

eolf-seql
SEQUENCE LISTING

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<110>  Laboratorios LETI SL
<120>  Molecule for treating an inflammatory disorder
<130>  P6032062PCT
<150>  EP 11165248.3
<151>  2011-05-09
<150>  US 61/484,67
<151>  2011-05-09
<160>  57
<170>  PatentIn version 3.3
<210>  1
<211>  267
<212>  PRT
<213>  Leishmania major
<400>  1

Met Thr Pro Leu Ser Leu Ser Ser Ser Arg His Ser Phe Lys Gln Asn
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Glu Thr Gln Asn Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ser
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Ser Ile Leu Gly Cys Gly Arg Ala Arg Val Trp Leu Asp Pro Asn Glu
      35      40      45

Ala Val Glu Ile Gln Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu
      50      55      60

Ile Lys Asp Gly Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg
65      70      75      80

Ala Arg Trp Arg Lys Met Lys Glu Ala Lys Asp Met Gly Arg His Asn
      85      90      95

Gly Val Gly Arg Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys
      100     105     110

Glu Leu Trp Met Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys
      115     120     125

Tyr Arg Ala Asp Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr
      130     135     140

Met Arg Ala Lys Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Val Glu
145     150     155     160

His Ile His Lys Ile Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala
      165     170     175

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Glu Gln Leu Ala Ala Lys His Leu Arg Asp Glu Gln Asn Arg Asn Lys
180 185 190

Ala Arg Lys Gln Glu Leu Lys Lys Arg Glu Lys Glu Arg Glu Arg Ala
195 200 205

Arg Arg Asp Asp Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Ala
210 215 220

Ala Lys Lys Ser Ala Ala Pro Ala Ala Lys Ser Ala Ala Pro Ala Ala
225 230 235 240

Lys Ala Ala Ala Pro Ala Thr Lys Ala Ala Ala Ala Pro Ala Thr
245 250 255

Lys Gly Ala Ala Pro Val Lys Lys Ser Lys Lys
260 265

<210> 2
<211> 804
<212> DNA
<213> Leishmania major

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gtgcgcaagc tgatcaagga tggcttcac atccgcaagc cgggtgaaggt gactcgcgc 240
gcgcggtggc gtaaaatgaa ggaggcgaag gacatggggc gccacaacgg cgttgggcgc 300
cgcgagggta gccgcgaggc ccgcatgccg agcaaggagt tgtggatgcg ccgcctgcgc 360
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cgcgacctgt acatgcgcgc gaagggtaac gtgttccgca acaagcgcaa cttgtggag 480
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aaggcggacg ccgcgaagaa gtccgccgcg cctgctgcga agtccgccgc gcctgccgcg 720
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<213> artificial

<220>
<223> primer

eolf-seql

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28

<210> 4
<211> 30
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<213> artificial

<220>
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<210> 5
<211> 250
<212> PRT
<213> Leishmania braziliensis

<400> 5

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20 25 30

Gln Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ala Arg Trp Arg
50 55 60

Lys Met Lys Glu Ala Lys Asp Met Gly Arg His Ser Gly Val Gly Arg
65 70 75 80

Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp
100 105 110

Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr Val Arg Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His Lys
130 135 140

Ile Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys His Gln Arg Asp Glu Gln His Arg Asn Lys Ala Arg Lys Gln
165 170 175

Glu Leu Lys Lys Arg Glu Lys Glu Arg Glu Arg Ala Arg Arg Asp Asp

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180

185

190

Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Val Ala Lys Lys Ser
195 200 205

Ala Ala Pro Ala Thr Lys Ala Ala Ala Val Ser Ala Ala Lys Ala Ala
210 215 220

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225 230 235 240

Pro Ala Val Pro Ala Lys Lys Ser Lys Lys
245 250

<210> 6

<211> 753

<212> DNA

<213> Leishmania braziliensis

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<211> 271

<212> PRT

<213> Leishmania braziliensis

<400> 7

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Cys Gly Arg Ala Arg Val Trp Leu Asp Pro Asn Glu Ala Met Glu Ile
20 25 30

Gln Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly

colf-seql

35

40

45

Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ala Arg Trp Arg
50 55 60

Lys Met Lys Glu Ala Lys Asp Met Gly Arg His Ser Gly Val Gly Arg
65 70 75 80

Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp
100 105 110

Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr Val Arg Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His Lys
130 135 140

Ile Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys His Gln Arg Asp Glu Gln His Arg Asn Lys Ala Arg Lys Gln
165 170 175

Glu Leu Lys Lys Arg Glu Lys Glu Arg Glu Arg Ala Arg Arg Asp Asp
180 185 190

Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Val Ala Lys Lys Ser
195 200 205

Ala Ala Pro Ala Thr Lys Ala Ala Ala Val Ser Ala Ala Lys Ala Ala
210 215 220

Ala Val Ser Ala Ala Lys Ala Ala Ala Val Ser Val Ser Arg Ala Ala
225 230 235 240

Ala Ala Val Ala Pro Ala Ala Lys Pro Ala Val Pro Ala Lys Ala Ala
245 250 255

Ala Pro Ala Ala Lys Gly Ala Val Pro Ala Lys Lys Ser Lys Lys
260 265 270

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<211> 816

<212> DNA

<213> Leishmania braziliensis

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cgcgagggta gccgcgaggc ccgcatgccg agcaaggagc tgtggatgcg ccgcctgcgc 300
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cgcgacctgt acgtgcgcgc gaagggtaac gtgttccgca acaagcgcaa ctttatggag 420
cacatccaca agatcaagaa cgagaagaag aaggagcggc agctggcgga gcagcttgcg 480
gcgaagcacc agcgcgacga gcagcaccgc aacaaggctc gcaagcagga gctgaagaag 540
cgcgagaagg agcgcgagcg cgcgaggcgc gacgacgctg ctgctgctgc gcagaagaag 600
aaggcggacg ttgcgaagaa gtctgctgcc cctgctacga aggctgctgc tgtctccgcc 660
gcgaaggctg ctgctgtctc cgccgcgaag gctgctgctg tctccgtctc gagggctgct 720
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aagggtgctg tgccggcgaa gaagtcgaag aagtaa 816

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 <212> PRT
 <213> Leishmania braziliensis

<400> 9

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 20 25 30

Lys Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His
 35 40 45

Lys Ile Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu
 50 55 60

Ala Ala Lys His Gln Arg Asp Glu Gln His Arg Asn Lys Ala Arg Lys
 65 70 75 80

Gln Glu Leu Lys Lys Arg Glu Lys Glu Arg Glu Arg Ala Arg Arg Asp
 85 90 95

Asp Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Val Ala Lys Lys
 100 105 110

Ser Ala Ala Pro Ala Thr Lys Ala Ala Ala Val Ser Ala Ala Lys Ala
 115 120 125

Ala Ala Val Ser Ala Ala Lys Ala Ala Ala Val Ser Val Ser Arg Ala
 130 135 140

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Ala Ala Ala Val Ala Pro Ala Ala Lys Pro Ala Val Pro Ala Lys Ala
145 150 155 160

Ala Ala Pro Ala Ala Lys Gly Ala Val Pro Ala Lys Lys Ser Lys Lys
165 170 175

<210> 10

<211> 531

<212> PRT

<213> Leishmania braziliensis

<400> 10

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Thr Thr Cys Thr Gly Cys Gly Thr Cys Gly Cys Cys Thr Gly Cys Thr
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Gly Cys Gly Cys Ala Ala Gly Thr Ala Cys Cys Gly Cys Gly Cys Gly
35 40 45

Gly Ala Cys Ala Ala Gly Ala Ala Gly Ala Thr Cys Gly Ala Cys Cys
50 55 60

Gly Cys Cys Ala Cys Gly Thr Gly Thr Ala Cys Cys Gly Cys Gly Ala
65 70 75 80

Cys Cys Thr Gly Thr Ala Cys Gly Thr Gly Cys Gly Cys Gly Cys Gly
85 90 95

Ala Ala Gly Gly Gly Thr Ala Ala Cys Gly Thr Gly Thr Thr Cys Cys
100 105 110

Gly Cys Ala Ala Cys Ala Ala Gly Cys Gly Cys Ala Ala Cys Cys Thr
115 120 125

Thr Ala Thr Gly Gly Ala Gly Cys Ala Cys Ala Thr Cys Cys Ala Cys
130 135 140

Ala Ala Gly Ala Thr Cys Ala Ala Gly Ala Ala Cys Gly Ala Gly Ala
145 150 155 160

Ala Gly Ala Ala Gly Ala Ala Gly Gly Ala Gly Cys Gly Gly Cys Ala
165 170 175

Gly Cys Thr Gly Gly Cys Gly Gly Ala Gly Cys Ala Gly Cys Thr Thr
180 185 190

Gly Cys Gly Gly Cys Gly Ala Ala Gly Cys Ala Cys Cys Ala Gly Cys
195 200 205

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Gly Cys Gly Ala Cys Gly Ala Gly Cys Ala Gly Cys Ala Cys Cys Gly
210 215 220

Cys Ala Ala Cys Ala Ala Gly Gly Cys Thr Cys Gly Cys Ala Ala Gly
225 230 235 240

Cys Ala Gly Gly Ala Gly Cys Thr Gly Ala Ala Gly Ala Ala Gly Cys
245 250 255

Gly Cys Gly Ala Gly Ala Ala Gly Gly Ala Gly Cys Gly Cys Gly Ala
260 265 270

Gly Cys Gly Cys Gly Cys Gly Ala Gly Gly Cys Gly Cys Gly Ala Cys
275 280 285

Gly Ala Cys Gly Cys Thr Gly Cys Thr Gly Cys Thr Gly Cys Thr Gly
290 295 300

Cys Gly Cys Ala Gly Ala Ala Gly Ala Ala Gly Ala Ala Gly Gly Cys
305 310 315 320

Gly Gly Ala Cys Gly Thr Thr Gly Cys Gly Ala Ala Gly Ala Ala Gly
325 330 335

Thr Cys Thr Gly Cys Thr Gly Cys Cys Cys Cys Thr Gly Cys Thr Ala
340 345 350

Cys Gly Ala Ala Gly Gly Cys Thr Gly Cys Thr Gly Cys Thr Gly Thr
355 360 365

Cys Thr Cys Cys Gly Cys Cys Gly Cys Gly Ala Ala Gly Gly Cys Thr
370 375 380

Gly Cys Thr Gly Cys Thr Gly Thr Cys Thr Cys Cys Gly Cys Cys Gly
385 390 395 400

Cys Gly Ala Ala Gly Gly Cys Thr Gly Cys Thr Gly Cys Thr Gly Thr
405 410 415

Cys Thr Cys Cys Gly Thr Cys Thr Cys Gly Ala Gly Gly Gly Cys Thr
420 425 430

Gly Cys Thr Gly Cys Thr Gly Cys Thr Gly Thr Gly Gly Cys Thr Cys
435 440 445

Cys Cys Gly Cys Thr Gly Cys Gly Ala Ala Gly Cys Cys Thr Gly Cys
450 455 460

Thr Gly Thr Gly Cys Cys Gly Gly Cys Gly Ala Ala Gly Gly Cys Thr
465 470 475 480

Gly Cys Gly Gly Cys Gly Cys Cys Thr ^{self-seq}Gly Cys Thr Gly Cys Gly Ala
 485 490 495
 Ala Gly Gly Gly Thr Gly Cys Thr Gly Thr Gly Cys Cys Gly Gly Cys
 500 505 510
 Gly Ala Ala Gly Ala Ala Gly Thr Cys Gly Ala Ala Gly Ala Ala Gly
 515 520 525
 Thr Ala Ala
 530

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

eof-seq1

180

185

190

Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Ala Ala Lys Lys Ser
195 200 205

Ala Ala Pro Ala Ala Lys Ser Ala Ala Pro Ala Ala Lys Ser Ala Ala
210 215 220

Pro Ala Ala Lys Val Ala Ala Pro Ala Thr Lys Gly Ala Ala Pro Val
225 230 235 240

Lys Lys Ser Lys Lys
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<211> 738
<212> DNA
<213> Leishmania infantum

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gtgcgcaagc tgatcaagga tggcttcata atccgcaagc cgggtgaaggc gcactcgcgc 180
gcgcggtggc gtaaaatgaa ggaggcgaag gacatggggc gccacaacgg cggtggccgc 240
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aagaagtcga agaagtaa 738

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<211> 238
<212> PRT
<213> Leishmania infantum

<400> 13

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Cys Gly Arg Ala Arg Val Trp Leu Asp Pro Asn Glu Ala Val Glu Ile
20 25 30

Gln Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly

eofl-seql

35

40

45

Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ala Arg Trp Arg
50 55 60

Lys Met Lys Glu Ala Lys Asp Met Gly Arg His Asn Gly Val Gly Arg
65 70 75 80

Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp
100 105 110

Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr Val Arg Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Val Glu His Ile His Lys
130 135 140

Ile Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys His Leu Arg Asp Glu Gln Asn Arg Asn Lys Ala Arg Lys Gln
165 170 175

Glu Leu Arg Lys Arg Glu Lys Glu Arg Glu Arg Ala Arg Arg Asp Asp
180 185 190

Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Ala Ala Lys Lys Ser
195 200 205

Ala Ala Pro Ala Ala Lys Ser Ala Ala Pro Ala Ala Lys Val Ala Ala
210 215 220

Pro Ala Thr Lys Gly Ala Ala Pro Val Lys Lys Ser Lys Lys
225 230 235

<210> 14
<211> 717
<212> DNA
<213> Leishmania infantum

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attctgcgcc gcctgctgcg caagtaccgc gcggacaaga agatcgaccg ccacgtgtac 360

eolf-seql

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gcgaagcacc tgcgcgacga gcagaaccgc aacaaggctc gcaagcagga gctgaggaag 540
cgcgagaagg agcgcgagcg cgcgaggcgc gacgacgctg ctgccgctgc gcagaagaag 600
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<210> 15
<211> 247
<212> PRT
<213> Leishmania mexicana

<400> 15

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ser Ser Ile Leu Ser
1 5 10 15

Cys Gly Arg Ala Arg Val Trp Leu Asp Pro Asn Glu Ala Met Glu Ile
20 25 30

Gln Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ala Arg Trp Arg
50 55 60

Lys Met Lys Glu Ala Lys Asp Met Gly Arg His Asn Gly Val Gly Arg
65 70 75 80

Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp
100 105 110

Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr Met Arg Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Val Glu Tyr Ile His Lys
130 135 140

Ile Lys Asn Glu Lys Lys Lys Ala Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys His Leu Arg Asp Glu Gln Asn Arg Asn Lys Ala Arg Lys Gln
165 170 175

Glu Leu Arg Lys Arg Glu Lys Glu Arg Glu Arg Ala Lys Arg Asp Asp
180 185 190

eolf-seql

Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Ala Ala Lys Lys Ser
195 200 205

Ala Ala Pro Ala Ala Lys Ser Ala Ala Pro Ala Ala Lys Ala Ala Ala
210 215 220

Pro Val Ala Lys Ala Ala Ala Ala Pro Ala Ala Lys Gly Ala Ala
225 230 235 240

Pro Val Lys Lys Ser Lys Lys
245

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<211> 744
<212> DNA
<213> Leishmania mexicana

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gcgcggtggc gtaaaatgaa ggaggcgaag gacatggggc gccacaacgg cgttggccgc 240
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<210> 17
<211> 247
<212> PRT
<213> Leishmania mexicana

<400> 17

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ser Ser Ile Leu Ser
1 5 10 15

Cys Gly Arg Ala Arg Val Trp Leu Asp Pro Asn Glu Ala Met Glu Ile
20 25 30

Gln Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

eolf-seql

Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ala Arg Trp Arg
50 55 60

Lys Met Lys Glu Ala Lys Asp Met Gly Arg His Asn Gly Val Gly Arg
65 70 75 80

Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp
100 105 110

Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr Met Arg Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Val Glu Tyr Ile His Lys
130 135 140

Ile Lys Asn Glu Lys Lys Lys Ala Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys His Leu Arg Asp Glu Gln Asn Arg Asn Lys Ala Arg Lys Gln
165 170 175

Glu Leu Arg Lys Arg Glu Lys Glu Arg Glu Arg Ala Lys Arg Asp Asp
180 185 190

Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Ala Ala Lys Lys Ser
195 200 205

Ala Ala Pro Ala Ala Lys Ser Ala Ala Pro Ala Ala Lys Ala Ala Ala
210 215 220

Pro Val Ala Lys Ala Ala Ala Ala Ala Pro Ala Ala Lys Gly Ala Ala
225 230 235 240

Pro Val Lys Lys Ser Lys Lys
245

<210> 18
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<212> DNA
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gtgcgcaagc tgatcaagga tggcttcata atccgcaagc cgggtgaagg gcaactcgcg 180
gcgcggtggc gtaaaatgaa ggaggcgaag gacatggggc gccacaacgg cggtggccgc 240
cgcgaggggta gccgcgaggc ccgcatgccg agcaaggagt tgtggatgcg ccgcctgcgc 300

eolf-seql

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cgagacctgt acatgcgcgc gaagggtaac gtgttccgca acaagcgcaa ccttgtggag    420
tacatccaca agatcaagaa tgagaagaag aaggcgcgcc agctggcgga gcagcttgcg    480
gcgaagcacc tgcgcgacga gcagaaccgc aacaaggctc gcaagcagga gctgcggaag    540
cgcgagaagg agcgcgagcg cggaagcgcg gacgacgctg ctgccgctgc gcagaagaag    600
aaggcggaag ccgcaagaa gtccgccgcg cctgctgcca agtccgccgc gcctgccgcg    660
aaggctgctg ccccgctgcg gaaggccgct gctgctgccc ccgcggcgaa ggggtgctgcg    720
ccggtgaaga agtcgaagaa gtaa                                           744

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<210> 19
 <211> 245
 <212> PRT
 <213> Leishmania donovani

<400> 19

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ser Ser Ile Leu Gly
 1 5 10 15

Cys Gly Arg Ala Arg Val Trp Leu Asp Pro Asn Glu Ala Val Glu Ile
 20 25 30

Gln Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
 35 40 45

Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ala Arg Trp Arg
 50 55 60

Lys Met Lys Glu Ala Lys Asp Met Gly Arg His Asn Gly Val Gly Arg
 65 70 75 80

Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
 85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp
 100 105 110

Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr Val Arg Ala Lys
 115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Val Glu His Ile His Lys
 130 135 140

Ile Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
 145 150 155 160

Ala Lys His Leu Arg Asp Glu Gln Asn Arg Asn Lys Ala Arg Lys Gln
 165 170 175

eolf-seql

Glu Leu Arg Lys Arg Glu Lys Glu Arg Glu Arg Ala Arg Arg Asp Asp
180 185 190

Ala Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Ala Ala Lys Lys Ser
195 200 205

Ala Ala Ser Ala Ala Lys Ser Ala Ala Pro Ala Ala Lys Ser Ala Ala
210 215 220

Pro Ala Ala Lys Val Ala Ala Pro Ala Thr Lys Gly Ala Ala Pro Val
225 230 235 240

Lys Lys Ser Lys Lys
245

<210> 20
<211> 738
<212> DNA
<213> Leishmania donovani

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gtgcgcaagc tgatcaagga tggcttcac atccgcaagc cgggtgaaggt gcaactcgcgc 180
gcgcggtggc gtaaaatgaa ggaggcgaag gacatggggc gccacaacgg cgttggccgc 240
cgcgagggta gccgcgaggc ccgcatgccg agcaaggagt tgtggatgcg ccgcctgcgc 300
attctgcgcc gcctgctgcg caagtaccgc gcggacaaga agatcgaccg ccacgtgtac 360
cgagacctgt acgtgcgcgc gaagggtaat gtgttcgcga acaagcgcaa cttgtggag 420
cacatccaca agatcaagaa tgagaagaag aaggagcgcc agctggcgga gcagcttgcg 480
gcgaagcacc tgcgcgacga gcagaaccgc aacaaggctc gcaagcagga gctgaggaag 540
cgcgagaagg agcgcgagcg cgcgaggcgc gacgacgctg ctgccgctgc gcagaagaag 600
aaggcggacg ccgcgaagaa gtctgccgcg tctgctgcga agtctgccgc gcctgctgcg 660
aagtctgccg cgctgcccgc gaaggttgct gccccgccca cgaagggtgc tgcgccggtg 720
aagaagtcga agaagtaa 738

<210> 21
<211> 372
<212> PRT
<213> Trypanosoma cruzi

<400> 21

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ala Asp Ile Leu Arg
1 5 10 15

Cys Gly Arg His Arg Val Trp Leu Asp Pro Asn Glu Ala Ser Glu Ile
20 25 30

eolf-seql

Ser Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

Leu Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ser Arg Trp Arg
50 55 60

His Met Lys Glu Ala Lys Ser Met Gly Arg His Glu Gly Ala Gly Arg
65 70 75 80

Arg Glu Gly Thr Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Glu Glu
100 105 110

Lys Lys Ile Asp Arg His Ile Tyr Arg Glu Leu Tyr Val Lys Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His Lys
130 135 140

Val Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys Arg Leu Lys Asp Glu Gln His Arg His Lys Ala Arg Lys Gln
165 170 175

Glu Leu Arg Lys Arg Glu Lys Asp Arg Glu Arg Ala Arg Arg Glu Asp
180 185 190

Ala Ala Ala Ala Ala Ala Ala Lys Gln Lys Ala Ala Ala Lys Lys Ala
195 200 205

Ala Ala Pro Ser Gly Lys Lys Ser Ala Lys Ala Ala Thr Ala Pro Ala
210 215 220

Lys Ala Ala Ala Ala Pro Ala Lys Ala Ala Ala Pro Ala Lys Ala
225 230 235 240

Ala Ala Ala Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys Ala Ala Ala
245 250 255

Ala Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala Ala Ala Pro
260 265 270

Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys
275 280 285

Ala Ala Ala Ala Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala
290 295 300

eolf-seql

Ala Ala Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala Ala Ala
305 310 315 320

Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala Ala Ala Pro Ala
325 330 335

Lys Ala Ala Ala Ala Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala
340 345 350

Ala Thr Ala Pro Ala Lys Ala Ala Thr Ala Pro Val Gly Lys Lys Ala
355 360 365

Gly Gly Lys Lys
370

<210> 22
<211> 1119
<212> DNA
<213> Trypanosoma cruzi

<400> 22
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gtgcgcaagt tgatcaagga tggcttgatt attcgcaagc ctgtcaaggt gcactcgcg 180
tcccgtggc gccacatgaa ggaggcgaag agcatgggcc gccacgaggg cgctggg 240
cgcgagggta cccgcgaagc ccgcatgccg agcaaggagc tgtggatgcg ccgtctg 300
attctccgcc gcctgctgcg caagtaccgc gaggagaaga agattgaccg ccacatctac 360
cgcgagctgt acgtgaaggc gaaggggaac gtgtttcgca acaagcgtaa cctcatggag 420
cacatccaca aggtgaagaa cgagaagaag aaggaaaggc agctggctga gcagctcg 480
gcgaagcgcc tgaaggatga gcagcaccgt cacaaggccc gcaagcagga gctgcgtaag 540
cgcgagaagg accgcgagcg tgcgcgtcgc gaagatgctg ccgctgccgc cgccggaag 600
cagaaagctg ctgcgaagaa ggccgctgct ccctctggca agaagtccgc gaaggctgct 660
actgcacctg cgaaggccgc tgctgcacct gcgaaggccg ctgctgcacc tgcgaaggct 720
gctgctgcac ctgcgaaggc tgctgctgca cctgcgaagg ctgctgctgc acctgcgaag 780
gctgctactg cacctgcgaa ggccgctgct gcacctgcga aggtgctac tgcacctg 840
aaggccgctg ctgcacctgc gaaggctgct gctgcacctg cgaaggctgc tactgcacct 900
gcgaaggccg ctgctgcacc tgcgaaggct gctactgcac ctgcgaaggc cgctgctgca 960
cctgcgaagg ctgctactgc acctgcgaag gccgctgctg cacctgcgaa ggccgctgct 1020
gcacctgcga aggtgctac tgcacctg 1080
actgcacccg ttggaagaa ggctggtggc aagaagtga 1119

<210> 23
<211> 356

eofl-seql

<212> PRT

<213> Trypanosoma cruzi

<400> 23

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ala Asp Ile Leu Arg
1 5 10 15

Cys Gly Arg His Arg Val Trp Leu Asp Pro Asn Glu Ala Ser Glu Ile
20 25 30

Ser Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

Leu Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ser Arg Trp Arg
50 55 60

His Met Lys Glu Ala Lys Ser Met Gly Arg His Glu Gly Ala Gly Arg
65 70 75 80

Arg Glu Gly Thr Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Glu Glu
100 105 110

Lys Lys Ile Asp Arg His Ile Tyr Arg Glu Leu Tyr Val Lys Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His Lys
130 135 140

Val Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys Arg Leu Lys Asp Glu Gln His Arg His Lys Ala Arg Lys Gln
165 170 175

Glu Leu Arg Lys Arg Glu Lys Asp Arg Glu Arg Ala Arg Arg Glu Asp
180 185 190

Ala Ala Ala Ala Ala Ala Lys Gln Lys Ala Ala Ala Lys Lys Ala
195 200 205

Ala Ala Pro Ser Gly Lys Lys Ser Ala Lys Ala Ala Ala Pro Ala Lys
210 215 220

Ala Ala Ala Ala Pro Ala Lys Ala Ala Ala Pro Pro Ala Lys Thr Ala
225 230 235 240

Ala Ala Pro Ala Lys Ala Ala Ala Pro Ala Lys Ala Ala Ala Pro Pro
245 250 255

eolf-seql

Ala Lys Ala Ala Ala Pro Pro Ala Lys Thr Ala Ala Pro Pro Ala Lys
260 265 270

Thr Ala Ala Pro Pro Ala Lys Ala Ala Ala Pro Pro Ala Lys Ala Ala
275 280 285

Ala Pro Pro Ala Lys Ala Ala Ala Pro Pro Ala Lys Ala Ala Ala Ala
290 295 300

Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys Ala Ala Ala Pro Pro Ala
305 310 315 320

Lys Ala Ala Ala Pro Pro Ala Lys Ala Ala Ala Pro Pro Ala Lys Ala
325 330 335

Ala Ala Pro Pro Ala Lys Ala Ala Ala Ala Pro Val Gly Lys Lys Ala
340 345 350

Gly Gly Lys Lys
355

<210> 24
<211> 1071
<212> DNA
<213> Trypanosoma cruzi

<400> 24
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gtgcgcaagt tgatcaagga tggctctgatt attcgcaagc ctgtcaaggt gcactcgcgc 180
tcccgtggc gccacatgaa ggaggcgaag agcatgggcc gccacgaggg cgctgggcgc 240
cgcgagggta cccgcgaagc ccgcatgccg agcaaggagc tgtggatgcg ccgtctgcgc 300
attctccgcc gcctgtctgc caagtaccgc gaggagaaga agattgaccg ccacatttac 360
cgcgagctgt acgtgaaggc gaaggggaac gtgtttcgca acaagcgtaa cctcatggag 420
cacatccaca aggtgaagaa cgagaagaag aaggaaaggc agctggctga gcagctcgcg 480
gcgaagcgcc tgaaggatga gcagcaccgt cacaaggccc gcaagcagga gctgcgtaag 540
cgcgagaagg accgcgagcg tgcgcgtcgc gaagatgctg ccgctgccgc cgccgcgaag 600
cagaaagctg ctgcgaagaa ggccgtgct ccctctggca agaagtccgc gaaggctgct 660
gcacccgcga aggctgtgc tgcacccgcg aaggccgctg ctccacccgc gaagaccgct 720
gctgcacccg cgaaggctgc tgcacctgcc aaggctgctg ctccacccgc gaaggctgct 780
gctccacccg cgaagaccgc tgctccacc gcgaagaccg ctgctccacc cgcaaggct 840
gctgtccac ccgcgaaggc cgctgtcca cccgcgaagg ccgctgtcc accgcgaag 900
gccgtgtg caccgcgaa ggccgtgct gcacccgcga aggtgtgtgc tccacccgcg 960
aaggccgctg ctccacccgc gaaggctgct gctccacccg cgaaggctgc tgctccacc 1020

eolf-seql

gcgaaggctg ctgctgctcc cgttggaaag aaggctggtg gcaagaagtg a

1071

<210> 25
<211> 343
<212> PRT
<213> Trypanosoma crusi

<400> 25

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ala Asp Ile Leu Arg
1 5 10 15

Cys Gly Arg His Arg Val Trp Leu Asp Pro Asn Glu Ala Ser Glu Ile
20 25 30

Ser Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

Leu Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ser Arg Trp Arg
50 55 60

His Met Lys Glu Ala Lys Ser Met Gly Arg His Glu Gly Ala Gly Arg
65 70 75 80

Arg Glu Gly Thr Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Glu Glu
100 105 110

Lys Lys Ile Asp Arg His Ile Tyr Arg Glu Leu Tyr Val Lys Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His Lys
130 135 140

Val Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys Arg Leu Lys Asp Glu Gln His Arg His Lys Ala Arg Lys Gln
165 170 175

Glu Leu Arg Lys Arg Glu Lys Asp Arg Glu Arg Ala Arg Arg Glu Asp
180 185 190

Ala Ala Ala Ala Ala Ala Lys Gln Lys Ala Ala Ala Lys Lys Ala
195 200 205

Ala Ala Pro Ser Gly Lys Lys Ser Ala Lys Ala Ala Ile Ala Pro Ala
210 215 220

Lys Ala Ala Ala Ala Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys Ala

eof-seq1

225 230 235 240

Ala Ala Ala Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys Ala Ala Ala
 245 250 255

Ala Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala Ala Ala Pro
 260 265 270

Ala Lys Thr Ala Ala Ala Pro Ala Lys Ala Ala Ala Pro Ala Lys Ala
 275 280 285

Ala Ala Ala Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala Ala
 290 295 300

Ala Pro Ala Lys Ala Ala Thr Ala Pro Ala Lys Ala Ala Thr Ala Pro
 305 310 315 320

Ala Lys Ala Ala Ala Ala Pro Ala Lys Ala Ala Thr Ala Pro Val Gly
 325 330 335

Lys Lys Ala Gly Gly Lys Lys
 340

<210> 26
 <211> 1032
 <212> DNA
 <213> Trypanosoma cruzi

<400> 26
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 gtgcgcaagt tgatcaagga tggctctgatt attcgcaagc ctgtcaagggt gcaactcgcg 180
 tcccgctggc gccacatgaa ggaggcgaag agcatgggcc gccacgaggg cgctgggcg 240
 cgcgagggta cccgcgaagc ccgcatgccg agcaaggagc tgtggatgcg ccgtctcgcg 300
 attctccgcc gcctgctgcg caagtaccgc gaggagaaga agattgaccg ccacatctac 360
 cgcgagctgt acgtgaaggc gaaggggaac gtgtttcgca acaagcgtaa cctcatggag 420
 cacatccaca aggtgaagaa cgagaagaag aaggaaaggc agctggctga gcagctcgcg 480
 gcgaagcgcc tgaaggatga gcagcaccgt cacaaggccc gcaagcagga gctgcgtaag 540
 cgcgagaagg accgcgagcg tgcgcgtcgc gaagatgctg ccgctgccgc cgccgcgaag 600
 cagaaagctg ctgcgaagaa ggccgctgct ccctctggca agaagtccgc gaaggctgct 660
 attgcacctg cgaaggccgc tgctgcacct gcgaaggccg ctgctgcacc tgcgaaggct 720
 gctgctgcac ctgcgaaggc cgctgctgca cctgcgaagg ctgctgctgc acctgcgaag 780
 gctgctactg cacctgcgaa ggctgctgct gcacctgcca agaccgctgc tgcacctgcg 840
 aaggctgctg cacctgcgaa ggccgctgct gcacctgcga aggccgctac tgcacctgcg 900
 aaggctgctg ctgcacctgc gaaggccgct actgcacctg cgaaggctgc tactgcacct 960

eolf-seql

gcgaaggctg ctgctgcacc tgcgaaggcc gctactgcac ccgttggaag gaaggctggt 1020
ggcaagaagt ga 1032

<210> 27
<211> 357
<212> PRT
<213> Trypanosoma cruzi

<400> 27

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ala Asp Ile Leu Arg
1 5 10 15

Cys Gly Arg His Arg Val Trp Leu Asp Pro Asn Glu Ala Ser Glu Ile
20 25 30

Ser Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

Leu Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ser Arg Trp Arg
50 55 60

His Met Lys Glu Ala Lys Ser Met Gly Arg His Glu Gly Ala Gly Arg
65 70 75 80

Arg Glu Gly Thr Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Glu Glu
100 105 110

Lys Lys Ile Asp Arg His Ile Tyr Arg Glu Leu Tyr Val Lys Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His Lys
130 135 140

Val Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys Arg Leu Lys Asp Glu Gln His Arg His Lys Ala Arg Lys Gln
165 170 175

Glu Leu Arg Lys Arg Glu Lys Asp Arg Glu Arg Ala Arg Arg Glu Asp
180 185 190

Ala Ala Ala Ala Ala Ala Lys Gln Lys Ala Ala Ala Lys Lys Ala
195 200 205

Ala Ala Pro Ser Gly Lys Lys Ser Ala Lys Ala Ala Ala Pro Ala Lys
210 215 220

eolf-seql

Ala Ala Ala Ala Pro Ala Lys Thr Ala Ala Pro Pro Ala Lys Ala Ala
225 230 235 240

Ala Pro Pro Ala Lys Ala Ala Ala Pro Pro Ala Lys Ala Ala Ala Pro
245 250 255

Pro Ala Lys Ala Ala Ala Pro Pro Ala Lys Ala Ala Ala Pro Pro Ala
260 265 270

Lys Ala Ala Ala Pro Pro Ala Lys Ala Ala Ala Pro Pro Ala Lys Ala
275 280 285

Ala Ala Pro Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys Thr Ala Ala
290 295 300

Pro Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys Thr Ala Ala Pro Pro
305 310 315 320

Ala Lys Thr Ala Ala Pro Pro Ala Lys Ala Ala Thr Pro Pro Ala Lys
325 330 335

Ala Ala Ala Pro Pro Ala Lys Ala Ala Ala Ala Pro Val Gly Lys Lys
340 345 350

Ala Gly Gly Lys Lys
355

<210> 28
<211> 1074
<212> DNA
<213> Trypanosoma cruzi

<400> 28
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gtgcgcaagt tgatcaagga tggctctgatt attcgcaagc ctgtcaaggt gcaactcgcg 180
tcccgcgtggc gccacatgaa ggaggcgaag agcatgggcc gccacgaggg cgctgggcg 240
cgcgagggtta cccgcgaagc ccgcatgccg agcaaggagc tgtggatgcg ccgtctgcgc 300
attctccgcc gcctgctgcg caagtaccgc gaggagaaga agattgaccg ccacatttac 360
cgcgagctgt acgtgaaggc gaaggggaac gtgtttcgca acaagcgtaa cctcatggag 420
cacatccaca aggtgaagaa cgagaagaag aaggaaaggc agctggctga gcagctcgcg 480
gcgaagcgcc tgaaggatga gcagcaccgt cacaaggccc gcaagcagga gctgcgtaag 540
cgcgagaagg accgcgagcg tgcgcgtcgc gaagatgctg ccgctgccgc cgccgcgaag 600
cagaaagctg ctgcgaagaa ggccgctgct ccctctggca agaagtccgc gaaggctgct 660
gcacctgcca aggctgctgc tgcacccgcg aagaccgctg ctccaccgcg gaaggccgct 720
gctccacccg cgaaggctgc tgctccacc gcgaaggctg ctgctccacc cgcgaggct 780

eof-seq1

gctgctccac ccgcgaaggc tgctgctcca ccgcgaagg ctgctgctcc acccgcaag 840
gctgctgctc caccgcgaa ggctgctgct ccaccgcga aggtgctgc tgcaccgcg 900
aagaccgctg ctccaccgc gaaggctgct gctgcaccgc cgaagaccgc tgctccacc 960
gcgaagaccg ctgctccacc cgcgaaggcc gctactccac ccgcgaaggc tgctgctcca 1020
ccgcgaagg ctgctgctgc tcccgttga aagaaggctg gtggcaagaa gtga 1074

<210> 29
<211> 260
<212> PRT
<213> Trypanosoma brucei

<400> 29

Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala Ala Asp Ile Leu Arg
1 5 10 15

Cys Gly Arg Gly Arg Val Trp Leu Asp Pro Asn Glu Ala Val Glu Ile
20 25 30

Arg Asn Ala Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly
35 40 45

Leu Val Met Arg Lys Pro Val Lys Val His Ser Arg Ser Arg Trp Arg
50 55 60

Gln Met Lys Leu Ala Lys Ser Met Gly Arg His Glu Gly Thr Gly Arg
65 70 75 80

Arg Glu Gly Thr Arg Glu Ala Arg Met Pro Ser Lys Asp Leu Trp Met
85 90 95

Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu Arg Lys Tyr Arg Glu Glu
100 105 110

Lys Lys Ile Asp Arg His Ile Tyr Arg Glu Leu Tyr Met Lys Ala Lys
115 120 125

Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Met Glu His Ile His Lys
130 135 140

Val Lys Asn Glu Lys Lys Lys Ala Arg Gln Leu Ala Glu Gln Leu Ala
145 150 155 160

Ala Lys Arg Leu Lys Asp Glu Gln Asn Arg Arg Lys Ala Arg Lys Gln
165 170 175

Glu Leu Lys Lys Arg Glu Lys Glu Arg Glu Arg Ala Arg Arg Asp Asp
180 185 190

Ala Ala Ala Ala Ala Ala Lys Gln Arg Ala Ala Ala Lys Lys Ala

eolf-seql

195

200

205

Ala Ala Pro Ala Ala Lys Lys Gly Gly Lys Ala Val Ala Pro Ala Thr
210 215 220

Pro Ala Lys Ala Ala Pro Ala Lys Ala Ala Ala Lys Val Ala Pro
225 230 235 240

Ala Lys Ala Ala Pro Ala Lys Ala Ala Ser Pro Ala Gly Lys Lys Ala
245 250 255

Ala Gly Lys Lys
260

<210> 30
<211> 783
<212> DNA
<213> Trypanosoma brucei

<400> 30
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cgcggtgtggt tggaccctaa cgaagcagta gagattcgca atgccaattc acgcaagagt 120
gtacgcaagt tgatcaaaga cggtttggtgta atgcgaaagc ctgttaaggt gcattcgcg 180
tcccgcgtggc gccagatgaa gttggcgaag agcatgggac gccacgaggg taccggccgc 240
cgcgaggggta ctcgcaagc acgcatgccc agcaaggacc tttggatgcg ccgacttcgc 300
attcttcgcc gtttgcttcg caagtaccgc gaagaaaaga agattgatcg gcacatctac 360
cgcgagctgt acatgaaggc aaagggcaac gtgttccgca acaagcgcaa ccttatggag 420
cacatccaca aggtgaagaa cgagaagaag aaggctcgtc agcttgctga gcaactcgcg 480
gcgaaacgcc taaaggacga gcagaaccgc cgcaaggcac gaaagcagga gctgaagaag 540
cgtgagaagg aacgtgagcg tgcacgccgt gacgatgccg ctgctgctgc cgctgccaaa 600
caacgagctg ccgcaagaa ggctgccgt cccgctgcc aagaagggtg caaggctgtt 660
gcccccgcca ctctgcgaa ggccgccct gcaaaggccg ccgctgcaaa ggttgcccca 720
gcgaaggcgg ctcccgcaaa ggccgccagc cctgccggga agaaggcagc gggtaagaag 780
tga 783

<210> 31
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 1

<400> 31

Met Thr Pro Leu Ser Leu Ser Ser Ser Arg His Ser Phe Lys Gln Asn
1 5 10 15

eolf-seql

Glu Thr Gln Asn
20

<210> 32
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 2

<400> 32

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

Ala Arg Leu Ala
20

<210> 33
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 3

<400> 33

Ser Leu Lys Leu Gln Ala Arg Leu Ala Ser Ser Ile Leu Gly Cys Gly
1 5 10 15

Arg Ala Arg Val
20

<210> 34
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 4

<400> 34

Ile Leu Gly Cys Gly Arg Ala Arg Val Trp Leu Asp Pro Asn Glu Ala
1 5 10 15

Val Glu Ile Gln
20

<210> 35
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 5

<400> 35

eolf-seql

Asp Pro Asn Glu Ala Val Glu Ile Gln Asn Ala Asn Ser Arg Lys Ser
1 5 10 15

Val Arg Lys Leu
20

<210> 36
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 6

<400> 36

Asn Ser Arg Lys Ser Val Arg Lys Leu Ile Lys Asp Gly Phe Ile Ile
1 5 10 15

Arg Lys Pro Val
20

<210> 37
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 7

<400> 37

Asp Gly Phe Ile Ile Arg Lys Pro Val Lys Val His Ser Arg Ala Arg
1 5 10 15

Trp Arg Lys Met
20

<210> 38
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 8

<400> 38

His Ser Arg Ala Arg Trp Arg Lys Met Lys Glu Ala Lys Asp Met Gly
1 5 10 15

Arg His Asn Gly
20

<210> 39
<211> 20
<212> PRT
<213> artificial

<220>

eolf-seql

<223> peptide 9

<400> 39

Ala Lys Asp Met Gly Arg His Asn Gly Val Gly Arg Arg Glu Gly Ser
1 5 10 15

Arg Glu Ala Arg
20

<210> 40

<211> 20

<212> PRT

<213> artificial

<220>

<223> peptide 10

<400> 40

Arg Arg Glu Gly Ser Arg Glu Ala Arg Met Pro Ser Lys Glu Leu Trp
1 5 10 15

Met Arg Arg Leu
20

<210> 41

<211> 20

<212> PRT

<213> artificial

<220>

<223> peptide 11

<400> 41

Ser Lys Glu Leu Trp Met Arg Arg Leu Arg Ile Leu Arg Arg Leu Leu
1 5 10 15

Arg Lys Tyr Arg
20

<210> 42

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<400> 42

Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp Lys Lys Ile Asp Arg
1 5 10 15

His Val Tyr Arg
20

<210> 43

<211> 20

eolf-seql

<212> PRT
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<220>
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<400> 43

Lys Lys Ile Asp Arg His Val Tyr Arg Asp Leu Tyr Met Arg Ala Lys
1 5 10 15

Gly Asn Val Phe
20

<210> 44
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<220>
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<400> 44

Tyr Met Arg Ala Lys Gly Asn Val Phe Arg Asn Lys Arg Asn Leu Val
1 5 10 15

Glu His Ile His
20

<210> 45
<211> 20
<212> PRT
<213> artificial

<220>
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<400> 45

Lys Arg Asn Leu Val Glu His Ile His Lys Ile Lys Asn Glu Lys Lys
1 5 10 15

Lys Glu Arg Gln
20

<210> 46
<211> 20
<212> PRT
<213> artificial

<220>
<223> peptide 16

<400> 46

Lys Asn Glu Lys Lys Lys Glu Arg Gln Leu Ala Glu Gln Leu Ala Ala
1 5 10 15

Lys His Leu Arg
20

eolf-seql

<210> 47
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<220>
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<400> 47

Glu Gln Leu Ala Ala Lys His Leu Arg Asp Glu Gln Asn Arg Asn Lys
 1 5 10 15

Ala Arg Lys Gln
 20

<210> 48
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<220>
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<400> 48

Gln Asn Arg Asn Lys Ala Arg Lys Gln Glu Leu Lys Lys Arg Glu Lys
 1 5 10 15

Glu Arg Glu Arg
 20

<210> 49
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<220>
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<400> 49

Lys Lys Arg Glu Lys Glu Arg Glu Arg Ala Arg Arg Asp Asp Ala Ala
 1 5 10 15

Ala Ala Ala Gln
 20

<210> 50
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<220>
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<400> 50

Arg Asp Asp Ala Ala Ala Ala Gln Lys Lys Lys Ala Asp Ala Ala
 1 5 10 15

eolf-seql

Lys Lys Ser Ala
20

<210> 51
<211> 20
<212> PRT
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<220>
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<400> 51

Lys Ala Asp Ala Ala Lys Lys Ser Ala Ala Pro Ala Ala Lys Ser Ala
1 5 10 15

Ala Pro Ala Ala
20

<210> 52
<211> 20
<212> PRT
<213> artificial

<220>
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<400> 52

Ala Ala Lys Ser Ala Ala Pro Ala Ala Lys Ala Ala Ala Pro Ala Thr
1 5 10 15

Lys Ala Ala Ala
20

<210> 53
<211> 20
<212> PRT
<213> artificial

<220>
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<400> 53

Ala Ala Pro Ala Thr Lys Ala Ala Ala Ala Ala Pro Ala Thr Lys Gly
1 5 10 15

Ala Ala Pro Val
20

<210> 54
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<220>
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eolf-seql

<400> 54

Pro Ala Thr Lys Gly Ala Ala Pro Val Lys Lys Ser Lys Lys
1 5 10

<210> 55

<211> 31

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<220>

<223> peptide 1-2

<400> 55

Met Thr Pro Leu Ser Leu Ser Ser Ser Arg His Ser Phe Lys Gln Asn
1 5 10 15

Glu Thr Gln Asn Met Val Ser Leu Lys Leu Gln Ala Arg Leu Ala
20 25 30

<210> 56

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<400> 56

Leu Arg Arg Leu Leu Arg Lys Tyr Arg Ala Asp Lys Lys Ile Asp Arg
1 5 10 15

His Val Tyr Arg Asp Leu Tyr Met Arg Ala Lys Gly Asn Val Phe Arg
20 25 30

Asn Lys Arg Asn Leu Val Glu His Ile His
35 40

<210> 57

<211> 25

<212> PRT

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<220>

<223> peptide 23-24

<400> 57

Ala Ala Pro Ala Thr Lys Ala Ala Ala Ala Ala Pro Ala Thr Lys Gly
1 5 10 15

Ala Ala Pro Val Lys Lys Ser Lys Lys
20 25