

Fig. 1

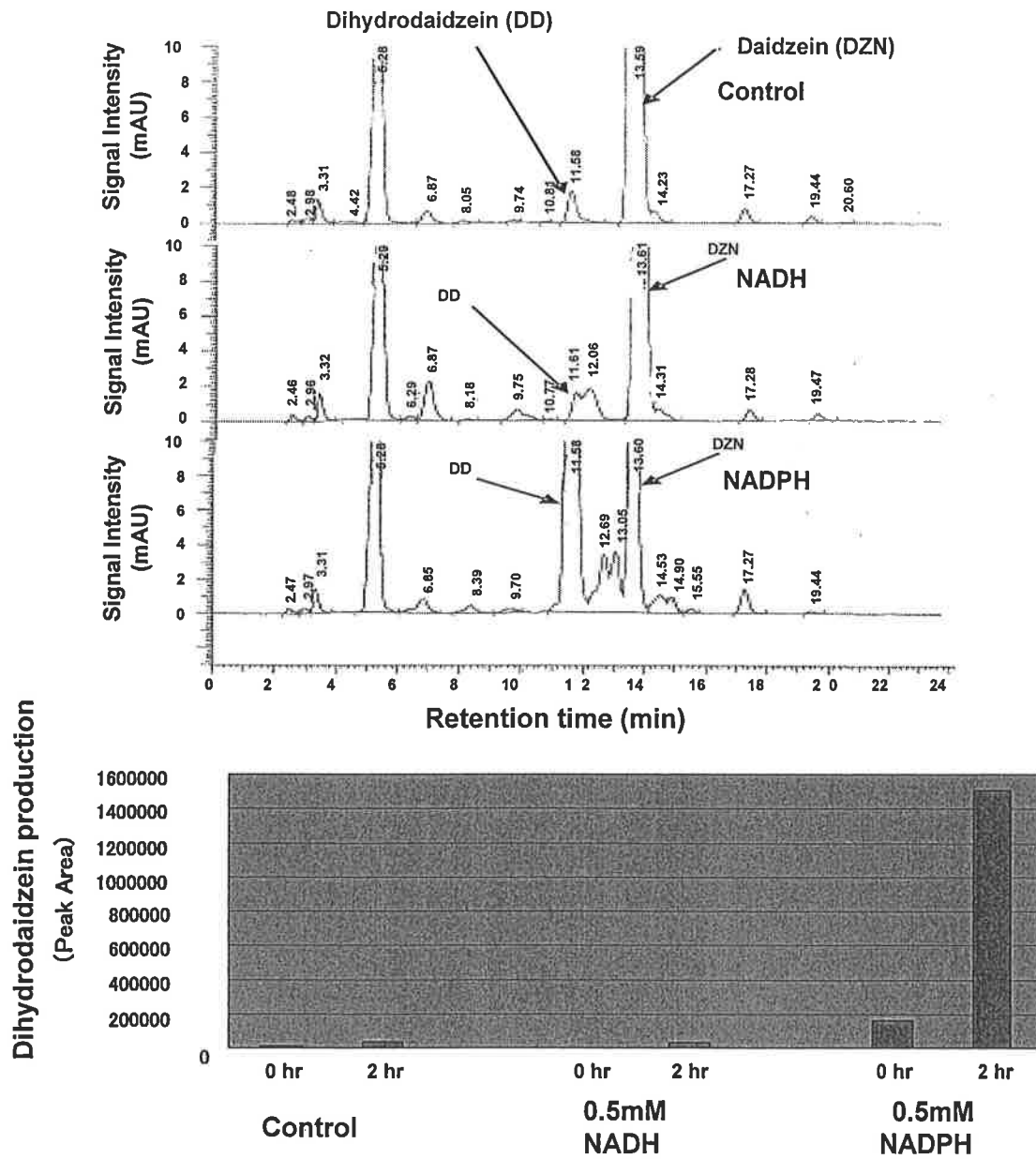


Fig. 2

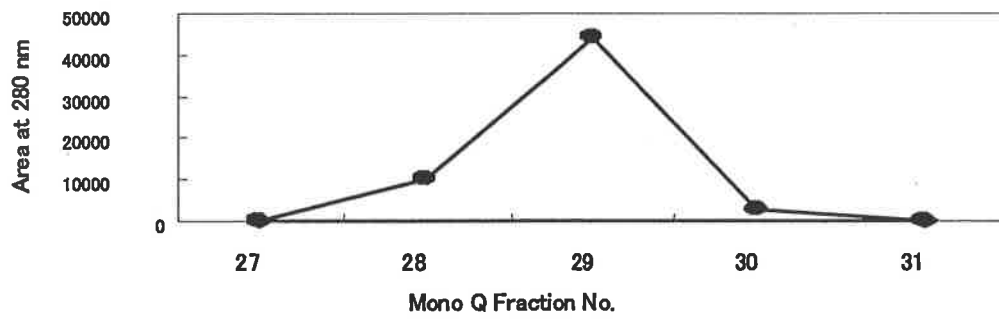
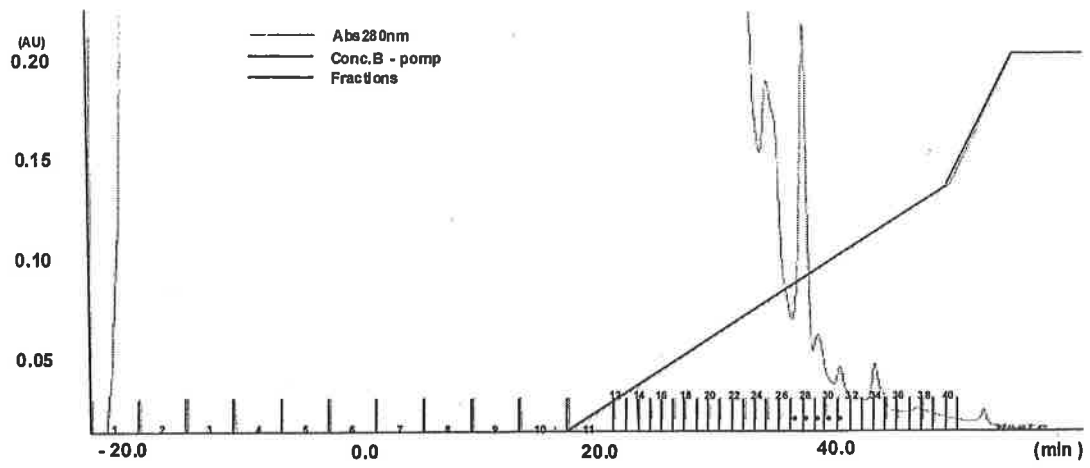


Fig. 3

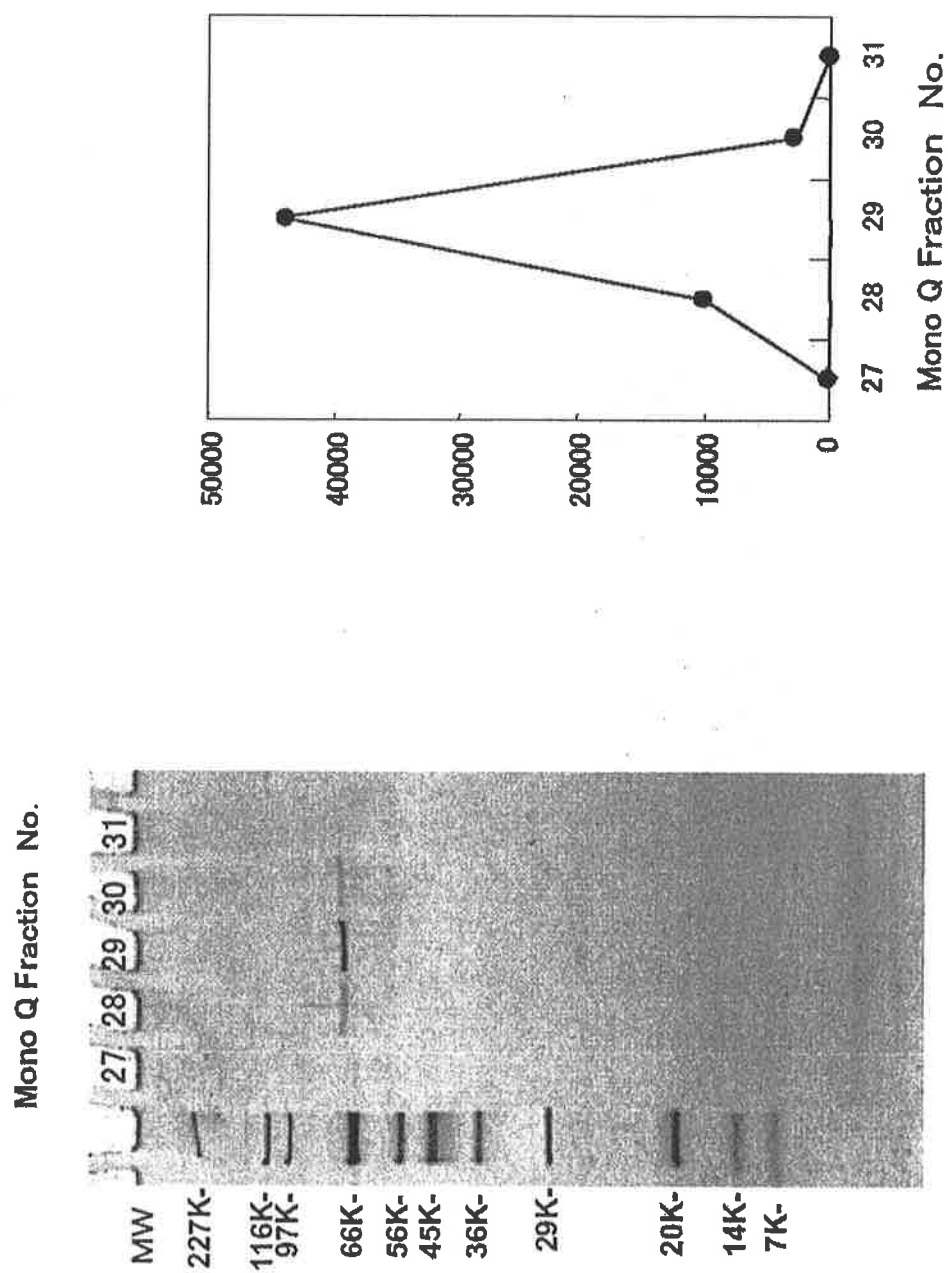


Fig. 4

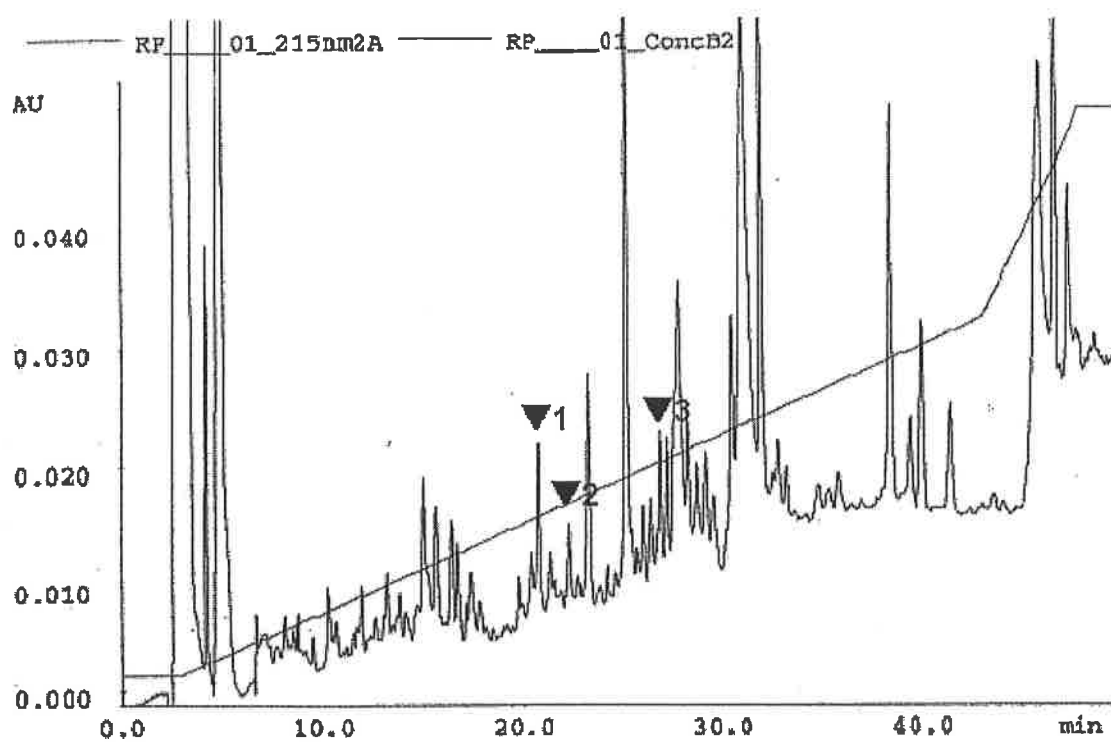


Fig. 5

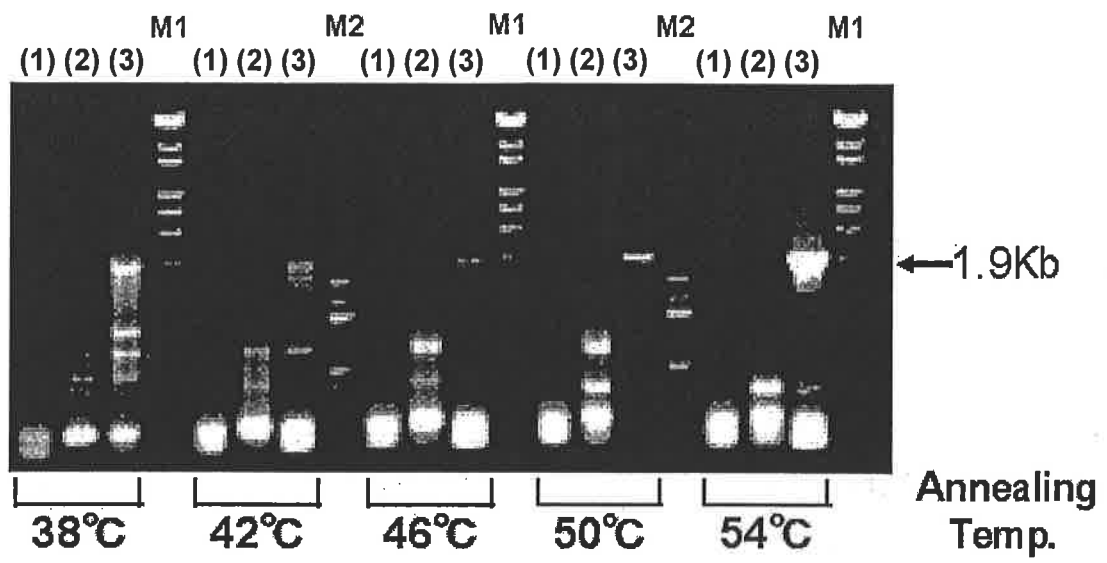


Fig. 6

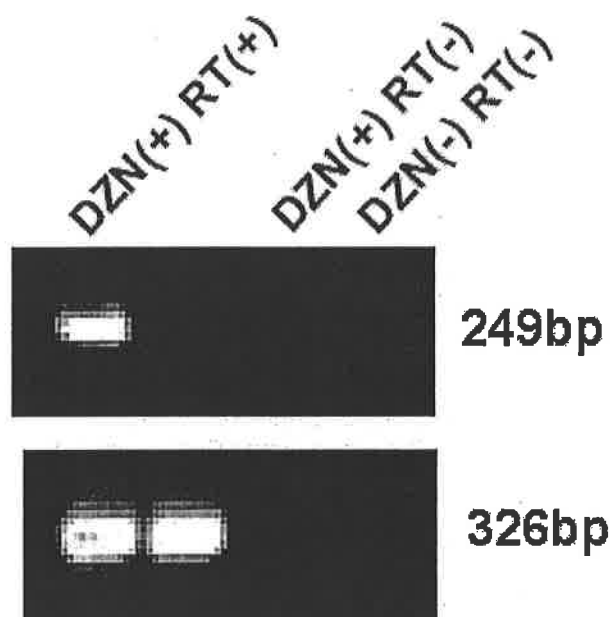


Fig. 7

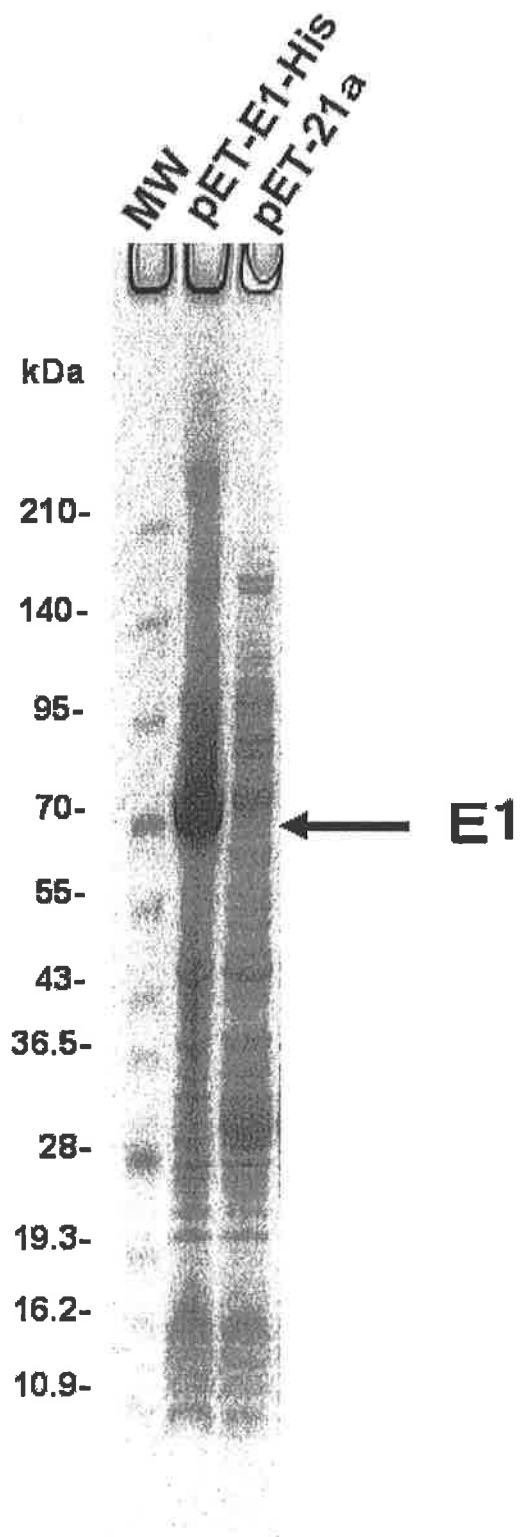


Fig. 8

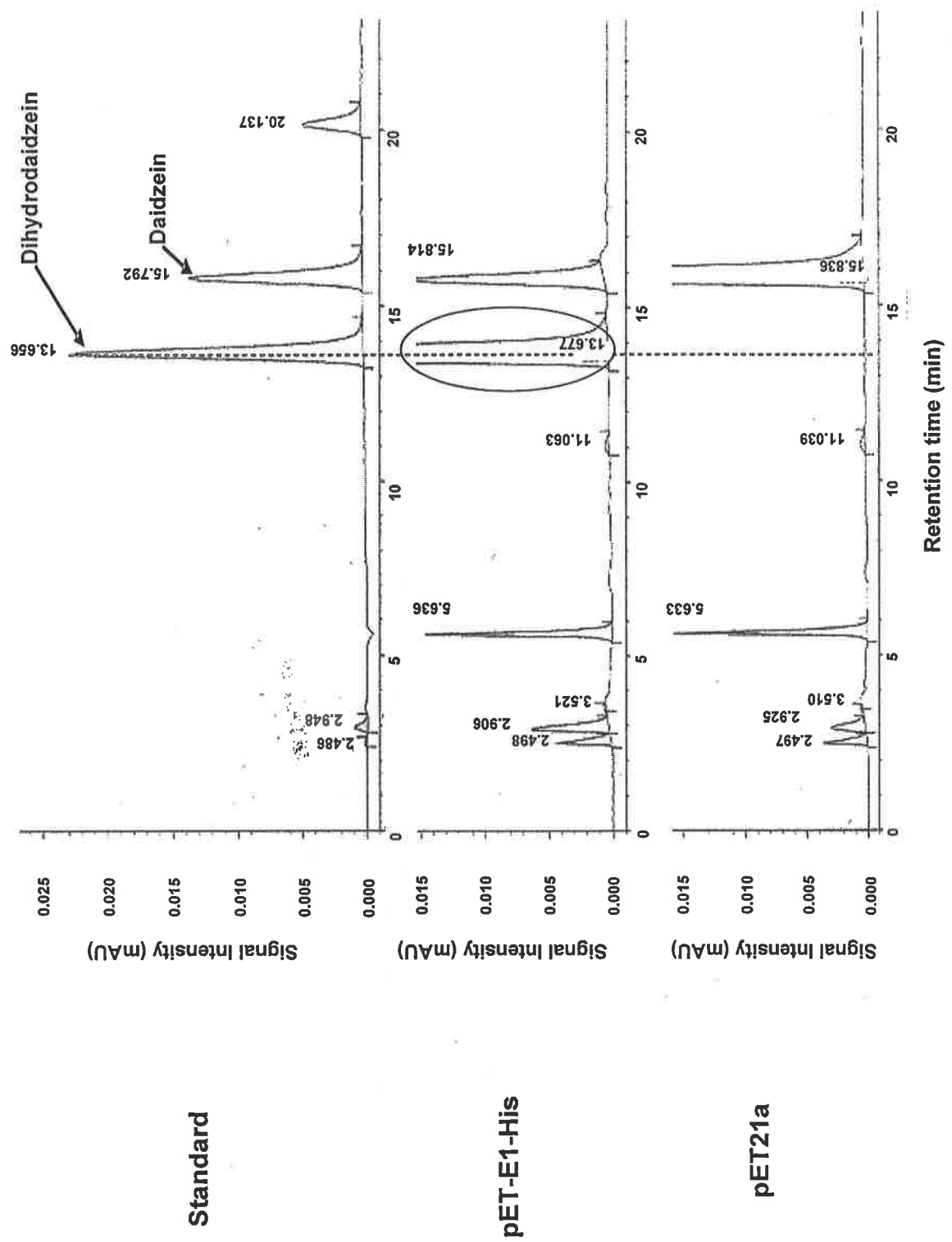


Fig. 9

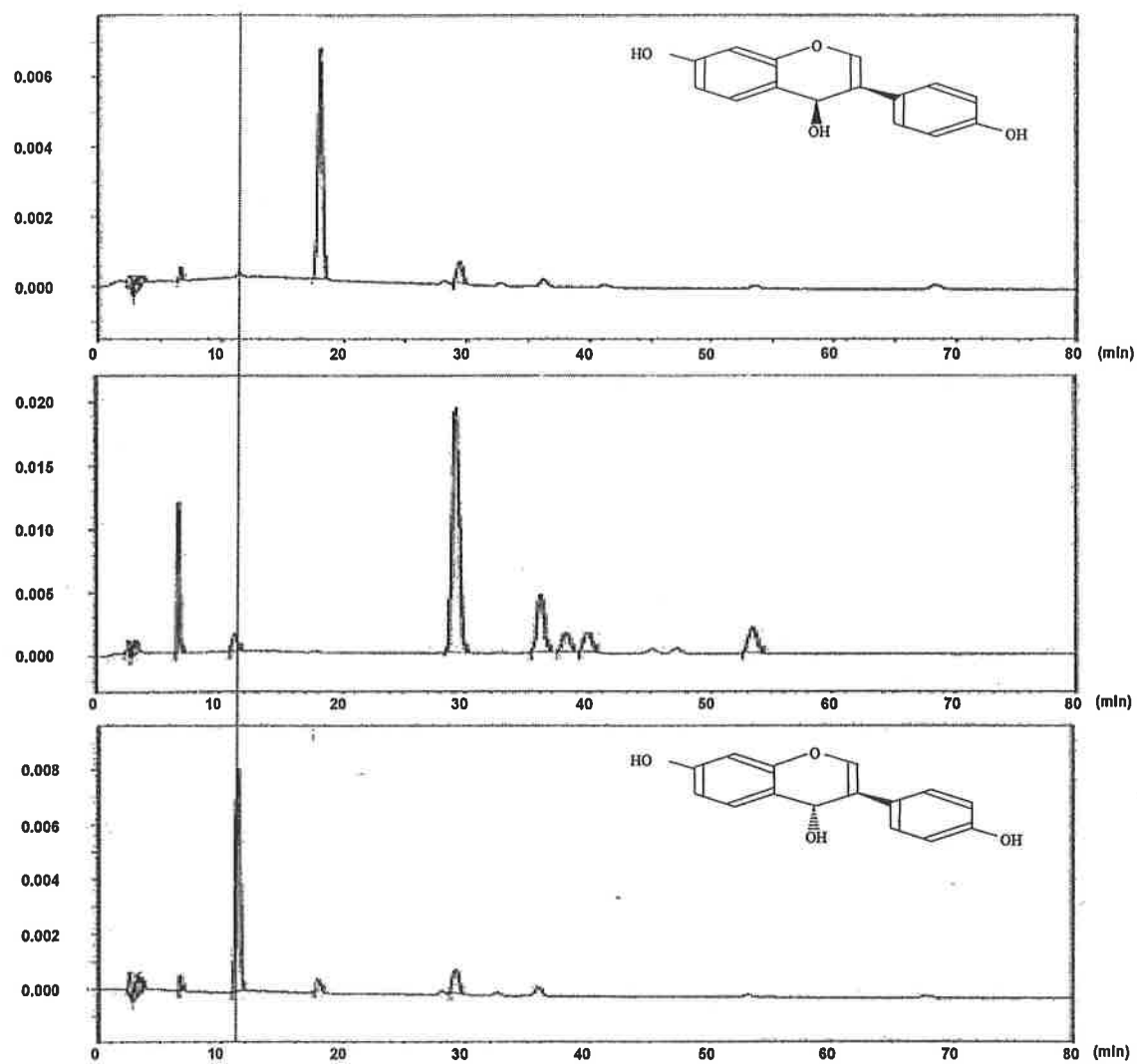


Fig. 10

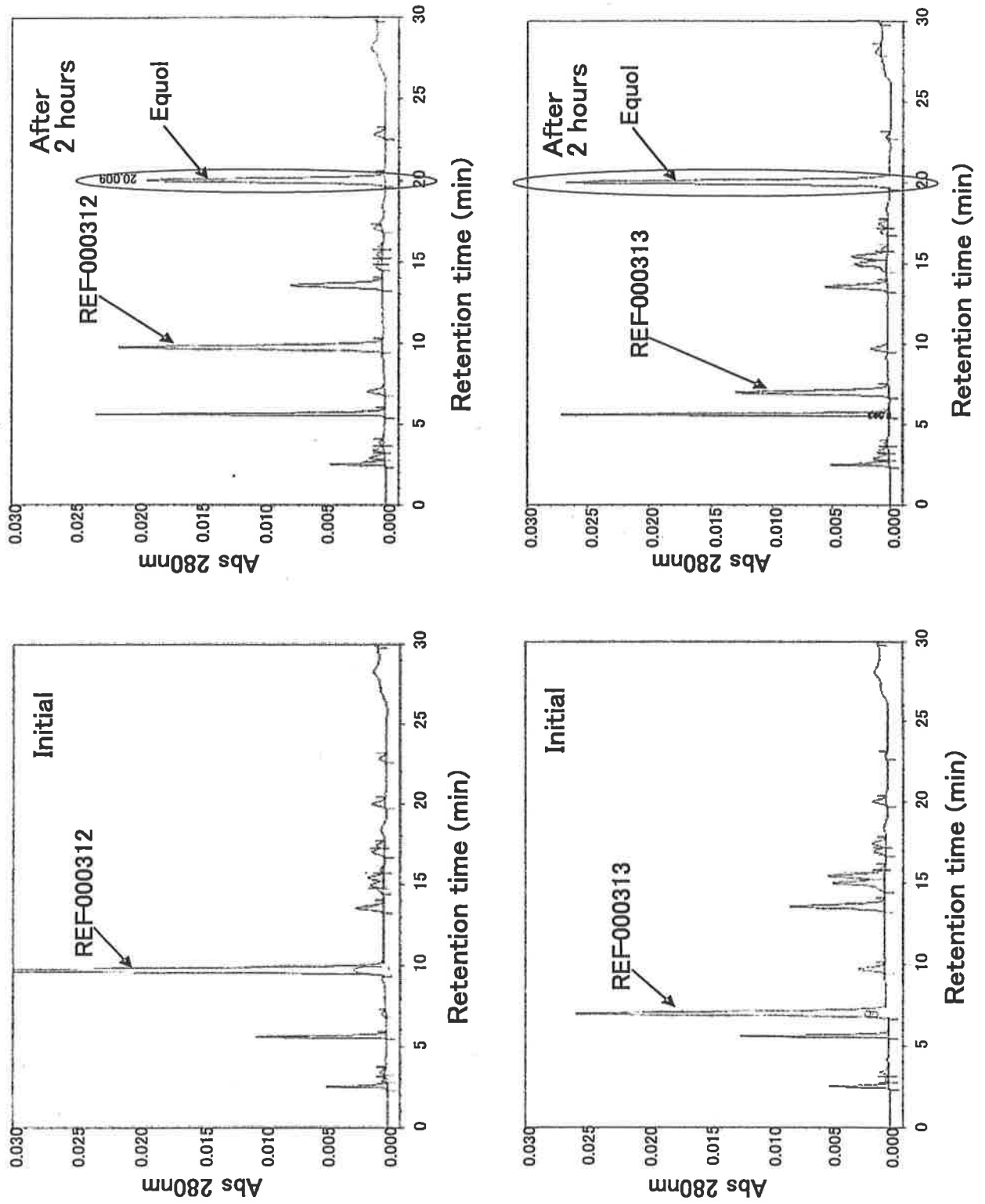


Fig. 11

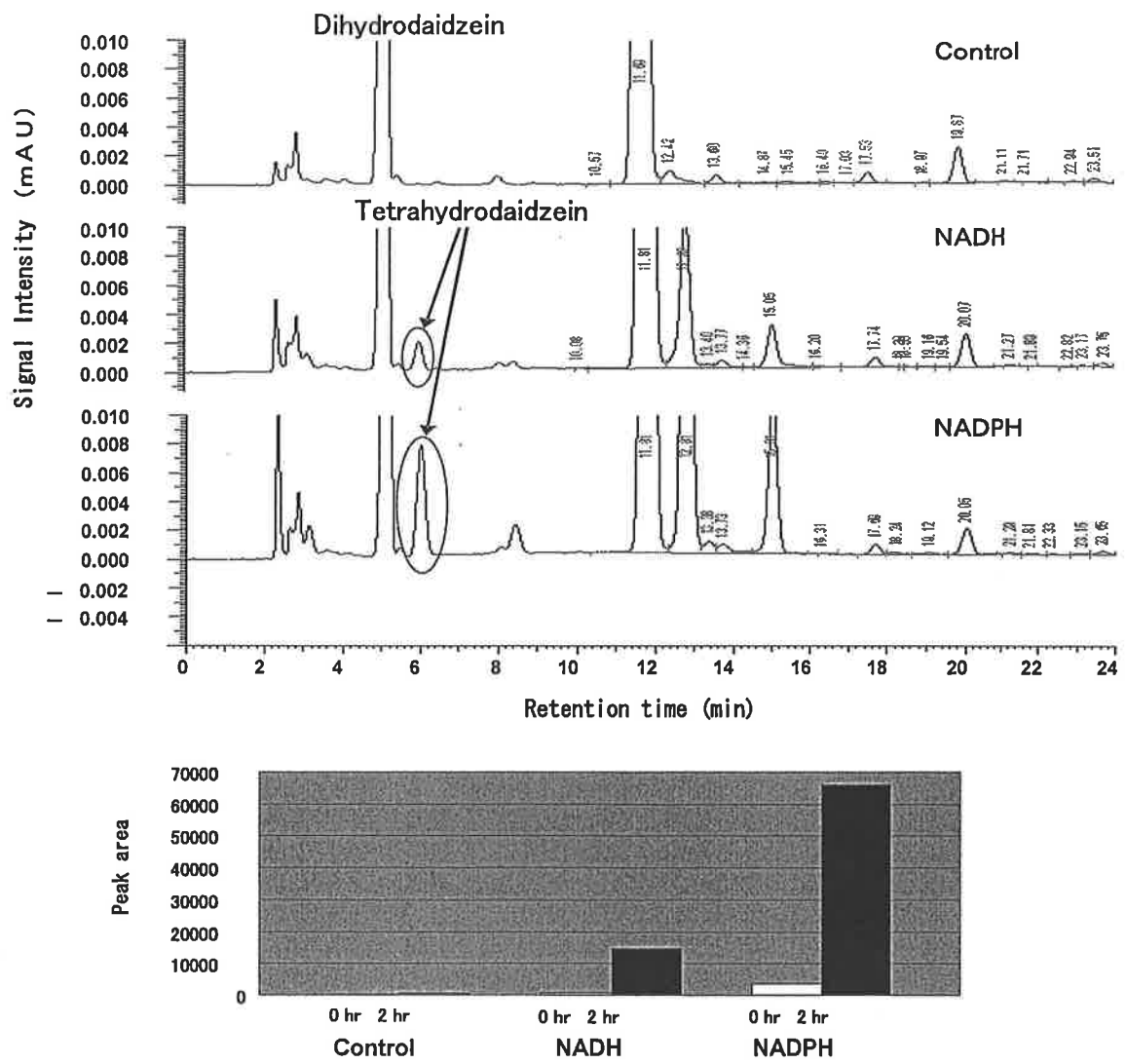


Fig. 12

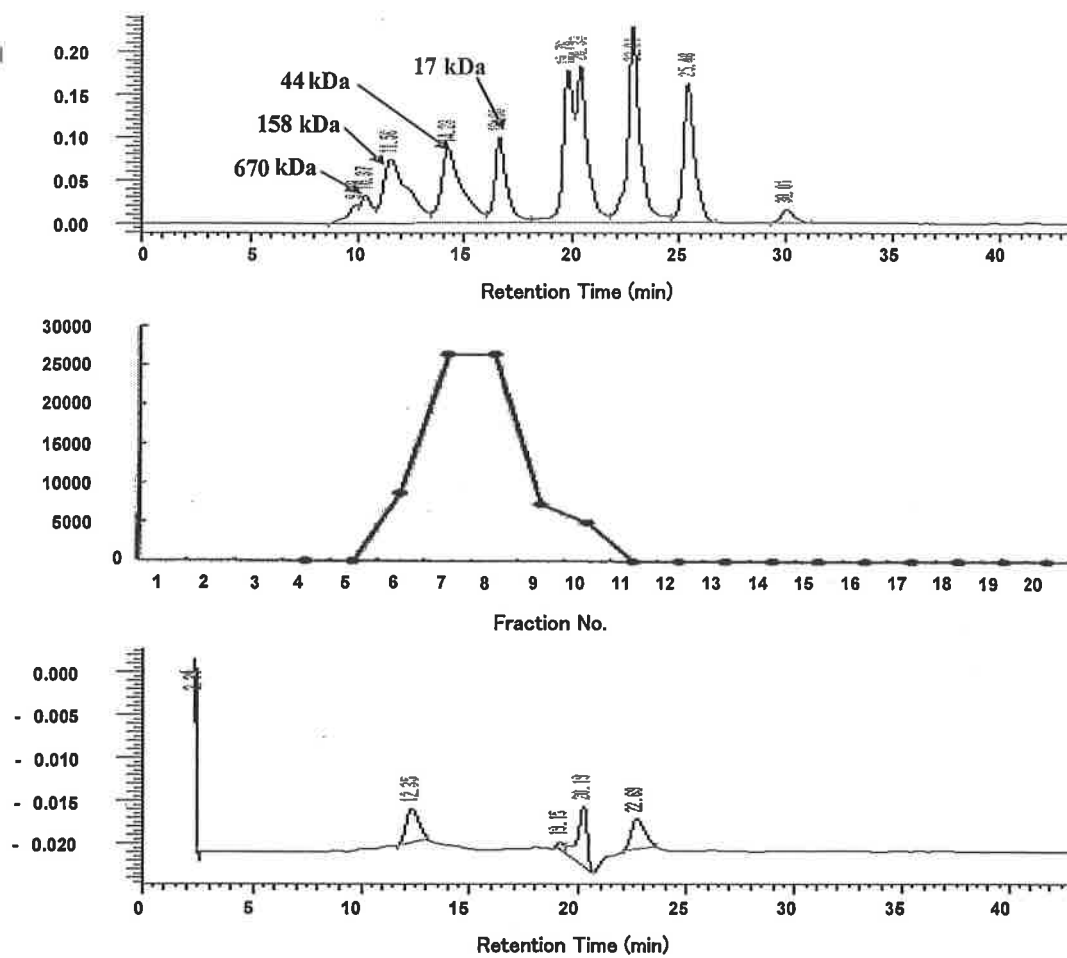


Fig. 13

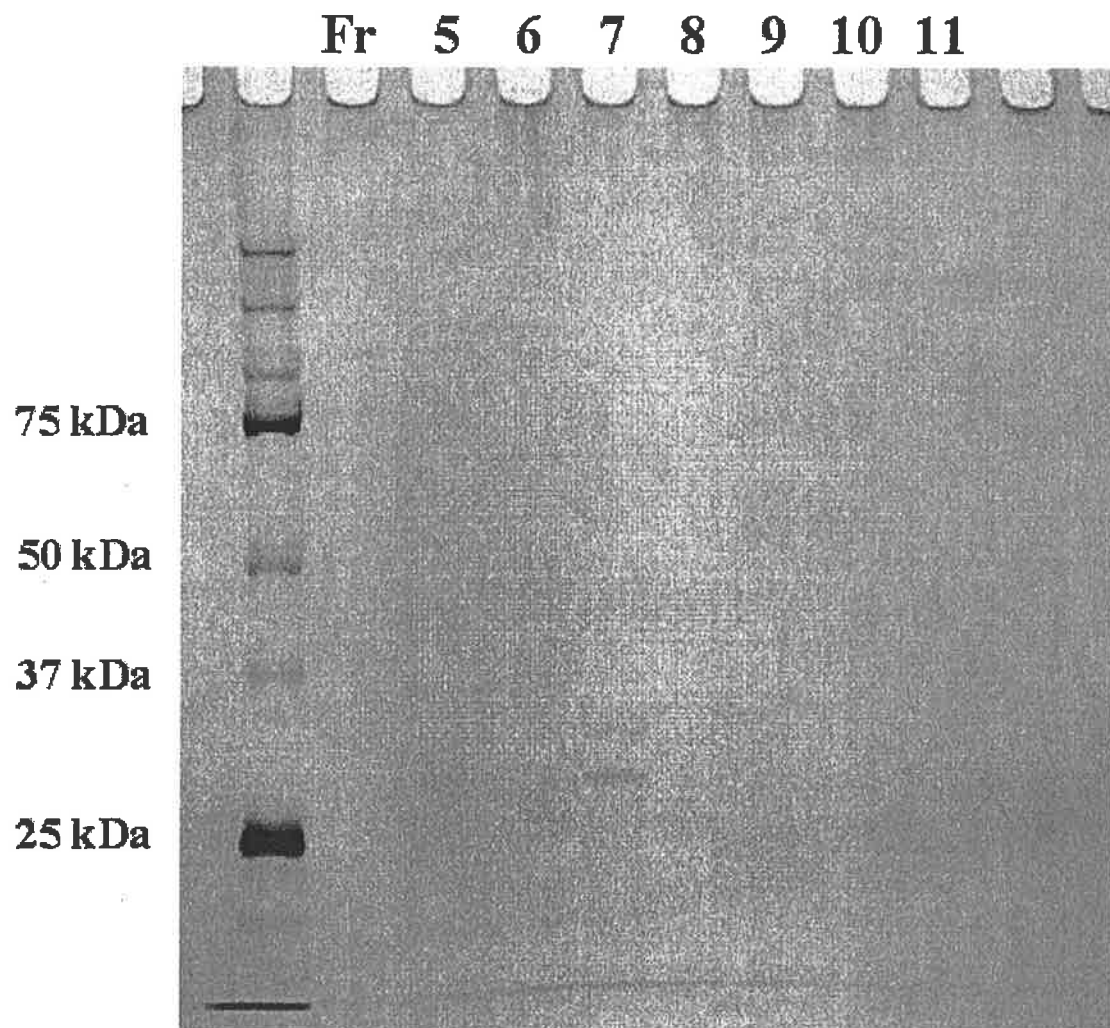


Fig. 14

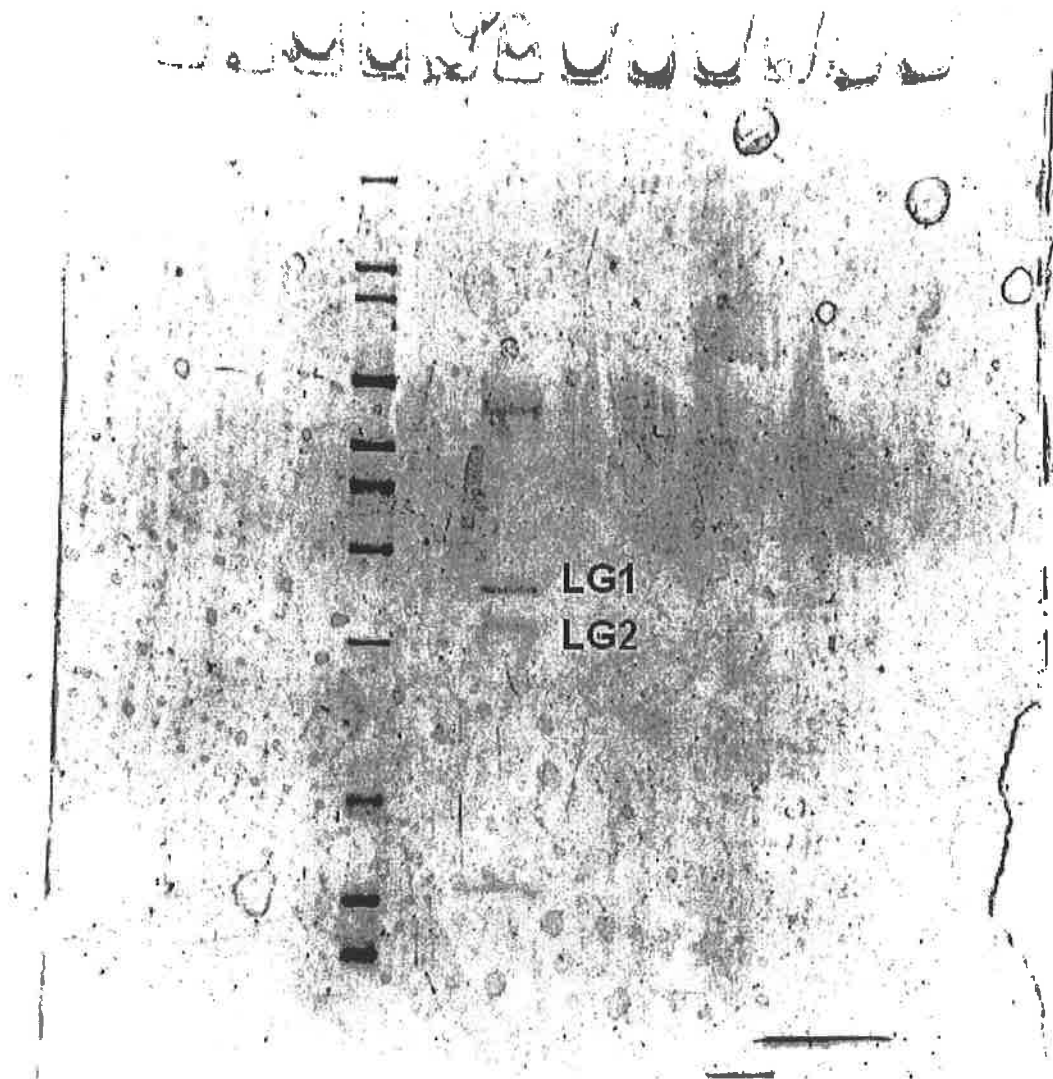


Fig. 15

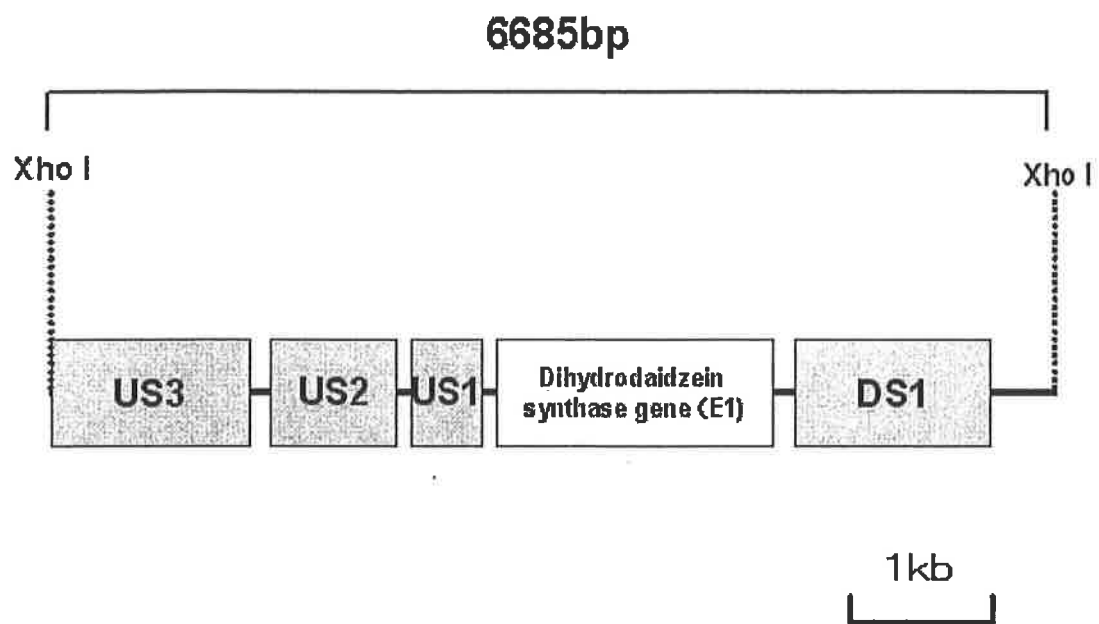


Fig. 16-1-a

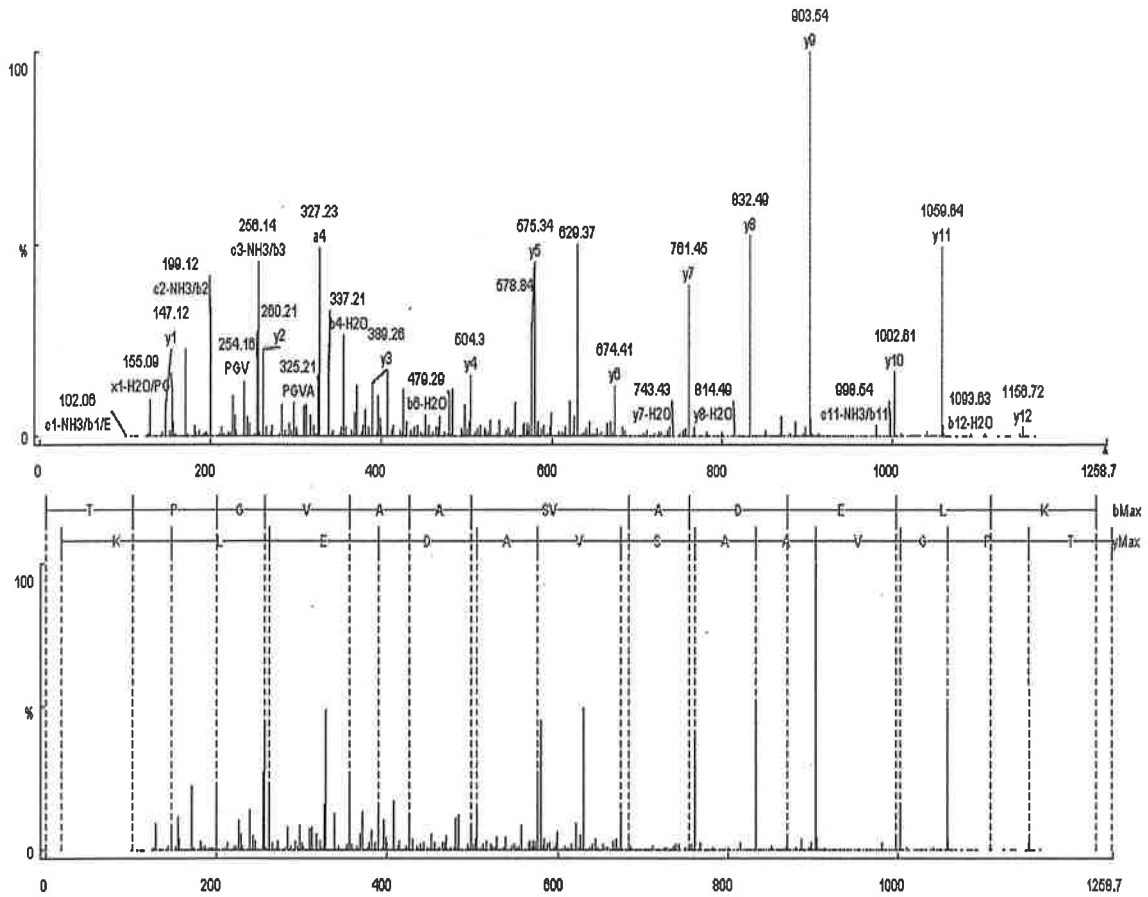


Fig. 16-1-b

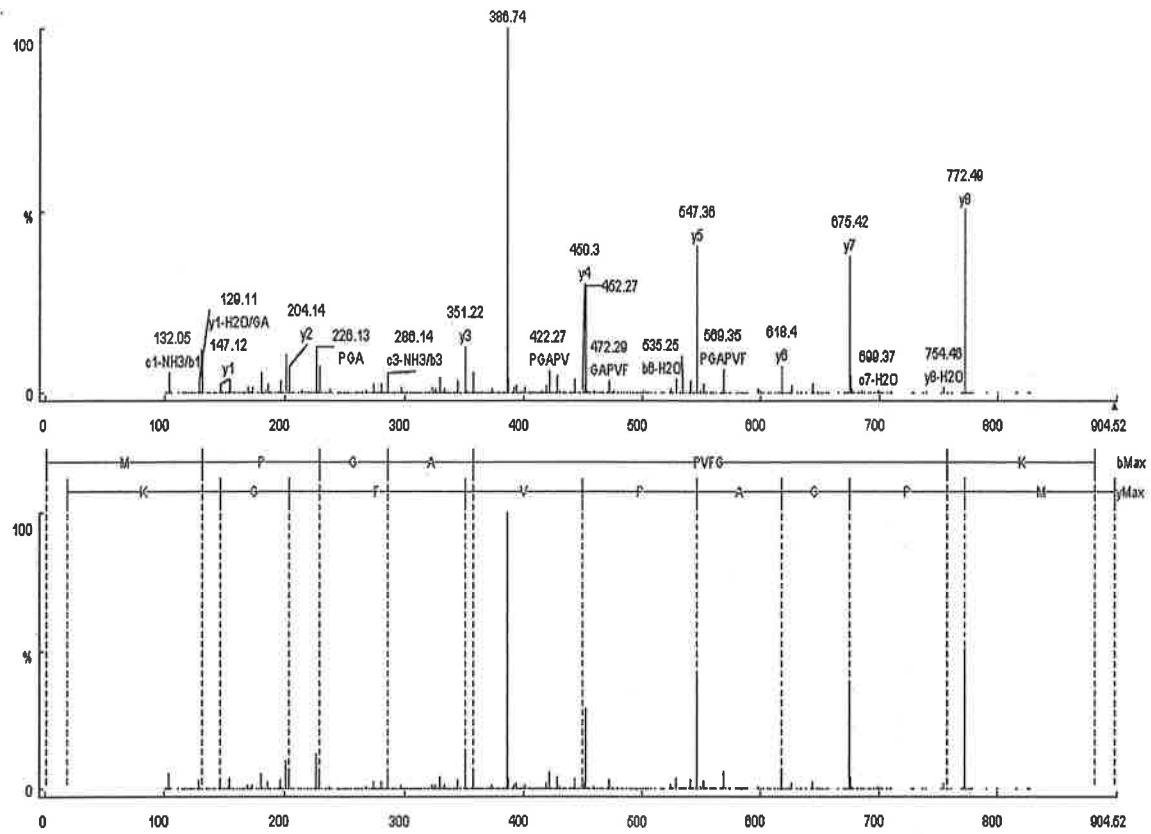


Fig. 16-2-a

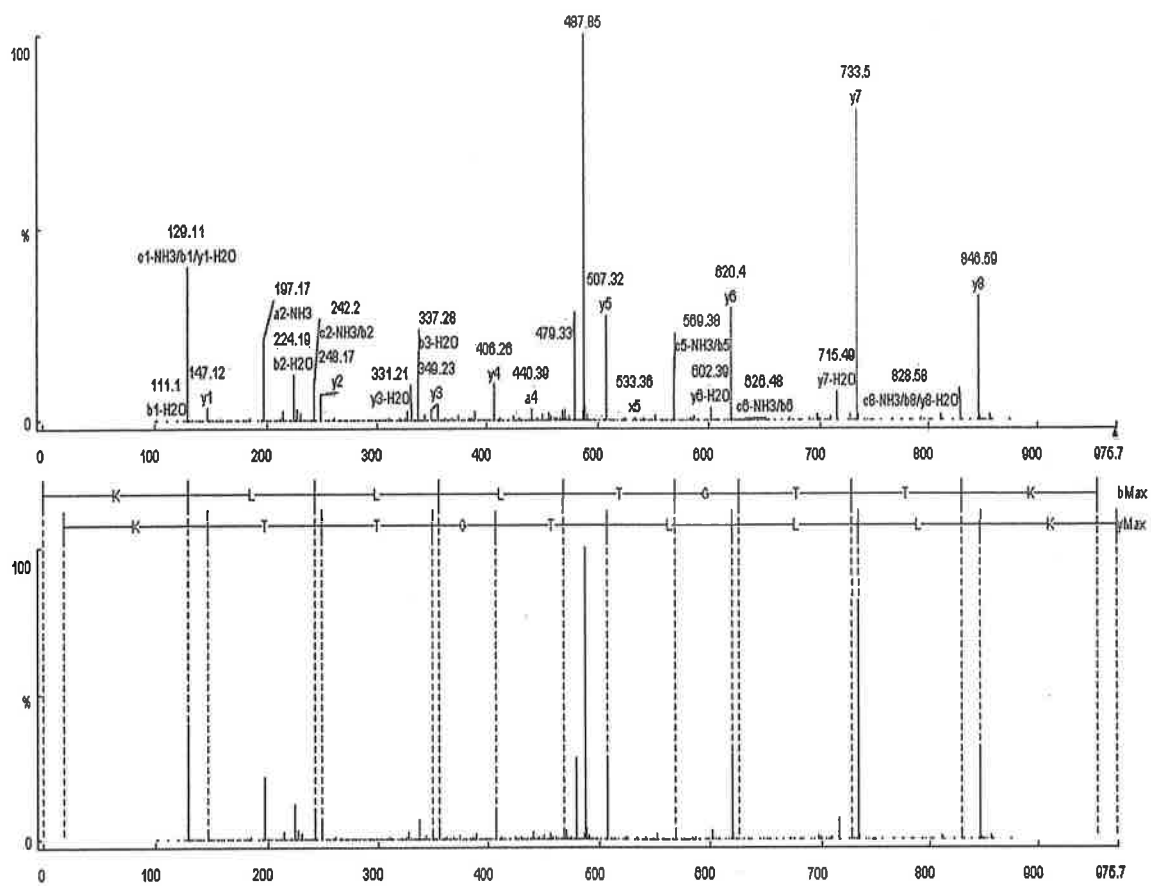


Fig. 16-2-b

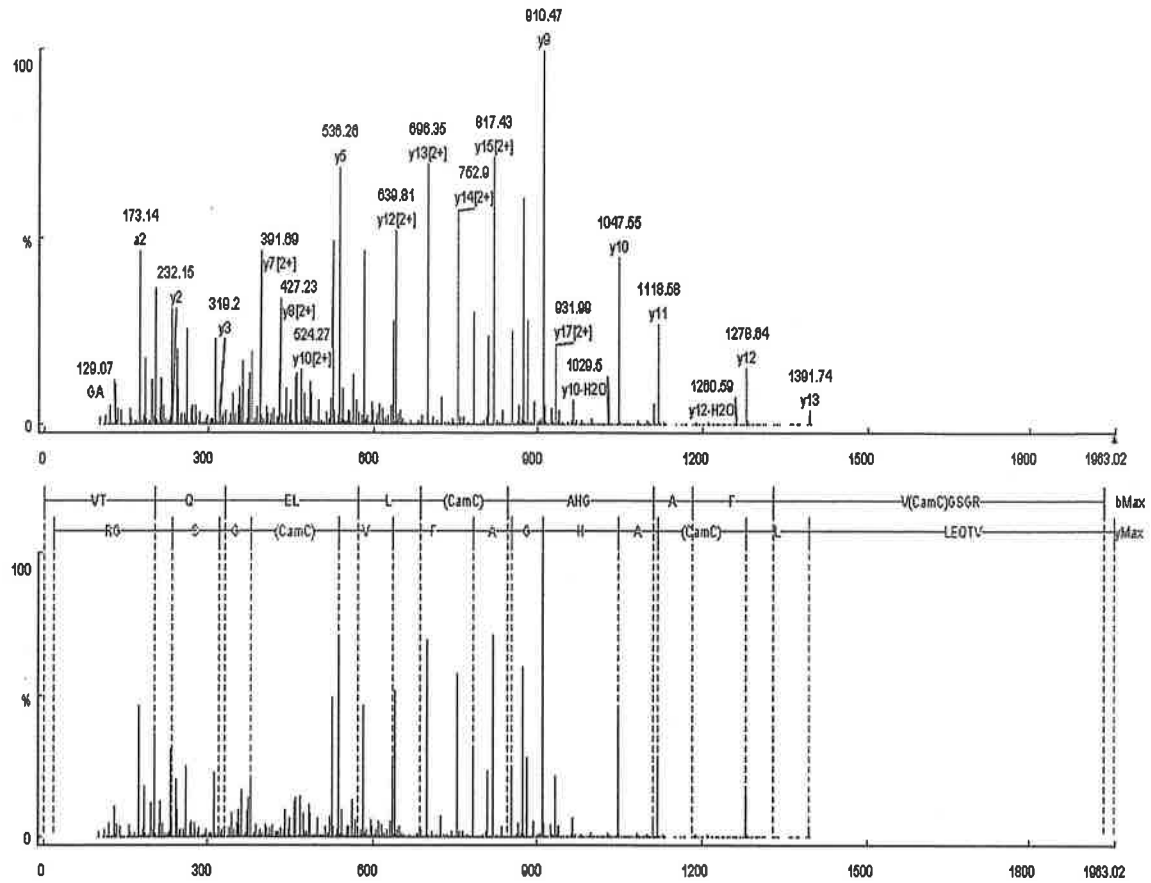


Fig. 16-3

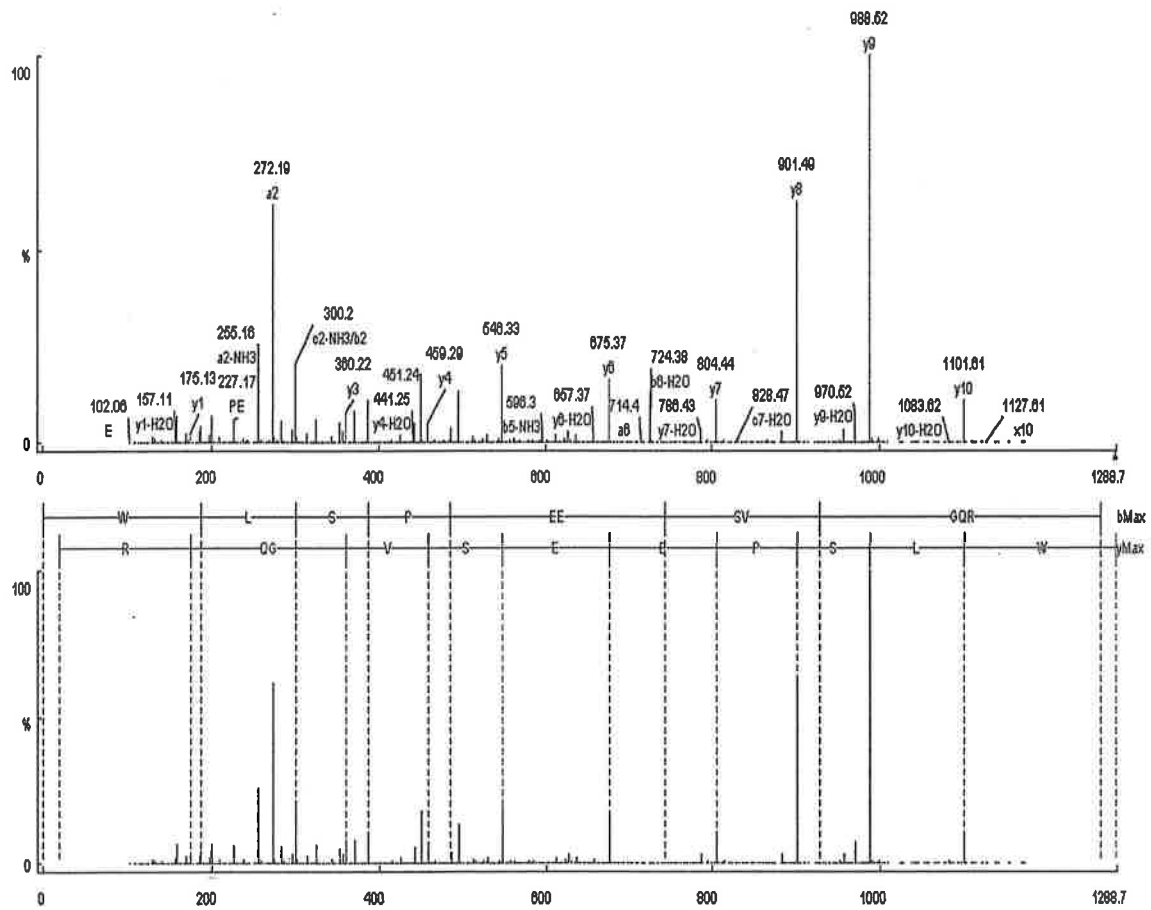


Fig. 17

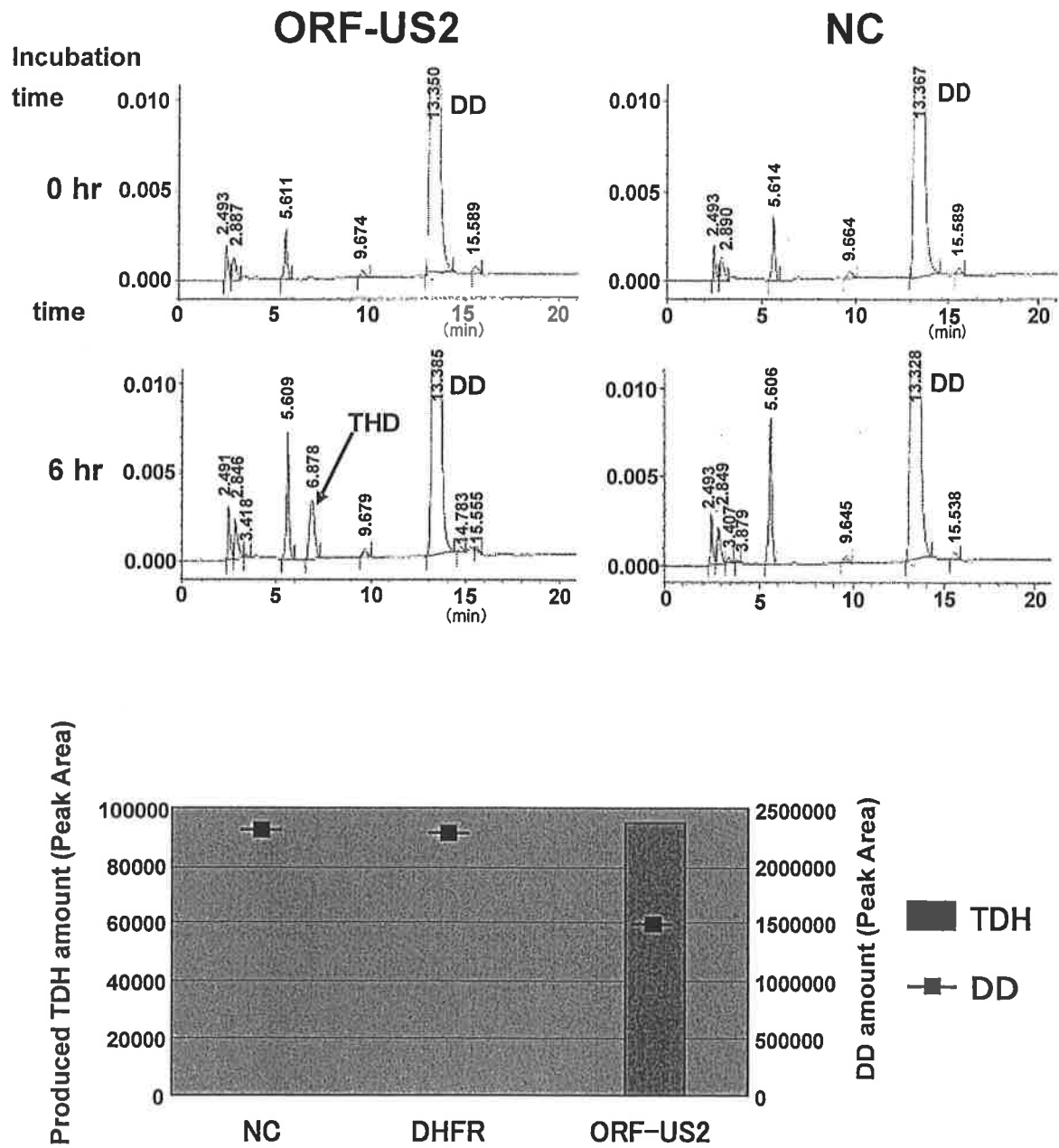


Fig. 18

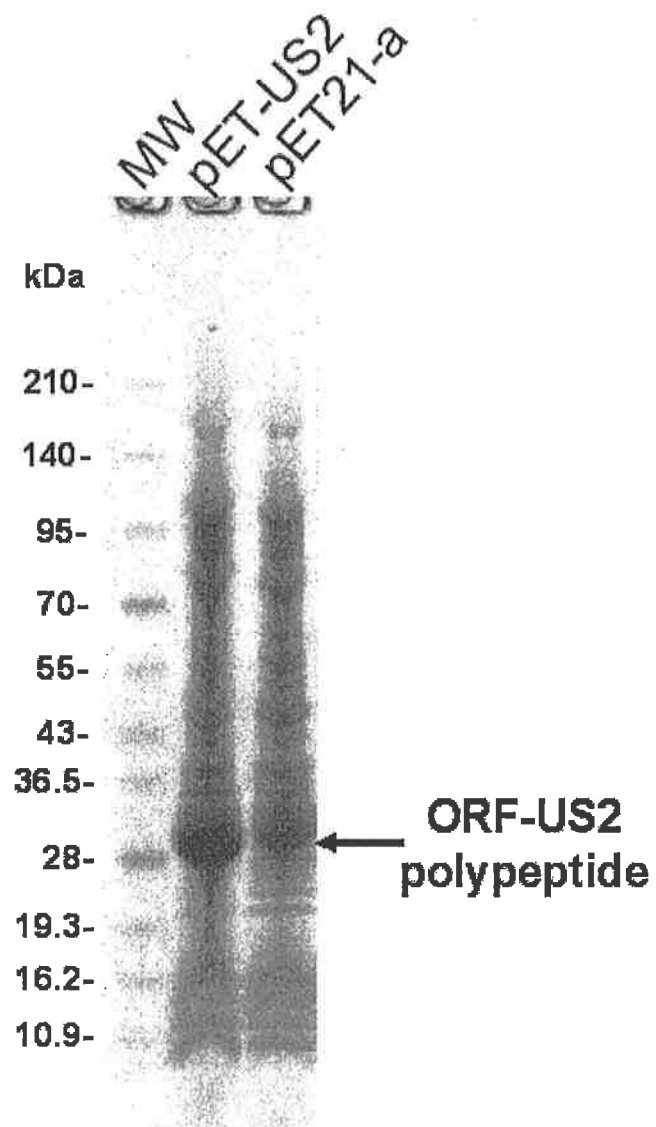


Fig. 19

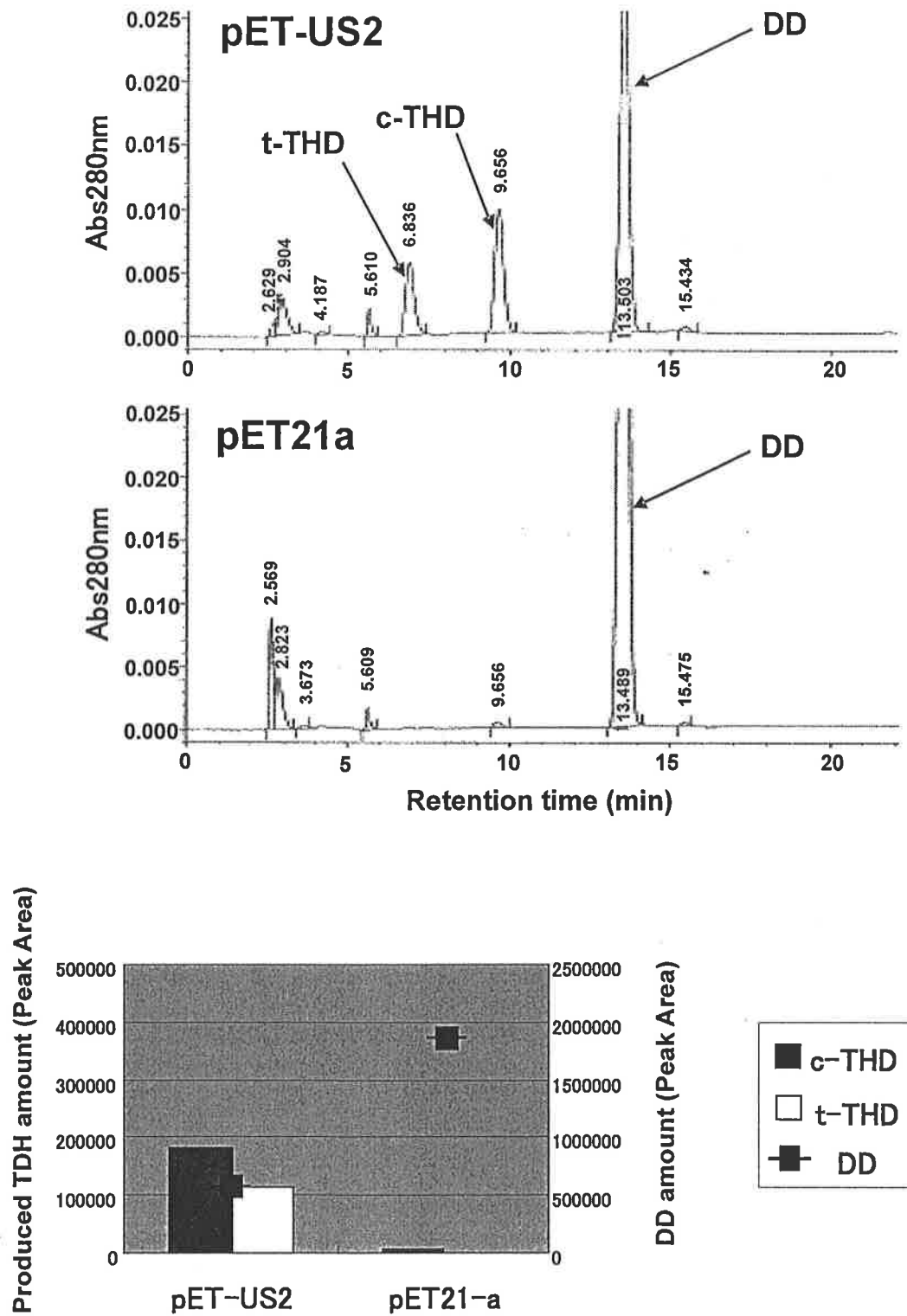


Fig. 20

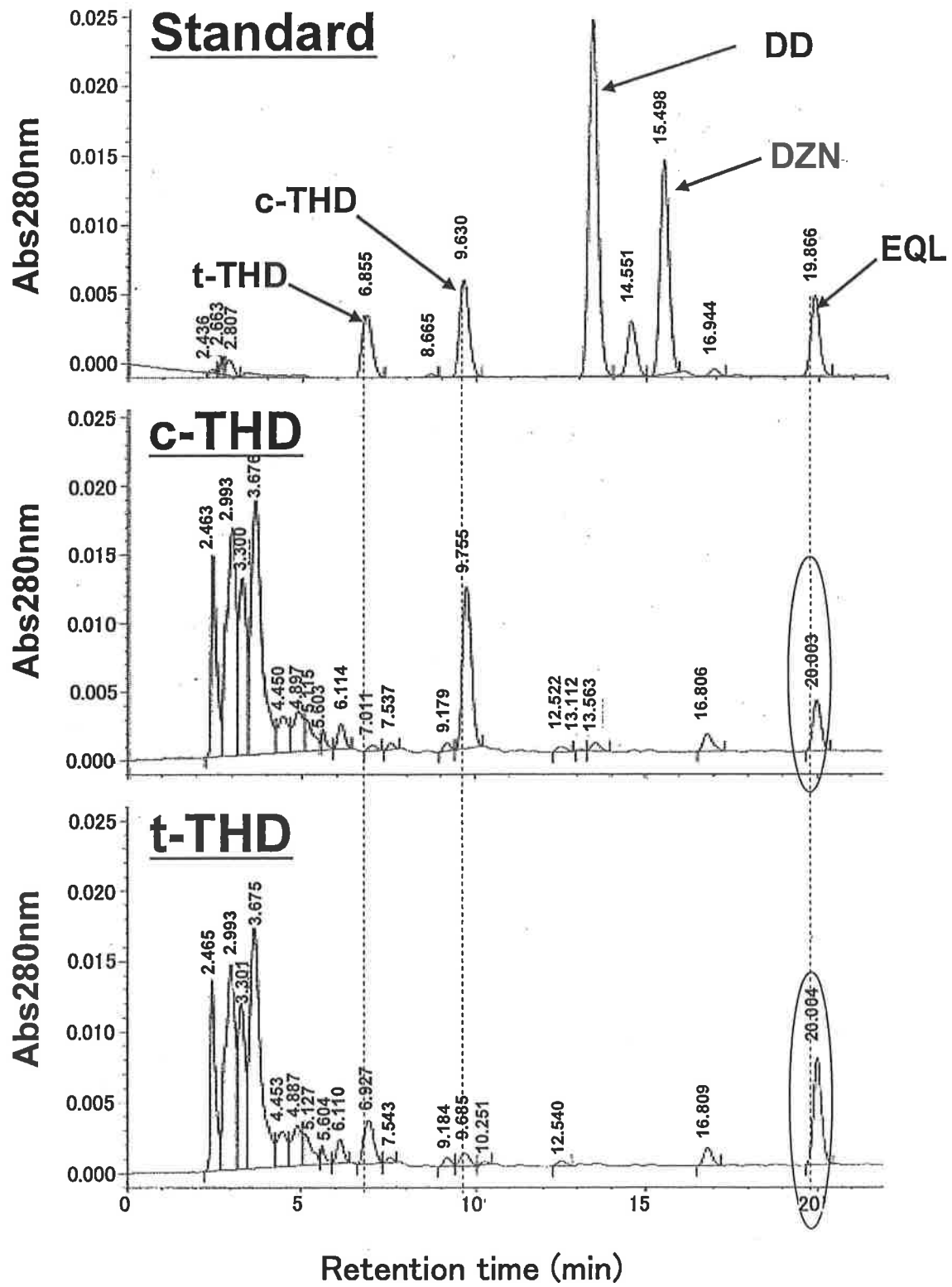


Fig. 21

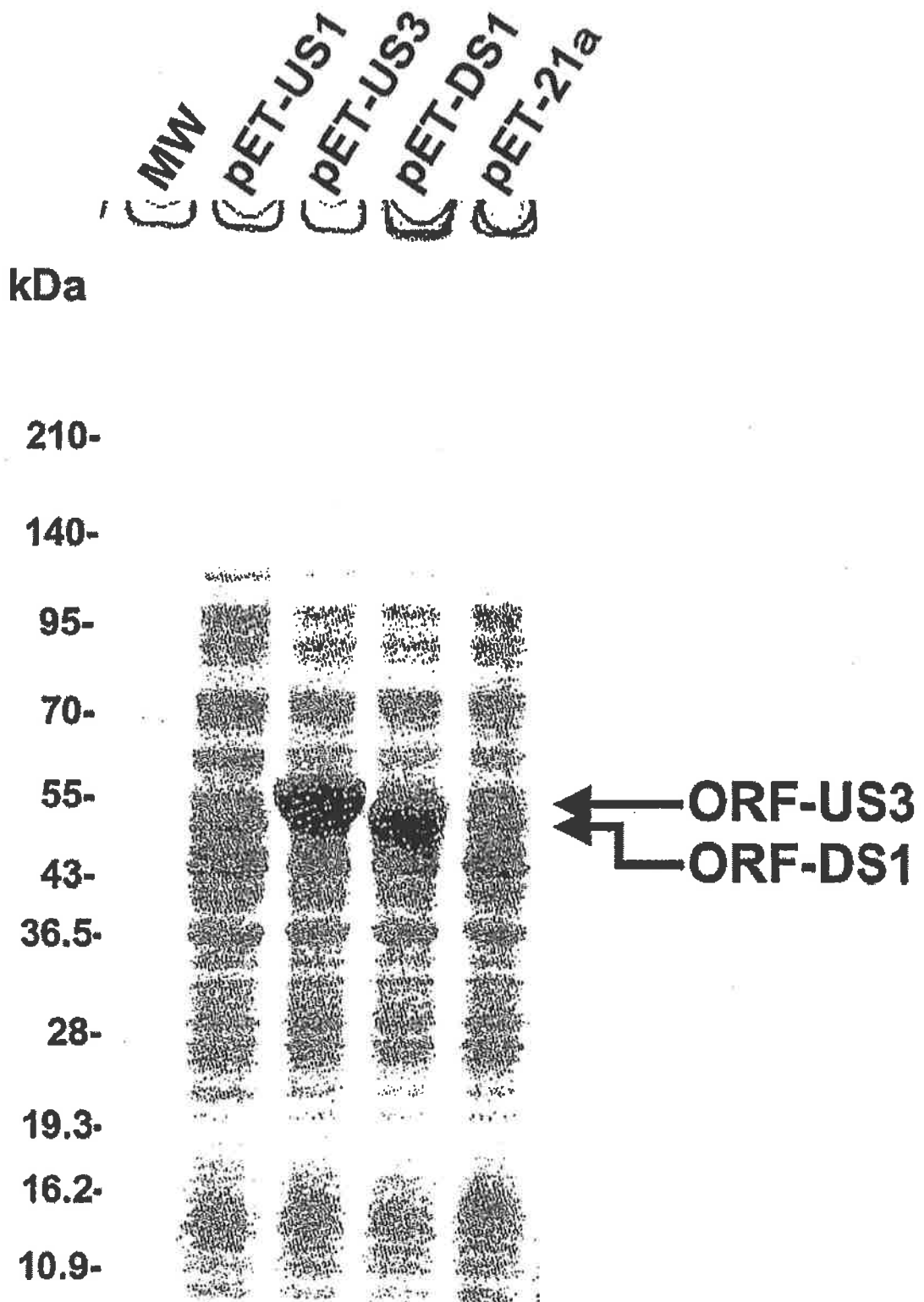


Fig. 22

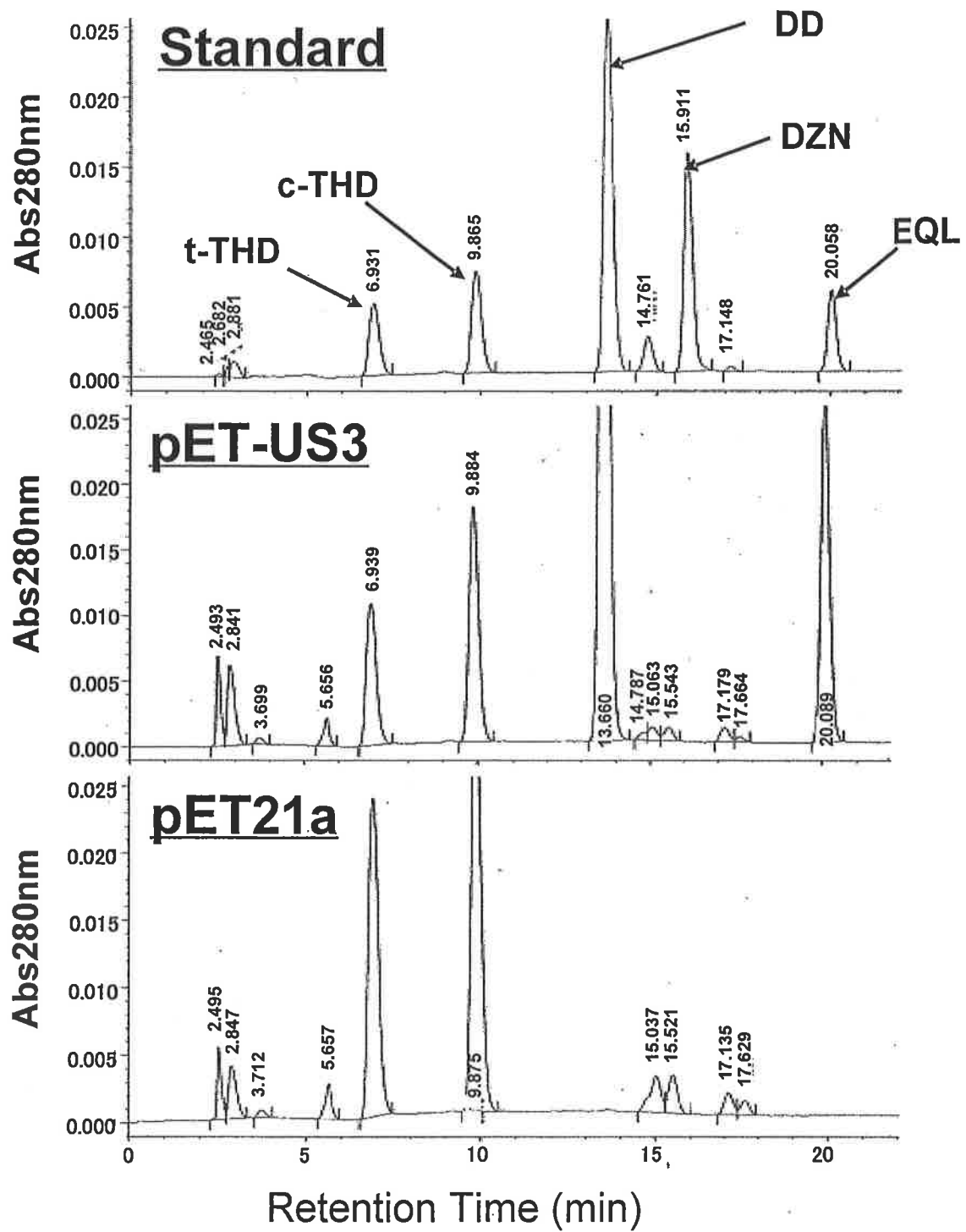


Fig. 23

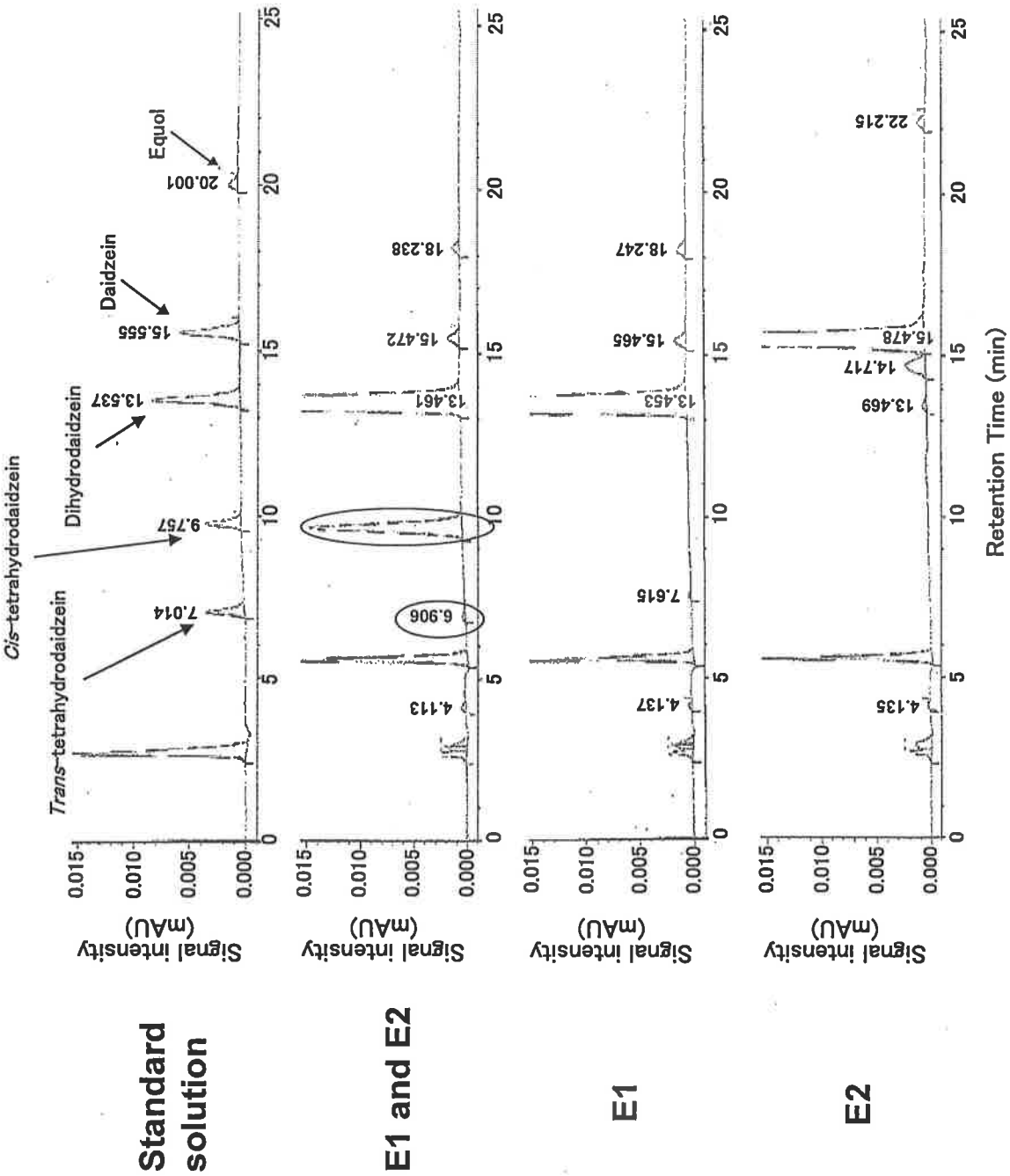


Fig. 24

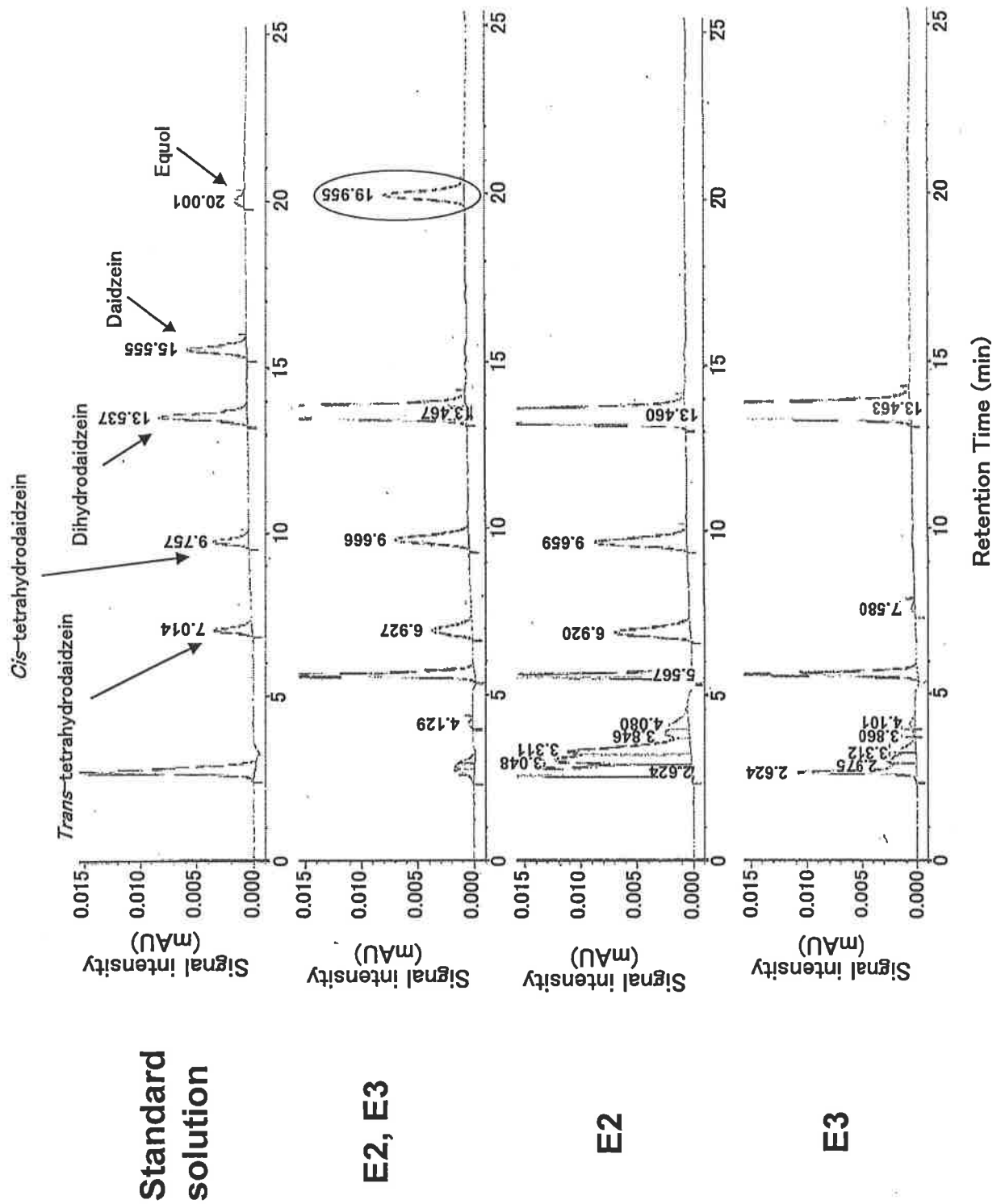


Fig. 25

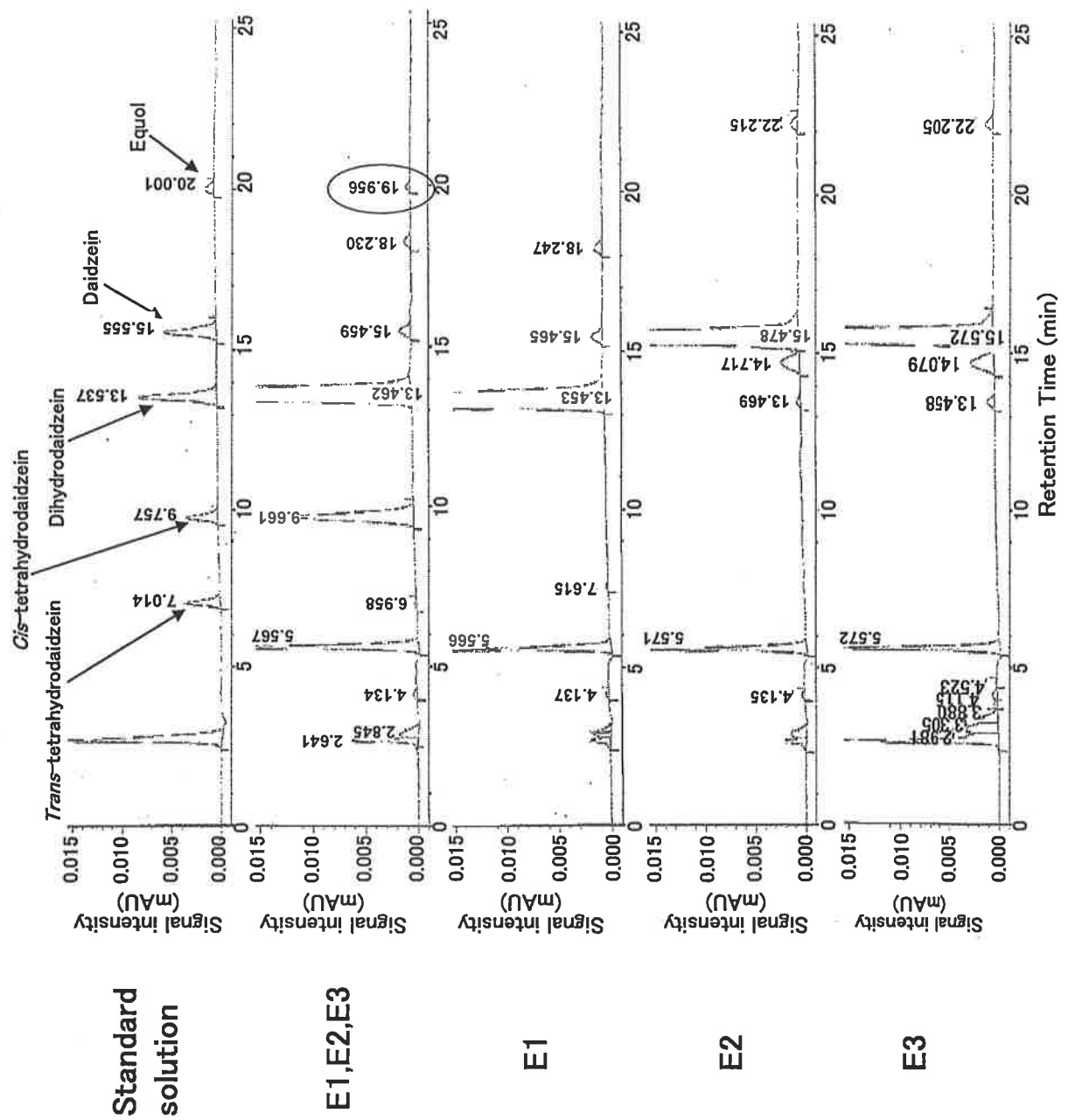


Fig. 26

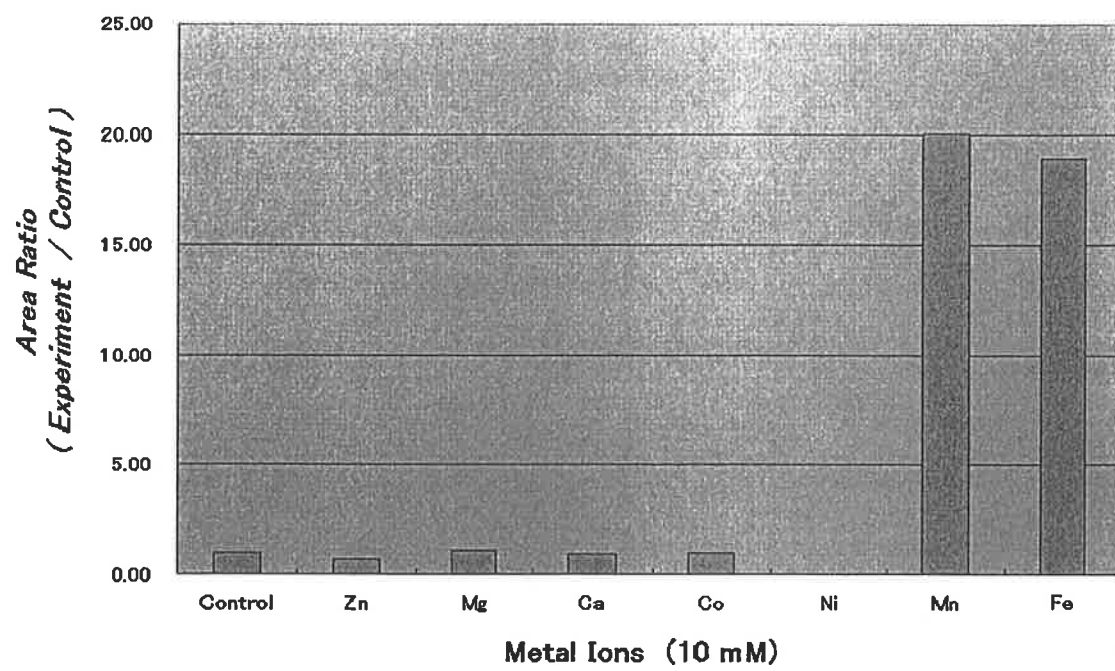


Fig. 27

Lactococcus_E1
 Bacteroides_E1
 Streptococcus_E1

NADPH binding domain
 MKNKFYPKTFERYIGNILEVENRAIRMPMGTELGNPDGSPSIWASLKAYAEADGGTGIVFMDNAGVTFHHVGLSLASDNVIGPMWSVLAKTIKONGAIPGLQIVHPGRDAFVRGDLIS
 MKNKFYPKTFERYIGNILEVENRAIRMPMGTELGNPDGSPSIWASLKAYAEADGGTGIVFMDNAGVTFHHVGLSLASDNVIGPMWSVLAKTIKONGAIPGLQIVHPGRDAFVRGDLIS
 MKNKFYPKTFERYIGNILEVENRAIRMPMGTELGNPDGSPSIWASLKAYAEADGGTGIVFMDNAGVTFHHVGLSLASDNVIGPMWSVLAKTIKONGAIPGLQIVHPGRDAFVRGDLIS

 OYE like FMN family sequence
 SSRIQWEPWYENGGAVPRELTIEEIHDFVGTGFCALRAQTAGEIVDVHAACGVLLSNFLSPRNTRNDIVYSSLHNRARFLLVIRDIKKKCPNLPLAIRLSGIDFEPDGIITEETCE
 SSRIQWEPWYENGGAVPRELTIEEIHDFVGTGFCALRAQTAGEIVDVHAACGVLLSNFLSPRNTRNDIVYSSLHNRARFLLVIRDIKKKCPNLPLAIRLSGIDFEPDGIITEETCE
 SSRIQWEPWYENGGAVPRELTIEEIHDFVGTGFCALRAQTAGEIVDVHAACGVLLSNFLSPRNTRNDIVYSSLHNRARFLLVIRDIKKKCPNLPLAIRLSGIDFEPDGIITEETCE

 Iron-Sulfur Protein, Fe/S4 Cluster
 VAKMCEAAGADAINITWGSAAEYINAAQLLSKHGHNHVEAAQMIKDAYSIPTMLCGGIIYSPEIGEKLLDGVODFIIGKPALADPMWAKKAAEGRPEDIRPCIGCGVGGCHDRGMLSGGV
 VAKMCEAAGADAINITWGSAAEYINAAQLLSKHGHNHVEAAQMIKDAYSIPTMLCGGIIYSPEIGEKLLDGVODFIIGKPALADPMWAKKAAEGRPEDIRPCIGCGVGGCHDRGMLSGGV
 VAKMCEAAGADAINITWGSAAEYINAAQLLSKHGHNHVEAAQMIKDAYSIPTMLCGGIIYSPEIGEKLLDGVODFIIGKPALADPMWAKKAAEGRPEDIRPCIGCGVGGCHDRGMLSGGV

 RAD-dependent pyridine nucleotide reduction signal
 VQCAVNAALYKFDPEVPYPOAEVPKKVIIGABPAGCEAAITAKKCGHDVTIYKRRKIGSVLKEATVSDSKEDLGRLLIYYETQLKKEGIEVITYEATADTVVAGGFDAIVACGATVRML
 VQCAVNAALYKFDPEVPYPOAEVPKKVIIGABPAGCEAAITAKKCGHDVTIYKRRKIGSVLKEATVSDSKEDLGRLLIYYETQLKKEGIEVITYEATADTVVAGGFDAIVACGATVRML
 VQCAVNAALYKFDPEVPYPOAEVPKKVIIGABPAGCEAAITAKKCGHDVTIYKRRKIGSVLKEATVSDSKEDLGRLLIYYETQLKKEGIEVITYEATADTVVAGGFDAIVACGATVRML

 RAD-dependent pyridine nucleotide reduction signal
 NIDGDDPSVYVYANDFLDNDCKSDADRVVYGGGIVGAETALILAERKQDVTITRSPFFVPSGVINGIAYNVRLGIMAGVTIKPSTOLVAVKDGKPMFAGPRGLETLVDYDQTISSGFVP
 NIDGDDPSVYVYANDFLDNDCKSDADRVVYGGGIVGAETALILAERKQDVTITRSPFFVPSGVINGIAYNVRLGIMAGVTIKPSTOLVAVKDGKPMFAGPRGLETLVDYDQTISSGFVP
 NIDGDDPSVYVYANDFLDNDCKSDADRVVYGGGIVGAETALILAERKQDVTITRSPFFVPSGVINGIAYNVRLGIMAGVTIKPSTOLVAVKDGKPMFAGPRGLETLVDYDQTISSGFVP

 Lactococcus_E1
 Bacteroides_E1
 Streptococcus_E1

TFNDFRAQIEEKCEDVRVIGIDCKASRNVDVAHVEGYIAGCNIL
 TFNDFRAQIEEKCEDVRVIGIDCKASRNVDVAHVEGYIAGCNIL
 TFNDFRAQIEEKCEDVRVIGIDCKASRNVDVAHVEGYIAGCNIL

† : FMN binding site (conserved)
 ‡ : FMN binding site (not conserved?)

Fig. 28

NADPH binding domain

Lactococcus_E2
Bacteroides_E2
Streptococcus_E2

MADEVKVKMPGAPVFGKWISPEESVQRLKGGKIILIGTTKGVGRVTOELLCAHGAFVCGSSRTP6VAASVADELKAKGYQAAGMDVDLSDYDAV
MSPHFASQIRWAKEDGPRGKEPTMADEVKVKMPGAPVFGKWISPEESVQRLKGGKIILIGTTKGVGRVTOELLCAHGAFVCGSSRTP6VAASVADELKAKGYQAAGMDVDLSDYDAV
MADEVKVKMPGAPVFGKWISPEESVQRLKGGKIILIGTTKGVGRVTOELLCAHGAFVCGSSRTP6VAASVADELKAKGYQAAGMDVDLSDYDAV

Alcohol dehydrogenase signature

Lactococcus_E2
Bacteroides_E2
Streptococcus_E2

KKWVEECHELIGGIDVVINNASHPGMAPFGEMTPEINWYGIKNELDLVYWCNCAMPYLOKAD-GASIIITSSVTVALQSSNSPQACHAACKGACLSLAROLAAEGGPFGRCHSVTPGLV
KKWVEECHELIGGIDVVINNASHPGMAPFGEMTPEINWYGIKNELDLVYWCNCAMPYLOKAD-GASIIITSSVTGLQSSNSPQACHAACKGACLSLAROLAAEGGPFGRCHSVTPGLV
KKWVOECHELIGGIDVVINNASHPGMAPFGEMTPEINWYGIKNELDLVYWCNCAMPYLOKAD-GASIIITSSVTGLQSSNSPQACHAACKGACLSLAROLAAEGGPFGRCHSVTPGLV

Active site

Glucose/habitat dehydrogenase family signature

Lactococcus_E2
Bacteroides_E2
Streptococcus_E2

WTEAMSNIPKEMASGLVAAQTTOQAVDPMDIAYAYLFLASDESRLITAANIPLYDGGAGAVTGGNGGEIEV
WTEAMSNIPKEMASGLVAAQTTOQAVDPMDIAYAYLFLASDESRLITAANIPLYDGGAGAVTGGNGGEIEV
WTEAMSNIPKEMASGLVAAQTTOQAVDPMDIAYAYLFLASDESRLITAANIPLYDGGAGAVTGGNGGEIEV

Glucose/habitat dehydrogenase family signature

Fig. 29

	FAD binding domain	
Lactococcus_E3	MAEFDVEYDLVWGGGASGKSAALIAAREGKRIVVLEKQIPETGGLSINVAE8TAAFESSIQNELGTPRLSKYHPTKQEGIEKFMGYSHORANDVVRFAFVENSAAETIDIVRDLGWYKAC	
Bacteroides_E3	MAQFDVEYDLVWGGGASGKSAALIAAREGKRIVVLEKQIPETGGLSINVAE8TAAFESSIQNELGTPRLSKYHPTKQEGIEKFMGYSHORANDVVRFAFVENSAAETIDIVRDLGWYKAC	
Streptococcus_E3	MAEFDVEYDLVWGGGASGKSAALIAAREGKRIVVLEKQIPETGGLSINVAE8TAAFESSIQNELGTPRLSKYHPTKQEGIEKFMGYSHORANDVVRFAFVENSAAETIDIVRDLGWYKAC	
Lactococcus_E3	DIAAEDDPNEVITFHLPEGLBAHCDEVLLDAIQKLDVDIFTSIPAKELIIDGAVV6VVAESDGEPLRV6GKAVILATGGNGSSPERIFKYSIFAPAAYNINNTLTPLONVGDGLDLALSA	
Bacteroides_E3	DIAAEDDPNEVITFHLPEGLBAHCDEVLLDAIQKLDVDIFTSIPAKELIIDGAVV6VVAESDGEPLRV6GKAVILATGGNGSSPERIFKYSIFAPAAYNINNTLTPLONVGDGLDLALSA	
Streptococcus_E3	DIAAEDDPSEVITFHLPEGLBAHCDEVLLDAIQKLDVDIFTSIPAKELIIDGAVV6VVAESDGEPLRV6GKAVILATGGNGSSPERIFKYSIFAPAAYNINNTLTPLONVGDGLDLALSA	
	Predicted oxidoreductase [General function prediction only] seq.	
Lactococcus_E3	GAADPTYITTCPIIAAGSRDMITNDSONV6GAGVNP6VWINKT6RRFAESVAENI6D16TTY6KOP6G6W6SILSDADIDRLVAESSEIAIGEFVYVYHKP6MERLPIDELAHLESGLVKKAGS	
Bacteroides_E3	GAADPTYITTCPIIAAGSRDMITNDSONV6GAGVNP6VWINKT6RRFAESVAENI6D16TTY6KOP6G6W6SILSDADIDRLVAESSEIAIGEFVYVYHKP6MERLPIDELAHLESGLVKKAGS	
Streptococcus_E3	GAADDTAITTCPIIAAGSRDMITNDSONV6GAGVNP6VWINKS6R6FCAESVAENI6D16TTY6KOP6G6I6V6SILSDADIDRLVNEESSEIAIGEFVYVYHKP6MERLPIDELAHLESGLVKKAGC	
Lactococcus_E3	FEELAAALIDVPVDITFVATMAQYNEACEKGYDADFHKCPDYLRFWVE6PFYAIPLAT6T6SSA66IRIN6N6QVVDADYNAIP6EL.YAV6L.DAT6L.Y6D6ST6N6EY6P6A6N6F.AHT6SR.IAAR	
Bacteroides_E3	FEELAAALIDVPVDITFVATMAQYNEACEKGYDADFHKCPDYLRFWVE6PFYAIPLAT6T6SSA66IRIN6N6QVVDADYNAIP6EL.YAV6L.DAT6L.Y6D6ST6N6EY6P6A6N6F.AHT6SR.IAAR	
Streptococcus_E3	FEELAEKUDWPAGAFVDITINAYNEACEKGYDADFHKCP6YLRAETDAPFYAIPLAT6T6SSA66IKIN6N6QVVDADYNAIP6EL.YAV6L.DAT6L.Y6D6ST6N6EY6P6A6N6F.AHT6SR.IAAR	
Lactococcus_E3	HAISTH-	
Bacteroides_E3	HAISTH-	
Streptococcus_E3	HALSTNE	

1/42

SEQUENCE LISTING

<110> OTSUKA PHARMACEUTICAL CO., LTD.

<120> Enzyme Relating to Equol Production

<130> P08-130

<150> JP2007-336227

<151> 2007-12-27

<150> JP2008-054874

<151> 2008-3-5

<150> JP2008-080570

<151> 2008-3-26

<160> 69

<170> PatentIn version 3.4

<210> 1

<211> 644

<212> PRT

<213> Lactococcus garvieae

<400> 1

Met Lys Asn Lys Phe Tyr Pro Lys Thr Phe Glu Arg Gly Tyr Ile Gly
1 5 10 15

Asn Leu Glu Val Glu Asn Arg Ala Ile Arg Met Pro Met Gly Thr Glu
20 25 30

Leu Gly Asn Pro Asp Gly Ser Pro Ser Trp Ala Ser Leu Lys Ala Tyr
35 40 45

Ala Glu Ala Ala Asp Gly Gly Thr Gly Ile Val Phe Met Asp Asn Ala
50 55 60

Gly Val Thr Gln Phe His His Val Gly Leu Ser Leu Ala Ser Asp Asn
65 70 75 80

Tyr Ile Gly Pro Met Ser Val Leu Ala Lys Thr Ile Lys Gln His Gly
85 90 95

Ala Ile Pro Gly Leu Gln Ile Val His Pro Gly Arg Asp Ala Ala Phe
100 105 110

Val Arg Gly Asp Asp Leu Ile Ser Ser Ser Arg Ile Gln Trp Glu Pro
115 120 125

Trp Tyr Glu Asn Gly Gly Ala Val Pro Arg Glu Leu Thr Ile Glu Glu
 130 135 140

Ile His Asp Phe Val Gly Tyr Phe Gly Asp Cys Ala Leu Arg Ala Gln
 145 150 155 160

Thr Ala Gly Phe Glu Ile Val Asp Val His Ala Ala Cys Gly Val Leu
 165 170 175

Leu Ser Asn Phe Leu Ser Pro Arg Asn Asn Thr Arg Asn Asp Met Tyr
 180 185 190

Gly Gly Ser Leu His Asn Arg Ala Arg Phe Leu Leu Glu Val Ile Arg
 195 200 205

Asp Ile Lys Lys Lys Cys Pro Asn Leu Pro Leu Ala Ile Arg Leu Ser
 210 215 220

Gly Ile Asp Phe Glu Pro Asp Gly Ile Thr Ile Glu Glu Thr Cys Glu
 225 230 235 240

Val Ala Lys Met Cys Glu Ala Ala Gly Ala Asp Ala Ile Asn Ile Thr
 245 250 255

Trp Gly Ser His Ala Glu Val Ile Asn Ala Ala Gly Leu Leu Ser Lys
 260 265 270

His Gly Ala Asn His Val Glu Ala Ala Lys Met Ile Lys Asp Ala Val
 275 280 285

Ser Ile Pro Thr Met Leu Cys Gly Gly Ile Tyr Ser Pro Glu Ile Gly
 290 295 300

Glu Lys Leu Leu Glu Asp Gly Val Cys Asp Phe Ile Gly Ile Gly Lys
 305 310 315 320

Pro Ala Leu Ala Asp Pro Met Trp Ala Lys Lys Ala Ala Glu Gly Arg
 325 330 335

Pro Glu Asp Ile Arg Pro Cys Ile Gly Cys Gly Val Gly Cys His Asp
 340 345 350

Arg Gly Met Leu Ser Gly Gly Val Val Gln Cys Ala Val Asn Ala Ala
355 360 365

Leu Tyr Lys Phe Asp Glu Pro Val Tyr Pro Gln Ala Glu Val Pro Lys
370 375 380

Lys Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Cys Glu Ala Ala Ile
385 390 395 400

Thr Ala Lys Lys Cys Gly His Asp Val Thr Ile Tyr Glu Lys Arg Lys
405 410 415

Ile Gly Gly Val Leu Lys Glu Ala Thr Val Ser Asp Ser Lys Glu Asp
420 425 430

Leu Gly Arg Leu Ile Thr Tyr Tyr Glu Thr Gln Leu Lys Lys Glu Gly
435 440 445

Ile Glu Val Ile Tyr Glu Glu Ala Thr Ala Asp Thr Val Val Ala Gly
450 455 460

Gly Phe Asp Val Ala Ile Val Ala Cys Gly Ala Thr Val Arg Asn Leu
465 470 475 480

Asn Ile Asp Gly Gln Asp Asp Pro Ser Val Val Tyr Ala Met Asp Phe
485 490 495

Leu Asp Asn Asp Cys Lys Ser Asp Ala Asp Arg Val Val Val Val Gly
500 505 510

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

Gly Lys Asp Val Thr Ile Thr Thr Arg Ser Pro Glu Phe Phe Val Ser
530 535 540

Gly Val Met Gly Ile Ala Tyr Met Val Arg Leu Gly Met Ala Gly Val
545 550 555 560

Thr Ile Lys Pro Ser Thr Gln Leu Val Ala Val Lys Asp Gly Lys Pro
565 570 575

Met Phe Ala Gly Pro Arg Gly Leu Glu Thr Leu Asp Val Asp Gln Thr

Val Arg Gly Asp Asp Leu Ile Ser Ser Ser Arg Ile Gln Trp Glu Pro
115 120 125

Trp Tyr Glu Asn Gly Gly Ala Val Pro Arg Glu Leu Thr Ile Glu Glu
130 135 140

Ile His Asp Phe Val Gly Tyr Phe Gly Asp Cys Ala Leu Arg Ala Gln
145 150 155 160

Thr Ala Gly Phe Glu Ile Val Asp Val His Ala Ala Cys Gly Val Leu
165 170 175

Leu Ser Asn Phe Leu Ser Pro Arg Asn Asn Thr Arg Asn Asp Met Tyr
180 185 190

Gly Gly Ser Leu His Asn Arg Ala Arg Phe Leu Leu Glu Val Ile Arg
195 200 205

Asp Ile Lys Lys Lys Cys Pro Asn Leu Pro Leu Ala Ile Arg Leu Ser
210 215 220

Gly Ile Asp Phe Glu Pro Asp Gly Ile Thr Ile Glu Glu Thr Cys Glu
225 230 235 240

Val Ala Lys Met Cys Glu Ala Ala Gly Ala Asp Ala Ile Asn Ile Thr
245 250 255

Trp Gly Ser His Ala Glu Val Ile Asn Ala Ala Gly Leu Leu Ser Lys
260 265 270

His Gly Ala Asn His Val Glu Ala Ala Lys Met Ile Lys Asp Ala Val
275 280 285

Ser Ile Pro Thr Met Leu Cys Gly Gly Ile Tyr Ser Pro Glu Ile Gly
290 295 300

Glu Lys Leu Leu Glu Asp Gly Val Cys Asp Phe Ile Gly Ile Gly Lys
305 310 315 320

Pro Ala Leu Ala Asp Pro Met Trp Ala Lys Lys Ala Ala Glu Gly Arg
325 330 335

Pro Glu Asp Ile Arg Pro Cys Ile Gly Cys Gly Val Gly Cys His Asp
340 345 350

Arg Gly Met Leu Ser Gly Gly Val Val Gln Cys Ala Val Asn Ala Ala
 355 360 365

Leu Tyr Lys Phe Asp Glu Pro Val Tyr Pro Gln Ala Glu Val Pro Lys
 370 375 380

Lys Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Cys Glu Ala Ala Ile
 385 390 395 400

Thr Ala Lys Lys Cys Gly His Asp Val Thr Ile Tyr Glu Lys Arg Lys
 405 410 415

Ile Gly Gly Val Leu Lys Glu Ala Thr Val Ser Asp Ser Lys Glu Asp
 420 425 430

Leu Gly Arg Leu Ile Thr Tyr Tyr Glu Thr Gln Leu Lys Lys Glu Gly
 435 440 445

Ile Glu Val Ile Tyr Glu Glu Ala Thr Ala Asp Thr Val Val Ala Gly
 450 455 460

Gly Phe Asp Val Ala Ile Val Ala Cys Gly Ala Thr Val Arg Asn Leu
 465 470 475 480

Asn Ile Asp Gly Gln Asp Asp Pro Ser Val Val Tyr Ala Met Asp Phe
 485 490 495

Leu Asp Asn Asp Cys Lys Ser Asp Ala Asp Arg Val Val Val Val Gly
 500 505 510

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

Gly Lys Asp Val Thr Ile Thr Thr Arg Ser Pro Glu Phe Phe Val Pro
 530 535 540

Gly Val Met Gly Ile Ala Tyr Met Val Arg Leu Gly Met Ala Gly Val
 545 550 555 560

Thr Ile Lys Pro Ser Thr Gln Leu Val Ala Val Lys Asp Gly Lys Pro
 565 570 575

Met Phe Ala Gly Pro Arg Gly Leu Glu Thr Leu Asp Val Asp Gln Thr

Val Arg Gly Asp Asp Leu Ile Ser Ser Ser Arg Ile Gln Trp Glu Pro
115 120 125

Trp Tyr Glu Asn Gly Gly Ala Val Pro Arg Glu Leu Thr Ile Glu Glu
 130 135 140

Ile His Asp Phe Val Gly Tyr Phe Gly Asp Cys Ala Leu Arg Ala Gln
 145 150 155 160

Thr Ala Gly Phe Glu Ile Ile Asp Val His Ala Ala Cys Gly Val Leu
 165 170 175

Leu Ser Asn Phe Leu Ser Pro Arg Asn Asn Thr Arg Asn Asp Met Tyr
 180 185 190

Gly Gly Ser Leu His Asn Arg Ala Arg Phe Leu Leu Glu Val Ile Arg
 195 200 205

Asp Ile Lys Lys Lys Cys Pro Asn Leu Pro Leu Ala Ile Arg Leu Ser
 210 215 220

Gly Ile Asp Phe Glu Pro Gly Gly Ile Thr Val Glu Glu Thr Cys Glu
 225 230 235 240

Val Ala Lys Met Cys Glu Ala Ala Gly Ala Asp Ala Ile Asn Ile Thr
 245 250 255

Trp Gly Ser His Ala Glu Val Ile Asn Ala Ala Gly Leu Leu Ser Lys
 260 265 270

His Gly Ala Asn His Val Glu Ala Ala Lys Met Ile Lys Asp Ala Val
 275 280 285

Ser Ile Pro Thr Met Leu Cys Gly Gly Ile Tyr Ser Pro Glu Ile Gly
 290 295 300

Glu Lys Leu Leu Glu Asp Gly Val Cys Asp Phe Ile Gly Ile Gly Lys
 305 310 315 320

Pro Ala Leu Ala Asp Pro Met Trp Ala Lys Lys Ala Ala Glu Gly Arg
 325 330 335

Pro Glu Asp Ile Arg Pro Cys Ile Gly Cys Gly Val Gly Cys His Asp
 340 345 350

Arg Gly Met Leu Ser Gly Gly Val Val Gln Cys Ala Val Asn Ala Ala
 355 360 365

Leu Tyr Lys Phe Asp Glu Pro Val Tyr Pro Gln Ala Glu Val Pro Lys
 370 375 380

Lys Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Cys Glu Ala Ala Ile
 385 390 395 400

Thr Ala Lys Lys Cys Gly His Asp Val Thr Ile Tyr Glu Lys Arg Lys
 405 410 415

Ile Gly Gly Val Leu Lys Glu Ala Thr Val Ser Asp Ser Lys Glu Asp
 420 425 430

Leu Gly Tyr Leu Ile Thr Tyr Tyr Glu Thr Gln Leu Lys Lys Glu Gly
 435 440 445

Ile Glu Val Ile Tyr Glu Glu Ala Thr Ala Ser Thr Val Ala Ala Gly
 450 455 460

Gly Phe Asp Val Ala Ile Val Ala Cys Gly Ala Thr Val Arg Asn Leu
 465 470 475 480

Asn Ile Asp Gly Gln Asp Asp Pro Ser Val Val Tyr Ala Met Asp Phe
 485 490 495

Leu Asp Asn Asp Cys Lys Ser Asp Ala Asp Arg Val Val Val Val Gly
 500 505 510

Gly Gly Ile Val Gly Ala Glu Thr Ala Leu Ile Leu Ala Glu Glu Gln
 515 520 525

Gly Lys Asp Val Thr Ile Thr Thr Arg Ser Pro Glu Phe Phe Val Pro
 530 535 540

Gly Val Met Gly Ile Ala Tyr Met Val Arg Leu Gly Met Ala Gly Val
 545 550 555 560

Thr Ile Lys Pro Ser Thr Gln Leu Val Ala Val Lys Asp Gly Lys Pro
 565 570 575

Met Phe Ala Gly Pro Arg Gly Leu Glu Thr Leu Asp Val Asp Gln Thr

580

585

590

Ile Ile Ser Ser Gly Phe Val Pro Thr Phe Asn Gln Phe Arg Ala Gln
 595 600 605

Ile Glu Glu Lys Cys Glu Asp Val Arg Val Ile Gly Ile Gly Asp Cys
 610 615 620

Lys Ala Ser Arg Met Val Met Asp Ala Val His Glu Gly Tyr Ile Ala
 625 630 635 640

Gly Cys Asn Leu

<210> 4
 <211> 1935
 <212> DNA
 <213> *Lactococcus garvieae*

<400> 4
 atgaagaaca agttctatcc gaagaccttc gagcgcggct acatcggtaa cctagaggtc 60
 gagaaccgag cgatccgcat gccgatgggc accgagctgg gcaaccgga cggctctccc 120
 agctgggcct ccctcaaggc gtacgctgag gctgccgacg gtggaaccgg catcgtgttc 180
 atggacaacg ccggcgtgac ccagttccac catgtcggac tgtccctggc cagcgacaac 240
 tacatcggcc ccatgtccgt cctcgcaaag accatcaagc agcacggggc catccccggc 300
 ctgcagatcg tccacccggg ccgcgacgcg gcgttcgtgc gcggtgacga cctgatctcc 360
 tcttcccgca tccagtggga gccctggtac gagaacggcg gcgctgttcc ccgcgagctc 420
 accatcgagg agatccacga cttcgtcggc tacttcggcg actgcgcact ccgcgcgacg 480
 accgcgggct tcgaaatcgt cgacgtccac gcggcatgcg gcgtcctgct gagcaacttc 540
 ctctcgccgc gcaacaacac ccgcaatgac atgtacggcg gaagcctgca caaccgcgcc 600
 cgcttcctgc tcgaggatc cgcgcacatc aagaagaagt gcccacacct cccgctggct 660
 atccgactct ccggcatcga cttcgaaccg gacggcatca ccatcgagga gacctgcgag 720
 gtcgccaaga tgtgcgaggc agccggtgcg gacgcatca acatcacctg gggttcccat 780
 gcagaggatc taaacgcggc cggcctgctc tccaagcacg gcgccaacca cgtcgaggca 840
 gcgaagatga tcaaggacgc tgtagcatc cccaccatgc tgtgcggcgg catctactcc 900
 cccgagatcg gcgagaagct gctcgaggac ggctctgctg acttcacatc catcggaag 960

cccgcgctcg ccgaccccat gtgggccaag aaggcagctg aggggcgctcc tgaggacatc 1020
 aggccctgca tcggttgagg cgtcggctgc catgaccgag gcatgctctc cggcggcgctc 1080
 gtccagtgcg ccgtcaacgc ggccctgtac aagttcgacg aaccggtcta cccgcaggct 1140
 gaggttccca agaaggtcat catcatcggc gcaggccccg ctggctgcga ggctgccatc 1200
 accgcgaaga agtgcggcca tgacgtcacc atctacgaga agcgcaagat cgggtggcggtt 1260
 ctgaaggagg ctaccgtctc cgacagcaag gaggacctcg gccgcctcat cacctactac 1320
 gagaccagc tcaagaagga gggcatcgag gtcattctac aggaggccac tgcagacacc 1380
 gttgtagccg gcggcttcga cgtcgccatc gtcgcctgcg gcgccaccgt gcgcaacctc 1440
 aacatcgacg gccaggacga cccctccgtc gtgtacgcga tggacttcct ggacaacgac 1500
 tgcaagagcg atgccgacag ggtcgtcggt gtcggcggtg gcatcgtggg tgccgagacc 1560
 gcgctgatcc tcgcggagga gcggggcaag gatgtcacca tcaccaccg ctccccggag 1620
 ttcttcgtct ccggcgctcat gggcatcgcc tacatggttc gcctgggtat ggcgggagtc 1680
 acgatcaagc cctccacca gctcgtcgcc gtcaaggatg gcaagcccat gttcgccggc 1740
 ccccgcggcc tggagaccct ggacgtcgac cagacaatca tctcctctgg ctctgtcccg 1800
 accttcaacc agttccgcgc ccagatcgag gagaagtgcg aggacgtcag ggtcatcggc 1860
 atcggcgact gcaaggcctc ccgcatggtc atggacgctg tccacgaggg ctacatcgct 1920
 ggctgcaacc ttag 1935

<210> 5

<211> 1935

<212> DNA

<213> Bacteroides ovatus

<400> 5

atgaagaaca agttctatcc gaagaccttc gagcgcggct acatcgga cctagaggtc 60
 gagaaccgag cgatccgcat gccgatgggc accgagctgg gcaaccggga cggctctccc 120
 agctgggcct ccttcaaggc gtacgtgag gctgccgacg gtggaaccgg catcgtgttc 180
 atggacaacg ccggcgtgac ccagttccac catgtcggac tgtccctggc cagcgacaac 240
 tacatcggcc ccatgtccgt cctcgcaaag accatcaagc agcacggggc catccccggc 300
 ctgcagatcg tccaccggg ccgcgacgcg gcgttcgtgc gcggtgacga cctgatctcc 360
 tcttcccgca tccagtggga gccctggtac gagaacggcg gcgctgttcc ccgcgagctc 420
 accatcgagg agatccacga ctctgtcggt tacttcggcg actgcgcact ccgcgcgcag 480

accgcgggct tcgaaatcgt cgacgtccac gcggcatgcg gcgtcctgct gagcaacttc 540
 ctctcgccgc gcaacaacac ccgtaacgac atgtacggcg gaagcctgca caaccgcgcc 600
 cgcttcctgc tcgaggtcat ccgcgacatc aagaagaagt gcccacacct cccgctggct 660
 atccgactct ccggcatcga cttcgaaccg gacggcatca ccatcgagga gacctgcgag 720
 gtgcgaaga tgtgcgagga agccggtgcg gacgcatca acatcacctg gggttcccat 780
 gcagagggtca taaacgcggc cggcctgctc tccaagcacg gcgccaacca cgtcgaggca 840
 gcgaagatga tcaaggacgc tgtagcatc cccaccatgc tgtgcggcgg catctactcc 900
 cccgagatcg gcgagaagct gctcgaggac gggtctgctg acttcacatcg catcggaag 960
 cccgcgctcg ccgaccccat gtgggccaag aaggcagctg aggggcgtcc tgaggacatc 1020
 aggcctgca tcggttgcg cgtcggctgc catgaccgcg gcatgctctc cggcggcgtc 1080
 gtccagtgcg ccgtcaacgc ggccctgtac aagttcgacg aaccgtcta cccgcaggct 1140
 gaggttccca agaaggtcat catcatcggc gcaggccccg ctggctgca ggctgccatc 1200
 accgcgaaga agtgcggcc tgacgtcacc atctacgaga agcgcaagat cgggtggcgtt 1260
 ctgaaggagg ctaccgtctc cgacagcaag gaggacctcg gccgcctcat cacctactac 1320
 gagaccagc tcaagaagga gggcatcgag gtcattctac aggaggccac tgcagacacc 1380
 gttgtagccg gcggcttcga cgtcgccatc gtcgcctgcg gcgccaccgt gcgcaacctc 1440
 aacatcgacg gccaggacga cccctccgtc gtgtacgca tggacttcct ggacaacgac 1500
 tgcaagagcg atgccgacag ggtcgtcgtt gtcggcgggtg gcatcgtggg cgcgagacc 1560
 gcgctgatcc tcgcggagga gcggggcaag gatgtcacca tcaccaccg ctccccggag 1620
 ttcttcgtcc ccggcgtcat gggcatcgcc tacatggttc gcctgggtat ggcgggagtc 1680
 acgatcaagc cctccaccca gctcgtcgcc gtcaaggacg gcaagcccat gttcgccggc 1740
 cccgcgggcc tggagaccct ggacgtcgac cagacaatca tctcctctgg cttcgtcccg 1800
 acctcaacc agttccgcgc ccagatcgag gagaagtgcg aggacgtcag ggtcatcggc 1860
 atcggcgact gcaaggcctc ccgcatggtc atggacgctg tccacgaggg ctacctcgt 1920
 ggctgcaacc ttag 1935

<210> 6
 <211> 1935
 <212> DNA
 <213> Streptococcus constellatus
 <400> 6

atgaaaaata agttctatcc gaagaccttc gagcgcggtt acatcggtaa cctagaggtc	60
gagaaccgag cgatccgcat gccgatgggc accgagctgg gcaaccggga cggctctccc	120
agctgggcct ccctcaaggc gtacgccgag gctgccgacg gcggtaccgg catcgtgttc	180
atggacaacg ccggcgtgac ccagttccac catgtcggac tttccctggc cagcgacaag	240
tacatcggcc ccatgtccgt cctcgctaag accatcaagc agcacggggc catccccggc	300
ctgcagatcg tccatccggg ccgcgacgcg gcgttcgtgc gcggtgacga cctgatctcc	360
tcctcccgca tccagtggga gccctggtag gagaacggcg gcgctgttcc ccgcgagctc	420
accatcgagg agatccacga cttcgtcggg tacttcggcg actgcgcact ccgcgcgcag	480
accgcgggct tcgaaatcat cgacgtccac gcggcatgcg gcgtcctgct gagcaacttc	540
ctctcgccgc gcaacaacac ccgcaacgac atgtacggcg gaagcctgca caaccgcgt	600
cgcttcctgc tcgaggtcat ccgcgacatc aagaagaagt gcccacacct cccgctggct	660
atccgactct ccggcatcga tttcgagccg ggccggcatca ccgtcgagga gacctgcgag	720
gtcgccaaga tgtgcgaggc agccggtgcg gacgccatca acatcacctg gggttcccat	780
gcagaggtca tcaacgcggc cggcctgctc tccaagcacg gcgccaacca cgtcgaggca	840
gcgaagatga tcaaggacgc tgtagcatc cccaccatgc tgtcgggcgg catctactcc	900
cccagatcgc gcgagaagct gctcgaggac gggtctctgc acttcacatcg catcggaag	960
ccagcgctcg ctgaccccat gtgggccaag aaggcggctg agggcggtcc tgaggacatc	1020
aggccctgca tcggttgccg cgtcggctgc catgaccgcg gcatgctctc cggcggcgctc	1080
gtccagtgcg ccgtcaacgc ggccctgtac aagttcgacg agcccgctta cccgcaggct	1140
gaggttccca agaaggttat catcatcggc gcaggtcccg ctggctgcga ggctgccatc	1200
accgcgaaga agtgcggcca tgacgtcacc atatacgaga agcgcaagat cggcggcggtt	1260
ctgaaggagg ctaccgtctc cgacagcaag gaggacctcg gctacctcat cacctactac	1320
gagaccacgc tcaagaagga gggcatcgag gtcactctac aggaggccac tgcaagcacc	1380
gttgacgccc gcggcttcga cgtcgccatc gtcgcctgcg gcgccaccgt gcgcaacctc	1440
aacatcgacg gccaggacga cccctccgtc gtgtacgcga tggacttcct ggacaacgac	1500
tgtaagagcg acgccgacag ggtcgtcgtt gtcggcggcg gcatcgtggg tgccgagacc	1560
gcgctgatcc tcgcggagga gcagggaag gacgtcacca tcactaccgc ctccccggag	1620
ttcttctgct ccggcgtcat gggtatcgcc tacatggttc gccttgcat ggcgggcgctc	1680
acgatcaagc cctccacca gctcgtcgcc gtcaaggacg gcaagcccat gttcgccggt	1740

ccccgcgggcc tggagaccct ggacgtcgac cagaccatca tctcctctgg cttcgtcccg 1800
 accttcaacc agttccgcgc ccagatcgag gagaagtgcg aggacgtcag ggtcatcggc 1860
 atcggcgact gcaaggcctc ccgtatggtc atggacgtg tccacgaggg ctacatcgct 1920
 ggctgcaacc tgtag 1935

<210> 7
 <211> 286
 <212> PRT
 <213> *Lactococcus garvieae*

<400> 7

Met Ala Gln Glu Val Lys Val Pro Lys Met Pro Gly Ala Pro Val Phe
1 5 10 15

Gly Lys Trp Ile Ser Pro Glu Glu Ser Val Gly Gln Arg Leu Lys Gly
20 25 30

Lys Lys Ile Leu Leu Thr Gly Thr Thr Lys Gly Val Gly Arg Val Thr
35 40 45

Gln Glu Leu Leu Cys Ala His Gly Ala Phe Val Cys Gly Ser Gly Arg
50 55 60

Thr Pro Gly Val Ala Ala Ser Val Ala Asp Glu Leu Lys Ala Lys Gly
65 70 75 80

Tyr Gln Ala Ala Gly Met Asp Val Asp Leu Ser Asp Tyr Asp Ala Val
85 90 95

Lys Lys Trp Val Glu Glu Cys Ala Glu Leu Met Gly Gly Ile Asp Val
100 105 110

Val Ile Asn Asn Ala Ser His Pro Gly Met Ala Pro Phe Gly Glu Met
115 120 125

Thr Pro Glu Ile Trp Asn Tyr Gly Ile Lys Asn Glu Leu Asp Leu Val
130 135 140

Tyr Asn Val Cys Asn Cys Ala Trp Pro Tyr Leu Gln Lys Ala Asp Gly
145 150 155 160

Ala Ser Ile Ile Ile Thr Ser Ser Thr Val Ala Leu Gln Gly Ser Asn
165 170 175

Ser Pro Gln Ala Cys His Ala Ala Cys Lys Gly Ala Cys Leu Ser Leu
180 185 190

Ala Arg Gln Leu Ala Ala Glu Gly Gly Pro Phe Gly Ile Arg Cys Asn
195 200 205

Ser Val Thr Pro Gly Leu Val Trp Thr Glu Ala Met Ser Asn Ile Pro
210 215 220

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

Val Asp Pro Met Asp Ile Ala Tyr Ala Tyr Leu Phe Leu Ala Ser Asp
245 250 255

Glu Ser Arg Gln Ile Thr Ala Ala Asn Ile Pro Val Asp Gly Gly Cys
260 265 270

Ala Gly Ala Val Thr Gly Gly Met Gln Gly Glu Ile Glu Val
275 280 285

<210> 8
<211> 310
<212> PRT
<213> Bacteroides ovatus

<400> 8

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

Pro Arg Gln Gly Lys Glu Pro Thr Met Ala Gln Glu Val Lys Val Pro
20 25 30

Lys Met Pro Gly Ala Pro Val Phe Gly Lys Trp Ile Ser Pro Glu Glu
35 40 45

Ser Val Gly Gln Arg Leu Lys Gly Lys Lys Ile Leu Leu Thr Gly Thr
50 55 60

Thr Lys Gly Val Gly Arg Val Thr Gln Glu Leu Leu Cys Ala His Gly
65 70 75 80

Ala Phe Val Cys Gly Ser Gly Arg Thr Pro Gly Val Ala Ala Ser Val
85 90 95

Ala Asp Glu Leu Lys Ala Lys Gly Tyr Gln Ala Ala Gly Met Asp Val
100 105 110

Asp Leu Ser Asp Tyr Asp Ala Val Lys Lys Trp Val Glu Glu Cys Ala
115 120 125

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

Gly Met Ala Pro Phe Gly Glu Met Thr Pro Glu Ile Trp Asn Tyr Gly
145 150 155 160

Val Lys Asn Glu Leu Asp Leu Val Tyr Asn Val Cys Asn Cys Ala Trp
165 170 175

Pro Tyr Leu Gln Lys Ala Asp Gly Ala Ser Ile Ile Ile Thr Ser Ser
180 185 190

Thr Val Gly Leu Gln Gly Ser Asn Ser Pro Gln Ala Cys His Ala Ala
195 200 205

Cys Lys Gly Ala Cys Leu Ser Leu Ala Arg Gln Leu Ala Ala Glu Gly
210 215 220

Gly Pro Phe Gly Ile Arg Cys Asn Ser Val Thr Pro Gly Leu Val Trp
225 230 235 240

Thr Glu Ala Met Ser Asn Ile Pro Lys Glu Met Ala Ser Gly Leu Val
245 250 255

Ala Ala Gln Thr Thr Gln Gln Ala Val Asp Pro Met Asp Ile Ala Tyr
260 265 270

Ala Tyr Leu Phe Leu Ala Ser Asp Glu Ser Arg Gln Ile Thr Ala Ala
275 280 285

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

Gln Gly Glu Ile Glu Val
305 310

<210> 9
<211> 287
<212> PRT
<213> Streptococcus constellatus

<400> 9

Met Ala Gln Glu Val Lys Cys Ala Lys Met Pro Gly Ala Pro Val Phe
1 5 10 15

Gly Lys Trp Ile Ser Pro Glu Glu Ser Ile Gly Gln Arg Leu Lys Gly
20 25 30

Lys Lys Ile Ile Leu Thr Gly Thr Thr Lys Gly Val Gly Lys Val Thr
35 40 45

Gln Glu Leu Leu Cys Ala His Gly Ala Phe Val Cys Gly Ser Gly Arg
50 55 60

Thr Pro Gly Val Ala Ala Ser Val Ala Asp Glu Leu Lys Ala Lys Gly
65 70 75 80

Tyr Gln Ala Ala Gly Met Asp Val Asp Leu Ser Asp Tyr Glu Ala Val
85 90 95

Lys Lys Trp Val Gln Glu Cys Ala Glu Leu Met Gly Gly Ile Asp Val
100 105 110

Val Ile Asn Asn Ala Ser His Pro Gly Met Ala Pro Phe Glu Glu Met
115 120 125

Thr Pro Glu Ile Trp Asn Tyr Gly Ile Lys Asn Glu Leu Asp Leu Val
130 135 140

Tyr Asn Val Cys Asn Cys Ala Trp Pro Tyr Leu Lys Glu Ala Glu Gly
145 150 155 160

Gly Ala Ser Ile Ile Ile Thr Ser Ser Thr Val Gly Leu Gln Gly Thr
165 170 175

Asn Ser Pro Gln Ala Cys His Ala Ala Ala Lys Gly Ala Cys Leu Ser

180

185

190

Leu Ala Arg Gln Leu Ala Ala Glu Gly Gly Pro Phe Gly Ile Arg Cys
 195 200 205

Asn Ser Val Thr Pro Gly Leu Val Trp Thr Glu Ala Met Ala Asn Ile
 210 215 220

Pro Lys Glu Met Ala Ser Gly Leu Val Gly Ala Gln Thr Thr Gln Gln
 225 230 235 240

Ala Ile Asp Pro Met Asp Ile Ala Tyr Ala Tyr Leu Phe Leu Ala Ser
 245 250 255

Asp Glu Ala Arg Gln Ile Thr Ala Ala Asn Leu Pro Val Asp Gly Gly
 260 265 270

Cys Ala Gly Ala Val Thr Gly Gly Met Gln Gly Glu Ile Glu Gly
 275 280 285

<210> 10

<211> 861

<212> DNA

<213> *Lactococcus garvieae*

<400> 10

atggcacagg aagtcaaagt cccaagatg cccggcgac ccgtgttcgg caagtggatc 60

tccccgagg agtccgtcgg ccagcgctg aagggaaga agatcctgct caccggcacc 120

accaagggcg tcggcagggt caccaggag ctgctgtgcg cacacggcgc cttcgtctgc 180

ggctccggcc gcacccccgg cgtggcagcc tccgtcgccg acgagctgaa ggccaagggc 240

taccaggccg ccggcatgga cgtcgacctg tctgactacg acgccgtgaa gaagtgggtt 300

gaggagtgcg ccgagctcat gggcggcatc gacgtcgtca tcaacaacgc gtcccacccc 360

ggcatggccc cttcggcga gatgacccg gagatctgga actacggcat caagaacgag 420

ctcgacctcg totacaacgt ctgcaactgc gcatggccct acctgcagaa ggcagacggc 480

gcctccatca tcatcacctc ctccaccgtc gccctccagg gcagcaactc ccctcaggcc 540

tgtcacgctg cctgcaaggg cgcctgcctg tccctggccc gccagctcgc cgctgagggc 600

ggccccttcg gcatccgctg caactccgtc acccggggcc tggctctggac cgaggccatg 660

tccaacatcc ccaaggagat ggcaagcggc ctggtcgcag ccagaccac ccagcaggct 720

gtcgacccga tggacatcgc ctacgcctac ctgttcctgg catccgacga gtcccgccag 780
 atcacccgtg ccaacatccc cgtcgacggc ggctgcgccg gcgctgtgac cggcggcatg 840
 cagggcgaga tcgaggtcta g 861

<210> 11
 <211> 933
 <212> DNA
 <213> Bacteroides ovatus

<400> 11
 atgagccgc attttgcgag ccaaagatgg gctgcaaagg aagacggccc aagacaagga 60
 aaggaaccaa ccatggcaca ggaagtcaaa gtccccaaga tgcccggcgc acccgtgttc 120
 ggcaagtgga tctcccccga ggagtccgtc ggccagcgcc tgaagggcaa gaagatcctg 180
 ctcaccggca ccaccaaggg cgtcggcagg gtcaccagg agctgctgtg cgcacacggc 240
 gccttctgtc ggggtccgg ccgcaccccc ggctggtgag cctccgtcgc cgacgagctg 300
 aaggccaagg gctaccaggc cgcgggcatg gacgtcgacc tgtctgacta cgacgccgtg 360
 aagaagtggg ttgaggagtg cgcgagctc atgggcggca tcgacgtcgt catcaacaac 420
 gcgtcccacc ccggcatggc ccccttcggc gagatgacct cggagatctg gaactacggc 480
 gtcaagaacg agctcgacct cgtctacaac gtctgcaact gcgcatggcc ctacctgcag 540
 aaggcagacg gcgcctccat catcatcacc tcctccaccg tcggcctcca gggcagcaac 600
 tcccctcagg cctgccacgc tgcttgaag ggccgctgcc tgtccctggc ccgccagctc 660
 gccgctgagg gcggcccctt cggcatccgc tgcaactcgc tcacccggg cctggtctgg 720
 accgaggcca tgtccaacat cccaaggag atggcaagcg gcctggtcgc agcccagacc 780
 acccagcagg ctgtcgacct gatggacatc gcctacgcct acctgttcct ggcatccgac 840
 gagtcccgcc agatcacgcg tgccaacatc cccgtcgacg gcggctgcgc cggcgtgtg 900
 accggcggca tgcagggcga gatcgaggtc taa 933

<210> 12
 <211> 864
 <212> DNA
 <213> Streptococcus constellatus

<400> 12
 atggcacagg aagtcaaatg cgccaagatg cccggagcgc ccgtcttcgg caagtggatc 60
 agccccgagg agtcgatcgg ccagcgcctc aagggaaga agatcattct caccggcacc 120
 actaagggcg tcggcaaggt caccgaagag ctgctgtgcg ccacggcgc cttcgtctgc 180

```

ggctccggtc gtacccccgg cgtggccgct tccgtggccg acgagctgaa ggccaagggc 240
taccaggccg ccggcatgga cgtcgacctg tccgactacg aggcctgtaa gaagtgggtc 300
caagagtgcg ccgagctcat gggcggcata gacgtcgtca tcaacaacgc ctcccaccgc 360
ggcatggccc ccttcgagga gatgaccccc gagatctgga actacggcat caagaacgag 420
ctcgacctgg tctacaacgt gtgcaactgc gcttggccgt acctgaagga agccgagggc 480
ggcgcttcca tcatcatcac ctctccacc gtcggcctcc agggcaccaa ctccccgcag 540
gcctgccacg ccgccgcaa gggcgcatgc ctgtccctgg ccgccagct ggcagctgaa 600
ggcggccccct tcggcatccg ctgcaactcc gtcacccccg gcctggtgtg gaccgaggcc 660
atggccaaca tcccgaagga aatggcatcc ggcttggtcg gtgcgcagac caccagcag 720
gctatcgacc ccatggacat cgcctacgt tacctcttcc tggcctccga tgaggctcgc 780
cagatcaccg cagcgaacct tccgctcgac ggcggctgcg ccggcgctgt gaccggcggc 840
atgcagggcg agatcgaagg ctaa 864

```

```

<210> 13
<211> 486
<212> PRT
<213> Lactococcus garvieae

```

```
<400> 13
```

```

Met Ala Glu Phe Asp Val Glu Tyr Asp Leu Val Val Val Gly Gly Gly
1           5           10           15

```

```

Ala Ser Gly Lys Ser Ala Ala Leu Ile Ala Ala Arg Glu Gly Lys Arg
          20           25           30

```

```

Val Val Val Leu Glu Lys Met Pro Glu Thr Gly Gly Leu Ser Met Tyr
          35           40           45

```

```

Ala Glu Gly Thr Ala Ala Phe Glu Ser Ser Ile Gln Asn Glu Leu Gly
          50           55           60

```

```

Thr Pro Arg Leu Ser Lys Tyr His Phe Pro Thr Lys Gln Glu Gly Ile
65           70           75           80

```

```

Glu Lys Phe Met Gly Tyr Ser His Gln Arg Ala Asn Tyr Asp Val Val
          85           90           95

```

21/42
Arg Ala Phe Val Glu Asn Ser Ala Glu Thr Ile Asp Ile Tyr Arg Asp
100 105 110

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

Asn Glu Val Trp Thr Phe His Leu Pro Glu Gly Leu Gly Ala His Cys
130 135 140

Gln Glu Val Leu Leu Asp Ala Ile Gln Lys Leu Asp Val Asp Ile Phe
145 150 155 160

Thr Ser Thr Pro Ala Lys Glu Leu Ile Ile Glu Asp Gly Ala Val Val
165 170 175

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

Ala Val Ile Leu Ala Thr Gly Gly Met Gly Ser Ser Pro Glu Arg Ile
195 200 205

Phe Lys Tyr Ser Trp Phe Ala Pro Ala Ala Tyr Asn Met Asn Thr Leu
210 215 220

Thr Pro Leu Gln Asn Val Gly Asp Gly Leu Asp Leu Ala Leu Ser Ala
225 230 235 240

Gly Ala Asp Pro Thr Tyr Ile Thr Thr Cys Pro Ile Leu Ala Ala Gly
245 250 255

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

Pro Gly Val Trp Ile Asn Lys Thr Gly Arg Arg Phe Ala Ala Glu Ser
275 280 285

Val Ala Glu Asn Ile Gly Asp Ile Gly Thr Tyr Tyr Gly Lys Gln Pro
290 295 300

Gly Gly Val Val Trp Ser Ile Leu Ser Gln Ala Asp Ile Asp Arg Leu
305 310 315 320

Val Ala Glu Gly Ser Glu Ile Ala Ile Gly Glu Phe Val Val Tyr His

325

330

335

Lys Pro Met Glu Arg Leu Pro Ile Glu Leu Glu Ala His Leu Glu Ser
 340 345 350

Gly Leu Val Lys Lys Ala Gly Ser Phe Glu Glu Leu Ala Ala Leu Ile
 355 360 365

Asp Val Pro Val Asp Thr Phe Val Ala Thr Met Ala Asp Tyr Asn Glu
 370 375 380

Ala Cys Glu Lys Gly Tyr Asp Asp Ala Phe Met Lys Lys Pro Gln Tyr
 385 390 395 400

Leu Arg Pro Met Val Glu Gly Pro Phe Tyr Ala Ile Pro Leu Ala Thr
 405 410 415

Gly Thr Met Gly Ser Ala Gly Gly Ile Arg Ile Asn Gly Asn Met Gln
 420 425 430

Val Val Asp Ala Asp Tyr Asn Ala Ile Pro Gly Leu Tyr Ala Val Gly
 435 440 445

Leu Asp Ala Thr Gly Leu Tyr Gly Asp Ser Tyr Asn Met Glu Val Pro
 450 455 460

Gly Ala Ala Asn Gly Phe Ala His Thr Ser Gly Arg Ile Ala Ala Arg
 465 470 475 480

His Ala Ile Ser Thr Met
 485

<210> 14

<211> 486

<212> PRT

<213> Bacteroides ovatus

<400> 14

Met Ala Gln Phe Asp Val Glu Tyr Asp Leu Val Val Val Gly Gly Gly
 1 5 10 15

Ala Ser Gly Lys Ser Ala Ala Leu Ile Ala Ala Arg Glu Gly Lys Arg
 20 25 30

Val Val Val Leu Glu Lys Met Pro Glu Thr Gly Gly Leu Ser Met Tyr
 35 40 45

Ala Glu Gly Thr Ala Ala Phe Glu Ser Ser Ile Gln Asn Glu Leu Gly
 50 55 60

Thr Pro Arg Leu Ser Lys Tyr His Phe Pro Thr Lys Gln Glu Gly Ile
 65 70 75 80

Glu Lys Phe Met Gly Tyr Ser His Gln Arg Ala Asn Tyr Asp Val Val
 85 90 95

Arg Ala Phe Val Glu Asn Ser Ala Glu Thr Ile Asp Ile Tyr Arg Asp
 100 105 110

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

Asn Glu Val Trp Thr Phe His Leu Pro Glu Gly Leu Gly Ala His Cys
 130 135 140

Gln Glu Val Leu Leu Asp Ala Ile Gln Lys Leu Asp Val Asp Ile Phe
 145 150 155 160

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

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

Ala Val Ile Leu Ala Thr Gly Gly Met Gly Ser Ser Pro Glu Arg Ile
 195 200 205

Phe Lys Tyr Ser Trp Phe Ala Pro Ala Ala Tyr Asn Met Asn Thr Leu
 210 215 220

Thr Pro Leu Gln Asn Val Gly Asp Gly Leu Asp Leu Ala Leu Ser Ala
 225 230 235 240

Gly Ala Asp Pro Thr Tyr Ile Thr Thr Cys Pro Ile Leu Ala Ala Gly
 245 250 255

24/42
Gly Arg Asp Met Thr Met Asp Ser Gln Val Gly Gly Ala Gly Val Asn
260 265 270

Pro Gly Val Trp Ile Asn Lys Thr Gly Arg Arg Phe Ala Ala Glu Ser
275 280 285

Val Ala Glu Asn Ile Gly Asp Ile Gly Thr Tyr Tyr Gly Lys Gln Pro
290 295 300

Gly Gly Val Val Trp Ser Ile Leu Ser Gln Ala Asp Ile Asp Arg Leu
305 310 315 320

Val Ala Glu Gly Ser Glu Ile Ala Ile Gly Glu Phe Val Val Tyr His
325 330 335

Lys Pro Met Glu Arg Leu Pro Ile Glu Leu Glu Ala His Leu Glu Ser
340 345 350

Gly Leu Val Lys Lys Ala Gly Ser Phe Glu Glu Leu Ala Ala Leu Ile
355 360 365

Asp Val Pro Val Asp Thr Phe Val Ala Thr Met Ala Asp Tyr Asn Glu
370 375 380

Ala Cys Glu Lys Gly Tyr Asp Asp Ala Phe Met Lys Lys Pro Gln Tyr
385 390 395 400

Leu Arg Pro Met Val Glu Gly Pro Phe Tyr Ala Ile Pro Leu Ala Thr
405 410 415

Gly Thr Met Gly Ser Ala Gly Gly Ile Arg Ile Asn Gly Asn Met Gln
420 425 430

Val Val Asp Ala Asp Tyr Asn Ala Ile Pro Gly Leu Tyr Ala Val Gly
435 440 445

Leu Asp Ala Thr Gly Leu Tyr Gly Asp Ser Tyr Asn Met Glu Val Pro
450 455 460

Gly Ala Ala Asn Gly Phe Ala His Thr Ser Gly Arg Ile Ala Ala Arg
465 470 475 480

His Ala Ile Ser Thr Met

<210> 15
 <211> 487
 <212> PRT
 <213> Streptococcus constellatus

<400> 15

Met Ala Glu Phe Asp Val Glu Tyr Asp Leu Val Val Val Gly Gly Gly
 1 5 10 15

Ala Ser Gly Lys Ser Ala Ala Leu Ile Ala Ala Arg Ala Gly Lys Ser
 20 25 30

Val Val Val Leu Glu Lys Met Pro Glu Thr Gly Gly Leu Ser Met Tyr
 35 40 45

Ala Glu Gly Thr Ala Ala Phe Glu Ser Ser Ile Gln Lys Glu Leu Gly
 50 55 60

Thr Pro Arg Leu Ser Lys Tyr His Phe Pro Thr Lys Gln Glu Gly Val
 65 70 75 80

Glu Lys Phe Met Gly Tyr Ser His Gln Arg Ala Ser Tyr Asp Val Val
 85 90 95

Arg Ala Phe Val Glu Asn Ser Ala Glu Thr Ile Asp Ile Tyr Arg Glu
 100 105 110

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

Ser Glu Val Trp Thr Phe His Leu Pro Glu Gly Leu Gly Ala His Cys
 130 135 140

Gln Glu Val Leu Leu Asp Ala Ile Gln Lys Leu Asp Val Asp Ile Phe
 145 150 155 160

Thr Ser Thr Pro Ala Lys Glu Leu Ile Ile Glu Asp Gly Lys Val Val
 165 170 175

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

Ala Val Ile Leu Ala Thr Gly Gly Met Gly Ser Asn Pro Asp Arg Ile
 195 200 205

Phe Lys Tyr Ser Trp Phe Ala Pro Ala Ala Tyr Asn Met Asn Val Leu
 210 215 220

Thr Pro Leu Gln Asn Met Gly Asp Gly Leu Asp Leu Ala Leu Ser Ala
 225 230 235 240

Gly Ala Asp Asp Thr Ala Ile Thr Thr Cys Pro Ile Leu Ala Ala Gly
 245 250 255

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

Pro Gly Val Trp Ile Asn Lys Ser Gly Lys Arg Phe Cys Ala Glu Ser
 275 280 285

Val Ala Glu Asn Ile Gly Asp Ile Gly Thr Tyr Tyr Gly Lys Gln Pro
 290 295 300

Gly Gly Ile Val Trp Ser Ile Leu Ser Gln Ala Asp Ile Asp Arg Leu
 305 310 315 320

Val Asn Glu Gly Ser Glu Ile Ala Ile Gly Glu Phe Val Val Tyr His
 325 330 335

Lys Pro Met Glu Arg Leu Pro Ile Glu Leu Asn Ala His Leu Glu Ser
 340 345 350

Gly Leu Val Lys Lys Ala Asp Cys Phe Glu Glu Leu Ala Glu Lys Met
 355 360 365

Asp Val Pro Ala Gly Ala Phe Val Asp Thr Met Asn Ala Tyr Asn Glu
 370 375 380

Ala Cys Glu Lys Gly Tyr Asp Asp Ala Phe Met Lys Lys Pro Glu Tyr
 385 390 395 400

Leu Arg Ala Glu Thr Gln Ala Pro Phe Tyr Ala Ile Pro Leu Ala Thr
 405 410 415

27/42

Gly Thr Met Gly Ser Ala Gly Gly Ile Lys Ile Asn Gly Asn Met Gln
 420 425 430

Val Ile Asp Ser Asp Ala Asn Pro Ile Pro Gly Leu Tyr Ala Val Gly
 435 440 445

Leu Asp Ala Thr Gly Leu Tyr Gly Asp Ser Tyr Asn Met Glu Val Pro
 450 455 460

Gly Ala Ala Asn Gly Phe Ala His Thr Ser Gly Arg Ile Ala Ala Arg
 465 470 475 480

His Ala Leu Ser Thr Met Glu
 485

<210> 16
 <211> 1461
 <212> DNA
 <213> *Lactococcus garvieae*

<400> 16
 atggcagaat tcgatgttga gtatgatctt gttgtcgttg gaggaggcgc ctctggaaag 60
 tctgcagcgc tgatgcgcgc ccgtgagggc aagcgcgtcg tgggtgctcga gaagatgccc 120
 gagaccggag gcctctccat gtacgccgaa ggcaccgctg ccttcgagtc ctctattcag 180
 aacgagctcg gcaccccgcg tctttccaag taccacttcc cgaccaagca ggagggcatc 240
 gagaagttca tgggctacag ccatcagcgc gcgaactacg acgtcgtccg cgctttcgtt 300
 gagaactcgc cagagaccat cgacatctac cgcgacctcg gcgtcgtcta caaggcctgc 360
 gacatgcgcg cagaggacga cccaacgag gtctggacct tccatctgcc cgagggcctc 420
 ggcgccatt gccaggaagt cctgctcgac gccatccaga agctcgacgt cgacatcttc 480
 acctccaccc ccgccaagga gtcacatcgc gaggacggcg ctgtcgtcgg tgtcgtcgcga 540
 gagtctgacg gcgagcccct gcgcgtcggc ggcaaggcgc ttatcctggc aaccggcggc 600
 atgggctcca gccgggagcg catottcaag tacagctggt tcgccccgcg tgcctacaac 660
 atgaacaccc tcaccccgct gcagaacgtc ggcgacggcc tcgacctcgc cctctccgcg 720
 ggcgagacc ccacctacat caccacctgc ccgattctcg cagcaggcgg ccgtgacatg 780
 accatggact ccaggtcggc cggcgcgggc gtcaaccccg gcgtgtggat caacaagacc 840
 ggcaggcgct tcgcggcoga gtccgttgcc gagaacatcg gcgacatcgg aacctactac 900
 ggcaagcagc ccggcggcgt ggtctggtcc atcctctccc aggcggacat cgaccgtctg 960

gtggccgagg gttccgagat cgcgatcggc gagttcgtcg tgtaccacaa gccgatggag 1020
 cgcctcccta tcgagctcga ggctcatctc gagtcgggc tggatgaaga ggctggcagc 1080
 ttcgaggagc tcgcagccct cattgacgtg cctgtagaca ccttcgtcgc aactatggcc 1140
 gactacaacg aggcatgcga gaagggtac gacgacgcct ttatgaaga gcccagtagc 1200
 ctccgcccga tggtcgaggg tcccttctat gccatccctc tggctaccgg caccatgggt 1260
 totgctggcg gcatccgcat taacggcaac atgcaggtcg tcgacgccga ctacaacgcc 1320
 attcccggtc tctacgggt cggctctggac gccacgggtc tctacggcga ttctacaac 1380
 atggagggtc ccggcgcagc aaacggttc gccacacct ccggacgcat cgcgcgccgc 1440
 cacgcgatct ccactatgta g 1461

<210> 17
 <211> 1461
 <212> DNA
 <213> Bacteroides ovatus

<400> 17
 atggcacaat tcgatgttga gtatgatctt gttgtcgttg gaggaggcgc ctctggaaag 60
 tctgcagcgc tgatcgccgc ccgtgagggc aagcgcgtcg tggatgctcga gaagatgccc 120
 gagaccggag gcctctccat gtacgccga ggcaccgtg ccttcgagtc ctctattcag 180
 aacgagctcg gcaccccgcg tctttccaag taccacttcc cgaccaagca ggagggcac 240
 gagaagttca tgggctacag ccatcagcgc gcgaactac acgtcgtccg cgctttcgtt 300
 gagaactccg cagagaccat cgacatctac cgcgacctcg gcgtcgtcta caaggcctgc 360
 gacatcgccg cagaggacga ccccaacgag gtctggacct tccatctgcc cgagggcctc 420
 ggcgcccatt gccaggaagt cctgctcgac gccatccaga agctcgacgt cgacatcttc 480
 acctcacccc ccgccaagga gctcatcatc gaggaaggcg ctgtcgtcgg tgtcgtcgca 540
 gagtctgacg gcgagcccct gcgcgtcggc ggcaaggcgc ttatcctggc aaccggcggc 600
 atgggctcca gcccgagcgc catcttcaag tacagctggt tcgccccgcg tgccataaac 660
 atgaacaccc tcaccccgct gcagaacgtc ggcgacggcc tcgacctcgc cctctccgcg 720
 ggcgagacc ccacctacat caccacctgc ccgattctcg cagcaggcgg ccgtgacatg 780
 accatggact ccaggtcgg cggcgcgggc gtcaaccccg gcgtgtggat caacaagacc 840
 ggcaaggcgt tcgcggccga gtccgttgcc gagaacatcg gcgacatcgg aacctactac 900
 ggcaagcagc ccggcggcgt ggtctggtcc atcctctccc aggggacat cgaccgtctg 960

gtggccgagg gttccgagat cgcgatcggc gagttcgtcg tgtaccacaa gccgatggag 1020
 cgcctcccta tcgagctcga ggctcatctc gaggccggcc tggatgaaga ggctggcagc 1080
 ttccgaggagc tcgcagccct cattgacgtg cctgtagaca ccttcgtcgc aactatggcc 1140
 gactacaacg aggcatgcga gaagggctac gacgacgcct ttatgaaga gccccagtac 1200
 ctccgcccga tggctgaggg tcccttctat gccatccctc tggctaccgg caccatgggt 1260
 tctgctggcg gcatccgcat taacggcaac atgcaggtcg tcgacgccga ctacaacgcc 1320
 attcccggtc tctacgcgtt cggctctggac gccacgggtc tctacggcga ctctacaac 1380
 atggagggtt ccggcgcagc aaacggtttt gccacacct ccggacgcat cgcgcgccgc 1440
 caccgatctt ccactatgta g 1461

<210> 18
 <211> 1464
 <212> DNA
 <213> Streptococcus constellatus

<400> 18
 atggctgagt tcgatgttga gtacgacctg gtcgtcgtcg gcggcggcgc atccggcaag 60
 tccgcggcct tgatcgcggc tcgcgccggc aagagcgtcg tcgttctcga gaagatgccc 120
 gagacgggcg gcctgtccat gtacgccgag gggaccgcgg cgttcgagtc ttccattcag 180
 aaggaactcg gtaccccccg tctgagcaag taccatttcc ccacgaagca agagggcgtg 240
 gagaagttca tgggatacag tcaccagcgc gcgagctacg acgtggtgcg cgccttcgtg 300
 gagaattccg ctgagaccat cgacatctac cgcgagctgg gcgtcgtcta caagacctgc 360
 gacatgcgcg cagaggacga tcccagcgag gtctggacct tccacctgcc cgagggcctc 420
 ggcgcccact gccaggaggt tctgctcgac gccatccaga agctcgacgt ggacatcttc 480
 acctccacgc ccgccaagga gctgattatc gaggacggca aggtcgtcgg cgtcgtggcc 540
 gaggccgacg gagagccgct gcgcgtcggc ggcaaggcgc tcctcctcgc gaccggcggc 600
 atgggctcga accccgaccg catcttcaag tacagctggt tcgccccgcg tgcctacaac 660
 atgaacgttc tgaccccgct gcagaatatg ggcgacggcc ttgatctggc cctgtccgca 720
 ggcgagatg acacggccat caccacctgc ccgattttgg cggctggcgg ccgtgacatg 780
 accatggatt cccaggctcg cggcgcaggc gtcaaccccg gcgtgtggat caacaagtcc 840
 ggcaagcgct tctgcgccga atccgtcgcc gagaacatcg gcgacatcg cactactac 900
 ggcaagcagc ccggcggcat cgtgtggtcc atcctctccc aggcgacat cgaccgcctg 960

gtcaacgagg gctccgaaat cgccatcggc gagttcgtcg tgtaccacaa gcccatggag 1020
 cgcctaccca tcgagctcaa tgcgcacctg gagtccggcc tggtaagaa ggccgactgc 1080
 ttogaagagc tggctgagaa gatggacgtt cccgccggcg ccttcgtaga caccatgaac 1140
 gcctacaacg aggcggtcga gaagggctac gacgacgcct tcatgaagaa gcccgagtac 1200
 ctgcgtgccg agaccaggc ccccttctac gccatccct tggcaacggg caccatgggc 1260
 tctgccggcg gcatcaagat caacggcaac atgcaggtca tcgattccga cgcgaacccc 1320
 atccccggcc tgtacgtgt gggcctggat gccaccggcc tgtacggcga ctctacaac 1380
 atggagggtc ccggcgccgc taacggcttt gccacacct ccggccgcat tgcggcacgc 1440
 cagccctct ccacgatgga gtaa 1464

<210> 19
 <211> 22
 <212> PRT
 <213> *Lactococcus garcieae*

<400> 19

Met Lys Asn Lys Phe Tyr Pro Lys Thr Phe Glu Arg Gly Tyr Ile Gly
 1 5 10 15

Asn Leu Glu Val Glu Asn
 20

<210> 20
 <211> 10
 <212> PRT
 <213> *Lactococcus garcieae*

<400> 20

Phe Asp Glu Pro Val Tyr Pro Gln Ala Glu
 1 5 10

<210> 21
 <211> 16
 <212> PRT
 <213> *Lactococcus garcieae*

<400> 21

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

<210> 22
 <211> 17
 <212> PRT
 <213> Lactococcus garcieae

<400> 22

Gly Tyr Ile Gly Asn Leu Glu Val Glu Asn Arg Ala Ile Arg Met Pro
 1 5 10 15

Met

<210> 23
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E1-N-terminal-31primer

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> n stands for inosine

<220>
 <221> misc_feature
 <222> (14)..(14)
 <223> n stands for inosine

<220>
 <221> misc_feature
 <222> (20)..(20)
 <223> n stands for adenine, guanine, cytosine or thymine

<220>
 <221> misc_feature
 <222> (26)..(26)
 <223> n stands for adenine, guanine, cytosine or thymine

<400> 23
 tgaagaataa nttntayccn aaracnttyg a

31

<210> 24
 <211> 37
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E1-N-terminal-37 primer

<220>
 <221> misc_feature
 <222> (11).. (11)
 <223> n stands for inosine

<220>
 <221> misc_feature
 <222> (14).. (14)
 <223> n stands for inosine

<220>
 <221> misc_feature
 <222> (20).. (20)
 <223> n stands for inosine

<220>
 <221> misc_feature
 <222> (26).. (26)
 <223> n stands for inosine

<220>
 <221> misc_feature
 <222> (35).. (35)
 <223> n stands for adenine, guanine, cytosine or thymine

<400> 24
 tgaagaataa nttntayccn aaracnttyg arrgnng

37

<210> 25
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E1-N-terminal-F32 primer

<220>
 <221> misc_feature
 <222> (21).. (21)
 <223> n stands for adenine, guanine, cytosine or thymine

<220>
 <221> misc_feature
 <222> (27).. (27)
 <223> n stands for adenine, guanine, cytosine or thymine

<400> 25
 atgaagaata agttttaycc naaracntty ga

32

<210> 26
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>

<223> E1-internal-RP1 primer

<220>

<221> misc_feature

<222> (24)..(24)

<223> n stands for adenine, guanine, cytosine or thymine

<220>

<221> misc_feature

<222> (33)..(33)

<223> n stands for adenine, guanine, cytosine or thymine

<400> 26

cctgcaatat aaccttcacg tacngcrtcc atnaccat

38

<210> 27

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> pUC19-FP-1 primer

<400> 27

acacaggaaa cagctatgac catgattacg

30

<210> 28

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> pUC19-RP-1 primer

<400> 28

agctggcgaa aggggggatgt gctgcaaggc

30

<210> 29

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> pUC19-FP-2 primer

<400> 29

atgattacgc caagcttgca tgccotgcagg

30

<210> 30

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> pUC19-RP-2 primer

<400> 30

ccagtcacga cgttgtaaaa cgacggccag

30

<210> 31

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> E1-RACE-N-P1 primer

<400> 31

atcgggatcg ctoggttctc gacctctagg ttac

34

<210> 32

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> E1-RACE-RP2-1 primer

<400> 32

atcgaggaga agtgcgagga cgtcagggtc atc

33

<210> 33

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> E1-RACE-N-P2 primer

<400> 33

ttctcgacct ctaggttacc gatgtagccg c

31

<210> 34

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> E1-RACE-RP2-2 primer

<400> 34

acgtcagggt catcggcata ggogactgca ag

32

<210> 35
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E1-conf-NP primer

<400> 35
 tgccgggtgca atggctgaca tcatgttcaa cctg 34

<210> 36
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E1-conf-CP primer

<400> 36
 tcctccatcg ttctccaat cagtaagaca cgcg 34

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E1-FP primer

<400> 37
 ctacatcgggt aacctagagg tcg 23

<210> 38
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E1-RP primer

<400> 38
 ccgtgctgct tgatggtott tgc 23

<210> 39
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Gar-16S-Ribo-FP primer

<400> 39

tgcgtagata tatggaggaa c 21

<210> 40
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Gar-16S-Ribo-RP primer

<400> 40
 cttatctcta aggatagcac g 21

<210> 41
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> exp.E1 pet F Nde primer

<400> 41
 agctcatatg aagaacaagt tctatccgaa 30

<210> 42
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> exp. E1 pet His primer

<400> 42
 aatcgaattc ctacaggttg cagccagcga tgt 33

<210> 43
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> RACE-N-P3-1

<400> 43
 atggagatag tgccgctggc aaggcaacgg cac 33

<210> 44
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>

<223> RACE-N-P3-2

<400> 44

tcaacgaaga ctcgatttga gcgagaggcg agg

33

<210> 45

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> E1-Bub-N-P1

<400> 45

acggtggaac cggcatcgtg ttcattggaca ac

32

<210> 46

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> E1-Bub-N-P2

<400> 46

gcgtgaccca gttccaccat gtcggactgt c

31

<210> 47

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> RACE-C-P3-1

<400> 47

gacatccgtg tcgagcgcag gatcacccat gag

33

<210> 48

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> RACE-C-P3-2

<400> 48

aggatcaccc atgagcgcac cgcattcatg gac

33

<210> 49

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> E1-Bub-C-P1

<400> 49

catcgctcatt gcagtcgttg tccaggaagt cc

32

<210> 50

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> E1-Bub-C-P2

<400> 50

ttgtccagga agtccatcgc gtacacgacg gag

33

<210> 51

<211> 13

<212> PRT

<213> Lactococcus garvieae

<220>

<221> MISC_FEATURE

<222> (12).. (12)

<223> Xaa stands for isoleucine or leucine

<400> 51

Thr	Pro	Gly	Val	Ala	Ala	Ser	Val	Ala	Asp	Glu	Xaa	Lys
1				5					10			

<210> 52

<211> 9

<212> PRT

<213> Lactococcus garvieae

<400> 52

Met	Pro	Gly	Ala	Pro	Val	Phe	Gly	Lys
1				5				

<210> 53

<211> 9

<212> PRT

<213> Lactococcus garvieae

<220>

<221> MISC_FEATURE

<222> (2)..(4)
 <223> Xaa stands for isoleucine or leucine

<400> 53

Lys Xaa Xaa Xaa Thr Gly Thr Thr Lys
 1 5

<210> 54
 <211> 18
 <212> PRT
 <213> Lactococcus garvieae

<220>
 <221> MISC_FEATURE
 <222> (5)..(6)
 <223> Xaa stands for isoleucine or leucine

<400> 54

Val Thr Gln Glu Xaa Xaa Cys Ala His Gly Ala Phe Val Cys Gly Ser
 1 5 10 15

Gly Arg

<210> 55
 <211> 11
 <212> PRT
 <213> Lactococcus garvieae

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Xaa stands for isoleucine or leucine

<400> 55

Trp Xaa Ser Pro Glu Glu Ser Val Gly Gln Arg
 1 5 10

<210> 56
 <211> 8
 <212> PRT
 <213> Lactococcus garvieae

<400> 56

Ala Gln Glu Val Lys Val Pro Lys
 1 5

<210> 57
 <211> 44
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E2-invitoTS-FP1

<400> 57
 actttaagaa ggagatatac caatggcaca ggaagtcaaa gtcc 44

<210> 58
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> E2-invitoTS-RP

<400> 58
 ctagacctcg atctcgccct gcatgcgg 28

<210> 59
 <211> 85
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Universal-Primer

<400> 59
 gaaattaata cgactcacta tagggagacc acaacgggtt ccctctagaa ataattttgt 60

ttaactttta gaaggagata tacca 85

<210> 60
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> exp.US2 pet F Nde

<400> 60
 tatacatatg gcacaggaag tcaaagtc 28

<210> 61
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>

<223> exp. US2 pet

<400> 61

aatcgaattc ctagacctcg atctcgccct gc

32

<210> 62

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> exp.US3 F primer

<400> 62

tatacatatg gcagaattcg atgttgag

28

<210> 63

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> exp.US3 R primer

<400> 63

cgcgaagctt ctacatagtg gagatcgctt gg

32

<210> 64

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> exp.US1 F primer

<400> 64

tatacatatg ttcaagggtc cacagggc

28

<210> 65

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> exp.US1 R primer

<400> 65

gctcgaattc ttagtgctgc tgtgcctttt cag

33

<210> 66

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> exp.DS1 F primer

<400> 66

atatacatat gcaggatatg gacttcatgg

30

<210> 67

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> exp.DS1 R primer

<400> 67

gctcgaattc tcatagtgac atcagcgctc cc

32

<210> 68

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> exp.E2 pet His primer

<400> 68

aatcgaattc gagacctcga tctcgccctg c

31

<210> 69

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> exp.E3 R His primer

<400> 69

cgcgaagctt gtacatagtg gagatcgcggt gg

32