

1336WOORD01 Sequence listing 2005-05-12.txt
SEQUENCE LISTING

<110> ALTANA Pharma AG

<120> Methode zur Identifizierung von PDE10-Antagonisten

<130> 1336WOORD01

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 884

<212> PRT

<213> Künstliche Sequenz

<220>

<221> PEPTIDE

<222> (1)..(884)

<223> PDE10/Cyab1 Chimäre

<400> 1

Met Leu Thr Asp Glu Lys Val Lys Ala Tyr Leu Ser Leu His Pro Gln
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Val Leu Asp Glu Phe Val Ser Glu Ser Val Ser Ala Glu Thr Val Glu
20 25 30

Lys Trp Leu Lys Arg Lys Asn Asn Lys Ser Glu Asp Glu Ser Ala Pro
35 40 45

Lys Glu Val Ser Arg Tyr Gln Asp Thr Asn Met Gln Gly Val Val Tyr
50 55 60

Glu Leu Asn Ser Tyr Ile Glu Gln Arg Leu Asp Thr Gly Gly Asp Asn
65 70 75 80

Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala Thr Lys
85 90 95

1336WOORD01 Sequence listing 2005-05-12.txt

Ala Asp Gly Phe Ala Leu Tyr Phe Leu Gly Glu Cys Asn Asn Ser Leu
100 105 110

Cys Ile Phe Thr Pro Pro Gly Ile Lys Glu Gly Lys Pro Arg Leu Ile
115 120 125

Pro Ala Gly Pro Ile Thr Gln Gly Thr Thr Val Ser Ala Tyr Val Ala
130 135 140

Lys Ser Arg Lys Thr Leu Leu Val Glu Asp Ile Leu Gly Asp Glu Arg
145 150 155 160

Phe Pro Arg Gly Thr Gly Leu Glu Ser Gly Thr Arg Ile Gln Ser Val
165 170 175

Leu Cys Leu Pro Ile Val Thr Ala Ile Gly Asp Leu Ile Gly Ile Leu
180 185 190

Glu Leu Tyr Arg His Trp Gly Lys Glu Ala Phe Cys Leu Ser His Gln
195 200 205

Glu Val Ala Thr Ala Asn Leu Ala Trp Ala Ser Val Ala Ile His Gln
210 215 220

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

Leu Leu Asp Val Ser Lys Thr Tyr Phe Asp Asn Ile Val Ala Ile Asp
245 250 255

Ser Leu Leu Glu His Ile Met Ile Tyr Ala Lys Asn Leu Val Asn Ala
260 265 270

Asp Arg Cys Ala Leu Phe Gln Val Asp His Lys Asn Lys Glu Leu Tyr
275 280 285

Ser Asp Leu Phe Asp Ile Gly Glu Glu Lys Glu Gly Lys Pro Val Phe
290 295 300

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

Gln Val Ala Arg Thr Gly Glu Val Leu Asn Ile Pro Asp Ala Tyr Ala
325 330 335

Asp Pro Arg Phe Asn Arg Glu Val Asp Leu Tyr Thr Gly Tyr Thr Thr
340 345 350

Arg Asn Ile Leu Cys Met Pro Ile Val Ser Arg Gly Ser Val Ile Gly
355 360 365

1336WOORD01 Sequence listing 2005-05-12.txt

Val Val Gln Met Val Asn Lys Ile Ser Gly Ser Ala Phe Ser Lys Thr
370 375 380

Asp Glu Asn Asn Phe Lys Met Phe Ala Val Phe Cys Ala Leu Ala Leu
385 390 395 400

His Cys Ala Asn Met Tyr His Arg Ile Arg Val Glu Lys Gln Tyr Gln
405 410 415

Lys Asp Ile Leu Gln Ser Leu Ser Asp Ala Val Ile Ser Thr Asp Met
420 425 430

Ala Gly Arg Ile Val Thr Ile Asn Asp Ala Ala Leu Glu Leu Leu Gly
435 440 445

Cys Pro Leu Gly Asp Ala Asn His Lys Ser Asn Lys Leu Leu Trp Glu
450 455 460

Gln Asn Leu Ile Gly Arg Val Val Trp Glu Ile Val Pro Ile Glu Asn
465 470 475 480

Leu Gln Met Arg Leu Glu Asp Ser Leu Lys Ser Gly Ala Lys His Tyr
485 490 495

Val Pro Glu Gln Ser Leu Ile Val Gly Ile Tyr Gln Leu Gln Met Ser
500 505 510

Glu Ser Arg Val Leu His Glu Thr Gln Asp Tyr Ser Ile Leu Thr Val
515 520 525

Arg Asp Arg Ile Asn Pro Asp Ile Phe Leu Pro Trp Asn Leu Pro Gln
530 535 540

Thr Pro Gln Ser Gln Phe Ile Thr Pro Glu Glu Val Gln Ile Leu Glu
545 550 555 560

Arg Ser Ile Asn Leu Thr Val Asn Pro Leu Thr Asn Pro Glu Gly Gly
565 570 575

Val Arg Gly Gly Leu Val Val Leu Glu Asp Ile Ser Gln Glu Lys Arg
580 585 590

Leu Lys Thr Thr Met Tyr Arg Tyr Leu Thr Pro His Val Ala Glu Gln
595 600 605

Val Met Ala Leu Gly Glu Asp Ala Leu Met Val Gly Glu Arg Lys Glu
610 615 620

Val Thr Val Leu Phe Ser Asp Ile Arg Gly Tyr Thr Thr Leu Thr Glu
625 630 635 640

Asn Leu Gly Ala Ala Glu Val Val Ser Leu Leu Asn Gln Tyr Phe Glu

Thr Met Val Glu Ala Val Phe Asn Tyr Glu Gly Thr Leu Asp Lys Phe
660 665 670

Ile Gly Asp Ala Leu Met Ala Val Phe Gly Ala Pro Leu Pro Leu Thr
675 680 685

Glu Asn His Ala Trp Gln Ala Val Gln Ser Ala Leu Asp Met Arg Gln
690 695 700

Arg Leu Lys Glu Phe Asn Gln Arg Arg Ile Ile Gln Ala Gln Pro Gln
705 710 715 720

Ile Lys Ile Gly Ile Gly Ile Ser Ser Gly Glu Val Val Ser Gly Asn
725 730 735

Ile Gly Ser His Lys Arg Met Asp Tyr Thr Val Ile Gly Asp Gly Val
740 745 750

Asn Leu Ser Ser Arg Leu Glu Thr Val Thr Lys Glu Tyr Gly Cys Asp
755 760 765

Ile Ile Leu Ser Glu Phe Thr Tyr Gln Leu Cys Ser Asp Arg Ile Trp
770 775 780

Val Arg Gln Leu Asp Lys Ile Arg Val Lys Gly Lys His Gln Ala Val
785 790 795 800

Asn Ile Tyr Glu Leu Ile Ser Asp Arg Ser Thr Pro Leu Asp Asp Asn
805 810 815

Thr Gln Glu Phe Leu Phe His Tyr His Asn Gly Arg Thr Ala Tyr Leu
820 825 830

Val Arg Asp Phe Thr Gln Ala Ile Ala Cys Phe Asn Ser Ala Lys His
835 840 845

Ile Arg Pro Thr Asp Gln Ala Val Asn Ile His Leu Glu Arg Ala Tyr
850 855 860

Asn Tyr Gln Gln Thr Pro Pro Pro Pro Gln Trp Asp Gly Val Trp Thr
865 870 875 880

Ile Phe Thr Lys

<210> 2

<211> 2655

<212> DNA

<213> Künstliche Sequenz

<220>

<221> CDS

<222> (1)..(2655)

<223> PDE10/CyaB1 Chimäre

<400> 2

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

1336WOORD01 Sequence listing 2005-05-12.txt

210	215	220	
gtg Val 225	cag Gln Val	tgc Cys	720
aga Arg	ggc Gly 230	ctt Leu	
gca Ala	aaa Lys	cag Gln	
aca Thr 235	gaa Glu	ttg Leu	
aat Asn	gac Asp	ttc Phe 240	
cta Leu	ctc Leu	gac Asp	768
gta Val	tca Ser 245	aaa Lys	
aca Thr	tat Tyr	ttt Phe	
gat Asp 250	aac Asn	ata Ile	
ggt Val	gca Ala	ata Ile 255	
aat Asn	gcc Ala		816
tct Ser	cta Leu	ctt Leu	
gaa Glu 260	cac His	ata Ile	
atg Met	ata Ile	tat Tyr 265	
gca Ala	aaa Lys	aac Asn	
ctg Leu	gtg Val 270	aat Asn	
gcc Ala			864
gat Asp	cgt Arg	tgt Cys 275	
gcg Ala	ctt Leu	ttc Phe	
cag Gln	gtg Val 280	gac Asp	
cat His	aag Lys	aac Asn	
aag Lys 285	gag Glu	tta Leu	
tat Tyr			912
tca Ser	gac Asp 290	ctt Leu	
ttt Phe	gat Asp	att Ile	
gga Gly 295	gag Glu	gaa Glu	
aag Lys	gaa Glu	gga Gly 300	
aaa Lys	cct Pro	gtc Val	
ttc Phe			960
aag Lys 305	aag Lys	acc Thr	
aaa Lys	gag Glu	ata Ile 310	
aga Arg	ttt Phe	tca Ser	
att Ile	gag Glu 315	aaa Lys	
gga Gly	att Ile	gct Ala	
ggc Gly 320			1008
caa Gln	gta Val	gca Ala	
aga Arg	aca Thr 325	ggg Gly	
gaa Glu	gtc Val	ctg Leu	
aac Asn 330	att Ile	cca Pro	
gat Asp	gcc Ala	tat Tyr 335	
gac Asp	cca Pro	cgc Arg	
ttt Phe 340	aac Asn	aga Arg	
gaa Glu	gta Val	gac Asp 345	
ttg Leu	tac Tyr	aca Thr	
ggc Gly 350	tac Tyr	acc Thr	
acg Thr			1056
cgg Arg	aac Asn	atc Ile 355	
ctg Leu	tgc Cys	atg Met	
ccc Pro	atc Ile 360	gtc Val	
agc Ser	cga Arg	ggc Gly	
agc Ser 365	gtg Val	ata Ile	
ggc Gly	ggt Gly		1104
gtg Val	gtg Val 370	cag Gln	
atg Met	gtc Val	aac Asn	
aaa Lys 375	atc Ile	agt Ser	
ggc Gly	agt Ser	gcc Ala 380	
ttc Phe	tgt Cys	gct Ala	
tta Leu	gcc Ala	tta Leu	
gaa Glu	ttg Leu	ggt Gly	
gac Asp	att Ile	tta Leu 420	
caa Gln	agc Ser	ttg Leu	
tca Ser	gat Asp 425	gct Ala	
gta Val	att Ile	gca Ala	
gaa Glu	ggt Gly	gac Asp	
gca Ala	gaa Glu	ttg Leu	
gca Ala	ttg Leu	gaa Glu 445	
ttg Leu	tta Leu	ctc Leu	
ggt Gly			1344
tgt Cys	cct Pro 450	tta Leu	
ggt Gly	gat Asp	gct Ala	
aat Asn 455	cat His	aaa Lys	
agt Ser	aat Asn	aag Lys 460	
ctg Leu	ctg Leu	tgg Trp	
gaa Glu			1392
caa Gln 465	aat Asn	tta Leu	
att Ile	ggt Gly	cgc Arg 470	
gta Val	gtt Val	tgg Trp	
gaa Glu	att Ile 475	gta Val	
cca Pro	att Ile	gaa Glu	
aat Asn	tat Tyr	caa Gln	
gac Asp	atg Met	gaa Glu 480	
ttt Phe			1440
ttg Leu	cag Gln	atg Met	
cgc Arg	tta Leu 485	gaa Glu	
gat Asp	agt Ser	tta Leu	
aaa Lys 490	agt Ser	ggt Gly	
gct Ala	aaa Lys	cat His	
tat Tyr			1488

1336WOORD01 Sequence listing 2005-05-12.txt

gtg	cca	gaa	caa	agt	ttg	ata	gtg	gga	att	tat	caa	tta	caa	atg	tct	1536
Val	Pro	Glu	Gln	Ser	Leu	Ile	Val	Gly	Ile	Tyr	Gln	Leu	Gln	Met	Ser	
			500					505					510			
gaa	agt	cgg	gtt	ttg	cat	gaa	act	caa	gac	tac	tct	att	ttg	aca	gta	1584
Glu	Ser	Arg	Val	Leu	His	Glu	Thr	Gln	Asp	Tyr	Ser	Ile	Leu	Thr	Val	
		515					520					525				
cgc	gat	cgc	atc	aac	cca	gat	att	ttt	ctc	ccc	tgg	aat	tta	ccc	caa	1632
Arg	Asp	Arg	Ile	Asn	Pro	Asp	Ile	Phe	Leu	Pro	Trp	Asn	Leu	Pro	Gln	
	530					535					540					
acc	ccc	cag	tcg	caa	ttt	atc	acc	ccg	gaa	gaa	gta	caa	atc	tta	gaa	1680
Thr	Pro	Gln	Ser	Gln	Phe	Ile	Thr	Pro	Glu	Glu	Val	Gln	Ile	Leu	Glu	
545					550				555						560	
cgc	agt	att	aat	ctt	acc	gtt	aat	cct	ttg	acg	aac	cca	gaa	ggc	ggg	1728
Arg	Ser	Ile	Asn	Leu	Thr	Val	Asn	Pro	Leu	Thr	Asn	Pro	Glu	Gly	Gly	
				565					570					575		
gtc	cgt	ggt	ggt	ttg	gta	gtt	ttg	gaa	gat	att	agt	caa	gag	aag	cgc	1776
Val	Arg	Gly	Gly	Leu	Val	Val	Leu	Glu	Asp	Ile	Ser	Gln	Glu	Lys	Arg	
			580					585					590			
ctc	aaa	act	act	atg	tat	cgc	tac	ctt	aca	ccc	cat	gta	gct	gaa	cag	1824
Leu	Lys	Thr	Thr	Met	Tyr	Arg	Tyr	Leu	Thr	Pro	His	Val	Ala	Glu	Gln	
		595					600					605				
gta	atg	gct	tta	ggg	gaa	gat	gcc	tta	atg	gtt	ggt	gaa	cgc	aag	gag	1872
Val	Met	Ala	Leu	Gly	Glu	Asp	Ala	Leu	Met	Val	Gly	Glu	Arg	Lys	Glu	
	610					615					620					
gtg	act	gtt	tta	ttt	tca	gat	atc	cga	ggc	tac	acc	aca	ctt	acg	gaa	1920
Val	Thr	Val	Leu	Phe	Ser	Asp	Ile	Arg	Gly	Tyr	Thr	Thr	Leu	Thr	Glu	
625					630					635					640	
aat	cta	ggt	gcg	gct	gaa	gtg	gta	tca	ctc	ctg	aac	caa	tat	ttt	gaa	1968
Asn	Leu	Gly	Ala	Ala	Glu	Val	Val	Ser	Leu	Leu	Asn	Gln	Tyr	Phe	Glu	
				645					650					655		
aca	atg	gtt	gaa	gca	gtt	ttc	aac	tat	gaa	ggc	aca	ctg	gat	aaa	ttt	2016
Thr	Met	Val	Glu	Ala	Val	Phe	Asn	Tyr	Glu	Gly	Thr	Leu	Asp	Lys	Phe	
			660					665					670			
atc	ggt	gat	gct	tta	atg	gct	gtt	ttt	ggt	gcg	cca	cta	cca	ctc	aca	2064
Ile	Gly	Asp	Ala	Leu	Met	Ala	Val	Phe	Gly	Ala	Pro	Leu	Pro	Leu	Thr	
		675					680					685				
gaa	aat	cat	gct	tgg	caa	gca	gta	cag	tca	gca	tta	gat	atg	cgc	caa	2112
Glu	Asn	His	Ala	Trp	Gln	Ala	Val	Gln	Ser	Ala	Leu	Asp	Met	Arg	Gln	
	690					695					700					
cgc	ctg	aag	gaa	ttt	aac	caa	cga	cgc	atc	att	cag	gca	caa	cca	caa	2160
Arg	Leu	Lys	Glu	Phe	Asn	Gln	Arg	Arg	Ile	Ile	Gln	Ala	Gln	Pro	Gln	
705					710					715					720	
atc	aaa	atc	ggt	att	ggt	att	agt	tct	gga	gaa	gta	gtt	tct	ggt	aac	2208
Ile	Lys	Ile	Gly	Ile	Gly	Ile	Ser	Ser	Gly	Glu	Val	Val	Ser	Gly	Asn	
				725					730					735		
atc	ggt	tct	cac	aag	cgt	atg	gat	tac	aca	gtc	att	ggt	gat	ggt	gtg	2256
Ile	Gly	Ser	His	Lys	Arg	Met	Asp	Tyr	Thr	Val	Ile	Gly	Asp	Gly	Val	
			740					745					750			
aat	tta	agt	tcc	cgc	ttg	gaa	act	gtc	acc	aaa	gaa	tat	ggc	tgt	gat	2304
Asn	Leu	Ser	Ser	Arg	Leu	Glu	Thr	Val	Thr	Lys	Glu	Tyr	Gly	Cys	Asp	
		755					760					765				

1336WOORD01 Sequence listing 2005-05-12.txt

att atc ctc agt gag ttt act tac caa tta tgc agc gat cgc att tgg ile ile leu ser glu phe thr tyr gln leu cys ser asp arg ile trp 770 775 780	2352
gta cgt cag tta gat aaa atc cga gtc aaa ggg aaa cac caa gct gtc val arg gln leu asp lys ile arg val lys gly lys his gln ala val 785 790 795 800	2400
aat atc tat gag ttg att agc gat cgc agt act ccc tta gat gac aac asn ile tyr glu leu ile ser asp arg ser thr pro leu asp asp asn 805 810 815	2448
acc caa gag ttc ctc ttt cac tat cat aat ggt cgg act gcc tac tta thr gln glu phe leu phe his tyr his asn gly arg thr ala tyr leu 820 825 830	2496
gtc cgc gat ttt acc cag gcg atc gct tgt ttt aac tca gct aaa cat val arg asp phe thr gln ala ile val cys phe asn ser ala lys his 835 840 845	2544
att cga ccc aca gac caa gct gtc aat att cac cta gaa cgc gcc tac ile arg pro thr asp gln ala val asn ile his leu glu arg ala tyr 850 855 860	2592
aat tat caa caa act cca cca cct cct caa tgg gac ggc gta tgg aca asn tyr gln gln thr pro pro pro pro gln trp asp gly val trp thr 865 870 875 880	2640
att ttc aca aag tag ile phe thr lys	2655

<210> 3

<211> 884

<212> PRT

<213> Künstliche Sequenz

<400> 3

Met Leu Thr Asp Glu Lys Val Lys Ala Tyr Leu Ser Leu His Pro Gln 1 5 10 15
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Val Leu Asp Glu Phe Val Ser Glu Ser Val Ser Ala Glu Thr Val Glu 20 25 30

Lys Trp Leu Lys Arg Lys Asn Asn Lys Ser Glu Asp Glu Ser Ala Pro 35 40 45

Lys Glu Val Ser Arg Tyr Gln Asp Thr Asn Met Gln Gly Val Val Tyr 50 55 60

Glu Leu Asn Ser Tyr Ile Glu Gln Arg Leu Asp Thr Gly Gly Asp Asn 65 70 75 80
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Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala Thr Lys 85 90 95

1336WOORD01 Sequence listing 2005-05-12.txt

Ala Asp Gly Phe 100 Ala Leu Tyr Phe 105 Leu Gly Glu Cys Asn 110 Asn Ser Leu

Cys Ile Phe 115 Thr Pro Pro Gly 120 Ile Lys Glu Gly Lys 125 Pro Arg Leu Ile

Pro Ala Gly 130 Pro Ile Thr 135 Gln Gly Thr Thr Val 140 Ser Ala Tyr Val Ala

Lys 145 Ser Arg Lys Thr 150 Leu Leu Val Glu Asp 155 Ile Leu Gly Asp Glu Arg 160

Phe Pro Arg Gly 165 Thr Gly Leu Glu Ser 170 Gly Thr Arg Ile Gln 175 Ser Val

Leu Cys Leu 180 Pro Ile Val Thr 185 Ala Ile Gly Asp Leu Ile 190 Gly Ile Leu

Glu Leu 195 Tyr Arg His Trp Gly 200 Lys Glu Ala Phe Cys 205 Leu Ser His Gln

Glu Val 210 Ala Thr Ala Asn 215 Leu Ala Trp Ala Ser 220 Val Ala Ile His Gln

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

Leu Leu Asp Val 245 Ser Lys Thr Tyr Phe 250 Asp Asn Ile Val Ala 255 Ile Asp

Ser Leu Leu 260 Glu His Ile Met Ile 265 Tyr Ala Lys Asn Leu 270 Val Asn Ala

Asp Arg 275 Cys Ala Leu Phe Gln 280 Val Asp His Lys Asn 285 Lys Glu Leu Tyr

Ser 290 Asp Leu Phe Asp Ile 295 Gly Glu Glu Lys Glu 300 Gly Lys Pro Val Phe

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

Gln Val Ala Arg 325 Thr Gly Glu Val Leu 330 Asn Ile Pro Asp Ala 335 Tyr Ala

Asp Pro Arg 340 Phe Asn Arg Glu Val 345 Asp Leu Tyr Thr Gly 350 Tyr Thr Thr

Arg Asn 355 Ile Leu Cys Met Pro 360 Ile Val Ser Arg Gly 365 Ser Val Ile Gly

Val Val Gln Met Val Asn Lys Ile Ser Gly Ser Ala Phe Ser Lys Thr

370

375

380

Asp Glu Asn Asn Phe Lys Met Phe Ala Val Phe Cys Ala Leu Ala Leu
 385 390 395 400

His Cys Ala Asn Met Tyr His Arg Ile Arg Val Glu Lys Gln Tyr Gln
 405 410 415

Lys Asp Ile Leu Gln Ser Leu Ser Asp Ala Val Ile Ser Thr Asp Met
 420 425 430

Ala Gly Arg Ile Val Thr Ile Asn Asp Ala Ala Leu Glu Leu Leu Gly
 435 440 445

Cys Pro Leu Gly Asp Ala Asn His Lys Ser Asn Lys Leu Leu Trp Glu
 450 455 460

Gln Asn Leu Ile Gly Arg Val Val Trp Glu Ile Val Pro Ile Glu Asn
 465 470 475 480

Leu Gln Met Arg Leu Glu Asp Ser Leu Lys Ser Gly Ala Lys His Tyr
 485 490 495

Val Pro Glu Gln Ser Leu Ile Val Gly Ile Tyr Gln Leu Gln Met Ser
 500 505 510

Glu Ser Arg Val Leu His Glu Thr Gln Asp Tyr Ser Ile Leu Thr Val
 515 520 525

Arg Asp Arg Ile Asn Pro Asp Ile Phe Leu Pro Trp Asn Leu Pro Gln
 530 535 540

Thr Pro Gln Ser Gln Phe Ile Thr Pro Glu Glu Val Gln Ile Leu Glu
 545 550 555 560

Arg Ser Ile Asn Leu Thr Val Asn Pro Leu Thr Asn Pro Glu Gly Gly
 565 570 575

Val Arg Gly Gly Leu Val Val Leu Glu Asp Ile Ser Gln Glu Lys Arg
 580 585 590

Leu Lys Thr Thr Met Tyr Arg Tyr Leu Thr Pro His Val Ala Glu Gln
 595 600 605

Val Met Ala Leu Gly Glu Asp Ala Leu Met Val Gly Glu Arg Lys Glu
 610 615 620

Val Thr Val Leu Phe Ser Asp Ile Arg Gly Tyr Thr Thr Leu Thr Glu
 625 630 635 640

Asn Leu Gly Ala Ala Glu Val Val Ser Leu Leu Asn Gln Tyr Phe Glu
 645 650 655

1336WOORD01 Sequence listing 2005-05-12.txt

Thr Met Val Glu Ala Val Phe Asn Tyr Glu Gly Thr Leu Asp Lys Phe
660 665 670

Ile Gly Asp Ala Leu Met Ala Val Phe Gly Ala Pro Leu Pro Leu Thr
675 680 685

Glu Asn His Ala Trp Gln Ala Val Gln Ser Ala Leu Asp Met Arg Gln
690 695 700

Arg Leu Lys Glu Phe Asn Gln Arg Arg Ile Ile Gln Ala Gln Pro Gln
705 710 715 720

Ile Lys Ile Gly Ile Gly Ile Ser Ser Gly Glu Val Val Ser Gly Asn
725 730 735

Ile Gly Ser His Lys Arg Met Asp Tyr Thr Val Ile Gly Asp Gly Val
740 745 750

Asn Leu Ser Ser Arg Leu Glu Thr Val Thr Lys Glu Tyr Gly Cys Asp
755 760 765

Ile Ile Leu Ser Glu Phe Thr Tyr Gln Leu Cys Ser Asp Arg Ile Trp
770 775 780

Val Arg Gln Leu Asp Lys Ile Arg Val Lys Gly Lys His Gln Ala Val
785 790 795 800

Asn Ile Tyr Glu Leu Ile Ser Asp Arg Ser Thr Pro Leu Asp Asp Asn
805 810 815

Thr Gln Glu Phe Leu Phe His Tyr His Asn Gly Arg Thr Ala Tyr Leu
820 825 830

Val Arg Asp Phe Thr Gln Ala Ile Ala Cys Phe Asn Ser Ala Lys His
835 840 845

Ile Arg Pro Thr Asp Gln Ala Val Asn Ile His Leu Glu Arg Ala Tyr
850 855 860

Asn Tyr Gln Gln Thr Pro Pro Pro Pro Gln Trp Asp Gly Val Trp Thr
865 870 875 880

Ile Phe Thr Lys

<210> 4

<211> 896

<212> PRT

<213> Künstliche Sequenz

<220>

<221> PEPTIDE

<222> (1)..(896)

<223> PDE10/CyaB1 Chimäre

<400> 4

Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Asp
1 5 10 15

Glu Lys Val Lys Ala Tyr Leu Ser Leu His Pro Gln Val Leu Asp Glu
20 25 30

Phe Val Ser Glu Ser Val Ser Ala Glu Thr Val Glu Lys Trp Leu Lys
35 40 45

Arg Lys Asn Asn Lys Ser Glu Asp Glu Ser Ala Pro Lys Glu Val Ser
50 55 60

Arg Tyr Gln Asp Thr Asn Met Gln Gly Val Val Tyr Glu Leu Asn Ser
65 70 75 80

Tyr Ile Glu Gln Arg Leu Asp Thr Gly Gly Asp Asn Gln Leu Leu Leu
85 90 95

Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala Thr Lys Ala Asp Gly Phe
100 105 110

Ala Leu Tyr Phe Leu Gly Glu Cys Asn Asn Ser Leu Cys Ile Phe Thr
115 120 125

Pro Pro Gly Ile Lys Glu Gly Lys Pro Arg Leu Ile Pro Ala Gly Pro
130 135 140

Ile Thr Gln Gly Thr Thr Val Ser Ala Tyr Val Ala Lys Ser Arg Lys
145 150 155 160

Thr Leu Leu Val Glu Asp Ile Leu Gly Asp Glu Arg Phe Pro Arg Gly
165 170 175

Thr Gly Leu Glu Ser Gly Thr Arg Ile Gln Ser Val Leu Cys Leu Pro
180 185 190

Ile Val Thr Ala Ile Gly Asp Leu Ile Gly Ile Leu Glu Leu Tyr Arg
195 200 205

His Trp Gly Lys Glu Ala Phe Cys Leu Ser His Gln Glu Val Ala Thr
210 215 220

1336WOORD01 Sequence listing 2005-05-12.txt

Ala Asn Leu Ala Trp Ala Ser Val Ala Ile His Gln Val Gln Val Cys
225 230 235 240

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

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

His Ile Met Ile Tyr Ala Lys Asn Leu Val Asn Ala Asp Arg Cys Ala
275 280 285

Leu Phe Gln Val Asp His Lys Asn Lys Glu Leu Tyr Ser Asp Leu Phe
290 295 300

Asp Ile Gly Glu Glu Lys Glu Gly Lys Pro Val Phe Lys Lys Thr Lys
305 310 315 320

Glu Ile Arg Phe Ser Ile Glu Lys Gly Ile Ala Gly Gln Val Ala Arg
325 330 335

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

Asn Arg Glu Val Asp Leu Tyr Thr Gly Tyr Thr Thr Arg Asn Ile Leu
355 360 365

Cys Met Pro Ile Val Ser Arg Gly Ser Val Ile Gly Val Val Gln Met
370 375 380

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

Phe Lys Met Phe Ala Val Phe Cys Ala Leu Ala Leu His Cys Ala Asn
405 410 415

Met Tyr His Arg Ile Arg Val Glu Lys Gln Tyr Gln Lys Asp Ile Leu
420 425 430

Gln Ser Leu Ser Asp Ala Val Ile Ser Thr Asp Met Ala Gly Arg Ile
435 440 445

Val Thr Ile Asn Asp Ala Ala Leu Glu Leu Leu Gly Cys Pro Leu Gly
450 455 460

Asp Ala Asn His Lys Ser Asn Lys Leu Leu Trp Glu Gln Asn Leu Ile
465 470 475 480

Gly Arg Val Val Trp Glu Ile Val Pro Ile Glu Asn Leu Gln Met Arg
485 490 495

1336WOORD01 Sequence listing 2005-05-12.txt

Leu Glu Asp Ser 500 Leu Lys Ser Gly Ala 505 Lys His Tyr Val 510 Pro Glu Gln
 Ser Leu Ile 515 Val Gly Ile Tyr Gln 520 Leu Gln Met Ser Glu 525 Ser Arg Val
 Leu His 530 Glu Thr Gln Asp Tyr 535 Ser Ile Leu Thr Val 540 Arg Asp Arg Ile
 Asn 545 Pro Asp Ile Phe Leu 550 Pro Trp Asn Leu Pro 555 Gln Thr Pro Gln Ser 560
 Gln Phe Ile Thr Pro 565 Glu Glu Val Gln Ile 570 Leu Glu Arg Ser Ile 575 Asn
 Leu Thr Val Asn 580 Pro Leu Thr Asn Pro 585 Glu Gly Gly Val Arg 590 Gly Gly
 Leu Val Val 595 Leu Glu Asp Ile Ser 600 Gln Glu Lys Arg Leu 605 Lys Thr Thr
 Met Tyr 610 Arg Tyr Leu Thr Pro 615 His Val Ala Glu Gln 620 Val Met Ala Leu
 Gly 625 Glu Asp Ala Leu Met 630 Val Gly Glu Arg Lys 635 Glu Val Thr Val Leu 640
 Phe Ser Asp Ile Arg 645 Gly Tyr Thr Thr Leu 650 Thr Glu Asn Leu Gly 655 Ala
 Ala Glu Val Val 660 Ser Leu Leu Asn Gln 665 Tyr Phe Glu Thr Met 670 Val Glu
 Ala Val Phe 675 Asn Tyr Glu Gly Thr 680 Leu Asp Lys Phe Ile 685 Gly Asp Ala
 Leu Met 690 Ala Val Phe Gly Ala 695 Pro Leu Pro Leu Thr 700 Glu Asn His Ala
 Trp 705 Gln Ala Val Gln Ser 710 Ala Leu Asp Met Arg 715 Gln Arg Leu Lys Glu 720
 Phe Asn Gln Arg Arg 725 Ile Ile Gln Ala Gln 730 Pro Gln Ile Lys Ile 735 Gly
 Ile Gly Ile Ser 740 Ser Gly Glu Val Val 745 Ser Gly Asn Ile Gly 750 Ser His
 Lys Arg Met 755 Asp Tyr Thr Val Ile 760 Gly Asp Gly Val Asn 765 Leu Ser Ser

1336WOORD01 Sequence listing 2005-05-12.txt

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

Glu Phe Thr Tyr Gln Leu Cys Ser Asp Arg Ile Trp Val Arg Gln Leu
785 790 795 800

Asp Lys Ile Arg Val Lys Gly Lys His Gln Ala Val Asn Ile Tyr Glu
805 810 815

Leu Ile Ser Asp Arg Ser Thr Pro Leu Asp Asp Asn Thr Gln Glu Phe
820 825 830

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

Thr Gln Ala Ile Ala Cys Phe Asn Ser Ala Lys His Ile Arg Pro Thr
850 855 860

Asp Gln Ala Val Asn Ile His Leu Glu Arg Ala Tyr Asn Tyr Gln Gln
865 870 875 880

Thr Pro Pro Pro Pro Gln Trp Asp Gly Val Trp Thr Ile Phe Thr Lys
885 890 895

<210> 5

<211> 462

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(462)

<223> GAF-A PDE10

<400> 5	
gac aac cag cta ctc ctc tat gaa ctg agc agc atc att aaa ata gcc	48
Asp Asn Gln Leu 5 Leu Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala	
1 10 15	
aca aaa gcc gat gga ttt gca ctg tat ttc ctt gga gag tgc aat aat	96
Thr Lys Ala Asp 20 Gly Phe Ala Leu Tyr 25 Phe Leu Gly Glu Cys Asn Asn	
30	
agc ctg tgt ata ttc acg cca cct ggg ata aag gaa gga aaa ccc cgc	144
Ser Leu Cys 35 Ile Phe Thr Pro 40 Gly Ile Lys Glu 45 Lys Pro Arg	
ctc atc cct gct ggg ccc atc act cag ggc acc acc gtc tct gct tat	192
Leu Ile Pro Ala Gly Pro 55 Ile Thr Gln Gly Thr 60 Val Ser Ala Tyr	
50 55 60	

1336WOORD01 Sequence listing 2005-05-12.txt

gtg gcc aag tcc agg aaa aca ctg cta gta gaa gac atc ctt gga gat	240
Val Ala Lys Ser Arg Lys Thr Leu Leu Val Glu Asp Ile Leu Gly Asp	
65 70 75 80	
gaa cga ttt cca aga ggc act gga ctg gaa tca ggg act cgt atc cag	288
Glu Arg Phe Pro Arg Gly Thr Gly Leu Glu Ser Gly Thr Arg Ile Gln	
85 90 95	
tct gtt ctt tgc tta cca att gtc act gca att ggt gac ttg att ggt	336
Ser Val Leu Cys Leu Pro Ile Val Thr Ala Ile Gly Asp Leu Ile Gly	
100 105 110	
att ctc gag ctg tat cgg cac tgg ggc aaa gaa gcc ttc tgt ctt agt	384
Ile Leu Glu Leu Tyr Arg His Trp Gly Lys Glu Ala Phe Cys Leu Ser	
115 120 125	
cac cag gag gtt gca aca gca aat ctt gcc tgg gct tca gta gca ata	432
His Gln Glu Val Ala Thr Ala Asn Leu Ala Trp Ser Val Ala Ile	
130 135 140	
cat cag gtg cag gta tgc aga ggc ctt gcc	462
His Gln Val Gln Val Cys Arg Gly Leu Ala	
145 150	

<210> 6

<211> 154

<212> PRT

<213> Homo sapiens

<400> 6

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

1336WOORD01 Sequence listing 2005-05-12.txt

His Gln Glu Val Ala Thr Ala Asn Leu Ala Trp Ala Ser Val Ala Ile
130 135 140

His Gln Val Gln Val Cys Arg Gly Leu Ala
145 150

<210> 7

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(471)

<223> GAF-B PDE10

<400> 7

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Ala Ile Asp Ser Leu Leu Glu His Ile Met Ile Tyr Ala Lys Asn Leu
1 5 10 15

gtg aat gcc gat cgt tgt gcg ctt ttc cag gtg gac cat aag aac aag 96
Val Asn Ala Asp Arg Cys Ala Leu Phe Gln Val Asp His Lys Asn Lys
20 25 30

gag tta tat tca gac ctt ttt gat att gga gag gaa aag gaa gga aaa 144
Glu Leu Tyr Ser Asp Leu Phe Asp Ile Gly Glu Glu Lys Glu Gly Lys
35 40 45

cct gtc ttc aag aag acc aaa gag ata aga ttt tca att gag aaa gga 192
Pro Val Phe Lys Lys Thr Lys Glu Ile Arg Phe Ser Ile Glu Lys Gly
50 55 60

att gct ggc caa gta gca aga aca ggg gaa gtc ctg aac att cca gat 240
Ile Ala Gly Gln Val Ala Arg Thr Gly Glu Val Leu Asn Ile Pro Asp
65 70 75 80

gcc tat gca gac cca cgc ttt aac aga gaa gta gac ttg tac aca ggc 288
Ala Tyr Ala Asp Pro Arg Phe Asn Arg Glu Val Asp Leu Tyr Thr Gly
85 90 95

tac acc acg cgg aac atc ctg tgc atg ccc atc gtc agc cga ggc agc 336
Tyr Thr Thr Arg Asn Ile Leu Cys Met Pro Ile Val Ser Arg Gly Ser
100 105 110

gtg ata ggt gtg gtg cag atg gtc aac aaa atc agt ggc agt gcc ttc 384
Val Ile Gly Val Val Gln Met Val Asn Lys Ile Ser Gly Ser Ala Phe
115 120 125

tct aaa aca gat gaa aac aac ttc aaa atg ttt gcc gtc ttt tgt gct 432
Ser Lys Thr Asp Glu Asn Asn Phe Lys Met Phe Ala Val Phe Cys Ala
130 135 140

tta gcc tta cac tgt gct aat atg tat cat aga att cgc 471
Leu Ala Leu His Cys Ala Asn Met Tyr His Arg Ile Arg
145 150 155

1336WOORD01 Sequence listing 2005-05-12.txt

<210> 8

<211> 157

<212> PRT

<213> Homo sapiens

<400> 8

Ala Ile Asp Ser Leu Leu Glu His Ile Met Ile Tyr Ala Lys Asn Leu
1 5 10 15

Val Asn Ala Asp Arg Cys Ala Leu Phe Gln Val Asp His Lys Asn Lys
20 25 30

Glu Leu Tyr Ser Asp Leu Phe Asp Ile Gly Glu Glu Lys Glu Gly Lys
35 40 45

Pro Val Phe Lys Lys Thr Lys Glu Ile Arg Phe Ser Ile Glu Lys Gly
50 55 60

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

Ala Tyr Ala Asp Pro Arg Phe Asn Arg Glu Val Asp Leu Tyr Thr Gly
85 90 95

Tyr Thr Thr Arg Asn Ile Leu Cys Met Pro Ile Val Ser Arg Gly Ser
100 105 110

Val Ile Gly Val Val Gln Met Val Asn Lys Ile Ser Gly Ser Ala Phe
115 120 125

Ser Lys Thr Asp Glu Asn Asn Phe Lys Met Phe Ala Val Phe Cys Ala
130 135 140

Leu Ala Leu His Cys Ala Asn Met Tyr His Arg Ile Arg
145 150 155

<210> 9

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1230)

1336WOORD01 Sequence listing 2005-05-12.txt

<223> GAF PDE10

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1 5 10 15

gta tta gat gaa ttt gta tct gaa agt gtt agt gca gag aca gta gag      96
Val Leu Asp Glu Phe Val Ser Glu Ser Val Ser Ala Glu Thr Val Glu
20 25 30

aaa tgg ctg aag agg aag aac aac aaa tca gaa gat gaa tca gct cct      144
Lys Trp Leu Lys Arg Lys Asn Asn Lys Ser Glu Asp Glu Ser Ala Pro
35 40 45

aag gaa gtc agc agg tac caa gat acg aat atg cag gga gtt gta tat      192
Lys Glu Val Ser Arg Tyr Gln Asp Thr Asn Met Gln Gly Val Val Tyr
50 55 60

gaa cta aac agc tat ata gaa caa cgg ttg gac aca gga gga gac aac      240
Glu Leu Asn Ser Tyr Ile Glu Gln Arg Leu Asp Thr Gly Gly Asp Asn
65 70 75 80

cag cta ctc ctc tat gaa ctg agc agc atc att aaa ata gcc aca aaa      288
Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala Thr Lys
85 90 95

gcc gat gga ttt gca ctg tat ttc ctt gga gag tgc aat aat agc ctg      336
Ala Asp Gly Phe Ala Leu Tyr Phe Leu Gly Glu Cys Asn Asn Ser Leu
100 105 110

tgt ata ttc acg cca cct ggg ata aag gaa gga aaa ccc cgc ctc atc      384
Cys Ile Phe Thr Pro Pro Gly Ile Lys Glu Gly Lys Pro Arg Leu Ile
115 120 125

cct gct ggg ccc atc act cag ggc acc acc gtc tct gct tat gtg gcc      432
Pro Ala Gly Pro Ile Thr Gln Gly Thr Thr Val Ser Ala Tyr Val Ala
130 135 140

aag tcc agg aaa aca ctg cta gta gaa gac atc ctt gga gat gaa cga      480
Lys Ser Arg Lys Thr Leu Leu Val Glu Asp Ile Leu Gly Asp Glu Arg
145 150 155 160

ttt cca aga ggc act gga ctg gaa tca ggg act cgt atc cag tct gtt      528
Phe Pro Arg Gly Thr Gly Leu Glu Ser Gly Thr Arg Ile Gln Ser Val
165 170 175

ctt tgc tta cca att gtc act gca att ggt gac ttg att ggt att ctc      576
Leu Cys Leu Pro Ile Val Thr Ala Ile Gly Asp Leu Ile Gly Ile Leu
180 185 190

gag ctg tat cgg cac tgg ggc aaa gaa gcc ttc tgt ctt agt cac cag      624
Glu Leu Tyr Arg His Trp Gly Lys Glu Ala Phe Cys Leu Ser His Gln
195 200 205

gag gtt gca aca gca aat ctt gcc tgg gct tca gta gca ata cat cag      672
Glu Val Ala Thr Ala Asn Leu Ala Trp Ala Ser Val Ala Ile His Gln
210 215 220

gtg cag gta tgc aga ggc ctt gcc aaa cag aca gaa ttg aat gac ttc      720
Val Gln Val Cys Arg Gly Leu Ala Lys Gln Thr Glu Leu Asn Asp Phe
225 230 235 240

cta ctc gac gta tca aaa aca tat ttt gat aac ata gtt gca ata gat      768
Leu Leu Asp Val Ser Lys Thr Tyr Phe Asp Asn Ile Val Ala Ile Asp
245 250 255

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1336WOORD01 Sequence listing 2005-05-12.txt

tct	cta	ctt	gaa	cac	ata	atg	ata	tat	gca	aaa	aac	ctg	gtg	aat	gcc	816
Ser	Leu	Leu	Glu	His	Ile	Met	Ile	Tyr	Ala	Lys	Asn	Leu	Val	Asn	Ala	
			260					265					270			
gat	cgt	tgt	gcg	ctt	ttc	cag	gtg	gac	cat	aag	aac	aag	gag	tta	tat	864
Asp	Arg	Cys	Ala	Leu	Phe	Gln	Val	Asp	His	Lys	Asn	Lys	Glu	Leu	Tyr	
		275					280					285				
tca	gac	ctt	ttt	gat	att	gga	gag	gaa	aag	gaa	gga	aaa	cct	gtc	ttc	912
Ser	Asp	Leu	Phe	Asp	Ile	Gly	Glu	Glu	Lys	Glu	Gly	Lys	Pro	Val	Phe	
	290					295					300					
aag	aag	acc	aaa	gag	ata	aga	ttt	tca	att	gag	aaa	gga	att	gct	ggc	960
Lys	Lys	Thr	Lys	Glu	Ile	Arg	Phe	Ser	Ile	Glu	Lys	Gly	Ile	Ala	Gly	
305					310					315					320	
caa	gta	gca	aga	aca	ggg	gaa	gtc	ctg	aac	att	cca	gat	gcc	tat	gca	1008
Gln	Val	Ala	Arg	Thr	Gly	Glu	Val	Leu	Asn	Ile	Pro	Asp	Ala	Tyr	Ala	
				325					330					335		
gac	cca	cgc	ttt	aac	aga	gaa	gta	gac	ttg	tac	aca	ggc	tac	acc	acg	1056
Asp	Pro	Arg	Phe	Asn	Arg	Glu	Val	Asp	Leu	Tyr	Thr	Gly	Tyr	Thr	Thr	
			340					345					350			
cgg	aac	atc	ctg	tgc	atg	ccc	atc	gtc	agc	cga	ggc	agc	gtg	ata	ggc	1104
Arg	Asn	Ile	Leu	Cys	Met	Pro	Ile	Val	Ser	Arg	Gly	Ser	Val	Ile	Gly	
		355					360					365				
gtg	gtg	cag	atg	gtc	aac	aaa	atc	agt	ggc	agt	gcc	ttc	tct	aaa	aca	1152
Val	Val	Gln	Met	Val	Asn	Lys	Ile	Ser	Gly	Ser	Ala	Phe	Ser	Lys	Thr	
	370					375					380					
gat	gaa	aac	aac	ttc	aaa	atg	ttt	gcc	gtc	ttt	tgt	gct	tta	gcc	tta	1200
Asp	Glu	Asn	Asn	Phe	Lys	Met	Phe	Ala	Val	Phe	Cys	Ala	Leu	Ala	Leu	
385					390					395					400	
cac	tgt	gct	aat	atg	tat	cat	aga	att	cgc							1230
His	Cys	Ala	Asn	Met	Tyr	His	Arg	Ile	Arg							
				405					410							

<210> 10

<211> 410

<212> PRT

<213> Homo sapiens

<400> 10

Met	Leu	Thr	Asp	Glu	Lys	Val	Lys	Ala	Tyr	Leu	Ser	Leu	His	Pro	Gln
1				5					10					15	
Val	Leu	Asp	Glu	Phe	Val	Ser	Glu	Ser	Val	Ser	Ala	Glu	Thr	Val	Glu
			20					25					30		
Lys	Trp	Leu	Lys	Arg	Lys	Asn	Asn	Lys	Ser	Glu	Asp	Glu	Ser	Ala	Pro
		35					40					45			
Lys	Glu	Val	Ser	Arg	Tyr	Gln	Asp	Thr	Asn	Met	Gln	Gly	Val	Val	Tyr
	50					55					60				

1336WOORD01 Sequence listing 2005-05-12.txt

Glu Leu Asn Ser Tyr Ile Glu Gln Arg Leu Asp Thr Gly Gly Asp Asn
65 70 75 80

Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala Thr Lys
85 90 95

Ala Asp Gly Phe Ala Leu Tyr Phe Leu Gly Glu Cys Asn Asn Ser Leu
100 105 110

Cys Ile Phe Thr Pro Pro Gly Ile Lys Glu Gly Lys Pro Arg Leu Ile
115 120 125

Pro Ala Gly Pro Ile Thr Gln Gly Thr Thr Val Ser Ala Tyr Val Ala
130 135 140

Lys Ser Arg Lys Thr Leu Leu Val Glu Asp Ile Leu Gly Asp Glu Arg
145 150 155 160

Phe Pro Arg Gly Thr Gly Leu Glu Ser Gly Thr Arg Ile Gln Ser Val
165 170 175

Leu Cys Leu Pro Ile Val Thr Ala Ile Gly Asp Leu Ile Gly Ile Leu
180 185 190

Glu Leu Tyr Arg His Trp Gly Lys Glu Ala Phe Cys Leu Ser His Gln
195 200 205

Glu Val Ala Thr Ala Asn Leu Ala Trp Ala Ser Val Ala Ile His Gln
210 215 220

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

Leu Leu Asp Val Ser Lys Thr Tyr Phe Asp Asn Ile Val Ala Ile Asp
245 250 255

Ser Leu Leu Glu His Ile Met Ile Tyr Ala Lys Asn Leu Val Asn Ala
260 265 270

Asp Arg Cys Ala Leu Phe Gln Val Asp His Lys Asn Lys Glu Leu Tyr
275 280 285

Ser Asp Leu Phe Asp Ile Gly Glu Glu Lys Glu Gly Lys Pro Val Phe
290 295 300

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

Gln Val Ala Arg Thr Gly Glu Val Leu Asn Ile Pro Asp Ala Tyr Ala
325 330 335

Asp Pro Arg Phe Asn Arg Glu Val Asp Leu Tyr Thr Gly Tyr Thr Thr
Page 21

Arg Asn Ile Leu Cys Met Pro Ile Val Ser Arg Gly Ser Val Ile Gly
355 360 365

Val Val Gln Met Val Asn Lys Ile Ser Gly Ser Ala Phe Ser Lys Thr
370 375 380

Asp Glu Asn Asn Phe Lys Met Phe Ala Val Phe Cys Ala Leu Ala Leu
385 390 395 400

His Cys Ala Asn Met Tyr His Arg Ile Arg
405 410

<210> 11

<211> 1425

<212> DNA

<213> Anabaena PCC7120

<220>

<221> CDS

<222> (1)..(1425)

<223> Katalytische Domäne CyaB1

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gta att tct aca gat atg gcc ggg aga att gtc aca att aat gat gca 96
Val Ile Ser Thr Asp Met Ala Gly Arg Ile Val Thr Ile Asn Asp Ala
20 25 30

gcc ttg gaa tta ctc ggt tgt cct tta ggt gat gct aat cat aaa agt 144
Ala Leu Glu Leu Leu Gly Cys Pro Leu Gly Asp Ala Asn His Lys Ser
35 40 45

aat aag ctg ctg tgg gaa caa aat tta att ggt cgc gta gtt tgg gaa 192
Asn Lys Leu Leu Trp Glu Gln Asn Leu Ile Gly Arg Val Val Trp Glu
50 55 60

att gta cca att gaa aat ttg cag atg cgc tta gaa gat agt tta aaa 240
Ile Val Pro Ile Glu Asn Leu Gln Met Arg Leu Glu Asp Ser Leu Lys
65 70 75 80

agt ggt gct aaa cat tat gtg cca gaa caa agt ttg ata gtg gga att 288
Ser Gly Ala Lys His Tyr Val Pro Glu Gln Ser Leu Ile Val Gly Ile
85 90 95

tat caa tta caa atg tct gaa agt cgg gtt ttg cat gaa act caa gac 336
Tyr Gln Leu Gln Met Ser Glu Ser Arg Val Leu His Glu Thr Gln Asp
100 105 110

tac tct att ttg aca gta cgc gat cgc atc aac cca gat att ttt ctc 384

1336WOORD01 Sequence listing 2005-05-12.txt

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

1336WOORD01 Sequence listing 2005-05-12.txt

385		390		395		400	
act ccc tta gat gac aac acc caa gag ttc ctc ttt cac tat cat aat	1248						
Thr Pro Leu Asp Asp Asn Thr Gln Glu Phe Leu Phe His Tyr His Asn							
	405	410	415				
ggt cgg act gcc tac tta gtc cgc gat ttt acc cag gcg atc gct tgt	1296						
Gly Arg Thr Ala Tyr Leu Val Arg Asp Phe Thr Gln Ala Ile Ala Cys							
	420	425	430				
ttt aac tca gct aaa cat att cga ccc aca gac caa gct gtc aat att	1344						
Phe Asn Ser Ala Lys His Ile Arg Pro Thr Asp Gln Ala Val Asn Ile							
	435	440	445				
cac cta gaa cgc gcc tac aat tat caa caa act cca cca cct cct caa	1392						
His Leu Glu Arg Ala Tyr Asn Tyr Gln Gln Thr Pro Pro Pro Pro Gln							
	450	455	460				
tgg gac ggc gta tgg aca att ttc aca aag tag	1425						
Trp Asp Gly Val Trp Thr Ile Phe Thr Lys							
	465	470					

<210> 12

<211> 474

<212> PRT

<213> Anabaena PCC7120

<400> 12

Val Glu Lys Gln Tyr Gln Lys Asp Ile Leu Gln Ser Leu Ser Asp Ala
1 5 10 15

Val Ile Ser Thr Asp Met Ala Gly Arg Ile Val Thr Ile Asn Asp Ala
20 25 30

Ala Leu Glu Leu Leu Gly Cys Pro Leu Gly Asp Ala Asn His Lys Ser
35 40 45

Asn Lys Leu Leu Trp Glu Gln Asn Leu Ile Gly Arg Val Val Trp Glu
50 55 60

Ile Val Pro Ile Glu Asn Leu Gln Met Arg Leu Glu Asp Ser Leu Lys
65 70 75 80

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

Tyr Gln Leu Gln Met Ser Glu Ser Arg Val Leu His Glu Thr Gln Asp
100 105 110

Tyr Ser Ile Leu Thr Val Arg Asp Arg Ile Asn Pro Asp Ile Phe Leu
115 120 125

Pro Trp Asn Leu Pro Gln Thr Pro Gln Ser Gln Phe Ile Thr Pro Glu
130 135 140

1336WOORD01 Sequence listing 2005-05-12.txt

Glu Val Gln Ile Leu Glu Arg Ser Ile Asn Leu Thr Val Asn Pro Leu
 145 150 155 160
 Thr Asn Pro Glu Gly Gly Val Arg Gly Gly Leu Val Val Leu Glu Asp
 165 170 175
 Ile Ser Gln Glu Lys Arg Leu Lys Thr Thr Met Tyr Arg Tyr Leu Thr
 180 185 190
 Pro His Val Ala Glu Gln Val Met Ala Leu Gly Glu Asp Ala Leu Met
 195 200 205
 Val Gly Glu Arg Lys Glu Val Thr Val Leu Phe Ser Asp Ile Arg Gly
 210 215 220
 Tyr Thr Thr Leu Thr Glu Asn Leu Gly Ala Ala Glu Val Val Ser Leu
 225 230 235 240
 Leu Asn Gln Tyr Phe Glu Thr Met Val Glu Ala Val Phe Asn Tyr Glu
 245 250 255
 Gly Thr Leu Asp Lys Phe Ile Gly Asp Ala Leu Met Ala Val Phe Gly
 260 265 270
 Ala Pro Leu Pro Leu Thr Glu Asn His Ala Trp Gln Ala Val Gln Ser
 275 280 285
 Ala Leu Asp Met Arg Gln Arg Leu Lys Glu Phe Asn Gln Arg Arg Ile
 290 295 300
 Ile Gln Ala Gln Pro Gln Ile Lys Ile Gly Ile Gly Ile Ser Ser Gly
 305 310 315 320
 Glu Val Val Ser Gly Asn Ile Gly Ser His Lys Arg Met Asp Tyr Thr
 325 330 335
 Val Ile Gly Asp Gly Val Asn Leu Ser Ser Arg Leu Glu Thr Val Thr
 340 345 350
 Lys Glu Tyr Gly Cys Asp Ile Ile Leu Ser Glu Phe Thr Tyr Gln Leu
 355 360 365
 Cys Ser Asp Arg Ile Trp Val Arg Gln Leu Asp Lys Ile Arg Val Lys
 370 375 380
 Gly Lys His Gln Ala Val Asn Ile Tyr Glu Leu Ile Ser Asp Arg Ser
 385 390 395 400
 Thr Pro Leu Asp Asp Asn Thr Gln Glu Phe Leu Phe His Tyr His Asn
 405 410 415

1336WOORD01 Sequence listing 2005-05-12.txt

Gly Arg Thr Ala Tyr Leu Val Arg Asp Phe Thr Gln Ala Ile Ala Cys
420 425 430

Phe Asn Ser Ala Lys His Ile Arg Pro Thr Asp Gln Ala Val Asn Ile
435 440 445

His Leu Glu Arg Ala Tyr Asn Tyr Gln Gln Thr Pro Pro Pro Pro Gln
450 455 460

Trp Asp Gly Val Trp Thr Ile Phe Thr Lys
465 470

<210> 13

<211> 1296

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1296)

<223> GAF PDE10

<400> 13

atg gaa gat gga cct tct aat aat gcg agc tgc ttc cga agg ctg acc	48
Met Glu Asp Gly Pro Ser Asn Asn Ala Ser Cys Phe Arg Arg Leu Thr	
1 5 10 15	

gag tgc ttc ctg agc ccc agt ttg aca gat gaa aaa gtg aag gca tat	96
Glu Cys Phe Leu Ser Pro Ser Leu Thr Asp Glu Lys Val Lys Ala Tyr	
20 25 30	

ctt tct ctt cac ccc cag gta tta gat gaa ttt gta tct gaa agt gtt	144
Leu Ser Leu His Pro Gln Val Leu Asp Glu Phe Val Ser Glu Ser Val	
35 40 45	

agt gca gag aca gta gag aaa tgg ctg aag agg aag aac aac aaa tca	192
Ser Ala Glu Thr Val Glu Lys Trp Leu Lys Arg Lys Asn Asn Lys Ser	
50 55 60	

gaa gat gaa tca gct cct aag gaa gtc agc agg tac caa gat acg aat	240
Glu Asp Glu Ser Ala Pro Lys Glu Val Ser Arg Tyr Gln Asp Thr Asn	
65 70 75 80	

atg cag gga gtt gta tat gaa cta aac agc tat ata gaa caa cgg ttg	288
Met Gln Gly Val Val Tyr Glu Leu Asn Ser Tyr Ile Glu Gln Arg Leu	
85 90 95	

gac aca gga gga gac aac cag cta ctc ctc tat gaa ctg agc agc atc	336
Asp Thr Gly Gly Asp Asn Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile	
100 105 110	

att aaa ata gcc aca aaa gcc gat gga ttt gca ctg tat ttc ctt gga	384
Ile Lys Ile Ala Thr Lys Ala Asp Gly Phe Ala Leu Tyr Phe Leu Gly	
115 120 125	

1336WOORD01 Sequence listing 2005-05-12.txt

gag Glu	tgc Cys 130	aat Asn	aat Asn	agc Ser	ctg Leu	tgt Cys 135	ata Ile	ttc Phe	acg Thr	cca Pro	cct Pro 140	ggg Gly	ata Ile	aag Lys	gaa Glu	432
gga Gly 145	aaa Lys	ccc Pro	cgc Arg	ctc Leu	atc Ile 150	cct Pro	gct Ala	ggg Gly	ccc Pro	atc Ile 155	act Thr	cag Gln	ggc Gly	acc Thr	acc Thr 160	480
gtc Val	tct Ser	gct Ala	tat Tyr	gtg Val 165	gcc Ala	aag Lys	tcc Ser	agg Arg	aaa Lys 170	aca Thr	ctg Leu	cta Leu	gta Val	gaa Glu 175	gac Asp	528
atc Ile	ctt Leu	gga Gly	gat Asp 180	gaa Glu	cga Arg	ttt Phe	cca Pro	aga Arg 185	ggg Gly	act Thr	gga Gly	ctg Leu	gaa Glu 190	tca Ser	ggg Gly	576
act Thr	cgt Arg	atc Ile 195	cag Gln	tct Ser	gtt Val	ctt Leu	tgc Cys 200	tta Leu	cca Pro	att Ile	gtc Val	act Thr 205	gca Ala	att Ile	ggg Gly	624
gac Asp	ttg Leu 210	att Ile	ggg Gly	att Ile	ctc Leu	gag Glu 215	ctg Leu	tat Tyr	cgg Arg	cac His	tgg Trp 220	ggc Gly	aaa Lys	gaa Glu	gcc Ala	672
ttc Phe 225	tgt Cys	ctt Leu	agt Ser	cac His	cag Gln 230	gag Glu	gtt Val	gca Ala	aca Thr	gca Ala 235	aat Asn	ctt Leu	gcc Ala	tgg Trp	gct Ala 240	720
tca Ser	gta Val	gca Ala	ata Ile	cat His 245	cag Gln	gtg Val	cag Gln	gta Val	tgc Cys 250	aga Arg	ggc Gly	ctt Leu	gcc Ala	aaa Lys 255	cag Gln	768
aca Thr	gaa Glu	ttg Leu	aat Asn 260	gac Asp	ttc Phe	cta Leu	ctc Leu	gac Asp 265	gta Val	tca Ser	aaa Lys	aca Thr	tat Tyr 270	ttt Phe	gat Asp	816
aac Asn	ata Ile	gtt Val 275	gca Ala	ata Ile	gat Asp	tct Ser	cta Leu 280	ctt Leu	gaa Glu	cac His	ata Ile	atg Met 285	ata Ile	tat Tyr	gca Ala	864
aaa Lys	aac Asn 290	ctg Leu	gtg Val	aat Asn	gcc Ala	gat Asp 295	cgt Arg	tgt Cys	gcg Ala	ctt Leu	ttc Phe 300	cag Gln	gtg Val	gac Asp	cat His	912
aag Lys 305	aac Asn	aag Lys	gag Glu	tta Leu	tat Tyr 310	tca Ser	gac Asp	ctt Leu	ttt Phe	gat Asp 315	att Ile	gga Gly	gag Glu	gaa Glu	aag Lys 320	960
gaa Glu	gga Gly	aaa Lys	cct Pro	gtc Val 325	ttc Phe	aag Lys	aag Lys	acc Thr	aaa Lys 330	gag Glu	ata Ile	aga Arg	ttt Phe	tca Ser 335	att Ile	1008
gag Glu	aaa Lys	gga Gly	att Ile 340	gct Ala	ggc Gly	caa Gln	gta Val	gca Ala 345	aga Arg	aca Thr	ggg Gly	gaa Glu	gtc Val 350	ctg Leu	aac Asn	1056
att Ile	cca Pro	gat Asp 355	gcc Ala	tat Tyr	gca Ala	gac Asp	cca Pro 360	cgc Arg	ttt Phe	aac Asn	aga Arg	gaa Glu 365	gta Val	gac Asp	ttg Leu	1104
tac Tyr	aca Thr 370	ggc Gly	tac Tyr	acc Thr	acg Thr	cgg Arg 375	aac Asn	atc Ile	ctg Leu	tgc Cys	atg Met 380	ccc Pro	atc Ile	gtc Val	agc Ser	1152
cga Arg 385	ggc Gly	agc Ser	gtg Val	ata Ile	ggg Gly 390	gtg Val	gtg Val	cag Gln	atg Met	gtc Val 395	aac Asn	aaa Lys	atc Ile	agt Ser	ggc Gly 400	1200

1336WOORD01 Sequence listing 2005-05-12.txt

agt gcc ttc tct aaa aca gat gaa aac aac ttc aaa atg ttt gcc gtc 1248
Ser Ala Phe Ser Lys Thr Asp Glu Asn Asn Phe Lys Met Phe Ala Val
405 410 415

ttt tgt gct tta gcc tta cac tgt gct aat atg tat cat aga att cgc 1296
Phe Cys Ala Leu Ala Leu His Cys Ala Asn Met Tyr His Arg Ile Arg
420 425 430

<210> 14

<211> 432

<212> PRT

<213> Homo sapiens

<400> 14

Met Glu Asp Gly Pro Ser Asn Asn Ala Ser Cys Phe Arg Arg Leu Thr
1 5 10 15

Glu Cys Phe Leu Ser Pro Ser Leu Thr Asp Glu Lys Val Lys Ala Tyr
20 25 30

Leu Ser Leu His Pro Gln Val Leu Asp Glu Phe Val Ser Glu Ser Val
35 40 45

Ser Ala Glu Thr Val Glu Lys Trp Leu Lys Arg Lys Asn Asn Lys Ser
50 55 60

Glu Asp Glu Ser Ala Pro Lys Glu Val Ser Arg Tyr Gln Asp Thr Asn
65 70 75 80

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

Asp Thr Gly Gly Asp Asn Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile
100 105 110

Ile Lys Ile Ala Thr Lys Ala Asp Gly Phe Ala Leu Tyr Phe Leu Gly
115 120 125

Glu Cys Asn Asn Ser Leu Cys Ile Phe Thr Pro Pro Gly Ile Lys Glu
130 135 140

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

Val Ser Ala Tyr Val Ala Lys Ser Arg Lys Thr Leu Leu Val Glu Asp
165 170 175

Ile Leu Gly Asp Glu Arg Phe Pro Arg Gly Thr Gly Leu Glu Ser Gly
180 185 190

1336WOORD01 Sequence listing 2005-05-12.txt

Thr Arg Ile Gln Ser Val Leu Cys Leu Pro Ile Val Thr Ala Ile Gly
195 200 205

Asp Leu Ile Gly Ile Leu Glu Leu Tyr Arg His Trp Gly Lys Glu Ala
210 215 220

Phe Cys Leu Ser His Gln Glu Val Ala Thr Ala Asn Leu Ala Trp Ala
225 230 235 240

Ser Val Ala Ile His Gln Val Gln Val Cys Arg Gly Leu Ala Lys Gln
245 250 255

Thr Glu Leu Asn Asp Phe Leu Leu Asp Val Ser Lys Thr Tyr Phe Asp
260 265 270

Asn Ile Val Ala Ile Asp Ser Leu Leu Glu His Ile Met Ile Tyr Ala
275 280 285

Lys Asn Leu Val Asn Ala Asp Arg Cys Ala Leu Phe Gln Val Asp His
290 295 300

Lys Asn Lys Glu Leu Tyr Ser Asp Leu Phe Asp Ile Gly Glu Glu Lys
305 310 315 320

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

Glu Lys Gly Ile Ala Gly Gln Val Ala Arg Thr Gly Glu Val Leu Asn
340 345 350

Ile Pro Asp Ala Tyr Ala Asp Pro Arg Phe Asn Arg Glu Val Asp Leu
355 360 365

Tyr Thr Gly Tyr Thr Thr Arg Asn Ile Leu Cys Met Pro Ile Val Ser
370 375 380

Arg Gly Ser Val Ile Gly Val Val Gln Met Val Asn Lys Ile Ser Gly
385 390 395 400

Ser Ala Phe Ser Lys Thr Asp Glu Asn Asn Phe Lys Met Phe Ala Val
405 410 415

Phe Cys Ala Leu Ala Leu His Cys Ala Asn Met Tyr His Arg Ile Arg
420 425 430

<210> 15

<211> 459

<212> DNA

<213> Homo sapiens

1336WOORD01 Sequence listing 2005-05-12.txt

<220>

<221> CDS

<222> (1)..(459)

<223> GAF-A PDE10

<400> 15

aac cag cta ctc ctc tat gaa ctg agc agc atc att aaa ata gcc aca 48
Asn Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala Thr
1 5 10 15

aaa gcc gat gga ttt gca ctg tat ttc ctt gga gag tgc aat aat agc 96
Lys Ala Asp Gly Phe Ala Leu Tyr Phe Leu Gly Glu Cys Asn Asn Ser
20 25 30

ctg tgt ata ttc acg cca cct ggg ata aag gaa gga aaa ccc cgc ctc 144
Leu Cys Ile Phe Thr Pro Pro Gly Ile Lys Glu Gly Lys Pro Arg Leu
35 40 45

atc cct gct ggg ccc atc act cag ggc acc acc gtc tct gct tat gtg 192
Ile Pro Ala Gly Pro Ile Thr Gln Gly Thr Thr Val Ser Ala Tyr Val
50 55 60

gcc aag tcc agg aaa aca ctg cta gta gaa gac atc ctt gga gat gaa 240
Ala Lys Ser Arg Lys Thr Leu Leu Val Glu Asp Ile Leu Gly Asp Glu
65 70 75 80

cga ttt cca aga ggc act gga ctg gaa tca ggg act cgt atc cag tct 288
Arg Phe Pro Arg Gly Thr Gly Leu Glu Ser Gly Thr Arg Ile Gln Ser
85 90 95

gtt ctt tgc tta cca att gtc act gca att ggt gac ttg att ggt att 336
Val Leu Cys Leu Pro Ile Val Thr Ala Ile Gly Asp Leu Ile Gly Ile
100 105 110

ctc gag ctg tat cgg cac tgg ggc aaa gaa gcc ttc tgt ctt agt cac 384
Leu Glu Leu Tyr Arg His Trp Gly Lys Glu Ala Phe Cys Leu Ser His
115 120 125

cag gag gtt gca aca gca aat ctt gcc tgg gct tca gta gca ata cat 432
Gln Glu Val Ala Thr Ala Asn Leu Ala Trp Ala Ser Val Ala Ile His
130 135 140

cag gtg cag gta tgc aga ggc ctt gcc 459
Gln Val Gln Val Cys Arg Gly Leu Ala
145 150

<210> 16

<211> 153

<212> PRT

<213> Homo sapiens

<400> 16

Asn Gln Leu Leu Leu Tyr Glu Leu Ser Ser Ile Ile Lys Ile Ala Thr
1 5 10 15

1336WOORD01 Sequence listing 2005-05-12.txt

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