

# Supplement materials

# Boosting Mouse Defense against Lethal *Toxoplasma gondii* Infection with Full-Length and Soluble SAG1 Recombinant Protein

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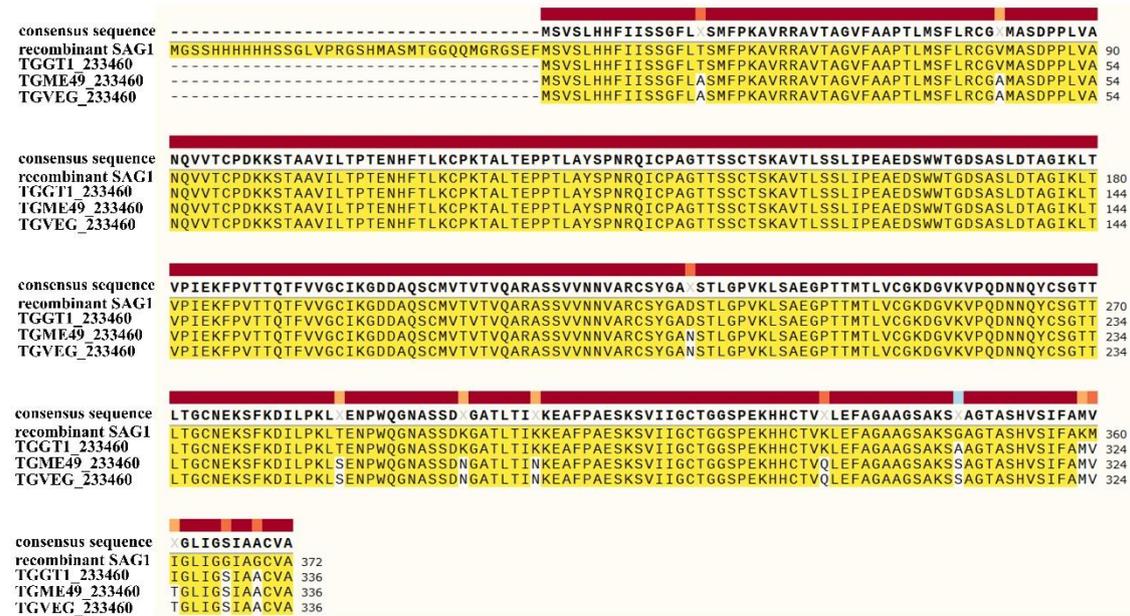
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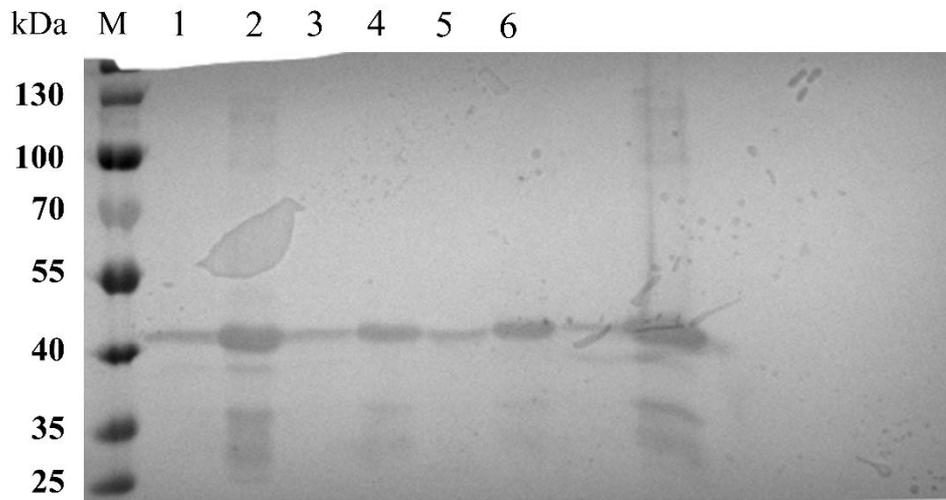
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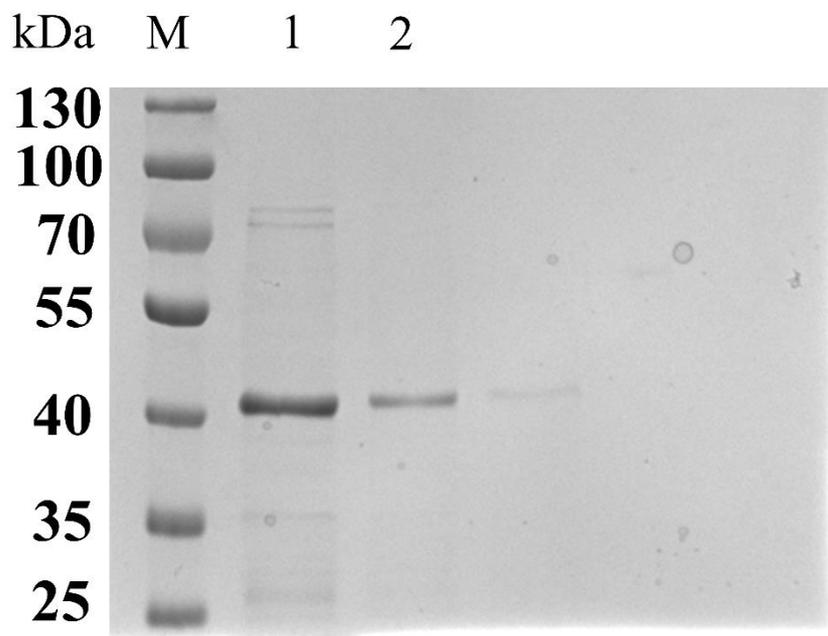
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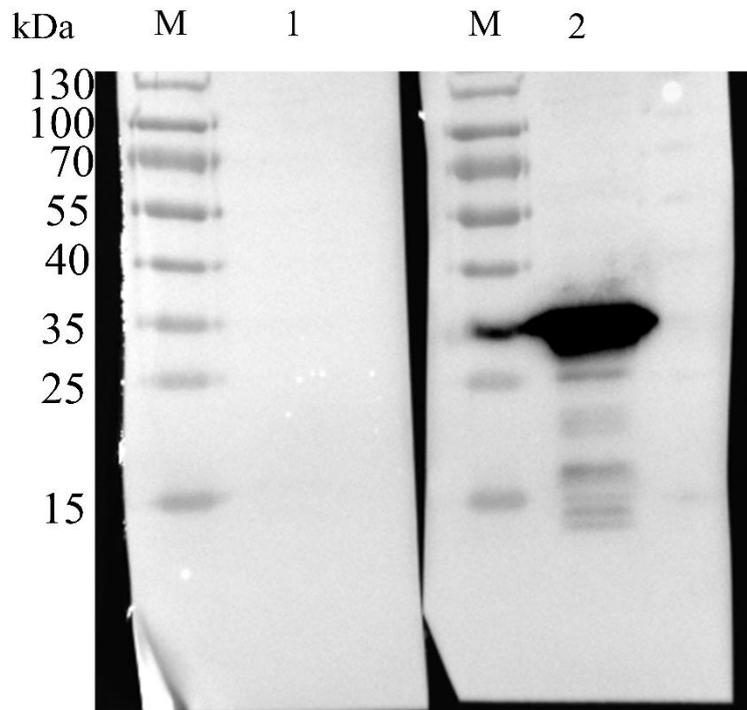
**Figure S1.** Sequence alignment between recombinant SAG1 protein and native SAG1 proteins of *T. gondii* types I and II strains. The amino acid sequence of the recombinant SAG1 was translated from the pET-28a-SAG1 sequence. The amino acid sequences of three native SAG1 were loaded from ToxoDB data.



**Figure S2.** The whole images of Figure 1 B. Identification of SAG1 recombinant protein expressed in *E. coli* Transetta (DE3) cells by western blot. 1,3,5: The soluble protein of interest in the cell lysates supernatant from three randomly selected single colonies ; 2,4,6: The insoluble protein of interest in cell lysate precipitation from three randomly selected single colonies; M: Stander protein marker.



**Figure S3.** The whole images of Figure 1 D. (D) Purified SAG1 recombinant protein identified by SDS-PAGE. 1,2: Target protein was in eluent buffer; M: Stander protein marker.



**Figure S4.** The whole images of Figure 2A. Western blot analysis for native SAG1 in TLA with the experimental mouse sera. 1: The reaction of TLA with the sera isolated from mice in the control group; 2: The reaction of TLA with the sera isolated from mice in the immunize group; M: Stander protein marker.

**Table S1.** Peptides with high score at C terminal of SAG1 protein binding to MHC class II molecules predicted by IEDB<sup>a</sup>.

Allele <sup>b</sup>	Start	End	Peptide <sup>c</sup>	Score <sup>d</sup>
H2-IA <sub>d</sub>	175	189	TVQARASSVNNVAR	0.519
<b>H2-IA<sub>d</sub></b>	<b>308</b>	<b>322</b>	<b>AKSAAGTASHVSIFA</b>	<b>0.4901</b>
H2-IA <sub>d</sub>	171	185	MVTVTVQARASSVN	0.4661
H2-IA <sub>d</sub>	296	310	TVKLEFAGAAGSAKS	0.4398
H2-IA <sub>d</sub>	169	183	SCMVTVTVQARASSV	0.4304
H2-IA <sub>d</sub>	170	184	CMVTVTVQARASSV	0.4233
<b>H2-IA<sub>d</sub></b>	<b>307</b>	<b>321</b>	<b>SAKSAAGTASHVSIF</b>	<b>0.4184</b>
H2-IA <sub>d</sub>	174	188	VTQARASSVNNVA	0.4077
H2-IA <sub>d</sub>	113	127	KAVTLSSLIPEAEDS	0.3972
<b>H2-IA<sub>d</sub></b>	<b>302</b>	<b>316</b>	<b>AGAAGSAKSAAGTAS</b>	<b>0.3781</b>
H2-IA <sub>d</sub>	240	254	EKSFKDILPKLTENP	0.3711
H2-IA <sub>d</sub>	168	182	QSCMVTVTVQARASS	0.3714
<b>H2-IA<sub>d</sub></b>	<b>295</b>	<b>309</b>	<b>CTVKLEFAGAAGSAK</b>	<b>0.3736</b>

<b>H2-IAd</b>	<b>306</b>	<b>320</b>	<b>GSAKSAAGTASHVSI</b>	<b>0.3635</b>
H2-IAd	297	311	VKLEFAGAAGSAKSA	0.3525
H2-IAd	63	77	KKSTAAVILTPTEH	0.3298
H2-IAd	61	75	PDKKSTAAVILTPTE	0.3298
<b>H2-IAd</b>	<b>301</b>	<b>315</b>	<b>FAGAAGSAKSAAGTA</b>	<b>0.3227</b>
H2-IAd	25	39	RAVTAGVFAAPTLMS	0.3234
H2-IAd	62	76	DKKSTAAVILTPTEH	0.3172

<sup>a</sup>The Immune Epitope Database (<http://tools.immuneepitope.org/mhcii>);

<sup>b</sup> H2-IAd alleles (mouse MHC class II molecules);

<sup>c</sup> 15 amino acids were chosen for analysis;

<sup>d</sup> High score indicates high level binding.