SEQUENCE LISTING

<110> ViGeneron GmbH

<120> An optimized acceptor splice site module for biological and biotechnological applications

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<151> 2018-12-20

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<223> pyrimidine tract

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<213> Unknown

<220>
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<210> 5
<211> 50
<212> DNA
<213> Unknown

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<223> ASS region

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<210> 6
<211> 38
<212> DNA
<213> Unknown

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<223> ASS region

<400> 6
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<210> 7
<211> 20
<212> DNA
<213> Unknown

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<223> ASS region

<400> 7
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<210> 8
<211> 39
<212> DNA
<213> Unknown

<220>
<223> ASS region

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<211> 166
<212> DNA
<213> Unknown

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<223> exon 3 of rhodopsin gene (containing the c.620T>G mutation

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gtacatcccc gagggcctgc agtgctcgtg tggaatcgac tactacacgc tcaagccgga 60

ggtcaacaac gagtcttttg tcatctacag gttcgtggtc cacttcacca tccccatgat 120

tatcatcttt ttctgctatg ggcagctcgt cttcaccgtc aaggag 166

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<211> 1213
<212> DNA
<213> Unknown

<220>
<223> mutated rhodopsin

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<223> pyrimidine tract

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<210> 12
<211> 14
<212> DNA
<213> Unknown

<220>
<223> pyrimidine tract

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tcttttgtca tcta 14

<210> 13
<211> 21
<212> DNA
<213> Unknown

<220>
<223> pyrimidine tract

<400> 13
caacgagtct tttgtcatct a 21

<210> 14
<211> 130
<212> DNA
<213> Unknown

<220>
<223> inverted repeat

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aggggttcct 130

<210> 15
<211> 130
<212> DNA
<213> Unknown

<220>
<223> inverted repeat

<400> 15
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ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgcag 130

<210> 16
<211> 82
<212> DNA
<213> Unknown

<220>
<223> poly A sequence

<400> 16
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tataagctgc aataaacaag tt 82

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<212> DNA
<213> Unknown

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<223> first binding domain

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attaaacagc aggatgcaaa aattcgcagg tggtcagatg 100

<210> 18
<211> 100
<212> DNA
<213> Unknown

<220>

<223> second binding domain

<400> 18
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gtctggcttt ttttcactga tgtgatcgcc ttgatgcact 100

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<211> 4455
<212> DNA
<213> Unknown

<220>
<223> Sequence shown in Fig 5

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aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180

aggaagatcg gaattcgccc ttaagggcgc gccgtttaaa tagctagcga cattgattat 240

tgactagtta ttaatagtaa tcaattacgg ggtcattagt tcatagccca tatatggagt 300

tccgcgttac ataacttacg gtaaatggcc cgcctggctg accgcccaac gacccccgcc 360

cattgacgtc aataatgacg tatgttccca tagtaacgcc aatagggact ttccattgac 420

gtcaatgggt ggagtattta cggtaaactg cccacttggc agtacatcaa gtgtatcata 480

tgccaagtac gccccctatt gacgtcaatg acggtaaatg gcccgcctgg cattatgccc 540

agtacatgac cttatgggac tttcctactt ggcagtacat ctacgtatta gtcatcgcta 600

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cactatttct cattaaaaac atcggcctgt ctgactcagt ggtctacctt ctgatcaact 1380

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cgagcgagcg cgcag 4455

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<211> 4855
<212> DNA
<213> Unknown

<220>
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aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180

aggaagatcg gaattcgccc ttaagggcgc gccgtttaaa tagctagcga cattgattat 240

tgactagtta ttaatagtaa tcaattacgg ggtcattagt tcatagccca tatatggagt 300

tccgcgttac ataacttacg gtaaatggcc cgcctggctg accgcccaac gacccccgcc 360

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tgccaagtac gccccctatt gacgtcaatg acggtaaatg gcccgcctgg cattatgccc 540

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<212> DNA
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<223> Sequence shown in Figure 7

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aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180

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<211> 4790
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<213> Unknown

<220>
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<213> Unknown

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<223> ASS sequence

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<210> 24
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<212> DNA
<213> Unknown

<220>
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<211> 50
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<213> Unknown

<220>
<223> ASS sequence

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<210> 26
<211> 27
<212> DNA
<213> Unknown

<220>
<223> ASS sequence

<400> 26
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<210> 27
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> binding domain BD_g

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cggcagccac cttggctgtt cccaagtccc tcacaggcag gg 102

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<212> DNA
<213> Artificial Sequence

<220>
<223> Binding domain BD_h+i

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gctcggcagc caccttggct gttcccaagt ccctcacagg cagggg 105

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<213> Artificial Sequence

<220>
<223> Binding domain PTM1, B2

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<220>
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<210> 31
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<220>
<223> ITR2 reverse primer

<400> 31
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<210> 32
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<212> DNA
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<223> Binding domain BD_j

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gtcaggcttt ctttcaaaga tgtgatcgcc ttgcagcact 100

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<220>
<223> Binding domain BD_I

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atttaaccgc cagtcaggct ttctttcaaa gatgtggatt 100

<210> 34
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Binding domain BD_m

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atttaaccgc ctgtctggct ttctttcaat gatgtggatt 100

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<212> DNA
<213> Artificial Sequence

<220>
<223> 5' cerulean + BD_g

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acgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg ccaatagggа 180

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<211> 1710
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' cerulean + BD_g

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