

SEQUENCE LISTING

<110> DSM IP Assets B.V.
Jansen, Mickel
Verwaal, René

<120> Low pH dicarboxylic acid production

<130> 26725-WO-PCT

<160> 10

<170> PatentIn version 3.5

<210> 1

<211> 3148

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct TDH1p-PCKa-TDH1t for expression in *S. cerevisiae*

<400> 1

ggatcccttc ccttttacag tgcttcggaa aagcacagcg ttgtccaagg gaacaatttt	60
tcttcaagtt aatgcataag aaatatcttt ttttatgttt agctaagtaa aagcagcttg	120
gagtaaaaaa aaaaatgagt aaatttctcg atggattagt ttctcacagg taacataaca	180
aaaaccaaga aaagcccgct tctgaaaact acagttgact tgtatgctaa agggccagac	240
taatgggagg agaaaaagaa acgaatgtat atgctcattt acactctata tcaccatagt	300
gaggataagt tgggctgagc ttctgatcca atttattcta tccattagtt gctgatatgt	360
cccaccagcc aacacttgat agtatctact cgccattcac ttccagcagc gccagtaggg	420
ttgttgagct tagtaaaaat gtgcgcacca caagcctaca tgactccacg tcacatgaaa	480
ccacaccgtg gggccttggt gcgctaggaa taggatatgc gacgaagacg cttctgctta	540
gtaaccacac cacatthttca gggggctgat ctgcttgctt cctttactgt cacgagcggc	600
ccataatcgc gctthttttt taaaaggcgc gagacagcaa acaggaagct cgggtttcaa	660
ccttcggagt ggtcgcagat ctggagactg gatctttaca atacagtaag gcaagccacc	720
atctgcttct taggtgcatg cgacgggtatc cacgtgcaga acaacatagt ctgaagaagg	780
gggggaggag catgttcatt ctctgtagca gtaagagctt ggtgataatg accaaaactg	840
gagtctcgaa atcatataaa tagacaatat attttcacac aatgagattt gtagtacagt	900
tctattctct ctcttgcata aataagaaat tcatcaagaa cttggtttga tatttcacca	960
acacacacaa aaaacagtac ttcaactaaat ttacacacaa aacaaaatga ccgatttgaa	1020

ccaattgact caagaattgg gtgctttggg tattcacgat gtccaagaag ttgtctacaa	1080
cccatcttac gaattgttgt ttgctgaaga aaccaagcca ggtttggaag gttacgaaaa	1140
gggtactgtt accaaccaag gtgctgttgc tgtcaacacc ggtatcttca ccggtcgttc	1200
tccaaaggac aaatacattg tcttgatga caagaccaag gacactgtct ggtggacttc	1260
tgaaaaggtc aagaacgaca acaaaccaat gtcccaagac acttggaact ctttaaaggg	1320
tttagtcgct gaccaattgt ctggtgaagag attattcgtt gtcgatgctt tctgtggtgc	1380
caacaaggac accagattag ctgtcagagt tgtcactgaa gttgcttggc aagctcactt	1440
cgttaccaac atgttcatca gaccatctgc tgaagaattg aaaggtttca agccagattt	1500
cgttgtcatg aacggtgcca aatgtaccaa cccaaactgg aaggaacaag gtttgaactc	1560
tgaaaacttt gttgctttca acatcactga aggtgttcaa ttgattggtg gtacctggta	1620
cggtggtgaa atgaagaagg gtatgttctc catgatgaac tacttcttgc cattgagagg	1680
tattgcttcc atgactgtt ctgccaatgt cggtaaggac ggtgacactg ccatcttctt	1740
cggctctatcc ggtaccggtg agaccacttt gtccactgac ccaaagagac aattgattgg	1800
tgatgacgaa cacggttggg atgacgaagg tgttttcaac tttgaagggtg gttgttacgc	1860
caagaccatc aacttatctg ctgaaaatga accagatata tacggtgcca tcaagcgtga	1920
cgtctatttg gaaaacgttg ttgttttggg caatggtgac gtcgattatg ctgacggttc	1980
caagactgaa aacaccagag tttcttacct aatctaccat attcaaaaca ttgtcaagcc	2040
agtttccaag gctggtccag ctaccaaagt tatcttcttg tctgctgatg ctttcggtgt	2100
tttgctcctt gtttccaagt tgactccaga acaaaccaag tactacttct tgtctggttt	2160
caccgccaag ttggctggta ctgaaagagg tatcactgaa ccaactccaa ctttctctgc	2220
ttgtttcggg gctgcctttt tgtctttgca cccaactcaa tacgctgaag ttttggtaaa	2280
gagaatgcaa gaatctggtg ctgaagctta cttggtcaac actggttggg acggtaccgg	2340
taagagaatc tccatcaaag ataccagagg tatcatcgat gccatcttgg atggttccat	2400
tgacaaggct gaaatgggtt ctttgccaat tttcgatttc tccattccaa aggccttgcc	2460
agggtgtcaac ccagccatct tagaccaag agacacctac gctgacaaag ctcaatggga	2520
agaaaaggct caagacttgg ctggtagatt cgtcaagaac ttcgaaaaat aactggtac	2580
tgctgaaggc caagctttgg ttgctgctgg tccaaaggcc taaggcccgg gcataaagca	2640
atcttgatga ggataatgat ttttttttga atatacataa atactaccgt ttttctgcta	2700

gattttgtga agacgtaaat aagtacatat tacttttttaa gccaaagacaa gattaagcat 2760
 taactttacc cttttctctt ctaagtttca atactagtta tcactgttta aaagttatgg 2820
 cgagaacgtc ggcggttaaa atatattacc ctgaacgtgg tgaattgaag ttctaggatg 2880
 gtttaaagat ttttcctttt tgggaaataa gtaacaata tattgctgcc tttgcaaaac 2940
 gcacataccc acaatatgtg actattggca aagaacgcat ttcctttga agaggtggat 3000
 actgatacta agagagtctc tattccggct ccacttttag tccagagatt acttgtcttc 3060
 ttacgtatca gaacaagaaa gcattttcaa agtaattgca tttgcccttg agcagtatat 3120
 atatactaag aaggcgcgcc gcggccgc 3148

<210> 2
 <211> 4959
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct TDH3p-FRDg-TDH3t for expression in *S. cerevisiae*

<400> 2
 ggatccggcg cgccctattt tcgaggacct tgtcaccttg agcccaagag agccaagatt 60
 taaattttcc tatgacttga tgcaaattcc caaagctaata aacatgcaag acacgtacgg 120
 tcaagaagac atatttgacc tcttaacagg ttcagacgcg actgcctcat cagtaagacc 180
 cgttgaaaag aacttacctg aaaaaaacga atatatacta gcgttgaaatg ttagcgtcaa 240
 caacaagaag tttaatgacg cggaggccaa ggcaaaaaga ttccttgatt acgtaaggga 300
 gttagaatca ttttgaataa aaaacacgct ttttcagttc gagtttatca ttatcaatac 360
 tgccatttca aagaatacgt aaataattaa tagtagtgat tttcctaact ttatttagtc 420
 aaaaaattag ccttttaatt ctgctgtaac ccgtacatgc ccaaaatagg gggcgggtta 480
 cacagaatat ataacatcgt aggtgtctgg gtgaacagtt tattcctggc atccactaaa 540
 tataatggag cccgcttttt aagctggcat ccagaaaaaa aaagaatccc agcaccaaaa 600
 tattgttttc ttcaccaacc atcagttcat aggtccattc tcttagcgca actacagaga 660
 acaggggcac aaacaggcaa aaaacgggca caacctcaat ggagtgatgc aacctgcctg 720
 gagtaaatga tgacacaagg caattgaccc acgcatgtat ctatctcatt ttcttacacc 780
 ttctattacc ttctgctctc tctgatttgg aaaaagctga aaaaaaagggt tgaaaccagt 840
 tcctgaaat tattccccta cttgactaat aagtatataa agacggtagg tattgattgt 900

aattctgtaa atctatattct taaacttctt aaattctact tttatagtta gtcttttttt	960
tagtttttaa acaccaagaa cttagtttctg aataaacaca cataaacaaa caaatgggt	1020
gatggtagat cttctgcttc cattgttgcc gttgaccag aaagagctgc cagagaaaga	1080
gatgctgctg ccagagcttt gttgcaagac tctccattgc acaccaccat gcaatacgt	1140
acctctgggt tggaaatgac tgttccatac gctttgaagg ttgttgcttc tgctgacact	1200
ttcgacagag ccaaggaagt tgctgatgaa gtcttgagat gtgcctggca attggctgac	1260
accgttttga actctttcaa cccaaactct gaagtctctt tagtcggtag attaccagtc	1320
ggcctaaaagc atcaaatgtc tgctccattg aaacgtgtca tggcttggtg tcaaagagtc	1380
tacaactcct ctgctgggtg tttcgaccca tccactgctc cagttgccaa ggctttgaga	1440
gaaattgctt tgggtaagga aagaaacaat gcttggttg aagctttgac tcaagcttgt	1500
accttgccaa actctttcgt cattgatctc gaagctggta ctatctccag aaagcacgaa	1560
cacgcttctt tggatttggtg tgggtgttcc aagggttaca tcgtcgatta cgtcattgac	1620
aacatcaatg ctgctggttt ccaaaacgtt ttctttgact ggggtgggtga ctgtcgtgcc	1680
tccggtatga acgccagaaa cactccatgg gttgtcggta tcactagacc tcttctcttg	1740
gacatgttgc caaacctcc aaaggaagct tcttacatct ccgtcatctc tttggacaat	1800
gaagcttttg ctacctctgg tgattacgaa aacttgatct acactgctga cgataaacca	1860
ttgacctgta cctacgattg gaaaggtaag gaattgatga agccatctca atccaatctc	1920
gctcaagttt ccgtcaagtg ttactctgcc atgtacgctg acgctttggc taccgcttgt	1980
ttcatcaagc gtgaccagc caaggctcaga caattggtg atgggtggag atacgttaga	2040
gacaccgtca gagattaccg tgtctacgtc agagaaaacg aaagagttgc caagatgttc	2100
gaaattgcca ctgaagatgc tgaaatgaga aagagaagaa tttccaacac tttaccagct	2160
cgtgtcattg ttgttggtg tggtttggtt ggtttgtccg ctgccattga agctgctggt	2220
tgtggtgctc aagttgttt gatggaaaag gaagccaagt tgggtggtaa ctctgccaag	2280
gctacctctg gtatcaacgg ttgggttact agagctcaag ctaaggcttc cattgtcgat	2340
ggtggtaagt acttcgaaag agatacctac aagtctggta tcggtggtaa caccgatcca	2400
gctttgggtta agactttgtc catgaaatct gctgacgcta tcggttggtt gacttctcta	2460
ggtgttccat tgactgttt gtcccaatta ggtggtcact ccagaaagag aactcacaga	2520
gctccagaca agaaggatgg tactccattg ccaattgggt tcaccatcat gaaaacttta	2580
gaagatcatg ttagaggtaa cttgtccggt agaataacca tcatggaaaa ctgttccgtt	2640

acctctttgt	tgtctgaaac	caaggaaaga	ccagacggta	ccaagcaa	cagagttacc	2700
ggtgtcgaat	tcactcaagc	tggttctggt	aagaccacca	ttttggctga	tgctgttatc	2760
ttggccaccg	gtggttttctc	caacgacaag	actgctgatt	ctttgttgag	agaacatgcc	2820
ccacacttgg	ttaacttccc	aaccaccaac	ggtccatggg	ctactgggtga	tggtgtcaag	2880
ttggctcaaa	gattaggtgc	tcaattgggc	gatattggaca	aggttcaatt	gcacccaact	2940
ggtttgatca	acccaaagga	cccagccaac	ccaaccaa	tcttgggtcc	agaagctcta	3000
agaggttctg	gtgggtgtttt	gttgaacaaa	caaggtaaga	gatttgtcaa	cgaattggat	3060
ttgagatctg	ttgtttccaa	ggccatcatg	gaacaagggtg	ctgaataccc	aggttctggt	3120
ggttccatgt	ttgcttactg	tgtcttgaac	gctgctgctc	aaaaattggt	tggtgtttcc	3180
tctcacgaat	tctactggaa	gaagatgggt	ttgttcgtca	aggctgacac	catgagagac	3240
ttggctgctt	tgattgggtg	tccagttgaa	tccgttcaac	aaactttaga	agaatacgaa	3300
agattatcca	tctctcaaag	atcttgtcca	attaccagaa	aatctgttta	cccatgtgtt	3360
ttgggtacca	aagggtccata	ctatgtcgcc	tttgtcactc	catctatcca	ctacaccatg	3420
ggtggttgtt	tgattttctcc	atctgctgaa	atccaaatga	agaacacttc	ttccagagct	3480
ccattgtccc	actccaaccc	aatcttgggt	ttattcgggtg	ctgggtgaagt	caccggtggt	3540
gtccacgggtg	gtaacagatt	aggtggtaac	tctttgttgg	aatgtgttgt	tttcggtaga	3600
attgccgggtg	acagagcttc	taccattttg	caaagaaagt	cctctgcttt	gtctttcaag	3660
gtctggacca	ctgttggtttt	gagagaagtc	agagaagggtg	gtgtctacgg	tgctggttcc	3720
cgtgtcttga	gattcaactt	accagggtgct	ctacaaagat	ctgggtctatc	cttgggtcaa	3780
ttcattgcca	tcagaggtga	ctgggacgggt	caacaattga	ttggttacta	ctctccaatc	3840
actttgccag	acgatttggg	tatgattgac	attttggcca	gatctgacaa	gggtacttta	3900
cgtgaatgga	tctctgcttt	ggaaccagggt	gacgctgtcg	aatgaaggc	ttgtgggtggt	3960
ttggctcatcg	aaagaagatt	atctgacaag	cacttcgttt	tcattgggtca	cattatcaac	4020
aagctatggt	tgattgctgg	tggtaccgggt	gttgcctcaa	tggtgcaa	catcaaggcc	4080
gctttcatga	agccattcat	cgacactttg	gaatccgtcc	acttgatcta	cgctgctgaa	4140
gatgtcactg	aattgactta	cagagaagtt	ttggaagaac	gtcgtcgtga	atccagaggt	4200
aaattcaaga	aaactttcgt	tttgaacaga	cctcctccat	tatggactga	cggtgtcgggt	4260
ttcatcgacc	gtgggtatctt	gaccaaccac	gttcaaccac	catctgacaa	cttattgggtt	4320

```

gccatctgtg gtccaccagt tatgcaaaga attgtcaagg ccactttaaa gacttttaggt      4380
tacaacatga acttggtcag aaccggtgac gaaactgaac catctggaag ttaaggcccg      4440
ggcgtgaatt tactttaaat cttgcattta aataaatttt ctttttatag ctttatgact      4500
tagtttcaat ttatatacta ttttaatgac attttcgatt cattgattga aagctttgtg      4560
ttttttcttg atgcgctatt gcattgttct tgtctttttc gccacatgta atatctgtag      4620
tagatacctg atacattgtg gatgctgagt gaaatttttag ttaataatgg aggcgctctt      4680
aataattttg gggatattgg cttttttttt taaagtttac aaatgaattt tttccgccag      4740
gataacgatt ctgaagttac tcttagcggt cctatcggtg cagccatcaa atcatgccta      4800
taaatcatgc ctatatgtgc gtgcagtcag tatcatctac atgaaaaaaaa ctcccgcaat      4860
ttcttataga atacgttgaa aattaaatgt acgcgccaaag ataagataac atatatctag      4920
atgcagtaat atacacagat tccggccggc cgcgccgcg      4959

```

```

<210> 3
<211> 2950
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Synthetic construct TDH1p-FUMR-TDH1t for expression in S.
      cerevisiae

```

```

<400> 3
ggatcccttc ccttttacag tgcttcggaa aagcacagcg ttgtccaagg gaacaatttt      60
tcttcaagtt aatgcataag aaatatcttt ttttatgttt agctaagtaa aagcagcttg      120
gagtaaaaaa aaaaatgagt aaatttctcg atggattagt ttctcacagg taacataaca      180
aaaaccaaga aaagcccgct tctgaaaact acagttgact tgtatgctaa agggccagac      240
taatgggagg agaaaaagaa acgaatgtat atgctcattt acactctata tcaccatatg      300
gaggataagt tgggctgagc ttctgatcca atttattcta tccattagtt gctgatatgt      360
cccaccagcc aacacttgat agtatctact cgccattcac ttccagcagc gccagtaggg      420
ttgttgagct tagtaaaaat gtgcgcacca caagcctaca tgactccacg tcacatgaaa      480
ccacaccgtg gggccttggt gcgctaggaa taggatatgc gacgaagacg cttctgctta      540
gtaaccacac cacattttca gggggctgat ctgcttgctt cctttactgt cagagcggc      600
ccataatcgc gctttttttt taaaaggcgc gagacagcaa acaggaagct cgggtttcaa      660
ccttcggagt ggtcgcagat ctggagactg gatctttaca atacagtaag gcaagccacc      720

```

atctgcttct taggtgcatg cgacggtatc cacgtgcaga acaacatagt ctgaagaagg	780
gggggaggag catgttcatt ctctgtagca gtaagagctt ggtgataatg accaaaactg	840
gagtctcgaa atcatataaa tagacaatat attttcacac aatgagattt gtagtacagt	900
tctattctct ctcttgcata aataagaaat tcatcaagaa cttgggttga tatttcacca	960
acacacacaa aaaacagtac ttactaaat ttacacacaa aacaaaatgt cctctgcttc	1020
tgctgctttg caaaaattca gagctgaaag agataccttc ggtgacttgc aagttccagc	1080
tgaccgttac tggggtgctc aaactcaaag atctttgcaa aactttgaca ttggtggtcc	1140
aactgaaaga atgccagaac cattaatcag agctttcggg gttttgaaga aggctgctgc	1200
caccgtcaac atgacctacg gtttggaacc aaagggttgg gaagccatcc aaaaggctgc	1260
tgacgaagtt atcgatgggt ctttgattga ccatttccca ttgggtgtct ggcaaaccgg	1320
ttctgggtact caaaccaaga tgaacgtcaa tgaagtcac tccaacagag ccattgaatt	1380
gttgggtggg gaattaggtt ccaaggctcc agtccaccca aacgatcatg tcaacatgtc	1440
tcaatcttcc aacgacactt tcccaactgc catgcacgtt gctgccgttg ttgaaattca	1500
cggtagattg attccagctt tgaccacttt gagagatgct ttgcaagcca aatctgctga	1560
attcgaacac atcatcaaga ttggtagaac ccacttgcaa gatgctacc cattgacttt	1620
agggtcaagaa ttctccgggt acaactcaaca attgacctac ggtattgctc gtgttcaagg	1680
tactttggaa agattataca acttgggtca aggtgggtact gctgtcggta ctggtttgaa	1740
caccagaaag ggtttcgatg ccaagggtgc tgaagccatt gcttccatca ctggtttacc	1800
attcaagacc gtcctaaaca aattcgaagc tttggctgct cacgacgctt tggttgaagc	1860
tcacgggtgct ttgaacaccg ttgcttggtc tttgatgaag attgccaacg atatccgtta	1920
cttgggttct ggtccaagat gtggtttagg tgaattgtct ctaccagaaa acgaaccagg	1980
ttcttccatc atgccaggta aggtcaaccc aactcaatgt gaagctatga ccatggtttg	2040
tgctcaagtc atgggtaaca aactgccat ctctgttgct ggttccaacg gtcaattcga	2100
attgaatgtc tttaaaccag tcatgatcaa gaacttgatc caatccatca gattaatctc	2160
tgacgcttcc atctctttca ccaagaactg tggtgtcggg attgaagcta acgaaaagaa	2220
gatctcctcc atcatgaacg aatctttgat gttgggtcact gctttgaacc ctcacattgg	2280
ttacgacaag gctgccaagt gtgccaagaa ggctcacaag gaaggtacca ctttgaaaga	2340
agctgctcta tctttgggtt acttgacctc tgaagaattc gaccaatggg ttagacctga	2400
ggacatgatt tctgccaagg attaaggccc gggcataaag caatcttgat gaggataatg	2460

```

attttttttt gaatatacat aaatactacc gtttttctgc tagattttgt gaagacgtaa      2520
ataagtacat attacttttt aagccaagac aagattaagc attaaacttta cccttttctc      2580
ttctaagttt caatactagt tatcactggt taaaagttat ggcgagaacg tcggcggtta      2640
aaatatatta ccctgaacgt ggtgaattga agttctagga tggtttaaag atttttcctt      2700
tttgggaaat aagtaaaca tatattgctg cctttgcaaa acgcacatac ccacaatatg      2760
tgactattgg caaagaacgc attatccttt gaagaggtgg atactgatac taagagagtc      2820
tctattccgg ctccactttt agtccagaga ttacttgtct tcttacgtat cagaacaaga      2880
aagcatttcc aaagtaattg catttgcctt tgagcagtat atatatacta agaaggcgcg      2940
ccgcggccgc                                     2950

```

```

<210> 4
<211> 1966
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Synthetic construct TDH3p-MDH3-TDH3t for expression in S.
      cerevisiae

```

```

<400> 4
ggatccggcg cgccacgcgt ggccggcctt agtcaaaaaa ttagcctttt aattctgctg      60
taacccttac atgccccaaa tagggggcgg gttacacaga atatataaca tcgtaggtgt      120
ctgggtgaac agttttattcc tggcatccac taaatataat ggagcccgct ttttaagctg      180
gcatccagaa aaaaaaagaa tcccagcacc aaaatattgt tttcttcacc aaccatcagt      240
tcataggtcc attctcttag cgcaactaca gagaacaggg gcacaaacag gcaaaaaacg      300
ggcacaacct caatggagtg atgcaacctg cctggagtaa atgatgacac aaggcaattg      360
accacgcat gtatctatct cattttctta caccttctat taccttctgc tctctctgat      420
ttggaaaaag ctgaaaaaaa aggttgaaac cagttccctg aaattattcc cctacttgac      480
taataagtat ataaagacgg taggtattga ttgtaattct gtaaattctat ttcttaaact      540
tcttaaattc tactttttata gttagtcttt tttttagttt taaaacacca agaacttagt      600
ttcgaataaa cacacataaa caaacaaaat ggttaagggt gccatcttag gtgcttctgg      660
tggtgtcggc caaccattat ctctattatt gaaattgtct ccatacgttt ctgaattggc      720
tttgtacgat atcagagctg ctgaaggat tggttaaggat ttgtcccaca tcaacaccaa      780
ctcctcttgt gttggttacg acaaggattc catcgaaaac actttgtcca atgctcaagt      840

```



```

tgtcttgatt ccagctggtg ttccaagaaa gccaggtttg accagagatg atttgttcaa      900
gatgaacgct ggtatcggtt agtctttggt tactgctgtc ggtaaatttg ccccaaacgc      960
tcgtatctta gtcactccca accctgttaa ctctttgggt ccaattgccg ttgaaacttt     1020
gaagaagatg ggtaagttca agccaggtaa cgttatgggt gtcaccaact tggatttggt     1080
cagagctgaa actttcttgg ttgactactt gatgttgaag aacccaaaga tcggtcaaga     1140
acaagacaag accaccatgc acagaaaggt caccgtcatc ggtggtcact ctggtgaaac     1200
catcattcca atcatcactg acaaatcctt ggttttccaa ttggacaagc aatacgaaca     1260
tttcatccac agagtccaat tcggtggtga cgaaattgtc aaggccaagc aaggtgccgg     1320
ttctgctacc ttgtccatgg ctttcgctgg tgccaaattt gctgaagaag tcttacgttc     1380
tttccacaac gaaaagccag aaactgaatc tttgtctgct ttcgtctact tgccaggttt     1440
gaagaacggt aagaaggctc aacaattagt cggtgacaac tccattgaat acttctcttt     1500
gccaatgtt ttgagaaacg gttccgttgt ttccattgac acttctgttt tggaaaaatt     1560
gtctccaaga gaagaacaat tggtaaacac tgctgtcaag gaattgagaa agaacattga     1620
aaagggtaa tctttcatct tggacagtta aggtgaattt actttaaatc ttgcatttaa     1680
ataaattttc tttttatagc tttatgactt agtttcaatt tatatactat tttaatgaca     1740
ttttcgattc attgattgaa agcttttgtt tttttcttga tgcgctattg cattgttctt     1800
gtctttttcg ccacatgtaa tatctgtagt agatacctga tacattgtgg atgctgagtg     1860
aaattttagt taataatgga ggcgctctta ataattttgg ggatattggc tttttttttt     1920
aaagtttaca aatgaatttt ttccgccagg atgggcccgcc ggccgc                    1966

```

<210> 5

<211> 2240

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct Enolp-SpMAE1-ENOt for expression in *S. cerevisiae*

<400> 5

```

ggatccggcg cgccccgcgg aaccgccaga tattcattac ttgacgcaaa agcgtttgaa      60
ataatgacga aaaagaagga agaaaaaaaa agaaaaatac cgcttctagg cgggttatct     120
actgatccga gttccacta ggatagcaac caaacacctg catatttgga cgacctttac     180
ttacaccacc aaaaaccact ttgcctctc ccgccctga taacgtccac taattgagcg     240

```

attacctgag	cggtcctctt	ttgtttgcag	catgagactt	gcatactgca	aatcgtaagt	300
agcaacgtct	caaggtcaaa	actgtatgga	aaccttgtca	cctcacttaa	ttctagctag	360
cctaccctgc	aagtcaagag	gtctccgtga	ttcctagcca	cctcaaggta	tgctctccc	420
cggaaactgt	ggccttttct	ggcacacatg	atctccacga	tttcaacata	taaatagctt	480
ttgataatgg	caatattaat	caaattttatt	ttactttctt	cttgtaacat	ctctcttgta	540
atcccttatt	ccttctagct	atttttcata	aaaaaccaag	caactgctta	tcaacacaca	600
aacactaaaa	caaaatgggt	gaattgaagg	aaatcttgaa	gcaacgttac	catgaattgt	660
tggactggaa	cgtcaaggct	ccacacgttc	cattgtctca	aagattgaag	catttcacct	720
ggccttggtt	tgcttgtaac	atggccactg	gtggtgtcgg	tttgatcatt	ggttctttcc	780
cattcagatt	ctacggtttg	aacaccattg	gtaagattgt	ctacatctta	caaatcttct	840
tattctcttt	gtttggttct	tgtatgttgt	tcagattcat	caaataccca	tctaccatca	900
aggactcctg	gaaccaccac	ttggaaaaat	tattcattgc	tacctgtttg	ctatccatct	960
ccactttcat	tgacatgttg	gccatctacg	cttaccacga	cactggtgaa	tggatggtct	1020
gggttatcag	aatcttatac	tacatctacg	ttgctgtctc	tttcatctac	tgtgtcatgg	1080
ctttcttcac	cattttcaac	aaccacgttt	acaccattga	aactgcttct	ccagcttggg	1140
tcttaccaat	tttcccacca	atgatctgtg	gtgtcattgc	tgggtgctgc	aactccactc	1200
aaccagctca	ccaattgaag	aacatggtta	tcttcggtat	cttattccaa	ggtttggggt	1260
tctgggttta	cttgttggtg	tttgctgtca	acgttttgag	attcttcacc	gttggtttgg	1320
ccaagcctca	agacagacca	ggtatgttca	tgtttggttg	tccaccagct	ttctccggtt	1380
tggctttgat	caacattgcc	cgtggtgcta	tgggttccag	accatacatt	ttcgtcggtg	1440
ccaattcttc	tgaatacttg	ggtttcgttt	ccactttcat	ggccattttc	atctgggggt	1500
tggctgcttg	gtgttactgt	ttggccatgg	tttctttctt	ggctggtttc	ttcaccagag	1560
ctccattgaa	atttgcttgt	ggttggtttg	ctttcatctt	cccaaacgtc	ggtttcgtta	1620
actgtaccat	tgaattgggt	aagatgattg	actccaaggc	cttccaaatg	ttcggtcaca	1680
tcacgggtgt	catcctatgt	atccaatgga	tcttggtgat	gtacttgatg	gtcagagctt	1740
tcttggtcaa	cgatttggtg	taccacagga	aggatgaaga	tgctcaccca	cctccaaagc	1800
caaacactgg	tgttttgaac	ccaactttcc	caccagaaaa	ggctccagct	tctttggaaa	1860
aggttgacac	ccacgttact	tccactgggtg	gtgaatctga	tcctccatct	tctgaacacg	1920

```

aaagcgttta agagcttttg attaagcctt ctagtccaaa aaacacgttt ttttgtcatt      1980
tatttcattt tcttagaata gtttagttta ttcattttat agtcacgaat gttttatgat      2040
tctatatagg gttgcaaaca agcatttttc attttatgtt aaaacaattt caggtttacc      2100
ttttattctg cttgtggtga cgcgggtatc cgcccgtctt tttggtcacc catgtattta      2160
attgcataaa taattcttaa aagtggagct agtctatttc tatttacata cctctcattt      2220
ctcatttcct ccgcggccgc                                                    2240

```

```

<210> 6
<211> 538
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Actinobacillus succinogenes phosphoenolpyruvate carboxykinase
      amino acid sequence, with EGY to DAF modification at pos 120 -
      122.

```

```

<400> 6

```

```

Met Thr Asp Leu Asn Lys Leu Val Lys Glu Leu Asn Asp Leu Gly Leu
1           5           10           15

```

```

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

```

```

Glu Glu Glu Thr Lys Pro Gly Leu Glu Gly Phe Asp Lys Gly Thr Leu
      35           40           45

```

```

Thr Thr Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly Arg
      50           55           60

```

```

Ser Pro Lys Asp Lys Tyr Ile Val Cys Asp Glu Thr Thr Lys Asp Thr
65           70           75           80

```

```

Val Trp Trp Asn Ser Glu Ala Ala Lys Asn Asp Asn Lys Pro Met Thr
      85           90           95

```

```

Gln Glu Thr Trp Lys Ser Leu Arg Glu Leu Val Ala Lys Gln Leu Ser
      100          105          110

```

```

Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Ser Glu Lys
      115          120          125

```

His Arg Ile Gly Val Arg Met Val Thr Glu Val Ala Trp Gln Ala His
 130 135 140

Phe Val Lys Asn Met Phe Ile Arg Pro Thr Asp Glu Glu Leu Lys Asn
 145 150 155 160

Phe Lys Ala Asp Phe Thr Val Leu Asn Gly Ala Lys Cys Thr Asn Pro
 165 170 175

Asn Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala Phe Asn
 180 185 190

Ile Thr Glu Gly Ile Gln Leu Ile Gly Gly Thr Trp Tyr Gly Gly Glu
 195 200 205

Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Phe Leu Pro Leu Lys
 210 215 220

Gly Val Ala Ser Met His Cys Ser Ala Asn Val Gly Lys Asp Gly Asp
 225 230 235 240

Val Ala Ile Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr Leu Ser
 245 250 255

Thr Asp Pro Lys Arg Gln Leu Ile Gly Asp Asp Glu His Gly Trp Asp
 260 265 270

Glu Ser Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys Thr Ile
 275 280 285

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

Asp Ala Leu Leu Glu Asn Val Val Val Arg Ala Asp Gly Ser Val Asp
 305 310 315 320

Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr Pro Ile
 325 330 335

Tyr His Ile Asp Asn Ile Val Arg Pro Val Ser Lys Ala Gly His Ala
 340 345 350

Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu Pro Pro

```

355                               360                               365

Val Ser Lys Leu Thr Pro Glu Gln Thr Glu Tyr Tyr Phe Leu Ser Gly
370                               375                               380

Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Val Thr Glu Pro Thr
385                               390                               395                               400

Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu His Pro
405                               410                               415

Ile Gln Tyr Ala Asp Val Leu Val Glu Arg Met Lys Ala Ser Gly Ala
420                               425                               430

Glu Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys Arg Ile
435                               440                               445

Ser Ile Lys Asp Thr Arg Gly Ile Ile Asp Ala Ile Leu Asp Gly Ser
450                               455                               460

Ile Glu Lys Ala Glu Met Gly Glu Leu Pro Ile Phe Asn Leu Ala Ile
465                               470                               475                               480

Pro Lys Ala Leu Pro Gly Val Asp Pro Ala Ile Leu Asp Pro Arg Asp
485                               490                               495

Thr Tyr Ala Asp Lys Ala Gln Trp Gln Val Lys Ala Glu Asp Leu Ala
500                               505                               510

Asn Arg Phe Val Lys Asn Phe Val Lys Tyr Thr Ala Asn Pro Glu Ala
515                               520                               525

Ala Lys Leu Val Gly Ala Gly Pro Lys Ala
530                               535

<210> 7
<211> 1139
<212> PRT
<213> Artificial Sequence

<220>
<223> Glycosomal Trypanosoma brucei fumarate reductase (FRDg) amino
acid sequence lacking 3 aa C-terminal targeting signal.

<400> 7

```

Met Val Asp Gly Arg Ser Ser Ala Ser Ile Val Ala Val Asp Pro Glu
1 5 10 15

Arg Ala Ala Arg Glu Arg Asp Ala Ala Ala Arg Ala Leu Leu Gln Asp
20 25 30

Ser Pro Leu His Thr Thr Met Gln Tyr Ala Thr Ser Gly Leu Glu Leu
35 40 45

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

Arg Ala Lys Glu Val Ala Asp Glu Val Leu Arg Cys Ala Trp Gln Leu
65 70 75 80

Ala Asp Thr Val Leu Asn Ser Phe Asn Pro Asn Ser Glu Val Ser Leu
85 90 95

Val Gly Arg Leu Pro Val Gly Gln Lys His Gln Met Ser Ala Pro Leu
100 105 110

Lys Arg Val Met Ala Cys Cys Gln Arg Val Tyr Asn Ser Ser Ala Gly
115 120 125

Cys Phe Asp Pro Ser Thr Ala Pro Val Ala Lys Ala Leu Arg Glu Ile
130 135 140

Ala Leu Gly Lys Glu Arg Asn Asn Ala Cys Leu Glu Ala Leu Thr Gln
145 150 155 160

Ala Cys Thr Leu Pro Asn Ser Phe Val Ile Asp Phe Glu Ala Gly Thr
165 170 175

Ile Ser Arg Lys His Glu His Ala Ser Leu Asp Leu Gly Gly Val Ser
180 185 190

Lys Gly Tyr Ile Val Asp Tyr Val Ile Asp Asn Ile Asn Ala Ala Gly
195 200 205

Phe Gln Asn Val Phe Phe Asp Trp Gly Gly Asp Cys Arg Ala Ser Gly
210 215 220

Met Asn Ala Arg Asn Thr Pro Trp Val Val Gly Ile Thr Arg Pro Pro
225 230 235 240

Ser Leu Asp Met Leu Pro Asn Pro Pro Lys Glu Ala Ser Tyr Ile Ser
245 250 255

Val Ile Ser Leu Asp Asn Glu Ala Leu Ala Thr Ser Gly Asp Tyr Glu
260 265 270

Asn Leu Ile Tyr Thr Ala Asp Asp Lys Pro Leu Thr Cys Thr Tyr Asp
275 280 285

Trp Lys Gly Lys Glu Leu Met Lys Pro Ser Gln Ser Asn Ile Ala Gln
290 295 300

Val Ser Val Lys Cys Tyr Ser Ala Met Tyr Ala Asp Ala Leu Ala Thr
305 310 315 320

Ala Cys Phe Ile Lys Arg Asp Pro Ala Lys Val Arg Gln Leu Leu Asp
325 330 335

Gly Trp Arg Tyr Val Arg Asp Thr Val Arg Asp Tyr Arg Val Tyr Val
340 345 350

Arg Glu Asn Glu Arg Val Ala Lys Met Phe Glu Ile Ala Thr Glu Asp
355 360 365

Ala Glu Met Arg Lys Arg Arg Ile Ser Asn Thr Leu Pro Ala Arg Val
370 375 380

Ile Val Val Gly Gly Gly Leu Ala Gly Leu Ser Ala Ala Ile Glu Ala
385 390 395 400

Ala Gly Cys Gly Ala Gln Val Val Leu Met Glu Lys Glu Ala Lys Leu
405 410 415

Gly Gly Asn Ser Ala Lys Ala Thr Ser Gly Ile Asn Gly Trp Gly Thr
420 425 430

Arg Ala Gln Ala Lys Ala Ser Ile Val Asp Gly Gly Lys Tyr Phe Glu
435 440 445

Arg Asp Thr Tyr Lys Ser Gly Ile Gly Gly Asn Thr Asp Pro Ala Leu

450		455		460
Val Lys Thr Leu Ser Met Lys Ser Ala Asp Ala Ile Gly Trp Leu Thr				
465		470		475
Ser Leu Gly Val Pro Leu Thr Val Leu Ser Gln Leu Gly Gly His Ser				
	485		490	495
Arg Lys Arg Thr His Arg Ala Pro Asp Lys Lys Asp Gly Thr Pro Leu				
	500		505	510
Pro Ile Gly Phe Thr Ile Met Lys Thr Leu Glu Asp His Val Arg Gly				
	515		520	525
Asn Leu Ser Gly Arg Ile Thr Ile Met Glu Asn Cys Ser Val Thr Ser				
	530		535	540
Leu Leu Ser Glu Thr Lys Glu Arg Pro Asp Gly Thr Lys Gln Ile Arg				
545		550		555
Val Thr Gly Val Glu Phe Thr Gln Ala Gly Ser Gly Lys Thr Thr Ile				
	565		570	575
Leu Ala Asp Ala Val Ile Leu Ala Thr Gly Gly Phe Ser Asn Asp Lys				
	580		585	590
Thr Ala Asp Ser Leu Leu Arg Glu His Ala Pro His Leu Val Asn Phe				
	595		600	605
Pro Thr Thr Asn Gly Pro Trp Ala Thr Gly Asp Gly Val Lys Leu Ala				
	610		615	620
Gln Arg Leu Gly Ala Gln Leu Val Asp Met Asp Lys Val Gln Leu His				
625		630		635
Pro Thr Gly Leu Ile Asn Pro Lys Asp Pro Ala Asn Pro Thr Lys Phe				
	645		650	655
Leu Gly Pro Glu Ala Leu Arg Gly Ser Gly Gly Val Leu Leu Asn Lys				
	660		665	670
Gln Gly Lys Arg Phe Val Asn Glu Leu Asp Leu Arg Ser Val Val Ser				
	675		680	685

Lys Ala Ile Met Glu Gln Gly Ala Glu Tyr Pro Gly Ser Gly Gly Ser
690 695 700

Met Phe Ala Tyr Cys Val Leu Asn Ala Ala Ala Gln Lys Leu Phe Gly
705 710 715 720

Val Ser Ser His Glu Phe Tyr Trp Lys Lys Met Gly Leu Phe Val Lys
725 730 735

Ala Asp Thr Met Arg Asp Leu Ala Ala Leu Ile Gly Cys Pro Val Glu
740 745 750

Ser Val Gln Gln Thr Leu Glu Glu Tyr Glu Arg Leu Ser Ile Ser Gln
755 760 765

Arg Ser Cys Pro Ile Thr Arg Lys Ser Val Tyr Pro Cys Val Leu Gly
770 775 780

Thr Lys Gly Pro Tyr Tyr Val Ala Phe Val Thr Pro Ser Ile His Tyr
785 790 795 800

Thr Met Gly Gly Cys Leu Ile Ser Pro Ser Ala Glu Ile Gln Met Lys
805 810 815

Asn Thr Ser Ser Arg Ala Pro Leu Ser His Ser Asn Pro Ile Leu Gly
820 825 830

Leu Phe Gly Ala Gly Glu Val Thr Gly Gly Val His Gly Gly Asn Arg
835 840 845

Leu Gly Gly Asn Ser Leu Leu Glu Cys Val Val Phe Gly Arg Ile Ala
850 855 860

Gly Asp Arg Ala Ser Thr Ile Leu Gln Arg Lys Ser Ser Ala Leu Ser
865 870 875 880

Phe Lys Val Trp Thr Thr Val Val Leu Arg Glu Val Arg Glu Gly Gly
885 890 895

Val Tyr Gly Ala Gly Ser Arg Val Leu Arg Phe Asn Leu Pro Gly Ala
900 905 910

Leu Gln Arg Ser Gly Leu Ser Leu Gly Gln Phe Ile Ala Ile Arg Gly
 915 920 925

Asp Trp Asp Gly Gln Gln Leu Ile Gly Tyr Tyr Ser Pro Ile Thr Leu
 930 935 940

Pro Asp Asp Leu Gly Met Ile Asp Ile Leu Ala Arg Ser Asp Lys Gly
 945 950 955 960

Thr Leu Arg Glu Trp Ile Ser Ala Leu Glu Pro Gly Asp Ala Val Glu
 965 970 975

Met Lys Ala Cys Gly Gly Leu Val Ile Glu Arg Arg Leu Ser Asp Lys
 980 985 990

His Phe Val Phe Met Gly His Ile Ile Asn Lys Leu Cys Leu Ile Ala
 995 1000 1005

Gly Gly Thr Gly Val Ala Pro Met Leu Gln Ile Ile Lys Ala Ala
 1010 1015 1020

Phe Met Lys Pro Phe Ile Asp Thr Leu Glu Ser Val His Leu Ile
 1025 1030 1035

Tyr Ala Ala Glu Asp Val Thr Glu Leu Thr Tyr Arg Glu Val Leu
 1040 1045 1050

Glu Glu Arg Arg Arg Glu Ser Arg Gly Lys Phe Lys Lys Thr Phe
 1055 1060 1065

Val Leu Asn Arg Pro Pro Pro Leu Trp Thr Asp Gly Val Gly Phe
 1070 1075 1080

Ile Asp Arg Gly Ile Leu Thr Asn His Val Gln Pro Pro Ser Asp
 1085 1090 1095

Asn Leu Leu Val Ala Ile Cys Gly Pro Pro Val Met Gln Arg Ile
 1100 1105 1110

Val Lys Ala Thr Leu Lys Thr Leu Gly Tyr Asn Met Asn Leu Val
 1115 1120 1125

Arg Thr Val Asp Glu Thr Glu Pro Ser Gly Ser
 1130 1135

<210> 8

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Rhizopus oryzae fumarase amino acid sequence, lacking the first
 23 N-terminal amino acids.

<400> 8

Met Ser Ser Ala Ser Ala Ala Leu Gln Lys Phe Arg Ala Glu Arg Asp
 1 5 10 15

Thr Phe Gly Asp Leu Gln Val Pro Ala Asp Arg Tyr Trp Gly Ala Gln
 20 25 30

Thr Gln Arg Ser Leu Gln Asn Phe Asp Ile Gly Gly Pro Thr Glu Arg
 35 40 45

Met Pro Glu Pro Leu Ile Arg Ala Phe Gly Val Leu Lys Lys Ala Ala
 50 55 60

Ala Thr Val Asn Met Thr Tyr Gly Leu Asp Pro Lys Val Gly Glu Ala
 65 70 75 80

Ile Gln Lys Ala Ala Asp Glu Val Ile Asp Gly Ser Leu Ile Asp His
 85 90 95

Phe Pro Leu Val Val Trp Gln Thr Gly Ser Gly Thr Gln Thr Lys Met
 100 105 110

Asn Val Asn Glu Val Ile Ser Asn Arg Ala Ile Glu Leu Leu Gly Gly
 115 120 125

Glu Leu Gly Ser Lys Ala Pro Val His Pro Asn Asp His Val Asn Met
 130 135 140

Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Met His Val Ala Ala
 145 150 155 160

Val Val Glu Ile His Gly Arg Leu Ile Pro Ala Leu Thr Thr Leu Arg
 165 170 175

Asp Ala Leu Gln Ala Lys Ser Ala Glu Phe Glu His Ile Ile Lys Ile
 180 185 190

Gly Arg Thr His Leu Gln Asp Ala Thr Pro Leu Thr Leu Gly Gln Glu
 195 200 205

Phe Ser Gly Tyr Thr Gln Gln Leu Thr Tyr Gly Ile Ala Arg Val Gln
 210 215 220

Gly Thr Leu Glu Arg Leu Tyr Asn Leu Ala Gln Gly Gly Thr Ala Val
 225 230 235 240

Gly Thr Gly Leu Asn Thr Arg Lys Gly Phe Asp Ala Lys Val Ala Glu
 245 250 255

Ala Ile Ala Ser Ile Thr Gly Leu Pro Phe Lys Thr Ala Pro Asn Lys
 260 265 270

Phe Glu Ala Leu Ala Ala His Asp Ala Leu Val Glu Ala His Gly Ala
 275 280 285

Leu Asn Thr Val Ala Cys Ser Leu Met Lys Ile Ala Asn Asp Ile Arg
 290 295 300

Tyr Leu Gly Ser Gly Pro Arg Cys Gly Leu Gly Glu Leu Ser Leu Pro
 305 310 315 320

Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr
 325 330 335

Gln Cys Glu Ala Met Thr Met Val Cys Ala Gln Val Met Gly Asn Asn
 340 345 350

Thr Ala Ile Ser Val Ala Gly Ser Asn Gly Gln Phe Glu Leu Asn Val
 355 360 365

Phe Lys Pro Val Met Ile Lys Asn Leu Ile Gln Ser Ile Arg Leu Ile
 370 375 380

Ser Asp Ala Ser Ile Ser Phe Thr Lys Asn Cys Val Val Gly Ile Glu
 385 390 395 400

Ala Asn Glu Lys Lys Ile Ser Ser Ile Met Asn Glu Ser Leu Met Leu
 405 410 415

Val Thr Ala Leu Asn Pro His Ile Gly Tyr Asp Lys Ala Ala Lys Cys
 420 425 430

Ala Lys Lys Ala His Lys Glu Gly Thr Thr Leu Lys Glu Ala Ala Leu
 435 440 445

Ser Leu Gly Tyr Leu Thr Ser Glu Glu Phe Asp Gln Trp Val Arg Pro
 450 455 460

Glu Asp Met Ile Ser Ala Lys Asp
 465 470

<210> 9

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Saccharomyces cerevisiae peroxisomal malate dehydrogenase (Mdh3)
 amino acid sequence, lacking the 3 C-terminal peroxisomal
 targeting sequence (SKL).

<400> 9

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

Leu Ser Leu Leu Leu Lys Leu Ser Pro Tyr Val Ser Glu Leu Ala Leu
 20 25 30

Tyr Asp Ile Arg Ala Ala Glu Gly Ile Gly Lys Asp Leu Ser His Ile
 35 40 45

Asn Thr Asn Ser Ser Cys Val Gly Tyr Asp Lys Asp Ser Ile Glu Asn
 50 55 60

Thr Leu Ser Asn Ala Gln Val Val Leu Ile Pro Ala Gly Val Pro Arg
 65 70 75 80

Lys Pro Gly Leu Thr Arg Asp Asp Leu Phe Lys Met Asn Ala Gly Ile
 85 90 95

Val Lys Ser Leu Val Thr Ala Val Gly Lys Phe Ala Pro Asn Ala Arg
 100 105 110

Ile Leu Val Ile Ser Asn Pro Val Asn Ser Leu Val Pro Ile Ala Val
 115 120 125

Glu Thr Leu Lys Lys Met Gly Lys Phe Lys Pro Gly Asn Val Met Gly
 130 135 140

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

Leu Met Leu Lys Asn Pro Lys Ile Gly Gln Glu Gln Asp Lys Thr Thr
 165 170 175

Met His Arg Lys Val Thr Val Ile Gly Gly His Ser Gly Glu Thr Ile
 180 185 190

Ile Pro Ile Ile Thr Asp Lys Ser Leu Val Phe Gln Leu Asp Lys Gln
 195 200 205

Tyr Glu His Phe Ile His Arg Val Gln Phe Gly Gly Asp Glu Ile Val
 210 215 220

Lys Ala Lys Gln Gly Ala Gly Ser Ala Thr Leu Ser Met Ala Phe Ala
 225 230 235 240

Gly Ala Lys Phe Ala Glu Glu Val Leu Arg Ser Phe His Asn Glu Lys
 245 250 255

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

Asn Gly Lys Lys Ala Gln Gln Leu Val Gly Asp Asn Ser Ile Glu Tyr
 275 280 285

Phe Ser Leu Pro Ile Val Leu Arg Asn Gly Ser Val Val Ser Ile Asp
 290 295 300

Thr Ser Val Leu Glu Lys Leu Ser Pro Arg Glu Glu Gln Leu Val Asn
 305 310 315 320

Thr Ala Val Lys Glu Leu Arg Lys Asn Ile Glu Lys Gly Lys Ser Phe

```

                                325                                330                                335

Ile Leu Asp Ser
                               340

<210>  10
<211> 438
<212>  PRT
<213>  Schizosaccharomyces pombe malate permease amino acid sequence.

<400>  10

Met Gly Glu Leu Lys Glu Ile Leu Lys Gln Arg Tyr His Glu Leu Leu
 1                               5                               10                               15

Asp Trp Asn Val Lys Ala Pro His Val Pro Leu Ser Gln Arg Leu Lys
                20                                25                                30

His Phe Thr Trp Ser Trp Phe Ala Cys Thr Met Ala Thr Gly Gly Val
    35                                40                                45

Gly Leu Ile Ile Gly Ser Phe Pro Phe Arg Phe Tyr Gly Leu Asn Thr
 50                               55                               60

Ile Gly Lys Ile Val Tyr Ile Leu Gln Ile Phe Leu Phe Ser Leu Phe
65                               70                               75                               80

Gly Ser Cys Met Leu Phe Arg Phe Ile Lys Tyr Pro Ser Thr Ile Lys
                85                                90                                95

Asp Ser Trp Asn His His Leu Glu Lys Leu Phe Ile Ala Thr Cys Leu
                100                               105                               110

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

Asp Thr Gly Glu Trp Met Val Trp Val Ile Arg Ile Leu Tyr Tyr Ile
    130                               135                               140

Tyr Val Ala Val Ser Phe Ile Tyr Cys Val Met Ala Phe Phe Thr Ile
145                               150                               155                               160

Phe Asn Asn His Val Tyr Thr Ile Glu Thr Ala Ser Pro Ala Trp Ile
                165                               170                               175

```

Leu Pro Ile Phe Pro Pro Met Ile Cys Gly Val Ile Ala Gly Ala Val
 180 185 190

Asn Ser Thr Gln Pro Ala His Gln Leu Lys Asn Met Val Ile Phe Gly
 195 200 205

Ile Leu Phe Gln Gly Leu Gly Phe Trp Val Tyr Leu Leu Leu Phe Ala
 210 215 220

Val Asn Val Leu Arg Phe Phe Thr Val Gly Leu Ala Lys Pro Gln Asp
 225 230 235 240

Arg Pro Gly Met Phe Met Phe Val Gly Pro Pro Ala Phe Ser Gly Leu
 245 250 255

Ala Leu Ile Asn Ile Ala Arg Gly Ala Met Gly Ser Arg Pro Tyr Ile
 260 265 270

Phe Val Gly Ala Asn Ser Ser Glu Tyr Leu Gly Phe Val Ser Thr Phe
 275 280 285

Met Ala Ile Phe Ile Trp Gly Leu Ala Ala Trp Cys Tyr Cys Leu Ala
 290 295 300

Met Val Ser Phe Leu Ala Gly Phe Phe Thr Arg Ala Pro Leu Lys Phe
 305 310 315 320

Ala Cys Gly Trp Phe Ala Phe Ile Phe Pro Asn Val Gly Phe Val Asn
 325 330 335

Cys Thr Ile Glu Ile Gly Lys Met Ile Asp Ser Lys Ala Phe Gln Met
 340 345 350

Phe Gly His Ile Ile Gly Val Ile Leu Cys Ile Gln Trp Ile Leu Leu
 355 360 365

Met Tyr Leu Met Val Arg Ala Phe Leu Val Asn Asp Leu Cys Tyr Pro
 370 375 380

Gly Lys Asp Glu Asp Ala His Pro Pro Pro Lys Pro Asn Thr Gly Val
 385 390 395 400

Leu Asn Pro Thr Phe Pro Pro Glu Lys Ala Pro Ala Ser Leu Glu Lys
405 410 415

Val Asp Thr His Val Thr Ser Thr Gly Gly Glu Ser Asp Pro Pro Ser
420 425 430

Ser Glu His Glu Ser Val
435