

50241PCT-sequence listing_ST25
SEQUENCE LISTING

<110> ETH Zürich

<120> RATIONAL DESIGN OF COMPONENTS OF THE
OLIGOSACCHARYLTRANSFERASE-CATALYSED ASPARAGINE-LINKED
GLYCOSYLATION

<130> 50241PCT

<160> 8

<170> PatentIn version 3.5

<210> 1

<211> 712

<212> PRT

<213> Campylobacter lari

<400> 1

Met Glu Leu Gln Gln Asn Phe Thr Asp Asn Asn Ser Ile Lys Tyr Thr
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Cys Ile Leu Ile Leu Ile Ala Phe Ala Phe Ser Val Leu Cys Arg Leu
20 25 30

Tyr Trp Val Ala Trp Ala Ser Glu Phe Tyr Glu Phe Phe Phe Asn Asp
35 40 45

Gln Leu Met Ile Thr Thr Asn Asp Gly Tyr Ala Phe Ala Glu Gly Ala
50 55 60

Arg Asp Met Ile Ala Gly Phe His Gln Pro Asn Asp Leu Ser Tyr Phe
65 70 75 80

Gly Ser Ser Leu Ser Thr Leu Thr Tyr Trp Leu Tyr Ser Ile Leu Pro
85 90 95

Phe Ser Phe Glu Ser Ile Ile Leu Tyr Met Ser Thr Phe Phe Ala Ser
100 105 110

Leu Ile Val Val Pro Ile Ile Leu Ile Ala Arg Glu Tyr Lys Leu Thr
115 120 125

Thr Tyr Gly Phe Ile Ala Ala Leu Leu Gly Ser Ile Ala Asn Ser Tyr
130 135 140

Tyr Asn Arg Thr Met Ser Gly Tyr Tyr Asp Thr Asp Met Leu Val Leu
145 150 155 160

Val Leu Pro Met Leu Ile Leu Leu Thr Phe Ile Arg Leu Thr Ile Asn
165 170 175

Lys Asp Ile Phe Thr Leu Leu Leu Ser Pro Ile Phe Ile Met Ile Tyr
180 185 190

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Leu Trp Trp Tyr Pro Ser Ser Tyr Ser Leu Asn Phe Ala Met Ile Gly
195 200 205

Leu Phe Gly Leu Tyr Thr Leu Val Phe His Arg Lys Glu Lys Ile Phe
210 215 220

Tyr Leu Ala Ile Ala Leu Met Ile Ile Ala Leu Ser Met Leu Ala Trp
225 230 235 240

Gln Tyr Lys Leu Ala Leu Ile Val Leu Leu Phe Ala Ile Phe Ala Phe
245 250 255

Lys Glu Glu Lys Ile Asn Phe Tyr Met Ile Trp Ala Leu Ile Phe Ile
260 265 270

Ser Ile Ser Ile Leu His Leu Ser Gly Gly Leu Asp Pro Val Leu Tyr
275 280 285

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

Asp Ala Ala Phe Met Tyr Phe Asn Val Asn Glu Thr Ile Met Glu Val
305 310 315 320

Asn Thr Ile Asp Pro Glu Val Phe Met Gln Arg Ile Ser Ser Ser Val
325 330 335

Leu Val Phe Ile Leu Ser Phe Ile Gly Phe Ile Leu Leu Cys Lys Asp
340 345 350

His Lys Ser Met Leu Leu Ala Leu Pro Met Leu Ala Leu Gly Phe Met
355 360 365

Ala Leu Arg Ala Gly Leu Arg Phe Thr Ile Tyr Ala Val Pro Val Met
370 375 380

Ala Leu Gly Phe Gly Tyr Phe Leu Tyr Ala Phe Phe Asn Phe Leu Glu
385 390 395 400

Lys Lys Gln Ile Lys Leu Ser Leu Arg Asn Lys Asn Ile Leu Leu Ile
405 410 415

Leu Ile Ala Phe Phe Ser Ile Ser Pro Ala Leu Met His Ile Tyr Tyr
420 425 430

Tyr Lys Ser Ser Thr Val Phe Thr Ser Tyr Glu Ala Ser Ile Leu Asn
435 440 445

Asp Leu Lys Asn Lys Ala Gln Arg Glu Asp Tyr Val Val Ala Trp Trp
450 455 460

Asp Tyr Gly Tyr Pro Ile Arg Tyr Tyr Ser Asp Val Lys Thr Leu Ile

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465 470 475 480

Asp Gly Gly Lys His Leu Gly Lys Asp Asn Phe Phe Ser Ser Phe Val
 485 490 495

Leu Ser Lys Glu Gln Ile Pro Ala Ala Asn Met Ala Arg Leu Ser Val
 500 505 510

Glu Tyr Thr Glu Lys Ser Phe Lys Glu Asn Tyr Pro Asp Val Leu Lys
 515 520 525

Ala Met Val Lys Asp Tyr Asn Gln Thr Ser Ala Lys Asp Phe Leu Glu
 530 535 540

Ser Leu Asn Asp Lys Asn Phe Lys Phe Asp Thr Asn Lys Thr Arg Asp
545 550 555 560

Val Tyr Ile Tyr Met Pro Tyr Arg Met Leu Arg Ile Met Pro Val Val
 565 570 575

Ala Gln Phe Ala Asn Thr Asn Pro Asp Asn Gly Glu Gln Glu Lys Ser
 580 585 590

Leu Phe Phe Ser Gln Ala Asn Ala Ile Ala Gln Asp Lys Thr Thr Gly
 595 600 605

Ser Val Met Leu Asp Asn Gly Val Glu Ile Ile Asn Asp Phe Arg Ala
610 615 620

Leu Lys Val Glu Gly Ala Ser Ile Pro Leu Lys Ala Phe Val Asp Ile
625 630 635 640

Glu Ser Ile Thr Asn Gly Lys Phe Tyr Tyr Asn Glu Ile Asp Ser Lys
 645 650 655

Ala Gln Ile Tyr Leu Leu Phe Leu Arg Glu Tyr Lys Ser Phe Val Ile
 660 665 670

Leu Asp Glu Ser Leu Tyr Asn Ser Ala Tyr Ile Gln Met Phe Leu Leu
 675 680 685

Asn Gln Tyr Asp Gln Asp Leu Phe Glu Gln Val Thr Asn Asp Thr Arg
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Ala Lys Ile Tyr Arg Leu Lys Arg
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<210> 2
<211> 6
<212> PRT
<213> Artificial sequence
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<223> Artificial hexapeptide substrate for OST

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<221> MISC_FEATURE

<222> (6)..(6)

<223> substituted with nitro group in para position

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Asp Gln Asn Ala Thr Phe
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<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Consensus sequon for bacterial OST

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<222> (1)..(1)

<223> Glu

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<221> VARIANT

<222> (2)..(2)

<223> Ala or Cys or Asp or Glu or Phe or Gly or His or Ile or Lys or
Leu or Met or Asn or Arg or Ser or Thr or Val or Trp or Tyr

<220>

<221> VARIANT

<222> (4)..(4)

<223> Cys or Asp or Glu or Phe or Gly or His or Ile or Lys or Leu or
Met or Asn or Gln or Arg or Ser or Thr or Val or Trp or Tyr

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<223> Ser

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Asp Gln Asn Ala Thr
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<210> 4

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Optimal substrate sequence for C. jejuni PglB OTS

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Asp Gln Asn Ala Thr
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<210> 5

<211> 6

<212> PRT

<213> Artificial Sequence

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<220>
<223> Hexapeptide substrate used in crystallization

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Asp Gln Asn Ala Thr Phe
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<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

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<223> Peptide used in crystallization

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<222> (1)..(1)
<223> ACETYLATION

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<400> 6

Asp Gln Asn Ala Thr Phe
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<223> Bacterial sequence motif

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Met or Asn or Pro or Gln or Arg or Ser or Thr or Val or Trp or
Tyr

<220>
<221> VARIANT
<222> (3)..(3)
<223> Cys or Asp or Glu or Phe or Gly or His or Ile or Lys or Leu or
Met or Asn or Pro or Gln or Arg or Ser or Thr or Val or Trp or
Tyr

<400> 7

Met Ala Ala Ile
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<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

50241PCT-sequence listing_ST25

<220>

<223> Pentapeptide substrate for OTS

<400> 8

Ala Gln Asn Ala Thr
1 5