

SEQUENCE LISTING

<110> Ezaki Glico Co., Ltd.

<120> Carotenoid compounds

<130> 21076W0

<150> JP2020-188462

<151> 2020-11-12

<160> 12

<170> PatentIn version 3.5

<210> 1

<211> 321

<212> DNA

<213> human

<400> 1

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tctcaaaaaa atgtagcctg taaaaatggc caaaccaact gttatcaatc atattccacc 180

atgtccatta ccgattgtcg cgaaacagga tcttccaaat atccaaattg tgcataataa 240

actaccaag cgaacaaaca tattatcgta gcatgtgaag gcaacccgta cgtacctgtc 300

cacttcgacg catcagtgta a 321

<210> 2

<211> 106

<212> PRT

<213> human

<400> 2

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1 5 10 15

Leu Thr Lys Asp Arg Cys Lys Pro Val Asn Thr Phe Val His Glu Ser
20 25 30

Leu Ala Asp Val Gln Ala Val Cys Ser Gln Lys Asn Val Ala Cys Lys
35 40 45

Asn Gly Gln Thr Asn Cys Tyr Gln Ser Tyr Ser Thr Met Ser Ile Thr

50

55

60

Asp Cys Arg Glu Thr Gly Ser Ser Lys Tyr Pro Asn Cys Ala Tyr Lys
 65 70 75 80

Thr Thr Gln Ala Asn Lys His Ile Ile Val Ala Cys Glu Gly Asn Pro
 85 90 95

Tyr Val Pro Val His Phe Asp Ala Ser Val
 100 105

<210> 3

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> S-Tag coding oligonucleotide with substitution at 34th to 36th position by phenylalanine coding sequence

<400> 3

aaagaaaccg ctgctgcgaa atttgaacgc cagttcatgg actcgtctac tagcgcagct 60

<210> 4

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> S-Tag amino sequence with substitution at 12th position by phenylalanine

<400> 4

Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln Phe Met Asp Ser Ser
 1 5 10 15

Thr Ser Ala Ala
 20

<210> 5

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> S-Tag introduced CaCCS

<400> 5

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gcgccgacca gcaaaccgga aagcctggat gtgaatatca gctgggttga taccgatctg	180
gatggcgccg aatttgatgt gattatcatt ggtaccggtc cggccggcct gcgtctggca	240
gaacaggtta gcaaatatgg tattaaagtg tgctgtgttg atccgagccc gctgagcatg	300
tggccgaaca attatggcgt gtgggttgat gaatttgaaa aactgggtct ggaagattgc	360
ctggatcata aatggccggt gagctgtgtt catatcagcg atcataaaac caaatatctg	420
gatcgcccgt atggctcgcgt gagccgtaaa aaactgaaac tgaaactgct gaacagctgc	480
gtggaaaacc gtgttaaatt ctacaaagcg aaagtgtga aagttaaaca tgaagaatth	540
gaaagcagca ttgtgtgtga tgatggccgc aaaatcagcg gtagcctgat tgttgatgcg	600
agcggctatg ccagcgatth tatcgaatat gataaaccgc gtaatcatgg ctatcaggtg	660
gcgcatggta ttctggccga agttgataat catccgtthg atctggataa aatgatgctg	720
atggattggc gcgatagcca tctgggtaac gaaccgtatc tgctgttgaa aaataccaaa	780
gaaccgacct ttctgtatgc gatgccgtth gatcgcaatc tgggtgtthct ggaagaaacc	840
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tttttcgatg ttgatccgaa atattggcat ggctttctga gcagccgcct gagcgtgaaa	1320
gaactggccg ttctgagcct gtacctgtth ggtcatgcga gcaacctggc ccgtctggat	1380
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ctgtaa	1446

<210> 6

<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> S-Tag introduced CaCCS

<400> 6

Met Ala Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln Phe Met Asp
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Ser Ser Thr Ser Ala Ala Met Phe His Tyr Arg Asn Lys Ser Ser Thr
20 25 30

His Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu Ser
35 40 45

Leu Asp Val Asn Ile Ser Trp Val Asp Thr Asp Leu Asp Gly Ala Glu
50 55 60

Phe Asp Val Ile Ile Ile Gly Thr Gly Pro Ala Gly Leu Arg Leu Ala
65 70 75 80

Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro Ser
85 90 95

Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu Phe
100 105 110

Glu Lys Leu Gly Leu Glu Asp Cys Leu Asp His Lys Trp Pro Val Ser
115 120 125

Cys Val His Ile Ser Asp His Lys Thr Lys Tyr Leu Asp Arg Pro Tyr
130 135 140

Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser Cys
145 150 155 160

Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Leu Lys Val Lys
165 170 175

His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Arg Lys Ile

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

Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Glu Gly Thr Arg Arg
405 410 415

Leu Phe Asp Ala Phe Phe Asp Val Asp Pro Lys Tyr Trp His Gly Phe
420 425 430

Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Ala Val Leu Ser Leu Tyr
435 440 445

Leu Phe Gly His Ala Ser Asn Leu Ala Arg Leu Asp Ile Val Thr Lys
450 455 460

Cys Thr Val Pro Leu Val Lys Leu Leu Gly Asn Leu Ala Ile Glu Ser
465 470 475 480

Leu

<210> 7
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> S-Tag introduced CaCCS via linker

<400> 7
atgtcgaaag aaaccgctgc tgcgaaattt gaacgccagt tcatggactc gtctactagt 60
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ggttcaatgt ttcattatcg taacaaaagc agcaccatt tttgcagctt tctggatctg 180
gcgccgacca gcaaaccgga aagcctggat gtgaatatca gctgggttga taccgatctg 240
gatggcgccg aatttgatgt gattatcatt ggtaccggtc cggccggcct gcgtctggca 300
gaacaggtta gcaaatatgg tattaaagtg tgctgtgttg atccgagccc gctgagcatg 360
tggccgaaca attatggcgt gtgggttgat gaatttgaaa aactgggtct ggaagattgc 420
ctggatcata aatggccggt gagctgtgtt catatcagcg atcataaaac caaatatctg 480
gatcgcccgt atggtcgctg gagccgtaaa aaactgaaac tgaaactgct gaacagctgc 540
gtggaaaacc gtgttaaatt ctacaaagcg aaagtgtga aagttaaaca tgaagaattt 600

gaaagcagca ttgtgtgtga tgatggccgc aaaatcagcg gtagcctgat tgttgatgcg	660
agcggctatg ccagcgattt tatcgaatat gataaaccgc gtaatcatgg ctatcaggtg	720
gcgcatggta ttctggccga agttgataat catccgtttg atctggataa aatgatgctg	780
atggattggc gcgatagcca tctgggtaac gaaccgtatc tgcgtgtgaa aaataccaaa	840
gaaccgacct ttctgtatgc gatgccgttt gatcgcaatc tgggtgtttct ggaagaaacc	900
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atgggaggcc cgctgccgcg tattccgcag aacgttatgg cgatcggcgg taccagcggc	1080
attgtgcatc cgagcagcgg ttatatggtt gcgcgcagca tggcgctggc accggtgctg	1140
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catcgcgtgt ggaatggctt gtggccgagc gatcgtcgcc gtgttcgtga atgctattgt	1260
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gaactggccg ttctgagcct gtacctgttt ggtcatgcga gcaacctggc ccgtctggat	1440
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ctgtaa	1506

<210> 8
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S-Tag introduced CaCCS via linker

<400> 8

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			20					25					30		

Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Met	Phe	His	Tyr	Arg	Asn
		35					40					45			

Lys Ser Ser Thr His Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser
50 55 60

Lys Pro Glu Ser Leu Asp Val Asn Ile Ser Trp Val Asp Thr Asp Leu
65 70 75 80

Asp Gly Ala Glu Phe Asp Val Ile Ile Ile Gly Thr Gly Pro Ala Gly
85 90 95

Leu Arg Leu Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys
100 105 110

Val Asp Pro Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp
115 120 125

Val Asp Glu Phe Glu Lys Leu Gly Leu Glu Asp Cys Leu Asp His Lys
130 135 140

Trp Pro Val Ser Cys Val His Ile Ser Asp His Lys Thr Lys Tyr Leu
145 150 155 160

Asp Arg Pro Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu
165 170 175

Leu Asn Ser Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val
180 185 190

Leu Lys Val Lys His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp
195 200 205

Gly Arg Lys Ile Ser Gly Ser Leu Ile Val Asp Ala Ser Gly Tyr Ala
210 215 220

Ser Asp Phe Ile Glu Tyr Asp Lys Pro Arg Asn His Gly Tyr Gln Val
225 230 235 240

Ala His Gly Ile Leu Ala Glu Val Asp Asn His Pro Phe Asp Leu Asp
245 250 255

Lys Met Met Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro

260

265

270

Tyr Leu Arg Val Lys Asn Thr Lys Glu Pro Thr Phe Leu Tyr Ala Met
 275 280 285

Pro Phe Asp Arg Asn Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser
 290 295 300

Arg Pro Met Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg
 305 310 315 320

Leu Arg His Leu Gly Ile Lys Val Arg Ser Val Leu Glu Glu Glu Lys
 325 330 335

Cys Val Ile Thr Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val
 340 345 350

Met Ala Ile Gly Gly Thr Ser Gly Ile Val His Pro Ser Ser Gly Tyr
 355 360 365

Met Val Ala Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile
 370 375 380

Val Glu Ser Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr
 385 390 395 400

His Arg Val Trp Asn Gly Leu Trp Pro Ser Asp Arg Arg Arg Val Arg
 405 410 415

Glu Cys Tyr Cys Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Glu
 420 425 430

Gly Thr Arg Arg Leu Phe Asp Ala Phe Phe Asp Val Asp Pro Lys Tyr
 435 440 445

Trp His Gly Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Ala Val
 450 455 460

Leu Ser Leu Tyr Leu Phe Gly His Ala Ser Asn Leu Ala Arg Leu Asp
 465 470 475 480

Ile Val Thr Lys Cys Thr Val Pro Leu Val Lys Leu Leu Gly Asn Leu
485 490 495

Ala Ile Glu Ser Leu
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<210> 9
<211> 2073
<212> DNA
<213> Artificial Sequence

<220>
<223> S-Tag introduced CaZEP

<400> 9
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ccgagcacca gcgtgttttag ccgcaaacag ctgccgctgc tgattagcaa agattttccg 180
gccgaactgt atcatagcct gccgtgcaaa agcctggaaa atggatcatat taagaaagtg 240
aaaggcggtta aagccaccct ggccgaagca ccggccaccc cgaccgaaaa atctaacagc 300
gaagtgccgc agaaaaaact gaaagtgctg gttgccggcg gtggcattgg tggcctgggtg 360
tttgcgctgg cggcgaaaaa gaaaggcttt gatgtgctgg tttttgaacg tgatctgagc 420
gccatccgcg gcgaaggcca gtatcgtggc ccgattcaga tccagagcaa tgccctggcg 480
gccctggaag cgattgatat ggatgtggcc gaagaaatca tgaacgcggg ttgcattacc 540
ggccagcgta tcaatggtct ggttgatggt attagcggca actggtattg taaatttgat 600
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gttcatgccca tgcagccgaa cctgggtcag ggcggttgta tggccattga agatagctat 1260
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ttcgtgaccg attttcagag cgaacatggt acctgggtta tcgataatga aggccgtcgc 1920
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aaagaagaac gtaaagtggg tggcaccgcg taa 2073

<210> 10
<211> 690
<212> PRT
<213> Artificial Sequence

<220>
<223> S-Tag introduced CaZEP

<400> 10

Met Ser Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln Phe Met Asp
1 5 10 15

Ser Ser Thr Ser Ala Ala Met Thr Met Ile Thr Asn Ser Met Tyr Ser
20 25 30

Thr Val Phe Tyr Thr Ser Val His Pro Ser Thr Ser Val Phe Ser Arg

35

40

45

Lys Gln Leu Pro Leu Leu Ile Ser Lys Asp Phe Pro Ala Glu Leu Tyr
 50 55 60

His Ser Leu Pro Cys Lys Ser Leu Glu Asn Gly His Ile Lys Lys Val
 65 70 75 80

Lys Gly Val Lys Ala Thr Leu Ala Glu Ala Pro Ala Thr Pro Thr Glu
 85 90 95

Lys Ser Asn Ser Glu Val Pro Gln Lys Lys Leu Lys Val Leu Val Ala
 100 105 110

Gly Gly Gly Ile Gly Gly Leu Val Phe Ala Leu Ala Ala Lys Lys Lys
 115 120 125

Gly Phe Asp Val Leu Val Phe Glu Arg Asp Leu Ser Ala Ile Arg Gly
 130 135 140

Glu Gly Gln Tyr Arg Gly Pro Ile Gln Ile Gln Ser Asn Ala Leu Ala
 145 150 155 160

Ala Leu Glu Ala Ile Asp Met Asp Val Ala Glu Glu Ile Met Asn Ala
 165 170 175

Gly Cys Ile Thr Gly Gln Arg Ile Asn Gly Leu Val Asp Gly Ile Ser
 180 185 190

Gly Asn Trp Tyr Cys Lys Phe Asp Thr Phe Thr Pro Ala Val Glu Arg
 195 200 205

Gly Leu Pro Val Thr Arg Val Ile Ser Arg Met Thr Leu Gln Gln Ile
 210 215 220

Leu Ala Arg Ala Val Gly Glu Asp Val Ile Met Asn Glu Ser Asn Val
 225 230 235 240

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

Gly Gln Arg Phe Thr Gly Asp Leu Leu Val Gly Ala Asp Gly Ile Arg
260 265 270

Ser Lys Val Arg Thr Asn Leu Phe Gly His Ser Glu Ala Thr Tyr Ser
275 280 285

Gly Tyr Thr Cys Tyr Thr Gly Ile Ala Asp Phe Val Pro Ala Asp Ile
290 295 300

Asp Thr Val Gly Tyr Arg Val Phe Leu Gly His Lys Gln Tyr Phe Val
305 310 315 320

Ser Ser Asp Val Gly Gly Gly Lys Met Gln Trp Tyr Ala Phe His Asn
325 330 335

Glu Pro Ala Gly Gly Val Asp Ala Pro Asn Gly Lys Lys Glu Arg Leu
340 345 350

Leu Lys Ile Phe Gly Gly Trp Cys Asp Asn Val Ile Asp Leu Leu Val
355 360 365

Ala Thr Asp Glu Asp Ala Ile Leu Arg Arg Asp Ile Tyr Asp Arg Pro
370 375 380

Pro Thr Phe Asn Trp Gly Arg Gly Arg Val Thr Leu Leu Gly Asp Ser
385 390 395 400

Val His Ala Met Gln Pro Asn Leu Gly Gln Gly Gly Cys Met Ala Ile
405 410 415

Glu Asp Ser Tyr Gln Leu Ala Leu Glu Leu Glu Lys Ala Trp Ser Arg
420 425 430

Ser Ala Glu Ser Gly Ser Pro Met Asp Val Ile Ser Ser Leu Arg Ser
435 440 445

Tyr Glu Ser Ala Arg Lys Leu Arg Val Gly Val Ile His Gly Leu Ala
450 455 460

Arg Met Ala Ala Ile Met Ala Ser Thr Tyr Lys Ala Tyr Leu Gly Val

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

<210> 11
<211> 2133
<212> DNA
<213> Artificial Sequence

<220>
<223> S-Tag introduced CaZEP via linker

<400> 11
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ggttcaatga ccatgattac gaattcgatg tatagcaccc tgttttatac cagcgttcat 180
ccgagcacca gcgtgttttag ccgcaaacag ctgccgctgc tgattagcaa agatthttccg 240
gccgaactgt atcatagcct gccgtgcaaa agcctggaaa atggtcatat taagaaagtg 300
aaaggcgtha aagccaccct ggccgaagca ccggccaccc cgaccgaaaa atctaacagc 360
gaagtgccgc agaaaaaact gaaagtgtg gttgccggcg gtggcattgg tggcctgggtg 420
tttgcgctgg cggcgaaaaa gaaaggctth gatgtgtctg tttttgaacg tgatctgagc 480
gccatccgcg gcgaaggcca gtatcgtggc ccgattcaga tccagagcaa tgccctggcg 540
gccctggaag cgattgatat ggatgtggcc gaagaaatca tgaacgcggg ttgcattacc 600
ggccagcgta tcaatggtct ggttgatggg attagcggca actgggtattg taaatttgat 660
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 <211> 710
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S-Tag introduced CaZEP via linker

<400> 12

Met	Ser	Lys	Glu	Thr	Ala	Ala	Ala	Lys	Phe	Glu	Arg	Gln	Phe	Met	Asp
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Ser	Ser	Thr	Ser	Ala	Ala	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser
			20					25					30		

Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Met	Thr	Met	Ile	Thr	Asn
		35					40				45				

Ser Met Tyr Ser Thr Val Phe Tyr Thr Ser Val His Pro Ser Thr Ser
50 55 60

Val Phe Ser Arg Lys Gln Leu Pro Leu Leu Ile Ser Lys Asp Phe Pro
65 70 75 80

Ala Glu Leu Tyr His Ser Leu Pro Cys Lys Ser Leu Glu Asn Gly His
85 90 95

Ile Lys Lys Val Lys Gly Val Lys Ala Thr Leu Ala Glu Ala Pro Ala
100 105 110

Thr Pro Thr Glu Lys Ser Asn Ser Glu Val Pro Gln Lys Lys Leu Lys
115 120 125

Val Leu Val Ala Gly Gly Gly Ile Gly Gly Leu Val Phe Ala Leu Ala
130 135 140

Ala Lys Lys Lys Gly Phe Asp Val Leu Val Phe Glu Arg Asp Leu Ser
145 150 155 160

Ala Ile Arg Gly Glu Gly Gln Tyr Arg Gly Pro Ile Gln Ile Gln Ser
165 170 175

Asn Ala Leu Ala Ala Leu Glu Ala Ile Asp Met Asp Val Ala Glu Glu
180 185 190

Ile Met Asn Ala Gly Cys Ile Thr Gly Gln Arg Ile Asn Gly Leu Val
195 200 205

Asp Gly Ile Ser Gly Asn Trp Tyr Cys Lys Phe Asp Thr Phe Thr Pro
210 215 220

Ala Val Glu Arg Gly Leu Pro Val Thr Arg Val Ile Ser Arg Met Thr
225 230 235 240

Leu Gln Gln Ile Leu Ala Arg Ala Val Gly Glu Asp Val Ile Met Asn
245 250 255

Glu Ser Asn Val Val Asn Phe Glu Asp Asp Gly Glu Lys Val Thr Val

260	265	270
Val Leu Glu Asn Gly Gln Arg Phe Thr Gly Asp Leu Leu Val Gly Ala		
275	280	285
Asp Gly Ile Arg Ser Lys Val Arg Thr Asn Leu Phe Gly His Ser Glu		
290	295	300
Ala Thr Tyr Ser Gly Tyr Thr Cys Tyr Thr Gly Ile Ala Asp Phe Val		
305	310	315
Pro Ala Asp Ile Asp Thr Val Gly Tyr Arg Val Phe Leu Gly His Lys		
325	330	335
Gln Tyr Phe Val Ser Ser Asp Val Gly Gly Gly Lys Met Gln Trp Tyr		
340	345	350
Ala Phe His Asn Glu Pro Ala Gly Gly Val Asp Ala Pro Asn Gly Lys		
355	360	365
Lys Glu Arg Leu Leu Lys Ile Phe Gly Gly Trp Cys Asp Asn Val Ile		
370	375	380
Asp Leu Leu Val Ala Thr Asp Glu Asp Ala Ile Leu Arg Arg Asp Ile		
385	390	395
Tyr Asp Arg Pro Pro Thr Phe Asn Trp Gly Arg Gly Arg Val Thr Leu		
405	410	415
Leu Gly Asp Ser Val His Ala Met Gln Pro Asn Leu Gly Gln Gly Gly		
420	425	430
Cys Met Ala Ile Glu Asp Ser Tyr Gln Leu Ala Leu Glu Leu Glu Lys		
435	440	445
Ala Trp Ser Arg Ser Ala Glu Ser Gly Ser Pro Met Asp Val Ile Ser		
450	455	460
Ser Leu Arg Ser Tyr Glu Ser Ala Arg Lys Leu Arg Val Gly Val Ile		
465	470	475
		480

His Gly Leu Ala Arg Met Ala Ala Ile Met Ala Ser Thr Tyr Lys Ala
485 490 495

Tyr Leu Gly Val Gly Leu Gly Pro Leu Ser Phe Leu Thr Lys Tyr Arg
500 505 510

Ile Pro His Pro Gly Arg Val Gly Gly Arg Val Phe Val Asp Leu Gly
515 520 525

Met Pro Leu Met Leu Ser Trp Val Leu Gly Gly Asn Gly Asp Lys Leu
530 535 540

Glu Gly Arg Ile Gln His Cys Arg Leu Ser Glu Lys Ala Asn Asp Gln
545 550 555 560

Leu Arg Arg Trp Phe Glu Asp Asp Asp Ala Leu Glu Arg Ala Thr Asp
565 570 575

Ala Glu Trp Leu Leu Leu Pro Ala Ala Asn Gly Asn Ser Ala Leu Glu
580 585 590

Thr Ile Val Leu Ser Arg Asp Glu Asp Val Pro Cys Thr Ile Gly Ser
595 600 605

Val Ser His Thr Asn Ile Pro Gly Lys Ser Val Val Leu Pro Leu Pro
610 615 620

Gln Val Ser Glu Met His Ala Gln Ile Ser Cys Lys Asn Asn Ala Phe
625 630 635 640

Phe Val Thr Asp Phe Gln Ser Glu His Gly Thr Trp Val Ile Asp Asn
645 650 655

Glu Gly Arg Arg Tyr Arg Val Ser Pro Asn Phe Pro Met Arg Phe His
660 665 670

Ser Ser Asp Val Ile Val Phe Gly Ser Asp Lys Ala Ala Phe Arg Val
675 680 685

Lys Thr Met Lys Phe Pro Ser Lys Thr Ala Glu Ala Lys Glu Glu Arg

690

695

700

Lys Val Val Gly Thr Ala
705 710