

146392026040SEQLIST

SEQUENCE LISTING

<110> Marc WONG
Liliana T. YEE
Amy LIM
Chris B. FONG

<120> ULTRAPURIFIED Dsba AND Dsbc AND METHODS OF MAKING AND USING THE SAME

<130> 146392026040

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> US 62/129,701

<151> 2015-03-06

<160> 6

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 189

<212> PRT

<213> E. coli

<400> 1

Ala	Gln	Tyr	Glu	Asp	Gly	Lys	Gln	Tyr	Thr	Thr	Leu	Glu	Lys	Pro	Val
1				5					10					15	
Ala	Gly	Ala	Pro	Gln	Val	Leu	Glu	Phe	Phe	Ser	Phe	Phe	Cys	Pro	His
			20					25					30		
Cys	Tyr	Gln	Phe	Glu	Glu	Val	Leu	His	Ile	Ser	Asp	Asn	Val	Lys	Lys
		35					40					45			
Lys	Leu	Pro	Glu	Gly	Val	Lys	Met	Thr	Lys	Tyr	His	Val	Asn	Phe	Met
	50					55					60				
Gly	Gly	Asp	Leu	Gly	Lys	Asp	Leu	Thr	Gln	Ala	Trp	Ala	Val	Ala	Met
65					70				75						80
Ala	Leu	Gly	Val	Glu	Asp	Lys	Val	Thr	Val	Pro	Leu	Phe	Glu	Gly	Val
				85					90					95	
Gln	Lys	Thr	Gln	Thr	Ile	Arg	Ser	Ala	Ser	Asp	Ile	Arg	Asp	Val	Phe
			100					105					110		
Ile	Asn	Ala	Gly	Ile	Lys	Gly	Glu	Tyr	Asp	Ala	Ala	Trp	Asn	Ser	
		115					120				125				
Phe	Val	Val	Lys	Ser	Leu	Val	Ala	Gln	Gln	Glu	Lys	Ala	Ala	Ala	Asp
	130					135					140				
Val	Gln	Leu	Arg	Gly	Val	Pro	Ala	Met	Phe	Val	Asn	Gly	Lys	Tyr	Gln
145					150				155					160	
Leu	Asn	Pro	Gln	Gly	Met	Asp	Thr	Ser	Asn	Met	Asp	Val	Phe	Val	Gln
			165						170					175	
Gln	Tyr	Ala	Asp	Thr	Val	Lys	Tyr	Leu	Ser	Glu	Lys	Lys			
			180					185							

<210> 2

<211> 627

<212> DNA

<213> E. coli

<400> 2

atgaaaaaga	tttggtgctggc	gctggctggt	ttagtttttag	cgtttagcgc	atcggcgggcg	60
cagtatgaag	atggtaaaca	gtacactacc	ctggaaaaac	cggtagctgg	cgcgccgcaa	120
gtgctggagt	ttttctcttt	cttctgcccc	cactgctatc	agtttgaaga	agttctgcat	180
atttctgata	atgtgaagaa	aaaactgccc	gaaggcgtga	agatgactaa	ataccacgtc	240
aacttcatgg	gtggtgacct	gggcaaagat	ctgactcagg	catgggctgt	ggcgatggcg	300
ctgggcgtgg	aagacaaagt	gactgttccg	ctgtttgaag	gcgtacagaa	aaccagacc	360
attcgttctg	cttctgatat	ccgcgatgta	tttatcaacg	caggtattaa	aggtgaagag	420
tacgacgcgg	cgtggaacag	cttcgtggtg	aaatctctgg	tcgctcagca	ggaaaaagct	480

146392026040SEQLIST

gcagctgacg tgcaattgcg tggcggttccg gcgatgtttg ttaacggtaa atatcagctg 540
aatccgcagg gtatggatac cagcaatatg gatgtttttg ttcagcagta tgctgataca 600
gtgaaatatc tgtccgagaa aaaataa 627

<210> 3
<211> 216
<212> PRT
<213> E. coli

<400> 3
Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met Gly Ile Lys Ser
1 5 10 15
Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys Thr Val Leu Thr
20 25 30
Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys His Ile Ile Gln
35 40 45
Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val Asn Val Thr Asn
50 55 60
Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys Glu Met Ile Val
65 70 75 80
Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val Phe Thr Asp Ile
85 90 95
Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met Ala Asp Tyr Asn
100 105 110
Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro Arg Gln Gly Leu
115 120 125
Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp Cys Ala Lys Asp
130 135 140
Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys Ser Val Ala Pro
145 150 155 160
Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala Leu Gly Val Gln
165 170 175
Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser Asn Gly Thr Leu
180 185 190
Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu
195 200 205
His Gln Lys Met Thr Ser Gly Lys
210 215

<210> 4
<211> 711
<212> DNA
<213> E. coli

<400> 4
atgaagaaag gttttatggt gtttactttg ttagcggcgt tttcaggctt tgctcaggct 60
gatgacgcgg caattcaaca aacgttagcc aaaatgggca tcaaaagcag cgatattcag 120
cccgcgcctg tagctggcat gaagacagtt ctgactaaca gcggcgtgtt gtacatcacc 180
gatgatggta aacatatcat tcagggggcca atgtatgacg ttagtggcac ggctccggtc 240
aatgtcacca ataagatgct gttaaagcag ttgaatgcgc ttgaaaaaga gatgatcggt 300
tataaagcgc cgcaggaaaa acacgtcatc accgtgttta ctgatattac ctgtgggttac 360
tgccacaaac tgcattagca aatggcagac tacaacgcgc tggggatcac cgtgcgttat 420
cttgctttcc cgcgccaggg gctggacagc gatgcagaga aagaaatgaa agctatctgg 480
tgtgcgaaag ataaaaacaa agcgtttgat gatgtgatgg caggtaaaag cgtcgacca 540
gccagttgcg acgtggatat tgccgaccat tacgcacttg gcgtccagct tggcgtagc 600
ggtactccgg cagttgtgct gagcaatggc acacttgttc cgggttacca gccgccgaaa 660
gagatgaaag aattcctcga cgaacaccaa aaaatgacca gcggtaaata a 711

<210> 5
<211> 208
<212> PRT
<213> E. coli

<400> 5
Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1 5 10 15
Ala Ser Ala Ala Gln Tyr Glu Asp Gly Lys Gln Tyr Thr Thr Leu Glu

146392026040SEQLIST

```

      20      25      30
Lys Pro Val Ala Gly Ala Pro Gln Val Leu Glu Phe Phe Ser Phe Phe
      35      40      45
Cys Pro His Cys Tyr Gln Phe Glu Glu Val Leu His Ile Ser Asp Asn
      50      55      60
Val Lys Lys Lys Leu Pro Glu Gly Val Lys Met Thr Lys Tyr His Val
      65      70      75
Asn Phe Met Gly Gly Asp Leu Gly Lys Asp Leu Thr Gln Ala Trp Ala
      85      90      95
Val Ala Met Ala Leu Gly Val Glu Asp Lys Val Thr Val Pro Leu Phe
      100      105      110
Glu Gly Val Gln Lys Thr Gln Thr Ile Arg Ser Ala Ser Asp Ile Arg
      115      120      125
Asp Val Phe Ile Asn Ala Gly Ile Lys Gly Glu Glu Tyr Asp Ala Ala
      130      135      140
Trp Asn Ser Phe Val Val Lys Ser Leu Val Ala Gln Gln Glu Lys Ala
      145      150      155
Ala Ala Asp Val Gln Leu Arg Gly Val Pro Ala Met Phe Val Asn Gly
      165      170      175
Lys Tyr Gln Leu Asn Pro Gln Gly Met Asp Thr Ser Asn Met Asp Val
      180      185      190
Phe Val Gln Gln Tyr Ala Asp Thr Val Lys Tyr Leu Ser Glu Lys Lys
      195      200      205

```

<210> 6
 <211> 236
 <212> PRT
 <213> E. coli

```

<400> 6
Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
  1      5      10      15
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
      20      25      30
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
      35      40      45
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
      50      55      60
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
      65      70      75
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
      85      90      95
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
      100      105      110
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
      115      120      125
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
      130      135      140
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
      145      150      155
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
      165      170      175
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
      180      185      190
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
      195      200      205
Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
      210      215      220
Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
      225      230      235

```