

SEQUENCE LISTING

<110> Lonza Ltd.

<120> novel tools for the production of glycosylated proteins in host cells

<130> 202148

<160> 61

<170> PatentIn version 3.4

<210> 1

<211> 1359

<212> DNA

<213> *Saccharomyces cerevisiae*

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<212> PRT

<213> *Saccharomyces cerevisiae*

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35 40 45

Asn Ser Gln Leu Thr Ala Ser Phe Phe Asp Val Lys Phe Tyr Pro Asp
50 55 60

Asn Asn Thr Val Ile Phe Asp Ile Asp Ala Thr Thr Thr Leu Asn Gly
65 70 75 80

Asn Val Thr Val Lys Ala Glu Leu Leu Thr Tyr Gly Leu Lys Val Leu
85 90 95

Asp Lys Thr Phe Asp Leu Cys Ser Leu Gly Gln Val Ser Leu Ser Pro
100 105 110

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Glu	Thr	Pro	Leu	Ala	Cys	Val	Gln	Ala	Ile	Leu	Ser	Asn	Gly	Lys	Thr	165	170	175
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Leu	Leu	Ala	Ile	Trp	Glu	Phe	Thr	Gln	Val	Asn	Ser	Pro	Ala	Ile	Val	420	425	430
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<212> DNA

<213> *Saccharomyces cerevisiae*

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<213> *Saccharomyces cerevisiae*

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 Ala Ala His Ile Ala Ser Asn Ser Ile Ser Leu Phe Ile Tyr Phe Gln
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 Asn Leu Ala Ile Thr Ala Met Met Gly Val Ser Arg Val Pro Pro Ile
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 325 330 335
 Val Ala Tyr Leu Ala Asn Ile Glu Leu Ser Asn Phe Phe Leu Thr Gly
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<213> *Saccharomyces cerevisiae*

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 35 40 45
 Asn Ser Gln Leu Thr Ala Ser Phe Phe Asp Val Lys Phe Tyr Pro Asp
 50 55 60
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 65 70 75 80
 Asn Val Thr Val Lys Ala Glu Leu Leu Thr Tyr Gly Leu Lys Val Leu
 85 90 95
 Asp Lys Thr Phe Asp Leu Cys Ser Leu Gly Gln Val Ser Leu Ser Pro
 100 105 110
 Leu Ser Ala Gly Arg Ile Asp Val Met Ser Thr Gln Val Ile Glu Ser
 115 120 125
 Ser Ile Thr Lys Gln Phe Pro Gly Ile Ala Tyr Thr Ile Pro Asp Leu
 130 135 140
 Asp Ala Gln Val Arg Val Val Ala Tyr Ala Gln Asn Asp Thr Glu Phe
 145 150 155 160
 Glu Thr Pro Leu Ala Cys Val Gln Ala Ile Leu Ser Asn Gly Lys Thr
 165 170 175
 Val Gln Thr Lys Tyr Ala Ala Trp Pro Ile Ala Ala Ile Ser Gly Val
 180 185 190
 Gly Val Leu Thr Ser Gly Phe Val Ser Val Ile Gly Tyr Ser Ala Thr
 195 200 205
 Ala Ala His Ile Ala Ser Asn Ser Ile Ser Leu Phe Ile Tyr Phe Gln
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<212> PRT

<213> *Saccharomyces cerevisiae*

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Asn Ser Ile Ser Leu Phe Ile Tyr Phe Gln Asn Leu Ala Ile Thr Ala
35 40 45

Met Met Gly Val Ser Arg Val Pro Pro Ile Ala Ala Ala Trp Thr Gln
50 55 60

Asn Phe Gln Trp Ser Met Gly Ile Ile Asn Thr Asn Phe Met Gln Lys
65 70 75 80

Ile Phe Asp Trp Tyr Val Gln Ala Thr Asn Gly Val Ser Asn Val Val
85 90 95

Val Ala Asn Lys Asp Val Leu Ser Ile Ser Val Gln Lys Arg Ala Ile
100 105 110

Ser Met Ala Ser Ser Ser Asp Tyr Asn Phe Asp Thr Ile Leu Asp Asp
115 120 125

Ser Asp Leu Tyr Thr Thr Ser Glu Lys Asp Pro Ser Asn Tyr Ser Ala
130 135 140

Lys Ile Leu Val Leu Arg Gly Ile Glu Arg Val Ala Tyr Leu Ala Asn
145 150 155 160

Ile Glu Leu Ser Asn Phe Phe Leu Thr Gly Ile Val Phe Phe Leu Phe
165 170 175

Phe Leu Phe Val Val Val Val Ser Leu Ile Phe Phe Lys Ala Leu Leu
180 185 190

Glu Val Leu Thr Arg Ala Arg Ile Leu Lys Glu Thr Ser Asn Phe Phe
195 200 205

Gln Tyr Arg Lys Asn Trp Gly Ser Ile Ile Lys Gly Thr Leu Phe Arg
210 215 220

Leu Ser Ile Ile Ala Phe Pro Gln Val Ser Leu Leu Ala Ile Trp Glu
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265

270

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 35 40 45
 Leu Ile Phe Phe Lys Ala Leu Leu Glu Val Leu Thr Arg Ala Arg Ile
 50 55 60
 Leu Lys Glu Thr Ser Asn Phe Phe Gln Tyr Arg Lys Asn Trp Gly Ser
 65 70 75 80
 Ile Ile Lys Gly Thr Leu Phe Arg Leu Ser Ile Ile Ala Phe Pro Gln
 85 90 95
 Val Ser Leu Leu Ala Ile Trp Glu Phe Thr Gln Val Asn Ser Pro Ala
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Ala Ser Ala Lys His Leu Gln Thr Thr Ser Leu Leu Thr Cys Met Asp
          35          40          45

Asn Ser Gln Leu Thr Ala Ser Phe Phe Asp Val Lys Phe Tyr Pro Asp
          50          55          60

Asn Asn Thr Val Ile Phe Asp Ile Asp Ala Thr Thr Thr Leu Asn Gly
65          70          75          80

Asn Val Thr Val Lys Ala Glu Leu Leu Thr Tyr Gly Leu Lys Val Leu
          85          90          95

Asp Lys Thr Phe Asp Leu Cys Ser Leu Gly Gln Val Ser Leu Ser Pro
          100          105          110

Leu Ser Ala Gly Arg Ile Asp Val Met Ser Thr Gln Val Ile Glu Ser
          115          120          125

Ser Ile Thr Lys Gln Phe Pro Gly Ile Ala Tyr Thr Ile Pro Asp Leu
          130          135          140

Asp Ala Gln Val Arg Val Val Ala Tyr Ala Gln Asn Asp Thr Glu Phe
145          150          155          160

Glu Thr Pro Leu Ala Cys Val Gln Ala Ile Leu Ser Asn Gly Lys Thr
          165          170          175

Val Gln Thr Lys Tyr Ala Ala Trp Pro Ile Ala Ala Ile Ser Gly Val
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Gly Val Leu Thr Ser Gly Phe Val Ser Val Ile Gly Tyr Ser
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<213> Saccharomyces cerevisiae
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Asn Ser Ile Ser Leu Phe Ile Tyr Phe Gln Asn Leu Ala Ile Thr Ala
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 50 55 60

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<212> DNA

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<211> 53

<212> PRT

<213> *Saccharomyces cerevisiae*

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 20 25 30

Thr Gly Ile Val Phe Phe Leu Phe Phe Leu Phe Val Val Val Val Ser
 35 40 45

Leu Ile Phe Phe Lys
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<210> 17

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<212> DNA

<213> *Saccharomyces cerevisiae*

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<212> PRT

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<213> Leishmania braziliensis

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<213> Leishmania braziliensis

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19

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<212> PRT
<213> Leishmania braziliensis
<400> 36

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 Glu Ile Gln Glu Met Leu Ala His Arg Val Pro Phe Asp Gln Met Gly
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 <213> Leishmania braziliensis
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<211> 854

<212> PRT

<213> *Leishmania brucei*

<400> 38

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Leu Thr Asp Glu Glu Glu Phe Val Gly Ile Phe Pro Cys Pro Phe Trp
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Pro Val Arg Phe Val Ile Thr Val Met Ala Leu Val Leu Leu Gly Ala
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Ser Cys Ile Arg Ala Phe Thr Ile Arg Met Leu Ser Val Gln Leu Tyr
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Gly Tyr Ile Ile His Glu Phe Asp Pro Trp Phe Asn Tyr Arg Ala Ala
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Glu Tyr Met Ser Ala His Gly Trp Ser Ala Phe Phe Ser Trp Phe Asp
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Tyr Met Ser Trp Tyr Pro Leu Gly Arg Pro Val Gly Thr Thr Thr Tyr
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Pro Gly Leu Gln Leu Thr Ala Val Ala Ile His Arg Ala Leu Ala Ala
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Ala Gly Val Pro Met Ser Leu Asn Asn Val Cys Val Leu Ile Pro Ala
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Trp Tyr Gly Ala Ile Ala Thr Ala Ile Leu Ala Leu Cys Ala Tyr Glu
180 185 190

Val Ser Arg Ser Met Val Ala Ala Ala Val Ala Ala Leu Ser Phe Ser
195 200 205

Ile Ile Pro Ala His Leu Met Arg Ser Met Ala Gly Glu Phe Asp Asn
210 215 220

Glu Cys Ile Ala Val Ala Ala Met Leu Leu Thr Phe Tyr Leu Trp Val
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Arg Ser Leu Arg Thr Arg Cys Ser Trp Pro Ile Gly Ile Leu Thr Gly
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Ile Ala Tyr Gly Tyr Met Val Ala Ala Trp Gly Gly Tyr Ile Phe Val
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Leu Asn Met Val Ala Met His Ala Gly Ile Ser Ser Met Val Asp Trp
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 His Pro Ala Ser Pro Glu Ala Met Trp Thr Phe Leu His Val Cys Gly
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 660 665 670
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<211> 2592

<212> DNA

<213> Leishmania infantum

<400> 39

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<211> 863

<212> PRT

<213> *Leishmania infantum*

<400> 40

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Asp Gly Ala Ala Val Asp Ser Ser Val Pro Pro Ser Gly Glu Thr Tyr
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Leu Phe His Cys Arg Ala Ala Pro Tyr Ser Lys Leu Ser Tyr Ala Phe
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Lys Gly Ile Met Ala Val Leu Ile Leu Cys Ala Leu Arg Ser Ala Tyr
65 70 75 80

Gln Val Arg Leu Leu Ser Val Gln Ile Tyr Gly Tyr Leu Ile His Glu
85 90 95

Phe Asp Pro Trp Phe Asn Tyr Arg Ala Ala Glu Tyr Met Ser Thr His
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Gly Trp Ser Ala Phe Phe Ser Trp Phe Asp Tyr Met Ser Trp Tyr Pro
115 120 125

Leu Gly Arg Pro Val Gly Ser Thr Thr Tyr Pro Gly Leu Gln Leu Thr
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Ala	Val	Ala	Ile	His	Arg	Ala	Leu	Ala	Ala	Ala	Gly	Met	Pro	Met	Ser	145	150	155	160
Leu	Asn	Asn	Val	Cys	Val	Leu	Met	Pro	Ala	Trp	Phe	Gly	Ala	Ile	Ala	165	170		175
Thr	Ala	Thr	Leu	Ala	Leu	Ile	Ala	Phe	Glu	Val	Ser	Glu	Ser	Ile	Cys	180	185		190
Met	Ala	Ala	Trp	Ala	Ala	Leu	Ser	Phe	Ser	Ile	Ile	Pro	Ala	His	Leu	195	200		205
Met	Arg	Ser	Met	Ala	Gly	Glu	Phe	Asp	Asn	Glu	Cys	Ile	Ala	Val	Ala	210	215		220
Ala	Met	Leu	Leu	Thr	Phe	Tyr	Cys	Trp	Val	Arg	Ser	Leu	Arg	Thr	Arg	225	230		235
Ser	Ser	Trp	Pro	Ile	Gly	Val	Leu	Thr	Gly	Val	Ala	Tyr	Gly	Tyr	Met	245	250		255
Val	Ala	Ala	Trp	Gly	Gly	Tyr	Ile	Phe	Val	Leu	Asn	Met	Val	Ala	Met	260	265		270
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Ala	Tyr	Leu	Asn	Tyr	Leu	His	Ile	Val	Tyr	Phe	Met	Trp	Ile	Phe	Ser	420	425		430
Phe	Pro	Val	Gln	Leu	Ile	Leu	Pro	Ser	Arg	Asn	Gln	Tyr	Ala	Val	Leu	435	440		445
Phe	Val	Phe	Val	Tyr	Ser	Phe	Met	Ala	Tyr	Tyr	Phe	Ser	Thr	Arg	Met	450	455		460
Val	Arg	Leu	Leu	Ile	Leu	Ala	Gly	Pro	Ala	Ala	Cys	Leu	Gly	Ala	Ser	465	470		475
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 Phe His Phe Ser Cys Val Ser Ser Ala Tyr Ser Phe Ala Gly Pro Arg
 595 600 605
 Ile Val Phe Gln Thr Gln Leu Arg Thr Gly Glu Gln Val Ile Val Lys
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 Asp Tyr Leu Glu Ala Tyr Glu Trp Leu Arg Asp Asn Thr Pro Glu Asp
 625 630 635 640
 Ala Arg Ile Leu Ala Trp Trp Asp Tyr Gly Tyr Gln Ile Thr Gly Ile
 645 650 655
 Gly Asn Arg Thr Ser Leu Ala Asp Gly Asn Thr Trp Asn His Glu His
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 Ile Ala Thr Ile Gly Lys Met Leu Thr Ser Pro Val Ala Glu Ala His
 675 680 685
 Ser Leu Val Arg His Met Ala Asp Tyr Val Leu Ile Trp Ala Gly Gln
 690 695 700
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 Val Tyr His Asp Ile Cys Pro His Asp Pro Leu Cys Gln Gln Phe Gly
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 Phe Tyr Arg Asn Asp Tyr Ser Arg Pro Thr Pro Met Met Arg Ala Ser
 740 745 750
 Leu Leu Tyr Asn Leu His Glu Val Gly Lys Thr Lys Gly Val Lys Val
 755 760 765
 Asp Pro Ser Leu Phe Gln Glu Val Tyr Ser Ser Lys Tyr Gly Leu Val
 770 775 780
 Arg Val Phe Lys Val Met Asn Val Ser Glu Glu Ser Lys Lys Trp Val
 785 790 795 800
 Ala Asp Pro Ala Asn Arg Val Cys His Pro Pro Gly Ser Trp Ile Cys
 805 810 815

Pro Gly Gln Tyr Pro Pro Ala Lys Glu Ile Gln Glu Met Leu Ala His
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Arg Val Pro Phe Asp Gln Val Gly Lys Asp Lys Lys Asp Lys Glu Ala
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<211> 2355

<212> DNA

<213> Leishmania infantum

<400> 41

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<211> 784

<212> PRT

<213> Leishmania infantum

<400> 42

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Gly	Trp	Ser	Ala	Phe	Phe	Ser	Trp	Phe	Asp	Tyr	Met	Ser	Trp	Tyr	Pro	50	55	60
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Ala	Val	Ala	Ile	His	Arg	Ala	Leu	Ala	Ala	Ala	Gly	Met	Pro	Met	Ser	85	90	95
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Ala	Met	Leu	Leu	Thr	Phe	Tyr	Cys	Trp	Val	Arg	Ser	Leu	Arg	Thr	Arg	165	170	175
Ser	Ser	Trp	Pro	Ile	Gly	Val	Leu	Thr	Gly	Val	Ala	Tyr	Gly	Tyr	Met	180	185	190
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His	Ala	Gly	Ile	Ser	Ser	Met	Val	Asp	Trp	Ala	Arg	Asn	Thr	Tyr	Asn	210	215	220
Pro	Ser	Leu	Leu	Arg	Ala	Tyr	Thr	Leu	Phe	Tyr	Val	Val	Gly	Thr	Ala	225	230	235
Ile	Ala	Val	Cys	Val	Pro	Pro	Val	Gly	Met	Ser	Pro	Phe	Lys	Ser	Leu	245	250	255
Glu	Gln	Leu	Gly	Ala	Leu	Leu	Val	Leu	Val	Phe	Leu	Cys	Gly	Leu	Gln	260	265	270
Ala	Cys	Glu	Val	Phe	Arg	Ala	Arg	Ala	Gly	Val	Glu	Val	Arg	Ser	Arg	275	280	285
Ala	Asn	Phe	Lys	Ile	Arg	Val	Arg	Val	Phe	Ser	Val	Met	Ala	Gly	Val	290	295	300
Ala	Ala	Leu	Ala	Ile	Ala	Val	Leu	Ala	Pro	Thr	Gly	Tyr	Phe	Gly	Pro	305	310	315
Leu	Ser	Val	Arg	Val	Arg	Ala	Leu	Phe	Val	Glu	His	Thr	Arg	Thr	Gly	325	330	335
Asn	Pro	Leu	Val	Asp	Ser	Val	Ala	Glu	His	Arg	Lys	Thr	Ser	Pro	Glu			

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Arg	Ile	Val	Phe	Gln	Thr	Gln	Leu	Arg	Thr	Gly	Glu	Gln	Val	Ile	Val
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Lys	Asp	Tyr	Leu	Glu	Ala	Tyr	Glu	Trp	Leu	Arg	Asp	Asn	Thr	Pro	Glu
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Asp	Ala	Arg	Ile	Leu	Ala	Trp	Trp	Asp	Tyr	Gly	Tyr	Gln	Ile	Thr	Gly
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Ile	Gly	Asn	Arg	Thr	Ser	Leu	Ala	Asp	Gly	Asn	Thr	Trp	Asn	His	Glu
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His	Ile	Ala	Thr	Ile	Gly	Lys	Met	Leu	Thr	Ser	Pro	Val	Ala	Glu	Ala
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Gln	Ser	Gly	Asp	Leu	Met	Lys	Ser	Pro	His	Met	Ala	Arg	Ile	Gly	Asn
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Ser	Val	Tyr	His	Asp	Ile	Cys	Pro	His	Asp	Pro	Leu	Cys	Gln	Gln	Phe
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Gly	Phe	Tyr	Arg	Asn	Asp	Tyr	Ser	Arg	Pro	Thr	Pro	Met	Met	Arg	Ala
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Ser Leu Leu Tyr Asn Leu His Glu Val Gly Lys Thr Lys Gly Val Lys
675 680 685

Val Asp Pro Ser Leu Phe Gln Glu Val Tyr Ser Ser Lys Tyr Gly Leu
690 695 700

Val Arg Val Phe Lys Val Met Asn Val Ser Glu Glu Ser Lys Lys Trp
705 710 715 720

Val Ala Asp Pro Ala Asn Arg Val Cys His Pro Pro Gly Ser Trp Ile
725 730 735

Cys Pro Gly Gln Tyr Pro Pro Ala Lys Glu Ile Gln Glu Met Leu Ala
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His Arg Val Pro Phe Asp Gln Met Gly Lys Asp Lys Lys Asp Lys Glu
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<210> 43

<211> 2382

<212> DNA

<213> Leishmania infantum

<400> 43

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<211> 794

<212> PRT

<213> Leishmania infantum

<400> 44

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Ser Thr Thr Tyr Pro Gly Leu Gln Leu Thr Ala Val Ala Ile His Arg
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Ala Leu Ala Ala Ala Gly Met Pro Met Ser Leu Asn Asn Val Cys Val
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Leu Met Pro Ala Trp Phe Ser Leu Val Ser Ser Ala Met Val Ala Leu
115 120 125

Leu Ala His Glu Leu Ser Gly Asn Met Ala Val Ala Ser Ile Ser Ser
130 135 140

Ile Leu Phe Ser Val Ile Pro Ala His Leu Met Arg Ser Met Ala Gly
145 150 155 160

Glu Phe Asp Asn Glu Cys Ile Ala Val Ala Ala Met Leu Leu Thr Phe
165 170 175

Tyr Cys Trp Val Arg Ser Leu Arg Thr Arg Ser Ser Trp Pro Ile Gly
180 185 190

Val Leu Thr Gly Val Ala Tyr Gly Tyr Met Val Ala Ala Trp Gly Gly
195 200 205

Tyr Ile Phe Val Leu Asn Met Val Ala Met His Ala Gly Ile Ser Ser
210 215 220

Met Val Asp Trp Ala Arg Asn Thr Tyr Asn Pro Ser Leu Leu Arg Ala
225 230 235 240

Tyr Thr Leu Phe Tyr Val Val Gly Thr Ala Ile Ala Val Cys Val Pro
245 250 255

Pro Val Gly Met Ser Pro Phe Lys Ser Leu Glu Gln Leu Gly Ala Leu
260 265 270

Leu Val Leu Leu Phe Ile Phe Gly Gln Ser Val Cys Glu Ala Gln Arg
275 280 285

Arg	Arg	Leu	Glu	Ile	Ala	Arg	Phe	Ser	Lys	Glu	Gly	Val	Ala	Leu	Leu	290	295	300
Ile	Arg	Ile	Tyr	Ala	Ala	Phe	Phe	Val	Gly	Ile	Val	Ala	Val	Ala	Thr	305	310	315
Ile	Ala	Pro	Ala	Gly	Phe	Phe	Lys	Pro	Leu	Ser	Leu	Gln	Ala	Ser	Ala	325	330	335
Ile	Ile	Thr	Gly	Val	Ser	Arg	Thr	Gly	Asn	Thr	Leu	Val	Asp	Thr	Leu	340	345	350
Ile	Ala	Gln	Asp	Ala	Ser	Asn	Leu	Leu	Ile	Val	Trp	Gln	Leu	Phe	Leu	355	360	365
Phe	Pro	Val	Phe	Gly	Trp	Val	Ala	Gly	Met	Ser	Ala	Phe	Leu	Thr	Glu	370	375	380
Leu	Val	Arg	Asn	Tyr	Thr	Tyr	Thr	Lys	Ser	Phe	Met	Leu	Met	Tyr	Gly	385	390	395
Val	Val	Gly	Leu	Tyr	Phe	Ala	Ser	Gln	Ser	Val	Arg	Met	Met	Val	Met	405	410	415
Met	Ala	Pro	Val	Ala	Cys	Ile	Phe	Thr	Ala	Leu	Leu	Phe	Arg	Trp	Ala	420	425	430
Leu	Asp	Tyr	Leu	Leu	Gly	Ser	Leu	Phe	Trp	Ala	Glu	Met	Pro	Pro	Cys	435	440	445
Phe	Asp	Thr	Asp	Ala	Gln	Arg	Gly	Arg	Gln	Gln	Gln	Thr	Ala	Glu	Glu	450	455	460
Ala	Glu	Ala	Glu	Thr	Lys	Arg	Lys	Glu	Glu	Glu	Tyr	Asn	Thr	Met	Gln	465	470	475
Val	Lys	Lys	Met	Thr	Thr	Arg	Met	Leu	Pro	Phe	Met	Phe	Leu	Leu	Leu	485	490	495
Leu	Phe	Arg	Leu	Ser	Gly	Phe	Ile	Glu	Asp	Val	Ala	Ala	Ile	Ser	Arg	500	505	510
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Val	Ser	Glu	Lys	Lys	Val	Asp	Asp	Tyr	Tyr	Ser	Gly	Tyr	Leu	Tyr	Leu	530	535	540
Arg	Asp	Asn	Thr	Pro	Glu	Asp	Ala	Arg	Ile	Leu	Ala	Trp	Trp	Asp	Tyr	545	550	555
Gly	Tyr	Gln	Ile	Thr	Gly	Ile	Gly	Asn	Arg	Thr	Ser	Leu	Ala	Asp	Gly	565	570	575
Asn	Thr	Trp	Asn	His	Glu	His	Ile	Ala	Thr	Ile	Gly	Lys	Met	Leu	Thr	580	585	590
Ser	Pro	Val	Ala	Glu	Ala	His	Ser	Leu	Val	Arg	His	Met	Ala	Asp	Tyr	595	600	605
Val	Leu	Ile	Phe	Ala	Gly	Asp	Thr	Tyr	Phe	Ser	Asp	Leu	Asn	Arg	Ser	610	615	620

Pro His Met Ala Arg Ile Gly Asn Ser Val Tyr Arg Asp Ile Cys Pro
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His Asp Pro Leu Cys Ser Arg Phe Val Leu Gln Lys Arg Pro Lys Ala
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Ala Ala Ala Lys Arg Ser Arg His Val Ser Val Asp Glu Leu Glu Glu
660 665 670

Glu Asp Asn Ala Glu His Val Val Tyr Glu Pro Ser Ser Leu Met Ala
675 680 685

Lys Ser Leu Ile Tyr His Leu His Ser Ala Gly Val Val Lys Gly Val
690 695 700

Thr Leu Asn Glu Thr Leu Phe Gln His Val Phe Thr Ser Ala Gln Gly
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Leu Ile Arg Ile Phe Lys Val Met Asn Val Ser Glu Glu Ser Lys Lys
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Trp Val Ala Asp Pro Ala Asn Arg Val Cys His Pro Pro Gly Ser Trp
740 745 750

Ile Cys Pro Gly Gln Tyr Pro Pro Ala Lys Glu Ile Gln Glu Met Leu
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<212> DNA

<213> Leishmania infantum

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<212> PRT

<213> Leishmania infantum

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Asp	Gly	Ala	Ala	Val	Asp	Ser	Thr	Leu	Pro	Pro	Ser	Asp	Glu	Thr	Tyr
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Leu	Phe	His	Cys	Arg	Ala	Ala	Pro	Tyr	Ser	Lys	Leu	Ser	Tyr	Ala	Phe
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Lys	Gly	Ile	Met	Thr	Val	Leu	Ile	Leu	Cys	Ala	Ile	Arg	Ser	Ala	Tyr
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Gln	Val	Arg	Leu	Ile	Ser	Val	Gln	Ile	Tyr	Gly	Tyr	Leu	Ile	His	Glu
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Phe	Asp	Pro	Trp	Phe	Asn	Tyr	Arg	Ala	Ala	Glu	Tyr	Met	Ser	Thr	His
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Gly	Trp	Ser	Ala	Phe	Phe	Ser	Trp	Phe	Asp	Tyr	Met	Ser	Trp	Tyr	Pro
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Leu	Gly	Arg	Pro	Val	Gly	Ser	Thr	Thr	Tyr	Pro	Gly	Leu	Gln	Leu	Thr
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Ala	Val	Ala	Ile	His	Arg	Ala	Leu	Ala	Ala	Ala	Gly	Met	Pro	Met	Ser
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Leu	Asn	Asn	Val	Cys	Val	Leu	Met	Pro	Ala	Trp	Phe	Gly	Ala	Ile	Ala
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Thr	Ala	Thr	Leu	Ala	Leu	Ile	Ala	Phe	Glu	Val	Ser	Glu	Ser	Ile	Cys
			180					185					190		

Met	Ala	Ala	Trp	Ala	Ala	Leu	Ser	Phe	Ser	Ile	Ile	Pro	Ala	His	Leu
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Met	Arg	Ser	Met	Ala	Gly	Glu	Phe	Asp	Asn	Glu	Cys	Ile	Ala	Val	Ala
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Ala	Met	Leu	Leu	Thr	Phe	Tyr	Cys	Trp	Val	Arg	Ser	Leu	Arg	Thr	Arg
225					230					235					240
Ser	Ser	Trp	Pro	Ile	Gly	Val	Leu	Thr	Gly	Val	Ala	Tyr	Gly	Tyr	Met
				245					250					255	
Ala	Ala	Ala	Trp	Gly	Gly	Tyr	Ile	Phe	Val	Leu	Asn	Met	Val	Ala	Met
			260					265					270		
His	Ala	Gly	Ile	Ser	Ser	Met	Val	Asp	Trp	Ala	Arg	Asn	Thr	Tyr	Asn
		275					280					285			
Pro	Ser	Leu	Leu	Arg	Ala	Tyr	Thr	Leu	Phe	Tyr	Val	Val	Gly	Thr	Ala
	290					295					300				
Ile	Ala	Val	Cys	Val	Pro	Pro	Val	Gly	Met	Ser	Pro	Phe	Lys	Ser	Leu
305					310					315					320
Glu	Gln	Leu	Gly	Ala	Leu	Leu	Val	Leu	Val	Phe	Leu	Cys	Gly	Leu	Gln
				325					330					335	
Val	Cys	Glu	Val	Leu	Arg	Ala	Arg	Ala	Gly	Val	Glu	Val	Arg	Ser	Arg
			340					345					350		
Ala	Asn	Phe	Lys	Ile	Arg	Val	Arg	Val	Phe	Ser	Val	Met	Ala	Gly	Val
		355					360					365			
Ala	Ala	Leu	Ala	Ile	Ser	Val	Leu	Ala	Pro	Thr	Gly	Tyr	Phe	Gly	Pro
		370				375					380				
Leu	Ser	Val	Arg	Val	Arg	Ala	Leu	Phe	Val	Glu	His	Thr	Arg	Thr	Gly
385					390					395					400
Asn	Pro	Leu	Val	Asp	Ser	Val	Ala	Glu	His	His	Pro	Ala	Asp	Ala	Leu
				405					410				415		
Ala	Tyr	Leu	Asn	Tyr	Leu	His	Ile	Val	His	Leu	Met	Trp	Ile	Cys	Ser
			420					425					430		
Leu	Pro	Val	Gln	Leu	Ile	Leu	Pro	Ser	Arg	Asn	Gln	Tyr	Ala	Val	Leu
		435					440					445			
Phe	Val	Leu	Val	Tyr	Ser	Phe	Met	Ala	Tyr	Tyr	Phe	Ser	Thr	Arg	Met
	450					455					460				
Val	Arg	Leu	Leu	Ile	Leu	Ala	Gly	Pro	Val	Ala	Cys	Leu	Gly	Ala	Ser
465					470					475					480
Glu	Val	Gly	Gly	Thr	Leu	Met	Glu	Trp	Cys	Phe	Gln	Gln	Leu	Phe	Trp
				485					490					495	
Asp	Asn	Gly	Met	Arg	Thr	Ala	Asp	Met	Val	Ala	Ala	Gly	Asp	Met	Pro
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Tyr	Gln	Lys	Asp	Asp	His	Thr	Ser	Arg	Gly	Ala	Gly	Ala	Arg	Gln	Lys
		515					520					525			

Gln Gln Lys Gln Lys Pro Gly Gln Val Ser Ala Arg Gly Ser Ser Thr
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 Ser Ser Glu Glu Arg Pro Tyr Arg Thr Leu Ile Pro Val Asp Phe Arg
 545 550 555 560
 Arg Asp Ala Gln Met Asn Arg Trp Ser Ala Gly Lys Thr Asn Ala Ala
 565 570 575
 Leu Ile Val Ala Leu Thr Ile Gly Val Leu Leu Pro Leu Ala Phe Val
 580 585 590
 Phe His Leu Ser Cys Ile Ser Ser Ala Tyr Ser Phe Ala Gly Pro Arg
 595 600 605
 Ile Val Phe Gln Thr Gln Leu His Thr Gly Glu Gln Val Ile Val Lys
 610 615 620
 Asp Tyr Leu Glu Ala Tyr Glu Trp Leu Arg Asp Ser Thr Pro Glu Asp
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 Ala Arg Val Leu Ala Trp Trp Asp Tyr Gly Tyr Gln Ile Thr Gly Ile
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 Gly Asn Arg Thr Ser Leu Ala Asp Gly Asn Thr Trp Asn His Glu His
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 Ile Ala Thr Ile Gly Lys Met Leu Thr Ser Pro Val Ala Glu Ala His
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 Ser Leu Val Arg His Met Ala Asp Tyr Val Leu Ile Trp Ala Gly Gln
 690 695 700
 Ser Gly Asp Leu Met Lys Ser Pro His Met Ala Arg Ile Gly Asn Ser
 705 710 715 720
 Val Tyr His Asp Ile Cys Pro Asp Asp Pro Leu Cys Gln Gln Phe Gly
 725 730 735
 Phe His Arg Asn Asp Tyr Ser Arg Pro Thr Pro Met Met Arg Ala Ser
 740 745 750
 Leu Leu Tyr Asn Leu His Glu Ala Gly Lys Thr Lys Gly Val Lys Val
 755 760 765
 Asn Pro Ser Leu Phe Gln Glu Val Tyr Ser Ser Lys Tyr Gly Leu Val
 770 775 780
 Arg Ile Phe Lys Val Met Asn Val Ser Ala Glu Ser Lys Lys Trp Val
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 Ala Asp Pro Ala Asn Arg Val Cys His Pro Pro Gly Ser Trp Ile Cys
 805 810 815
 Pro Gly Gln Tyr Pro Pro Ala Lys Glu Ile Gln Glu Met Leu Ala His
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 His His Lys Ala
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 Phe Asp Pro Trp Phe Asn Tyr Arg Ala Ala Glu Tyr Met Ser Thr His
 35 40 45
 Gly Trp Ser Ala Phe Phe Ser Trp Phe Asp Tyr Met Ser Trp Tyr Pro
 50 55 60

Leu	Gly	Arg	Pro	Val	Gly	Ser	Thr	Thr	Tyr	Pro	Gly	Leu	Gln	Leu	Thr	65	70	75	80
Ala	Val	Ala	Ile	His	Arg	Ala	Leu	Ala	Ala	Ala	Gly	Met	Pro	Met	Ser		85	90	95
Leu	Asn	Asn	Val	Cys	Val	Leu	Met	Pro	Ala	Trp	Phe	Gly	Ala	Ile	Ala	100	105		110
Thr	Ala	Thr	Leu	Ala	Leu	Met	Thr	Tyr	Glu	Met	Ser	Gly	Ser	Gly	Ile	115	120		125
Ala	Ala	Ala	Ile	Ala	Ala	Phe	Ile	Phe	Ser	Ile	Ile	Pro	Ala	His	Leu	130	135		140
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Ser	Ser	Trp	Pro	Ile	Gly	Val	Leu	Thr	Gly	Val	Ala	Tyr	Gly	Tyr	Met	180	185		190
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Glu	Gln	Leu	Gly	Ala	Leu	Leu	Val	Leu	Val	Phe	Leu	Cys	Gly	Leu	Gln		260	265	270
Val	Cys	Glu	Val	Leu	Arg	Ala	Arg	Ala	Gly	Val	Glu	Val	Arg	Ser	Arg	275	280		285
Ala	Asn	Phe	Lys	Ile	Arg	Val	Arg	Val	Phe	Ser	Val	Met	Ala	Gly	Val	290	295		300
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Leu	Ser	Val	Arg	Val	Arg	Ala	Leu	Phe	Val	Glu	His	Thr	Arg	Thr	Gly		325	330	335
Asn	Pro	Leu	Val	Asp	Ser	Val	Ala	Glu	His	Arg	Met	Thr	Ser	Pro	Lys	340	345		350
Ala	Tyr	Ala	Phe	Phe	Leu	Asp	Phe	Thr	Tyr	Pro	Val	Trp	Leu	Leu	Gly	355	360		365
Thr	Val	Leu	Gln	Leu	Leu	Gly	Ala	Phe	Met	Gly	Ser	Arg	Lys	Glu	Ala	370	375		380
Arg	Leu	Phe	Met	Gly	Leu	His	Ser	Leu	Ala	Thr	Tyr	Tyr	Phe	Ala	Asp	385	390	395	400

Arg	Met	Ser	Arg	Leu	Ile	Val	Leu	Ala	Gly	Pro	Ala	Ala	Ala	Ala	Met	405	410	415
Thr	Ala	Gly	Ile	Leu	Gly	Leu	Val	Tyr	Glu	Trp	Cys	Trp	Ala	Gln	Leu	420	425	430
Thr	Gly	Trp	Ala	Ser	Pro	Gly	Leu	Ser	Ala	Ala	Gly	Ser	Gly	Gly	Met	435	440	445
Asp	Asp	Phe	Asp	Asn	Lys	Arg	Gly	Gln	Thr	Gln	Ile	Gln	Ser	Ser	Thr	450	455	460
Ala	Asn	Arg	Asn	Arg	Gly	Val	Arg	Ala	His	Ala	Ile	Ala	Ala	Val	Lys	465	470	475
Ser	Ile	Lys	Ala	Gly	Val	Asn	Leu	Leu	Pro	Leu	Val	Leu	Arg	Val	Gly	485	490	495
Val	Ala	Val	Ala	Ile	Leu	Ala	Val	Thr	Val	Gly	Thr	Pro	Tyr	Val	Ser	500	505	510
Gln	Phe	Gln	Ala	Arg	Cys	Ile	Gln	Ser	Ala	Tyr	Ser	Phe	Ala	Gly	Pro	515	520	525
Arg	Ile	Val	Phe	Gln	Ala	Gln	Leu	His	Thr	Gly	Glu	Gln	Val	Ile	Val	530	535	540
Lys	Asp	Tyr	Leu	Glu	Ala	Tyr	Glu	Trp	Leu	Arg	Asp	Ser	Thr	Pro	Glu	545	550	555
Asp	Ala	Arg	Val	Leu	Ala	Trp	Trp	Asp	Tyr	Gly	Tyr	Gln	Ile	Thr	Gly	565	570	575
Ile	Gly	Asn	Arg	Thr	Ser	Leu	Ala	Asp	Gly	Asn	Thr	Trp	Asn	His	Glu	580	585	590
His	Ile	Ala	Thr	Ile	Gly	Lys	Met	Leu	Thr	Ser	Pro	Val	Ala	Glu	Ala	595	600	605
His	Ser	Leu	Val	Arg	His	Met	Ala	Asp	Tyr	Val	Leu	Ile	Trp	Ala	Gly	610	615	620
Gln	Ser	Gly	Asp	Leu	Met	Lys	Ser	Pro	His	Met	Ala	Arg	Ile	Gly	Asn	625	630	635
Ser	Val	Tyr	His	Asp	Ile	Cys	Pro	Asp	Asp	Pro	Leu	Cys	Gln	Gln	Phe	645	650	655
Gly	Phe	His	Arg	Asn	Asp	Tyr	Ser	Arg	Pro	Thr	Pro	Met	Met	Arg	Ala	660	665	670
Ser	Leu	Leu	Tyr	Asn	Leu	His	Glu	Ala	Gly	Lys	Thr	Lys	Gly	Val	Lys	675	680	685
Val	Asn	Pro	Ser	Leu	Phe	Gln	Glu	Val	Tyr	Ser	Ser	Lys	Tyr	Gly	Leu	690	695	700
Val	Arg	Ile	Phe	Lys	Val	Met	Asn	Val	Ser	Ala	Glu	Ser	Lys	Lys	Trp	705	710	715
Val	Ala	Asp	Pro	Ala	Asn	Arg	Val	Cys	His	Pro	Pro	Gly	Ser	Trp	Ile	725	730	735

Cys Pro Gly Gln Tyr Pro Pro Ala Lys Glu Ile Gln Glu Met Leu Ala
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His Arg Val Pro Phe Asp Gln Met Asp Lys His Lys Gln His Lys Glu
755 760 765

Thr His His Lys Ala
770

<210> 49
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<212> DNA
<213> Leishmania infantum
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<210> 50
<211> 790
<212> PRT
<213> Leishmania infantum
<400> 50

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

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 355 360 365
 Phe Pro Phe Leu Gly Trp Val Ala Gly Met Ser Ala Phe Leu Arg Glu
 370 375 380
 Leu Ile Arg Asn Tyr Thr Tyr Ala Lys Ser Phe Ile Leu Met Tyr Gly
 385 390 395 400
 Val Val Gly Met Tyr Phe Ala Ser Gln Ser Val Arg Met Met Val Met
 405 410 415
 Met Ala Pro Val Ala Cys Ile Phe Thr Ala Leu Leu Phe Arg Trp Ala
 420 425 430
 Leu Asp Tyr Leu Leu Gly Ser Leu Phe Trp Ala Glu Met Pro Pro Ser
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 Phe Asp Thr Asp Ala Gln Arg Gly Arg Gln Gln Gln Thr Ala Glu Glu
 450 455 460
 Ser Glu Ala Glu Thr Lys Arg Lys Glu Glu Glu Tyr Asn Thr Met Gln
 465 470 475 480
 Val Lys Lys Met Ser Val Arg Met Leu Pro Phe Met Leu Leu Leu Leu
 485 490 495
 Leu Phe Arg Leu Ser Gly Phe Ile Glu Asp Val Ala Ala Ile Ser Arg
 500 505 510
 Lys Met Glu Ala Pro Gly Ile Val Phe Pro Ser Glu Gln Val Gln Gly
 515 520 525
 Val Ser Glu Lys Lys Val Asp Asp Tyr Tyr Ala Gly Tyr Leu Tyr Leu
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 Arg Asp Ser Thr Pro Glu Asp Ala Arg Val Leu Ala Trp Trp Asp Tyr
 545 550 555 560
 Gly Tyr Gln Ile Thr Gly Ile Gly Asn Arg Thr Ser Leu Ala Asp Gly
 565 570 575
 Asn Thr Trp Asn His Glu His Ile Ala Thr Ile Gly Lys Met Leu Thr
 580 585 590
 Ser Pro Val Ala Glu Ala His Ser Leu Val Arg His Met Ala Asp Tyr
 595 600 605
 Val Leu Ile Ser Ala Gly Asp Thr Tyr Phe Ser Asp Leu Asn Arg Ser
 610 615 620
 Pro Met Met Ala Arg Ile Gly Asn Ser Val Tyr His Asp Ile Cys Pro
 625 630 635 640
 Asp Asp Pro Leu Cys Ser Gln Phe Val Leu Gln Lys Arg Pro Lys Ala
 645 650 655
 Ala Ala Ala Lys Arg Ser Arg His Val Ser Val Asp Ala Leu Glu Glu
 660 665 670
 Asp Asp Thr Ala Glu His Met Val Tyr Glu Pro Ser Ser Leu Ile Ala
 675 680 685

Lys Ser Leu Ile Tyr His Leu His Ser Thr Gly Val Val Thr Gly Val
 690 695 700
 Thr Leu Asn Glu Thr Leu Phe Gln His Val Phe Thr Ser Pro Gln Gly
 705 710 715 720
 Leu Met Arg Ile Phe Lys Val Met Asn Val Ser Thr Glu Ser Lys Lys
 725 730 735
 Trp Val Ala Asp Ser Ala Asn Arg Val Cys His Pro Pro Gly Ser Trp
 740 745 750
 Ile Cys Pro Gly Gln Tyr Pro Pro Ala Lys Glu Ile Gln Glu Met Leu
 755 760 765
 Ala His Gln His Thr Asn Phe Lys Asp Leu Leu Asp Pro Arg Thr Thr
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 Trp Ser Gly Ser Arg Arg
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<210> 51

<211> 2574

<212> DNA

<213> *Leishmania infantum*

<400> 51

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<210> 52

<211> 857

<212> PRT

<213> Leishmania infantum

<400> 52

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Thr Lys Thr Ala Ser Pro Pro Ala Lys Val Ile Leu Leu Pro Lys Thr
35          40          45

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Leu Thr Asp Glu Lys Asp Phe Ile Gly Ile Phe Pro Phe Pro Phe Trp
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Pro Val His Phe Val Leu Thr Val Val Ala Leu Phe Val Leu Ala Ala
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Ser Cys Phe Gln Ala Phe Thr Val Arg Met Ile Ser Val Gln Ile Tyr
85          90          95

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Gly Tyr Leu Ile His Glu Phe Asp Pro Trp Phe Asn Tyr Arg Ala Ala
100         105         110

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Glu Tyr Met Ser Thr His Gly Trp Ser Ala Phe Phe Ser Trp Phe Asp
115         120         125

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Tyr Met Ser Trp Tyr Pro Leu Gly Arg Pro Val Gly Ser Thr Thr Tyr
130         135         140

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Pro Gly Leu Gln Leu Thr Ala Val Ala Ile His Arg Ala Leu Ala Ala
145         150         155         160

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Ala Gly Met Pro Met Ser Leu Asn Asn Val Cys Val Leu Met Pro Ala
165         170         175

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Trp Phe Gly Ala Ile Ala Thr Ala Thr Leu Ala Phe Cys Thr Tyr Glu
180         185         190

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Ala Ser Gly Ser Thr Val Ala Ala Ala Ala Ala Ala Leu Ser Phe Ser
195         200         205

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Ile Ile Pro Ala His Leu Met Arg Ser Met Ala Gly Glu Phe Asp Asn
210         215         220

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Glu Cys Ile Ala Val Ala Ala Met Leu Leu Thr Phe Tyr Cys Trp Val
225         230         235         240

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Arg Ser Leu Arg Thr Arg Ser Ser Trp Pro Ile Gly Val Leu Thr Gly
245         250         255

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Val Ala Tyr Gly Tyr Met Ala Ala Ala Trp Gly Gly Tyr Ile Phe Val
260         265         270

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Leu Asn Met Val Ala Met His Ala Gly Ile Ser Ser Met Val Asp Trp
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 Ala Arg Asn Thr Tyr Asn Pro Ser Leu Leu Arg Ala Tyr Thr Leu Phe
 290 295 300
 Tyr Val Val Gly Thr Ala Ile Ala Val Cys Val Pro Pro Val Gly Met
 305 310 315 320
 Ser Pro Phe Lys Ser Leu Glu Gln Leu Gly Ala Leu Leu Val Leu Val
 325 330 335
 Phe Leu Cys Gly Leu Gln Val Cys Glu Val Leu Arg Ala Arg Ala Gly
 340 345 350
 Val Glu Val Arg Ser Arg Ala Asn Phe Lys Ile Arg Val Arg Val Phe
 355 360 365
 Ser Val Met Ala Gly Val Ala Ala Leu Ala Ile Ser Val Leu Ala Pro
 370 375 380
 Thr Gly Tyr Phe Gly Pro Leu Ser Val Arg Val Arg Ala Leu Phe Val
 385 390 395 400
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 405 410 415
 Gln Pro Ala Ser Pro Glu Ala Met Trp Ala Phe Leu His Val Cys Gly
 420 425 430
 Val Thr Trp Gly Leu Gly Ser Ile Val Leu Ala Val Ser Thr Phe Val
 435 440 445
 His Tyr Ser Pro Ser Lys Val Phe Trp Leu Leu Asn Ser Gly Ala Val
 450 455 460
 Tyr Tyr Phe Ser Thr Arg Met Ala Arg Leu Leu Leu Leu Ser Gly Pro
 465 470 475 480
 Ala Ala Cys Leu Ser Thr Gly Ile Phe Val Gly Thr Ile Leu Glu Ala
 485 490 495
 Ala Val Gln Leu Ser Phe Trp Asp Ser Asp Ala Thr Lys Ala Lys Lys
 500 505 510
 Gln Gln Lys Gln Ala Gln Arg His Gln Arg Gly Ala Gly Lys Gly Ser
 515 520 525
 Gly Arg Asp Asp Ala Lys Asn Ala Thr Thr Ala Arg Ala Phe Cys Asp
 530 535 540
 Val Phe Ala Gly Ser Ser Leu Ala Trp Gly His Arg Met Val Leu Ser
 545 550 555 560
 Ile Ala Met Trp Ala Leu Val Thr Thr Thr Ala Val Ser Phe Phe Ser
 565 570 575
 Ser Glu Phe Ala Ser His Ser Thr Lys Phe Ala Glu Gln Ser Ser Asn
 580 585 590
 Pro Met Ile Val Phe Ala Ala Val Val Gln Asn Arg Ala Thr Gly Lys
 595 600 605

Pro Met Asn Leu Leu Val Asp Asp Tyr Leu Lys Ala Tyr Glu Trp Leu
 610 615 620
 Arg Asp Ser Thr Pro Glu Asp Ala Arg Val Leu Ala Trp Trp Asp Tyr
 625 630 635 640
 Gly Tyr Gln Ile Thr Gly Ile Gly Asn Arg Thr Ser Leu Ala Asp Gly
 645 650 655
 Asn Thr Trp Asn His Glu His Ile Ala Thr Ile Gly Lys Met Leu Thr
 660 665 670
 Ser Pro Val Ala Glu Ala His Ser Leu Val Arg His Met Ala Asp Tyr
 675 680 685
 Val Leu Ile Trp Ala Gly Gln Ser Gly Asp Leu Met Lys Ser Pro His
 690 695 700
 Met Ala Arg Ile Gly Asn Ser Val Tyr His Asp Ile Cys Pro Asp Asp
 705 710 715 720
 Pro Leu Cys Gln Gln Phe Gly Phe His Arg Asn Asp Tyr Ser Arg Pro
 725 730 735
 Thr Pro Met Met Arg Ala Ser Leu Leu Tyr Asn Leu His Glu Ala Gly
 740 745 750
 Lys Arg Lys Gly Val Lys Val Asn Pro Ser Leu Phe Gln Glu Val Tyr
 755 760 765
 Ser Ser Lys Tyr Gly Leu Val Arg Ile Phe Lys Val Met Asn Val Ser
 770 775 780
 Ala Glu Ser Lys Lys Trp Val Ala Asp Pro Ala Asn Arg Val Cys His
 785 790 795 800
 Pro Pro Gly Ser Trp Ile Cys Pro Gly Gln Tyr Pro Pro Ala Lys Glu
 805 810 815
 Ile Gln Glu Met Leu Ala His Arg Val Pro Phe Asp Gln Val Thr Asn
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 850 855

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<211> 2406

<212> DNA

<213> Trypanosoma brucei

<400> 53

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<213> Trypanosoma brucei
<400> 54

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35          40          45

Val Ser Thr Ile Val Ser Ala Val Ile Leu Ile Tyr Ser Val His Arg
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Ala Tyr Asp Ile Arg Leu Thr Ser Val Arg Leu Tyr Gly Glu Leu Ile
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His Glu Phe Asp Pro Trp Phe Asn Tyr Arg Ala Thr Gln Tyr Leu Ser
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Asp Asn Gly Trp Arg Ala Phe Phe Gln Trp Tyr Asp Tyr Met Ser Trp
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Tyr Pro Leu Gly Arg Pro Val Gly Thr Thr Ile Phe Pro Gly Met Gln
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Asn	Arg	Val	Cys	Asp	Pro	Pro	Gly	Ser	Trp	Ile	Cys	Ala	Gly	Gln	Tyr	770	775	780	
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<211> 2466
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<213> Trypanosoma brucei
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Pro	Val	Lys	Glu	Ser	His	Ala	Leu	Ile	Arg	His	Leu	Ala	Asp	Tyr	Val	645	650	655	
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<212> DNA

<213> Trypanosoma brucei

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<210> 58

<211> 821

<212> PRT

<213> Trypanosoma brucei

<400> 58

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Asn Asn Thr Pro Glu Asp Ala Arg Ile Leu Ser Trp Trp Asp Tyr Gly
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 Pro Val Lys Glu Ser His Ala Leu Ile Arg His Leu Ala Asp Tyr Val
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 Met Ala Arg Ile Gly Asn Ser Val Tyr Arg Asp Met Cys Ser Glu Asp
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 Asp Pro Leu Cys Thr Gln Phe Gly Phe Tyr Ser Gly Asp Phe Asn Lys
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 740 745 750
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 755 760 765
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 770 775 780
 Lys Glu Ile Gln Asp Met Leu Ala Lys Arg Ile Asp Tyr Glu Gln Leu
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<210> 59

<211> 2397

<212> DNA

<213> Trypanosoma cruzi

<400> 59

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<210> 60

<211> 798

<212> PRT

<213> Trypanosoma cruzi

<400> 60

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20              25              30

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Leu Ala Ile Tyr Arg Ala Tyr Ser Ile Arg Met Ile Ser Ile Arg Val
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Tyr Gly Lys Val Ile His Glu Phe Asp Pro Trp Phe Asn Phe Arg Ala
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Ser Glu Tyr Leu Asp Glu His Gly Trp Asp Ala Phe Phe His Trp Tyr
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Asp Tyr Met Ser Trp Tyr Pro Leu Gly Arg Pro Val Gly Thr Thr Ile
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Glu Thr Trp Gly Ser Phe Ser Gly Ala Ala Met Thr Ala Gly Leu Phe
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Trp	Met	Arg	Gly	Arg	Tyr	Asp	Ala	Ser	Leu	Leu	Trp	Ala	Tyr	Ser	Leu	
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Lys	Gly	Ser	Pro	Thr	Ile	Arg	Ser	Lys	Lys	Leu	Glu	Lys	Lys	Gly	His	
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Phe Ala Ala Leu Leu Phe Asn Pro Met Ala Arg Ser Tyr Asn Glu Asp
515 520 525

Ser Ile Lys Met Ala His Thr Leu Ser Asn Pro Arg Ile Met Trp Tyr
530 535 540

Ser Met Thr Glu Gln Asn Thr Pro Val Leu Val Asp Asp Tyr Tyr Val
545 550 555 560

Ser Tyr Leu Trp Leu Arg Asn Asn Thr Pro Ala Asp Ala Arg Ile Leu
565 570 575

Ala Trp Trp Asp Tyr Gly Tyr Gln Ile Thr Gly Ile Gly Asn Arg Thr
580 585 590

Ser Leu Ala Asp Gly Asn Thr Trp Asn His Glu His Ile Ala Thr Ile
595 600 605

Gly Lys Leu Leu Thr Ser Pro Val Ala Lys Ala His Leu Leu Ile Arg
610 615 620

His Leu Ala Asp Tyr Val Leu Ile Trp Thr Gly Ser Arg Ala Glu Asp
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Leu Met Lys Ser Pro His Met Ala Arg Ile Gly Asn Ser Val Tyr Arg
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Asp Ile Cys Pro Glu Asp Asp Pro Leu Cys Ser Asn Phe Gly Phe Glu
660 665 670

Asp Tyr Asp Leu Ser Arg Pro Thr Pro Met Met Arg Met Ser Leu Leu
675 680 685

Tyr Asn Leu His Val Ser Gly Glu Ser Pro Ser Pro Ala Ile Asp Asn
690 695 700

Met Phe Arg Leu Ala Tyr Arg Ser Arg His Gly Leu Val Lys Ile Tyr
705 710 715 720

Lys Val Met Asn Val Ser Ala Glu Ser Lys Ala Trp Val Ala Asp Pro
725 730 735

Lys Asn Arg Lys Cys Asp Ala Pro Gly Ser Trp Leu Cys Thr Gly Gln
740 745 750

Tyr Pro Pro Ala Lys Glu Ile Gln Glu Met Leu Ala Arg Arg Ile Asp
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<210> 61

<211> 402

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 61

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