

CYA-B-0002-PCT1-SEQ-1\_ST25  
SEQUENCE LISTING

<110> CYANIMAL IP  
x, x

<120> CyaA polypeptides as immune enhancer

<130> CYA-B-0002-PCT1

<150> EP16002451.9

<151> 2016-11-17

<160> 10

<170> PatentIn version 3.5

<210> 1

<211> 1706

<212> PRT

<213> Bordetella pertussis

<400> 1

Met Gln Gln Ser His Gln Ala Gly Tyr Ala Asn Ala Ala Asp Arg Glu  
1 5 10 15

Ser Gly Ile Pro Ala Ala Val Leu Asp Gly Ile Lys Ala Val Ala Lys  
20 25 30

Glu Lys Asn Ala Thr Leu Met Phe Arg Leu Val Asn Pro His Ser Thr  
35 40 45

Ser Leu Ile Ala Glu Gly Val Ala Thr Lys Gly Leu Gly Val His Ala  
50 55 60

Lys Ser Ser Asp Trp Gly Leu Gln Ala Gly Tyr Ile Pro Val Asn Pro  
65 70 75 80

Asn Leu Ser Lys Leu Phe Gly Arg Ala Pro Glu Val Ile Ala Arg Ala  
85 90 95

Asp Asn Asp Val Asn Ser Ser Leu Ala His Gly His Thr Ala Val Asp  
100 105 110

Leu Thr Leu Ser Lys Glu Arg Leu Asp Tyr Leu Arg Gln Ala Gly Leu  
115 120 125

Val Thr Gly Met Ala Asp Gly Val Val Ala Ser Asn His Ala Gly Tyr  
130 135 140

Glu Gln Phe Glu Phe Arg Val Lys Glu Thr Ser Asp Gly Arg Tyr Ala  
145 150 155 160

Val Gln Tyr Arg Arg Lys Gly Gly Asp Asp Phe Glu Ala Val Lys Val  
165 170 175

Ile Gly Asn Ala Ala Gly Ile Pro Leu Thr Ala Asp Ile Asp Met Phe  
Pge p

## CYA-B-0002-PCT1-SEQ-1\_ST25

180

185

190

Ala Ile Met Pro His Leu Ser Asn Phe Arg Asp Ser Ala Arg Ser Ser  
195 200 205

Val Thr Ser Gly Asp Ser Val Thr Asp Tyr Leu Ala Arg Thr Arg Arg  
210 215 220

Ala Ala Ser Glu Ala Thr Gly Gly Leu Asp Arg Glu Arg Ile Asp Leu  
225 230 235 240

Leu Trp Lys Ile Ala Arg Ala Gly Ala Arg Ser Ala Val Gly Thr Glu  
245 250 255

Ala Arg Arg Gln Phe Arg Tyr Asp Gly Asp Met Asn Ile Gly Val Ile  
260 265 270

Thr Asp Phe Glu Leu Glu Val Arg Asn Ala Leu Asn Arg Arg Ala His  
275 280 285

Ala Val Gly Ala Gln Asp Val Val Gln His Gly Thr Glu Gln Asn Asn  
290 295 300

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

Glu Ser Gln Met Leu Thr Arg Gly Gln Leu Lys Glu Tyr Ile Gly Gln  
325 330 335

Gln Arg Gly Glu Gly Tyr Val Phe Tyr Glu Asn Arg Ala Tyr Gly Val  
340 345 350

Ala Gly Lys Ser Leu Phe Asp Asp Gly Leu Gly Ala Ala Pro Gly Val  
355 360 365

Pro Ser Gly Arg Ser Lys Phe Ser Pro Asp Val Leu Glu Thr Val Pro  
370 375 380

Ala Ser Pro Gly Leu Arg Arg Pro Ser Leu Gly Ala Val Glu Arg Gln  
385 390 395 400

Asp Ser Gly Tyr Asp Ser Leu Asp Gly Val Gly Ser Arg Ser Phe Ser  
405 410 415

Leu Gly Glu Val Ser Asp Met Ala Ala Val Glu Ala Ala Glu Leu Glu  
420 425 430

Met Thr Arg Gln Val Leu His Ala Gly Ala Arg Gln Asp Asp Ala Glu  
435 440 445

Pro Gly Val Ser Gly Ala Ser Ala His Trp Gly Gln Arg Ala Leu Gln

## CYA-B-0002-PCT1-SEQ-1\_ST25

450

455

460

Gly Ala Gln Ala Val Ala Ala Ala Gln Arg Leu Val His Ala Ile Ala  
465 470 475 480

Leu Met Thr Gln Phe Gly Arg Ala Gly Ser Thr Asn Thr Pro Gln Glu  
485 490 495

Ala Ala Ser Leu Ser Ala Ala Val Phe Gly Leu Gly Glu Ala Ser Ser  
500 505 510

Ala Val Ala Glu Thr Val Ser Gly Phe Phe Arg Gly Ser Ser Arg Trp  
515 520 525

Ala Gly Gly Phe Gly Val Ala Gly Gly Ala Met Ala Leu Gly Gly Gly  
530 535 540

Ile Ala Ala Ala Val Gly Ala Gly Met Ser Leu Thr Asp Asp Ala Pro  
545 550 555 560

Ala Gly Gln Lys Ala Ala Ala Gly Ala Glu Ile Ala Leu Gln Leu Thr  
565 570 575

Gly Gly Thr Val Glu Leu Ala Ser Ser Ile Ala Leu Ala Leu Ala Ala  
580 585 590

Ala Arg Gly Val Thr Ser Gly Leu Gln Val Ala Gly Ala Ser Ala Gly  
595 600 605

Ala Ala Ala Gly Ala Leu Ala Ala Ala Leu Ser Pro Met Glu Ile Tyr  
610 615 620

Gly Leu Val Gln Gln Ser His Tyr Ala Asp Gln Leu Asp Lys Leu Ala  
625 630 635 640

Gln Glu Ser Ser Ala Tyr Gly Tyr Glu Gly Asp Ala Leu Leu Ala Gln  
645 650 655

Leu Tyr Arg Asp Lys Thr Ala Ala Glu Gly Ala Val Ala Gly Val Ser  
660 665 670

Ala Val Leu Ser Thr Val Gly Ala Ala Val Ser Ile Ala Ala Ala Ala  
675 680 685

Ser Val Val Gly Ala Pro Val Ala Val Val Thr Ser Leu Leu Thr Gly  
690 695 700

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

Leu Ala Asn Asp Tyr Ala Arg Lys Ile Asp Glu Leu Gly Gly Pro Gln  
Pge p

## CYA-B-0002-PCT1-SEQ-1\_ST25

725

730

735

Ala Tyr Phe Glu Lys Asn Leu Gln Ala Arg His Glu Gln Leu Ala Asn  
740 745 750

Ser Asp Gly Leu Arg Lys Met Leu Ala Asp Leu Gln Ala Gly Trp Asn  
755 760 765

Ala Ser Ser Val Ile Gly Val Gln Thr Thr Glu Ile Ser Lys Ser Ala  
770 775 780

Leu Glu Leu Ala Ala Ile Thr Gly Asn Ala Asp Asn Leu Lys Ser Val  
785 790 795 800

Asp Val Phe Val Asp Arg Phe Val Gln Gly Glu Arg Val Ala Gly Gln  
805 810 815

Pro Val Val Leu Asp Val Ala Ala Gly Gly Ile Asp Ile Ala Ser Arg  
820 825 830

Lys Gly Glu Arg Pro Ala Leu Thr Phe Ile Thr Pro Leu Ala Ala Pro  
835 840 845

Gly Glu Glu Gln Arg Arg Arg Thr Lys Thr Gly Lys Ser Glu Phe Thr  
850 855 860

Thr Phe Val Glu Ile Val Gly Lys Gln Asp Arg Trp Arg Ile Arg Asp  
865 870 875 880

Gly Ala Ala Asp Thr Thr Ile Asp Leu Ala Lys Val Val Ser Gln Leu  
885 890 895

Val Asp Ala Asn Gly Val Leu Lys His Ser Ile Lys Leu Asp Val Ile  
900 905 910

Gly Gly Asp Gly Asp Asp Val Val Leu Ala Asn Ala Ser Arg Ile His  
915 920 925

Tyr Asp Gly Gly Ala Gly Thr Asn Thr Val Ser Tyr Ala Ala Leu Gly  
930 935 940

Arg Gln Asp Ser Ile Thr Val Ser Ala Asp Gly Glu Arg Phe Asn Val  
945 950 955 960

Arg Lys Gln Leu Asn Asn Ala Asn Val Tyr Arg Glu Gly Val Ala Thr  
965 970 975

Gln Thr Thr Ala Tyr Gly Lys Arg Thr Glu Asn Val Gln Tyr Arg His  
980 985 990

Val Glu Leu Ala Arg Val Gly Gln Leu Val Glu Val Asp Thr Leu Glu  
Pge p

995 CYA-B-0002-PCT1-SEQ-1\_ST25  
1000 1005

His	Val	Gln	His	Ile	Ile	Gly	Gly	Ala	Gly	Asn	Asp	Ser	Ile	Thr
	1010					1015					1020			
Gly	Asn	Ala	His	Asp	Asn	Phe	Leu	Ala	Gly	Gly	Ser	Gly	Asp	Asp
	1025					1030					1035			
Arg	Leu	Asp	Gly	Gly	Ala	Gly	Asn	Asp	Thr	Leu	Val	Gly	Gly	Glu
	1040					1045					1050			
Gly	Gln	Asn	Thr	Val	Ile	Gly	Gly	Ala	Gly	Asp	Asp	Val	Phe	Leu
	1055					1060					1065			
Gln	Asp	Leu	Gly	Val	Trp	Ser	Asn	Gln	Leu	Asp	Gly	Gly	Ala	Gly
	1070					1075					1080			
Val	Asp	Thr	Val	Lys	Tyr	Asn	Val	His	Gln	Pro	Ser	Glu	Glu	Arg
	1085					1090					1095			
Leu	Glu	Arg	Met	Gly	Asp	Thr	Gly	Ile	His	Ala	Asp	Leu	Gln	Lys
	1100					1105					1110			
Gly	Thr	Val	Glu	Lys	Trp	Pro	Ala	Leu	Asn	Leu	Phe	Ser	Val	Asp
	1115					1120					1125			
His	Val	Lys	Asn	Ile	Glu	Asn	Leu	His	Gly	Ser	Arg	Leu	Asn	Asp
	1130					1135					1140			
Arg	Ile	Ala	Gly	Asp	Asp	Gln	Asp	Asn	Glu	Leu	Trp	Gly	His	Asp
	1145					1150					1155			
Gly	Asn	Asp	Thr	Ile	Arg	Gly	Arg	Gly	Gly	Asp	Asp	Ile	Leu	Arg
	1160					1165					1170			
Gly	Gly	Leu	Gly	Leu	Asp	Thr	Leu	Tyr	Gly	Glu	Asp	Gly	Asn	Asp
	1175					1180					1185			
Ile	Phe	Leu	Gln	Asp	Asp	Glu	Thr	Val	Ser	Asp	Asp	Ile	Asp	Gly
	1190					1195					1200			
Gly	Ala	Gly	Leu	Asp	Thr	Val	Asp	Tyr	Ser	Ala	Met	Ile	His	Pro
	1205					1210					1215			
Gly	Arg	Ile	Val	Ala	Pro	His	Glu	Tyr	Gly	Phe	Gly	Ile	Glu	Ala
	1220					1225					1230			
Asp	Leu	Ser	Arg	Glu	Trp	Val	Arg	Lys	Ala	Ser	Ala	Leu	Gly	Val
	1235					1240					1245			
Asp	Tyr	Tyr	Asp	Asn	Val	Arg	Asn	Val	Glu	Asn	Val	Ile	Gly	Thr

CYA-B-0002-PCT1-SEQ-1\_ST25

1250						1255					1260
Ser	Met	Lys	Asp	Val	Leu	Ile	Gly	Asp	Ala	Gln	Ala
	1265					1270					1275
Met	Gly	Gln	Gly	Gly	Asp	Asp	Thr	Val	Arg	Gly	Gly
	1280					1285					1290
Asp	Leu	Leu	Phe	Gly	Gly	Asp	Gly	Asn	Asp	Met	Leu
	1295					1300					1305
Ala	Gly	Asn	Asp	Thr	Leu	Tyr	Gly	Gly	Leu	Gly	Asp
	1310					1315					1320
Glu	Gly	Gly	Ala	Gly	Asn	Asp	Trp	Phe	Gly	Gln	Thr
	1325					1330					1335
Glu	His	Asp	Val	Leu	Arg	Gly	Gly	Asp	Gly	Val	Asp
	1340					1345					1350
Tyr	Ser	Gln	Thr	Gly	Ala	His	Ala	Gly	Ile	Ala	Ala
	1355					1360					1365
Gly	Leu	Gly	Ile	Leu	Ala	Asp	Leu	Gly	Ala	Gly	Arg
	1370					1375					1380
Leu	Gly	Glu	Ala	Gly	Ser	Ser	Ala	Tyr	Asp	Thr	Val
	1385					1390					1395
Glu	Asn	Val	Val	Gly	Thr	Glu	Leu	Ala	Asp	Arg	Ile
	1400					1405					1410
Ala	Gln	Ala	Asn	Val	Leu	Arg	Gly	Ala	Gly	Gly	Ala
	1415					1420					1425
Ala	Gly	Gly	Glu	Gly	Asp	Asp	Val	Leu	Leu	Gly	Gly
	1430					1435					1440
Asp	Gln	Leu	Ser	Gly	Asp	Ala	Gly	Arg	Asp	Arg	Leu
	1445					1450					1455
Ala	Gly	Asp	Asp	Trp	Phe	Phe	Gln	Asp	Ala	Ala	Asn
	1460					1465					1470
Leu	Leu	Asp	Gly	Gly	Asp	Gly	Arg	Asp	Thr	Val	Asp
	1475					1480					1485
Pro	Gly	Arg	Gly	Leu	Asp	Ala	Gly	Ala	Lys	Gly	Val
	1490					1495					1500
Leu	Gly	Lys	Gly	Phe	Ala	Ser	Leu	Met	Asp	Glu	Pro
											Glu
											Thr
											Ser

CYA-B-0002-PCT1-SEQ-1\_ST25  
 1505 1510 1515

Asn Val Leu Arg Asn Ile Glu Asn Ala Val Gly Ser Ala Arg Asp  
 1520 1525 1530

Asp Val Leu Ile Gly Asp Ala Gly Ala Asn Val Leu Asn Gly Leu  
 1535 1540 1545

Ala Gly Asn Asp Val Leu Ser Gly Gly Ala Gly Asp Asp Val Leu  
 1550 1555 1560

Leu Gly Asp Glu Gly Ser Asp Leu Leu Ser Gly Asp Ala Gly Asn  
 1565 1570 1575

Asp Asp Leu Phe Gly Gly Gln Gly Asp Asp Thr Tyr Leu Phe Gly  
 1580 1585 1590

Val Gly Tyr Gly His Asp Thr Ile Tyr Glu Ser Gly Gly Gly His  
 1595 1600 1605

Asp Thr Ile Arg Ile Asn Ala Gly Ala Asp Gln Leu Trp Phe Ala  
 1610 1615 1620

Arg Gln Gly Asn Asp Leu Glu Ile Arg Ile Leu Gly Thr Asp Asp  
 1625 1630 1635

Ala Leu Thr Val His Asp Trp Tyr Arg Asp Ala Asp His Arg Val  
 1640 1645 1650

Glu Ile Ile His Ala Ala Asn Gln Ala Val Asp Gln Ala Gly Ile  
 1655 1660 1665

Glu Lys Leu Val Glu Ala Met Ala Gln Tyr Pro Asp Pro Gly Ala  
 1670 1675 1680

Ala Ala Ala Ala Pro Pro Ala Ala Arg Val Pro Asp Thr Leu Met  
 1685 1690 1695

Gln Ser Leu Ala Val Asn Trp Arg  
 1700 1705

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 <213> Bordetella bronchiseptica

<400> 2

Met Gln Gln Ser His Gln Ala Gly Tyr Ala Asn Ala Ala Asp Arg Glu  
 1 5 10 15

Ser Gly Ile Pro Ala Ala Val Leu Asp Gly Ile Lys Ala Val Ala Lys  
 20 25 30

CYA-B-0002-PCT1-SEQ-1\_ST25

Glu Lys Asn Ala Thr Leu Met Phe Arg Leu Val Asn Pro His Ser Thr  
 35 40 45  
 Ser Leu Ile Ala Glu Gly Val Ala Thr Lys Gly Leu Gly Val His Ala  
 50 55 60  
 Lys Ser Ser Asp Trp Gly Leu Gln Ala Gly Tyr Ile Pro Val Asn Pro  
 65 70 75 80  
 Asn Leu Ser Lys Leu Phe Gly Arg Ala Pro Glu Val Ile Ala Arg Ala  
 85 90 95  
 Asn Asn Asp Val Asn Ser Ser Leu Ala His Gly His Thr Ala Val Asp  
 100 105 110  
 Leu Thr Leu Ser Lys Glu Arg Leu Asp Tyr Leu Arg Gln Ala Gly Leu  
 115 120 125  
 Val Thr Gly Met Ala Asp Gly Val Val Ala Ser Asn His Ala Gly Tyr  
 130 135 140  
 Glu Gln Phe Glu Phe Arg Val Lys Glu Thr Ser Asp Gly Arg Tyr Ala  
 145 150 155 160  
 Val Gln Tyr Arg Arg Lys Gly Gly Asp Asp Phe Glu Ala Val Lys Val  
 165 170 175  
 Ile Gly Asn Ala Ala Gly Ile Pro Leu Thr Ala Asp Ile Asp Met Phe  
 180 185 190  
 Ala Ile Met Pro His Leu Ser Asn Phe Arg Asp Ser Ala Arg Ser Ser  
 195 200 205  
 Val Thr Ser Gly Asp Ser Val Thr Asp Tyr Leu Ala Arg Thr Arg Arg  
 210 215 220  
 Ala Ala Ser Glu Ala Thr Gly Gly Leu Asp Pro Glu Arg Ile Asp Leu  
 225 230 235 240  
 Leu Trp Lys Ile Ala Arg Ala Gly Ala Arg Ser Ala Val Gly Thr Glu  
 245 250 255  
 Ala Arg Arg Gln Phe Arg Tyr Asp Gly Asp Met Asn Ile Gly Val Ile  
 260 265 270  
 Thr Asp Phe Glu Leu Glu Val Arg Asn Ala Leu Asn Arg Arg Ala His  
 275 280 285  
 Ala Val Gly Ala Gln Asp Val Val Gln His Gly Thr Glu Gln Asn Asn  
 290 295 300



## CYA-B-0002-PCT1-SEQ-1\_ST25

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

## CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Gly Thr Val Glu Leu Ala Ser Ser Ile Ala Leu Ala Leu Ala Ala  
 580 585 590  
 Ala Arg Gly Val Thr Ser Gly Leu Gln Val Ala Gly Ala Ser Ala Gly  
 595 600 605  
 Ala Ala Ala Gly Ala Leu Ala Ala Ala Leu Ser Pro Met Glu Ile Tyr  
 610 615 620  
 Gly Leu Val Gln Gln Ser His Tyr Ala Asp Gln Leu Asp Lys Leu Ala  
 625 630 635 640  
 Gln Glu Ser Ser Ala Tyr Gly Tyr Glu Gly Asp Ala Leu Leu Ala Gln  
 645 650 655  
 Leu Tyr Arg Asp Lys Thr Ala Ala Glu Gly Ala Val Ala Gly Val Ser  
 660 665 670  
 Ala Val Leu Ser Thr Val Gly Ala Ala Val Ser Ile Ala Ala Ala Ala  
 675 680 685  
 Ser Val Val Gly Ala Pro Val Ala Val Val Thr Ser Leu Leu Thr Gly  
 690 695 700  
 Ala Leu Asn Gly Ile Leu Arg Gly Val Gln Gln Pro Ile Ile Glu Lys  
 705 710 715 720  
 Leu Ala Asn Asp Tyr Ala Arg Lys Ile Asp Glu Leu Gly Gly Pro Gln  
 725 730 735  
 Ala Tyr Phe Glu Lys Asn Leu Gln Ala Arg His Glu Gln Leu Ala Asn  
 740 745 750  
 Ser Asp Gly Leu Arg Lys Met Leu Ala Asp Leu Gln Ala Gly Trp Asn  
 755 760 765  
 Ala Ser Ser Val Ile Gly Val Gln Thr Thr Glu Ile Ser Lys Ser Ala  
 770 775 780  
 Leu Glu Leu Ala Ala Ile Thr Gly Asn Ala Asp Asn Leu Lys Ser Ala  
 785 790 795 800  
 Asp Val Phe Val Asp Arg Phe Ile Gln Gly Glu Arg Val Ala Gly Gln  
 805 810 815  
 Pro Val Val Leu Asp Val Ala Ala Gly Gly Ile Asp Ile Ala Ser Arg  
 820 825 830  
 Lys Gly Glu Arg Pro Ala Leu Thr Phe Ile Thr Pro Leu Ala Ala Pro  
 835 840 845

CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Glu Glu Gln Arg Arg Arg Thr Lys Thr Gly Lys Ser Glu Phe Thr  
 850 855 860  
 Thr Phe Val Glu Ile Val Gly Lys Gln Asp Arg Trp Arg Ile Arg Asp  
 865 870 875 880  
 Gly Ala Ala Asp Thr Thr Ile Asp Leu Ala Lys Val Val Ser Gln Leu  
 885 890 895  
 Val Asp Ala Asn Gly Val Leu Lys His Ser Ile Lys Leu Glu Val Ile  
 900 905 910  
 Gly Gly Asp Gly Asp Asp Val Val Leu Ala Asn Ala Ser Arg Ile His  
 915 920 925  
 Tyr Asp Gly Gly Ala Gly Thr Asn Thr Val Ser Tyr Ala Ala Leu Gly  
 930 935 940  
 Arg Gln Asp Ser Ile Thr Val Ser Ala Asp Gly Glu Arg Phe Asn Val  
 945 950 955 960  
 Arg Lys Gln Leu Asn Asn Ala Asn Val Tyr Arg Glu Gly Val Ala Thr  
 965 970 975  
 Gln Lys Thr Ala Tyr Gly Lys Arg Thr Glu Asn Val Gln Tyr Arg His  
 980 985 990  
 Val Glu Leu Ala Arg Val Gly Gln Leu Val Glu Val Asp Thr Leu Glu  
 995 1000 1005  
 His Val Gln His Ile Ile Gly Gly Ala Gly Asn Asp Ser Ile Thr  
 1010 1015 1020  
 Gly Asn Ala His Asp Asn Phe Leu Ala Gly Gly Ala Gly Asp Asp  
 1025 1030 1035  
 Arg Leu Asp Gly Gly Ala Gly Asn Asp Thr Leu Val Gly Gly Glu  
 1040 1045 1050  
 Gly His Asn Thr Val Val Gly Gly Ala Gly Asp Asp Val Phe Leu  
 1055 1060 1065  
 Gln Asp Leu Gly Val Trp Ser Asn Gln Leu Asp Gly Gly Ala Gly  
 1070 1075 1080  
 Val Asp Thr Val Lys Tyr Asn Val His Gln Pro Ser Glu Glu Arg  
 1085 1090 1095  
 Leu Glu Arg Met Gly Glu Thr Gly Ile His Ala Asp Leu Gln Lys  
 1100 1105 1110

## CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Thr Val Glu Lys Trp Pro Ala Leu Asn Leu Phe Ser Val Asp  
 1115 1120 1125  
 His Val Lys Asn Ile Glu Asn Leu His Gly Ser Ser Leu Asn Asp  
 1130 1135 1140  
 Ser Ile Ala Gly Asp Asp Arg Asp Asn Glu Leu Trp Gly Asp Asp  
 1145 1150 1155  
 Gly Asn Asp Thr Ile His Gly Arg Gly Gly Asp Asp Ile Leu Arg  
 1160 1165 1170  
 Gly Gly Leu Gly Leu Asp Thr Leu Tyr Gly Glu Asp Gly Asn Asp  
 1175 1180 1185  
 Ile Phe Leu Gln Asp Asp Glu Thr Val Ser Asp Asp Ile Asp Gly  
 1190 1195 1200  
 Gly Ala Gly Leu Asp Thr Val Asp Tyr Ser Ala Met Ile His Ala  
 1205 1210 1215  
 Gly Lys Ile Val Ala Pro His Glu Tyr Gly Phe Gly Ile Glu Ala  
 1220 1225 1230  
 Asp Leu Ser Arg Glu Trp Val Arg Lys Ala Ser Ala Leu Gly Val  
 1235 1240 1245  
 Asp Tyr Tyr Asp Ser Val Arg Asn Val Glu Asn Val Ile Gly Thr  
 1250 1255 1260  
 Ser Met Lys Asp Val Leu Ile Gly Asp Ala Gln Ala Asn Thr Leu  
 1265 1270 1275  
 Met Gly Gln Gly Gly Asp Asp Thr Val Arg Gly Gly Asp Gly Asp  
 1280 1285 1290  
 Asp Leu Leu Phe Gly Gly Asp Gly Asn Asp Met Leu Tyr Gly Asp  
 1295 1300 1305  
 Ala Gly Asn Asp Thr Leu Tyr Gly Gly Leu Gly Asp Asp Thr Leu  
 1310 1315 1320  
 Glu Gly Gly Ala Gly Asn Asp Trp Phe Gly Gln Thr Pro Ala Arg  
 1325 1330 1335  
 Glu His Asp Val Leu Arg Gly Gly Ala Gly Val Asp Thr Val Asp  
 1340 1345 1350  
 Tyr Ser Gln Ala Gly Ala His Ala Gly Val Ala Thr Gly Arg Ile  
 1355 1360 1365

## CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Leu Gly Ile Leu Ala Asp Leu Gly Ala Gly Arg Val Asp Lys  
 1370 1375 1380  
 Leu Gly Glu Ala Gly Ser Ser Ala Tyr Asp Thr Val Ser Gly Ile  
 1385 1390 1395  
 Glu Asn Val Val Gly Thr Glu Leu Ala Asp Arg Ile Thr Gly Asp  
 1400 1405 1410  
 Ala Gln Ala Asn Val Leu Arg Gly Ala Gly Gly Ala Asp Val Leu  
 1415 1420 1425  
 Ala Gly Gly Glu Gly Asp Asp Val Leu Leu Gly Gly Glu Gly Asp  
 1430 1435 1440  
 Asp Gln Leu Ser Gly Asp Ala Gly Arg Asp Arg Leu Tyr Gly Glu  
 1445 1450 1455  
 Ala Gly Asp Asp Trp Phe Phe Gln Asp Ala Ala Asn Ala Gly Asn  
 1460 1465 1470  
 Leu Leu Asp Gly Gly Asp Gly Asn Asp Thr Val Asp Phe Ser Gly  
 1475 1480 1485  
 Pro Gly Arg Gly Leu Asp Ala Gly Ala Lys Gly Val Phe Leu Ser  
 1490 1495 1500  
 Leu Gly Lys Gly Phe Ala Ser Leu Met Asp Glu Pro Glu Thr Ser  
 1505 1510 1515  
 Asn Val Leu Arg His Ile Glu Asn Ala Val Gly Ser Val Arg Asp  
 1520 1525 1530  
 Asp Val Leu Ile Gly Asp Ala Gly Ala Asn Val Leu Asn Gly Leu  
 1535 1540 1545  
 Ala Gly Asn Asp Val Leu Ser Gly Gly Ala Gly Asp Asp Val Leu  
 1550 1555 1560  
 Leu Gly Asp Glu Gly Ser Asp Leu Leu Ser Gly Asp Ala Gly Asn  
 1565 1570 1575  
 Asp Asp Leu Phe Gly Gly Gln Gly Asp Asp Thr Tyr Leu Phe Gly  
 1580 1585 1590  
 Ala Gly Tyr Gly His Asp Thr Ile Tyr Glu Ser Gly Gly Gly His  
 1595 1600 1605  
 Asp Thr Ile Arg Ile Asn Ala Gly Ala Asp Gln Leu Trp Phe Ala  
 1610 1615 1620

CYA-B-0002-PCT1-SEQ-1\_ST25

Arg Gln Gly Asn Asp Leu Glu Ile Arg Ile Leu Gly Thr Asp Asp  
1625 1630 1635

Ala Leu Thr Val His Asp Trp Tyr Arg Asp Ala Asp His Arg Val  
1640 1645 1650

Glu Ala Ile His Ala Ala Asn Gln Ala Ile Asp Pro Ala Gly Ile  
1655 1660 1665

Glu Lys Leu Val Glu Ala Met Ala Gln Tyr Pro Asp Pro Gly Ala  
1670 1675 1680

Ala Ala Ala Ala Pro Pro Ala Ala Arg Val Pro Asp Thr Leu Met  
1685 1690 1695

Gln Ser Leu Ala Val Asn Trp Arg  
1700 1705

<210> 3  
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<213> Bordetella parapertussis

<400> 3

Met Gln Gln Ser His Gln Ala Gly Tyr Ala Asn Ala Ala Asp Arg Glu  
1 5 10 15

Ser Gly Ile Pro Ala Ala Val Leu Asp Gly Ile Lys Ala Val Ala Lys  
20 25 30

Glu Lys Asn Ala Thr Leu Met Phe Arg Leu Val Asn Pro His Ser Thr  
35 40 45

Ser Leu Ile Ala Glu Gly Val Ala Thr Lys Gly Leu Gly Val His Ala  
50 55 60

Lys Ser Ser Asp Trp Gly Leu Gln Ala Gly Tyr Ile Pro Val Asn Pro  
65 70 75 80

Asn Leu Ser Lys Leu Phe Gly Arg Ala Pro Glu Val Ile Ala Arg Ala  
85 90 95

Asp Asn Asp Val Asn Ser Ser Leu Ala His Gly His Thr Ala Val Asp  
100 105 110

Leu Thr Leu Ser Lys Glu Arg Leu Asp Tyr Leu Arg Gln Ala Gly Leu  
115 120 125

Val Thr Gly Met Ala Asp Gly Val Val Ala Ser Asn His Ala Gly Tyr  
130 135 140

## CYA-B-0002-PCT1-SEQ-1\_ST25

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

## CYA-B-0002-PCT1-SEQ-1\_ST25

Leu Gly Glu Val Ser Asp Met Ala Ala Val Glu Ala Ala Glu Leu Glu  
 420 425 430  
 Met Thr Arg Gln Val Leu His Ala Gly Ala Arg Gln Asp Asp Ala Glu  
 435 440 445  
 Pro Gly Val Ser Gly Ala Ser Ala His Trp Gly Gln Arg Ala Leu Gln  
 450 455 460  
 Gly Ala Gln Ala Val Ala Ala Ala Gln Arg Leu Val His Ala Ile Ala  
 465 470 475 480  
 Leu Met Thr Gln Phe Gly Arg Ala Gly Ser Thr Asn Thr Pro Gln Glu  
 485 490 495  
 Ala Ala Ser Leu Ser Ala Ala Val Phe Gly Leu Gly Glu Ala Ser Ser  
 500 505 510  
 Ala Val Ala Glu Thr Val Ser Gly Phe Phe Arg Gly Ser Ser Arg Trp  
 515 520 525  
 Ala Gly Gly Phe Gly Val Ala Gly Gly Ala Met Ala Leu Gly Gly Gly  
 530 535 540  
 Ile Ala Ala Ala Val Gly Ala Gly Met Ser Leu Thr Asp Asp Ala Pro  
 545 550 555 560  
 Ala Gly Gln Lys Ala Ala Val Gly Ala Glu Ile Ala Leu Gln Leu Thr  
 565 570 575  
 Gly Gly Thr Val Glu Leu Ala Ser Ser Ile Ala Leu Ala Leu Ala Ala  
 580 585 590  
 Ala Arg Gly Val Thr Ser Gly Leu Gln Val Ala Gly Ala Ser Ala Gly  
 595 600 605  
 Ala Ala Ala Gly Ala Leu Ala Ala Ala Leu Ser Pro Met Glu Ile Tyr  
 610 615 620  
 Gly Leu Val Gln Gln Ser His Tyr Ala Asp Gln Leu Asp Lys Leu Ala  
 625 630 635 640  
 Gln Glu Ser Ser Ala Tyr Gly Tyr Glu Gly Asp Ala Leu Leu Ala Gln  
 645 650 655  
 Leu Tyr Arg Asp Lys Thr Ala Ala Glu Gly Ala Val Ala Gly Val Ser  
 660 665 670  
 Ala Val Leu Ser Thr Val Gly Ala Ala Val Ser Ile Ala Ala Ala Ala  
 675 680 685



## CYA-B-0002-PCT1-SEQ-1\_ST25

Ser Val Val Gly Ala Pro Val Ala Val Val Thr Ser Leu Leu Thr Gly  
 690 695 700  
 Ala Leu Asn Gly Ile Leu Arg Gly Val Gln Gln Pro Ile Ile Glu Lys  
 705 710 715 720  
 Leu Ala Asn Asp Tyr Ala Arg Lys Ile Asp Glu Leu Gly Gly Pro Gln  
 725 730 735  
 Ala Tyr Phe Glu Lys Asn Leu Gln Ala Arg His Glu Gln Leu Ala Asn  
 740 745 750  
 Ser Asp Gly Leu Arg Lys Met Leu Ala Asp Leu Gln Ala Gly Trp Asn  
 755 760 765  
 Ala Ser Ser Val Ile Gly Val Gln Thr Thr Glu Ile Ser Lys Ser Ala  
 770 775 780  
 Leu Glu Leu Ala Ala Ile Thr Gly Asn Ala Asp Asn Leu Lys Ser Ala  
 785 790 795 800  
 Asp Val Phe Val Asp Arg Phe Ile Gln Gly Glu Arg Val Ala Gly Gln  
 805 810 815  
 Pro Val Val Leu Asp Val Ala Ala Gly Gly Ile Asp Ile Ala Ser Arg  
 820 825 830  
 Lys Gly Glu Arg Pro Ala Leu Thr Phe Ile Thr Pro Leu Ala Ala Pro  
 835 840 845  
 Gly Glu Glu Gln Arg Arg Arg Thr Lys Thr Gly Lys Ser Glu Phe Thr  
 850 855 860  
 Thr Phe Val Glu Ile Val Gly Lys Gln Asp Arg Trp Arg Ile Arg Asp  
 865 870 875 880  
 Gly Ala Ala Asp Thr Thr Ile Asp Leu Ala Lys Val Val Ser Gln Leu  
 885 890 895  
 Val Asp Ala Asn Gly Val Leu Lys His Ser Ile Lys Leu Glu Val Ile  
 900 905 910  
 Gly Gly Asp Gly Asp Asp Val Val Leu Ala Asn Ala Ser Arg Ile His  
 915 920 925  
 Tyr Asp Gly Gly Ala Gly Thr Asn Thr Val Ser Tyr Ala Ala Leu Gly  
 930 935 940  
 Arg Gln Asp Ser Ile Thr Val Ser Ala Asp Gly Glu Arg Phe Asn Val  
 945 950 955 960

## CYA-B-0002-PCT1-SEQ-1\_ST25

Arg Lys Gln Leu Asn Asn Ala Asn Val Tyr Arg Glu Gly Val Ala Thr  
 965 970 975  
 Gln Lys Thr Ala Tyr Gly Lys Arg Thr Glu Asn Val Gln Tyr Arg His  
 980 985 990  
 Val Glu Leu Ala Arg Val Gly Gln Leu Val Glu Val Asp Thr Leu Glu  
 995 1000 1005  
 His Val Gln His Ile Ile Gly Gly Ala Gly Asn Asp Ser Ile Thr  
 1010 1015 1020  
 Gly Asn Ala His Asp Asn Phe Leu Ala Gly Gly Ala Gly Asp Asp  
 1025 1030 1035  
 Arg Leu Asp Gly Gly Ala Gly Asn Asp Thr Leu Val Gly Gly Glu  
 1040 1045 1050  
 Gly His Asn Thr Val Val Gly Gly Ala Gly Asp Asp Val Phe Leu  
 1055 1060 1065  
 Gln Asp Leu Gly Val Trp Ser Asn Gln Leu Asp Gly Gly Ala Gly  
 1070 1075 1080  
 Val Asp Thr Val Lys Tyr Asn Val His Gln Pro Ser Glu Glu Arg  
 1085 1090 1095  
 Leu Glu Arg Met Gly Asp Thr Gly Ile His Ala Asp Leu Gln Lys  
 1100 1105 1110  
 Gly Thr Val Glu Lys Trp Pro Ala Leu Asn Leu Phe Ser Val Asp  
 1115 1120 1125  
 His Val Lys Asn Ile Glu Asn Leu His Gly Ser Ser Leu Asn Asp  
 1130 1135 1140  
 Ser Ile Ala Gly Asp Asp Arg Asp Asn Glu Leu Trp Gly Asp Asp  
 1145 1150 1155  
 Gly Asn Asp Thr Ile His Gly Arg Gly Gly Asp Asp Ile Leu Arg  
 1160 1165 1170  
 Gly Gly Leu Gly Leu Asp Thr Leu Tyr Gly Glu Asp Gly Asn Asp  
 1175 1180 1185  
 Ile Phe Leu Gln Asp Asp Glu Thr Val Ser Asp Asp Ile Asp Gly  
 1190 1195 1200  
 Gly Ala Gly Leu Asp Thr Val Asp Tyr Ser Ala Met Ile His Ala  
 1205 1210 1215

## CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Lys Ile Val Ala Pro His Glu Tyr Gly Phe Gly Ile Glu Ala  
 1220 1225 1230  
 Asp Leu Ser Glu Gly Trp Val Arg Lys Ala Ala Arg Arg Gly Met  
 1235 1240 1245  
 Gly Tyr Tyr Asp Ser Val Arg Ser Val Glu Asn Val Ile Gly Thr  
 1250 1255 1260  
 Ser Met Lys Asp Val Leu Ile Glu Asp Ala Gln Ala Asn Thr Leu  
 1265 1270 1275  
 Met Gly Gln Gly Gly Asp Asp Thr Val Arg Gly Gly Asp Gly Asp  
 1280 1285 1290  
 Asp Leu Leu Phe Gly Gly Asp Gly Asn Asp Met Leu Tyr Gly Asp  
 1295 1300 1305  
 Ala Gly Asn Asp Thr Leu Tyr Gly Gly Leu Gly Asp Asp Thr Leu  
 1310 1315 1320  
 Glu Gly Gly Ala Gly Asn Asp Trp Phe Gly Gln Thr Pro Ala Arg  
 1325 1330 1335  
 Glu His Asp Val Leu Arg Gly Gly Ala Gly Val Asp Thr Val Asp  
 1340 1345 1350  
 Tyr Ser Gln Ala Gly Ala His Ala Gly Val Ala Thr Gly Arg Ile  
 1355 1360 1365  
 Gly Leu Gly Ile Leu Ala Asp Leu Gly Ala Gly Arg Val Asp Lys  
 1370 1375 1380  
 Leu Gly Glu Ala Gly Ser Ser Ala Tyr Asp Thr Val Ser Gly Ile  
 1385 1390 1395  
 Glu Asn Val Val Gly Thr Glu Leu Ala Asp Arg Ile Thr Gly Asp  
 1400 1405 1410  
 Ala Gln Ala Asn Val Leu Arg Gly Ala Gly Gly Ala Asp Val Leu  
 1415 1420 1425  
 Ala Gly Gly Glu Gly Asp Asp Val Leu Leu Gly Gly Glu Gly Asp  
 1430 1435 1440  
 Asp Gln Leu Ser Gly Asp Ala Gly Arg Asp Arg Leu Tyr Gly Glu  
 1445 1450 1455  
 Ala Gly Asp Asp Trp Phe Phe Gln Asp Ala Ala Asn Ala Gly Asn  
 1460 1465 1470

## CYA-B-0002-PCT1-SEQ-1\_ST25

Leu Leu Asp Gly Gly Asp Gly Asn Asp Thr Val Asp Phe Ser Gly  
 1475 1480 1485  
 Pro Gly Arg Gly Leu Asp Ala Gly Ala Lys Gly Val Phe Leu Ser  
 1490 1495 1500  
 Leu Gly Lys Gly Phe Ala Ser Leu Met Asp Glu Pro Glu Thr Ser  
 1505 1510 1515  
 Asn Val Leu Arg His Ile Glu Asn Ala Val Gly Ser Val Arg Asp  
 1520 1525 1530  
 Asp Val Leu Ile Gly Asp Ala Gly Ala Asn Val Leu Asn Gly Leu  
 1535 1540 1545  
 Ala Gly Asn Asp Val Leu Ser Gly Gly Ala Gly Asp Asp Val Leu  
 1550 1555 1560  
 Leu Gly Asp Glu Gly Ser Asp Leu Leu Ser Gly Asp Ala Gly Asn  
 1565 1570 1575  
 Asp Asp Leu Phe Gly Gly Gln Gly Asp Asp Thr Tyr Leu Phe Gly  
 1580 1585 1590  
 Ala Gly Tyr Gly His Asp Thr Ile Tyr Glu Ser Gly Gly Gly His  
 1595 1600 1605  
 Asp Thr Ile Arg Ile Asn Ala Gly Ala Asp Gln Leu Trp Phe Ala  
 1610 1615 1620  
 Arg Gln Gly Asn Asp Leu Glu Ile Arg Ile Leu Gly Thr Asp Asp  
 1625 1630 1635  
 Ala Leu Thr Val His Asp Trp Tyr Arg Asp Ala Asp His Arg Val  
 1640 1645 1650  
 Glu Ala Ile His Ala Ala Asn Gln Ala Ile Asp Pro Ala Gly Ile  
 1655 1660 1665  
 Glu Lys Leu Val Glu Ala Met Ala Gln Tyr Pro Asp Pro Gly Ala  
 1670 1675 1680  
 Ala Ala Ala Ala Pro Pro Ala Ala Arg Val Pro Asp Thr Leu Met  
 1685 1690 1695  
 Gln Ser Leu Ala Val Asn Trp Arg  
 1700 1705

<210> 4  
 <211> 373  
 <212> PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; AC domain

&lt;400&gt; 4

Met Gln Gln Ser His Gln Ala Gly Tyr Ala Asn Ala Ala Asp Arg Glu  
1 5 10 15

Ser Gly Ile Pro Ala Ala Val Leu Asp Gly Ile Lys Ala Val Ala Lys  
20 25 30

Glu Lys Asn Ala Thr Leu Met Phe Arg Leu Val Asn Pro His Ser Thr  
35 40 45

Ser Leu Ile Ala Glu Gly Val Ala Thr Lys Gly Leu Gly Val His Ala  
50 55 60

Lys Ser Ser Asp Trp Gly Leu Gln Ala Gly Tyr Ile Pro Val Asn Pro  
65 70 75 80

Asn Leu Ser Lys Leu Phe Gly Arg Ala Pro Glu Val Ile Ala Arg Ala  
85 90 95

Asp Asn Asp Val Asn Ser Ser Leu Ala His Gly His Thr Ala Val Asp  
100 105 110

Leu Thr Leu Ser Lys Glu Arg Leu Asp Tyr Leu Arg Gln Ala Gly Leu  
115 120 125

Val Thr Gly Met Ala Asp Gly Val Val Ala Ser Asn His Ala Gly Tyr  
130 135 140

Glu Gln Phe Glu Phe Arg Val Lys Glu Thr Ser Asp Gly Arg Tyr Ala  
145 150 155 160

Val Gln Tyr Arg Arg Lys Gly Gly Asp Asp Phe Glu Ala Val Lys Val  
165 170 175

Ile Gly Asn Ala Ala Gly Ile Pro Leu Thr Ala Asp Ile Asp Met Phe  
180 185 190

Ala Ile Met Pro His Leu Ser Asn Phe Arg Asp Ser Ala Arg Ser Ser  
195 200 205

Val Thr Ser Gly Asp Ser Val Thr Asp Tyr Leu Ala Arg Thr Arg Arg  
210 215 220

Ala Ala Ser Glu Ala Thr Gly Gly Leu Asp Arg Glu Arg Ile Asp Leu  
225 230 235 240

Leu Trp Lys Ile Ala Arg Ala Gly Ala Arg Ser Ala Val Gly Thr Glu

## CYA-B-0002-PCT1-SEQ-1\_ST25

245

250

255

Ala Arg Arg Gln Phe Arg Tyr Asp Gly Asp Met Asn Ile Gly Val Ile  
260 265 270

Thr Asp Phe Glu Leu Glu Val Arg Asn Ala Leu Asn Arg Arg Ala His  
275 280 285

Ala Val Gly Ala Gln Asp Val Val Gln His Gly Thr Glu Gln Asn Asn  
290 295 300

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

Glu Ser Gln Met Leu Thr Arg Gly Gln Leu Lys Glu Tyr Ile Gly Gln  
325 330 335

Gln Arg Gly Glu Gly Tyr Val Phe Tyr Glu Asn Arg Ala Tyr Gly Val  
340 345 350

Ala Gly Lys Ser Leu Phe Asp Asp Gly Leu Gly Ala Ala Pro Gly Val  
355 360 365

Pro Gly Gly Arg Ser  
370

<210> 5

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Hly linking segment

<400> 5

Lys Ser Ser Pro Asp Val Leu Glu Thr Val Pro Ala Ser Pro Gly Leu  
1 5 10 15

Arg Arg Pro Ser Leu Gly Ala Val Glu Arg Gln Asp Ser Gly Tyr Asp  
20 25 30

Ser Leu Asp Gly Val Gly Ser Arg Ser Phe Ser Leu Gly Glu Val Ser  
35 40 45

Asp Met Ala Ala Val Glu Ala Ala Glu Leu Glu Met Thr Arg Gln Val  
50 55 60

Leu His Ala Gly Ala Arg Gln Asp Asp Ala Glu Pro Gly Val Ser Gly  
65 70 75 80

Ala Ser Ala His Trp Gly Gln Arg Ala Leu Gln Gly Ala Gln Ala Val  
85 90 95

CYA-B-0002-PCT1-SEQ-1\_ST25

Ala Ala Ala Gln Arg Leu Val His Ala Ile Ala Leu Met Thr Gln Phe  
100 105 110

Gly Arg Ala Gly Ser Thr Asn Thr Pro Gln Glu Ala Ala Ser Leu  
115 120 125

<210> 6  
<211> 205  
<212> PRT  
<213> Bordetella bronchiseptica  
<400> 6

Met Thr Ile Asp Leu Gly Val Ser Leu Thr Ser Gln Ala Gly Gly Leu  
1 5 10 15

Gln Gly Ile Asp Leu Lys Ser Met Asp Ile Gln Thr Leu Met Val Tyr  
20 25 30

Val Gln Gly Arg Arg Ala Glu Leu Leu Thr Ala Gln Met Gln Thr Gln  
35 40 45

Ala Glu Val Val Gln Lys Ala Asn Glu Arg Met Ala Gln Leu Asn Glu  
50 55 60

Val Leu Ser Ala Leu Ser Arg Ala Lys Ala Glu Phe Pro Pro Asn Pro  
65 70 75 80

Lys Pro Gly Asp Thr Ile Pro Gly Trp Asp Asn Gln Lys Val Ser Arg  
85 90 95

Ile Glu Val Pro Leu Asn Asp Ala Leu Arg Ala Ala Gly Leu Thr Gly  
100 105 110

Met Phe Glu Ala Arg Asp Gly Gln Val Thr Ala Pro Gly Gly Arg Gly  
115 120 125

Thr Gln Val Val Asn Gly Thr Gly Val Met Ala Gly Ser Thr Thr Tyr  
130 135 140

Lys Glu Leu Glu Ser Ala Tyr Thr Thr Val Lys Gly Met Leu Asp Thr  
145 150 155 160

Ala Ser Asn Thr Gln Gln Met Asp Met Ile Arg Leu Gln Ala Ala Ser  
165 170 175

Asn Lys Arg Asn Glu Ala Phe Glu Val Met Thr Asn Thr Glu Lys Arg  
180 185 190

Arg Ser Asp Leu Asn Ser Ser Ile Thr Asn Asn Met Arg  
195 200 205

## CYA-B-0002-PCT1-SEQ-1\_ST25

&lt;210&gt; 7

&lt;211&gt; 312

&lt;212&gt; PRT

<213> *Leishmania infantum*

&lt;400&gt; 7

Met Asn Tyr Glu Gly His Leu Lys Gly His Arg Gly Trp Val Thr Ser  
 1 5 10 15

Leu Ala Cys Pro Gln Gln Ala Gly Ser Tyr Ile Lys Val Val Ser Thr  
 20 25 30

Ser Arg Asp Gly Thr Ala Ile Ser Trp Lys Ala Asn Pro Asp Arg His  
 35 40 45

Ser Val Asp Ser Asp Tyr Gly Leu Pro Ser His Arg Leu Glu Gly His  
 50 55 60

Thr Gly Phe Val Ser Cys Val Ser Leu Ala His Ala Thr Asp Tyr Ala  
 65 70 75 80

Leu Thr Ala Ser Trp Asp Arg Ser Ile Arg Met Trp Asp Leu Arg Asn  
 85 90 95

Gly Gln Cys Gln Arg Lys Phe Leu Lys His Thr Lys Asp Val Leu Ala  
 100 105 110

Val Ala Phe Ser Pro Asp Asp Arg Leu Ile Val Ser Ala Gly Arg Asp  
 115 120 125

Asn Val Ile Arg Val Trp Asn Val Ala Gly Glu Cys Met His Glu Phe  
 130 135 140

Leu Arg Asp Gly His Glu Asp Trp Val Ser Ser Ile Cys Phe Ser Pro  
 145 150 155 160

Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp Asn Thr Ile  
 165 170 175

Lys Val Trp Asn Val Asn Gly Gly Lys Cys Glu Arg Thr Leu Lys Gly  
 180 185 190

His Ser Asn Tyr Val Ser Thr Val Thr Val Ser Pro Asp Gly Ser Leu  
 195 200 205

Cys Ala Ser Gly Gly Lys Asp Gly Ala Ala Leu Leu Trp Asp Leu Ser  
 210 215 220

Thr Gly Glu Gln Leu Phe Lys Ile Asn Val Glu Ser Pro Ile Asn Gln  
 225 230 235 240

Ile Ala Phe Ser Pro Asn Arg Phe Trp Met Cys Val Ala Thr Glu Arg  
 Pge p



## CYA-B-0002-PCT1-SEQ-1\_ST25

245

250

255

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

Thr Pro Asp Gly Ala Lys Pro Ser Glu Cys Ile Ser Ile Ala Trp Ser  
275 280 285

Ala Asp Gly Asn Thr Leu Tyr Ser Gly His Lys Asp Asn Leu Ile Arg  
290 295 300

Val Trp Ser Ile Ser Asp Ala Glu  
305 310

&lt;210&gt; 8

&lt;211&gt; 1335

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polypeptide

&lt;400&gt; 8

Arg Ser Lys Phe Ser Pro Asp Val Leu Glu Thr Val Pro Ala Ser Pro  
1 5 10 15

Gly Leu Arg Arg Pro Ser Leu Gly Ala Val Glu Arg Gln Asp Ser Gly  
20 25 30

Tyr Asp Ser Leu Asp Gly Val Gly Ser Arg Ser Phe Ser Leu Gly Glu  
35 40 45

Val Ser Asp Met Ala Ala Val Glu Ala Ala Glu Leu Glu Met Thr Arg  
50 55 60

Gln Val Leu His Ala Gly Ala Arg Gln Asn Asn Ala Gln Pro Gly Val  
65 70 75 80

Ser Gly Ala Ser Ala His Trp Gly Gln Arg Ala Leu Gln Gly Ala Gln  
85 90 95

Ala Val Ala Ala Ala Gln Arg Leu Val His Ala Ile Ala Leu Met Thr  
100 105 110

Gln Phe Gly Arg Ala Gly Ser Thr Asn Thr Pro Gln Glu Ala Ala Ser  
115 120 125

Leu Ser Ala Ala Val Phe Gly Leu Gly Glu Ala Ser Ser Ala Val Ala  
130 135 140

Glu Thr Val Ser Gly Phe Phe Arg Gly Ser Ser Arg Trp Ala Gly Gly  
145 150 155 160

## CYA-B-0002-PCT1-SEQ-1\_ST25

Phe Gly Val Ala Gly<sub>165</sub> Gly Ala Met Ala Leu<sub>170</sub> Gly Gly Gly Ile Ala<sub>175</sub> Ala  
 Ala Val Gly Ala<sub>180</sub> Gly Met Ser Leu Thr<sub>185</sub> Asp Asp Ala Pro Ala<sub>190</sub> Gly Gln  
 Lys Ala Ala<sub>195</sub> Ala Gly Ala Glu Ile<sub>200</sub> Ala Leu Gln Leu Thr<sub>205</sub> Gly Gly Thr  
 Val Glu<sub>210</sub> Leu Ala Ser Ser Ile<sub>215</sub> Ala Leu Ala Leu Ala<sub>220</sub> Ala Ala Arg Gly  
 Val<sub>225</sub> Thr Ser Gly Leu Gln<sub>230</sub> Val Ala Gly Ala Ser<sub>235</sub> Ala Gly Ala Ala Ala  
 Gly Ala Leu Ala Ala<sub>245</sub> Ala Leu Ser Pro Met<sub>250</sub> Glu Ile Tyr Gly Leu<sub>255</sub> Val  
 Gln Gln Ser His<sub>260</sub> Tyr Ala Asp Gln Leu<sub>265</sub> Asp Lys Leu Ala Gln<sub>270</sub> Glu Ser  
 Ser Ala Tyr<sub>275</sub> Gly Tyr Glu Gly Asp<sub>280</sub> Ala Leu Leu Ala Gln<sub>285</sub> Leu Tyr Arg  
 Asp Lys<sub>290</sub> Thr Ala Ala Glu Gly<sub>295</sub> Ala Val Ala Gly Val<sub>300</sub> Ser Ala Val Leu  
 Ser<sub>305</sub> Thr Val Gly Ala Ala<sub>310</sub> Val Ser Ile Ala Ala<sub>315</sub> Ala Ala Ser Val Val<sub>320</sub>  
 Gly Ala Pro Val Ala<sub>325</sub> Val Val Thr Ser Leu<sub>330</sub> Leu Thr Gly Ala Leu<sub>335</sub> Asn  
 Gly Ile Leu Arg<sub>340</sub> Gly Val Gln Gln Pro<sub>345</sub> Ile Ile Glu Lys Leu<sub>350</sub> Ala Asn  
 Asp Tyr Ala<sub>355</sub> Arg Lys Ile Asp Glu<sub>360</sub> Leu Gly Gly Pro Gln<sub>365</sub> Ala Tyr Phe  
 Glu Lys<sub>370</sub> Asn Leu Gln Ala Arg<sub>375</sub> His Glu Gln Leu Ala<sub>380</sub> Asn Ser Asp Gly  
 Leu Arg Lys Met Leu Ala<sub>390</sub> Asp Leu Gln Ala Gly<sub>395</sub> Trp Asn Ala Ser Ser<sub>400</sub>  
 Val Ile Gly Val Gln<sub>405</sub> Thr Thr Glu Ile Ser<sub>410</sub> Lys Ser Ala Leu Glu<sub>415</sub> Leu  
 Ala Ala Ile Thr<sub>420</sub> Gly Asn Ala Asp Asn<sub>425</sub> Leu Lys Ser Val Asp<sub>430</sub> Val Phe

## CYA-B-0002-PCT1-SEQ-1\_ST25

Val Asp Arg Phe Val Gln Gly Glu Arg Val Ala Gly Gln Pro Val Val  
 435 440 445  
 Leu Asp Val Ala Ala Gly Gly Ile Asp Ile Ala Ser Arg Lys Gly Glu  
 450 455 460  
 Arg Pro Ala Leu Thr Phe Ile Thr Pro Leu Ala Ala Pro Gly Glu Glu  
 465 470 475 480  
 Gln Arg Arg Arg Thr Lys Thr Gly Lys Ser Glu Phe Thr Thr Phe Val  
 485 490 495  
 Glu Ile Val Gly Lys Gln Asp Arg Trp Arg Ile Arg Asp Gly Ala Ala  
 500 505 510  
 Asp Thr Thr Ile Asp Leu Ala Lys Val Val Ser Gln Leu Val Asp Ala  
 515 520 525  
 Asn Gly Val Leu Lys His Ser Ile Lys Leu Asp Val Ile Gly Gly Asp  
 530 535 540  
 Gly Asp Asp Val Val Leu Ala Asn Ala Ser Arg Ile His Tyr Asp Gly  
 545 550 555 560  
 Gly Ala Gly Thr Asn Thr Val Ser Tyr Ala Ala Leu Gly Arg Gln Asp  
 565 570 575  
 Ser Ile Thr Val Ser Ala Asp Gly Glu Arg Phe Asn Val Arg Lys Gln  
 580 585 590  
 Leu Asn Asn Ala Asn Val Tyr Arg Glu Gly Val Ala Thr Gln Thr Thr  
 595 600 605  
 Ala Tyr Gly Lys Arg Thr Glu Asn Val Gln Tyr Arg His Val Glu Leu  
 610 615 620  
 Ala Arg Val Gly Gln Leu Val Glu Val Asp Thr Leu Glu His Val Gln  
 625 630 635 640  
 His Ile Ile Gly Gly Ala Gly Asn Asp Ser Ile Thr Gly Asn Ala His  
 645 650 655  
 Asp Asn Phe Leu Ala Gly Gly Ser Gly Asp Asp Arg Leu Asp Gly Gly  
 660 665 670  
 Ala Gly Asn Asp Thr Leu Val Gly Gly Glu Gly Gln Asn Thr Val Ile  
 675 680 685  
 Gly Gly Ala Gly Asp Asp Val Phe Leu Gln Asp Leu Gly Val Trp Ser  
 690 695 700

CYA-B-0002-PCT1-SEQ-1\_ST25

Asn Gln Leu Asp Gly Gly Ala Gly Val Asp Thr Val Lys Tyr Asn Val  
 705 710 715 720  
 His Gln Pro Ser Glu Glu Arg Leu Glu Arg Met Gly Asp Thr Gly Ile  
 725 730 735  
 His Ala Asp Leu Gln Lys Gly Thr Val Glu Lys Trp Pro Ala Leu Asn  
 740 745 750  
 Leu Phe Ser Val Asp His Val Lys Asn Ile Glu Asn Leu His Gly Ser  
 755 760 765  
 Arg Leu Asn Asp Arg Ile Ala Gly Asp Asp Gln Asp Asn Glu Leu Trp  
 770 775 780  
 Gly His Asp Gly Asn Asp Thr Ile Arg Gly Arg Gly Gly Asp Asp Ile  
 785 790 795 800  
 Leu Arg Gly Gly Leu Gly Leu Asp Thr Leu Tyr Gly Glu Asp Gly Asn  
 805 810 815  
 Asp Ile Phe Leu Gln Asp Asp Glu Thr Val Ser Asp Asp Ile Asp Gly  
 820 825 830  
 Gly Ala Gly Leu Asp Thr Val Asp Tyr Ser Ala Met Ile His Pro Gly  
 835 840 845  
 Arg Ile Val Ala Pro His Glu Tyr Gly Phe Gly Ile Glu Ala Asp Leu  
 850 855 860  
 Ser Arg Glu Trp Val Arg Lys Ala Ser Ala Leu Gly Val Asp Tyr Tyr  
 865 870 875 880  
 Asp Asn Val Arg Asn Val Glu Asn Val Ile Gly Thr Ser Met Lys Asp  
 885 890 895  
 Val Leu Ile Gly Asp Ala Gln Ala Asn Thr Leu Met Gly Gln Gly Gly  
 900 905 910  
 Asp Asp Thr Val Arg Gly Gly Asp Gly Asp Asp Leu Leu Phe Gly Gly  
 915 920 925  
 Asp Gly Asn Asp Met Leu Tyr Gly Asp Ala Gly Asn Asp Thr Leu Tyr  
 930 935 940  
 Gly Gly Leu Gly Asp Asp Thr Leu Glu Gly Gly Ala Gly Asn Asp Trp  
 945 950 955 960  
 Phe Gly Gln Thr Gln Ala Arg Glu His Asp Val Leu Arg Gly Gly Asp  
 965 970 975

## CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Val Asp Thr Val Asp Tyr Ser Gln Thr Gly Ala His Ala Gly Ile  
 980 985 990  
 Ala Ala Gly Arg Ile Gly Leu Gly Ile Leu Ala Asp Leu Gly Ala Gly  
 995 1000 1005  
 Arg Val Asp Lys Leu Gly Glu Ala Gly Ser Ser Ala Tyr Asp Thr  
 1010 1015 1020  
 Val Ser Gly Ile Glu Asn Val Val Gly Thr Glu Leu Ala Asp Arg  
 1025 1030 1035  
 Ile Thr Gly Asp Ala Gln Ala Asn Val Leu Arg Gly Ala Gly Gly  
 1040 1045 1050  
 Ala Asp Val Leu Ala Gly Gly Glu Gly Asp Asp Val Leu Leu Gly  
 1055 1060 1065  
 Gly Asp Gly Asp Asp Gln Leu Ser Gly Asp Ala Gly Arg Asp Arg  
 1070 1075 1080  
 Leu Tyr Gly Glu Ala Gly Asp Asp Trp Phe Phe Gln Asp Ala Ala  
 1085 1090 1095  
 Asn Ala Gly Asn Leu Leu Asp Gly Gly Asp Gly Arg Asp Thr Val  
 1100 1105 1110  
 Asp Phe Ser Gly Pro Gly Arg Gly Leu Asp Ala Gly Ala Lys Gly  
 1115 1120 1125  
 Val Phe Leu Ser Leu Gly Lys Gly Phe Ala Ser Leu Met Asp Glu  
 1130 1135 1140  
 Pro Glu Thr Ser Asn Val Leu Arg Asn Ile Glu Asn Ala Val Gly  
 1145 1150 1155  
 Ser Ala Arg Asp Asp Val Leu Ile Gly Asp Ala Gly Ala Asn Val  
 1160 1165 1170  
 Leu Asn Gly Leu Ala Gly Asn Asp Val Leu Ser Gly Gly Ala Gly  
 1175 1180 1185  
 Asp Asp Val Leu Leu Gly Asp Glu Gly Ser Asp Leu Leu Ser Gly  
 1190 1195 1200  
 Asp Ala Gly Asn Asp Asp Leu Phe Gly Gly Gln Gly Asp Asp Thr  
 1205 1210 1215  
 Tyr Leu Phe Gly Val Gly Tyr Gly His Asp Thr Ile Tyr Glu Ser  
 1220 1225 1230

CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Gly Gly His Asp Thr Ile Arg Ile Asn Ala Gly Ala Asp Gln  
 1235 1240 1245  
 Leu Trp Phe Ala Arg Gln Gly Asn Asp Leu Glu Ile Arg Ile Leu  
 1250 1255 1260  
 Gly Thr Asp Asp Ala Leu Thr Val His Asp Trp Tyr Arg Asp Ala  
 1265 1270 1275  
 Asp His Arg Val Glu Ile Ile His Ala Ala Asn Gln Ala Val Asp  
 1280 1285 1290  
 Gln Ala Gly Ile Glu Lys Leu Val Glu Ala Met Ala Gln Tyr Pro  
 1295 1300 1305  
 Asp Pro Gly Ala Ala Ala Ala Ala Pro Pro Ala Ala Arg Val Pro  
 1310 1315 1320  
 Asp Thr Leu Met Gln Ser Leu Ala Val Asn Trp Arg  
 1325 1330 1335

<210> 9  
 <211> 1590  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> CyaA Bordetella B - Bsp22 antigen  
 <400> 9

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

CYA-B-0002-PCT1-SEQ-1\_ST25

115

120

125

Thr Ile Pro Gly Trp Asp Asn Gln Lys Val Ser Arg Ile Glu Val Pro  
130 135 140  
Leu Asn Asp Ala Leu Arg Ala Ala Gly Leu Thr Gly Met Phe Glu Ala  
145 150 155 160  
Arg Asp Gly Gln Val Thr Ala Pro Gly Gly Arg Gly Thr Gln Val Val  
165 170 175  
Asn Gly Thr Gly Val Met Ala Gly Ser Thr Thr Tyr Lys Glu Leu Glu  
180 185 190  
Ser Ala Tyr Thr Thr Val Lys Gly Met Leu Asp Thr Ala Ser Asn Thr  
195 200 205  
Gln Gln Met Asp Met Ile Arg Leu Gln Ala Ala Ser Asn Lys Arg Asn  
210 215 220  
Glu Ala Phe Glu Val Met Thr Asn Thr Glu Lys Arg Arg Ser Asp Leu  
225 230 235 240  
Asn Ser Ser Ile Thr Asn Asn Met Arg Thr Gly Ala Ala Pro Ser Arg  
245 250 255  
Ser Lys Phe Ser Pro Asp Val Leu Glu Thr Val Pro Ala Ser Pro Gly  
260 265 270  
Leu Arg Arg Pro Ser Leu Gly Ala Val Glu Arg Gln Asp Ser Gly Tyr  
275 280 285  
Asp Ser Leu Asp Gly Val Gly Ser Arg Ser Phe Ser Leu Gly Glu Val  
290 295 300  
Ser Asp Met Ala Ala Val Glu Ala Ala Glu Leu Glu Met Thr Arg Gln  
305 310 315 320  
Val Leu His Ala Gly Ala Arg Gln Asp Asp Ala Glu Pro Gly Val Ser  
325 330 335  
Gly Ala Ser Ala His Trp Gly Gln Arg Ala Leu Gln Gly Ala Gln Ala  
340 345 350  
Val Ala Ala Ala Gln Arg Leu Val His Ala Ile Ala Leu Met Thr Gln  
355 360 365  
Phe Gly Arg Ala Gly Ser Thr Asn Thr Pro Gln Glu Ala Ala Ser Leu  
370 375 380  
Ser Ala Ala Val Phe Gly Leu Gly Glu Ala Ser Ser Ala Val Ala Glu  
Pge p





## CYA-B-0002-PCT1-SEQ-1\_ST25

660

665

670

Ala Ile Thr Gly Asn Ala Asp Asn Leu Lys Ser Val Asp Val Phe Val  
675 680 685

Asp Arg Phe Val Gln Gly Glu Arg Val Ala Gly Gln Pro Val Val Leu  
690 695 700

Asp Val Ala Ala Gly Gly Ile Asp Ile Ala Ser Arg Lys Gly Glu Arg  
705 710 715 720

Pro Ala Leu Thr Phe Ile Thr Pro Leu Ala Ala Pro Gly Glu Glu Gln  
725 730 735

Arg Arg Arg Thr Lys Thr Gly Lys Ser Glu Phe Thr Thr Phe Val Glu  
740 745 750

Ile Val Gly Lys Gln Asp Arg Trp Arg Ile Arg Asp Gly Ala Ala Asp  
755 760 765

Thr Thr Ile Asp Leu Ala Lys Val Val Ser Gln Leu Val Asp Ala Asn  
770 775 780

Gly Val Leu Lys His Ser Ile Lys Leu Asp Val Ile Gly Gly Asp Gly  
785 790 795 800

Asp Asp Val Val Leu Ala Asn Ala Ser Arg Ile His Tyr Asp Gly Gly  
805 810 815

Ala Gly Thr Asn Thr Val Ser Tyr Ala Ala Leu Gly Arg Gln Asp Ser  
820 825 830

Ile Thr Val Ser Ala Asp Gly Glu Arg Phe Asn Val Arg Lys Gln Leu  
835 840 845

Asn Asn Ala Asn Val Tyr Arg Glu Gly Val Ala Thr Gln Thr Thr Ala  
850 855 860

Tyr Gly Lys Arg Thr Glu Asn Val Gln Tyr Arg His Val Glu Leu Ala  
865 870 875 880

Arg Val Gly Gln Val Val Glu Val Asp Thr Leu Glu His Val Gln His  
885 890 895

Ile Ile Gly Gly Ala Gly Asn Asp Ser Ile Thr Gly Asn Ala His Asp  
900 905 910

Asn Phe Leu Ala Gly Gly Ser Gly Asp Asp Arg Leu Asp Gly Gly Ala  
915 920 925

Gly Asn Asp Thr Leu Val Gly Gly Glu Gly Gln Asn Thr Val Ile Gly

## CYA-B-0002-PCT1-SEQ-1\_ST25

930

935

940

Gly Ala Gly Asp Asp Val Phe Leu Gln Asp Leu Gly Val Trp Ser Asn  
 945 950 955 960

Gln Leu Asp Gly Gly Ala Gly Val Asp Thr Val Lys Tyr Asn Val His  
 965 970 975

Gln Pro Ser Glu Glu Arg Leu Glu Arg Met Gly Asp Thr Gly Ile His  
 980 985 990

Ala Asp Leu Gln Lys Gly Thr Val Glu Lys Trp Pro Ala Leu Asn Leu  
 995 1000 1005

Phe Ser Val Asp His Val Lys Asn Ile Glu Asn Leu His Gly Ser  
 1010 1015 1020

Arg Leu Asn Asp Arg Ile Ala Gly Asp Asp Gln Asp Asn Glu Leu  
 1025 1030 1035

Trp Gly His Asp Gly Asn Asp Thr Ile Arg Gly Arg Gly Gly Asp  
 1040 1045 1050

Asp Ile Leu Arg Gly Gly Leu Gly Leu Asp Thr Leu Tyr Gly Glu  
 1055 1060 1065

Asp Gly Asn Asp Ile Phe Leu Gln Asp Asp Glu Thr Val Ser Asp  
 1070 1075 1080

Asp Ile Asp Gly Lys Ala Gly Leu Asp Thr Val Asp Tyr Ser Ala  
 1085 1090 1095

Met Ile His Pro Gly Arg Ile Val Ala Pro His Glu Tyr Gly Phe  
 1100 1105 1110

Gly Ile Glu Ala Asp Leu Ser Arg Glu Trp Val Arg Lys Ala Ser  
 1115 1120 1125

Ala Leu Gly Val Asp Tyr Tyr Asp Asn Val Arg Asn Val Glu Asn  
 1130 1135 1140

Val Ile Gly Thr Ser Met Lys Asp Val Leu Ile Gly Asp Ala Gln  
 1145 1150 1155

Ala Asn Thr Leu Met Gly Gln Gly Gly Asp Asp Thr Val Arg Gly  
 1160 1165 1170

Gly Asp Gly Asp Asp Leu Leu Phe Gly Gly Asp Gly Asn Asp Met  
 1175 1180 1185

Leu Tyr Gly Asp Ala Gly Asn Asp Thr Leu Tyr Gly Gly Leu Gly

CYA-B-0002-PCT1-SEQ-1\_ST25

1190											
Asp	Asp	Thr	Leu	Glu	Gly	Gly	Ala	Gly	Asn	Asp	Trp
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Thr	Gln	Ala	Arg	Glu	His	Asp	Val	Leu	Arg	Gly	Gly
1220						1225					1230
Asp	Thr	Val	Asp	Tyr	Ser	Gln	Thr	Gly	Ala	His	Ala
1235						1240					1245
Ala	Gly	Arg	Ile	Gly	Leu	Gly	Ile	Leu	Ala	Asp	Leu
1250						1255					1260
Arg	Val	Asp	Lys	Leu	Gly	Glu	Ala	Gly	Ser	Ser	Ala
1265						1270					1275
Val	Ser	Gly	Ile	Glu	Asn	Val	Val	Gly	Thr	Glu	Leu
1280						1285					1290
Ile	Thr	Gly	Asp	Ala	Gln	Ala	Asn	Val	Leu	Arg	Gly
1295						1300					1305
Ala	Asp	Val	Leu	Ala	Gly	Gly	Glu	Gly	Asp	Asp	Val
1310						1315					1320
Gly	Asp	Gly	Asp	Asp	Gln	Leu	Ser	Gly	Asp	Ala	Gly
1325						1330					1335
Leu	Tyr	Gly	Glu	Ala	Gly	Asp	Asp	Trp	Phe	Phe	Gln
1340						1345					1350
Asn	Ala	Gly	Asn	Leu	Leu	Asp	Gly	Gly	Asp	Gly	Arg
1355						1360					1365
Asp	Phe	Ser	Gly	Pro	Gly	Arg	Gly	Leu	Asp	Ala	Gly
1370						1375					1380
Val	Phe	Leu	Ser	Leu	Gly	Lys	Gly	Phe	Ala	Ser	Leu
1385						1390					1395
Pro	Glu	Thr	Ser	Asn	Val	Leu	Arg	Asn	Ile	Glu	Asn
1400						1405					1410
Ser	Ala	Arg	Asp	Asp	Val	Leu	Ile	Gly	Asp	Ala	Gly
1415						1420					1425
Leu	Asn	Gly	Leu	Ala	Gly	Asn	Asp	Val	Leu	Ser	Gly
1430						1435					1440
Asp	Asp	Val	Leu	Leu	Gly	Asp	Glu	Gly	Ser	Asp	Leu

## 1445

1450

Q=1\_3  
1455

1480

11e  
1485Ile  
1495Gly  
1500Gly  
151011e  
15151hr  
1525

tyr  
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1540GIN  
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1555Ala  
1560Ala  
1570Ala  
1575Leu  
1585Arg  
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<213> Art

<220>

<223> Chimeric protein CyaA-P36

<400> 10

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18  
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Se  
25GI  
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35

40

SE  
4561  
50

55

60

65

se  
70

75

AS  
80

## CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Thr Ala Ile Ser Trp Lys Ala Asn Pro Asp Arg His Ser Val Asp  
 85 90 95  
 Ser Asp Tyr Gly Leu Pro Ser His Arg Leu Glu Gly His Thr Gly Phe  
 100 105 110  
 Val Ser Cys Val Ser Leu Ala His Ala Thr Asp Tyr Ala Leu Thr Ala  
 115 120 125  
 Ser Trp Asp Arg Ser Ile Arg Met Trp Asp Leu Arg Asn Gly Gln Cys  
 130 135 140  
 Gln Arg Lys Phe Leu Lys His Thr Lys Asp Val Leu Ala Val Ala Phe  
 145 150 155 160  
 Ser Pro Asp Asp Arg Leu Ile Val Ser Ala Gly Arg Asp Asn Val Ile  
 165 170 175  
 Arg Val Trp Asn Val Ala Gly Glu Cys Met His Glu Phe Leu Arg Asp  
 180 185 190  
 Gly His Glu Asp Trp Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu  
 195 200 205  
 His Pro Ile Val Val Ser Gly Ser Trp Asp Asn Thr Ile Lys Val Trp  
 210 215 220  
 Asn Val Asn Gly Gly Lys Cys Glu Arg Thr Leu Lys Gly His Ser Asn  
 225 230 235 240  
 Tyr Val Ser Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala Ser  
 245 250 255  
 Gly Gly Lys Asp Gly Ala Ala Leu Leu Trp Asp Leu Ser Thr Gly Glu  
 260 265 270  
 Gln Leu Phe Lys Ile Asn Val Glu Ser Pro Ile Asn Gln Ile Ala Phe  
 275 280 285  
 Ser Pro Asn Arg Phe Trp Met Cys Val Ala Thr Glu Arg Ser Leu Ser  
 290 295 300  
 Val Tyr Asp Leu Glu Ser Lys Ala Val Ile Ala Glu Leu Thr Pro Asp  
 305 310 315 320  
 Gly Ala Lys Pro Ser Glu Cys Ile Ser Ile Ala Trp Ser Ala Asp Gly  
 325 330 335  
 Asn Thr Leu Tyr Ser Gly His Lys Asp Asn Leu Ile Arg Val Trp Ser  
 340 345 350

## CYA-B-0002-PCT1-SEQ-1\_ST25

Ile Ser Asp Ala Glu Thr Gly Ala Ala Pro Ser Arg Ser Lys Phe Ser  
 355 360 365  
 Pro Asp Val Leu Glu Thr Val Pro Ala Ser Pro Gly Leu Arg Arg Pro  
 370 375 380  
 Ser Leu Gly Ala Val Glu Arg Gln Asp Ser Gly Tyr Asp Ser Leu Asp  
 385 390 395 400  
 Gly Val Gly Ser Arg Ser Phe Ser Leu Gly Glu Val Ser Asp Met Ala  
 405 410 415  
 Ala Val Glu Ala Ala Glu Leu Glu Met Thr Arg Gln Val Leu His Ala  
 420 425 430  
 Gly Ala Arg Gln Asp Asp Ala Glu Pro Gly Val Ser Gly Ala Ser Ala  
 435 440 445  
 His Trp Gly Gln Arg Ala Leu Gln Gly Ala Gln Ala Val Ala Ala Ala  
 450 455 460  
 Gln Arg Leu Val His Ala Ile Ala Leu Met Thr Gln Phe Gly Arg Ala  
 465 470 475 480  
 Gly Ser Thr Asn Thr Pro Gln Glu Ala Ala Ser Leu Ser Ala Ala Val  
 485 490 495  
 Phe Gly Leu Gly Glu Ala Ser Ser Ala Val Ala Glu Thr Val Ser Gly  
 500 505 510  
 Phe Phe Arg Gly Ser Ser Arg Trp Ala Gly Gly Phe Gly Val Ala Gly  
 515 520 525  
 Gly Ala Met Ala Leu Gly Gly Gly Ile Ala Ala Ala Val Gly Ala Gly  
 530 535 540  
 Met Ser Leu Thr Asp Asp Ala Pro Ala Gly Gln Lys Ala Ala Ala Gly  
 545 550 555 560  
 Ala Glu Ile Ala Leu Gln Leu Thr Gly Gly Thr Val Glu Leu Ala Ser  
 565 570 575  
 Ser Ile Ala Leu Ala Leu Ala Ala Ala Arg Gly Val Thr Ser Gly Leu  
 580 585 590  
 Gln Val Ala Gly Ala Ser Ala Gly Ala Ala Ala Gly Ala Leu Ala Ala  
 595 600 605  
 Ala Leu Ser Pro Met Glu Ile Tyr Gly Leu Val Gln Gln Ser His Tyr  
 610 615 620

## CYA-B-0002-PCT1-SEQ-1\_ST25

Ala Asp Gln Leu Asp Lys Leu Ala Gln Glu Ser Ser Ala Tyr Gly Tyr  
 625 630 635 640  
 Glu Gly Asp Ala Leu Leu Ala Gln Leu Tyr Arg Asp Lys Thr Ala Ala  
 645 650 655  
 Glu Gly Ala Val Ala Gly Val Ser Ala Val Leu Ser Thr Val Gly Ala  
 660 665 670  
 Ala Val Ser Ile Ala Ala Ala Ala Ser Val Val Gly Ala Pro Val Ala  
 675 680 685  
 Val Val Thr Ser Leu Leu Thr Gly Ala Leu Asn Gly Ile Leu Arg Gly  
 690 695 700  
 Val Gln Gln Pro Ile Ile Glu Lys Leu Ala Asn Asp Tyr Ala Arg Lys  
 705 710 715 720  
 Ile Asp Glu Leu Gly Gly Pro Gln Ala Tyr Phe Glu Lys Asn Leu Gln  
 725 730 735  
 Ala Arg His Glu Gln Leu Ala Asn Ser Asp Gly Leu Arg Lys Met Leu  
 740 745 750  
 Ala Asp Leu Gln Ala Gly Trp Asn Ala Ser Ser Val Ile Gly Val Gln  
 755 760 765  
 Thr Thr Glu Ile Ser Lys Ser Ala Leu Glu Leu Ala Ala Ile Thr Gly  
 770 775 780  
 Asn Ala Asp Asn Leu Lys Ser Val Asp Val Phe Val Asp Arg Phe Val  
 785 790 795 800  
 Gln Gly Glu Arg Val Ala Gly Gln Pro Val Val Leu Asp Val Ala Ala  
 805 810 815  
 Gly Gly Ile Asp Ile Ala Ser Arg Lys Gly Glu Arg Pro Ala Leu Thr  
 820 825 830  
 Phe Ile Thr Pro Leu Ala Ala Pro Gly Glu Glu Gln Arg Arg Arg Thr  
 835 840 845  
 Lys Thr Gly Lys Ser Glu Phe Thr Thr Phe Val Glu Ile Val Gly Lys  
 850 855 860  
 Gln Asp Arg Trp Arg Ile Arg Asp Gly Ala Ala Asp Thr Thr Ile Asp  
 865 870 875 880  
 Leu Ala Lys Val Val Ser Gln Leu Val Asp Ala Asn Gly Val Leu Lys  
 885 890 895

## CYA-B-0002-PCT1-SEQ-1\_ST25

His Ser Ile Lys Leu Asp Val Ile Gly Gly Asp Gly Asp Asp Val Val  
 900 905 910  
 Leu Ala Asn Ala Ser Arg Ile His Tyr Asp Gly Gly Ala Gly Thr Asn  
 915 920 925  
 Thr Val Ser Tyr Ala Ala Leu Gly Arg Gln Asp Ser Ile Thr Val Ser  
 930 935 940  
 Ala Asp Gly Glu Arg Phe Asn Val Arg Lys Gln Leu Asn Asn Ala Asn  
 945 950 955 960  
 Val Tyr Arg Glu Gly Val Ala Thr Gln Thr Thr Ala Tyr Gly Lys Arg  
 965 970 975  
 Thr Glu Asn Val Gln Tyr Arg His Val Glu Leu Ala Arg Val Gly Gln  
 980 985 990  
 Val Val Glu Val Asp Thr Leu Glu His Val Gln His Ile Ile Gly Gly  
 995 1000 1005  
 Ala Gly Asn Asp Ser Ile Thr Gly Asn Ala His Asp Asn Phe Leu  
 1010 1015 1020  
 Ala Gly Gly Ser Gly Asp Asp Arg Leu Asp Gly Gly Ala Gly Asn  
 1025 1030 1035  
 Asp Thr Leu Val Gly Gly Glu Gly Gln Asn Thr Val Ile Gly Gly  
 1040 1045 1050  
 Ala Gly Asp Asp Val Phe Leu Gln Asp Leu Gly Val Trp Ser Asn  
 1055 1060 1065  
 Gln Leu Asp Gly Gly Ala Gly Val Asp Thr Val Lys Tyr Asn Val  
 1070 1075 1080  
 His Gln Pro Ser Glu Glu Arg Leu Glu Arg Met Gly Asp Thr Gly  
 1085 1090 1095  
 Ile His Ala Asp Leu Gln Lys Gly Thr Val Glu Lys Trp Pro Ala  
 1100 1105 1110  
 Leu Asn Leu Phe Ser Val Asp His Val Lys Asn Ile Glu Asn Leu  
 1115 1120 1125  
 His Gly Ser Arg Leu Asn Asp Arg Ile Ala Gly Asp Asp Gln Asp  
 1130 1135 1140  
 Asn Glu Leu Trp Gly His Asp Gly Asn Asp Thr Ile Arg Gly Arg  
 1145 1150 1155



## CYA-B-0002-PCT1-SEQ-1\_ST25

Gly Gly Asp Asp Ile Leu Arg Gly Gly Leu Gly Leu Asp Thr Leu  
 1160 1165 1170  
 Tyr Gly Glu Asp Gly Asn Asp Ile Phe Leu Gln Asp Asp Glu Thr  
 1175 1180 1185  
 Val Ser Asp Asp Ile Asp Gly Gly Ala Gly Leu Asp Thr Val Asp  
 1190 1195 1200  
 Tyr Ser Ala Met Ile His Pro Gly Arg Ile Val Ala Pro His Glu  
 1205 1210 1215  
 Tyr Gly Phe Gly Ile Glu Ala Asp Leu Ser Arg Glu Trp Val Arg  
 1220 1225 1230  
 Lys Ala Ser Ala Leu Gly Val Asp Tyr Tyr Asp Asn Val Arg Asn  
 1235 1240 1245  
 Val Glu Asn Val Ile Gly Thr Ser Met Lys Asp Val Leu Ile Gly  
 1250 1255 1260  
 Asp Ala Gln Ala Asn Thr Leu Met Gly Gln Gly Gly Asp Asp Thr  
 1265 1270 1275  
 Val Arg Gly Gly Asp Gly Asp Asp Leu Leu Phe Gly Gly Asp Gly  
 1280 1285 1290  
 Asn Asp Met Leu Tyr Gly Asp Ala Gly Asn Asp Thr Leu Tyr Gly  
 1295 1300 1305  
 Gly Leu Gly Asp Asp Thr Leu Glu Gly Gly Ala Gly Asn Asp Trp  
 1310 1315 1320  
 Phe Gly Gln Thr Gln Ala Arg Glu His Asp Val Leu Arg Gly Gly  
 1325 1330 1335  
 Asp Gly Val Asp Thr Val Asp Tyr Ser Gln Thr Gly Ala His Ala  
 1340 1345 1350  
 Gly Ile Ala Ala Gly Arg Ile Gly Leu Gly Ile Leu Ala Asp Leu  
 1355 1360 1365  
 Gly Ala Gly Arg Val Asp Lys Leu Gly Glu Ala Gly Ser Ser Ala  
 1370 1375 1380  
 Tyr Asp Thr Val Ser Gly Ile Glu Asn Val Val Gly Thr Glu Leu  
 1385 1390 1395  
 Ala Asp Arg Ile Thr Gly Asp Ala Gln Ala Asn Val Leu Arg Gly  
 1400 1405 1410

## CYA-B-0002-PCT1-SEQ-1\_ST25

Ala	Gly	Gly	Ala	Asp	Val	Leu	Ala	Gly	Gly	Glu	Gly	Asp	Asp	Val
	1415					1420					1425			
Leu	Leu	Gly	Gly	Asp	Gly	Asp	Asp	Gln	Leu	Ser	Gly	Asp	Ala	Gly
	1430					1435					1440			
Arg	Asp	Arg	Leu	Tyr	Gly	Glu	Ala	Gly	Asp	Asp	Trp	Phe	Phe	Gln
	1445					1450					1455			
Asp	Ala	Ala	Asn	Ala	Gly	Asn	Leu	Leu	Asp	Gly	Gly	Asp	Gly	Arg
	1460					1465					1470			
Asp	Thr	Val	Asp	Phe	Ser	Gly	Pro	Gly	Arg	Gly	Leu	Asp	Ala	Gly
	1475					1480					1485			
Ala	Lys	Gly	Val	Phe	Leu	Ser	Leu	Gly	Lys	Gly	Phe	Ala	Ser	Leu
	1490					1495					1500			
Met	Asp	Glu	Pro	Glu	Thr	Ser	Asn	Val	Leu	Arg	Asn	Ile	Glu	Asn
	1505					1510					1515			
Ala	Val	Gly	Ser	Ala	Arg	Asp	Asp	Val	Leu	Ile	Gly	Asp	Ala	Gly
	1520					1525					1530			
Ala	Asn	Val	Leu	Asn	Gly	Leu	Ala	Gly	Asn	Asp	Val	Leu	Ser	Gly
	1535					1540					1545			
Gly	Ala	Gly	Asp	Asp	Val	Leu	Leu	Gly	Asp	Glu	Gly	Ser	Asp	Leu
	1550					1555					1560			
Leu	Ser	Gly	Asp	Ala	Gly	Asn	Asp	Asp	Leu	Phe	Gly	Gly	Gln	Gly
	1565					1570					1575			
Asp	Asp	Thr	Tyr	Leu	Phe	Gly	Val	Gly	Tyr	Gly	His	Asp	Thr	Ile
	1580					1585					1590			
Tyr	Glu	Ser	Gly	Gly	Gly	His	Asp	Thr	Ile	Arg	Ile	Asn	Ala	Gly
	1595					1600					1605			
Ala	Asp	Gln	Leu	Trp	Phe	Ala	Arg	Gln	Gly	Asn	Asp	Leu	Glu	Ile
	1610					1615					1620			
Arg	Ile	Leu	Gly	Thr	Asp	Asp	Ala	Leu	Thr	Val	His	Asp	Trp	Tyr
	1625					1630					1635			
Arg	Asp	Ala	Asp	His	Arg	Val	Glu	Ile	Ile	His	Ala	Ala	Asn	Gln
	1640					1645					1650			
Ala	Val	Asp	Gln	Ala	Gly	Ile	Glu	Lys	Leu	Val	Glu	Ala	Met	Ala
	1655					1660					1665			

CYA-B-0002-PCT1-SEQ-1\_ST25

Gln Tyr Pro Asp Pro Gly Ala Ala Ala Ala Ala Pro Pro Ala Ala  
1670 1675 1680

Arg Val Pro Asp Thr Leu Met Gln Ser Leu Ala Val Asn Trp Arg  
1685 1690 1695