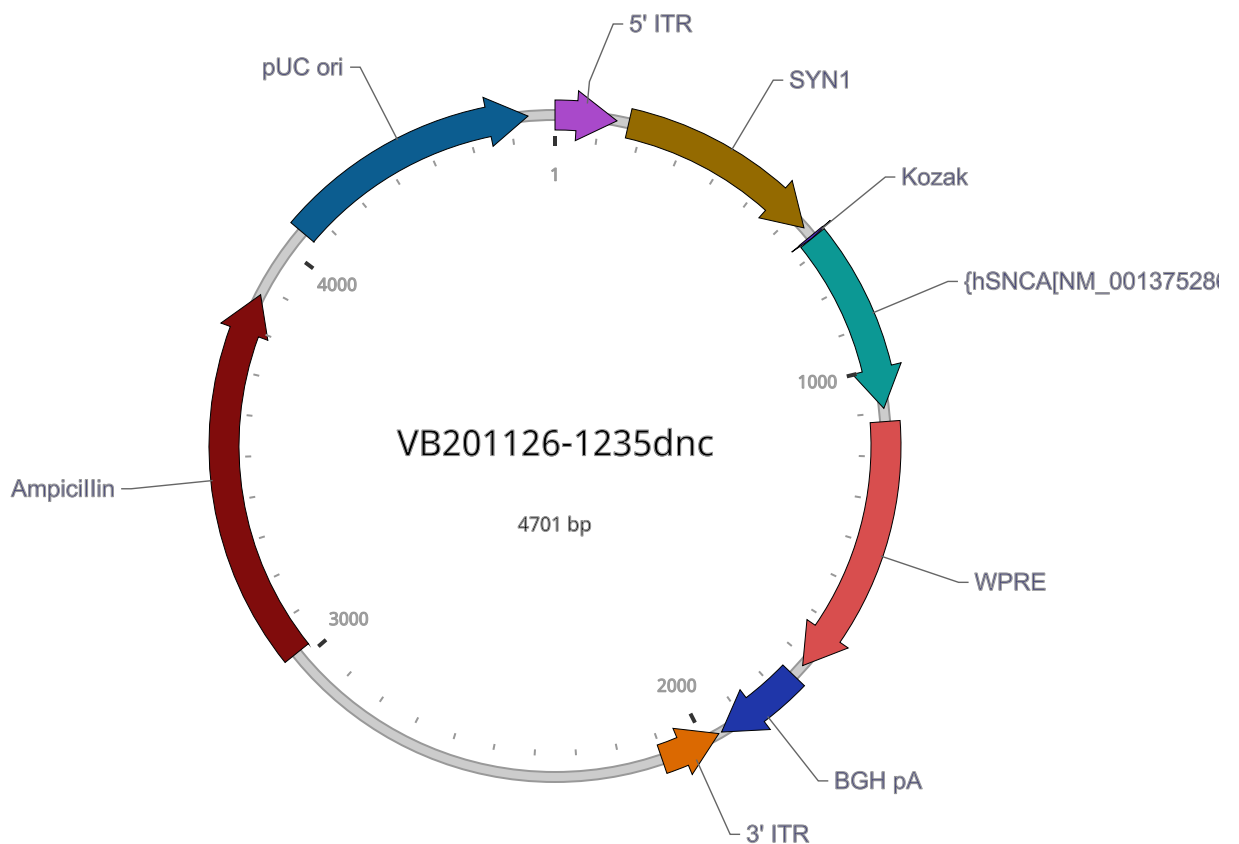


## Vector Summary

Vector ID	VB201126-1235dnc
Vector Name	pAAV[Exp]-SYN1>{hSNCA[NM_001375286.1]*(A53T)}:WPRE
Vector Size	4701 bp
Viral Genome Size	2104 bp
Vector Type	Mammalian Gene Expression AAV Vector
Inserted Promoter	SYN1
Inserted ORF	{hSNCA[NM_001375286.1]*(A53T)}
Inserted Regulatory Element	WPRE
Plasmid Copy Number	High
Antibiotic Resistance	Ampicillin
Cloning Host	VB UltraStable (or alternative strain)

## Vector Map



## Vector Components

Name	Position	Size (bp)	Type	Description	Application notes
5' ITR	■ 1-141	141	ITR	AAV 5' inverted terminal repeat (functional equivalent of wild-type 5' ITR)	Allows replication of the viral genome and its packaging into virus.
<b>SYN1</b>	■ 169-637	469	Promoter	Human synapsin I promoter	Tissue specificity: Brain. Cell type specificity: Mature neurons.
Kozak	■ 662-667	6	Miscellaneous	Kozak translation initiation sequence	Facilitates translation initiation of ATG start codon downstream of the Kozak sequence.
{hSNCA[NM_001375286.1]* (A53T)}	■ 668-1090	423	ORF	<i>None</i>	<i>None</i>
<b>WPRE</b>	■ 1121-1718	598	Miscellaneous	Woodchuck hepatitis virus posttranscriptional regulatory element	Enhances virus stability in packaging cells, leading to higher titer of packaged virus; enhances higher expression of transgenes.
BGH pA	■ 1749-1956	208	PolyA_signal	Bovine growth hormone polyadenylation signal	Allows transcription termination and polyadenylation of mRNA transcribed by Pol II RNA polymerase.
3' ITR	■ complement (1964-2104)	141	ITR	AAV 3' inverted terminal repeat	Allows replication of the viral genome and its packaging into virus.
Ampicillin	■ 3021-3881	861	ORF	Ampicillin resistance gene	Allows E. coli to be resistant to ampicillin.

Name	Position	Size (bp)	Type	Description	Application notes
pUC ori	■ 4052-4640	589	Rep_origin	pUC origin of replication	Facilitates plasmid replication in E. coli; regulates high-copy plasmid number (500-700).

Note: Components added by user are listed in **bold red** text.

## Vector Sequence

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1  CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG CCCGGGCGTC GGGCGACCTT TGGTCGCCCC
81  GCCTCAGTGA GCGAGCGAGC GCGCAGAGAG GGAGTGGCCA ACTCCATCAC TAGGGGTTC TTAGACAA CTTTGTATAG
161  AAAAGTTGCT GCAGAGGGCC CTGCGTATGA GTGCAAGTGG GTTTTAGGAC CAGGATGAGG CGGGGTGGGG GTGCCTACCT
241  GACGACCGAC CCCGACCCAC TGGACAAGCA CCCAACCCCC ATTCCCCAAA TTGCGCATCC CCTATCAGAG AGGGGGAGGG
321  GAAACAGGAT GCGGCGAGGC GCGTGCACAC TGCCAGCTTC AGCACCCGCG ACAGTGCCTT CGCCCCGCC TGGCGGCGCG
401  CGCCACCGCC GCCTCAGCAC TGAAGGCGCG CTGACGTCAC TCGCCGGTCC CCCGCAAAC CCCCTTCCCG GCCACCTTGG
481  TCGCGTCCGC GCCGCCGCCG GCCCAGCCGG ACCGCACCAC GCGAGGCGCG AGATAGGGGG GCACGGGCGC GACCATCTGC
561  GCTGCGGCGC CGGCGACTCA GCGCTGCCTC AGTCTGCGGT GGGCAGCGGA GGAGTCGTGT CGTGCCTGAG AGCGCAGCAA
641  GTTTGTACAA AAAAGCAGGC TGCCACCATG GATGTATTCA TGAAAGGACT TTCAAAGGCC AAGGAGGGAG TTGTGGCTGC
721  TGCTGAGAAA ACCAAACAGG GTGTGGCAGA AGCAGCAGGA AAGACAAAAG AGGGTGTCT CTATGTAGGC TCCAAAACCA
801  AGGAGGGAGT GGTGCATGGT GTGACAACAG TGGCTGAGAA GACCAAAGAG CAAGTGACAA ATGTTGGAGG AGCAGTGGTG
881  ACGGGTGTGA CAGCAGTAGC CCAGAAGACA GTGGAGGGAG CAGGGAGCAT TGCAGCAGCC ACTGGCTTTG TCAAAAAGGA
961  CCAGTTGGGC AAGAATGAAG AAGGAGCCCC ACAGGAAGGA ATTCTGGAAG ATATGCCTGT GGATCCTGAC AATGAGGCTT
1041  ATGAAATGCC TTCTGAGGAA GGGTATCAAG ACTACGAACC TGAAGCCTAA ACCCAGCTTT CTTGTACAAA GTGGGAATTC
1121  CGATAATCAA CCTCTGGATT ACAAATTTG TGAAAGATTG ACTGGTATTC TTAACATATG TGCTCCTTTT ACGCTATGTG
1201  GATACGCTGC TTTAATGCCT TTGTATCATG CTATTGCTTC CCGTATGGCT TTCATTTTCT CCTCCTTGTA TAAATCCTGG
1281  TTGCTGTCTC TTTATGAGGA GTTGTGGCCC GTTGTGAGGC AACGTGGCGT GGTGTGCACT GTGTTTGCTG ACGCAACCCC
1361  CACTGGTTGG GGCATTGCCA CCACCTGTCA GCTCCTTTCC GGGACTTTCG CTTTCCCCCT CCCTATTGCC ACGGCGGAAC
1441  TCATCGCCGC CTGCCTTGCC CGCTGCTGGA CAGGGGCTCG GCTGTTGGGC ACTGACAATT CCGTGGTGTG GTCGGGGAAG
1521  CTGACGTCTT TTCATAGGCT GCTCGCCTGT GTTGCCACCT GGATTCTGCG CGGGACGTCC TTCTGCTACG TCCCTTCGGC
1601  CCTCAATCCA GCGGACCTTC CTTCCCGCGG CTTGCTGCCG GCTCTGCGGC CTCTTCCGCG TCTTCGCTT CGCCCTCAGA
1681  CGAGTCGGAT CTCCTTTTGG GCCGCCTCCC CGCATCGGGA ATTCTAGAG CTCGCTGATC AGCCTCGACT GTGCCTTCTA
1761  GTTGCCAGCC ATCTGTTGTT TGCCCCTCCC CCGTGCCTTC CTGACCCTG GAAGGTGCCA CTCCCCTGT CTTTCTTAA
1841  TAAAATGAGG AAATTGCATC GCATTGTCTG AGTAGGTGTC ATTCTATTCT GGGGGGTGGG GTGGGGCAGG ACAGCAAGGG
1921  GGAGGATTGG GAAGAGAATA GCAGGCATGC TGGGGAGGGC CGCAGGAACC CCTAGTGATG GAGTTGGCCA CTCCCTCTCT
2001  GCGCGCTCGC TCGCTCACTG AGGCCGGGCG ACCAAAGGTC GCCCGACGCC CGGGCTTTGC CCGGGCGGCC TCAGTGAGCG
2081  AGCGAGCGCG CAGCTGCCTG CAGGGGCGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTTT ACACCGCATA
2161  CGTCAAAGCA ACCATAGTAC GCGCCCTGTA GCGGCGCATT AAGCGCGGCG GGGGTGGTGG TTACGCGCAG CGTGACCGCT
2241  AACTTGCCA GCGCCTTAGC GCCCGTCTCT TCGCTTTTCT TCCCTTCTT TCTCGCCACG TTCGCGGCT TTCCCCGTCA
2321  AGCTCTAAAT CGGGGCTCC CTTTAGGGTT CCGATTTAGT GCTTTACGGC ACCTCGACCC CAAAAAACTT GATTTGGGTG
2401  ATGGTTCACG TAGTGGGCCA TCGCCCTGAT AGACGGTTTT TCGCCCTTTG ACGTTGGAGT CCACGTTCTT TAATAGTGGA
2481  CTCTTGTTCC AAAGTGAAC AACACTCAAC TCTATCTCGG GCTATTCTTT TGATTTATAA GGGATTTTGC CGATTTCCGT
2561  CTATTGGTTA AAAAATGAGC TGATTTAACA AAAATTTAAC GCGAATTTTA ACAAATATT AACGTTTACA ATTTTATGGT
2641  GACTCTCAG TACAATCTGC TCTGATGCCG CATAGTTAAG CCAGCCCCGA CACCCGCCAA CACCCGCTGA CGCGCCCTGA
2721  CGGGCTTGTC TGCTCCCGGC ATCCGCTTAC AGACAAGCTG TGACCGTCTC CGGGAGCTGC ATGTGTCAGA GGTTTTACC

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2801  GTCATCACCG AAACGCGCGA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTAA  TGTCATGATA ATAATGGTTT
2881  CTTAGACGTC AGGTGGCACT TTTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG
2961  TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG
3041  TGTCGCCCTT ATTCCTTTT TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG
3121  CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC
3201  GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA
3281  GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG
3361  GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC
3441  GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT
3521  GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAAGTG
3601  GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC
3681  TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGAAGC CGCGGTATCA TTGCAGCACT
3761  GGGGCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC
3841  AGATCGTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
3921  TTAAACTTC ATTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAATCC CTTAACGTGA
4001  GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT
4081  GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG
4161  GTAAGTGGCT TCAGCAGAGC GCAGATACCA AATACTGTTC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAAGTC
4241  TGTAGCACCG CCTACATAAC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG
4321  GGTTGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG
4401  GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC
4481  GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT
4561  ATAGTCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA
4641  AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG T

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Deleted from original sequence:

▼ 824-1247

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## Validation by Restriction Enzyme Digestion

Restriction Enzymes	Cutting Sites	DNA Fragments (bp)
NcoI	667, 1534	867, 3834
ApaI	1335, 2640, 3137, 4383	1305, 497, 1246, 1653
DraIII	2413	4701
ApaI+NcoI	667, 1335, 1534, 2640, 3137, 4383	668, 199, 1106, 497, 1246, 985
ApaI+DraIII	1335, 2413, 2640, 3137, 4383	1078, 227, 497, 1246, 1653