

51 426 K.ST25
SEQUENCE LISTING

<110> PAION Deutschland GmbH
Inserm Transfer

<120> Treatment of neurological or neurodegenerative disorders

<130> 51 426 K

<160> 7

<170> PatentIn version 3.3

<210> 1

<211> 82

<212> PRT

<213> Homo sapiens

<220>

<221> Kringle DOMAIN

<222> (1)..(82)

<223> t-PA_kringle 1

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Cys Tyr Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala
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Glu Ser Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln
20 25 30

Lys Pro Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly
35 40 45

Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys
50 55 60

Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro
65 70 75 80

Ala Cys

<210> 2

<211> 82

<212> PRT

<213> homo sapiens

<220>

<221> Kringle DOMAIN

<222> (1)..(82)

<223> t-PA_kringle 2

<400> 2

Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His Ser Leu Thr
1 5 10 15

51 426 K.ST25
 Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile Leu Ile Gly
 20 25 30
 Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu Gly
 35 40 45
 Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys
 50 55 60
 His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro
 65 70 75 80

Ser Cys

<210> 3
 <211> 82
 <212> PRT
 <213> Desmodus rotundus

<220>
 <221> Kringle DOMAIN
 <222> (1)..(82)
 <223> kringle domain of DSPA alpha 1

<400> 3

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

Val Cys

<210> 4
 <211> 353
 <212> PRT
 <213> Rattus norvegicus

<220>
 <221> N-terminal sequence without signal peptide
 <222> (1)..(353)
 <223> as 19 to 371 of rat NR1-1a (NP_058706.1)

<400> 4

Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val Leu Ser
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 Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln Ala Asn
 20 25 30
 Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser Val Thr
 35 40 45
 His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu Asp Leu
 50 55 60
 Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro Thr Pro
 65 70 75 80
 Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly Phe Tyr
 85 90 95
 Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr Ser Asp
 100 105 110
 Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr Ser His
 115 120 125
 Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Asn Trp Asn His
 130 135 140
 Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala Gln Lys
 145 150 155 160
 Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu Lys Val
 165 170 175
 Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu
 180 185 190
 Ala Arg Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp
 195 200 205
 Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly
 210 215 220
 Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly Asn Ala
 225 230 235 240
 Leu Arg Tyr Ala Pro Asp Gly Ile Ile Gly Leu Gln Leu Ile Asn Gly
 245 250 255
 Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln
 260 265 270

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Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg
275 280 285

Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys
290 295 300

Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val
305 310 315 320

Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met
325 330 335

Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr
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His

<210> 5
<211> 353
<212> PRT
<213> homo sapiens

<220>
<221> N-terminal sequence without sequence peptide
<222> (1)..(353)
<223> as 19 to 371 of human NR1-1 (NP_000823.4)

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Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln Ala Asn
20 25 30

Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser Val Thr
35 40 45

His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu Asp Leu
50 55 60

Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro Thr Pro
65 70 75 80

Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly Phe Tyr
85 90 95

Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr Ser Asp
100 105 110

Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr Ser His
Seite 4

115

120

125

Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp Asn His
 130 135 140

Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala Gln Lys
 145 150 155 160

Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu Lys Val
 165 170 175

Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu
 180 185 190

Ala Arg Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp
 195 200 205

Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly
 210 215 220

Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly Asn Ala
 225 230 235 240

Leu Arg Tyr Ala Pro Asp Gly Ile Ile Gly Leu Gln Leu Ile Asn Gly
 245 250 255

Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln
 260 265 270

Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg
 275 280 285

Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys
 290 295 300

Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val
 305 310 315 320

Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met
 325 330 335

Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr
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His

<210> 6
 <211> 1059
 <212> DNA
 <213> rattus norvegicus

<220>
 <221> N-terminal_domain_without_signal_sequence
 <222> (1)..(1059)
 <223> nt 320 - 1378 of NM_017010.1| Rattus norvegicus glutamate
 receptor, ionotropic, N-methyl D-aspartate 1 (Grin1), mRNA

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tgtgaggacc tcattcttag ccaggcttac gctatcctag ttagccaccc gcctactccc    240
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<210> 7
 <211> 1059
 <212> DNA
 <213> homo sapiens

<220>
 <221> N-terminal_sequence_without_signal_peptide
 <222> (1)..(1059)
 <223> nt 388 - 1442 of NM_000832.5, Homo sapiens glutamate receptor,
 ionotropic, N-methyl D-aspartate 1 (GRIN1), transcript variant
 NR1-1, mRNA

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cagctcaatg ccacctcgt cacgcacaag cccaacgcca tccagatggc tctgtcgggtg    180
tgcgaggacc tcattctccag ccaggcttac gccatcctag ttagccatcc acctaccccc    240
aacgaccact tactccac ccctgtctcc tacacagccg gcttctaccg catacccgtg    300
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ctggggctga ccacccgcat gtccatctac tcggacaaga gcatccacct gagcttcctg	360
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agctggaacc acatcatcct gctggtcagc gacgaccacg agggccgggc ggctcagaaa	480
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