

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> A Method of Averting Opioid Addiction

<130> REGN-025W0

<140> TBA (Filed Herewith)

<141> 2017-11-28

<150> 62/427,365

<151> 2016-11-29

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> DNA

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cctggaaaag  ggcttgagtg  gatgggaggt  tttgatcctg  aagatgggtg  aacaatctac  180
gcacagaagt  tccagggcag  agtcaccatg  accgaggaca  catctacaga  cacagcctac  240
atggagctga  ccagcctgag  atcggaagac  acggccgtgt  attactgttc  aacgattttt  300
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 20            25            30
Ser Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35            40            45
Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
 50            55            60
Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 65            70            75            80
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Met	Glu	Leu	Thr	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ser	Thr	Ile	Phe	Gly	Val	Val	Thr	Asn	Phe	Asp	Asn	Trp	Gly	Gln	Gly
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Thr	Leu	Val	Thr	Val	Ser	Ser									
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24

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 Gly Phe Thr Leu Thr Glu Leu Ser
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<210> 5
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<400> 5
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<220>
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<210> 7
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<211> 12
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gggaaagccc ctaagcgcct gatctatgct gcattcaatt tgcaaagtgg ggtcccatca 180
agattcagcg gcagtggatc tgggacagaa ttcactctca caatcagtag cctgcagcct 240
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20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile

		35				40				45					
Tyr	Ala	Ala	Phe	Asn	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Glu	Asp	Leu	Ala	Ser	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Arg	Tyr	Pro	Trp
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Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg				
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<220>
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<400> 11
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<400> 12
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<400> 13
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acaggcgga ccacactcag agagcaatgt ccctgcagga cacaccatcc cccaagccca 180
ctggactaaa cttcagcatt cccttgacac tgcccttcgc agagcccgca gcgccccggc 240
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agctgcagac actcaggatc tggacttcga ggtcgggtgt gctgccccct tcaacaggac 420
tcacaggagc aagcgggtcat catcccatcc catcttccac aggggcgaat tctcgggtgtg 480
tgacagtgtc agcgtgtggg ttggggataa gaccaccgcc acagacatca agggcaagga 540
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gaccaagtgc cgggacccaa atcccgttga cagcgggtgc cggggcattg actcaaagca 660
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gcagggtgcc tggcggttta tccggataga tacggcctgt atgtgtgtgc tcagcaggaa 780
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<212> PRT

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<400> 18

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			20					25					30				
Val	Met	Val	Leu	Gly	Glu	Val	Asn	Ile	Asn	Asn	Ser	Val	Phe	Lys	Gln		
			35				40					45					
Tyr	Phe	Phe	Glu	Thr	Lys	Cys	Arg	Asp	Pro	Asn	Pro	Val	Asp	Ser	Gly		
	50					55					60						
Cys	Arg	Gly	Ile	Asp	Ser	Lys	His	Trp	Asn	Ser	Tyr	Cys	Thr	Thr	Thr		
65					70					75					80		
His	Thr	Phe	Ala	Leu	Thr	Met	Asp	Gly	Lys	Gln	Ala	Ala	Trp	Arg	Phe		
			85					90						95			
Ile	Arg	Ile	Asp	Thr	Ala	Cys	Val	Cys	Val	Leu	Ser	Arg	Lys	Ala	Val		
			100					105					110				
Arg	Arg	Ala															
		115															