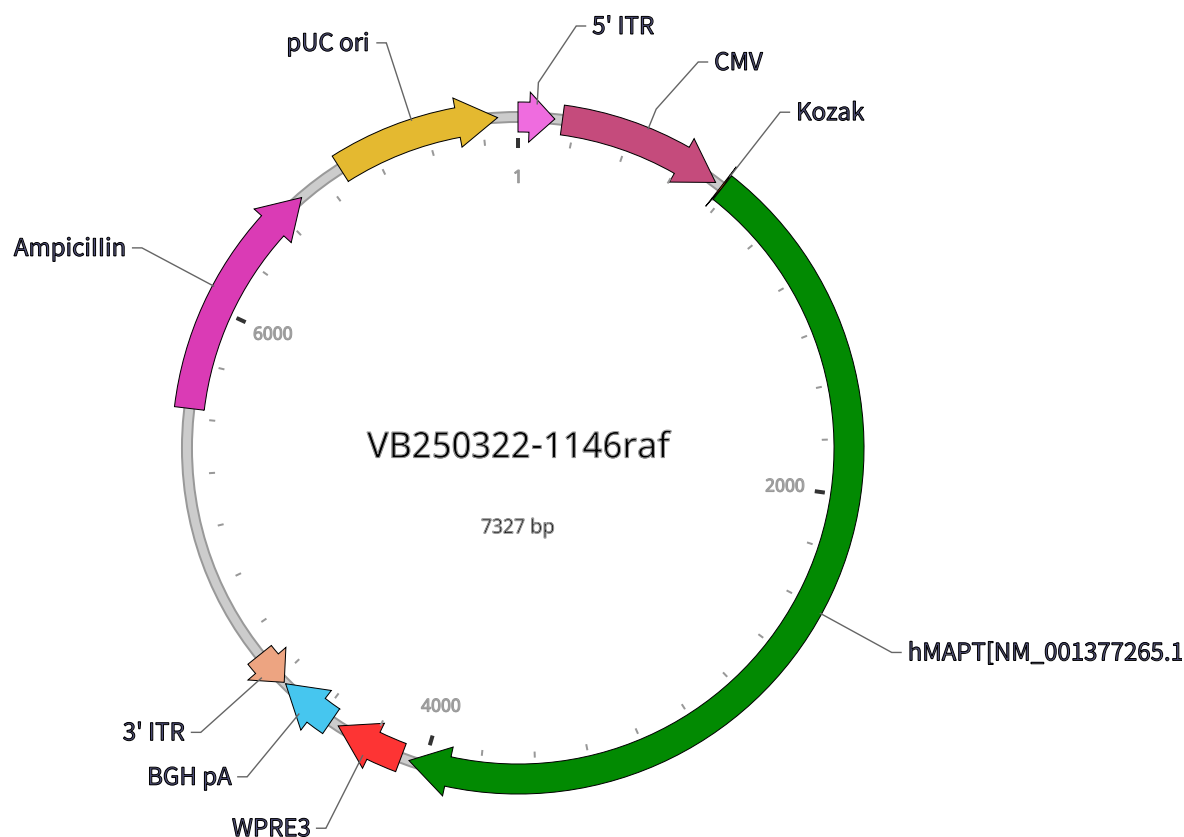


Vector Summary

Vector ID	VB250322-1146raf
Vector Name	pAAV[Exp]-CMV>hMAPT[NM_001377265.1]/T2A/EGFP:WPRE3
Vector Size	7327 bp
Viral Genome Size	4708 bp
Vector Type	Mammalian Gene Expression AAV Vector
Inserted Promoter	CMV
Inserted ORF	hMAPT[NM_001377265.1]/T2A/EGFP
Inserted Regulatory Element	WPRE3
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	■ 1-130	130	ITR	AAV 5' inverted terminal repeat (functional equivalent of wild-type 5' ITR)	Allows rescue of virus from recombinant plasmid and replication of the viral genome; this ITR is identical to that of the wild-type AAV2 genome.
CMV	■ 158-746	589	Promoter	Human cytomegalovirus immediate early enhancer/promoter	Strong promoter; may have variable strength in some cell types.
Kozak	■ 771-776	6	Miscellaneous	Kozak translation initiation sequence	Facilitates translation initiation of ATG start codon downstream of the Kozak sequence.
hMAPT[NM_001377265.1]/T2A/EGFP	■ 777-4055	3279	CDS	None	None
WPRES	■ 4086-4333	248	Miscellaneous	Truncated short version of woodchuck hepatitis virus posttranscriptional regulatory element (248 bp)	Contained only minimal gamma and alpha subunits of WPRES. Slightly weaker effective compared to WPRES.
BGH pA	■ 4364-4571	208	Regulatory Elements	Bovine growth hormone polyadenylation signal	Allows transcription termination and polyadenylation of mRNA transcribed by Pol II RNA polymerase.
3' ITR	■ complement (4579-4708)	130	ITR	AAV 3' inverted terminal repeat	Allows rescue of virus from recombinant plasmid and replication of the viral genome; this ITR is identical to that of the wild-type AAV2 genome.
Ampicillin	■ 5636-6496	861	CDS	Ampicillin resistance gene	Allows E. coli to be resistant to ampicillin.
pUC ori	■ 6667-7255	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  CTGCGCGCTC GCTCGCTCAC TGAGGCCGCC CGGGCAAAGC CCGGGCGTCG GGCGACCTTT GGTGCCCCGG CCTCAGTGAG
81  CGAGCGAGCG CGCAGAGAGG GAGTGGCCAA CTCCATCACT AGGGGTTCTT TCTAGACAAC TTTGTATAGA AAAGTTGTAG
161 TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAATG
241 GCGCGCTGG CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTC CCATAGTAAC GCCAATAGGG
321 ACTTTCATT GACGTCAATG GGTGGAGTAT TTACGGTAAA CTGCCCACTT GGCAGTACAT CAAGTGTATC ATATGCCAAG
401 TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCGCC TGGCATTATG CCCAGTACAT GACCTTATGG GACTTTCCTA
481 CTTGGCAGTA CATCTACGTA TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG GCGTGGATAG
561 CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATG ACGTCAATGG GAGTTTGTTC TGGCACCAAA ATCAACGGGA
641 CTTTCAAAA TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGTA GGCCTGTACG GTGGGAGGTC TATATAAGCA
721 GAGCTGGTTT AGTGAACCGT CAGATCCAAG TTTGTACAAA AAAGCAGGCT GCCACCATGG CTGAGCCCCG CCAGGAGTTC
801 GAAGTGATGG AAGATCACGC TGGGACGTAC GGGTTGGGGG ACAGGAAAGA TCAGGGGGGC TACACCATGC ACCAAGACCA
881 AGAGGGTGAC ACGGACGCTG GCCTGAAAGA ATCTCCCTG CAGACCCCCA CTGAGGACGG ATCTGAGGAA CCGGGCTCTG
961 AAACCTCTGA TGCTAAGAGC ACTCCAACAG CGGAAGCTGA AGAAGCAGGC ATTGGAGACA CCCCAGCCT GGAAGACGAA
1041 GCTGCTGGTC ACGTGACCCA AGAGGAGTTG AGAGTTCCGG GCCGGCAGAG GAAGGCGCCT GAAAGGCCCC TGGCCAATGA
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1201 AAGCTCCCGT CCCGCTGACC GCGAGCCTTC CTCAGACCG TCCGTTTGC CCAGCGCCTC CTCCAACAGG AGGCCCTCAG
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Validation by Restriction Enzyme Digestion

Restriction Enzymes	Cutting Sites	DNA Fragments (bp)
NaeI	1084, 4922	3838, 3489
NheI	3234	7327
ApaI	5255, 5752, 6998	497, 1246, 5584
ApaI+NheI	3234, 5255, 5752, 6998	2021, 497, 1246, 3563
ApaI+NaeI	1084, 4922, 5255, 5752, 6998	3838, 333, 497, 1246, 1413