

**Helbing Laboratory eDNA Technical Bulletin**All eDNA tools are validated through a rigorous multi-step evaluation protocol that includes tests of DNA target specificity and amplification sensitivity<sup>1-3</sup>.**General eDNA Assay Information**

Target Species: Green sturgeon (*Acipenser medirostris*) eDNA qPCR Tool: eACME3 Gene Target: MT-Dloop  
 Species Code: te-ACME eDNA qPCR Format: TaqMan Published in: \_\_\_\_\_

**eDNA Assay Sensitivity Test Summary using gBlocks™ Synthetic DNA**

LOD 0.2 95% CI 0.2-0.4 Copies/Rxn LOQ 0.9 95% CI 0.6-1.6 Copies/Rxn LOB 0 hits/8  
 LOQ<sub>continuous</sub> 4 Copies/Rxn

Binomial-Poisson model for 8 technical replicates determined using eLowQuant R code<sup>4</sup>. When the LOQ < LOD, use the LOD for the LOQ. Enzyme: QIAcuity**eDNA Assay Specificity Test Information**

Each qPCR reaction in the specificity assay contained 10 picograms of voucher target gDNA (n=25 technical replicates)

Species	Common Name ( <i>Species</i> )	Detection	# Voucher		Sample Sources/Locations
			Specimens		
te-ACFU	Lake sturgeon/yellow sturgeon ( <i>Acipenser fulvescens</i> )	No	2		British Columbia
te-ACME	Green sturgeon ( <i>Acipenser medirostris</i> )	Yes	5		California
te-ACR	White sturgeon ( <i>Acipenser transmontanus</i> )	No	1		British Columbia
te-CACA	Longnose sucker ( <i>Catostomus catostomus</i> )	No	1		British Columbia
te-CACO	White sucker ( <i>Catostomus commersonii</i> )	No	1		Ontario
te-COAR	Cisco/Tullibee ( <i>Coregonus artedii</i> )	No	1		British Columbia
te-COCL	Lake whitefish ( <i>Coregonus clupeaformis</i> )	No	1		Alberta
te-ESLU	Northern pike ( <i>Esox lucius</i> )	No	1		British Columbia
te-LOLO	Burbot ( <i>Lota lota</i> )	No	1		Yukon
te-ONCLle	Westslope cutthroat trout ( <i>Oncorhynchus clarkii lewisi</i> )	No	1		Alberta
te-ONKE	Chum salmon ( <i>Oncorhynchus keta</i> )	No	1		British Columbia
te-ONKI	Coho salmon ( <i>Oncorhynchus kisutch</i> )	No	1		British Columbia
te-ONMY	Rainbow (steelhead) trout ( <i>Oncorhynchus mykiss</i> )	No	1		Alberta
te-ONNE	Sockeye salmon ( <i>Oncorhynchus nerka</i> )	No	1		British Columbia
te-ONTS	Chinook salmon ( <i>Oncorhynchus tshawytscha</i> )	No	1		British Columbia
te-SACO	Bull trout ( <i>Salvelinus confluentus</i> )	No	1		Alberta
te-SAFO	Brook trout ( <i>Salvelinus fontinalis</i> )	No	1		Alberta
te-SANA	Lake trout ( <i>Salvelinus namaycush</i> )	No	1		Alberta
te-SASA	Atlantic salmon ( <i>Salmo salar</i> )	No	1		Nova Scotia
ma-CALUfa	Dog ( <i>Canis lupus familiaris</i> )	No	1		British Columbia
ma-FECA	Cat (domestic) ( <i>Felis catus</i> )	No	1		British Columbia
ma-HOSA	Human ( <i>Homo sapiens</i> )	No	1		Netherlands

**References**

- Hobbs, J, Adams, IT, Round, JM, Goldberg, CS, Allison, MJ, Bergman, LC, Mirabzadeh, A, Allen, H, Helbing, CC (2020) Revising the range of Rocky Mountain tailed frog, *Ascaphus montanus*, in British Columbia, Canada, using environmental DNA methods. Environmental DNA, 2: 350-361. <https://doi.org/10.1002/edn3.82>
- Hobbs, J, Round, JM, Allison, MJ, Helbing, CC (2019) Expansion of the known distribution of the coastal tailed frog, *Ascaphus truei*, in British Columbia, Canada, using robust eDNA detection methods. PLOS ONE 14(3): e0213849. <https://doi.org/10.1371/journal.pone.0213849>
- Langlois, VS, Allison, MJ, Bergman, LC, To, TA, and Helbing, CC (2020) The need for robust qPCR-based eDNA detection assays in environmental monitoring and risk assessments. Environmental DNA, 3: 519-527. doi: 10.1002/edn3.164
- Lesperance, M, Allison, MJ, Bergman, LC, Hocking, MD, and Helbing, CC (2021) A statistical model for calibration and computation of detection and quantification limits for low copy number environmental DNA samples. Environmental DNA, 3: 970-981. doi: 10.1002/edn3.220

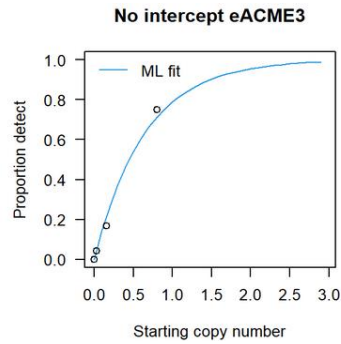
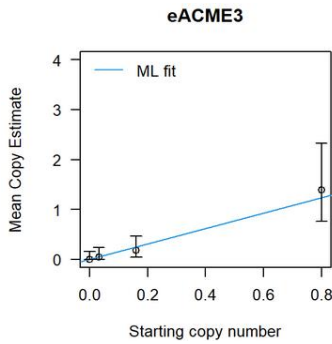


eDNA Assay Sensitivity Test Details using gBlocks™ synthetic DNA

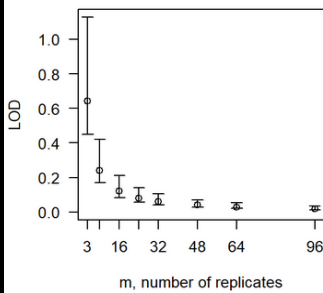
To calculate tables for different numbers of replicates, raw csv data files can be accessed here:  
<https://onlineacademiccommunity.uvic.ca/helbinglab/edna/>

From 8 Technical Replicates

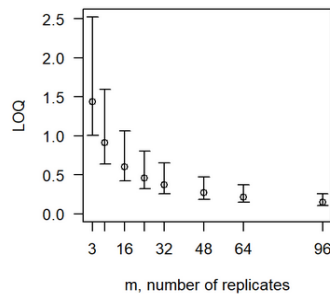
# Detects	# Copies	SE
0	0	0
1	0.086	0.088
2	0.185	0.138
3	0.303	0.188
4	0.446	0.248
5	0.631	0.325
6	0.892	0.44
7	1.338	0.67



Limits detect - no intercept eACME3

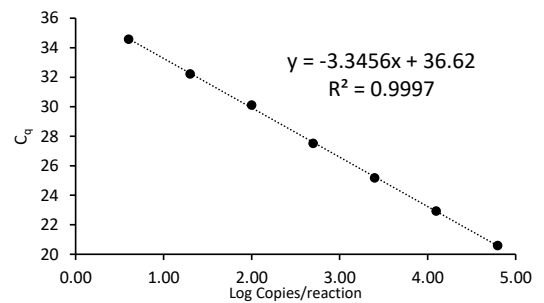


Limits quant - no intercept eACME3



Determined using eLowQuant R code<sup>4</sup>.

Applied to reactions with  $\geq 95\%$  positive hits



Efficiency 99%

Binomial-Poisson model: No intercept  
Determined using eLowQuant R code<sup>4</sup>.  
Based on a 2  $\mu\text{L}$  DNA input in a total 15  $\mu\text{L}$  reaction

Field Sample Validation

Sample Type	Known		Detected	Location
	Presence	# Samples		

Abbreviations

95% CI	95% Confidence interval	LOQ	Limit of quantification
eDNA	Environmental DNA	MT-Dloop	Mitochondrial displacement loop (D-loop) gene
gDNA	Total genomic DNA extracted from voucher specimen	NTC	qPCR no template control
LOB	Limit of blank	qPCR	Quantitative real-time polymerase chain reaction
LOD	Limit of detection	SE	Standard error