

SEQUENCE LISTING

<110> Eli Lilly and Company

<120> 2,3-DIHYDRO-1H-INDOLE COMPOUNDS

<130> X21056

<150> 62/348457

<151> 2016-06-10

<160> 13

<170> PatentIn version 3.5

<210> 1

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 1

Met	Arg	Ile	Phe	Ala	Val	Phe	Ile	Phe	Met	Thr	Tyr	Trp	His	Leu	Leu
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Asn	Ala	Phe	Thr	Val	Thr	Val	Pro	Lys	Asp	Leu	Tyr	Val	Val	Glu	Tyr
			20					25					30		

Gly	Ser	Asn	Met	Thr	Ile	Glu	Cys	Lys	Phe	Pro	Val	Glu	Lys	Gln	Leu
		35					40					45			

Asp	Leu	Ala	Ala	Leu	Ile	Val	Tyr	Trp	Glu	Met	Glu	Asp	Lys	Asn	Ile
	50					55					60				

Ile	Gln	Phe	Val	His	Gly	Glu	Glu	Asp	Leu	Lys	Val	Gln	His	Ser	Ser
65					70					75					80

Tyr	Arg	Gln	Arg	Ala	Arg	Leu	Leu	Lys	Asp	Gln	Leu	Ser	Leu	Gly	Asn
				85					90					95	

Ala	Ala	Leu	Gln	Ile	Thr	Asp	Val	Lys	Leu	Gln	Asp	Ala	Gly	Val	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
115 120 125

Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
130 135 140

Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
145 150 155 160

Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
165 170 175

Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
180 185 190

Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
195 200 205

Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
210 215 220

Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225 230 235 240

Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
245 250 255

Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
260 265 270

Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
275 280 285

Glu Thr
290

<210> 2
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser
1 5 10

<210> 3
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 3

Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 4
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 4

Ala Arg Ser Pro Asp Tyr Ser Pro Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 5
<211> 13
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 5

Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn
1 5 10

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 6

Tyr Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 7

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 7

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val
1 5 10

<210> 8

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 8

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr	20	25	30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35	40	45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe	50	55	60
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr	65	70	75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Arg Ser Pro Asp Tyr Ser Pro Tyr Tyr Tyr Tyr Gly Met Asp Val	100	105	110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	115	120	

<210> 9
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 9

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln	1	5	10	15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn	20	25	30	
Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu				

35

40

45

Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu
 85 90 95

Ser Gly Ser Val Phe Gly Gly Gly Ile Lys Leu Thr Val Leu Gly
 100 105 110

<210> 10

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 10

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Ser Pro Asp Tyr Ser Pro Tyr Tyr Tyr Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
 210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 225 230 235 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser
325 330 335

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 11
<211> 216
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 11

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu
85 90 95

Ser Gly Ser Val Phe Gly Gly Gly Ile Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His

180

185

190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205

Thr Val Ala Pro Ala Glu Cys Ser
 210 215

<210> 12
 <211> 1359
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 12
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 ccagggcagg gtctggagtg gatgggcgga atcattccca tcttcgggac cgccaactac 180
 gctcagaagt ttcagggaag ggtcactatt accgccgaca aaagcacatc tactgcttat 240
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 gactatagcc cttactatta ctatggcatg gatgtctggg gccagggaac cacagtgaca 360
 gtctcatccg ctagcaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 420
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 gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaagcc 720
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 ttcaactggt atgtggacgg cgtggagggt cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca agactggctg	960
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccatcctc catcgagaaa	1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	1080
cgggaggaga tgaccaagaa ccaagtcagc ctgacctgcc tggtaaagg cttctatccc	1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1200
cctcccgatg tggactccga cggctccttc ttcctctatt ccaagctcac cgtggacaag	1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac	1320
cactacacgc agaagagcct ctccctgtct ccgggcaaa	1359

<210> 13
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 13	
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cccggcacag cacctaagct gctgatctat ggaaactcaa ataggccatc cggagtcccc	180
gaccgggttct ctggtagtaa atcaggcact tccgccagcc tggctattag cgggctgcag	240
tctgaggacg aagccgatta ctattgccag tcttacgatt ccagcctgtc tgggaagtgtg	300
tttggcggag ggatcaagct gaccgtcctg ggccagccta aggctgcccc ctcggtcact	360
ctgttccccg cctcctctga ggagcttcaa gccaacaagg ccacactggg gtgtctcata	420
agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtaag	480
gcgggagtg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc	540
tacctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg	600
catgaaggga gcaccgtgga gaagacagtg gcccctgcag aatgctct	648