**Supplementary material**

**Table 1S The specific primers to *Ts*serpin genes**

|  |  |  |
| --- | --- | --- |
| Name of Primers | sequences(5'to3') | Enzyme cleavage site |
| Ts12383-F | 5'CGCGGATCCATGTTTGCCAAGGATAGCTTC3' | *BamH* I |
| Ts12384-R | 5'CCCAAGCTTGGTACTTGCTTTCCGGTTCG3' | *Hind* III |
| TsEP45-F | 5'CGAGCTCATGATTTCTCTACGTATGAGAGAC3' | *Sac* I |
| TsEP45-R | 5'CCCAAGCTTGCTAGTGGCAGAGTGTGGAG3' | *Hind* III |
| Ts4848-F | 5'CGCGGATCCATGTCCCCACTGAGCATA3' | *BamH* I |
| Ts4848-R | 5'CCCAAGCTTGGTACTTGCTTTCCGGTTC3' | *Hind* III |
| Ts570-F | 5'CGCGGATCCATGAGAGAGAAAACTCTGAAC3' | *BamH* I |
| Ts570-R | 5'CCCAAGCTTG ATAGCGAGGATCGGTAATGC3' | *Hind* III |
| TsB6-F | 5'CGCGGATCCATGCTAGATGAATATTACTTTAATCACC3' | *BamH* I |
| TsB6-R | 5'CCCAAGCTTGGCAGGCCAGGGGATTGAC3' | *Hind* III |

**Table 2S Sequences alignment of RCLs of *Ts*serpins with other species serpins.** Residues marked blue refer to the consensus sequence of RCL. The boxed residues representing the scissile-bond and bold-face residues were predicted P1. TsB6, Ts570, TsEP45, Ts4848, Ts12383 (*Taenia solium*), Em (*Echinococcus multilocularis*), SjB10 (*Schistosoma japonicum*), SjB6 (*Schistosoma japonicum*), Sm1 and Sm2 (*Schistosoma mansoni*), Csi (*Clonorchis sinensis*), Pwe (*Paragonimus westermani*), Bm-1 and Bm-2 (*Brugia malayi*), Hco (*Haemonchus contorus*), Tvi(*Trichostrongylus vitrinus*), A1AT (Human α1-antitrypsin)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ID | P17 | P16 | P15 | P14 | P13 | P12 | P11 | P10 | P9 | P8 | P7 | P6 | P5 | P4 | P3 | P2 | P1 | P1' | P2' | P3' | P4' |
| TsB6 | E | E | G | A | E | A | A | A | A | T | G | M | A | I | A | P | **M** | C | L | C | P |
| Ts12383 | E | E | G | A | E | A | A | A | A | T | G | M | V | M | M | C | **R** | C | M | P | M |
| Ts4848 | E | E | G | A | E | A | A | A | A | T | G | M | V | M | M | C | **R** | C | M | P | M |
| Ts570 | E | A | G | V | K | A | A | A | V | S | S | I | A | I | V | P | **M** | S | L | P | P |
| TsEP45 | R | S | G | I | R | L | L | S | V | G | T | L | N | L | E | T | **N** | Q | H | Q | F |
| Emu | E | E | G | A | E | A | A | A | A | T | A | M | P | M | M | V | **R** | C | M | P | A |
| SjB10 | E | S | G | I | E | A | A | S | V | T | S | P | I | I | V | P | **I** | S | A | L | I |
| SjB6 | E | E | G | A | V | A | A | A | A | S | A | T | V | M | L | K | **C** | S | A | I | R |
| Sm1 | E | K | G | A | V | A | A | A | A | T | A | T | Q | M | V | R | **C** | T | A | F | I |
| Sm2 | E | K | G | A | V | A | A | A | A | T | A | T | R | M | I | R | **C** | T | A | F | I |
| Csi | E | E | G | A | T | A | A | A | S | T | A | G | M | M | V | S | **M** | M | M | G | P |
| Pwe | E | E | G | A | T | A | A | A | A | T | A | V | M | M | N | M | **R** | C | A | M | M |
| Bma1 | E | K | G | T | E | S | T | A | A | T | V | V | D | L | I | D | **R** | M | G | T | Q |
| Bma2 | E | K | G | T | E | S | A | A | A | T | I | I | E | L | E | D | **R** | M | G | S | S |
| Hco | E | D | G | T | T | A | A | G | A | T | V | F | C | K | F | E | **S** | M | S | A | I |
| Tsp | E | E | G | T | E | A | A | V | S | T | A | V | R | I | V | P | **M** | S | G | V | M |
| Tvi | E | E | G | T | T | A | A | A | A | R | C | G | K | W | Y | H | **C** | R | L | C | W |
| A1AT | E | K | G | T | E | A | A | G | A | M | F | L | E | A | I | P | **M** | S | I | P | P |

**Table 3S Predicted post-translational modification (PTM) sites of the putative *Ts*serpin proteins**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | position | | | | |
| PTM site | TsB6 | Ts4848 | TsEP45 | Ts570 | Ts12383 |
| cAMP- and cGMP-dependent protein kinase | 140-143 | 175-178 | 299-302 | 84-87、149-152 | 203-206 |
| Casein kinase II | 43-46、70-73、76-79、94-97、121-124、185-188、205-208、258-261、263-266、306-309 | 17-22、 21-24、33-36、52-55、59-62、 97-100、 105-108、152-155、164-167、267-270 | 15-18、82-85、105-108、109-112、171-174、234-237、319-322、347-350、356-359、 | 19-22、65-68、104-107、156-159、163-166、175-178、386-389 | 21-24、45-48、49-52、61-64、80-83、87-89、125-128、133-136、180-183、192-195、295-298 |
| N-myristoylation | 162-172、275-280 | 30-35、101-106、158-163、264-269、302-307 | 75-80、100-105、164-169、222-227、292-297 | 36-41、100-105、350-355 | 58-63、129-134、186-191、292-297、330-335 |
| Protein kinase C | 17-19、40-42、80-82、138-140、168-170、306-308 | 33-35、40-42、144-146、154-156 | 3-5、27-29、56-58、65-67、150-152、160-162、170-172、223-225、244-246、253-255、300-302、338-340、356-358 | 31-33、57-59、65-67、104-106 | 61-63、68-70、172-174、182-184 |
| Tyrosine kinase | 252-260 |  | 288-295 |  |  |

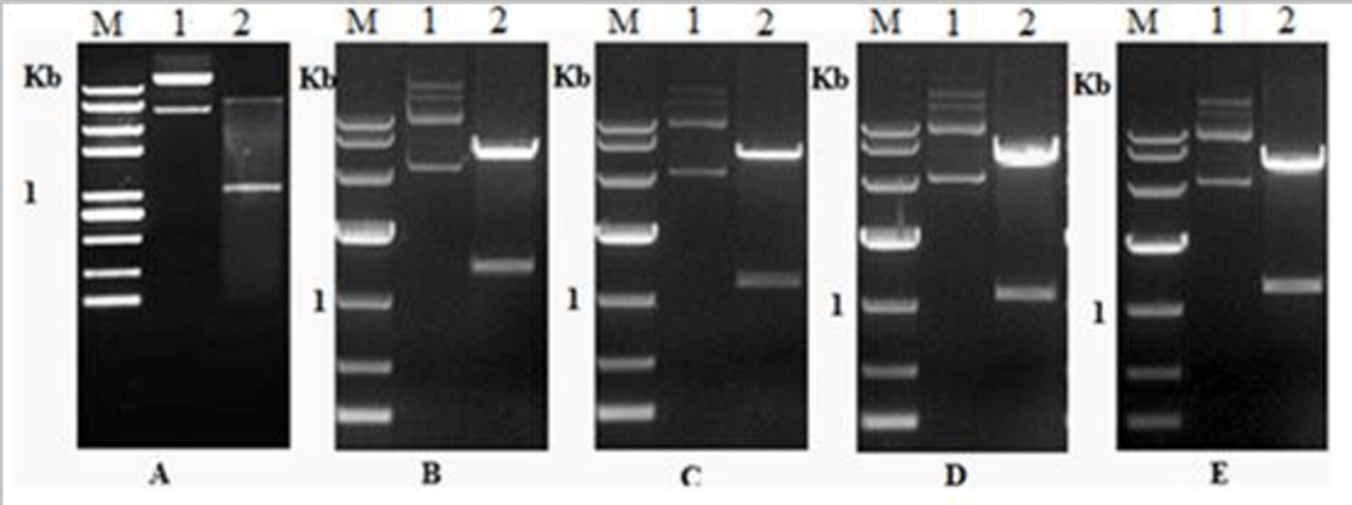
**Table 4S****Potential B cell epitope positions and sequences of *Ts*serpins**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| TsB6 | | Ts4848 | | TsEP45 | | Ts570 | | Ts12383 | |
| sequences | position | sequences | position | sequences | position | sequences | position | sequences | position |
| LVLFPRGSKK | 10-19 | ALAGSEGDTR | 13-22 | ISLRMRDKG | 2-10 | ALLTSKGPE | 54-62 | AQLQSSEGE | 16-24 |
| SLALSGSSGR | 33-42 | QAVTSSDAK | 49-57 | AAASEPERPKSTFS | 12-25 | EAIVGEREKKTC | 71-82 | ALAGSEGDTR | 41-50 |
| DAVSDGDTG | 73-81 | LDFSSDPEGSR | 93-103 | INDITKKSGHS | 52-62 | IGVANSRREDN | 99-109 | QAVTSSDAK | 77-85 |
| SNAEKAR | 121-127 | EWISENTK | 108-115 | KAARGTS | 77-83 | NDWARSST | 158-165 | LDFSSDPEGSR | 121-131 |
| LMTRESI | 145-151 | WKWKFEKSETDR | 145-156 | QALSTTNSRD | 89-98 | EQFLKSN | 170-176 | EWISENTK | 136-143 |
| ADFSRITKKE | 300-309 | HTLSKGD | 161-167 | VVWTQTSRK | 165-173 |  |  | WKWKFEKSETDR | 173-184 |
|  |  | IVLPEKR | 203-209 | KWLSKVS | 180-186 |  |  | HTLSKGD | 189-195 |
|  |  | PRFSLGGRNMKLKESL | 245-260 | LELYGSSKGS | 218-227 |  |  | IVLPEKR | 231-237 |
|  |  | HVVEPES | 347-353 | IYYKDTK | 248-254 |  |  | PRFSLGGRNMKLKESL | 273-283 |
|  |  |  |  | NPFDSDR | 334-340 |  |  | HVVEPES | 375-381 |
|  |  |  |  | LHINSGKE | 352-359 |  |  |  |  |
|  |  |  |  | AFLQVSRSG | 361-369 |  |  |  |  |
|  |  |  |  | ILIDRES | 421-427 |  |  |  |  |

**Fig 1S.****Amplification of the serpins from *T.solium* by PCR.** 4A: *Ts*B6 (1131bp); 4B: *Ts*EP45 (1350bp); 4C: *Ts*570 (1206bp); 4D: *Ts*4848 (1065bp); 4E: *Ts*12383 (1149bp)

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**Fig 2S.** **Identification of recombinant plasmid pET-30a (+)-*Ts*serpins by enzyme digestion.** M: DNA Marker; 5A: 1, Recombinant plasmid of pET-30a (+)-*Ts*B6; 2, Enzyme digestion of pET-30a (+)-*Ts*B6. 5B: 1, Recombinant plasmid of pET-30a (+)-*Ts*EP45; 2, Enzyme digestion of pET-30a (+)-*Ts*EP45. 5C: 1, Recombinant plasmid of pET-30a (+)-*Ts*570; 2, Enzyme digestion of pET-30a (+)-*Ts*570. 5D: 1, Recombinant plasmid of pET-30a (+)-*Ts*4848; 2, Enzyme digestion of pET-30a (+)-*Ts*4848. 5E: 1, Recombinant plasmid of pET-30a (+)-*Ts*12383; 2, Enzyme digestion of pET-30a (+)-*Ts*12383.

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**Fig 3S.** **Expression of recombinant *Ts*serpins proteins.** M: Protein molecular weight Markers; 6A:Recombinant proteins of the *Ts*serpins induced expression: 1, 3, 5, 7, 9: Expression products without inducement of *Ts*EP45, *Ts*4848, *Ts*12383, *Ts*570, *Ts*B6, respectively; 2, 4, 6, 8, 10: Expression products with inducement of *Ts*EP45, *Ts*4848, *Ts*12383, *Ts*570, *Ts*B6, respectively.

