

***Toxoplasma gondii*, Strain RH  $\Delta ku80::DiCre:T2A:CAT$**

**Catalog No. NR-51627**

**Product Description:**

*Toxoplasma gondii* (*T. gondii*), strain RH  $\Delta ku80::DiCre:T2A:CAT$  was deposited to BEI Resources as a transgenic, chloramphenicol-resistant strain, derived from the virulent Type I strain RH. Strain RH  $\Delta ku80::DiCre:T2A:CAT$  was engineered by transfection of the RH  $\Delta ku80$  strain with a DiCre\_T2A construct, which expresses two dimerizable Cre (DiCre) recombinase subunits from a single promoter using T2A skip peptides. A chloramphenicol acetyltransferase (CAT) selectable marker is located between the two DiCre subunits to prevent the loss of the recombinase.

**Lot: 70026739<sup>1</sup>**

**Manufacturing Date: 24JUN2019**

TEST	SPECIFICATIONS	RESULTS
<b>Cell Morphology<sup>2</sup></b>	Report results	Crescent-shaped and refractile
<b>Genotypic Analysis<sup>3</sup></b> Sequencing of 850 locus (~ 700 base pairs)	≥ 99% sequence identity to <i>T. gondii</i> , strain RH KT850 (GenBank: GU249505)	100% sequence identity to <i>T. gondii</i> , strain RH KT850 (GenBank: GU249505) (Figure 1)
Sequencing of Cre recombinase (~ 250 base pairs)	Consistent with Cre recombinase	Consistent with Cre recombinase (Figure 2)
<b>PCR Assay of Extracted DNA<sup>3,4</sup></b> 850 locus Cre recombinase <i>ku80</i> gene	~ 770 base pair amplicon ~ 260 base pair amplicon No amplicon detected	~ 770 base pair amplicon ~ 260 base pair amplicon No amplicon detected
<b>Viable Cell Count by Hemacytometry<sup>3</sup></b>	> 10 <sup>6</sup> cells per mL	5.6 × 10 <sup>7</sup> cells per mL
<b>Viability (post-freeze)<sup>2,5</sup></b>	Growth	Growth
<b>Sterility (21-day incubation)<sup>2</sup></b> Harpo's HTYE broth, 37°C and 26°C, aerobic <sup>6</sup> Trypticase soy broth, 37°C and 26°C, aerobic Sabouraud broth, 37°C and 26°C, aerobic DMEM with 10% FBS, 37°C, aerobic Sheep blood agar, 37°C, aerobic Sheep blood agar, 37°C, anaerobic Thioglycollate broth, 37°C, anaerobic	No growth No growth No growth No growth No growth No growth No growth	No growth No growth No growth No growth No growth No growth No growth
<b>Mycoplasma Contamination<sup>2</sup></b> DNA Detection by PCR	None detected	None detected

<sup>1</sup>NR-51627 was produced by cultivation of the deposited material in human foreskin fibroblast cells (ATCC® CRL-1634™) with cell cultivation medium for parasites (ATCC® medium 2222: Dulbecco's Minimal Essential Medium adjusted to contain 10% heat-inactivated fetal bovine serum). The culture was propagated for 3 days at 37°C in an aerobic atmosphere with 5% CO<sub>2</sub> until lysis of the host cell monolayer was reached.

<sup>2</sup>Testing completed on vial, post-freeze material.

<sup>3</sup>Testing completed on bulk material prior to vialing and freezing.

<sup>4</sup>Primer sequences and PCR conditions are available upon request.

<sup>5</sup>Viable cells were seen after 3 days at 27°C in an aerobic atmosphere in DMEM supplemented with 10% heat-inactivated fetal bovine serum.

<sup>6</sup>Atlas, Ronald M. *Handbook of Microbiological Media*. 3rd ed. Ed. Lawrence C. Parks. Boca Raton: CRC Press, 2004, p. 798.

**Figure 1: 850 Locus Amplicon Sequence**

CCTTCTCCAG CATCTGGGGG GAAACCCGTA GAGGCGCCTT TACATTCCAC ACCTGCAACG GGGAGTCCTT CAGAGACTGT CCGTGTACCA  
 GCAGACACAC AAAGTCCGTG CTGCGGCGCA AAGGGCTCGC TTCCAAAGGA AACATCCCCG AAAAGCGACA TCGGAACACA CGTTCCCGGA  
 AAACGTTTCG CGCCATCACC GTCCCCACTG CAAGGCCCGC GTCTTGCTTC ATTTTTCGTG GGCTCTGAGG GCGGGCCAGA GGGTGACGTC  
 GTCATAATCC ACTCAGGTGG GCCTTCTTCG TCGTCAGGCA GCAGCGGCTT GGGCGACAGC TCAGTTTCAC CGTCAGATGG TGACTIONACC  
 ACGCCAAGCG CTCCTGCACG AGGCATGCAG CAAGAGGGAC CTGTGGGGGG CAGCAGCTCA CCGGAGCAAG GAGGGAGGCA GGCACAGGCA  
 CCCATTAGTG CCACTACTGC TTCTCCCCA CAAACAGGGA TGCTCCAGG GAAAGCAGCG CCGACACCCA GAAGCGATGG CAAGCCGTCG  
 CCAGGGCGAA CGGGCGTCGA TAAGGTCGGA GGGCCTTCTC GTGGAAGAGG GTCGCCTTCG CGTAGCCCCG GTAGCCGGTT GAGCCTTTTA  
 AAGACCCAC GGGGACCAGT TGCTCACC ACAGGGGGG TACGAGGAAG GGGTGGCAGC CATGCAGCAT CG

**Figure 2: Cre Recombinase Amplicon Sequence**

AGTGC GTTCA AAGGCCAGGG CCTGCTTGGC TCTCTCCCCA GCATCCACAT TCTCCTTTCT GATTCTCCTC ATCACCAGGG ACACAGCATT  
 GGAGTCAGAA GGGCGAGGCA GGCCAGATCT CCTGTGCAGC ATGTTGAGCT GGCCAGGTG CTGTTGGATG GTCTTCACAG CCAGGCCTCT  
 GGCTTGACAG TACAGGAGGT AGTCCCTCAC ATCCTCAGGT TCAGCAGGGA ACCATTTTCT GTTGGATCC

/Heather Couch/  
 Heather Couch

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