



5' AGCTTATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGG 75
 3' TCGAATAGCTGACGTGCCACGTGGTTACGAAGACCGCAGTCCGTCGGTAGCCTTCGACACCATAACCGACACGTCC

TCGTAAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCC GTTCTGGATAATGTTTTTTGCGCCGACATCAT 150
 AGCATTTAGTGACGTATTAAGCACAGCGAGTTCGCGTGAGGGCAAGACCTATTACAAAAACGCGGCTGTAGTA

AACGGTTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAG 225
 TTGCCAAGACCGTTTATAAGACTTTACTCGACA ACTGTTAATTAGTAGCCGAGCATATTACACACCTTAACACTC

tac promoter lac operator

CGGATAACAATTTACACAGGAAACAGTATTCATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGC 300
 GCCTATTGTTAAAGTGTGTCCTTTGTCATAAGTACAGGGGATATGATCCAATAACCTTTTAATTCCCGGAACAG

lac operator

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	

GST

AACCCACTCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTGTATGAGCGGATGAAGGTGATA 375
 TTGGGTGAGCTGAAGAAAACCTTATAGA ACTTCTTTTATACTTCTCGTAAACATACTCGCGCTACTTCCACTAT

15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
Gln	Pro	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	His	Leu	Tyr	Glu	Arg	Asp	Glu	Gly	Asp			

GST

AATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAT 450
 TTACCGCTTTGTTTTTCAA ACTTAACCCAAACCTCAAAGGGTTAGAAGGAATAATATACTACCACTACAATTTA

40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65
Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	

GST

TAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAACATGTTGGGTGGTTGTCCAAAAGAGCGTG
ATTGTGTCAGATACCGGTAGTATGCAATATATCGACTGTTCTGTGTTGTACAACCCACCAACAGGTTTTCTCGCAC

525

65 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg
GST

CAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACT
GTCTCTAAAGTTACGAACCTCCTCGCCAAAACCTATAATCTATGCCACAAAGCTCTTAACGTATATCATTCTGA

600

90 Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp
GST

TTGAAACTCTCAAAGTTGATTTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCATA
AACTTTGAGAGTTTCAACTAAAAGAATCGTTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACAGTAT

675

115 Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His
GST

AAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACA
TTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCGAGAACTACAACAAAATATGT

750

140 Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr
GST

TGGACCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTGTTTTAAAAACGTATTGAAGCTATCCACAAATTG
ACCTGGGTTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTGCATAACTTCGATAGGGTGTGTTAAC

825

165 Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile
GST

ATAAGTACTTCAAATCCAGCAAGTATATAGCATGGCCTTTCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACC
TATTCATGAACCTTTAGGTCGTTTCATATATCGTACCGGAAACGTCCCGACCGTTTCGGTGCAAACCACCACCGCTGG

900

190 Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp
GST

ATCCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCTGGGATCCCCGAATTCCCGGGTCGACTCGAGCG
TAGGAGGTTTTAGCCTAGACCTTCAAGACAAGGTCCCGGGGACCCTAGGGGCTTAAGGGCCAGCTGAGCTCGC

975

215 His Pro Pro Lys Ser Asp Leu Glu Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Asn Ser Arg Val Asp Ser Ser
GST HRV 3C site (in frame with HRV 3C site) MCS

GCCGCATCGTGACTGACTGACGATCTGCCTCGCGCGTTTTGGTGATGACGGTGAAAACCTCTGACACATGCAGCT
CGGCGTAGCACTGACTGACTGCTAGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCTGA

1050

Gly Arg Ile Val Thr Asp *
-- (in frame with HRV 3C site) ▶

MCS