macrophages to enhance the cellular response. Examples of such agents include polymer surfactants described by BASF Wyandotte publications, e.g., Schmolka, *J. Am. Oil. Chem. Soc.* 54:110, 1977, and Hunter et al., *J. Immunol* 129:1244, 1981, PLURONICTM L62LF, L101, and L64, PEG1000, and TETRONICTM 1501, 150R1, 701, 901, 1301, and 130R1. The chemical structures of such agents are well known in the art. In one embodiment, the agent is chosen to have a hydrophile-lipophile balance (HLB) of between 0 and 2, as defined by

Hunter and Bennett, *J. Immun.* 133:3167, 1984. The agent can be provided in an effective amount, for example between 0.5 and 10%, or in an amount between 1.25 and 5%.

In one example oil is included in the composition. Examples of such oils include squalene, Squalane, EICOSANETM, tetratetracontane, glycerol, and peanut oil or other vegetable oils. In one specific, non-limiting example, the oil is provided in an amount between 1 and 10%, or between 2.5 and 5%. The oil should be both biodegradable and biocompatible so that the body can break down the oil over time, and so that no adverse affects, such as granulomas, are evident upon use of the oil.

In one embodiment, the adjuvant in the composition is a mixture of stabilizing detergents, micelle-forming agent, and oil available under the name PROVAX[®] (IDEC Pharmaceuticals, San Diego, Calif.). An adjuvant can also be an immunostimulatory nucleic acid, such as a nucleic acid including a CpG motif, or a biological adjuvant (see above).

Controlled release parenteral formulations can be made as implants, oily injections, or as particulate systems. For a broad overview of protein delivery systems, see Banga, *Therapeutic Peptides and Proteins: Formulation, Processing, and Delivery Systems*, Technomic Publishing Company, Inc., Lancaster, Pa., 1995. Particulate systems include microspheres, microparticles, microcapsules, nanocapsules, nanospheres, and nanoparticles. Microcapsules contain the therapeutic protein as a central core. In microspheres, the therapeutic agent is dispersed throughout the particle. Particles, microspheres, and microcapsules smaller than about 1 μ m are generally referred to as nanoparticles, nanospheres, and nanocapsules, respectively. Capillaries have a diameter of approximately 5 μ m so that only nanoparticles are administered intravenously. Microparticles are typically around 100 μ m in diameter and are administered subcutaneously or intramuscularly (see Kreuter, *Colloidal Drug Delivery Systems*, J. Kreuter, ed., Marcel Dekker, Inc., New York, N.Y., pp. 219-342, 1994; Tice & Tabibi, *Treatise on Controlled Drug Delivery*, A. Kydonieus, ed., Marcel Dekker, Inc. New York, N.Y., pp. 315-339, 1992).

In particular examples, at least 10² CFU of the TS bacteria disclosed herein are administered per dose, such as at least 10³ CFU, at least 10⁴ CFU, at least 10⁵ CFU, at least 10⁶ CFU, at least 10⁷ CFU, at least 10⁸ CFU, such as 10² to 10⁸ CFU or 10⁴ to 10⁸ CFU. In particular examples, such dosages are administered intradermal or intranasal.

Single or multiple administrations of the compositions are administered depending on the dosage and frequency as required and tolerated by the subject. In one embodiment, the dosage is administered once as a bolus, but in another embodiment can be applied periodically until a therapeutic result is achieved. In one embodiment, the dose is sufficient to treat or ameliorate symptoms or signs of bacterial infection without producing unacceptable toxicity to the subject. In another embodiment, the dose is sufficient to prevent infection with a bacterium upon subsequent exposure to the bacterium (such as *M. tuberculosis*). In a further embodiment, the dose is sufficient to prevent a symptom of bacterial infection (e.g., tuberculosis) in a subject with a latent bacterial infection. Systemic or local administration can be utilized.

Thus the disclosure provides methods for producing an immune response to a bacterium in a subject. The method can include administering to the subject a therapeutically effective amount of a TS bacterium, wherein the temperature-sensitive bacterium expresses a psychrophilic TS essential protein or nucleic acid molecule provided herein (such as a nucleic acid coding sequence in a vector), thereby inducing an immune response to the bacterium. The method can further

include administering other agents, such as an adjuvant or antimicrobial agent (such as an antibiotic). In some examples, the immune response is a protective immune response. The subject may have a bacterial infection, be at risk for acquiring a bacterial infection, or have a latent bacterial infection. Exemplary bacterial infections include infections with *M. tuberculosis*, *Salmonella* or *Francisella*.

Methods of measuring an immune response following stimulation with a bacterial antigen, such as a cytokine response, are known in the art. In some examples, the method further includes measuring an immune response following administration of the therapeutic compositions provided herein. In one example, a cytokine response is increased following administration of the composition provided herein, such as an increase relative to the absence of administration of the composition. In one example, cytokine production increases by at least 20%, such as at least 40%, at least 50%, at least 75%, at least 90%, or at least 95% following administration of the composition, relative to the cytokine response in the absence of administration of the composition.

The disclosure is illustrated by the following non-limiting Examples.

EXAMPLE 1

This example pertains to an exemplary method to create recombinant psychrophilic genes joined to flanking DNA of a mesophilic host.

FIG. 1a exemplifies the fusion PCR (also known as, “extension overlap PCR”, “overlap PCR” or “splice overlap PCR”) strategy used to incorporate the *C. psychrerythraea* essential gene (C2) into the wt *F. novicida* genome. The *C. psychrerythraea* genes were engineered with overlap PCR to contain the ribosome binding site (RBS) and the initial three codons and stop codon of the surrounding *F. novicida* genes (F1 and F3) to promote translation of the C2 gene at normal levels for *F. novicida*. The fusion PCR product was ligated to an erythromycin resistant sacB cassette (Em^R -sacB) prior to its transformation into *F. novicida*. Em^R colonies containing the fusion PCR product were grown in the presence of sucrose and colonies were screened for the loss of Em^R , the *F. novicida* essential gene (F2), and the presence of C2.

FIG. 1b illustrates the introduction of the psychrophilic gene fusion construct into the target organism’s chromosome via a single crossover event. Furthermore, it illustrates that the excision can be enhanced using the counter-selectable sacB marker. For genes that are not a part of a multi-cistronic operon the upstream pathogen genomic region was fused to the psychrophilic structural gene from codon 4 through to the stop codon. A similar approach was used when substituting a psychrophilic allele into the middle of an operon. However, as one skilled in the art can appreciate, depending on the nature of the operon, some of the codons at the C terminus of the host homologue remained if they were important for translation of the downstream cistron.

EXAMPLE 2

This example pertains to an exemplary method to insert the psychrophilic allele into the mesophilic bacteria.

FIG. 2a illustrates the substitution region for the psychrophilic ligA gene, corresponding to SEQ ID NO: 1. Additionally, it illustrates its incorporation into the wt *F. novicida* chromosome. FIGS. 2b-e illustrate the integration point for the psychrophilic ligA genes of *C. psychrerythraea*, *S. frigid-marina*, *P. haloplanktis* 1, and *P. haloplanktis* 2 respectively. The first three codons for *F. novicida* were retained in order to

maximize the potential for ligA expression levels. FIG. 2a-e illustrates that in most cases the integration and excision events result in a simple substitution of the psychrophilic gene for the mesophilic host homologue. However, the integration and excision events may also lead to the formation of a hybrid gene as illustrated in FIG. 1b.

EXAMPLE 3

This example pertains to an exemplary method to determine the maximal growth temperature of each bacterial strain and to show its growth properties at restrictive temperatures.

Each bacterial strain was tested on agar plates placed in a highly stable ($\pm 1^\circ \text{C.}$) incubator; the restrictive temperatures were defined as the lowest temperatures that did not permit the formation of isolated colonies on an agar streak plate. The growth properties at different temperatures of four different transgenic strains of *F. novicida* carrying psychrophilic ligA substitutions and the growth properties of wt *F. novicida* are shown in FIGS. 3-6. The psychrophilic ligA genes are ligA_{Cp}, ligA_{Sf}, ligA_{Ph} and ligA_{Ph2}, as represented by SEQ ID NOs: 1, 7, 3, and 5 respectively. In the first panels in FIGS. 3-6, growth is shown at a permissive temperature, i.e., a temperature below the restrictive temperature. In subsequent panels, growth of both the transgenic and wt strains is shown before and after a shift to the restrictive temperature or higher.

Extended growth curves of both the *F. novicida* transgenic and wt strains are shown as inserts in select panels of FIG. 3-6. These curves were generated by taking a fully grown culture, diluting it, and monitoring its growth in fresh growth media. More specifically, the wt and TS transgenic *F. novicida* cultures were grown at restrictive temperatures until they reached stationary phase at which point, they were diluted and re-incubated for growth at the restrictive temperatures again. The additional growth curves demonstrate that the cessation of growth exhibited by the transgenic strain is a real phenomenon, as opposed to a temporary adjustment to the temperature shift.

EXAMPLE 4

This pertains to an exemplary method used to determine the frequency of mutations that permit bacterial growth at temperatures higher than the restrictive temperature of TS *F. novicida* transgenic strains.

Cultures were grown to late logarithmic phase at the permissive growth temperature, they were then diluted in a series of 10^9 - 10^5 cells/plate on agar and incubated at temperatures about 3°C. above the restrictive temperature, as well as at temperatures about 3°C. below the restrictive temperature. From this dilution series the rate of mutations that allow for growth at higher temperatures were calculated, Table 2 exemplifies the frequency of mutation to temperature resistance in *F. novicida*. Remarkably, some of the psychrophilic genes are unable to mutate to forms that will function above their restrictive temperature. One skilled in the art may hypothesize that the millions of years required to adapt to a cold climate renders some of the psychrophilic essential gene products unable to adopt simple changes allowing them to function in temperatures typical to their mesophilic counterparts. These include ligA_{Cp}, ligA_{Ph}, hemC_{Cp}, dnaK_{Cp}, fnt_{Cp}, and dnaK_{Sf}.

EXAMPLE 5

This example pertains to an exemplary method to determine the duration of viability of the recombinant TS bacterial strains at the restrictive temperature.

An exemplary culture of a TS transgenic strain that has a maximal growth temperature of about 33° C., was grown at about 30° C. and a sample of the culture was incubated at about 37° C. to mimic the typical temperature of human body core tissues. Samples were taken at varying time points between 0-24 hours, and the individual samples were re-diluted, plated on to growth media, and then cultured at about 30° C. to determine the death rate above the restrictive temperature. As a control, the same experiment was carried out with the wt bacterium.

The persistence of *F. tularensis* strains carrying the psychrophilic essential genes within their macrophages was determined. Transgenic strains were cultured at about 30° C. and used to infect macrophages at about 37° C. in 24 well tissue culture plates using standard methods known to those skilled in these arts. For several days monitoring the infected macrophages a subset of cells were lysed and the bacteria were plated onto agar medium and incubated at about 30° C. The data generated in these experiments showed the lifespan of transgene strains during an infection with macrophages at a restrictive temperature and helped to predict the persistence of TS strains during infections.

This example can be extrapolated to provide an in vitro correlation for what can occur in a mammal. A TS transgenic strain will grow in a cool part of the body such as the skin. Replication of the strain at and about this cool site will constantly cause the TS transgenic strain progeny to be moved into the draining lymph nodes. Depending on the locations of the lymph nodes and the restrictive temperature of the TS transgenic strain, the TS progeny will die over a period of several hours. The presence of the TS transgenic strain both in its live and dead states will stimulate an immune response.

EXAMPLE 6

This pertains to an exemplary method to determine the ability of a TS essential gene from a psychrophile to impart its TS phenotype on a mesophilic bacterium. Specifically, it provides a method for transferring a psychrophilic essential gene encoding a TS product to a variety of bacteria as well as the transfer of the TS essential gene between mesophiles.

Several psychrophilic essential genes were substituted into the genome of the mesophilic bacterium *F. novicida*. Multiple approaches can be used to inserting a psychrophilic essential gene into a given bacterium in place of its mesophilic homologue. Furthermore, it can be appreciated that one can substitute a given psychrophilic essential gene into many different bacteria. The following three methods exemplify various ways of substituting ligA_{CP} into three different bacteria. A common approach to gene substitution is illustrated in FIG. 1b, and involves the integration of a foreign gene in a bacterium that is in close proximity to the hosts' homologous gene through PCR. Following integration, a counter selective marker, such as sacB, can be used to help identify the results of the integration and excision events. Specifically this approach was used to replace the *F. novicida* ligA gene with the psychrophilic ligA_{CP} gene.

An alternate approach was used to replace the *S. enterica* ligA. The strain of *S. enterica* used had a bacteriophage Mu insertion in the chromosomal copy of ligA (Park et al., 1989. *J. Bacterial.* 171: 2173-80). A wt copy of the bacteriophage T4 DNA ligase was carried on the ampicillin resistant plasmid, pBR313. The ligA_{CP} gene was introduced on the compatible chloramphenicol resistant plasmid, pSUP2716, and the recombinant *S. enterica* strain was cultured in the absence of ampicillin and the presence of chloramphenicol. These growth conditions allow the pBR313:T4 DNA ligase recom-

binant plasmid to be lost. *S. enterica* strains that had lost the plasmid encoding the T4 DNA ligase, rendering them ampicillin sensitive, were dependant on the ligA_{CP} for viability and were TS.

Another alternate approach can be employed when introducing a psychrophilic essential gene into Gram-positive bacteria. The method of insertion of ligA_{CP} into *M. smegmatis* described herein exemplifies this method. A version of ligA_{CP} (SEQ ID NOS: 17 and 18) designed with optimal codons was cloned into the mycobacterial plasmid, pSM1; this a precautionary step due to the low G+C content in the ligA_{CP} gene when compared to that of the *M. smegmatis* and *M. tuberculosis* ligA genes. The recombinant pSMT3:ligA_{CP} was electroporated into *M. smegmatis*. Subsequently a large fragment of the *M. smegmatis* ligA gene was deleted resulting in a strain dependent on ligA_{CP} for viability. This strain was TS at about 34° C. This temperature is reflective of the TS nature of the *F. novicida* transgene strain encoding ligA_{CP}.

This example illustrates the use of a mesophilic tester strain which contains a psychrophilic essential gene to predict the TS phenotype when said psychrophilic essential gene is used to construct a transgene strain of another mesophilic bacterium. In this example, the tester strain was *F. novicida*. The substitution of ligA_{CP} for the *F. novicida* ligA homologue showed that ligA_{CP} functioned in the mesophile and imparted a TS phenotype having a restrictive temperature of about 34° C. The phenotype of the transgenic strain of *F. novicida* carrying ligA_{CP} predicted that substitution of the ligA_{CP} gene into other mesophiles (destination hosts) would result in viable bacteria that had a restrictive temperature of 34° C. The phenotype of the *Salmonella* and *Mycobacteria* transgene strains carrying ligA_{CP} showed that the inter-genus transfer of a TS psychrophilic essential gene could result in a phenotype seen in the tester strain.

EXAMPLE 7

This example describes an exemplary method to combine psychrophilic genes or fragments thereof (as represented by SEQ ID NO 1-24) or mutant essential psychrophilic genes to create gene products with desired TS properties.

Combining about 30%, at the 5'-end, of the *novicida* pyrG gene with about 2/3 of the 3'-end of the *C. psychrerythraea* pyrG gene (pyrG_{CP}) in the region of codon 157-159 created a recombinant gene that was TS at 37° C. The *F. novicida* and *C. psychrerythraea* pyrG genes are identical at codons 157-159 inclusive. Additionally, the single point mutation at amino acid residue 149 in ligA_{PH} from an asparagine ("N") residue to a lysine ("K") residue changes the restrictive temperature from 37° C. to 28° C.

This approach could be applied to different psychrophilic genes by using either in vitro or in vivo recombinant technologies to combine two or more homologues of the same gene.

EXAMPLE 8

This example pertains to an exemplary method to determine the distribution of a transgenic strain from a site of infection in a mammal.

F. novicida (a.k.a. *F. tularensis* subspecies *novicida*) carrying a psychrophilic transgene was used. One skilled in the art will appreciate that similar methods can be used to generate and examine TS strains of *F. tularensis*. *F. novicida* is highly virulent in mice. The infection of mice by *F. novicida*

serves as a model for the infection of larger mammals with *F. tularensis*. Most strains of *F. tularensis* are highly virulent in most mammals.

The distribution of *F. novicida* transgenic strains from the site of infection was assessed either by injecting the recombinant strains through the skin, or by introduction via the nose, and measuring the amount of viable *F. novicida* cells in internal organs such as the lung, liver and spleen about three to ten days after the inoculation. It was found that TS *F. novicida* transgenic strains did not spread significantly from the site of inoculation. A direct correlation between the inactivation temperature of the psychrophilic essential gene and the level of distribution throughout the system was observed; the dissemination of TS *F. novicida* strains is Lewis Rats is outlined in Table 3.

TABLE 3

<i>F. novicida</i> strain	Restrictive Temp. (° C.)	CFU/Tail injection site	CFU/Spleen
wt ⁻	45	$9.7 \times 10^3/7.1 \times 10^3$	$3.7 \times 10^6/2.2 \times 10^6$
ligA _{CP}	34	$5 \times 10^2/3 \times 10^2$	0/0
ligA _{Ph}	36.8	$3 \times 10^2/2 \times 10^2$	0/0
dnaK _{CP}	38.2	$1.5 \times 10^4/7.6 \times 10^4$	$5.0 \times 10^2/0$
fnt _{CP}	41	$5.2 \times 10^3/2.4 \times 10^3$	$3.5 \times 10^3/2.1 \times 10^5$

As a further example, one of the psychrophilic essential genes (ligA_{CP}) was substituted into the genome of *M. tuberculosis* to create a transgenic strain. Some psychrophilic essential genes originate in bacteria with DNA with low G+C content. Thus the genes were optimized with codons for *M. tuberculosis* prior to inserting the psychrophilic genes into the pathogenic bacteria (SEQ ID NOS: 17 and 18 provide the optimized sequences). Codon optimization is a method well known to those skilled in these arts and can be accomplished using freely available bioinformatic tools. The codon optimized psychrophilic essential genes were inserted into *M. tuberculosis* by methods that are well described in Examples 1 and 2. *M. tuberculosis*, like *M. smegmatis*, are Gram-positive bacteria.

Another exemplary method pertains to an exemplary method the distribution of a Gram-negative pathogenic strain. A psychrophilic essential gene was introduced into *S. enterica*. Upon introduction of the ligA_{CP} psychrophilic essential gene into *S. enterica*, the result was a transgenic strain that was unable to grow at 37° C., as illustrated in FIG. 8. Furthermore, this strain was unable to disperse from the site of inoculation in infected mice, as evidenced by the inability of the strain to migrate to the lungs, liver or spleen.

EXAMPLE 9

This example pertains to an exemplary method to determine the level of protective immune response generated from the inoculation of a mammal with a TS transgenic bacterial strain. Methods of inoculation are known in the art, and can include i.v., i.m., s.c., or i.p. injection, as well as inhalation, oral, and transdermal routes of delivery. One skilled in the art will appreciate that methods similar to those described in this example can be used to test any transgenic TS bacterial strain that includes one or more psychrophilic essential nucleic acid sequences.

Inoculation of mice with a TS *F. novicida* transgenic strain (Fn-ligA_{Ph}, Fn-ligA_{CP} or Fn-dnaK_{CP}) caused the cells of their immune systems to be stimulated (as measured by reduced bacterial organ burdens) resulting in protection against infec-

tion with wt *F. novicida* (FIGS. 10a-d). Mice were initially inoculated with the TS transgenic strain and then challenged with an inoculation three weeks later of the wt *F. novicida* strain. This resulted in reduced growth in the livers and spleens of mice infected with the wt strains as compared to mice that had not been inoculated with recombinant *F. novicida*. Furthermore, decreases in the morbidity and mortalities were observed among the inoculated group of mice resulting in the conclusion that immune protection was achieved.

Similarly, mice vaccinated with *M. tuberculosis* and *S. enterica* transgenic strains (ligA_{Ph}) were shown to be more resistant to infections with the wt pathogens than were unvaccinated mice.

EXAMPLE 10

This example pertains to an exemplary method of discovering novel psychrophilic essential genes.

Psychrophilic bacterium can be isolated from a cold environment, for example ocean waters near the Earth's poles. Essential genes can be identified by using degenerate PCR or other standard techniques to find highly conserved genes, such as bacterial essential genes. Once these genes have been identified, they can be substituted into the genome of a mesophile using the methods provided herein or known in the art, displacing the host homologue of the gene. The resulting strain can then be tested for temperature sensitivity as described herein.

EXAMPLE 11

This example pertains to an exemplary method of using TS transgene strains in drug discovery research. Although a TS *F. tularensis* strain is exemplified, one skilled in the art will appreciate that similar methods can be used for other TS strains generated using the methods provided herein.

A TS transgenic strain of *F. tularensis* (ligA_{Ph}) that was inoperable above about 37° C. was used to infect cell line macrophages grown in microtiter plates at 34° C. A library of antimicrobial drug candidates was introduced to individual wells that contained the infected macrophages, and the effect of the drug candidates on the killing of *F. tularensis* was measured by lysing the macrophages at various time points and determining the number of viable TS transgenic *F. tularensis* by plating on agar plates. Wt *F. tularensis* is extremely infectious and causes a deadly disease. The use of the TS transgenic *F. tularensis* strain allowed one to use greatly relaxed biological containment conditions because the strain is incapable of causing disease in humans.

EXAMPLE 12

This example pertains to an exemplary method of generating and using TS strains of *Mycobacterium* containing temperature-sensitive essential nucleic acid molecules from psychrophilic bacteria to develop an immunogenic composition, which for example can be used to stimulate an immune response in a mammal, to protect or treat an *M. tuberculosis* infection in the mammal.

The ligA_{Ph} and pryG_{CP} genes will separately be introduced into *M. tuberculosis* H37Rv using an integration/excision approach. The counter-selectable marker sacB will be used to enhance the generation of excision events that can be detected. C57BL/6 mice will be vaccinated by introducing

10,000 bacteria subcutaneously at the base of the tail. Negative controls mice injected with PBS and positive control mice injected with the BCG strain will be processed at the same time. The mice will be rested for 30 days. Following this period all of the mice will be exposed to an aerosol of *M. tuberculosis* H37Rv that deposits 150 bacteria into the lungs. At weeks 0, 4, 8, 16 and 32 following exposure to *M. tuberculosis* H37Rv, the mice will be euthanized and the number of *M. tuberculosis* H37Rv in the lungs and spleens determined. If the transgenes TS *M. tuberculosis* strains are successful at inducing a protective immune response, the number of bac-

teria in the mice organs will be less than that of the negative control. Subsequent experiments will be performed in a guinea pig model of tuberculosis.

In view of the many possible embodiments to which the principles of our invention may be applied, it should be recognized that illustrated embodiments are only examples of the invention and should not be considered a limitation on the scope of the invention. Rather, the scope of the invention is defined by the following claims. We therefore claim as our invention all that comes within the scope and spirit of these claims.

SEQUENCE LISTING

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<223> OTHER INFORMATION: ligACp hybrid

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<222> LOCATION: (1)..(2070)

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<221> NAME/KEY: misc_feature

<222> LOCATION: (569)..(569)

<223> OTHER INFORMATION: k at location 569 is g or t/u

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1460)..(1460)

<223> OTHER INFORMATION: y at location 1460 is t/u or c

<400> SEQUENCE: 1

atg act cca gtc gaa aag aaa att agc caa ctg caa cag cag ctt aat	48
Met Thr Pro Val Glu Lys Lys Ile Ser Gln Leu Gln Gln Leu Asn	
1 5 10 15	
caa tat aat cat gaa tat tat gta tta gac caa cct agt gtg cct gat	96
Gln Tyr Asn His Glu Tyr Tyr Val Leu Asp Gln Pro Ser Val Pro Asp	
20 25 30	
gca gaa tat gac cga tta atg aca gca tta atc gat tta gaa aag act	144
Ala Glu Tyr Asp Arg Leu Met Thr Ala Leu Ile Asp Leu Glu Lys Thr	
35 40 45	
aat cct gag ctt aag act att gac tca cct agc caa aaa gtt ggc ggt	192
Asn Pro Glu Leu Lys Thr Ile Asp Ser Pro Ser Gln Lys Val Gly Gly	
50 55 60	
cag gca tta aaa tct ttc act caa gta act cat cag ctg ccg atg ctt	240
Gln Ala Leu Lys Ser Phe Thr Gln Val Thr His Gln Leu Pro Met Leu	
65 70 75 80	
tct ctt gat aat gtt ttt tct tta gat gat ttt cac gca ttt gtt aaa	288
Ser Leu Asp Asn Val Phe Ser Leu Asp Asp Phe His Ala Phe Val Lys	
85 90 95	
cgc gta aaa gat agg tta aat gac aat caa gcg ata gtc ttt tgt gcc	336
Arg Val Lys Asp Arg Leu Asn Asp Asn Gln Ala Ile Val Phe Cys Ala	
100 105 110	
gag cct aaa tta gac ggt tta gca gtg agt tta cgt tat gag cac ggg	384
Glu Pro Lys Leu Asp Gly Leu Ala Val Ser Leu Arg Tyr Glu His Gly	
115 120 125	
cag tta ata caa gcg gct aca cgt ggc gat ggt agt gta ggg gag aat	432
Gln Leu Ile Gln Ala Ala Thr Arg Gly Asp Gly Ser Val Gly Glu Asn	
130 135 140	
att acg act aac att cgt aca ata aaa tct att ccg ctt aag tta atg	480
Ile Thr Thr Asn Ile Arg Thr Ile Lys Ser Ile Pro Leu Lys Leu Met	
145 150 155 160	
ggc aca cca ggt aaa gat ttt cct gat atc gtt gaa gtc cgc ggt gaa	528

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Gly	Thr	Pro	Gly	Lys	Asp	Phe	Pro	Asp	Ile	Val	Glu	Val	Arg	Gly	Glu	
			165						170					175		
gtt	ttt	atg	cct	aag	gca	agt	ttt	gac	gca	tta	aat	aca	tkg	gct	aaa	576
Val	Phe	Met	Pro	Lys	Ala	Ser	Phe	Asp	Ala	Leu	Asn	Thr	Xaa	Ala	Lys	
			180					185					190			
aaa	cgt	ggc	gag	aaa	ggg	ttt	gca	aat	cca	cgt	aat	gca	gcg	gcg	gga	624
Lys	Arg	Gly	Glu	Lys	Gly	Phe	Ala	Asn	Pro	Arg	Asn	Ala	Ala	Ala	Gly	
		195					200					205				
agt	tta	cga	caa	ctt	gat	tct	aaa	atc	acc	gct	aaa	cgt	aat	tta	gct	672
Ser	Leu	Arg	Gln	Leu	Asp	Ser	Lys	Ile	Thr	Ala	Lys	Arg	Asn	Leu	Ala	
	210						215					220				
ttt	tac	gct	tat	agc	ctt	gga	ttt	gta	ggg	aaa	ctg	tct	gat	gga	ggc	720
Phe	Tyr	Ala	Tyr	Ser	Leu	Gly	Phe	Val	Gly	Lys	Leu	Ser	Asp	Gly	Gly	
	225				230					235				240		
gct	gaa	agt	acc	gat	tta	acc	aat	gac	ttt	ttt	gct	aac	tct	cat	cat	768
Ala	Glu	Ser	Thr	Asp	Leu	Thr	Asn	Asp	Phe	Phe	Ala	Asn	Ser	His	His	
			245					250						255		
gaa	aga	cta	tgt	cag	ctt	aaa	agg	ttg	ggg	ttg	cct	atg	tgt	cca	gaa	816
Glu	Arg	Leu	Cys	Gln	Leu	Lys	Arg	Leu	Gly	Leu	Pro	Met	Cys	Pro	Glu	
		260						265					270			
gta	cgc	tta	ctt	gaa	agt	gag	caa	gcc	tgt	gat	gcg	ttt	tat	caa	gat	864
Val	Arg	Leu	Leu	Glu	Ser	Glu	Gln	Ala	Cys	Asp	Ala	Phe	Tyr	Gln	Asp	
	275						280						285			
atc	tta	gca	aag	cgt	agt	gcc	ttg	agt	tat	gaa	att	gat	ggc	act	gta	912
Ile	Leu	Ala	Lys	Arg	Ser	Ala	Leu	Ser	Tyr	Glu	Ile	Asp	Gly	Thr	Val	
	290					295					300					
tta	aaa	gtt	gat	gaa	atc	tct	ttg	cag	aaa	cgt	tta	ggg	ttt	gtc	gca	960
Leu	Lys	Val	Asp	Glu	Ile	Ser	Leu	Gln	Lys	Arg	Leu	Gly	Phe	Val	Ala	
	305				310					315				320		
cgt	gcc	cca	cgt	tgg	gct	att	gct	tat	aaa	ttc	cct	gcg	gaa	gaa	gaa	1008
Arg	Ala	Pro	Arg	Trp	Ala	Ile	Ala	Tyr	Lys	Phe	Pro	Ala	Glu	Glu	Glu	
				325					330					335		
tta	acc	tgt	gtt	gaa	gat	gtc	gag	ttt	caa	gta	ggg	cgt	acc	ggc	gcg	1056
Leu	Thr	Cys	Val	Glu	Asp	Val	Glu	Phe	Gln	Val	Gly	Arg	Thr	Gly	Ala	
		340						345					350			
att	act	ccc	gta	gca	cgt	ttg	aaa	ccg	gta	ttt	gtt	ggg	ggc	gta	aca	1104
Ile	Thr	Pro	Val	Ala	Arg	Leu	Lys	Pro	Val	Phe	Val	Gly	Gly	Val	Thr	
		355					360					365				
gtt	tct	aat	gcc	aca	tta	cat	aac	caa	gat	gaa	ata	acc	cga	tta	ggg	1152
Val	Ser	Asn	Ala	Thr	Leu	His	Asn	Gln	Asp	Glu	Ile	Thr	Arg	Leu	Gly	
	370					375					380					
ctg	aaa	gtg	aat	gat	ttc	gtg	gtt	atc	cgc	cgt	gcc	ggg	gat	gtt	att	1200
Leu	Lys	Val	Asn	Asp	Phe	Val	Val	Ile	Arg	Arg	Ala	Gly	Asp	Val	Ile	
	385				390					395				400		
cct	caa	att	gtt	agc	gta	gta	ctt	gat	aaa	cga	cca	gat	aat	gcc	gtc	1248
Pro	Gln	Ile	Val	Ser	Val	Val	Leu	Asp	Lys	Arg	Pro	Asp	Asn	Ala	Val	
			405						410					415		
gat	ata	gtc	ttt	cct	acc	agt	tgc	cct	gtt	tgt	gac	tct	gca	gtg	gct	1296
Asp	Ile	Val	Phe	Pro	Thr	Ser	Cys	Pro	Val	Cys	Asp	Ser	Ala	Val	Ala	
		420						425					430			
aaa	cct	gaa	ggg	gaa	gcc	gta	ctg	aga	tgt	acc	gcc	gga	ctt	ttc	tgt	1344
Lys	Pro	Glu	Gly	Glu	Ala	Val	Leu	Arg	Cys	Thr	Ala	Gly	Leu	Phe	Cys	
		435				440						445				
gcg	gcg	caa	aga	aaa	gaa	gct	att	aaa	cat	ttt	gct	tct	cga	aaa	gca	1392
Ala	Ala	Gln	Arg	Lys	Glu	Ala	Ile	Lys	His	Phe	Ala	Ser	Arg	Lys	Ala	
	450					455					460					
cat	gat	gtt	gat	ggg	tta	ggg	gac	aaa	cta	gta	gag	caa	ctt	gta	gat	1440
His	Asp	Val	Asp	Gly	Leu	Gly	Asp	Lys	Leu	Val	Glu	Gln	Leu	Val	Asp	
	465				470					475				480		

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gaa aag tta att aat acg cgc gct gat tta ttc aaa tta acc gaa ata	1488
Glu Lys Leu Ile Asn Thr Xaa Ala Asp Leu Phe Lys Leu Thr Glu Ile	
485 490 495	
caa gtt agt act ata gat cgt atg ggt aaa aaa tca gcg acc aat tta	1536
Gln Val Ser Thr Ile Asp Arg Met Gly Lys Lys Ser Ala Thr Asn Leu	
500 505 510	
att aat gga ctt gag cag gct aaa agt acc aca cta gca aaa ttt att	1584
Ile Asn Gly Leu Glu Gln Ala Lys Ser Thr Thr Leu Ala Lys Phe Ile	
515 520 525	
tat ggt ctg ggc ata cgc gaa gtc ggt gaa gca act gct gct aat cta	1632
Tyr Gly Leu Gly Ile Arg Glu Val Gly Glu Ala Thr Ala Ala Asn Leu	
530 535 540	
gca aat cat ttt tat acc tta gcg gca att gaa agt gct tct ctt gaa	1680
Ala Asn His Phe Tyr Thr Leu Ala Ala Ile Glu Ser Ala Ser Leu Glu	
545 550 555 560	
gac tta caa aat gtt tca gat gtt ggc gaa gtc gtt gcc aaa aat att	1728
Asp Leu Gln Asn Val Ser Asp Val Gly Glu Val Val Ala Lys Asn Ile	
565 570 575	
att aat ttc ttt aaa gaa gag cat aac tta gcg atc gtt tct gga cta	1776
Ile Asn Phe Phe Lys Glu Glu His Asn Leu Ala Ile Val Ser Gly Leu	
580 585 590	
agt gaa gta atg cac tgg cca act att gaa ata aag tca gct gag gag	1824
Ser Glu Val Met His Trp Pro Thr Ile Glu Ile Lys Ser Ala Glu Glu	
595 600 605	
tta ccg ctt gca gag cag ata ttt gtt tta aca ggc aca tta acc caa	1872
Leu Pro Leu Ala Glu Gln Ile Phe Val Leu Thr Gly Thr Leu Thr Gln	
610 615 620	
atg gga aga act gaa gct aaa aca gcc tta cag tcc ttg gga gct aaa	1920
Met Gly Arg Thr Glu Ala Lys Thr Ala Leu Gln Ser Leu Gly Ala Lys	
625 630 635 640	
gta tca ggt agt gtc tcg aag aat aca cac ttc gtt gtt gca ggt gat	1968
Val Ser Gly Ser Val Ser Lys Asn Thr His Phe Val Val Ala Gly Asp	
645 650 655	
aaa gcg gga tct aaa ctg act aag gct cag gat tta ggt atc tca gtg	2016
Lys Ala Gly Ser Lys Leu Thr Lys Ala Gln Asp Leu Gly Ile Ser Val	
660 665 670	
ctt acc gaa gat ggg tta gta gcg tta ctt gcc gaa cat ggc ata act	2064
Leu Thr Glu Asp Gly Leu Val Ala Leu Leu Ala Glu His Gly Ile Thr	
675 680 685	
att tga	2070
Ile	

<210> SEQ ID NO 2

<211> LENGTH: 689

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (190)..(190)

<223> OTHER INFORMATION: The 'Xaa' at location 190 stands for Trp, or Leu.

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (487)..(487)

<223> OTHER INFORMATION: The 'Xaa' at location 487 stands for Pro, or Leu.

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 2

Met Thr Pro Val Glu Lys Lys Ile Ser Gln Leu Gln Gln Gln Leu Asn
1 5 10 15

Gln Tyr Asn His Glu Tyr Tyr Val Leu Asp Gln Pro Ser Val Pro Asp

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20							25					30				
Ala	Glu	Tyr	Asp	Arg	Leu	Met	Thr	Ala	Leu	Ile	Asp	Leu	Glu	Lys	Thr	
		35					40					45				
Asn	Pro	Glu	Leu	Lys	Thr	Ile	Asp	Ser	Pro	Ser	Gln	Lys	Val	Gly	Gly	
	50					55					60					
Gln	Ala	Leu	Lys	Ser	Phe	Thr	Gln	Val	Thr	His	Gln	Leu	Pro	Met	Leu	
65					70					75					80	
Ser	Leu	Asp	Asn	Val	Phe	Ser	Leu	Asp	Asp	Phe	His	Ala	Phe	Val	Lys	
			85						90					95		
Arg	Val	Lys	Asp	Arg	Leu	Asn	Asp	Asn	Gln	Ala	Ile	Val	Phe	Cys	Ala	
		100						105					110			
Glu	Pro	Lys	Leu	Asp	Gly	Leu	Ala	Val	Ser	Leu	Arg	Tyr	Glu	His	Gly	
		115					120					125				
Gln	Leu	Ile	Gln	Ala	Ala	Thr	Arg	Gly	Asp	Gly	Ser	Val	Gly	Glu	Asn	
	130					135						140				
Ile	Thr	Thr	Asn	Ile	Arg	Thr	Ile	Lys	Ser	Ile	Pro	Leu	Lys	Leu	Met	
145					150					155					160	
Gly	Thr	Pro	Gly	Lys	Asp	Phe	Pro	Asp	Ile	Val	Glu	Val	Arg	Gly	Glu	
			165						170					175		
Val	Phe	Met	Pro	Lys	Ala	Ser	Phe	Asp	Ala	Leu	Asn	Thr	Xaa	Ala	Lys	
		180						185					190			
Lys	Arg	Gly	Glu	Lys	Gly	Phe	Ala	Asn	Pro	Arg	Asn	Ala	Ala	Ala	Gly	
	195					200						205				
Ser	Leu	Arg	Gln	Leu	Asp	Ser	Lys	Ile	Thr	Ala	Lys	Arg	Asn	Leu	Ala	
	210					215						220				
Phe	Tyr	Ala	Tyr	Ser	Leu	Gly	Phe	Val	Gly	Lys	Leu	Ser	Asp	Gly	Gly	
225					230					235					240	
Ala	Glu	Ser	Thr	Asp	Leu	Thr	Asn	Asp	Phe	Phe	Ala	Asn	Ser	His	His	
			245						250					255		
Glu	Arg	Leu	Cys	Gln	Leu	Lys	Arg	Leu	Gly	Leu	Pro	Met	Cys	Pro	Glu	
		260						265					270			
Val	Arg	Leu	Leu	Glu	Ser	Glu	Gln	Ala	Cys	Asp	Ala	Phe	Tyr	Gln	Asp	
	275						280					285				
Ile	Leu	Ala	Lys	Arg	Ser	Ala	Leu	Ser	Tyr	Glu	Ile	Asp	Gly	Thr	Val	
	290					295						300				
Leu	Lys	Val	Asp	Glu	Ile	Ser	Leu	Gln	Lys	Arg	Leu	Gly	Phe	Val	Ala	
305					310					315					320	
Arg	Ala	Pro	Arg	Trp	Ala	Ile	Ala	Tyr	Lys	Phe	Pro	Ala	Glu	Glu	Glu	
			325						330					335		
Leu	Thr	Cys	Val	Glu	Asp	Val	Glu	Phe	Gln	Val	Gly	Arg	Thr	Gly	Ala	
		340						345					350			
Ile	Thr	Pro	Val	Ala	Arg	Leu	Lys	Pro	Val	Phe	Val	Gly	Gly	Val	Thr	
	355						360						365			
Val	Ser	Asn	Ala	Thr	Leu	His	Asn	Gln	Asp	Glu	Ile	Thr	Arg	Leu	Gly	
	370					375						380				
Leu	Lys	Val	Asn	Asp	Phe	Val	Val	Ile	Arg	Arg	Ala	Gly	Asp	Val	Ile	
385					390					395					400	
Pro	Gln	Ile	Val	Ser	Val	Val	Leu	Asp	Lys	Arg	Pro	Asp	Asn	Ala	Val	
			405						410					415		
Asp	Ile	Val	Phe	Pro	Thr	Ser	Cys	Pro	Val	Cys	Asp	Ser	Ala	Val	Ala	
		420						425					430			
Lys	Pro	Glu	Gly	Glu	Ala	Val	Leu	Arg	Cys	Thr	Ala	Gly	Leu	Phe	Cys	
	435						440						445			

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Ala Ala Gln Arg Lys Glu Ala Ile Lys His Phe Ala Ser Arg Lys Ala
 450 455 460

His Asp Val Asp Gly Leu Gly Asp Lys Leu Val Glu Gln Leu Val Asp
 465 470 475 480

Glu Lys Leu Ile Asn Thr Xaa Ala Asp Leu Phe Lys Leu Thr Glu Ile
 485 490 495

Gln Val Ser Thr Ile Asp Arg Met Gly Lys Lys Ser Ala Thr Asn Leu
 500 505 510

Ile Asn Gly Leu Glu Gln Ala Lys Ser Thr Thr Leu Ala Lys Phe Ile
 515 520 525

Tyr Gly Leu Gly Ile Arg Glu Val Gly Glu Ala Thr Ala Ala Asn Leu
 530 535 540

Ala Asn His Phe Tyr Thr Leu Ala Ala Ile Glu Ser Ala Ser Leu Glu
 545 550 555 560

Asp Leu Gln Asn Val Ser Asp Val Gly Glu Val Val Ala Lys Asn Ile
 565 570 575

Ile Asn Phe Phe Lys Glu Glu His Asn Leu Ala Ile Val Ser Gly Leu
 580 585 590

Ser Glu Val Met His Trp Pro Thr Ile Glu Ile Lys Ser Ala Glu Glu
 595 600 605

Leu Pro Leu Ala Glu Gln Ile Phe Val Leu Thr Gly Thr Leu Thr Gln
 610 615 620

Met Gly Arg Thr Glu Ala Lys Thr Ala Leu Gln Ser Leu Gly Ala Lys
 625 630 635 640

Val Ser Gly Ser Val Ser Lys Asn Thr His Phe Val Val Ala Gly Asp
 645 650 655

Lys Ala Gly Ser Lys Leu Thr Lys Ala Gln Asp Leu Gly Ile Ser Val
 660 665 670

Leu Thr Glu Asp Gly Leu Val Ala Leu Leu Ala Glu His Gly Ile Thr
 675 680 685

Ile

<210> SEQ ID NO 3
 <211> LENGTH: 2022
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: ligAph hybrid
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(2022)

<400> SEQUENCE: 3

atg act cca agc att agt gag caa ata aac cat ctt cgt agt acg ctt	48
Met Thr Pro Ser Ile Ser Glu Gln Ile Asn His Leu Arg Ser Thr Leu	
1 5 10 15	
 gaa cag cac agt tac aat tat tat gta ctt gat acc ccc agt att cct	96
Glu Gln His Ser Tyr Asn Tyr Tyr Val Leu Asp Thr Pro Ser Ile Pro	
20 25 30	
 gat gct gaa tac gac cgt tta tta caa caa ctc agc gca cta gaa act	144
Asp Ala Glu Tyr Asp Arg Leu Leu Gln Gln Leu Ser Ala Leu Glu Thr	
35 40 45	
 cag cac cca gaa tta ata act gcc gac tca cca acc caa aaa gtg ggc	192
Gln His Pro Glu Leu Ile Thr Ala Asp Ser Pro Thr Gln Lys Val Gly	
50 55 60	
 ggg gct gcg cta agt aaa ttt gag caa gta gcg cac caa gtg cct atg	240
Gly Ala Ala Leu Ser Lys Phe Glu Gln Val Ala His Gln Val Pro Met	

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65	70	75	80	
tta tcg ctt gat aac gcc ttt agc gaa gat gag ttt att gcc ttt aat				288
Leu Ser Leu Asp Asn Ala Phe Ser Glu Asp Glu Phe Ile Ala Phe Asn	85	90	95	
cgc cgt ata aaa gag cgt tta atg agt acc gaa gag ctt act ttt tgt				336
Arg Arg Ile Lys Glu Arg Leu Met Ser Thr Glu Glu Leu Thr Phe Cys	100	105	110	
tgt gag cca aaa cta gat gcc tta gct gtg tcg att att tat cgt gat				384
Cys Glu Pro Lys Leu Asp Gly Leu Ala Val Ser Ile Ile Tyr Arg Asp	115	120	125	
ggc gta cta gtg caa gcc gcg acc cga ggt gat ggg ttg acg gga gaa				432
Gly Val Leu Val Gln Ala Ala Thr Arg Gly Asp Gly Leu Thr Gly Glu	130	135	140	
aat gta act caa aac gtt aaa aca att cgt aat gtg cca ctt aaa tta				480
Asn Val Thr Gln Asn Val Lys Thr Ile Arg Asn Val Pro Leu Lys Leu	145	150	155	160
cga ggt agc gat tat cct gct gaa cta gaa gtg cgc ggc gaa gtg ttt				528
Arg Gly Ser Asp Tyr Pro Ala Glu Leu Glu Val Arg Gly Glu Val Phe	165	170	175	
atg gat aat gca gcc ttt gaa aag ttt aac att gaa gct gaa aaa cgt				576
Met Asp Asn Ala Gly Phe Glu Lys Phe Asn Ile Glu Ala Glu Lys Arg	180	185	190	
ggg gaa aaa gta ttt gta aac cca cgc aac gcc gcc gca ggt agc ctg				624
Gly Glu Lys Val Phe Val Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu	195	200	205	
cgc cag ctt gac tct aaa att acg gct aaa cgc cca ctg atg ttt tat				672
Arg Gln Leu Asp Ser Lys Ile Thr Ala Lys Arg Pro Leu Met Phe Tyr	210	215	220	
gcc tac agc aca ggt ctt gta gcc gac ggt agc att gca gag gat cat				720
Ala Tyr Ser Thr Gly Leu Val Ala Asp Gly Ser Ile Ala Glu Asp His	225	230	235	240
tat cag caa tta gaa aaa ttg act gat tgg ggg tta cca ctt tgc cct				768
Tyr Gln Gln Leu Glu Lys Leu Thr Asp Trp Gly Leu Pro Leu Cys Pro	245	250	255	
gaa aca aaa tta gta gaa gcc cca caa gct gca ctg gct tat tat act				816
Glu Thr Lys Leu Val Glu Gly Pro Gln Ala Ala Leu Ala Tyr Tyr Thr	260	265	270	
gac att tta acg cgc cgt gcc gag ctt aaa tat gaa ata gat gcc gtg				864
Asp Ile Leu Thr Arg Arg Gly Glu Leu Lys Tyr Glu Ile Asp Gly Val	275	280	285	
gta ata aaa ata aat caa aaa gcc tta caa gag cgt tta gcc ttt gta				912
Val Ile Lys Ile Asn Gln Lys Ala Leu Gln Glu Arg Leu Gly Phe Val	290	295	300	
gca cgc gct ccg cgt tgg gct att gct tat aag ttc ccg gcc caa gaa				960
Ala Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Phe Pro Ala Gln Glu	305	310	315	320
gaa ata acc aaa tta ctc gat gta gag ttt cag gtg ggg cgt acg gga				1008
Glu Ile Thr Lys Leu Asp Val Glu Phe Gln Val Gly Arg Thr Gly	325	330	335	
gca att aca ccg gtt gca cgc tta gag ccg gta ttt gtt ggt ggt gtt				1056
Ala Ile Thr Pro Val Ala Arg Leu Glu Pro Val Phe Val Gly Gly Val	340	345	350	
act gta tca aac gct acc ttg cac aat gcc gat gaa ata gcg cgc tta				1104
Thr Val Ser Asn Ala Thr Leu His Asn Gly Asp Glu Ile Ala Arg Leu	355	360	365	
ggc gta aaa gtg gcc gac acg gta att att cgc cgt gca ggg gac gta				1152
Gly Val Lys Val Gly Asp Thr Val Ile Ile Arg Arg Ala Gly Asp Val	370	375	380	
att cca caa ata acg caa gta gta ctt gag cgc cgc cct gat gat gcc				1200

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Ile Pro Gln Ile Thr Gln Val Val Leu Glu Arg Arg Pro Asp Asp Ala 385 390 395 400	
cgc gat att gag ttt ccg gta act tgc cca att tgt gac tcc cat gta Arg Asp Ile Glu Phe Pro Val Thr Cys Pro Ile Cys Asp Ser His Val 405 410 415	1248
gaa aaa gta gaa ggt gaa gcc gta gcg cgt tgt act ggt ggt tta gtg Glu Lys Val Glu Gly Glu Ala Val Ala Arg Cys Thr Gly Gly Leu Val 420 425 430	1296
tgc ccg gcg caa cgt aaa caa gcg att aaa cac ttt gca tcg cgc aaa Cys Pro Ala Gln Arg Lys Gln Ala Ile Lys His Phe Ala Ser Arg Lys 435 440 445	1344
gca ctc gat att gac ggc ctt ggc gat aaa att gtt gat caa ctc gtc Ala Leu Asp Ile Asp Gly Leu Gly Asp Lys Ile Val Asp Gln Leu Val 450 455 460	1392
gac aga gag ctg att aaa acc cct gca gat ttg ttt att tta aag caa Asp Arg Glu Leu Ile Lys Thr Pro Ala Asp Leu Phe Ile Leu Lys Gln 465 470 475 480	1440
gga cat ttt gaa tcg ctt gag cgt atg ggg cca aag tcg gct aaa aat Gly His Phe Glu Ser Leu Glu Arg Met Gly Pro Lys Ser Ala Lys Asn 485 490 495	1488
ttg gtt act gcg ctt caa gac gct aaa gca aca act ttg gct aag ttt Leu Val Thr Ala Leu Gln Asp Ala Lys Ala Thr Thr Leu Ala Lys Phe 500 505 510	1536
tta tac tca ttg ggt att cgt gaa gcg ggt gag gca acc aca caa aat Leu Tyr Ser Leu Gly Ile Arg Glu Ala Gly Glu Ala Thr Thr Gln Asn 515 520 525	1584
tta gct aat cat ttc tta acc ctt gaa aac gta ata aat gcc agc att Leu Ala Asn His Phe Leu Thr Leu Glu Asn Val Ile Asn Ala Ser Ile 530 535 540	1632
gat agt tta act caa gta agt gat gtg ggc gaa ata gta gca acc cat Asp Ser Leu Thr Gln Val Ser Asp Val Gly Glu Ile Val Ala Thr His 545 550 555 560	1680
gta cgt agc ttt ttt gcc gaa cag cat aat tta gat gtt gta aat gcg Val Arg Ser Phe Phe Ala Glu Gln His Asn Leu Asp Val Val Asn Ala 565 570 575	1728
ctg gta gag caa ggt att aat tgg cct gaa ctt act cca cct tca gcg Leu Val Glu Gln Gly Ile Asn Trp Pro Glu Leu Thr Pro Pro Ser Ala 580 585 590	1776
caa gag cag cca tta gct ggc ctt gtt tat gtg ctt acc ggt acc tta Gln Glu Gln Pro Leu Ala Gly Leu Val Tyr Val Leu Thr Gly Thr Leu 595 600 605	1824
aac aca tta aac cgt aat gac gcc aaa gca cgt ttg caa cag tta ggt Asn Thr Leu Asn Arg Asn Asp Ala Lys Ala Arg Leu Gln Gln Leu Gly 610 615 620	1872
gct aaa gtg tcg ggt agt gtg tcg gct aaa acc gat gcg tta gta gca Ala Lys Val Ser Gly Ser Val Ser Ala Lys Thr Asp Ala Leu Val Ala 625 630 635 640	1920
ggc gaa aag gcc ggc tct aaa cta act aag gca caa gac tta ggt ata Gly Glu Lys Ala Gly Ser Lys Leu Thr Lys Ala Gln Asp Leu Gly Ile 645 650 655	1968
gat gta ctg aca gaa gaa gat tta att aat tta tta gag caa cat aat Asp Val Leu Thr Glu Glu Asp Leu Ile Asn Leu Leu Glu Gln His Asn 660 665 670	2016
ggc tga Gly	2022

<210> SEQ ID NO 4

<211> LENGTH: 673

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 4

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Met Thr Pro Ser Ile Ser Glu Gln Ile Asn His Leu Arg Ser Thr Leu
1      5      10      15

Glu Gln His Ser Tyr Asn Tyr Tyr Val Leu Asp Thr Pro Ser Ile Pro
20      25      30

Asp Ala Glu Tyr Asp Arg Leu Leu Gln Gln Leu Ser Ala Leu Glu Thr
35      40      45

Gln His Pro Glu Leu Ile Thr Ala Asp Ser Pro Thr Gln Lys Val Gly
50      55      60

Gly Ala Ala Leu Ser Lys Phe Glu Gln Val Ala His Gln Val Pro Met
65      70      75      80

Leu Ser Leu Asp Asn Ala Phe Ser Glu Asp Glu Phe Ile Ala Phe Asn
85      90      95

Arg Arg Ile Lys Glu Arg Leu Met Ser Thr Glu Glu Leu Thr Phe Cys
100     105     110

Cys Glu Pro Lys Leu Asp Gly Leu Ala Val Ser Ile Ile Tyr Arg Asp
115     120     125

Gly Val Leu Val Gln Ala Ala Thr Arg Gly Asp Gly Leu Thr Gly Glu
130     135     140

Asn Val Thr Gln Asn Val Lys Thr Ile Arg Asn Val Pro Leu Lys Leu
145     150     155     160

Arg Gly Ser Asp Tyr Pro Ala Glu Leu Glu Val Arg Gly Glu Val Phe
165     170     175

Met Asp Asn Ala Gly Phe Glu Lys Phe Asn Ile Glu Ala Glu Lys Arg
180     185     190

Gly Glu Lys Val Phe Val Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
195     200     205

Arg Gln Leu Asp Ser Lys Ile Thr Ala Lys Arg Pro Leu Met Phe Tyr
210     215     220

Ala Tyr Ser Thr Gly Leu Val Ala Asp Gly Ser Ile Ala Glu Asp His
225     230     235     240

Tyr Gln Gln Leu Glu Lys Leu Thr Asp Trp Gly Leu Pro Leu Cys Pro
245     250     255

Glu Thr Lys Leu Val Glu Gly Pro Gln Ala Ala Leu Ala Tyr Tyr Thr
260     265     270

Asp Ile Leu Thr Arg Arg Gly Glu Leu Lys Tyr Glu Ile Asp Gly Val
275     280     285

Val Ile Lys Ile Asn Gln Lys Ala Leu Gln Glu Arg Leu Gly Phe Val
290     295     300

Ala Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Phe Pro Ala Gln Glu
305     310     315     320

Glu Ile Thr Lys Leu Leu Asp Val Glu Phe Gln Val Gly Arg Thr Gly
325     330     335

Ala Ile Thr Pro Val Ala Arg Leu Glu Pro Val Phe Val Gly Gly Val
340     345     350

Thr Val Ser Asn Ala Thr Leu His Asn Gly Asp Glu Ile Ala Arg Leu
355     360     365

Gly Val Lys Val Gly Asp Thr Val Ile Ile Arg Arg Ala Gly Asp Val
370     375     380

Ile Pro Gln Ile Thr Gln Val Val Leu Glu Arg Arg Pro Asp Asp Ala
385     390     395     400

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cag	cac	cca	gaa	tta	ata	act	gcc	gac	tca	cca	acc	caa	aaa	gtg	ggc	192
Gln	His	Pro	Glu	Leu	Ile	Thr	Ala	Asp	Ser	Pro	Thr	Gln	Lys	Val	Gly	
50						55					60					
ggt	gct	gcg	cta	agt	aaa	ttt	gag	caa	gta	gcg	cac	caa	gtg	cct	atg	240
Gly	Ala	Ala	Leu	Ser	Lys	Phe	Glu	Gln	Val	Ala	His	Gln	Val	Pro	Met	
65					70				75					80		
tta	tcg	ctt	gat	aac	gcc	ttt	agc	gaa	gat	gag	ttt	att	gcc	ttt	aat	288
Leu	Ser	Leu	Asp	Asn	Ala	Phe	Ser	Glu	Asp	Glu	Phe	Ile	Ala	Phe	Asn	
			85						90					95		
cgc	cgt	ata	aaa	gag	cgt	tta	atg	agt	acc	gaa	gag	ctt	act	ttt	tgt	336
Arg	Arg	Ile	Lys	Glu	Arg	Leu	Met	Ser	Thr	Glu	Glu	Leu	Thr	Phe	Cys	
			100					105					110			
tgt	gag	cca	aaa	cta	gat	ggc	tta	gct	gtg	tcg	att	att	tat	cgt	gat	384
Cys	Glu	Pro	Lys	Leu	Asp	Gly	Leu	Ala	Val	Ser	Ile	Ile	Tyr	Arg	Asp	
			115				120						125			
ggc	gta	cta	gtg	caa	gcc	gcg	acc	cga	ggt	gat	ggg	ttg	acg	gga	gaa	432
Gly	Val	Leu	Val	Gln	Ala	Ala	Thr	Arg	Gly	Asp	Gly	Leu	Thr	Gly	Glu	
			130				135					140				
aat	gta	act	caa	aaa	ggt	aaa	aca	att	cgt	aat	gtg	cca	ctt	aaa	tta	480
Asn	Val	Thr	Gln	Lys	Val	Lys	Thr	Ile	Arg	Asn	Val	Pro	Leu	Lys	Leu	
					150					155					160	
cga	ggt	agc	gat	tat	cct	gct	gaa	cta	gaa	gtg	cgc	ggc	gaa	gtg	ttt	528
Arg	Gly	Ser	Asp	Tyr	Pro	Ala	Glu	Leu	Glu	Val	Arg	Gly	Glu	Val	Phe	
			165						170					175		
atg	gat	aat	gca	ggc	ttt	gaa	aag	ttt	aac	att	gaa	gct	gaa	aaa	cgt	576
Met	Asp	Asn	Ala	Gly	Phe	Glu	Lys	Phe	Asn	Ile	Glu	Ala	Glu	Lys	Arg	
			180					185					190			
ggt	gaa	aaa	gta	ttt	gta	aac	cca	cgc	aac	gcc	gcc	gca	ggt	agc	ctg	624
Gly	Glu	Lys	Val	Phe	Val	Asn	Pro	Arg	Asn	Ala	Ala	Ala	Gly	Ser	Leu	
			195				200					205				
cgc	cag	ctt	gac	tct	aaa	att	acg	gct	aaa	cgc	cca	ctg	atg	ttt	tat	672
Arg	Gln	Leu	Asp	Ser	Lys	Ile	Thr	Ala	Lys	Arg	Pro	Leu	Met	Phe	Tyr	
			210			215					220					
gcc	tac	agc	aca	ggt	ctt	gta	gcc	gac	ggt	agc	att	gca	gag	gat	cat	720
Ala	Tyr	Ser	Thr	Gly	Leu	Val	Ala	Asp	Gly	Ser	Ile	Ala	Glu	Asp	His	
					230				235					240		
tat	cag	caa	tta	gaa	aaa	ttg	act	gat	tgg	ggg	tta	cca	ctt	tgc	cct	768
Tyr	Gln	Gln	Leu	Glu	Lys	Leu	Thr	Asp	Trp	Gly	Leu	Pro	Leu	Cys	Pro	
					245				250					255		
gaa	aca	aaa	tta	gta	gaa	ggc	cca	caa	gct	gca	ctg	gct	tat	tat	act	816
Glu	Thr	Lys	Leu	Val	Glu	Gly	Pro	Gln	Ala	Ala	Leu	Ala	Tyr	Tyr	Thr	
			260					265					270			
gac	att	tta	acg	cgc	cgt	ggc	gag	ctt	aaa	tat	gaa	ata	gat	ggc	gtg	864
Asp	Ile	Leu	Thr	Arg	Arg	Gly	Glu	Leu	Lys	Tyr	Glu	Ile	Asp	Gly	Val	
			275				280						285			
gta	ata	aaa	ata	aat	caa	aaa	gcc	tta	caa	gag	cgt	tta	ggc	ttt	gta	912
Val	Ile	Lys	Ile	Asn	Gln	Lys	Ala	Leu	Gln	Glu	Arg	Leu	Gly	Phe	Val	
			290				295					300				
gca	cgc	gct	ccg	cgt	tgg	gct	att	gct	tat	aag	ttc	ccg	gcc	caa	gaa	960
Ala	Arg	Ala	Pro	Arg	Trp	Ala	Ile	Ala	Tyr	Lys	Phe	Pro	Ala	Gln	Glu	
			305			310				315				320		
gaa	ata	acc	aaa	tta	ctc	gat	gta	gag	ttt	cag	gtg	ggg	cgt	acg	gga	1008
Glu	Ile	Thr	Lys	Leu	Leu	Asp	Val	Glu	Phe	Gln	Val	Gly	Arg	Thr	Gly	
				325					330					335		
gca	att	aca	ccg	ggt	gca	cgc	tta	gag	ccg	gta	ttt	ggt	ggt	ggt	ggt	1056
Ala	Ile	Thr	Pro	Val	Ala	Arg	Leu	Glu	Pro	Val	Phe	Val	Gly	Gly	Val	
				340				345						350		
act	gta	tca	aac	gct	acc	ttg	cac	aat	ggc	gat	gaa	ata	gcg	cgc	tta	1104
Thr	Val	Ser	Asn	Ala	Thr	Leu	His	Asn	Gly	Asp	Glu	Ile	Ala	Arg	Leu	
			355				360						365			

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ggc gta aaa gtg ggc gac acg gta att att cgc cgt gca ggg gac gta Gly Val Lys Val Gly Asp Thr Val Ile Ile Arg Arg Ala Gly Asp Val 370 375 380	1152
att cca caa ata acg caa gta gta ctt gag cgc cgc cct gat gat gcc Ile Pro Gln Ile Thr Gln Val Val Leu Glu Arg Arg Pro Asp Asp Ala 385 390 395 400	1200
cgc gat att gag ttt ccg gta act tgc cca att tgt gac tcc cat gta Arg Asp Ile Glu Phe Pro Val Thr Cys Pro Ile Cys Asp Ser His Val 405 410 415	1248
gaa aaa gta gaa ggt gaa gcc gta gcg cgt tgt act ggt ggt tta gtg Glu Lys Val Glu Gly Glu Ala Val Ala Arg Cys Thr Gly Gly Leu Val 420 425 430	1296
tgc ccg gcg caa cgt aaa caa gcg att aaa cac ttt gca tcg cgc aaa Cys Pro Ala Gln Arg Lys Gln Ala Ile Lys His Phe Ala Ser Arg Lys 435 440 445	1344
gca ctc gat att gac ggc ctt ggc gat aaa att gtt gat caa ctc gtc Ala Leu Asp Ile Asp Gly Leu Gly Asp Lys Ile Val Asp Gln Leu Val 450 455 460	1392
gac aga gag ctg att aaa acc cct gca gat ttg ttt att tta aag caa Asp Arg Glu Leu Ile Lys Thr Pro Ala Asp Leu Phe Ile Leu Lys Gln 465 470 475 480	1440
gga cat ttt gaa tcg ctt gag cgt atg ggg cca aag tcg gct aaa aat Gly His Phe Glu Ser Leu Glu Arg Met Gly Pro Lys Ser Ala Lys Asn 485 490 495	1488
ttg gtt act gcg ctt caa gac gct aaa gca aca act ttg gct aag ttt Leu Val Thr Ala Leu Gln Asp Ala Lys Ala Thr Thr Leu Ala Lys Phe 500 505 510	1536
tta tac tca ttg ggt att cgt gaa gcg ggt gag gca acc aca caa aat Leu Tyr Ser Leu Gly Ile Arg Glu Ala Gly Glu Ala Thr Thr Gln Asn 515 520 525	1584
tta gct aat cat ttc tta acc ctt gaa aac gta ata aat gcc agc att Leu Ala Asn His Phe Leu Thr Leu Glu Asn Val Ile Asn Ala Ser Ile 530 535 540	1632
gat agt tta act caa gta agt gat gtg ggc gaa ata gta gca acc cat Asp Ser Leu Thr Gln Val Ser Asp Val Gly Glu Ile Val Ala Thr His 545 550 555 560	1680
gta cgt agc ttt ttt gcc gaa cag cat aat tta gat gtt gta aat gcg Val Arg Ser Phe Phe Ala Glu Gln His Asn Leu Asp Val Val Asn Ala 565 570 575	1728
ctg gta gag caa ggt att aat tgg cct gaa ctt act cca cct tca gcg Leu Val Glu Gln Gly Ile Asn Trp Pro Glu Leu Thr Pro Pro Ser Ala 580 585 590	1776
caa gag cag cca tta gct ggc ctt gtt tat gtg ctt acc ggt acc tta Gln Glu Gln Pro Leu Ala Gly Leu Val Tyr Val Leu Thr Gly Thr Leu 595 600 605	1824
aac aca tta aac cgt aat gac gcc aaa gca cgt ttg caa cag tta ggt Asn Thr Leu Asn Arg Asn Asp Ala Lys Ala Arg Leu Gln Gln Leu Gly 610 615 620	1872
gct aaa gtg tcg ggt agt gtg tcg gct aaa acc gat gcg tta gta gca Ala Lys Val Ser Gly Ser Val Ser Ala Lys Thr Asp Ala Leu Val Ala 625 630 635 640	1920
ggc gaa aag gcc ggc tct aaa cta act aag gca caa gac tta ggt ata Gly Glu Lys Ala Gly Ser Lys Leu Thr Lys Ala Gln Asp Leu Gly Ile 645 650 655	1968
gat gta ctg aca gaa gaa gat tta att aat tta tta gag caa cat aat Asp Val Leu Thr Glu Glu Asp Leu Ile Asn Leu Leu Glu Gln His Asn 660 665 670	2016
ggc tga Gly	2022

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<210> SEQ ID NO 6
<211> LENGTH: 673
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 6
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1          5          10          15
Glu Gln His Ser Tyr Asn Tyr Tyr Val Leu Asp Thr Pro Ser Ile Pro
20          25          30
Asp Ala Glu Tyr Asp Arg Leu Leu Gln Gln Leu Ser Ala Leu Glu Thr
35          40          45
Gln His Pro Glu Leu Ile Thr Ala Asp Ser Pro Thr Gln Lys Val Gly
50          55          60
Gly Ala Ala Leu Ser Lys Phe Glu Gln Val Ala His Gln Val Pro Met
65          70          75          80
Leu Ser Leu Asp Asn Ala Phe Ser Glu Asp Glu Phe Ile Ala Phe Asn
85          90          95
Arg Arg Ile Lys Glu Arg Leu Met Ser Thr Glu Glu Leu Thr Phe Cys
100         105         110
Cys Glu Pro Lys Leu Asp Gly Leu Ala Val Ser Ile Ile Tyr Arg Asp
115         120         125
Gly Val Leu Val Gln Ala Ala Thr Arg Gly Asp Gly Leu Thr Gly Glu
130         135         140
Asn Val Thr Gln Lys Val Lys Thr Ile Arg Asn Val Pro Leu Lys Leu
145         150         155         160
Arg Gly Ser Asp Tyr Pro Ala Glu Leu Glu Val Arg Gly Glu Val Phe
165         170         175
Met Asp Asn Ala Gly Phe Glu Lys Phe Asn Ile Glu Ala Glu Lys Arg
180         185         190
Gly Glu Lys Val Phe Val Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
195         200         205
Arg Gln Leu Asp Ser Lys Ile Thr Ala Lys Arg Pro Leu Met Phe Tyr
210         215         220
Ala Tyr Ser Thr Gly Leu Val Ala Asp Gly Ser Ile Ala Glu Asp His
225         230         235         240
Tyr Gln Gln Leu Glu Lys Leu Thr Asp Trp Gly Leu Pro Leu Cys Pro
245         250         255
Glu Thr Lys Leu Val Glu Gly Pro Gln Ala Ala Leu Ala Tyr Tyr Thr
260         265         270
Asp Ile Leu Thr Arg Arg Gly Glu Leu Lys Tyr Glu Ile Asp Gly Val
275         280         285
Val Ile Lys Ile Asn Gln Lys Ala Leu Gln Glu Arg Leu Gly Phe Val
290         295         300
Ala Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Phe Pro Ala Gln Glu
305         310         315         320
Glu Ile Thr Lys Leu Leu Asp Val Glu Phe Gln Val Gly Arg Thr Gly
325         330         335
Ala Ile Thr Pro Val Ala Arg Leu Glu Pro Val Phe Val Gly Gly Val
340         345         350
Thr Val Ser Asn Ala Thr Leu His Asn Gly Asp Glu Ile Ala Arg Leu
355         360         365

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Gly Val Lys Val Gly Asp Thr Val Ile Ile Arg Arg Ala Gly Asp Val
 370 375 380
 Ile Pro Gln Ile Thr Gln Val Val Leu Glu Arg Arg Pro Asp Asp Ala
 385 390 395 400
 Arg Asp Ile Glu Phe Pro Val Thr Cys Pro Ile Cys Asp Ser His Val
 405 410 415
 Glu Lys Val Glu Gly Glu Ala Val Ala Arg Cys Thr Gly Gly Leu Val
 420 425 430
 Cys Pro Ala Gln Arg Lys Gln Ala Ile Lys His Phe Ala Ser Arg Lys
 435 440 445
 Ala Leu Asp Ile Asp Gly Leu Gly Asp Lys Ile Val Asp Gln Leu Val
 450 455 460
 Asp Arg Glu Leu Ile Lys Thr Pro Ala Asp Leu Phe Ile Leu Lys Gln
 465 470 475 480
 Gly His Phe Glu Ser Leu Glu Arg Met Gly Pro Lys Ser Ala Lys Asn
 485 490 495
 Leu Val Thr Ala Leu Gln Asp Ala Lys Ala Thr Thr Leu Ala Lys Phe
 500 505 510
 Leu Tyr Ser Leu Gly Ile Arg Glu Ala Gly Glu Ala Thr Thr Gln Asn
 515 520 525
 Leu Ala Asn His Phe Leu Thr Leu Glu Asn Val Ile Asn Ala Ser Ile
 530 535 540
 Asp Ser Leu Thr Gln Val Ser Asp Val Gly Glu Ile Val Ala Thr His
 545 550 555 560
 Val Arg Ser Phe Phe Ala Glu Gln His Asn Leu Asp Val Val Asn Ala
 565 570 575
 Leu Val Glu Gln Gly Ile Asn Trp Pro Glu Leu Thr Pro Pro Ser Ala
 580 585 590
 Gln Glu Gln Pro Leu Ala Gly Leu Val Tyr Val Leu Thr Gly Thr Leu
 595 600 605
 Asn Thr Leu Asn Arg Asn Asp Ala Lys Ala Arg Leu Gln Gln Leu Gly
 610 615 620
 Ala Lys Val Ser Gly Ser Val Ser Ala Lys Thr Asp Ala Leu Val Ala
 625 630 635 640
 Gly Glu Lys Ala Gly Ser Lys Leu Thr Lys Ala Gln Asp Leu Gly Ile
 645 650 655
 Asp Val Leu Thr Glu Glu Asp Leu Ile Asn Leu Leu Glu Gln His Asn
 660 665 670

Gly

<210> SEQ ID NO 7
 <211> LENGTH: 2013
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: LigAsf hybrid
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(2013)

<400> SEQUENCE: 7

atg act cca att caa act gaa atg gat caa ctt act cac acc att aac
 Met Thr Pro Ile Gln Thr Glu Met Asp Gln Leu Thr His Thr Ile Asn
 1 5 10 15
 caa cat aat att cgt tat tac gtt gat gat gct ccg tca ata ccc gat
 Gln His Asn Ile Arg Tyr Tyr Val Asp Asp Ala Pro Ser Ile Pro Asp

48

96

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20	25	30	
gct gaa tac gac aga tta att aag cgc tta act gag tta gaa cgt gac Ala Glu Tyr Asp Arg Leu Ile Lys Arg Leu Thr Glu Leu Glu Arg Asp 35 40 45			144
tat ccg caa ttt aaa tcg gta gat tca ccg aca caa cgc gtc ggt ggt Tyr Pro Gln Phe Lys Ser Val Asp Ser Pro Thr Gln Arg Val Gly Gly 50 55 60			192
ata gca tta caa aaa ttt gct caa att acc cac ctt aaa ccg atg tta Ile Ala Leu Gln Lys Phe Ala Gln Ile Thr His Leu Lys Pro Met Leu 65 70 75 80			240
agt ctc gac aat gcg ttt gaa caa gcc gat ttt gca gca ttt aat aag Ser Leu Asp Asn Ala Phe Glu Gln Ala Asp Phe Ala Ala Phe Asn Lys 85 90 95			288
cgt ata act gat aaa gtc gat agc gtc gat tat gtt tgc gaa cca aaa Arg Ile Thr Asp Lys Val Asp Ser Val Asp Tyr Val Cys Glu Pro Lys 100 105 110			336
cta gac gga ttg gcc gtg agt att act tat cgt ttt ggc gtt ctt gaa Leu Asp Gly Leu Ala Val Ser Ile Thr Tyr Arg Phe Gly Val Leu Glu 115 120 125			384
cgc gcc gca acg cga ggt gat gcc agt gtc gcc gaa gat att acc gct Arg Ala Ala Thr Arg Gly Asp Gly Ser Val Gly Glu Asp Ile Thr Ala 130 135 140			432
aat gtg cgt act att cgt tca att cct ctt aag tta cgc ggt gaa gga Asn Val Arg Thr Ile Arg Ser Ile Pro Leu Lys Leu Arg Gly Glu Gly 145 150 155 160			480
ttt cca gat tta gtt gaa gta cgt gcc gaa gtg ttt atg cct aaa gcg Phe Pro Asp Leu Val Glu Val Arg Gly Glu Val Phe Met Pro Lys Ala 165 170 175			528
gca ttt gag gca tta aac cag cgt caa atc agc aaa ggt gac aaa gtc Ala Phe Glu Ala Leu Asn Gln Arg Gln Ile Ser Lys Gly Asp Lys Val 180 185 190			576
ttt gtt aat cct cgc aac gca gct gcc gcc agt ttg cgc caa tta gac Phe Val Asn Pro Arg Asn Ala Ala Gly Ser Leu Arg Gln Leu Asp 195 200 205			624
agt aaa att acc gct tca agg gct ctt ggg ttt tat gct tat gca tta Ser Lys Ile Thr Ala Ser Arg Ala Leu Gly Phe Tyr Ala Tyr Ala Leu 210 215 220			672
ggt gta gtc gaa gcc gag tca caa ccg atg caa aca agc cac tat gcc Gly Val Val Glu Gly Glu Ser Gln Pro Met Gln Thr Ser His Tyr Gly 225 230 235 240			720
caa cta aca cag ctg caa caa tgg ggt att ccc gtt agt agt gaa gtg Gln Leu Thr Gln Leu Gln Gln Trp Gly Ile Pro Val Ser Ser Glu Val 245 250 255			768
aaa gtg act gat tta tta gaa aaa gtc tat gca tat tac gcc gat att Lys Val Thr Asp Leu Leu Glu Lys Val Tyr Ala Tyr Tyr Ala Asp Ile 260 265 270			816
atg gcc aga cga agt gcg ctt gaa tat gaa att gac gcc gtc gtc ata Met Ala Arg Arg Ser Ala Leu Glu Tyr Glu Ile Asp Gly Val Val Ile 275 280 285			864
aag gtt aat gac att gcc aag caa caa aca ctt ggt ttt gtg gct aaa Lys Val Asn Asp Ile Ala Lys Gln Gln Thr Leu Gly Phe Val Ala Lys 290 295 300			912
gct cct cga tgg gcc ata gcc tat aaa ttt cca gcc cag gaa gaa atg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Phe Pro Ala Gln Glu Glu Met 305 310 315 320			960
acc ttg tta gag tct gtt gac ttt cag gtt gcc cga acg ggt gct gtt Thr Leu Leu Glu Ser Val Asp Phe Gln Val Gly Arg Thr Gly Ala Val 325 330 335			1008
acc cct gtc gct cgc ctc aaa ccg ata ttt gtc ggt gcc gtg act gtg			1056

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Thr	Pro	Val	Ala	Arg	Leu	Lys	Pro	Ile	Phe	Val	Gly	Gly	Val	Thr	Val	
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tcg	aat	gcg	acc	ttg	cac	aat	gct	gat	gaa	att	gcc	cgt	ctt	ggg	gtg	1104
Ser	Asn	Ala	Thr	Leu	His	Asn	Ala	Asp	Glu	Ile	Ala	Arg	Leu	Gly	Val	
		355					360					365				
aaa	ata	ggc	gat	aca	gtg	att	att	cgc	cgc	gca	ggg	gac	gtt	atc	cgc	1152
Lys	Ile	Gly	Asp	Thr	Val	Ile	Ile	Arg	Arg	Ala	Gly	Asp	Val	Ile	Pro	
		370					375					380				
caa	att	gtt	gct	atc	gtg	cca	gaa	aag	cgc	cct	gat	gat	gca	caa	gat	1200
Gln	Ile	Val	Ala	Ile	Val	Pro	Glu	Lys	Arg	Pro	Asp	Asp	Ala	Gln	Asp	
		385				390				395					400	
att	atc	ttt	cca	ctg	cat	tgt	cct	gtg	tgc	caa	agc	att	gtt	gag	cgt	1248
Ile	Ile	Phe	Pro	Leu	His	Cys	Pro	Val	Cys	Gln	Ser	Ile	Val	Glu	Arg	
				405					410					415		
tta	gaa	ggg	gaa	gct	gta	gcg	cgt	tgt	agt	ggg	gga	ctt	ttt	tgt	gaa	1296
Leu	Glu	Gly	Glu	Ala	Val	Ala	Arg	Cys	Ser	Gly	Gly	Leu	Phe	Cys	Glu	
			420					425					430			
gcg	caa	cgt	aaa	gag	gcg	att	aaa	cat	ttt	gca	tcc	cgt	aaa	gca	tta	1344
Ala	Gln	Arg	Lys	Glu	Ala	Ile	Lys	His	Phe	Ala	Ser	Arg	Lys	Ala	Leu	
		435					440					445				
aat	att	gat	ggc	atg	ggc	gat	aaa	atc	gtt	gag	caa	tta	att	gat	aaa	1392
Asn	Ile	Asp	Gly	Met	Gly	Asp	Lys	Ile	Val	Glu	Gln	Leu	Ile	Asp	Lys	
		450				455					460					
gaa	cta	gtc	aaa	acg	cca	gca	gac	ttg	ttt	tcc	ctt	acc	gct	tct	agc	1440
Glu	Leu	Val	Lys	Thr	Pro	Ala	Asp	Leu	Phe	Ser	Leu	Thr	Ala	Ser	Ser	
					470					475					480	
atc	acg	atg	tta	gat	cgc	atg	gcg	atg	aag	tca	gcc	aca	aat	att	gtc	1488
Ile	Thr	Met	Leu	Asp	Arg	Met	Ala	Met	Lys	Ser	Ala	Thr	Asn	Ile	Val	
				485					490					495		
gcg	gcg	att	aaa	cac	gct	aaa	gcc	act	aca	tta	gcg	cgt	ttt	tta	tat	1536
Ala	Ala	Ile	Lys	His	Ala	Lys	Ala	Thr	Thr	Leu	Ala	Arg	Phe	Leu	Tyr	
			500					505						510		
agt	ctt	ggg	atc	cgc	gaa	gtc	ggc	gaa	gct	acc	gcc	gct	aat	tta	gcc	1584
Ser	Leu	Gly	Ile	Arg	Glu	Val	Gly	Glu	Ala	Thr	Ala	Ala	Asn	Leu	Ala	
		515					520					525				
caa	cac	ttt	gcc	gaa	ttt	gag	cgt	att	cga	act	gct	agc	gtt	gaa	caa	1632
Gln	His	Phe	Ala	Glu	Phe	Glu	Arg	Ile	Arg	Thr	Ala	Ser	Val	Glu	Gln	
		530					535				540					
ctg	ctc	gaa	gtc	gct	gat	gtt	ggg	gac	att	gta	gca	aaa	cac	att	cga	1680
Leu	Leu	Glu	Val	Ala	Asp	Val	Gly	Asp	Ile	Val	Ala	Lys	His	Ile	Arg	
		545				550				555					560	
caa	ttt	ttt	gca	cag	cca	cat	aac	att	gaa	gta	ata	gag	caa	ttg	ctt	1728
Gln	Phe	Phe	Ala	Gln	Pro	His	Asn	Ile	Glu	Val	Ile	Glu	Gln	Leu	Leu	
				565					570					575		
gaa	gcc	ggc	att	act	tgg	cct	gtt	att	gaa	caa	gct	gac	gaa	tcg	cag	1776
Glu	Ala	Gly	Ile	Thr	Trp	Pro	Val	Ile	Glu	Gln	Ala	Asp	Glu	Ser	Gln	
			580					585					590			
ctt	agt	ctt	aaa	ggg	caa	acg	tgg	gtg	tta	act	ggg	acg	cta	act	caa	1824
Leu	Ser	Leu	Lys	Gly	Gln	Thr	Trp	Val	Leu	Thr	Gly	Thr	Leu	Thr	Gln	
		595					600					605				
ctt	aat	cgt	aac	gat	gcc	aaa	gcc	caa	tta	cag	gct	ttg	ggc	gcc	aaa	1872
Leu	Asn	Arg	Asn	Asp	Ala	Lys	Ala	Gln	Leu	Gln	Ala	Leu	Gly	Ala	Lys	
		610				615					620					
gtg	gct	ggc	agt	gtt	tcg	aaa	aat	act	gat	tgc	ctt	gtt	gct	ggg	gaa	1920
Val	Ala	Gly	Ser	Val	Ser	Lys	Asn	Thr	Asp	Cys	Leu	Val	Ala	Gly	Glu	
		625				630				635					640	
gca	gcg	ggg	tct	aaa	tta	gca	aaa	gct	gaa	gaa	ttg	ggc	gtt	aag	gtg	1968
Ala	Ala	Gly	Ser	Lys	Leu	Ala	Lys	Ala	Glu	Glu	Leu	Gly	Val	Lys	Val	
				645					650					655		

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ata gat gaa caa gct ctg atg gat tta ttg aat gcg gct aac tga	2013
Ile Asp Glu Gln Ala Leu Met Asp Leu Leu Asn Ala Ala Asn	
660 665 670	

<210> SEQ ID NO 8
 <211> LENGTH: 670
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 8

Met Thr Pro Ile Gln Thr Glu Met Asp Gln Leu Thr His Thr Ile Asn	
1 5 10 15	
Gln His Asn Ile Arg Tyr Tyr Val Asp Asp Ala Pro Ser Ile Pro Asp	
20 25 30	
Ala Glu Tyr Asp Arg Leu Ile Lys Arg Leu Thr Glu Leu Glu Arg Asp	
35 40 45	
Tyr Pro Gln Phe Lys Ser Val Asp Ser Pro Thr Gln Arg Val Gly Gly	
50 55 60	
Ile Ala Leu Gln Lys Phe Ala Gln Ile Thr His Leu Lys Pro Met Leu	
65 70 75 80	
Ser Leu Asp Asn Ala Phe Glu Gln Ala Asp Phe Ala Ala Phe Asn Lys	
85 90 95	
Arg Ile Thr Asp Lys Val Asp Ser Val Asp Tyr Val Cys Glu Pro Lys	
100 105 110	
Leu Asp Gly Leu Ala Val Ser Ile Thr Tyr Arg Phe Gly Val Leu Glu	
115 120 125	
Arg Ala Ala Thr Arg Gly Asp Gly Ser Val Gly Glu Asp Ile Thr Ala	
130 135 140	
Asn Val Arg Thr Ile Arg Ser Ile Pro Leu Lys Leu Arg Gly Glu Gly	
145 150 155 160	
Phe Pro Asp Leu Val Glu Val Arg Gly Glu Val Phe Met Pro Lys Ala	
165 170 175	
Ala Phe Glu Ala Leu Asn Gln Arg Gln Ile Ser Lys Gly Asp Lys Val	
180 185 190	
Phe Val Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Leu Asp	
195 200 205	
Ser Lys Ile Thr Ala Ser Arg Ala Leu Gly Phe Tyr Ala Tyr Ala Leu	
210 215 220	
Gly Val Val Glu Gly Glu Ser Gln Pro Met Gln Thr Ser His Tyr Gly	
225 230 235 240	
Gln Leu Thr Gln Leu Gln Gln Trp Gly Ile Pro Val Ser Ser Glu Val	
245 250 255	
Lys Val Thr Asp Leu Leu Glu Lys Val Tyr Ala Tyr Tyr Ala Asp Ile	
260 265 270	
Met Ala Arg Arg Ser Ala Leu Glu Tyr Glu Ile Asp Gly Val Val Ile	
275 280 285	
Lys Val Asn Asp Ile Ala Lys Gln Gln Thr Leu Gly Phe Val Ala Lys	
290 295 300	
Ala Pro Arg Trp Ala Ile Ala Tyr Lys Phe Pro Ala Gln Glu Glu Met	
305 310 315 320	
Thr Leu Leu Glu Ser Val Asp Phe Gln Val Gly Arg Thr Gly Ala Val	
325 330 335	
Thr Pro Val Ala Arg Leu Lys Pro Ile Phe Val Gly Gly Val Thr Val	
340 345 350	

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Ser Asn Ala Thr Leu His Asn Ala Asp Glu Ile Ala Arg Leu Gly Val
 355 360 365

Lys Ile Gly Asp Thr Val Ile Ile Arg Arg Ala Gly Asp Val Ile Pro
 370 375 380

Gln Ile Val Ala Ile Val Pro Glu Lys Arg Pro Asp Asp Ala Gln Asp
 385 390 395 400

Ile Ile Phe Pro Leu His Cys Pro Val Cys Gln Ser Ile Val Glu Arg
 405 410 415

Leu Glu Gly Glu Ala Val Ala Arg Cys Ser Gly Gly Leu Phe Cys Glu
 420 425 430

Ala Gln Arg Lys Glu Ala Ile Lys His Phe Ala Ser Arg Lys Ala Leu
 435 440 445

Asn Ile Asp Gly Met Gly Asp Lys Ile Val Glu Gln Leu Ile Asp Lys
 450 455 460

Glu Leu Val Lys Thr Pro Ala Asp Leu Phe Ser Leu Thr Ala Ser Ser
 465 470 475 480

Ile Thr Met Leu Asp Arg Met Ala Met Lys Ser Ala Thr Asn Ile Val
 485 490 495

Ala Ala Ile Lys His Ala Lys Ala Thr Thr Leu Ala Arg Phe Leu Tyr
 500 505 510

Ser Leu Gly Ile Arg Glu Val Gly Glu Ala Thr Ala Ala Asn Leu Ala
 515 520 525

Gln His Phe Ala Glu Phe Glu Arg Ile Arg Thr Ala Ser Val Glu Gln
 530 535 540

Leu Leu Glu Val Ala Asp Val Gly Asp Ile Val Ala Lys His Ile Arg
 545 550 555 560

Gln Phe Phe Ala Gln Pro His Asn Ile Glu Val Ile Glu Gln Leu Leu
 565 570 575

Glu Ala Gly Ile Thr Trp Pro Val Ile Glu Gln Ala Asp Glu Ser Gln
 580 585 590

Leu Ser Leu Lys Gly Gln Thr Trp Val Leu Thr Gly Thr Leu Thr Gln
 595 600 605

Leu Asn Arg Asn Asp Ala Lys Ala Gln Leu Gln Ala Leu Gly Ala Lys
 610 615 620

Val Ala Gly Ser Val Ser Lys Asn Thr Asp Cys Leu Val Ala Gly Glu
 625 630 635 640

Ala Ala Gly Ser Lys Leu Ala Lys Ala Glu Glu Leu Gly Val Lys Val
 645 650 655

Ile Asp Glu Gln Ala Leu Met Asp Leu Leu Asn Ala Ala Asn
 660 665 670

<210> SEQ ID NO 9
 <211> LENGTH: 1638
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PyrGCP hybrid
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1638)

<400> SEQUENCE: 9

atg aat tct aac act aaa att att ttc gtc aca ggt ggg gta gta tca	48
Met Asn Ser Asn Thr Lys Ile Ile Phe Val Thr Gly Gly Val Val Ser	
1 5 10 15	
tca ctt ggt aag ggt gta act gcg gca tct ttg gct act ctc tta gaa	96

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Ser	Leu	Gly	Lys	Gly	Val	Thr	Ala	Ala	Ser	Leu	Ala	Thr	Leu	Leu	Glu	
			20					25					30			
agt	cgt	ggg	ctt	aat	gta	aca	atg	atg	aag	ctt	gat	cca	tac	atc	aat	144
Ser	Arg	Gly	Leu	Asn	Val	Thr	Met	Met	Lys	Leu	Asp	Pro	Tyr	Ile	Asn	
		35					40					45				
ggt	gat	cca	ggg	act	atg	agt	cca	ttg	caa	cat	ggg	gaa	ggt	ttt	gta	192
Val	Asp	Pro	Gly	Thr	Met	Ser	Pro	Leu	Gln	His	Gly	Glu	Val	Phe	Val	
	50					55					60					
acc	gaa	gat	ggc	gca	gag	act	gat	ctt	gat	tta	ggg	cat	tat	gag	cgc	240
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
	65				70					75				80		
ttt	atc	cgc	aat	aag	atg	act	caa	gca	aat	aac	ttc	aca	acc	ggg	aaa	288
Phe	Ile	Arg	Asn	Lys	Met	Thr	Gln	Ala	Asn	Asn	Phe	Thr	Thr	Gly	Lys	
			85						90					95		
gta	tac	cag	agt	gtg	tta	aga	aga	gag	cgt	aag	ggg	gat	tat	cta	ggg	336
Val	Tyr	Gln	Ser	Val	Leu	Arg	Arg	Glu	Arg	Lys	Gly	Asp	Tyr	Leu	Gly	
		100						105					110			
gct	act	atc	cag	gtg	att	cca	cat	atc	att	gat	gag	atc	aaa	agg	cgt	384
Ala	Thr	Ile	Gln	Val	Ile	Pro	His	Ile	Ile	Asp	Glu	Ile	Lys	Arg	Arg	
	115					120						125				
att	tgt	agt	ggg	att	gct	gat	gat	gtt	gat	gtt	gcg	att	gtt	gag	att	432
Ile	Cys	Ser	Gly	Ile	Ala	Asp	Asp	Val	Asp	Val	Ala	Ile	Val	Glu	Ile	
	130					135					140					
ggg	ggg	act	gtt	ggg	gat	atc	gag	tca	caa	cca	ttt	tta	gaa	gct	att	480
Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	Phe	Leu	Glu	Ala	Ile	
	145			150					155					160		
cgt	caa	ttg	gca	tta	gag	gta	ggg	cgt	gat	cgt	gct	atg	ttt	atg	cat	528
Arg	Gln	Leu	Ala	Leu	Glu	Val	Gly	Arg	Asp	Arg	Ala	Met	Phe	Met	His	
			165					170					175			
ttg	acc	tta	gtg	cca	tat	tta	gca	gca	gca	ggg	gaa	atc	aaa	act	aaa	576
Leu	Thr	Leu	Val	Pro	Tyr	Leu	Ala	Ala	Ala	Gly	Glu	Ile	Lys	Thr	Lys	
			180					185					190			
cca	aca	cag	cac	tca	gta	aaa	gat	tta	cgc	tct	atc	ggg	att	ttt	cct	624
Pro	Thr	Gln	His	Ser	Val	Lys	Asp	Leu	Arg	Ser	Ile	Gly	Ile	Phe	Pro	
		195				200						205				
gac	att	tta	gta	tgt	cgt	tca	gac	cgc	gct	att	cct	aac	gcc	gaa	cgc	672
Asp	Ile	Leu	Val	Cys	Arg	Ser	Asp	Arg	Ala	Ile	Pro	Asn	Ala	Glu	Arg	
	210				215						220					
gct	aaa	ata	tct	ctc	ttc	act	aat	gtt	gaa	gag	aaa	gcg	gtt	gta	tca	720
Ala	Lys	Ile	Ser	Leu	Phe	Thr	Asn	Val	Glu	Glu	Lys	Ala	Val	Val	Ser	
	225				230					235				240		
atg	cgt	gat	gta	gac	agt	att	tat	aag	att	cct	gct	tta	tta	aaa	gct	768
Met	Arg	Asp	Val	Asp	Ser	Ile	Tyr	Lys	Ile	Pro	Ala	Leu	Leu	Lys	Ala	
			245					250						255		
caa	ggg	acc	gat	gaa	ata	gtt	gtt	aag	cga	ttt	ggg	tta	gat	gta	cct	816
Gln	Gly	Thr	Asp	Glu	Ile	Val	Val	Lys	Arg	Phe	Gly	Leu	Asp	Val	Pro	
			260					265					270			
gaa	gcc	gac	tta	act	gaa	tggt	gaa	gaa	gtg	ctt	tac	cat	gaa	gca	aat	864
Glu	Ala	Asp	Leu	Thr	Glu	Trp	Glu	Glu	Val	Leu	Tyr	His	Glu	Ala	Asn	
		275				280						285				
cct	atc	ggg	gaa	gtg	act	att	ggg	atg	gtt	ggg	aaa	tac	act	gaa	tta	912
Pro	Ile	Gly	Glu	Val	Thr	Ile	Gly	Met	Val	Gly	Lys	Tyr	Thr	Glu	Leu	
	290					295					300					
cct	gat	gag	tac	aaa	tca	gta	aac	gaa	gag	tta	aaa	cat	gca	ggg	ctt	960
Pro	Asp	Ala	Tyr	Lys	Ser	Val	Asn	Glu	Ala	Leu	Lys	His	Ala	Gly	Leu	
	305				310					315				320		
aaa	aac	caa	gtc	act	gta	aat	att	aaa	tac	att	gac	tcg	caa	gat	gta	1008
Lys	Asn	Gln	Val	Thr	Val	Asn	Ile	Lys	Tyr	Ile	Asp	Ser	Gln	Asp	Val	
			325					330						335		

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gaa gtc aaa ggt gtt gaa atc tta gct aac ttg gat gct att tta gtt Glu Val Lys Gly Val Glu Ile Leu Ala Asn Leu Asp Ala Ile Leu Val 340 345 350	1056
cct ggt ggt ttc ggt gaa cgt ggt gtt gaa ggt aaa att tta acg gca Pro Gly Gly Phe Gly Glu Arg Gly Val Glu Gly Lys Ile Leu Thr Ala 355 360 365	1104
caa tat gcg cgt gaa aac aaa gta cct tat tta ggt att tgt tta ggt Gln Tyr Ala Arg Glu Asn Lys Val Pro Tyr Leu Gly Ile Cys Leu Gly 370 375 380	1152
atg caa gta gcc tta att gaa ttt gct cgt aat gtt gcc ggt tta act Met Gln Val Ala Leu Ile Glu Phe Ala Arg Asn Val Ala Gly Leu Thr 385 390 395 400	1200
gat gcg cac agt act gaa ttt aat agc gaa act cca cac cca gtg gtt Asp Ala His Ser Thr Glu Phe Asn Ser Glu Thr Pro His Pro Val Val 405 410 415	1248
ggt tta atc agt gaa tgg tta gac gaa gaa ggc caa gtt gag tac cga Gly Leu Ile Ser Glu Trp Leu Asp Glu Glu Gly Gln Val Glu Tyr Arg 420 425 430	1296
aat gag caa tca gat tta ggt ggt act atg cgt tta ggt tca caa ttg Asn Glu Gln Ser Asp Leu Gly Gly Thr Met Arg Leu Gly Ser Gln Leu 435 440 445	1344
tgc cac ttg gtg aaa ggt acc aag gct tgc gac gta tat ggt agt gaa Cys His Leu Val Lys Gly Thr Lys Ala Cys Asp Val Tyr Gly Ser Glu 450 455 460	1392
aca atc aat gag aga cac cgt cat cgt ttt gag gta aat aat aac tac Thr Ile Asn Glu Arg His Arg Phe Glu Val Asn Asn Asn Tyr 465 470 475 480	1440
cga gaa caa tta agc aaa gca ggt ttg att ttc tcg ggt tta tcg tca Arg Glu Gln Leu Ser Lys Ala Gly Leu Ile Phe Ser Gly Leu Ser Ser 485 490 495	1488
gat aaa agt tta gtt gag gtg att gaa ata gcg gat cat cca tgg ttt Asp Lys Ser Leu Val Glu Val Ile Glu Ile Ala Asp His Pro Trp Phe 500 505 510	1536
att gcg ggt caa ttc cat cct gag ttt aat tct act cca cgt gat ggt Ile Ala Gly Gln Phe His Pro Glu Phe Asn Ser Thr Pro Arg Asp Gly 515 520 525	1584
cac ccg tta ttc gaa agc ttt gtt gca gcg agt ttt aaa ctg caa aat His Pro Leu Phe Glu Ser Phe Val Ala Ala Ser Phe Lys Leu Gln Asn 530 535 540	1632
aat tag Asn 545	1638

<210> SEQ ID NO 10

<211> LENGTH: 545

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 10

Met Asn Ser Asn Thr Lys Ile Ile Phe Val Thr Gly Gly Val Val Ser
1 5 10 15

Ser Leu Gly Lys Gly Val Thr Ala Ala Ser Leu Ala Thr Leu Leu Glu
20 25 30

Ser Arg Gly Leu Asn Val Thr Met Met Lys Leu Asp Pro Tyr Ile Asn
35 40 45

Val Asp Pro Gly Thr Met Ser Pro Leu Gln His Gly Glu Val Phe Val
50 55 60

Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg

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65	70	75	80
Phe Ile Arg Asn Lys Met Thr Gln Ala Asn Asn Phe Thr Thr Gly Lys	85	90	95
Val Tyr Gln Ser Val Leu Arg Arg Glu Arg Lys Gly Asp Tyr Leu Gly	100	105	110
Ala Thr Ile Gln Val Ile Pro His Ile Ile Asp Glu Ile Lys Arg Arg	115	120	125
Ile Cys Ser Gly Ile Ala Asp Asp Val Asp Val Ala Ile Val Glu Ile	130	135	140
Gly Gly Thr Val Gly Asp Ile Glu Ser Gln Pro Phe Leu Glu Ala Ile	145	150	155
Arg Gln Leu Ala Leu Glu Val Gly Arg Asp Arg Ala Met Phe Met His	165	170	175
Leu Thr Leu Val Pro Tyr Leu Ala Ala Gly Glu Ile Lys Thr Lys	180	185	190
Pro Thr Gln His Ser Val Lys Asp Leu Arg Ser Ile Gly Ile Phe Pro	195	200	205
Asp Ile Leu Val Cys Arg Ser Asp Arg Ala Ile Pro Asn Ala Glu Arg	210	215	220
Ala Lys Ile Ser Leu Phe Thr Asn Val Glu Glu Lys Ala Val Val Ser	225	230	235
Met Arg Asp Val Asp Ser Ile Tyr Lys Ile Pro Ala Leu Leu Lys Ala	245	250	255
Gln Gly Thr Asp Glu Ile Val Val Lys Arg Phe Gly Leu Asp Val Pro	260	265	270
Glu Ala Asp Leu Thr Glu Trp Glu Glu Val Leu Tyr His Glu Ala Asn	275	280	285
Pro Ile Gly Glu Val Thr Ile Gly Met Val Gly Lys Tyr Thr Glu Leu	290	295	300
Pro Asp Ala Tyr Lys Ser Val Asn Glu Ala Leu Lys His Ala Gly Leu	305	310	315
Lys Asn Gln Val Thr Val Asn Ile Lys Tyr Ile Asp Ser Gln Asp Val	325	330	335
Glu Val Lys Gly Val Glu Ile Leu Ala Asn Leu Asp Ala Ile Leu Val	340	345	350
Pro Gly Gly Phe Gly Glu Arg Gly Val Glu Gly Lys Ile Leu Thr Ala	355	360	365
Gln Tyr Ala Arg Glu Asn Lys Val Pro Tyr Leu Gly Ile Cys Leu Gly	370	375	380
Met Gln Val Ala Leu Ile Glu Phe Ala Arg Asn Val Ala Gly Leu Thr	385	390	395
Asp Ala His Ser Thr Glu Phe Asn Ser Glu Thr Pro His Pro Val Val	405	410	415
Gly Leu Ile Ser Glu Trp Leu Asp Glu Glu Gly Gln Val Glu Tyr Arg	420	425	430
Asn Glu Gln Ser Asp Leu Gly Gly Thr Met Arg Leu Gly Ser Gln Leu	435	440	445
Cys His Leu Val Lys Gly Thr Lys Ala Cys Asp Val Tyr Gly Ser Glu	450	455	460
Thr Ile Asn Glu Arg His Arg His Arg Phe Glu Val Asn Asn Asn Tyr	465	470	475
Arg Glu Gln Leu Ser Lys Ala Gly Leu Ile Phe Ser Gly Leu Ser Ser	485	490	495

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Asp Lys Ser Leu Val Glu Val Ile Glu Ile Ala Asp His Pro Trp Phe
500 505 510

Ile Ala Gly Gln Phe His Pro Glu Phe Asn Ser Thr Pro Arg Asp Gly
515 520 525

His Pro Leu Phe Glu Ser Phe Val Ala Ala Ser Phe Lys Leu Gln Asn
530 535 540

Asn
545

<210> SEQ ID NO 11

<211> LENGTH: 954

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: hemCCp hybrid

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(954)

<400> SEQUENCE: 11

atg aaa caa act aca gta cga att gcc acg cgt aaa agc gcc ctc gcc 48
Met Lys Gln Thr Thr Val Arg Ile Ala Thr Arg Lys Ser Ala Leu Ala
1 5 10 15

tta tgg caa gca gaa tat gtt aaa gcg caa ctt gag cat ttt cat gac 96
Leu Trp Gln Ala Glu Tyr Val Lys Ala Gln Leu Glu His Phe His Asp
20 25 30

ggt att aat gtt gaa tta gtg cct atg aca acg aaa ggc gac atc att 144
Gly Ile Asn Val Glu Leu Val Pro Met Thr Thr Lys Gly Asp Ile Ile
35 40 45

tta gac acg cct tta gcc aaa gtc ggc ggt aaa ggt tta ttt gtt aaa 192
Leu Asp Thr Pro Leu Ala Lys Val Gly Gly Lys Gly Leu Phe Val Lys
50 55 60

gag ctt gaa gta gca atg ctt gaa gac cgt gct gat att gct gtt cat 240
Glu Leu Glu Val Ala Met Leu Glu Asp Arg Ala Asp Ile Ala Val His
65 70 75 80

tca atg aaa gat gtt cct gtc gat ttt cca gaa ggc tta gga tta gaa 288
Ser Met Lys Asp Val Pro Val Asp Phe Pro Glu Gly Leu Gly Leu Glu
85 90 95

gtc att tgt cct cgt gaa gat ccc cgt gat gct ttt gtt tct aat acc 336
Val Ile Cys Pro Arg Glu Asp Pro Arg Asp Ala Phe Val Ser Asn Thr
100 105 110

atc aaa tca tta agt gat tta cca caa ggc tct att gtt ggc acc tca 384
Ile Lys Ser Leu Ser Asp Leu Pro Gln Gly Ser Ile Val Gly Thr Ser
115 120 125

agc tta cgc cgt cag tgt caa tta aaa gca agc cgc cct gat tta gat 432
Ser Leu Arg Arg Gln Cys Gln Leu Lys Ala Ser Arg Pro Asp Leu Asp
130 135 140

att cgt gat tta cgt ggc aat gta aat acc cgc cta aga aaa tta gat 480
Ile Arg Asp Leu Arg Gly Asn Val Asn Thr Arg Leu Arg Lys Leu Asp
145 150 155 160

gaa ggt cag tac gac gct att ata tta gcc gct gca ggc cta att cgc 528
Glu Gly Gln Tyr Asp Ala Ile Ile Leu Ala Ala Gly Leu Ile Arg
165 170 175

tta gaa atg agc gag cgt att gca cag ttt atc gaa cca gaa gaa atg 576
Leu Glu Met Ser Glu Arg Ile Ala Gln Phe Ile Glu Pro Glu Glu Met
180 185 190

ctt cct gca aat ggc caa ggc gct gtt ggc att gaa tgt cgt aat gat 624
Leu Pro Ala Asn Gly Gln Gly Ala Val Gly Ile Glu Cys Arg Asn Asp
195 200 205

gat gcg aca att aaa gcc tta tta gca cca tta gaa tgt gct acc acc 672

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Asp	Ala	Thr	Ile	Lys	Ala	Leu	Leu	Ala	Pro	Leu	Glu	Cys	Ala	Thr	Thr		
210						215					220						
cgt	att	cgt	gtt	ctt	gca	gaa	cgt	gca	atg	aat	aga	gca	tta	caa	ggc		720
Arg	Ile	Arg	Val	Leu	Ala	Glu	Arg	Ala	Met	Asn	Arg	Ala	Leu	Gln	Gly		
225					230					235				240			
ggc	tgc	cag	gtt	cct	atc	ggc	agc	tat	ggc	gtt	att	tct	gct	gat	ggc		768
Gly	Cys	Gln	Val	Pro	Ile	Gly	Ser	Tyr	Gly	Val	Ile	Ser	Ala	Asp	Gly		
			245						250					255			
aaa	aat	atc	cac	tta	cgt	ggc	tta	gtt	ggc	tct	gtc	gat	ggc	agt	gaa		816
Lys	Asn	Ile	His	Leu	Arg	Gly	Leu	Val	Gly	Ser	Val	Asp	Gly	Ser	Glu		
			260				265						270				
atg	ata	gaa	agt	gaa	atc	acc	ggc	cct	gtt	gaa	gaa	ggc	gaa	gcg	ctc		864
Met	Ile	Glu	Ser	Glu	Ile	Thr	Gly	Pro	Val	Glu	Glu	Gly	Glu	Ala	Leu		
		275				280						285					
ggc	aat	aaa	ctc	gcg	caa	gag	tta	cta	agc	cga	ggc	gca	gat	aaa	att		912
Gly	Asn	Lys	Leu	Ala	Gln	Glu	Leu	Leu	Ser	Arg	Gly	Ala	Asp	Lys	Ile		
		290				295					300						
tta	cag	caa	gtt	tat	tca	gaa	aat	gat	atc	aaa	gag	agt	taa				954
Leu	Gln	Gln	Val	Tyr	Ser	Glu	Asn	Asp	Ile	Lys	Glu	Ser					
305					310					315							

<210> SEQ ID NO 12
 <211> LENGTH: 317
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 12

Met	Lys	Gln	Thr	Thr	Val	Arg	Ile	Ala	Thr	Arg	Lys	Ser	Ala	Leu	Ala		
1				5					10					15			
Leu	Trp	Gln	Ala	Glu	Tyr	Val	Lys	Ala	Gln	Leu	Glu	His	Phe	His	Asp		
		20					25						30				
Gly	Ile	Asn	Val	Glu	Leu	Val	Pro	Met	Thr	Thr	Lys	Gly	Asp	Ile	Ile		
		35					40					45					
Leu	Asp	Thr	Pro	Leu	Ala	Lys	Val	Gly	Gly	Lys	Gly	Leu	Phe	Val	Lys		
		50				55				60							
Glu	Leu	Glu	Val	Ala	Met	Leu	Glu	Asp	Arg	Ala	Asp	Ile	Ala	Val	His		
				70					75					80			
Ser	Met	Lys	Asp	Val	Pro	Val	Asp	Phe	Pro	Glu	Gly	Leu	Gly	Leu	Glu		
			85					90						95			
Val	Ile	Cys	Pro	Arg	Glu	Asp	Pro	Arg	Asp	Ala	Phe	Val	Ser	Asn	Thr		
			100				105						110				
Ile	Lys	Ser	Leu	Ser	Asp	Leu	Pro	Gln	Gly	Ser	Ile	Val	Gly	Thr	Ser		
		115				120						125					
Ser	Leu	Arg	Arg	Gln	Cys	Gln	Leu	Lys	Ala	Ser	Arg	Pro	Asp	Leu	Asp		
		130			135				140								
Ile	Arg	Asp	Leu	Arg	Gly	Asn	Val	Asn	Thr	Arg	Leu	Arg	Lys	Leu	Asp		
		145			150				155					160			
Glu	Gly	Gln	Tyr	Asp	Ala	Ile	Ile	Leu	Ala	Ala	Ala	Gly	Leu	Ile	Arg		
				165				170						175			
Leu	Glu	Met	Ser	Glu	Arg	Ile	Ala	Gln	Phe	Ile	Glu	Pro	Glu	Glu	Met		
			180				185					190					
Leu	Pro	Ala	Asn	Gly	Gln	Gly	Ala	Val	Gly	Ile	Glu	Cys	Arg	Asn	Asp		
		195				200						205					
Asp	Ala	Thr	Ile	Lys	Ala	Leu	Leu	Ala	Pro	Leu	Glu	Cys	Ala	Thr	Thr		
		210				215					220						

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Arg Ile Arg Val Leu Ala Glu Arg Ala Met Asn Arg Ala Leu Gln Gly
 225 230 235 240

Gly Cys Gln Val Pro Ile Gly Ser Tyr Gly Val Ile Ser Ala Asp Gly
 245 250 255

Lys Asn Ile His Leu Arg Gly Leu Val Gly Ser Val Asp Gly Ser Glu
 260 265 270

Met Ile Glu Ser Glu Ile Thr Gly Pro Val Glu Glu Gly Glu Ala Leu
 275 280 285

Gly Asn Lys Leu Ala Gln Glu Leu Leu Ser Arg Gly Ala Asp Lys Ile
 290 295 300

Leu Gln Gln Val Tyr Ser Glu Asn Asp Ile Lys Glu Ser
 305 310 315

<210> SEQ ID NO 13
 <211> LENGTH: 984
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: fmtCp hybrid
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) .. (984)

<400> SEQUENCE: 13

atg aaa aaa cca cta aat atc att ttt gca ggt act cct gaa ttc gct	48
Met Lys Lys Pro Leu Asn Ile Ile Phe Ala Gly Thr Pro Glu Phe Ala	
1 5 10 15	
gcc caa cat tta gca gcg tta att aat tct gaa cat aat att gtc gcc	96
Ala Gln His Leu Ala Ala Leu Ile Asn Ser Glu His Asn Ile Val Ala	
20 25 30	
gtt tat tgt ccc cct gat aaa cca gct ggc cgc ggt aaa aaa cta aca	144
Val Tyr Cys Pro Pro Asp Lys Pro Ala Gly Arg Gly Lys Lys Leu Thr	
35 40 45	
gct tgt gca aca aag tta ctc gca ata gag cac gac att att gtt gag	192
Ala Cys Ala Thr Lys Leu Leu Ala Ile Glu His Asp Ile Ile Val Glu	
50 55 60	
caa cct att aac ttt aaa aat gag gaa gac caa caa caa tta gcg aaa	240
Gln Pro Ile Asn Phe Lys Asn Glu Glu Asp Gln Gln Gln Leu Ala Lys	
65 70 75 80	
tat aac gct gat atc atg gtt gtt gtt gct tat ggt ctg cta tta cct	288
Tyr Asn Ala Asp Ile Met Val Val Val Ala Tyr Gly Leu Leu Leu Pro	
85 90 95	
gaa gtc att tta aac tct cca cgt tta ggc tgc att aac gta cat ggc	336
Glu Val Ile Leu Asn Ser Pro Arg Leu Gly Cys Ile Asn Val His Gly	
100 105 110	
tca att cta cca aaa tgg cgt ggt gca gca cct att caa cgt tct ctt	384
Ser Ile Leu Pro Lys Trp Arg Gly Ala Ala Pro Ile Gln Arg Ser Leu	
115 120 125	
gaa gct gga gat aag aaa acc ggt gtc acc att atg caa atg gat aaa	432
Glu Ala Gly Asp Lys Lys Thr Gly Val Thr Ile Met Gln Met Asp Lys	
130 135 140	
ggg tta gac acg gga gac atg att cta tcc gct gag tgc gaa ata gaa	480
Gly Leu Asp Thr Gly Asp Met Ile Leu Ser Ala Glu Cys Glu Ile Glu	
145 150 155 160	
aat aca gat acc agt gca agt ctt tat gaa aaa ctt gcc aac tta ggg	528
Asn Thr Asp Thr Ser Ala Ser Leu Tyr Glu Lys Leu Ala Asn Leu Gly	
165 170 175	
cca act gcc tta gtt aat aca tta act att atg gct gaa cct gat tat	576
Pro Thr Ala Leu Val Asn Thr Leu Thr Ile Met Ala Glu Pro Asp Tyr	
180 185 190	

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caa gcc agt aat cat aat atc gct caa gat gat gaa tta gcg act tat	624
Gln Ala Ser Asn His Asn Ile Ala Gln Asp Asp Glu Leu Ala Thr Tyr	
195 200 205	
gcc aag aaa ctt gat aaa act gaa gca gag ctt aac tgg caa ttc agt	672
Ala Lys Lys Leu Asp Lys Thr Glu Ala Glu Leu Asn Trp Gln Phe Ser	
210 215 220	
gct gat gaa cta cat cga aaa att cgt gct tat att cct tgg cca gtt	720
Ala Asp Glu Leu His Arg Lys Ile Arg Ala Tyr Ile Pro Trp Pro Val	
225 230 235 240	
gct caa ttt acc ttt aca gaa tct gaa ggt aag cag cat agg tta cgc	768
Ala Gln Phe Thr Phe Thr Glu Ser Glu Gly Lys Gln His Arg Leu Arg	
245 250 255	
ata tgg caa gca tcc gtg caa gaa tat cga ggc aat gct gat cca ggc	816
Ile Trp Gln Ala Ser Val Gln Glu Tyr Arg Gly Asn Ala Asp Pro Gly	
260 265 270	
acg ata ata aag gca gac aaa gaa ggg ata gaa gta gca aca acc agt	864
Thr Ile Ile Lys Ala Asp Lys Glu Gly Ile Glu Val Ala Thr Thr Ser	
275 280 285	
ggg tgg tta cga cta gaa gtc att caa ctt cca ggg aaa aaa gca tta	912
Gly Ser Leu Arg Leu Glu Val Ile Gln Leu Pro Gly Lys Lys Ala Leu	
290 295 300	
gcc gta aaa gac atc cta aat ggt cgc agc gat tgg ttc gtt gtt ggc	960
Ala Val Lys Asp Ile Leu Asn Gly Arg Ser Asp Trp Phe Val Val Gly	
305 310 315 320	
agc act att aac aag cta gga taa	984
Ser Thr Ile Asn Lys Leu Gly	
325	

<210> SEQ ID NO 14
 <211> LENGTH: 327
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 14

Met Lys Lys Pro Leu Asn Ile Ile Phe Ala Gly Thr Pro Glu Phe Ala	
1 5 10 15	
Ala Gln His Leu Ala Ala Leu Ile Asn Ser Glu His Asn Ile Val Ala	
20 25 30	
Val Tyr Cys Pro Pro Asp Lys Pro Ala Gly Arg Gly Lys Lys Leu Thr	
35 40 45	
Ala Cys Ala Thr Lys Leu Leu Ala Ile Glu His Asp Ile Ile Val Glu	
50 55 60	
Gln Pro Ile Asn Phe Lys Asn Glu Glu Asp Gln Gln Gln Leu Ala Lys	
65 70 75 80	
Tyr Asn Ala Asp Ile Met Val Val Val Ala Tyr Gly Leu Leu Leu Pro	
85 90 95	
Glu Val Ile Leu Asn Ser Pro Arg Leu Gly Cys Ile Asn Val His Gly	
100 105 110	
Ser Ile Leu Pro Lys Trp Arg Gly Ala Ala Pro Ile Gln Arg Ser Leu	
115 120 125	
Glu Ala Gly Asp Lys Lys Thr Gly Val Thr Ile Met Gln Met Asp Lys	
130 135 140	
Gly Leu Asp Thr Gly Asp Met Ile Leu Ser Ala Glu Cys Glu Ile Glu	
145 150 155 160	
Asn Thr Asp Thr Ser Ala Ser Leu Tyr Glu Lys Leu Ala Asn Leu Gly	
165 170 175	

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Pro Thr Ala Leu Val Asn Thr Leu Thr Ile Met Ala Glu Pro Asp Tyr
 180 185 190

Gln Ala Ser Asn His Asn Ile Ala Gln Asp Asp Glu Leu Ala Thr Tyr
 195 200 205

Ala Lys Lys Leu Asp Lys Thr Glu Ala Glu Leu Asn Trp Gln Phe Ser
 210 215 220

Ala Asp Glu Leu His Arg Lys Ile Arg Ala Tyr Ile Pro Trp Pro Val
 225 230 235 240

Ala Gln Phe Thr Phe Thr Glu Ser Glu Gly Lys Gln His Arg Leu Arg
 245 250 255

Ile Trp Gln Ala Ser Val Gln Glu Tyr Arg Gly Asn Ala Asp Pro Gly
 260 265 270

Thr Ile Ile Lys Ala Asp Lys Glu Gly Ile Glu Val Ala Thr Thr Ser
 275 280 285

Gly Ser Leu Arg Leu Glu Val Ile Gln Leu Pro Gly Lys Lys Ala Leu
 290 295 300

Ala Val Lys Asp Ile Leu Asn Gly Arg Ser Asp Trp Phe Val Val Gly
 305 310 315 320

Ser Thr Ile Asn Lys Leu Gly
 325

<210> SEQ ID NO 15
 <211> LENGTH: 1164
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: murGCp hybrid
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) .. (1164)

<400> SEQUENCE: 15

atg agt cta aat cat ggc caa ggt aat aaa gat tta gca aaa act ttg Met Ser Leu Asn His Gly Gln Gly Asn Lys Asp Leu Ala Lys Thr Leu 1 5 10 15	48
tta gtc atg gct ggt ggc acc ggt gga cat ata ttc cct ggt att gcg Leu Val Met Ala Gly Gly Thr Gly His Ile Phe Pro Gly Ile Ala 20 25 30	96
gtc gcc gat gag ctg aaa gcg caa gga tgg aaa atc cat tgg ttg gga Val Ala Asp Glu Leu Lys Ala Gln Gly Trp Lys Ile His Trp Leu Gly 35 40 45	144
act gcc gat cgt atg gaa gct caa att gta cct atg cat ggt tat gat Thr Ala Asp Arg Met Glu Ala Gln Ile Val Pro Met His Gly Tyr Asp 50 55 60	192
att tcg ttt atc aat ata agt ggt ctg cgt ggt aaa aat cta tta aca Ile Ser Phe Ile Asn Ile Ser Gly Leu Arg Gly Lys Asn Leu Leu Thr 65 70 75 80	240
acg ctt gtt atg cct ttt aaa ttg tta agg tcg ctt ttt caa gcg aga Thr Leu Val Met Pro Phe Lys Leu Leu Arg Ser Leu Phe Gln Ala Arg 85 90 95	288
cgc gtg att aaa aca gtg aaa cct gat gtt gtt ata ggc atg ggt ggc Arg Val Ile Lys Thr Val Lys Pro Asp Val Val Ile Gly Met Gly Gly 100 105 110	336
tat gca agt gct ccg ggt ggt ttg gcc gct tgg cta agt aaa ata ccg Tyr Ala Ser Ala Pro Gly Gly Leu Ala Ala Trp Leu Ser Lys Ile Pro 115 120 125	384
cta atc gtt cat gaa caa aat gct gct gcc gga tta agt aat cgc ttg Leu Ile Val His Glu Gln Asn Ala Ala Ala Gly Leu Ser Asn Arg Leu 130 135 140	432

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tta gcg cgt atc gcc aat aaa gta tgc tgc gcc ttt cct aat gca ttt	480
Leu Ala Arg Ile Ala Asn Lys Val Cys Cys Ala Phe Pro Asn Ala Phe	
145 150 155 160	
ggt agc gga att gat gtt gaa gtg gtt ggt aat cct tta cgc gcg tca	528
Val Ser Gly Ile Asp Val Glu Val Val Gly Asn Pro Leu Arg Ala Ser	
165 170 175	
atc ggt cag caa gca ctg gtt tca gaa aat ata gat caa agc cac gaa	576
Ile Gly Gln Gln Ala Leu Val Ser Glu Asn Ile Asp Gln Ser His Glu	
180 185 190	
ggt agt aaa aat att cta gtg gta ggt ggt agt tta ggc gct caa gtc	624
Gly Ser Lys Asn Ile Leu Val Val Gly Gly Ser Leu Gly Ala Gln Val	
195 200 205	
tta aat aag gtg atg ccg gat agc ttt aag gat tta tca gaa agt gat	672
Leu Asn Lys Val Met Pro Asp Ser Phe Lys Asp Leu Ser Glu Ser Asp	
210 215 220	
gag aaa tat tgt ata tgg cac caa acg ggc gac aat aac caa gca cta	720
Glu Lys Tyr Cys Ile Trp His Gln Thr Gly Asp Asn Asn Gln Ala Leu	
225 230 235 240	
gtc acc gca tct tat aaa cag gaa tat att gat act gga aaa gtg aga	768
Val Thr Ala Ser Tyr Lys Gln Glu Tyr Ile Asp Thr Gly Lys Val Arg	
245 250 255	
ggt acc gaa ttt att act gat att gct gct gca tat cag tgg gct gat	816
Val Thr Glu Phe Ile Thr Asp Ile Ala Ala Ala Tyr Gln Trp Ala Asp	
260 265 270	
ata gtg att tgt cgt gcg gga gcg cta acc gtt tca gaa tta gcc atg	864
Ile Val Ile Cys Arg Ala Gly Ala Leu Thr Val Ser Glu Leu Ala Met	
275 280 285	
gca gca aca cca gcc att ttt gta cca cta ccg cat gca gta gat gat	912
Ala Ala Thr Pro Ala Ile Phe Val Pro Leu Pro His Ala Val Asp Asp	
290 295 300	
cat caa aca aaa aat gcg ttg tac ctc gta aag cga gat gca gca aag	960
His Gln Thr Lys Asn Ala Leu Tyr Leu Val Lys Arg Asp Ala Ala Lys	
305 310 315 320	
tta ttg cca cag gca gaa cta aat aat gag agt atc acg tcg tta ata	1008
Leu Leu Pro Gln Ala Glu Leu Asn Asn Glu Ser Ile Thr Ser Leu Ile	
325 330 335	
atc gag ctg ttt gat cag cct caa act tta gct gac atg gct aaa gct	1056
Ile Glu Leu Phe Asp Gln Pro Gln Thr Leu Ala Asp Met Ala Lys Ala	
340 345 350	
tct ttg agt gct gca act agt gat gca agt cag aaa gta gca aaa ttg	1104
Ser Leu Ser Ala Ala Thr Ser Asp Ala Ser Gln Lys Val Ala Lys Leu	
355 360 365	
tgc caa cag ctt tca ata tcg aat ggc gca aaa ctt aga aat aat gaa	1152
Cys Gln Gln Leu Ser Ile Ser Asn Gly Ala Lys Leu Arg Asn Asn Glu	
370 375 380	
gag aac aaa taa	1164
Glu Asn Lys	
385	

<210> SEQ ID NO 16

<211> LENGTH: 387

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 16

Met Ser Leu Asn His Gly Gln Gly Asn Lys Asp Leu Ala Lys Thr Leu
1 5 10 15

Leu Val Met Ala Gly Gly Thr Gly Gly His Ile Phe Pro Gly Ile Ala
20 25 30

-continued

Val Ala Asp Glu Leu Lys Ala Gln Gly Trp Lys Ile His Trp Leu Gly
 35 40 45
 Thr Ala Asp Arg Met Glu Ala Gln Ile Val Pro Met His Gly Tyr Asp
 50 55 60
 Ile Ser Phe Ile Asn Ile Ser Gly Leu Arg Gly Lys Asn Leu Leu Thr
 65 70 75 80
 Thr Leu Val Met Pro Phe Lys Leu Leu Arg Ser Leu Phe Gln Ala Arg
 85 90 95
 Arg Val Ile Lys Thr Val Lys Pro Asp Val Val Ile Gly Met Gly Gly
 100 105 110
 Tyr Ala Ser Ala Pro Gly Gly Leu Ala Ala Trp Leu Ser Lys Ile Pro
 115 120 125
 Leu Ile Val His Glu Gln Asn Ala Ala Ala Gly Leu Ser Asn Arg Leu
 130 135 140
 Leu Ala Arg Ile Ala Asn Lys Val Cys Cys Ala Phe Pro Asn Ala Phe
 145 150 155 160
 Val Ser Gly Ile Asp Val Glu Val Val Gly Asn Pro Leu Arg Ala Ser
 165 170 175
 Ile Gly Gln Gln Ala Leu Val Ser Glu Asn Ile Asp Gln Ser His Glu
 180 185 190
 Gly Ser Lys Asn Ile Leu Val Val Gly Gly Ser Leu Gly Ala Gln Val
 195 200 205
 Leu Asn Lys Val Met Pro Asp Ser Phe Lys Asp Leu Ser Glu Ser Asp
 210 215 220
 Glu Lys Tyr Cys Ile Trp His Gln Thr Gly Asp Asn Asn Gln Ala Leu
 225 230 235 240
 Val Thr Ala Ser Tyr Lys Gln Glu Tyr Ile Asp Thr Gly Lys Val Arg
 245 250 255
 Val Thr Glu Phe Ile Thr Asp Ile Ala Ala Ala Tyr Gln Trp Ala Asp
 260 265 270
 Ile Val Ile Cys Arg Ala Gly Ala Leu Thr Val Ser Glu Leu Ala Met
 275 280 285
 Ala Ala Thr Pro Ala Ile Phe Val Pro Leu Pro His Ala Val Asp Asp
 290 295 300
 His Gln Thr Lys Asn Ala Leu Tyr Leu Val Lys Arg Asp Ala Ala Lys
 305 310 315 320
 Leu Leu Pro Gln Ala Glu Leu Asn Asn Glu Ser Ile Thr Ser Leu Ile
 325 330 335
 Ile Glu Leu Phe Asp Gln Pro Gln Thr Leu Ala Asp Met Ala Lys Ala
 340 345 350
 Ser Leu Ser Ala Ala Thr Ser Asp Ala Ser Gln Lys Val Ala Lys Leu
 355 360 365
 Cys Gln Gln Leu Ser Ile Ser Asn Gly Ala Lys Leu Arg Asn Asn Glu
 370 375 380
 Glu Asn Lys
 385

<210> SEQ ID NO 17

<211> LENGTH: 2067

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Codon optimized ligACp optimized for M. tuberculosis

<220> FEATURE:

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<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (2067)

<400> SEQUENCE: 17

gtg agc gag aag gag aag aaa ata tcc cag ctg caa cag caa ctg aac	48
Val Ser Glu Lys Glu Lys Lys Ile Ser Gln Leu Gln Gln Gln Leu Asn	
1 5 10 15	
caa tat aac cat gag tac tat gtc ctc gac cag cca tcg gtc ccc gat	96
Gln Tyr Asn His Glu Tyr Tyr Val Leu Asp Gln Pro Ser Val Pro Asp	
20 25 30	
gcg gag tac gat cgc ctg atg acc gcg tta atc gat ctg gaa aag acc	144
Ala Glu Tyr Asp Arg Leu Met Thr Ala Leu Ile Asp Leu Glu Lys Thr	
35 40 45	
aac ccg gag ttg aag acg atc gac agt ccg tcg cag aag gtg ggc ggt	192
Asn Pro Glu Leu Lys Thr Ile Asp Ser Pro Ser Gln Lys Val Gly Gly	
50 55 60	
cag gcc ctg aag agc ttc acc caa gtg acg cat cag ctg ccc atg ctc	240
Gln Ala Leu Lys Ser Phe Thr Gln Val Thr His Gln Leu Pro Met Leu	
65 70 75 80	
tcg ctt gac aac gtc ttt tcg ctg gat gac ttc cac gcc ttc gtc aag	288
Ser Leu Asp Asn Val Phe Ser Leu Asp Asp Phe His Ala Phe Val Lys	
85 90 95	
agg gtc aaa gac cgt ctc aat gac aac cag gcg atc gtg ttc tgt gcc	336
Arg Val Lys Asp Arg Leu Asn Asp Asn Gln Ala Ile Val Phe Cys Ala	
100 105 110	
gag ccg aag ctg gac ggc ctc gcg gta tcg ctc cgc tac gag cat ggc	384
Glu Pro Lys Leu Asp Gly Leu Ala Val Ser Leu Arg Tyr Glu His Gly	
115 120 125	
cag ctc atc cag gcg gcc acg cgg ggc gac ggc tca gtc ggg gag aat	432
Gln Leu Ile Gln Ala Ala Thr Arg Gly Asp Gly Ser Val Gly Glu Asn	
130 135 140	
atc acc acg aac atc cgg acg atc aag tcc atc ccc ctg aag ctc atg	480
Ile Thr Thr Asn Ile Arg Thr Ile Lys Ser Ile Pro Leu Lys Leu Met	
145 150 155 160	
ggc act ccc ggc aaa gac ttt cca gac att gtg gaa gtc cgg ggc gaa	528
Gly Thr Pro Gly Lys Asp Phe Pro Asp Ile Val Glu Val Arg Gly Glu	
165 170 175	
gtg ttc atg ccg aag gcc tcg ttc gac gcg ctg aac acc ctg gct aag	576
Val Phe Met Pro Lys Ala Ser Phe Asp Ala Leu Asn Thr Leu Ala Lys	
180 185 190	
aaa cgg ggg gag aag ggc ttc gct aac ccg cgg aac gcg gca gcc ggc	624
Lys Arg Gly Glu Lys Gly Phe Ala Asn Pro Arg Asn Ala Ala Gly	
195 200 205	
agt ctg cgt cag ctg gac agc aag atc acg gcc aag cgc aac ctg gcg	672
Ser Leu Arg Gln Leu Asp Ser Lys Ile Thr Ala Lys Arg Asn Leu Ala	
210 215 220	
ttc tat gcc tac agc cta ggt ttc gtg ggg aaa ctg agc gac ggg ggc	720
Phe Tyr Ala Tyr Ser Leu Gly Phe Val Gly Lys Leu Ser Asp Gly Gly	
225 230 235 240	
gcg gaa agc acc gac ttg acg aac gac ttt ttc gcg aac tcg cac cat	768
Ala Glu Ser Thr Asp Leu Thr Asn Asp Phe Phe Ala Asn Ser His His	
245 250 255	
gag cga ttg tgt caa ttg aag cga ctg ggt ttg ccg atg tgt ccg gag	816
Glu Arg Leu Cys Gln Leu Lys Arg Leu Gly Leu Pro Met Cys Pro Glu	
260 265 270	
gtg ccg ctg cta gaa tcg gag cag gct tgc gac gcg ttc tac cag gac	864
Val Arg Leu Leu Glu Ser Glu Gln Ala Cys Asp Ala Phe Tyr Gln Asp	
275 280 285	
atc ctc gcg aag cgc tcg gct ctt tca tac gaa atc gac ggt acc gtt	912
Ile Leu Ala Lys Arg Ser Ala Leu Ser Tyr Glu Ile Asp Gly Thr Val	

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290	295	300	
ttg aag gtt gac gag atc tcc ctc cag aag cgc ctg ggt ttc gtg gcg Leu Lys Val Asp Glu Ile Ser Leu Gln Lys Arg Leu Gly Phe Val Ala 305 310 315 320			960
cgg gca ccg cgc tgg gcc atc gcc tac aag ttc cca gca gag gaa gag Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Phe Pro Ala Glu Glu Glu 325 330 335			1008
ctg acc tgc gtg gag gac gta gaa ttt caa gtg ggc cgc acc ggt gcc Leu Thr Cys Val Glu Asp Val Glu Phe Gln Val Gly Arg Thr Gly Ala 340 345 350			1056
atc acc ccg gtt gcc cgc ctg aag cct gtc ttc gtg ggc ggt gtc acc Ile Thr Pro Val Ala Arg Leu Lys Pro Val Phe Val Gly Gly Val Thr 355 360 365			1104
gtg agc aac gct acc ctt cat aac cag gac gag atc aca cgt ctg ggg Val Ser Asn Ala Thr Leu His Asn Gln Asp Glu Ile Thr Arg Leu Gly 370 375 380			1152
ctg aag gtc aac gat ttc gtc gtg att cgc cgg gca ggc gac gtt att Leu Lys Val Asn Asp Phe Val Val Ile Arg Arg Ala Gly Asp Val Ile 385 390 395 400			1200
ccg cag atc gtg tgc gtg gtc ctg gac aaa agg ccg gat aac gcc gtc Pro Gln Ile Val Ser Val Val Leu Asp Lys Arg Pro Asp Asn Ala Val 405 410 415			1248
gat atc gtc ttc ccc acg tgc tgc ccg gtg tgc gac tgc gcc gtg gcc Asp Ile Val Phe Pro Thr Ser Cys Pro Val Cys Asp Ser Ala Val Ala 420 425 430			1296
aag ccc gaa ggc gag gca gtc ctg cgg tgc aca gcc ggg ctc ttc tgt Lys Pro Glu Gly Glu Ala Val Leu Arg Cys Thr Ala Gly Leu Phe Cys 435 440 445			1344
gcg gcc cag cgc aag gaa gcc atc aag cac ttc gcc tcc cgc aag gcc Ala Ala Gln Arg Lys Glu Ala Ile Lys His Phe Ala Ser Arg Lys Ala 450 455 460			1392
cac gac gtc gac gga ctg ggc gac aag ctc gtc gag cag ctt gta gac His Asp Val Asp Gly Leu Gly Asp Lys Leu Val Glu Gln Leu Val Asp 465 470 475 480			1440
gag aag ctg atc aac acc ccc gcg gat ctg ttc aag ctc acc gaa atc Glu Lys Leu Ile Asn Thr Pro Ala Asp Leu Phe Lys Leu Thr Glu Ile 485 490 495			1488
cag gtg agt acc att gac aga atg gga aag aag tct gcc acc aac ctg Gln Val Ser Thr Ile Asp Arg Met Gly Lys Lys Ser Ala Thr Asn Leu 500 505 510			1536
ata aat ggt ctg gag cag gcg aag agc act acg ctg gcg aag ttc att Ile Asn Gly Leu Glu Gln Ala Lys Ser Thr Thr Leu Ala Lys Phe Ile 515 520 525			1584
tac gcc ctg ggg atc cgg gaa gtg gga gag gcc acg gcc gcg aac ctg Tyr Gly Leu Gly Ile Arg Glu Val Gly Glu Ala Thr Ala Ala Asn Leu 530 535 540			1632
gcc aac cac ttc tac acc ctc gcc gcg atc gag agc gcc agc ttg gag Ala Asn His Phe Tyr Thr Leu Ala Ala Ile Glu Ser Ala Ser Leu Glu 545 550 555 560			1680
gat ctg cag aac gta tcc gac gtg ggt gag gtc gtg gca aag aac atc Asp Leu Gln Asn Val Ser Asp Val Gly Glu Val Val Ala Lys Asn Ile 565 570 575			1728
att aat ttc ttc aag gaa gag cac aac ctg gcg atc gtc agc ggt ttg Ile Asn Phe Phe Lys Glu Glu His Asn Leu Ala Ile Val Ser Gly Leu 580 585 590			1776
agc gaa gtg atg cac tgg ccc acc atc gag atc aag tgc gcc gag gag Ser Glu Val Met His Trp Pro Thr Ile Glu Ile Lys Ser Ala Glu Glu 595 600 605			1824
ctt cct ctg gcg gag cag atc ttc gtc ctc acc gga act ctc acc cag			1872

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Leu	Pro	Leu	Ala	Glu	Gln	Ile	Phe	Val	Leu	Thr	Gly	Thr	Leu	Thr	Gln		
610						615					620						
atg	ggc	cgc	acg	gag	gcg	aag	acc	gcc	ttg	caa	tcc	ctg	ggc	gct	aag	1920	
Met	Gly	Arg	Thr	Glu	Ala	Lys	Thr	Ala	Leu	Gln	Ser	Leu	Gly	Ala	Lys		
625					630					635				640			
gtc	tcg	ggc	tcc	gtc	tcc	aag	aac	acc	cac	ttc	gtg	ggt	gcg	ggc	gac	1968	
Val	Ser	Gly	Ser	Val	Ser	Lys	Asn	Thr	His	Phe	Val	Val	Ala	Gly	Asp		
				645					650					655			
aag	gct	ggc	agc	aag	ctg	acg	aag	gcg	cag	gac	ctc	ggc	atc	tca	gtc	2016	
Lys	Ala	Gly	Ser	Lys	Leu	Thr	Lys	Ala	Gln	Asp	Leu	Gly	Ile	Ser	Val		
				660				665					670				
ctg	aca	gag	gat	ggc	ctg	gtc	gcc	ctg	ctg	gca	gag	cac	ggc	atc	acc	2064	
Leu	Thr	Glu	Asp	Gly	Leu	Val	Ala	Leu	Leu	Ala	Glu	His	Gly	Ile	Thr		
		675					680					685					
att																2067	
Ile																	

<210> SEQ ID NO 18
 <211> LENGTH: 689
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 18

Val	Ser	Glu	Lys	Glu	Lys	Lys	Ile	Ser	Gln	Leu	Gln	Gln	Gln	Leu	Asn		
1				5				10						15			
Gln	Tyr	Asn	His	Glu	Tyr	Tyr	Val	Leu	Asp	Gln	Pro	Ser	Val	Pro	Asp		
		20					25						30				
Ala	Glu	Tyr	Asp	Arg	Leu	Met	Thr	Ala	Leu	Ile	Asp	Leu	Glu	Lys	Thr		
		35				40						45					
Asn	Pro	Glu	Leu	Lys	Thr	Ile	Asp	Ser	Pro	Ser	Gln	Lys	Val	Gly	Gly		
		50			55						60						
Gln	Ala	Leu	Lys	Ser	Phe	Thr	Gln	Val	Thr	His	Gln	Leu	Pro	Met	Leu		
65					70					75					80		
Ser	Leu	Asp	Asn	Val	Phe	Ser	Leu	Asp	Asp	Phe	His	Ala	Phe	Val	Lys		
			85					90						95			
Arg	Val	Lys	Asp	Arg	Leu	Asn	Asp	Asn	Gln	Ala	Ile	Val	Phe	Cys	Ala		
		100				105							110				
Glu	Pro	Lys	Leu	Asp	Gly	Leu	Ala	Val	Ser	Leu	Arg	Tyr	Glu	His	Gly		
		115				120						125					
Gln	Leu	Ile	Gln	Ala	Ala	Thr	Arg	Gly	Asp	Gly	Ser	Val	Gly	Glu	Asn		
		130				135					140						
Ile	Thr	Thr	Asn	Ile	Arg	Thr	Ile	Lys	Ser	Ile	Pro	Leu	Lys	Leu	Met		
145				150						155					160		
Gly	Thr	Pro	Gly	Lys	Asp	Phe	Pro	Asp	Ile	Val	Glu	Val	Arg	Gly	Glu		
			165					170						175			
Val	Phe	Met	Pro	Lys	Ala	Ser	Phe	Asp	Ala	Leu	Asn	Thr	Leu	Ala	Lys		
		180						185					190				
Lys	Arg	Gly	Glu	Lys	Gly	Phe	Ala	Asn	Pro	Arg	Asn	Ala	Ala	Ala	Gly		
		195					200					205					
Ser	Leu	Arg	Gln	Leu	Asp	Ser	Lys	Ile	Thr	Ala	Lys	Arg	Asn	Leu	Ala		
		210				215					220						
Phe	Tyr	Ala	Tyr	Ser	Leu	Gly	Phe	Val	Gly	Lys	Leu	Ser	Asp	Gly	Gly		
225					230					235					240		
Ala	Glu	Ser	Thr	Asp	Leu	Thr	Asn	Asp	Phe	Phe	Ala	Asn	Ser	His	His		
				245					250					255			

Glu 260	Arg	Leu	Cys	Gln	Leu	Lys	Arg	Leu	Gly	Leu	Pro	Met	Cys	Pro	Glu
Val 275	Arg	Leu	Leu	Glu	Ser	Glu	Gln	Ala	Cys	Asp	Ala	Phe	Tyr	Gln	Asp
Ile 290	Leu	Ala	Lys	Arg	Ser	Ala	Leu	Ser	Tyr	Glu	Ile	Asp	Gly	Thr	Val
Leu 305	Lys	Val	Asp	Glu	Ile	Ser	Leu	Gln	Lys	Arg	Leu	Gly	Phe	Val	Ala
Arg	Ala	Pro	Arg	Trp	Ala	Ile	Ala	Tyr	Lys	Phe	Pro	Ala	Glu	Glu	Glu
Leu	Thr	Cys	Val	Glu	Asp	Val	Glu	Phe	Gln	Val	Gly	Arg	Thr	Gly	Ala
Ile	Thr	Pro	Val	Ala	Arg	Leu	Lys	Pro	Val	Phe	Val	Gly	Gly	Val	Thr
Val	Ser	Asn	Ala	Thr	Leu	His	Asn	Gln	Asp	Glu	Ile	Thr	Arg	Leu	Gly
Leu 385	Lys	Val	Asn	Asp	Phe	Val	Val	Ile	Arg	Arg	Ala	Gly	Asp	Val	Ile
Pro	Gln	Ile	Val	Ser	Val	Val	Leu	Asp	Lys	Arg	Pro	Asp	Asn	Ala	Val
Asp	Ile	Val	Phe	Pro	Thr	Ser	Cys	Pro	Val	Cys	Asp	Ser	Ala	Val	Ala
Lys	Pro	Glu	Gly	Glu	Ala	Val	Leu	Arg	Cys	Thr	Ala	Gly	Leu	Phe	Cys
Ala	Ala	Gln	Arg	Lys	Glu	Ala	Ile	Lys	His	Phe	Ala	Ser	Arg	Lys	Ala
His 465	Asp	Val	Asp	Gly	Leu	Gly	Asp	Lys	Leu	Val	Glu	Gln	Leu	Val	Asp
Glu	Lys	Leu	Ile	Asn	Thr	Pro	Ala	Asp	Leu	Phe	Lys	Leu	Thr	Glu	Ile
Gln	Val	Ser	Thr	Ile	Asp	Arg	Met	Gly	Lys	Lys	Ser	Ala	Thr	Asn	Leu
Ile	Asn	Gly	Leu	Glu	Gln	Ala	Lys	Ser	Thr	Thr	Leu	Ala	Lys	Phe	Ile
Tyr	Gly	Leu	Gly	Ile	Arg	Glu	Val	Gly	Glu	Ala	Thr	Ala	Ala	Asn	Leu
Ala 545	Asn	His	Phe	Tyr	Thr	Leu	Ala	Ala	Ile	Glu	Ser	Ala	Ser	Leu	Glu
Asp	Leu	Gln	Asn	Val	Ser	Asp	Val	Gly	Glu	Val	Val	Ala	Lys	Asn	Ile
Ile	Asn	Phe	Phe	Lys	Glu	Glu	His	Asn	Leu	Ala	Ile	Val	Ser	Gly	Leu
Ser	Glu	Val	Met	His	Trp	Pro	Thr	Ile	Glu	Ile	Lys	Ser	Ala	Glu	Glu
Leu	Pro	Leu	Ala	Glu	Gln	Ile	Phe	Val	Leu	Thr	Gly	Thr	Leu	Thr	Gln
Met 625	Gly	Arg	Thr	Glu	Ala	Lys	Thr	Ala	Leu	Gln	Ser	Leu	Gly	Ala	Lys
Val	Ser	Gly	Ser	Val	Ser	Lys	Asn	Thr	His	Phe	Val	Val	Ala	Gly	Asp
Lys	Ala	Gly	Ser	Lys	Leu	Thr	Lys	Ala	Gln	Asp	Leu	Gly	Ile	Ser	Val

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Leu Thr Glu Asp Gly Leu Val Ala Leu Leu Ala Glu His Gly Ile Thr
675 680 685

Ile

<210> SEQ ID NO 19
 <211> LENGTH: 1917
 <212> TYPE: DNA
 <213> ORGANISM: Colwellia psychroerythrus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1917)
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (556)..(556)
 <223> OTHER INFORMATION: s at location 556 is g or c

<400> SEQUENCE: 19

atg gga aaa att att ggt att gac cta gga aca act aac tca tgt gtt	48
Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val	
1 5 10 15	
gct gtt tta gat ggc gac agt gta cgt gtt att gaa aat gca gaa ggc	96
Ala Val Leu Asp Gly Asp Ser Val Arg Val Ile Glu Asn Ala Glu Gly	
20 25 30	
gat cgt aca act cct tct att att ggt tat aca gcc gaa ggc gaa aca	144
Asp Arg Thr Thr Pro Ser Ile Ile Gly Tyr Thr Ala Glu Gly Glu Thr	
35 40 45	
tta gta ggt caa cct gct aag cgt caa tct gta act aac cca gaa aac	192
Leu Val Gly Gln Pro Ala Lys Arg Gln Ser Val Thr Asn Pro Glu Asn	
50 55 60	
act tta tat gca att aaa cgc tta atc ggt cgt cgt ttc gaa gat aaa	240
Thr Leu Tyr Ala Ile Lys Arg Leu Ile Gly Arg Arg Phe Glu Asp Lys	
65 70 75 80	
gaa aca caa cgt gac atc gat att atg cca ttt ggt att gtt aaa gcg	288
Glu Thr Gln Arg Asp Ile Asp Ile Met Pro Phe Gly Ile Val Lys Ala	
85 90 95	
gat aac ggt gat gct tgg gtt caa gta aaa ggc gag aaa att gct ccg	336
Asp Asn Gly Asp Ala Trp Val Gln Val Lys Gly Glu Lys Ile Ala Pro	
100 105 110	
cca caa gtt tca gct gaa gtt ctt aag aaa atg aaa aag act gct gaa	384
Pro Gln Val Ser Ala Glu Val Leu Lys Lys Met Lys Lys Thr Ala Glu	
115 120 125	
gac ttc tta ggt gaa acc gta act gaa gct gtt att act gta cct gct	432
Asp Phe Leu Gly Glu Thr Val Thr Glu Ala Val Ile Thr Val Pro Ala	
130 135 140	
tac ttt aac gat tca caa cgc caa gca acg aaa gat gct ggt cgt att	480
Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Arg Ile	
145 150 155 160	
gct ggt ctt gaa gtc aaa cgt att atc aac gaa cct act gct gct gcc	528
Ala Gly Leu Glu Val Lys Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala	
165 170 175	
ctt gct tac ggc atg gac aaa caa gaa sgt gac aaa gtt gtt gca gtt	576
Leu Ala Tyr Gly Met Asp Lys Gln Glu Xaa Asp Lys Val Val Ala Val	
180 185 190	
tac gat tta ggt ggt ggt aca ttc gat att tca atc att gaa att gat	624
Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Ile Glu Ile Asp	
195 200 205	
gaa atg gat ggc gaa cac act ttt gaa gta tta gcg act aac ggt gat	672
Glu Met Asp Gly Glu His Thr Phe Glu Val Leu Ala Thr Asn Gly Asp	
210 215 220	
act cac tta ggt ggt gaa gat ttt gat aac cgt tta atc aac tac ctt	720
Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu Ile Asn Tyr Leu	
225 230 235 240	

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gta gct gaa ttc aaa aaa gac caa ggc atg gac tta acg tct gat cct Val Ala Glu Phe Lys Lys Asp Gln Gly Met Asp Leu Thr Ser Asp Pro 245 250 255	768
tta gca atg cag cgt tta aaa gaa gca gca gaa aaa gct aaa tgt gaa Leu Ala Met Gln Arg Leu Lys Glu Ala Ala Glu Lys Ala Lys Cys Glu 260 265 270	816
ctt tct tca gca caa caa aca gat gta aac tta cct tac atc act gct Leu Ser Ser Ala Gln Gln Thr Asp Val Asn Leu Pro Tyr Ile Thr Ala 275 280 285	864
gat ggt tca ggt cct aag cac atg aac atc aaa gtg act cgt gct aag Asp Gly Ser Gly Pro Lys His Met Asn Ile Lys Val Thr Arg Ala Lys 290 295 300	912
tta gaa tca cta gtt gaa gat atg gtt aaa gca aca tta gag ccg ctt Leu Glu Ser Leu Val Glu Asp Met Val Lys Ala Thr Leu Glu Pro Leu 305 310 315 320	960
aaa caa gcg ctt aaa gat gca gac tta tca gta agc aag att gat gat Lys Gln Ala Leu Lys Asp Ala Asp Leu Ser Val Ser Lys Ile Asp Asp 325 330 335	1008
gtt att tta gtt ggt ggt caa tct cgt atg cca cta gtt caa aaa act Val Ile Leu Val Gly Gly Gln Ser Arg Met Pro Leu Val Gln Lys Thr 340 345 350	1056
gtt act gat ttc ttc ggt aaa gag cca cgt aaa gat gtt aac cct gat Val Thr Asp Phe Phe Gly Lys Glu Pro Arg Lys Asp Val Asn Pro Asp 355 360 365	1104
gaa gca gta gct tct ggt gcg gcg att caa gcg ggt gtt ctt tct ggt Glu Ala Val Ala Ser Gly Ala Ala Ile Gln Ala Gly Val Leu Ser Gly 370 375 380	1152
gat gtg act gac gtt ctt tta tta gac gtt aca cca cta tca tta ggt Asp Val Thr Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu Gly 385 390 395 400	1200
atc gaa act atg ggc ggt gtg atg act aag gtt atc gac aaa aac act Ile Glu Thr Met Gly Gly Val Met Thr Lys Val Ile Asp Lys Asn Thr 405 410 415	1248
act atc cca act aag caa tca caa act ttc tct aca gct gat gat aac Thr Ile Pro Thr Lys Gln Ser Gln Thr Phe Ser Thr Ala Asp Asp Asn 420 425 430	1296
caa gct gca gta act gtt cat gtt tgt cag ggt gag cgt aag caa gct Gln Ala Ala Val Thr Val His Val Cys Gln Gly Glu Arg Lys Gln Ala 435 440 445	1344
tca gca aac aaa tct tta ggt caa ttt aac ctt gaa ggt att gaa cca Ser Ala Asn Lys Ser Leu Gly Gln Phe Asn Leu Glu Gly Ile Glu Pro 450 455 460	1392
gca caa cgt ggt aca cca caa atc gaa gta act ttt gat att gat gct Ala Gln Arg Gly Thr Pro Gln Ile Glu Val Thr Phe Asp Ile Asp Ala 465 470 475 480	1440
gat ggt atc ttg cac gtt acg gct aaa gat aag aat act ggt aaa gag Asp Gly Ile Leu His Val Thr Ala Lys Asp Lys Asn Thr Gly Lys Glu 485 490 495	1488
caa aaa atc act atc aaa gcc tct tct ggt tta tct gat gaa gaa gta Gln Lys Ile Thr Ile Lys Ala Ser Ser Gly Leu Ser Asp Glu Glu Val 500 505 510	1536
gag cag atg gta cgt gat gca gaa gct aac gct gat gct gat gct aaa Glu Gln Met Val Arg Asp Ala Glu Ala Asn Ala Asp Ala Asp Ala Lys 515 520 525	1584
ttt gaa gag cta gta act gca cgt aat caa gct gat ggc atg att cac Phe Glu Glu Leu Val Thr Ala Arg Asn Gln Ala Asp Gly Met Ile His 530 535 540	1632
gcg act cgc aag caa gtt gaa gaa gca ggc gaa gag tta cca agc gaa Ala Thr Arg Lys Gln Val Glu Glu Ala Gly Glu Glu Leu Pro Ser Glu 545 550 555	1680

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545	550	555	560	
gat aaa gaa aaa att gaa gca gca tta act gag ctt gaa gaa gca gtt				1728
Asp Lys Glu Lys Ile Glu Ala Ala Leu Thr Glu Leu Glu Glu Ala Val	565	570	575	
aaa ggt gat gat aaa gaa gta att gaa gct aaa act caa gca ctt atg				1776
Lys Gly Asp Asp Lys Glu Val Ile Glu Ala Lys Thr Gln Ala Leu Met	580	585	590	
gaa gca tca gct aag tta atg gaa att gct caa gct aaa gaa caa gct				1824
Glu Ala Ser Ala Lys Leu Met Glu Ile Ala Gln Ala Lys Glu Gln Ala	595	600	605	
caa agc gct cct gaa ggt gct caa gaa gct gac gca gct cct gca gac				1872
Gln Ser Ala Pro Glu Gly Ala Gln Glu Ala Asp Ala Ala Pro Ala Asp	610	615	620	
gat gtt gtt gat gct gag ttt gaa gaa gtt aaa gac aaa aaa taa				1917
Asp Val Val Asp Ala Glu Phe Glu Glu Val Lys Asp Lys Lys	625	630	635	

<210> SEQ ID NO 20

<211> LENGTH: 638

<212> TYPE: PRT

<213> ORGANISM: Colwellia psychroerythrus

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (186)..(186)

<223> OTHER INFORMATION: The 'Xaa' at location 186 stands for Gly, or Arg.

<400> SEQUENCE: 20

Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val			
1 5 10 15			
Ala Val Leu Asp Gly Asp Ser Val Arg Val Ile Glu Asn Ala Glu Gly			
20 25 30			
Asp Arg Thr Thr Pro Ser Ile Ile Gly Tyr Thr Ala Glu Gly Glu Thr			
35 40 45			
Leu Val Gly Gln Pro Ala Lys Arg Gln Ser Val Thr Asn Pro Glu Asn			
50 55 60			
Thr Leu Tyr Ala Ile Lys Arg Leu Ile Gly Arg Arg Phe Glu Asp Lys			
65 70 75 80			
Glu Thr Gln Arg Asp Ile Asp Ile Met Pro Phe Gly Ile Val Lys Ala			
85 90 95			
Asp Asn Gly Asp Ala Trp Val Gln Val Lys Gly Glu Lys Ile Ala Pro			
100 105 110			
Pro Gln Val Ser Ala Glu Val Leu Lys Lys Met Lys Lys Thr Ala Glu			
115 120 125			
Asp Phe Leu Gly Glu Thr Val Thr Glu Ala Val Ile Thr Val Pro Ala			
130 135 140			
Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Arg Ile			
145 150 155 160			
Ala Gly Leu Glu Val Lys Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala			
165 170 175			
Leu Ala Tyr Gly Met Asp Lys Gln Glu Xaa Asp Lys Val Val Ala Val			
180 185 190			
Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Ile Glu Ile Asp			
195 200 205			
Glu Met Asp Gly Glu His Thr Phe Glu Val Leu Ala Thr Asn Gly Asp			
210 215 220			
Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu Ile Asn Tyr Leu			
225 230 235 240			

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<210> SEQ ID NO 21
<211> LENGTH: 1220
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: tyrS hybrid
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (11)..(1207)

<400> SEQUENCE: 21

tataaatata atg tcg agc ttt aac caa gca ttc gcc gaa cta aaa cgc      49
      Met Ser Ser Phe Asn Gln Ala Phe Ala Glu Leu Lys Arg
        1             5             10

gga gca gaa gaa ata tta gta gaa gaa gaa tta tta aca aag ctt aag      97
Gly Ala Glu Glu Ile Leu Val Glu Glu Glu Leu Thr Lys Leu Lys
  15             20             25

aca ggt aag ccg cta aaa atc aaa gcg ggt ttt gat cct act gcg cct     145
Thr Gly Lys Pro Leu Lys Ile Lys Ala Gly Phe Asp Pro Thr Ala Pro
  30             35             40             45

gac tta cat tta ggc cac acg gta tta att aac aag ctt cgt caa ttc     193
Asp Leu His Leu Gly His Thr Val Leu Ile Asn Lys Leu Arg Gln Phe
      50             55             60

caa caa tta ggt cat gaa gtt att ttc ttg att ggt gac ttc acc gga     241
Gln Gln Leu Gly His Glu Val Ile Phe Leu Ile Gly Asp Phe Thr Gly
      65             70             75

atg att ggt gat cca acg ggt aaa aat gtg acg cgt aag gca ctc act     289
Met Ile Gly Asp Pro Thr Gly Lys Asn Val Thr Arg Lys Ala Leu Thr
      80             85             90

aaa gaa gac gta tta gcc aat gct gaa acg tat aaa gag caa gtc ttt     337
Lys Glu Asp Val Leu Ala Asn Ala Glu Thr Tyr Lys Glu Gln Val Phe
      95             100            105

aaa ata tta gat ccc gct aaa aca acc gtt gcc ttt aac tct act tgg     385
Lys Ile Leu Asp Pro Ala Lys Thr Thr Val Ala Phe Asn Ser Thr Trp
  110             115            120            125

atg gat aaa tta ggc gcg gca ggt atg tta caa ctt gcc tct cgt caa     433
Met Asp Lys Leu Gly Ala Ala Gly Met Leu Gln Leu Ala Ser Arg Gln
      130            135            140

acg gtt gcc cgt atg atg gag cgt gac gac ttt aaa aaa cgt tat gct     481
Thr Val Ala Arg Met Met Glu Arg Asp Asp Phe Lys Lys Arg Tyr Ala
      145            150            155

aac ggc cag gcc att gct att cat gag ttt atg tac cct tta gta caa     529
Asn Gly Gln Ala Ile Ala Ile His Glu Phe Met Tyr Pro Leu Val Gln
      160            165            170

ggt tgg gat tca gtt gcg ctt gag gct gat gtt gag ctg ggt ggt acc     577
Gly Trp Asp Ser Val Ala Leu Glu Ala Asp Val Glu Leu Gly Gly Thr
      175            180            185

gac caa aag ttt aat tta tta atg ggt cgt gag tta caa aaa tct gaa     625
Asp Gln Lys Phe Asn Leu Leu Met Gly Arg Glu Leu Gln Lys Ser Glu
      190            195            200            205

ggc cag cgt cca caa aca gta tta atg atg cca tta ctt gaa ggc cta     673
Gly Gln Arg Pro Gln Thr Val Leu Met Met Pro Leu Leu Glu Gly Leu
      210            215            220

gat ggc gtt cag aaa atg tct aag tca tta ggc aac tac att ggc att     721
Asp Gly Val Gln Lys Met Ser Lys Ser Leu Gly Asn Tyr Ile Gly Ile
      225            230            235

act gat acg cct acc gac atg ttt ggc aaa ata atg tca att tca gat     769
Thr Asp Thr Pro Thr Asp Met Phe Gly Lys Ile Met Ser Ile Ser Asp
      240            245            250

gta tta atg tgg cgt tac tac gag tta ctt agc ttt aaa ccg ctt gaa     817
Val Leu Met Trp Arg Tyr Tyr Glu Leu Leu Ser Phe Lys Pro Leu Glu
      255            260            265

gaa att gaa ggt tat aaa acc gag ata gaa aat ggc aaa aat cct cgt     865

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Glu Ile Glu Gly Tyr Lys Thr Glu Ile Glu Asn Gly Lys Asn Pro Arg	
270 275 280 285	
gat gtt aaa att gat tta gcc aaa gaa ttg att gct cgt ttt cat gat	913
Asp Val Lys Ile Asp Leu Ala Lys Glu Leu Ile Ala Arg Phe His Asp	
290 295 300	
gaa gct gct gca caa gct gcc cat gat gaa ttc atc aat cgt ttc caa	961
Glu Ala Ala Ala Gln Ala Ala His Asp Glu Phe Ile Asn Arg Phe Gln	
305 310 315	
aaa ggt gcg tta cct gat gat atg ccg gaa tta acg att acc act gaa	1009
Lys Gly Ala Leu Pro Asp Asp Met Pro Glu Leu Thr Ile Thr Thr Glu	
320 325 330	
aat ggt gaa ata gcc att gct aac ttg ctt aaa gat gca gga tta gtc	1057
Asn Gly Glu Ile Ala Ile Ala Asn Leu Leu Lys Asp Ala Gly Leu Val	
335 340 345	
ggg agt act tct gat gcc ttt aga atg atc aaa caa ggg gcg gct aaa	1105
Gly Ser Thr Ser Asp Ala Phe Arg Met Ile Lys Gln Gly Ala Ala Lys	
350 355 360 365	
att gat agc gaa aaa gta act gac cgt agc tta gtt att agc gct ggc	1153
Ile Asp Ser Glu Lys Val Thr Asp Arg Ser Leu Val Ile Ser Ala Gly	
370 375 380	
acg acg gca gtt tat caa gtc ggc aaa cgt aaa ttt gct cgt att acc	1201
Thr Thr Ala Val Tyr Gln Val Gly Lys Arg Lys Phe Ala Arg Ile Thr	
385 390 395	
ata aaa taaggggttg taa	1220
Ile Lys	

<210> SEQ ID NO 22

<211> LENGTH: 399

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 22

Met Ser Ser Phe Asn Gln Ala Phe Ala Glu Leu Lys Arg Gly Ala Glu	
1 5 10 15	
Glu Ile Leu Val Glu Glu Glu Leu Thr Lys Leu Lys Thr Gly Lys	
20 25 30	
Pro Leu Lys Ile Lys Ala Gly Phe Asp Pro Thr Ala Pro Asp Leu His	
35 40 45	
Leu Gly His Thr Val Leu Ile Asn Lys Leu Arg Gln Phe Gln Gln Leu	
50 55 60	
Gly His Glu Val Ile Phe Leu Ile Gly Asp Phe Thr Gly Met Ile Gly	
65 70 75 80	
Asp Pro Thr Gly Lys Asn Val Thr Arg Lys Ala Leu Thr Lys Glu Asp	
85 90 95	
Val Leu Ala Asn Ala Glu Thr Tyr Lys Glu Gln Val Phe Lys Ile Leu	
100 105 110	
Asp Pro Ala Lys Thr Thr Val Ala Phe Asn Ser Thr Trp Met Asp Lys	
115 120 125	
Leu Gly Ala Ala Gly Met Leu Gln Leu Ala Ser Arg Gln Thr Val Ala	
130 135 140	
Arg Met Met Glu Arg Asp Asp Phe Lys Lys Arg Tyr Ala Asn Gly Gln	
145 150 155 160	
Ala Ile Ala Ile His Glu Phe Met Tyr Pro Leu Val Gln Gly Trp Asp	
165 170 175	
Ser Val Ala Leu Glu Ala Asp Val Glu Leu Gly Gly Thr Asp Gln Lys	
180 185 190	

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Phe Asn Leu Leu Met Gly Arg Glu Leu Gln Lys Ser Glu Gly Gln Arg
 195 200 205
 Pro Gln Thr Val Leu Met Met Pro Leu Leu Glu Gly Leu Asp Gly Val
 210 215 220
 Gln Lys Met Ser Lys Ser Leu Gly Asn Tyr Ile Gly Ile Thr Asp Thr
 225 230 235 240
 Pro Thr Asp Met Phe Gly Lys Ile Met Ser Ile Ser Asp Val Leu Met
 245 250 255
 Trp Arg Tyr Tyr Glu Leu Leu Ser Phe Lys Pro Leu Glu Glu Ile Glu
 260 265 270
 Gly Tyr Lys Thr Glu Ile Glu Asn Gly Lys Asn Pro Arg Asp Val Lys
 275 280 285
 Ile Asp Leu Ala Lys Glu Leu Ile Ala Arg Phe His Asp Glu Ala Ala
 290 295 300
 Ala Gln Ala Ala His Asp Glu Phe Ile Asn Arg Phe Gln Lys Gly Ala
 305 310 315 320
 Leu Pro Asp Asp Met Pro Glu Leu Thr Ile Thr Thr Glu Asn Gly Glu
 325 330 335
 Ile Ala Ile Ala Asn Leu Leu Lys Asp Ala Gly Leu Val Gly Ser Thr
 340 345 350
 Ser Asp Ala Phe Arg Met Ile Lys Gln Gly Ala Ala Lys Ile Asp Ser
 355 360 365
 Glu Lys Val Thr Asp Arg Ser Leu Val Ile Ser Ala Gly Thr Thr Ala
 370 375 380
 Val Tyr Gln Val Gly Lys Arg Lys Phe Ala Arg Ile Thr Ile Lys
 385 390 395

<210> SEQ ID NO 23
 <211> LENGTH: 741
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: cmk hybrid
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (51)..(731)

<400> SEQUENCE: 23

aagtctagaa gatgtcgaaa aacttgtaga gtttatgcag gaatttgaga atg aac 56
 Met Asn
 1
 aat agc aca cca gtt ata acc att gat ggc cca agt ggg gct ggt aaa 104
 Asn Ser Thr Pro Val Ile Thr Ile Asp Gly Pro Ser Gly Ala Gly Lys
 5 10 15
 gga acc gtt gca agg ata gtt gcg gac caa tta ggt tgg cac ctt ctt 152
 Gly Thr Val Ala Arg Ile Val Ala Asp Gln Leu Gly Trp His Leu Leu
 20 25 30
 gac agt ggg gct att tac cgc gtc tta gct gtt gcc att caa cat cac 200
 Asp Ser Gly Ala Ile Tyr Arg Val Leu Ala Val Ala Ile Gln His His
 35 40 45 50
 caa ctt tca tta gat gat gaa gag cct ctt atc cct atg gct gca cat 248
 Gln Leu Ser Leu Asp Asp Glu Glu Pro Leu Ile Pro Met Ala Ala His
 55 60 65
 tta gat gtt caa ttt gaa att aat agt caa ggt gaa gct aaa gtt att 296
 Leu Asp Val Gln Phe Glu Ile Asn Ser Gln Gly Glu Ala Lys Val Ile
 70 75 80
 tta gaa ggt gaa aat gtt act gaa att att cgt act gaa gaa gtt ggc 344
 Leu Glu Gly Glu Asn Val Thr Glu Ile Ile Arg Thr Glu Glu Val Gly

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85	90	95	
gga tta gca tcg aaa gta gca gca ttt cca cgt gtt aga gaa gcg cta			392
Gly Leu Ala Ser Lys Val Ala Ala Phe Pro Arg Val Arg Glu Ala Leu			
100	105	110	
tta cga aga caa cgt gca ttt agc gtt agc cct ggc tta att gca gat			440
Leu Arg Arg Gln Arg Ala Phe Ser Val Ser Pro Gly Leu Ile Ala Asp			
115	120	125	130
ggt cgc gac atg gga acc gtt gtt ttt ccg aaa gct cca gta aaa ata			488
Gly Arg Asp Met Gly Thr Val Val Phe Pro Lys Ala Pro Val Lys Ile			
135	140	145	
ttt tta act gct agt gct gaa gaa cga gct gac cga aga ttt aat cag			536
Phe Leu Thr Ala Ser Ala Glu Glu Arg Ala Asp Arg Arg Phe Asn Gln			
150	155	160	
ttg aaa gaa aaa gga att gat gtt aac atc ggg cgc ctt ttg gat gac			584
Leu Lys Glu Lys Gly Ile Asp Val Asn Ile Gly Arg Leu Leu Asp Asp			
165	170	175	
ata cgt caa cga gat gag cga gat caa aac cgc aag gta gct cct ctt			632
Ile Arg Gln Arg Asp Glu Arg Asp Gln Asn Arg Lys Val Ala Pro Leu			
180	185	190	
atc ccg gca gaa gga gcg tta act att gat tct act gat att tct att			680
Ile Pro Ala Glu Gly Ala Leu Thr Ile Asp Ser Thr Asp Ile Ser Ile			
195	200	205	210
aca gaa gtc gtc aat aaa atc ctt atg ttt gcc aat ggc aaa tta acg			728
Thr Glu Val Val Asn Lys Ile Leu Met Phe Ala Asn Gly Lys Leu Thr			
215	220	225	
tag atatttttagc			741

<210> SEQ ID NO 24

<211> LENGTH: 226

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 24

Met Asn Asn Ser Thr Pro Val Ile Thr Ile Asp Gly Pro Ser Gly Ala			
1	5	10	15
Gly Lys Gly Thr Val Ala Arg Ile Val Ala Asp Gln Leu Gly Trp His			
20	25	30	
Leu Leu Asp Ser Gly Ala Ile Tyr Arg Val Leu Ala Val Ala Ile Gln			
35	40	45	
His His Gln Leu Ser Leu Asp Asp Glu Glu Pro Leu Ile Pro Met Ala			
50	55	60	
Ala His Leu Asp Val Gln Phe Glu Ile Asn Ser Gln Gly Glu Ala Lys			
65	70	75	80
Val Ile Leu Glu Gly Glu Asn Val Thr Glu Ile Ile Arg Thr Glu Glu			
85	90	95	
Val Gly Gly Leu Ala Ser Lys Val Ala Ala Phe Pro Arg Val Arg Glu			
100	105	110	
Ala Leu Leu Arg Arg Gln Arg Ala Phe Ser Val Ser Pro Gly Leu Ile			
115	120	125	
Ala Asp Gly Arg Asp Met Gly Thr Val Val Phe Pro Lys Ala Pro Val			
130	135	140	
Lys Ile Phe Leu Thr Ala Ser Ala Glu Glu Arg Ala Asp Arg Arg Phe			
145	150	155	160
Asn Gln Leu Lys Glu Lys Gly Ile Asp Val Asn Ile Gly Arg Leu Leu			
165	170	175	

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Asp Asp Ile Arg Gln Arg Asp Glu Arg Asp Gln Asn Arg Lys Val Ala
 180 185 190
 Pro Leu Ile Pro Ala Glu Gly Ala Leu Thr Ile Asp Ser Thr Asp Ile
 195 200 205
 Ser Ile Thr Glu Val Val Asn Lys Ile Leu Met Phe Ala Asn Gly Lys
 210 215 220
 Leu Thr
 225

<210> SEQ ID NO 25
 <211> LENGTH: 1937
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: dnaKsf hybrid
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (11)..(1927)

<400> SEQUENCE: 25

ggagaatcaa atg gga aaa att att ggt atc gat tta ggc aca aca aac	49
Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn	
1 5 10	
tcg tgt gta gca gtc ctt gat ggc ggc aaa gca cgc gta att gaa aac	97
Ser Cys Val Ala Val Leu Asp Gly Gly Lys Ala Arg Val Ile Glu Asn	
15 20 25	
gca gag ggt gat cgc aca acc cca tca att atc gct tat acc gat gat	145
Ala Glu Gly Asp Arg Thr Thr Pro Ser Ile Ile Ala Tyr Thr Asp Asp	
30 35 40 45	
gaa att att gta ggc cag cca gca aag cgt cag gct gta acc aac cca	193
Glu Ile Ile Val Gly Gln Pro Ala Lys Arg Gln Ala Val Thr Asn Pro	
50 55 60	
aca aac aca ttc ttt gcc atc aag cgt tta atc ggt cgt cgt ttt aaa	241
Thr Asn Thr Phe Phe Ala Ile Lys Arg Leu Ile Gly Arg Arg Phe Lys	
65 70 75	
gat gac gaa gtt caa cgt gat gtg aac atc atg cca ttc aaa att atc	289
Asp Asp Glu Val Gln Arg Asp Val Asn Ile Met Pro Phe Lys Ile Ile	
80 85 90	
gca gct gat aat ggt gat gca tgg gtt gag tca cgt ggt aac aaa atg	337
Ala Ala Asp Asn Gly Asp Ala Trp Val Glu Ser Arg Gly Asn Lys Met	
95 100 105	
gca cca cca caa gtt tca gct gaa atc ttg aaa aag atg aaa aag act	385
Ala Pro Pro Gln Val Ser Ala Glu Ile Leu Lys Lys Met Lys Lys Thr	
110 115 120 125	
gct gaa gac ttt tta ggt gaa gaa gtg act gaa gcg gtt att acc gtt	433
Ala Glu Asp Phe Leu Gly Glu Glu Val Thr Glu Ala Val Ile Thr Val	
130 135 140	
cct gct tac ttt aac gat tca caa cgt caa gcc act aaa gat gct ggt	481
Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly	
145 150 155	
cgt atc gca ggt ctt gat gtt aag cgt att atc aac gaa cct act gct	529
Arg Ile Ala Gly Leu Asp Val Lys Arg Ile Ile Asn Glu Pro Thr Ala	
160 165 170	
gct gca ctt gca tac ggt atc gac aag aaa caa ggc gac aac att gtt	577
Ala Ala Leu Ala Tyr Gly Ile Asp Lys Lys Gln Gly Asp Asn Ile Val	
175 180 185	
gct gta tac gat tta ggt ggt ggt aca ttc gat atc tct atc atc gaa	625
Ala Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Ile Glu	
190 195 200 205	
att gac agc aac gat ggt gac caa aca ttt gaa gta cta gca acc aat	673
Ile Asp Ser Asn Asp Gly Asp Gln Thr Phe Glu Val Leu Ala Thr Asn	

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210				215				220				
ggt gat act cac tta ggt ggt gaa gac ttt gat aac cgt atg att aac	721											
Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Met Ile Asn												
225	230				235							
tat tta gct gat gaa ttc aaa aaa gac caa ggc tta gat ctt cgt aga	769											
Tyr Leu Ala Asp Glu Phe Lys Lys Asp Gln Gly Leu Asp Leu Arg Arg												
240	245				250							
gat cct tta gca atg caa cgt ttg aaa gaa gcc gct gaa aaa gca aaa	817											
Asp Pro Leu Ala Met Gln Arg Leu Lys Glu Ala Ala Glu Lys Ala Lys												
255	260				265							
atc gag ctt tca agc act aac cac act gaa gtt aac ttg cct tac atc	865											
Ile Glu Leu Ser Ser Thr Asn His Thr Glu Val Asn Leu Pro Tyr Ile												
270	275				280				285			
act gct gat gca tca ggt cct aag cat tta gtg gtt aaa att act cgt	913											
Thr Ala Asp Ala Ser Gly Pro Lys His Leu Val Val Lys Ile Thr Arg												
290	295				300							
gct aag tta gag tca tta gtt gaa gat tta att caa cgt act cta gag	961											
Ala Lys Leu Glu Ser Leu Val Glu Asp Leu Ile Gln Arg Thr Leu Glu												
305	310				315							
ccg ctt aaa gtt gca cta gct gat gct gat tta tca ata tca gat atc	1009											
Pro Leu Lys Val Ala Leu Ala Asp Ala Asp Leu Ser Ile Ser Asp Ile												
320	325				330							
aat gaa gtg att ctt gtg ggt ggt cag act cgt atg cct aaa gta caa	1057											
Asn Glu Val Ile Leu Val Gly Gly Gln Thr Arg Met Pro Lys Val Gln												
335	340				345							
gaa gca gtc act aac ttc ttt ggc aaa gag cct cgt aaa gat gtt aac	1105											
Glu Ala Val Thr Asn Phe Phe Gly Lys Glu Pro Arg Lys Asp Val Asn												
350	355				360				365			
cct gat gaa gcg gtt gct gtt ggt gcg gcg att cag gct ggc gta ctt	1153											
Pro Asp Glu Ala Val Ala Val Gly Ala Ala Ile Gln Ala Gly Val Leu												
370	375				380							
tct ggt gaa gtg aaa gac gta ctt cta ctt gac gtt acc cca cta tct	1201											
Ser Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser												
385	390				395							
ctt ggt att gaa acc atg ggc agt gtg atg aca aag ctt atc gag aag	1249											
Leu Gly Ile Glu Thr Met Gly Ser Val Met Thr Lys Leu Ile Glu Lys												
400	405				410							
aac acc act atc ccg act aaa gct cag caa gta ttc tca aca gct gac	1297											
Asn Thr Thr Ile Pro Thr Lys Ala Gln Gln Val Phe Ser Thr Ala Asp												
415	420				425							
gac aac caa agt gcc gtg act att cac gta ctt caa ggt gaa cgt aag	1345											
Asp Asn Gln Ser Ala Val Thr Ile His Val Leu Gln Gly Glu Arg Lys												
430	435				440				445			
caa gcg agt gct aac aag tca tta ggt caa ttt aac ctt gaa ggt att	1393											
Gln Ala Ser Ala Asn Lys Ser Leu Gly Gln Phe Asn Leu Glu Gly Ile												
450	455				460							
gag cca gca cca cgt ggc caa cca cag gtt gaa gtg atg ttc gac att	1441											
Glu Pro Ala Pro Arg Gly Gln Pro Gln Val Glu Val Met Phe Asp Ile												
465	470				475							
gat gct gat ggt atc tta cat gtg tct gca aca gac aag aaa aca ggt	1489											
Asp Ala Asp Gly Ile Leu His Val Ser Ala Thr Asp Lys Lys Thr Gly												
480	485				490							
aag aaa caa aac att act atc aaa gcc tct tca ggt tta tct gat gaa	1537											
Lys Lys Gln Asn Ile Thr Ile Lys Ala Ser Ser Gly Leu Ser Asp Glu												
495	500				505							
gaa gtt gaa caa atg gta cgt gat gca gaa gct cat gct gat gaa gat	1585											
Glu Val Glu Gln Met Val Arg Asp Ala Glu Ala His Ala Asp Glu Asp												
510	515				520				525			
gct aaa ttt gaa gag tta gtt aaa gcg cgt aat caa gca gat ggt tta	1633											

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Ala Lys Phe Glu Glu Leu Val Lys Ala Arg Asn Gln Ala Asp Gly Leu	
530 535 540	
gct cat tca act aaa aaa caa gtt gaa gaa gct ggc gat gca cta gct	1681
Ala His Ser Thr Lys Lys Gln Val Glu Glu Ala Gly Asp Ala Leu Ala	
545 550 555	
agt gac gaa aaa gaa aag att gaa gca gca atc gca act tta gaa act	1729
Ser Asp Glu Lys Glu Lys Ile Glu Ala Ala Ile Ala Thr Leu Glu Thr	
560 565 570	
gcc ata aaa ggc aaa gat aaa gaa gcc att gat aca gca act caa gcg	1777
Ala Ile Lys Gly Lys Asp Lys Glu Ala Ile Asp Thr Ala Thr Gln Ala	
575 580 585	
cta atc gaa gcg tct gct aag tta atg gaa att gct caa gct aaa gct	1825
Leu Ile Glu Ala Ser Ala Lys Leu Met Glu Ile Ala Gln Ala Lys Ala	
590 595 600 605	
caa ggt gaa gca gaa ggt caa gcg cac gat gct ggc caa gaa aag cct	1873
Gln Gly Glu Ala Glu Gly Gln Ala His Asp Ala Gly Gln Glu Lys Pro	
610 615 620	
gct gat gat gtt gtt gat gct gag ttc gaa gaa gtt aaa gac gac aaa	1921
Ala Asp Asp Val Val Asp Ala Glu Phe Glu Glu Val Lys Asp Asp Lys	
625 630 635	
aaa taa ataatctttt	1937
Lys	

<210> SEQ ID NO 26
 <211> LENGTH: 638
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 26

Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val	
1 5 10 15	
Ala Val Leu Asp Gly Gly Lys Ala Arg Val Ile Glu Asn Ala Glu Gly	
20 25 30	
Asp Arg Thr Thr Pro Ser Ile Ile Ala Tyr Thr Asp Asp Glu Ile Ile	
35 40 45	
Val Gly Gln Pro Ala Lys Arg Gln Ala Val Thr Asn Pro Thr Asn Thr	
50 55 60	
Phe Phe Ala Ile Lys Arg Leu Ile Gly Arg Arg Phe Lys Asp Asp Glu	
65 70 75 80	
Val Gln Arg Asp Val Asn Ile Met Pro Phe Lys Ile Ile Ala Ala Asp	
85 90 95	
Asn Gly Asp Ala Trp Val Glu Ser Arg Gly Asn Lys Met Ala Pro Pro	
100 105 110	
Gln Val Ser Ala Glu Ile Leu Lys Lys Met Lys Lys Thr Ala Glu Asp	
115 120 125	
Phe Leu Gly Glu Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr	
130 135 140	
Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Arg Ile Ala	
145 150 155 160	
Gly Leu Asp Val Lys Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Leu	
165 170 175	
Ala Tyr Gly Ile Asp Lys Lys Gln Gly Asp Asn Ile Val Ala Val Tyr	
180 185 190	
Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Ile Glu Ile Asp Ser	
195 200 205	

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Asn	Asp	Gly	Asp	Gln	Thr	Phe	Glu	Val	Leu	Ala	Thr	Asn	Gly	Asp	Thr
210						215					220				
His	Leu	Gly	Gly	Glu	Asp	Phe	Asp	Asn	Arg	Met	Ile	Asn	Tyr	Leu	Ala
225					230					235					240
Asp	Glu	Phe	Lys	Lys	Asp	Gln	Gly	Leu	Asp	Leu	Arg	Arg	Asp	Pro	Leu
			245						250					255	
Ala	Met	Gln	Arg	Leu	Lys	Glu	Ala	Ala	Glu	Lys	Ala	Lys	Ile	Glu	Leu
			260					265					270		
Ser	Ser	Thr	Asn	His	Thr	Glu	Val	Asn	Leu	Pro	Tyr	Ile	Thr	Ala	Asp
		275					280					285			
Ala	Ser	Gly	Pro	Lys	His	Leu	Val	Val	Lys	Ile	Thr	Arg	Ala	Lys	Leu
	290					295					300				
Glu	Ser	Leu	Val	Glu	Asp	Leu	Ile	Gln	Arg	Thr	Leu	Glu	Pro	Leu	Lys
305					310					315					320
Val	Ala	Leu	Ala	Asp	Ala	Asp	Leu	Ser	Ile	Ser	Asp	Ile	Asn	Glu	Val
			325						330					335	
Ile	Leu	Val	Gly	Gly	Gln	Thr	Arg	Met	Pro	Lys	Val	Gln	Glu	Ala	Val
			340					345					350		
Thr	Asn	Phe	Phe	Gly	Lys	Glu	Pro	Arg	Lys	Asp	Val	Asn	Pro	Asp	Glu
		355					360					365			
Ala	Val	Ala	Val	Gly	Ala	Ala	Ile	Gln	Ala	Gly	Val	Leu	Ser	Gly	Glu
		370				375					380				
Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val	Thr	Pro	Leu	Ser	Leu	Gly	Ile
385					390					395					400
Glu	Thr	Met	Gly	Ser	Val	Met	Thr	Lys	Leu	Ile	Glu	Lys	Asn	Thr	Thr
			405						410					415	
Ile	Pro	Thr	Lys	Ala	Gln	Gln	Val	Phe	Ser	Thr	Ala	Asp	Asp	Asn	Gln
			420					425					430		
Ser	Ala	Val	Thr	Ile	His	Val	Leu	Gln	Gly	Glu	Arg	Lys	Gln	Ala	Ser
		435					440					445			
Ala	Asn	Lys	Ser	Leu	Gly	Gln	Phe	Asn	Leu	Glu	Gly	Ile	Glu	Pro	Ala
	450					455					460				
Pro	Arg	Gly	Gln	Pro	Gln	Val	Glu	Val	Met	Phe	Asp	Ile	Asp	Ala	Asp
465					470					475					480
Gly	Ile	Leu	His	Val	Ser	Ala	Thr	Asp	Lys	Lys	Thr	Gly	Lys	Lys	Gln
			485						490					495	
Asn	Ile	Thr	Ile	Lys	Ala	Ser	Ser	Gly	Leu	Ser	Asp	Glu	Glu	Val	Glu
		500						505					510		
Gln	Met	Val	Arg	Asp	Ala	Glu	Ala	His	Ala	Asp	Glu	Asp	Ala	Lys	Phe
		515					520					525			
Glu	Glu	Leu	Val	Lys	Ala	Arg	Asn	Gln	Ala	Asp	Gly	Leu	Ala	His	Ser
	530					535					540				
Thr	Lys	Lys	Gln	Val	Glu	Glu	Ala	Gly	Asp	Ala	Leu	Ala	Ser	Asp	Glu
545					550					555					560
Lys	Glu	Lys	Ile	Glu	Ala	Ala	Ile	Ala	Thr	Leu	Glu	Thr	Ala	Ile	Lys
			565						570					575	
Gly	Lys	Asp	Lys	Glu	Ala	Ile	Asp	Thr	Ala	Thr	Gln	Ala	Leu	Ile	Glu
		580						585					590		
Ala	Ser	Ala	Lys	Leu	Met	Glu	Ile	Ala	Gln	Ala	Lys	Ala	Gln	Gly	Glu
		595				600						605			
Ala	Glu	Gly	Gln	Ala	His	Asp	Ala	Gly	Gln	Glu	Lys	Pro	Ala	Asp	Asp
	610					615					620				
Val	Val	Asp	Ala	Glu	Phe	Glu	Glu	Val	Lys	Asp	Asp	Lys	Lys		

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625                               630                               635

<210> SEQ ID NO 27
<211> LENGTH: 1175
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: ftsZ hybrid
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1155)

<400> SEQUENCE: 27

atg ttt gat ttt aac gat tca atg gtt tca aat gcc ata att aaa gtt      48
Met Phe Asp Phe Asn Asp Ser Met Val Ser Asn Ala Ile Ile Lys Val
1           5           10           15

gtc ggt gtt ggt gcc ggt gcc ggt aat gct gta caa cat atg tgt gaa      96
Val Gly Val Gly Gly Gly Gly Asn Ala Val Gln His Met Cys Glu
20          25          30

gaa gtt tct gat gtt gag ttt ttt gcc cta aat aca gat ggt caa gca      144
Glu Val Ser Asp Val Glu Phe Phe Ala Leu Asn Thr Asp Gly Gln Ala
35          40          45

tta tca aaa tca aaa gtt caa aat ata tta caa att ggt aca aac cta      192
Leu Ser Lys Ser Lys Val Gln Asn Ile Leu Gln Ile Gly Thr Asn Leu
50          55          60

aca aaa ggt tta ggt gct ggt gcg aat cct gaa att ggt aag aga gct      240
Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Ile Gly Lys Arg Ala
65          70          75          80

gca act gaa gat aga gcg aaa atc gag caa ctt tta gag ggt gct gat      288
Ala Thr Glu Asp Arg Ala Lys Ile Glu Gln Leu Leu Glu Gly Ala Asp
85          90          95

atg gtt ttc atc act gct ggt atg ggt ggt ggt aca ggt aca ggt gga      336
Met Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Thr Gly Gly
100         105         110

gct cct gta gtt gca gaa gtt gca aaa gag atg ggt ata ctt aca gta      384
Ala Pro Val Val Ala Glu Val Ala Lys Glu Met Gly Ile Leu Thr Val
115         120         125

gct gta gtt act aag cct ttc cct ttt gaa gga cca aga aga atg aaa      432
Ala Val Val Thr Lys Pro Phe Pro Phe Glu Gly Pro Arg Arg Met Lys
130         135         140

gca gca gag caa ggt att gag ttt tta tct aaa agt gtt gat tca ctg      480
Ala Ala Glu Gln Gly Ile Glu Phe Leu Ser Lys Ser Val Asp Ser Leu
145         150         155         160

att act att cct aac gaa aag tta ctg aaa gta ctt ggc cct gga aca      528
Ile Thr Ile Pro Asn Glu Lys Leu Leu Lys Val Leu Gly Pro Gly Thr
165         170         175

agc tta tta gat gcc ttt aaa gca gca aat aac gtg cta ctt ggc gcc      576
Ser Leu Leu Asp Ala Phe Lys Ala Ala Asn Asn Val Leu Leu Gly Ala
180         185         190

gtt cag ggt att gca gaa tta att act cgt cct ggt ttg ata aat gtc      624
Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Ile Asn Val
195         200         205

gat ttt gct gat gta cgt acc gtt atg tct gag atg ggt act gcc atg      672
Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Thr Ala Met
210         215         220

atg ggt tct ggt act gct tct ggc gat gat aga gca caa gaa gct gct      720
Met Gly Ser Gly Thr Ala Ser Gly Asp Asp Arg Ala Gln Glu Ala Ala
225         230         235         240

gat gct gct att tca agt cct tta tta gag gat gtg gat tta gct ggt      768
Asp Ala Ala Ile Ser Ser Pro Leu Leu Glu Asp Val Asp Leu Ala Gly
245         250         255

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gca cgc ggg atc tta gtt aat att acc gca ggt atg gat att agt atc	816
Ala Arg Gly Ile Leu Val Asn Ile Thr Ala Gly Met Asp Ile Ser Ile	
260 265 270	
gat gag ttt gaa act gtt ggt aat gcc gtt aaa gct ttc gct tct gaa	864
Asp Glu Phe Glu Thr Val Gly Asn Ala Val Lys Ala Phe Ala Ser Glu	
275 280 285	
aat gcg act gtt gtt gtt ggt gct gtt att gat atg gat atg aca gat	912
Asn Ala Thr Val Val Val Gly Ala Val Ile Asp Met Asp Met Thr Asp	
290 295 300	
gag ctt cgt gtg act gtt gtt gct acg ggt att ggc gct gaa agt aag	960
Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile Gly Ala Glu Ser Lys	
305 310 315 320	
cct gat att acg tta gta aat cct atg cca atg gct gaa gca aaa gtt	1008
Pro Asp Ile Thr Leu Val Asn Pro Met Pro Met Ala Glu Ala Lys Val	
325 330 335	
gtc ggt ggg gat tat aca cca gct gca cca cag gca aat tta gcg act	1056
Val Gly Gly Asp Tyr Thr Pro Ala Ala Pro Gln Ala Asn Leu Ala Thr	
340 345 350	
gaa gca ata gct atg act gat agc aat gcg cag aaa gca gca gca acc	1104
Glu Ala Ile Ala Met Thr Asp Ser Asn Ala Gln Lys Ala Ala Ala Thr	
355 360 365	
gac tta gat act tat tta gat att cct gct ttt tta cgt aag caa gcg	1152
Asp Leu Asp Thr Tyr Leu Asp Ile Pro Ala Phe Leu Arg Lys Gln Ala	
370 375 380	
gat taataaaaaac caaaattaag	1175
Asp	
385	

<210> SEQ ID NO 28

<211> LENGTH: 385

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 28

Met Phe Asp Phe Asn Asp Ser Met Val Ser Asn Ala Ile Ile Lys Val	
1 5 10 15	
Val Gly Val Gly Gly Gly Gly Asn Ala Val Gln His Met Cys Glu	
20 25 30	
Glu Val Ser Asp Val Glu Phe Phe Ala Leu Asn Thr Asp Gly Gln Ala	
35 40 45	
Leu Ser Lys Ser Lys Val Gln Asn Ile Leu Gln Ile Gly Thr Asn Leu	
50 55 60	
Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Ile Gly Lys Arg Ala	
65 70 75 80	
Ala Thr Glu Asp Arg Ala Lys Ile Glu Gln Leu Leu Glu Gly Ala Asp	
85 90 95	
Met Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Thr Gly Gly	
100 105 110	
Ala Pro Val Val Ala Glu Val Ala Lys Glu Met Gly Ile Leu Thr Val	
115 120 125	
Ala Val Val Thr Lys Pro Phe Pro Phe Glu Gly Pro Arg Arg Met Lys	
130 135 140	
Ala Ala Glu Gln Gly Ile Glu Phe Leu Ser Lys Ser Val Asp Ser Leu	
145 150 155 160	
Ile Thr Ile Pro Asn Glu Lys Leu Leu Lys Val Leu Gly Pro Gly Thr	
165 170 175	

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Ser Leu Leu Asp Ala Phe Lys Ala Ala Asn Asn Val Leu Leu Gly Ala
180 185 190

Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Ile Asn Val
195 200 205

Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Thr Ala Met
210 215 220

Met Gly Ser Gly Thr Ala Ser Gly Asp Asp Arg Ala Gln Glu Ala Ala
225 230 235 240

Asp Ala Ala Ile Ser Ser Pro Leu Leu Glu Asp Val Asp Leu Ala Gly
245 250 255

Ala Arg Gly Ile Leu Val Asn Ile Thr Ala Gly Met Asp Ile Ser Ile
260 265 270

Asp Glu Phe Glu Thr Val Gly Asn Ala Val Lys Ala Phe Ala Ser Glu
275 280 285

Asn Ala Thr Val Val Val Gly Ala Val Ile Asp Met Asp Met Thr Asp
290 295 300

Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile Gly Ala Glu Ser Lys
305 310 315 320

Pro Asp Ile Thr Leu Val Asn Pro Met Pro Met Ala Glu Ala Lys Val
325 330 335

Val Gly Gly Asp Tyr Thr Pro Ala Ala Pro Gln Ala Asn Leu Ala Thr
340 345 350

Glu Ala Ile Ala Met Thr Asp Ser Asn Ala Gln Lys Ala Ala Ala Thr
355 360 365

Asp Leu Asp Thr Tyr Leu Asp Ile Pro Ala Phe Leu Arg Lys Gln Ala
370 375 380

Asp
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The invention claimed is:

1. A method of making a recombinant temperature sensitive (TS) bacteria comprising an essential peptide, comprising:

screening a psychrophilic microbial genome for detection
therein of an essential polynucleotide that confers temperature sensitivity to a bacterium upon expression of a
protein from the essential polynucleotide that is inactivated at a temperature greater than 30° C.;

isolating said essential polynucleotide;

constructing a nucleic acid construct comprising the essential
polynucleotide and one or more control sequences operably linked to the essential polynucleotide;

inserting the nucleic acid construct into the genome of a
selected mesophilic bacterial host cell thereby functionally replacing the selected mesophilic bacterial host
cell's homologue of the essential polynucleotide whereby the essential polynucleotide encodes a protein
that is operable at a temperature less than 30° C. and inoperable at a temperature greater than 30° C.;

culturing the mesophilic bacterial host cell comprising the
essential polynucleotide at a temperature less than 30° C. to confirm the viability of the mesophilic bacterial
host cell comprising the essential polynucleotide;

further culturing the mesophilic bacterial host cell comprising
the essential polynucleotide at a temperature greater than 30° C. to determine if the mesophilic bacterial
host cell comprising the essential polynucleotide is killed; and

if the mesophilic bacterial host cell comprising the essential
polynucleotide is killed, inserting the nucleic acid construct into the genome of a selected destination
mesophilic bacterial host cell, thereby functionally replacing the selected destination mesophilic bacterial
host cell's homologue of the essential polynucleotide, thereby generating a recombinant TS bacteria.

2. The method of claim 1, wherein the selected mesophilic
bacterial host cell is a *Francisella novicida* cell.

3. The method of claim 1, wherein the wherein the psychrophilic
microbial genome is from *Colwellia* sp., *Pseudoalteromonas* sp., or *Shewanella* sp.

4. The method of claim 1, wherein the psychrophilic microbial
genome is from *Pseudoalteromonas haloplanktis*.

5. The method of claim 1, wherein the psychrophilic microbial
genome is from *C. psychrophila*.

6. The method of claim 1, wherein the selected destination
mesophilic bacterial host cell is *Salmonella* sp. or *Mycobacterium* sp.

7. The method of claim 1, wherein the selected destination
mesophilic bacterial host cell is *Haemophilus* sp., *Vibrio* sp., *Escherichia* sp., *Streptococcus* sp., *Burkholderia* sp., *Campylobacter* sp., *Neisseria* sp., *Helicobacter* sp. or *Francisella* sp.

8. The method of claim 1, wherein screening the psychrophilic
microbial genome detects a polynucleotide sequence comprising the nucleotide sequence shown in SEQ ID NO: 1,
3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 or 27.

9. The method of claim 1, wherein screening the psychrophilic
microbial genome detects a polynucleotide sequence

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encoding a protein comprising the amino acid sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, or 28.

10. The method of claim 1, wherein the protein encoded by the essential polynucleotide is operable at a temperature of 4° 5 C. to 30° C.

11. The method of claim 1, wherein the nucleic acid construct comprising the essential polynucleotide comprises a vector.

12. The method of claim 1, wherein screening the psychro- 10 philic microbial genome detects a polynucleotide sequence selected from the group consisting of ligA, pyrG, hemC, ftsZ, cmk, murG, fnt, tyrS, or dnaK.

13. The method of claim 1, wherein screening the psychro- 15 philic microbial genome detects a polynucleotide sequence comprising the ligA polynucleotide sequence.

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