

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
1 5 10 15

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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501-1219 EF Sequence																
				H5cAng_57125												
465				470				475				480				
Asp	Gly	Gly	Lys	His 485	Leu	Gly	Lys	Asp	Asn 490	Phe	Phe	Ser	Ser	Phe 495	Val	
Leu	Ser	Lys	Glu 500	Gln	Ile	Pro	Ala	Ala 505	Asn	Met	Ala	Arg	Leu 510	Ser	Val	
Glu	Tyr	Thr 515	Glu	Lys	Ser	Phe	Lys 520	Glu	Asn	Tyr	Pro	Asp 525	Val	Leu	Lys	
Ala	Met 530	Val	Lys	Asp	Tyr	Asn 535	Gln	Thr	Ser	Ala	Lys 540	Asp	Phe	Leu	Glu	
Ser 545	Leu	Asn	Asp	Lys	Asn 550	Phe	Lys	Phe	Asp	Thr 555	Asn	Lys	Thr	Arg	Asp 560	
Val	Tyr	Ile	Tyr	Met 565	Pro	Tyr	Arg	Met	Leu 570	Arg	Ile	Met	Pro	Val 575	Val	
Ala	Gln	Phe	Ala 580	Asn	Thr	Asn	Pro	Asp 585	Asn	Gly	Glu	Gln	Glu 590	Lys	Ser	
Leu	Phe	Phe 595	Ser	Gln	Ala	Asn	Ala 600	Ile	Ala	Gln	Asp	Lys 605	Thr	Thr	Gly	
Ser	Val 610	Met	Leu	Asp	Asn	Gly 615	Val	Glu	Ile	Ile	Asn 620	Asp	Phe	Arg	Ala	
Leu 625	Lys	Val	Glu	Gly	Ala 630	Ser	Ile	Pro	Leu	Lys 635	Ala	Phe	Val	Asp	Ile 640	
Glu	Ser	Ile	Thr	Asn 645	Gly	Lys	Phe	Tyr	Tyr 650	Asn	Glu	Ile	Asp	Ser 655	Lys	
Ala	Gln	Ile	Tyr 660	Leu	Leu	Phe	Leu	Arg 665	Glu	Tyr	Lys	Ser	Phe 670	Val	Ile	
Leu	Asp	Glu 675	Ser	Leu	Tyr	Asn	Ser 680	Ala	Tyr	Ile	Gln	Met 685	Phe	Leu	Leu	
Asn	Gln 690	Tyr	Asp	Gln	Asp	Leu 695	Phe	Glu	Gln	Val	Thr 700	Asn	Asp	Thr	Arg	
Ala 705	Lys	Ile	Tyr	Arg	Leu 710	Lys	Arg									

<210>	2
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<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

<400> 2

Asp Gln Asn Ala Thr Phe
1 5

<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Consensus sequon for bacterial OST

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<221> VARIANT

<222> (1)..(1)

<223> Glu

<220>

<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

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<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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<221> VARIANT

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<223> Ser

<400> 3

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

<400> 4

Asp Gln Asn Ala Thr
1 5

<210> 5

<211> 6

<212> PRT

<213> Artificial Sequence

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<220>
<223> Hexapeptide substrate used in crystallization

<400> 5

Asp Gln Asn Ala Thr Phe
1 5

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

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<223> Peptide used in crystallization

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<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> substituted with nitro group in para position

<400> 6

Asp Gln Asn Ala Thr Phe
1 5

<210> 7
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<212> PRT
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<220>
<223> Bacterial sequence motif

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<221> VARIANT
<222> (2)..(2)
<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

<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