

eolf-seql
SEQUENCE LISTING

<110> Givaudan SA

<120> Process

<130> 30875PCT

<150> GB1618090.3

<151> 2016-10-26

<160> 4

<170> PatentIn version 3.3

<210> 1

<211> 631

<212> PRT

<213> Alicyclobacillus acidocaldarius

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

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Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145 150 155 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
165 170 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
180 185 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
195 200 205

Gly Ala Lys Gly Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Ala
210 215 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225 230 235 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
245 250 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
260 265 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
275 280 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
290 295 300

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

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
325 330 335

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Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
340 345 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
355 360 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
370 375 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385 390 395 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
420 425 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
435 440 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
450 455 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465 470 475 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
485 490 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
515 520 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
530 535 540

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Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 2

<211> 631

<212> PRT

<213> Artificial sequence

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<223> Synthetic AacSHC Derivative

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Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
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Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
50 55 60

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Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
100 105 110

Ala Leu Arg Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser Ser Arg Val
115 120 125

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
145 150 155 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
165 170 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
180 185 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
195 200 205

Gly Ala Lys Gly Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Ala
210 215 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
225 230 235 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
245 250 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
260 265 270

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Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
 275 280 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
 290 295 300

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

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
 325 330 335

Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
 340 345 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
 355 360 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
 370 375 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
 385 390 395 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
 405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
 420 425 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
 435 440 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
 450 455 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
 465 470 475 480

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Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
485 490 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
515 520 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
530 535 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Tyr Pro Gly Asp Phe Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630

<210> 3

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<212> DNA

<213> Artificial sequence

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<223> Synthetic AacSHC Derivative

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gactgggtcg agcagcatca gaaccggac ggcggtggg gcgaggactg ccgctcgtac	1620
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<210> 4

<211> 631

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<213> Artificial sequence

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<223> Synthetic AacSHC Derivative

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Met Ala Glu Gln Leu Val Glu Ala Pro Ala Tyr Ala Arg Thr Leu Asp
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Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
          20          25          30

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Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
      35          40          45

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Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
      50          55          60

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Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
65          70          75          80

```

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Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
      85          90          95

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Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
      100         105         110

```

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Ala Leu Arg Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser Ser Arg Val
      115         120         125

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Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
 130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
 145 150 155 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
 165 170 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
 180 185 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
 195 200 205

Gly Ala Lys Gly Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Ala
 210 215 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
 225 230 235 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
 245 250 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
 260 265 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
 275 280 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
 290 295 300

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

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
 325 330 335

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Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
340 345 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
355 360 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
370 375 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
385 390 395 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
420 425 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
435 440 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
450 455 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
465 470 475 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
485 490 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
515 520 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
530 535 540

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Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Trp Tyr Leu Gly
595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
610 615 620

Lys Gln Ala Ile Glu Arg Arg
625 630