

**Figure S1.** Double digestion analysis of the recombinant plasmid pET32a/H2A1. Lane M: DNA molecular weight marker DL5000; Line 1: plasmid pET32a/H2A1 digested by *Eco* RI and *Hind* III.

□ <u>Downl</u>	oad	GenBank Graphics					
		a gondii ME49 histone					
Sequence	D:	KM_002365227.2 Length	n: 1173 Number of Ma	tches: 1			
Range 1	: 1 t	o 543 GenBank Graphics			<u> </u>	Next Match A Pre	vious Match
Score 1003 bit	s(54		entities 3/543(100%)	Gaps 0/543(0%)	Str. Plu	and s/Plus	
Query 1	1	ATGTGGTTGTGCGATTGGGCA	AAGGAACCAGAAGTATCAT	TCTTCGACTCTTACA	TTAAA	60	
Sbjct 1	1	ATGTGGTTGTGCGATTGGGCA	AAGGAACCAGAAGTATCAT	TCTTCGACTCTTACA	TTAAA	60	
Query 6	ŝ1	TCCGCGGGCAATACACACACG	TGTTTCCCTACACGAGGTC	CGTCTTCTCCCTGttt	ttttG	120	
Sbjct 6	ŝ1	TCCGCGGGCAATACACACACG	TGTTTCCCTACACGAGGTC	CTCTTCTCCCTGTTT	TTTTG	120	
Query 1	121	GGTTCCTTCCTCCACTCCGTT	TCCCTCGTAGACAAGATGT	CGGCCAAAGGCAAGG	GCGGT	180	
Sbjct 1	121	GGTTCCTTCCTCCACTCCGTT	TCCCTCGTAGACAAGATGT	CGGCCAAAGGCAAGG	GCGGT	180	
Query 1	181	CGCGCGAAGAAGTCCGGCAAG		AGGCCGGTCTTCAGT	TCCCT	240	
Sbjct 1	181	CGCGCGAAGAAGTCCGGCAAG		AGGCCGGTCTTCAGT	TCCCT	240	
Query 2	241	GTGGGAAGAATCGGTCGCTAC	TTGAAGAAGGGCAGATACG	CCAAGCGTGTTGGTG	CTGGC	300	
Sbjct 2	241	GTGGGAAGAATCGGTCGCTAC	TTGAAGAAGGGCAGATACG	CCAAGCGTGTTGGTG	CTGGC	300	
Query 3	301	GCCCCTGTTTACATGGCTGCC	GTTCTCGAGTACCTGTGCG	CTGAGATCCTCGAGT	TGGCG	360	
Sbjct 3	301	GCCCCTGTTTACATGGCTGCC	GTTCTCGAGTACCTGTGCG	CTGAGATCCTCGAGT	TGGCG	360	
Query 3	361	GGCAACGCCGCTCGTGACCAC		CTCGTCACATCCAGC	TGGCC	420	
Sbjct 3	361	GGCAACGCCGCTCGTGACCAC		CTCGTCACATCCAGC	TĠĠĊĊ	420	
Query 4	421	GTCCGCAACGACGAGGAACTC	TCCAAGTTCCTCGGCGGAG	TGACCATCGCAAGCG	GTGGT	480	
Sbjct 4	421	GTCCGCAACGACGAGGAACTC	TCCAAGTTCCTCGGCGGAG	TGACCATCGCAAGCG	ĠŦĠĠŦ	480	
Query (	481	GTCATGCCTAACGTCCACTCT	GTGCTCCTCCCCAAGAAGA	GCAAGGGCAAGAAGT	CTCAG	540	
Sbjct 4	481	GTCATGCCTAACGTCCACTCT	GTGCTCCTCCCAAGAAGA	GCAAGGGCAAGAAGT		540	
Query 5	541	TAA 543					
Sbjct 5	541	TAA 543					

**Figure S2.** Sequence alignment results of the recombinant plasmid pET32a/H2A1. Compared with the nucleotide sequences of H2A1 gene (Genbank: XM\_002365227), sequence analysis was conducted through the Blast program online (http://www.blast.ncbi.nlm.nih.gov/blast.cgi).

**Table S1.** Effects on proliferation at different concentrations (0, 5, 10, 20, 40, 80  $\mu$ g/ml) of rTgH2A1 on the murine macrophages. Results were evaluated using one-way ANOVA analysis followed by Dunnett's test and shown as mean of the OD450  $\pm$  standard deviation.

Group	OD value	P value <sup>a</sup>	P value <sup>b</sup>
Blank	$0.401 \pm 0.016$	-	0.9980
Control	$0.408 \pm 0.018$	0.9980	-
5 μg/mL rTgH2A1	$0.391 \pm 0.015$	0.9892	0.8892
10 μg/mL rTgH2A1	$0.402 \pm 0.017$	> 0.9999	0.9982
20 μg/mL rTgH2A1	$0.446 \pm 0.019$	0.1614	0.2857
40 μg/mL rTgH2A1	$0.474 \pm 0.030$	0.0111	0.0218
80 μg/mL rTgH2A1	$0.367 \pm 0.017$	0.3665	0.2134

<sup>&</sup>lt;sup>a</sup> and <sup>b</sup> were compared with blank group and His tagged protein group, respectively.