



Synthetic Nucleic Acids

How do you research microorganisms that don't grow reliably *in vitro*?"

Go straight to synthetic nucleic acids. ATCC has identified the need for nucleic acids that represent clinically relevant organisms that cannot be reliably cultured *in vitro*, such as:

- Hepatitis C
- Mycoplasma genitalium
- Treponema pallidum
- Norovirus

How do you know you don't have anything viable in your nucleic acids?

Go straight to synthetic nucleic acids. Choose from a growing list of ready-to-use, Biosafety Level 1 nucleic acids that serve as molecular models for organisms, such as:

- Eastern equine encephalitis virus (EEEV)
- St. Louis encephalitis virus (SLEV)
- Dengue virus
- Sapovirus

How do you know your synthetic nucleic acids are going to yield the right results?

Trust ATCC for your synthetic nucleic acid needs.

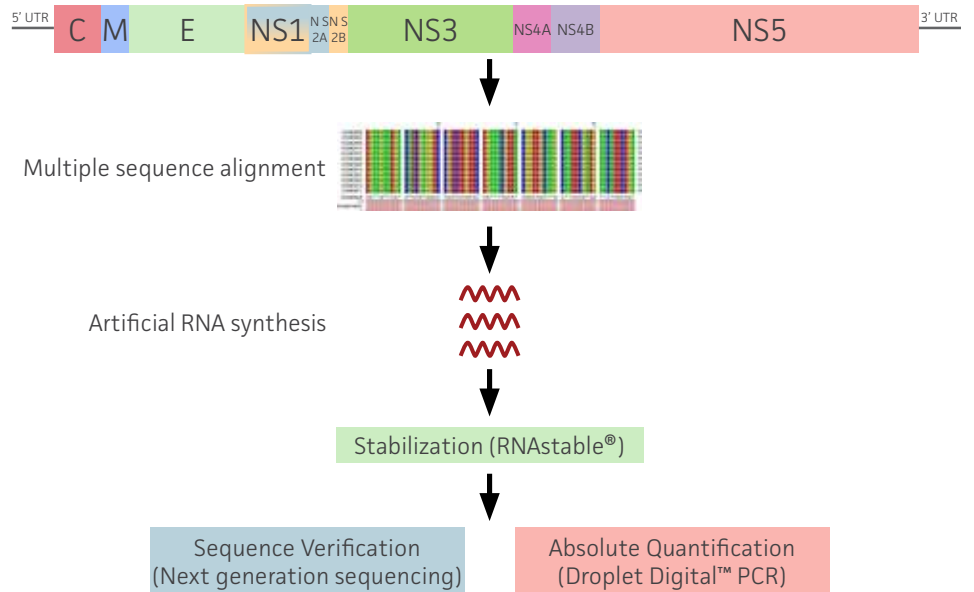
ATCC synthetic nucleic acids are quantified by genome copy number using Droplet Digital™ PCR, and produced under ISO 9001:2008 certified as well as ISO/IEC 17025:2005 and ISO 13485:2003 accredited processes, so you can trust the accuracy of your results. What's more, each DNA or RNA preparation is stabilized using a DNA- or RNA-based BioMātrica® stabilization matrix (DNAstable®, RNAstable®) to ensure consistent results run after run.



How does the ATCC developmental process work?

ATCC performs extensive research on select organisms, and works with collaborators to identify key target regions within the genome that are compatible with primers used in molecular-based assays. Multiple sequence alignment allows for the development of a consensus sequence that is used to synthetically build the finished product. Each synthetic preparation is then extensively tested to ensure:

- Identity
- Stability
- Functionality
- Quantification



To learn more about our synthetic molecular standards, visit us online at www.atcc.org/GenuineNucleics.

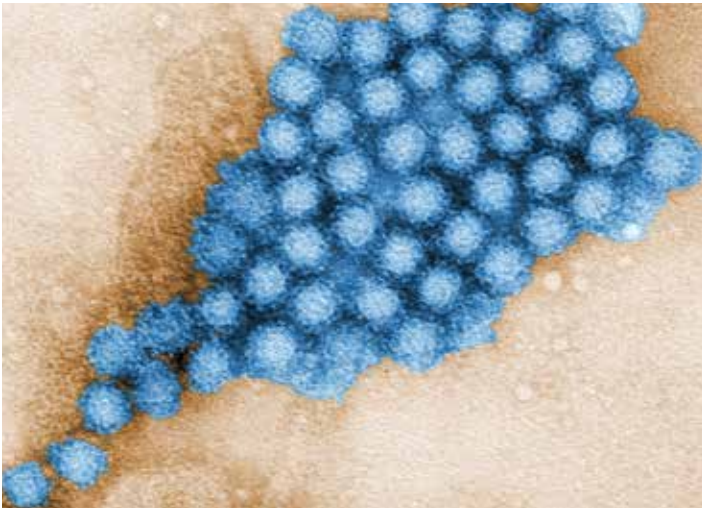


Image courtesy of Charles D. Humphrey, PhD, CDC

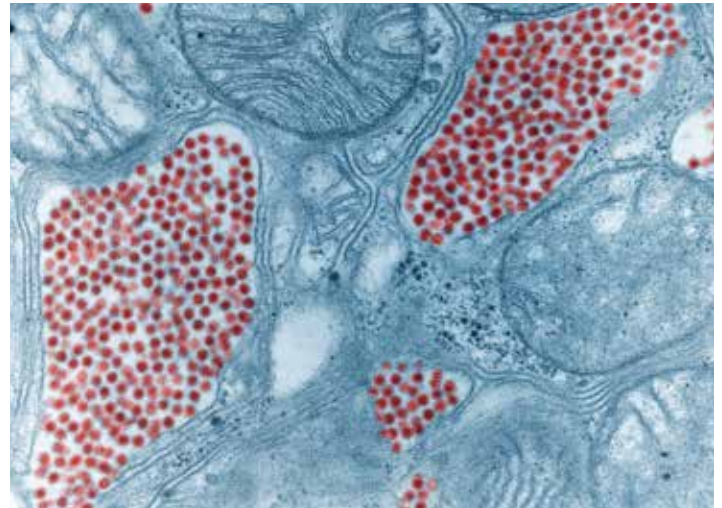


Image courtesy of Fred Murphy and Sylvia Whitfield, CDC

TABLE 1. Blood-Borne Disease

ATCC® No.	Synthetic Genome	Genetic Target
VR-3249SD™	BK virus	Full length genome of BK virus derived from a plasmid clone
VR-3232SD™	Hepatitis B virus	Fragments from the highly conserved precore, core, P, S and X regions
VR-3233SD™	Hepatitis C virus	Fragments from 5'UTR and X-tail region (3'UTR)
VR-3247SD™	Human gammaherpesvirus 4 (Epstein-Barr virus)	Fragments from LMP2, BNRF-1, EBER-1, BAMH1W (1 copy, virus genome contains 7), EBNA-2, BHRF-1, EBNA-1 Region (BERF3, BKRF1), BXLF-1, BALF-5, and LMP-1.
VR-3245SD™	Human immunodeficiency virus 1	Fragments from the 5' LTR, <i>gag</i> gene, <i>pol</i> gene (including protease, reverse transcriptase, and integrase regions), <i>tat</i> gene, <i>rev</i> gene, and <i>nef</i> gene
VR-3259SD™	Human T-cell leukemia virus 2	Proviral genome sequence of HTLV-2 except the long terminal repeats (LTRs)

TABLE 2. Digestive System Disease

ATCC® No.	Synthetic Genome	Genetic Target
VR-3238SD™	Astrovirus	Fragments from ORF1a, ORF1b, ORF2, and 3' UTR regions
PRA-3000SD™	<i>Cyclospora cayetanensis</i>	Full 18S rRNA gene sequence, and full ITS1 and ITS2 sequences
VR-3257SD™	Hepatitis A virus	Fragments from the 5' untranslated region, viral capsid proteins (VP1- 4), self-cleaving peptide 2A, proteinase 3C, and 3D RNA polymerase regions
VR-3258SD™	Hepatitis E virus	Fragments from the 5' untranslated region, methyl transferase, Y domain, X domain, helicase, RNA-directed RNA polymerase, and open reading frames 2 and 3 (ORF2 and ORF3) regions
VR-3255SD™	Murine Norovirus	Fragments from the 5'UTR, NS1/2, NS5, NS6, NS7, Gp1, VF1, GP2, GP3, and 3'UTR
VR-3234SD™	Norovirus GI	Fragments from the RNA-dependent RNA polymerase and VP1 regions
VR-3235SD™	Norovirus GII	Fragments from the RNA-dependent RNA polymerase, VP1, and VP2 regions
VR-3237SD™	Sapovirus	Fragments from the RNA-dependent RNA polymerase, VP1, and polyprotein regions

TABLE 3. Respiratory Disease


ATCC® No.	Synthetic Genome	Genetic Target
VR-3251SD™	Human bocavirus	Fragments from the 5'UTR, NS1, NP1, VP1, VP2, and 3' UTR genes
VR-3248SD™	Middle East respiratory syndrome coronavirus	Fragments from the ORF1ab, ORF5, upper envelope (upE), ORF8b, nucleocapsid (N) protein gene, and 3' UTR regions
VR-3250SD™	Human metapneumovirus	Fragments from the N gene (mRNA-Nucleoprotein), P gene (mRNA-Phosphoprotein), M gene (mRNA-Matrix Protein), F gene (mRNA-Fusion Glycoprotein), and L gene (mRNA-RNA Dependent RNA Polymerase)

TABLE 4. Sexually transmitted infections (STI)

ATCC® No.	Synthetic Genome	Genetic Target
VR-3232SD™	Hepatitis B virus	Fragments from the highly conserved precore, core, P, S and X regions
VR-3245SD™	Human immunodeficiency virus 1	Fragments from the 5' LTR, <i>gag</i> gene, <i>pol</i> gene (including protease, reverse transcriptase, and integrase regions), <i>tat</i> gene, <i>rev</i> gene, and <i>nef</i> gene
VR-3240SD™	Human papillomavirus 16	Full length genome of HPV 16 derived from a plasmid clone
VR-3241SD™	Human papillomavirus 18	Full length genome of HPV 18 derived from a plasmid clone
VR-3256SD™	Human papillomavirus 31	Full length genome of HPV 31 derived from a plasmid clone
VR-3259SD™	Human T-cell leukemia virus 2	Proviral genome sequence of HTLV-2 except the long terminal repeats (LTRs)
BAA-2641SD™	<i>Mycoplasma genitalium</i>	Fragments from the 16S gene, <i>mgpA</i> , and <i>gap</i>
BAA-2642SD™	<i>Treponema pallidum</i>	Fragments from the <i>poIA</i> , <i>tpr</i> , 23S gene, <i>arp</i> , 16S gene, <i>flaA</i> , 47kDa protein gene, and <i>bmp</i>

TABLE 5. Vector-borne disease

ATCC® No.	Synthetic Genome	Genetic Target
VR-3246SD™	Chikungunya virus	Fragments from the 5' UTR, nsP1, nsP2, nsP3, nsP4, E2, and E1 genes
VR-3228SD™	Dengue virus type 1	Fragments from the capsid, membrane, and envelope regions
VR-3229SD™	Dengue virus type 2	Fragments from the capsid, membrane, and envelope regions
VR-3230SD™	Dengue virus type 3	Fragments from the capsid, membrane, and envelope regions
VR-3231SD™	Dengue virus type 4	Fragments from the capsid, membrane, and envelope regions
VR-3239SD™	Eastern equine encephalitis virus	Fragments from the capsid, NSP1, NSP3, 3' UTR, E1 envelope glycoprotein, and the E2 envelope glycoprotein regions
PRA-3001SD™	<i>Plasmodium malariae</i>	Fragments from the the 18S rRNA gene, untranslated region (UTR), cyclooxygenase 1 and 3 (Cox1 & Cox3), and Cytochrome B (Cytb) regions
VR-3254SD™	Rift Valley fever virus	Fragments from the long, medium, and small genome segments, including the Gn gene and the nonstructural genes (NSs and NSm)
VR-3236SD™	St. Louis encephalitis virus	Fragments from the NS1 gene, pre-membrane, envelope, NS5 gene, and 3' UTR regions
VR-3198SD™	West Nile virus	Fragments from the 5' UTR, capsid protein C, membrane glycoprotein precursor prM, envelope protein E, nonstructural proteins NS1, NS2A, NS3, and NS5, and the 3' UTR regions
VR-3253SD™	Yellow fever virus	Fragments from the capsid protein C, Pre-M, Envelope protein, NS1, NS2A, NS3, and NS5 regions.
VR-3252SD™	Zika virus	Fragments from the Membrane glycoprotein precursor M, Envelope, NS1, NS2B, NS3, NS4B, and NS5 regions

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