

TcSERPIN	-Q <sup>1</sup> DVTL <sup>2</sup> SLTKHVLQ-TE---AKDSNLAF <sup>3</sup> SPLSIHVVL <sup>4</sup> SMIAAG <sup>5</sup> STGPTLDQLLSFLKS---ASN
AtSerp1	-QNQVSMNLAKHVIT-TV---SQNSNVIFSPASINVVL <sup>6</sup> SIIAAGSAGATKDQILSFLKF---SST
CmPS-1	---DVAMAITKRILQHDE---AKGSNVVISPLSIYVLLSLVAAGSKGRPLDQLLSFLKS---NSI
ZXA	HQTSFALRLAAALSSPAHPAGGAGRNVA <sup>7</sup> FSPLSLHVALSLVAAGAGGATRDQLASALGG--PGSA
BSZx	HQTRFAVRLASAISSPSHAKGSS-GNAAF <sup>8</sup> SPLSLHVALSLVAAGAA-ATRDQLAATLGAAEKGDA
WSZ2A	HQTRFGFRLASTISSNPE---STANNVAFSPVSLHVALSLITAGAGGATRDQLVATLGE---GEA
TcSERPIN	DHLGSFSSELV <sup>9</sup> SVVFADGSPAGGPRL <sup>10</sup> SFANGVWIDKSLPLKPSFKQVVDNVYKAASNQVDFQTKA
AtSerp1	DQLNSFSSEIVSAVLADGSANGGPKLSVANGAWIDKSL <sup>11</sup> SFKPSFKQLLED <sup>12</sup> SYKAASNQAD <sup>13</sup> FQSKA
CmPS-1	DNLNAFASHIIDKV <sup>14</sup> FADASSCGGPRLAFVNGVWIDQSL <sup>15</sup> SLKSS <sup>16</sup> FQQVVDKYYKAELRQVDFLTKA
ZXA	EGLHAFAEQLVQVLV <sup>17</sup> LADASGAGGPRVAFADGVFVDASL <sup>18</sup> SLKKT <sup>19</sup> FGDVAVGKYKAETHSVDFQTKA
BSZx	EGLHALAEQVVQVVLADASGAGGPRSF--ANVFVDSSLK <sup>20</sup> KLKPSFKDLVVGKYKGETQSVDFQTKA
WSZ2A	ERLHALAEQVVQFVLADASYADSPRVTFANGVFVDASL <sup>21</sup> PLKPSFQELAVCKYKAEAQSVDFQTKA
TcSERPIN	VQVAGEVNLWAEKETSGLIKQLLPPGSVDG <sup>22</sup> STR <sup>23</sup> LIFANALYFKGAW <sup>24</sup> NETFDASKTKENDF <sup>25</sup> YL <sup>26</sup> VN <sup>27</sup> G
AtSerp1	VEVIAEVNSWAEKETNGLITEVLPEGSADSMTKLIFANALYFKGTWNEKFDES <sup>28</sup> LTQEGEFHLLDG
CmPS-1	NEVISEVNSWVEKNTYGLIREILPAGSVGSSTQ <sup>29</sup> LVLANALYFKA <sup>30</sup> AWQQA <sup>31</sup> FDASITMKRDFYLIDG
ZXA	AEVASQVNSWVEKVTSGLIKEILPPGSVDHTTRLVLGNALYFKGAWTEKFDASKTKDGEFHLLDG
BSZx	PEVAGQVNSWVEKITTTGLIKEILPAGSVDSTTRLVLGNALYFKGSWTEKFDASKTKDEKFHLLDG
WSZ2A	AEVTAQVNSWVEKVTTGLIKDILPAGSISNTTRLVLGNALYFKGAWTDQ <sup>32</sup> FSRVTKSDYFYLLDG
TcSERPIN	S <sup>33</sup> SVKAPFMT <sup>34</sup> SQKKQAVGAYDGFKVLGLPYKQGGDKRRF <sup>35</sup> SMYFFLPDAKDGLPAIVEKV <sup>36</sup> SSE <sup>37</sup> SGFL
AtSerp1	NKVTAPFMTSKKKQYVSAYDGFKVLGLPYLQGD <sup>38</sup> KRQFSMYFYLPDANNGLSDLLDKIVSTPGFL
CmPS-1	SSVKAPFMSGEKDQYVAVFDGFKVLALPYSQGPDP <sup>39</sup> RRFSMYFFLPDRKDG <sup>40</sup> LASLIEKLDSEPGFI
ZXA	KSVQAPFMSTSKKQYILSYDNLKVLKLPYQ <sup>41</sup> GGDKRQFSMYILLPEAQDGLWSLAEKLNSEPEFL
BSZx	SSVQTPFMSSTKKQYISSYDNLKVLKLPYQ <sup>42</sup> GGDKRQFSMYILLPEAQDGLWNLANKLSTEPEFM
WSZ2A	SSIQTPFMYSSEEQYISSDGLKVLKLPYKQGGDKRQFSMYILLPEAPSGIWSLAEKLSAPELL
TcSERPIN	ERHLPYEPVKVGEFRIPRFKISFGFEASEVLKRLGLVLPF <sup>43</sup> SGEGGL <sup>44</sup> TEMVDSP-LGQSL <sup>45</sup> VVSNIF
AtSerp1	DNHIPRRQVKVREFKIPKFKFSFGFDASNVLKGLGLTSPFSGE <sup>46</sup> EGLTEMVESPEMGKNLCVSNIF
CmPS-1	DRHIPCKKQELGGFLIPKFKISFGIEVSDVLKKLGLVLPFT-EGGL <sup>47</sup> LGMVESP-VAQNLRVSNIF
ZXA	EKHIPTRQVTVGQFKLPKFKISFGFEASDLLKSLGLHLPFSSEADLTEMVDSP-EGKNLFVSSVF
BSZx	EKHMPMQKVPVGQFKLPKFKISFGFEASDMLKGLGLQLPFSSEADLSEMVDSP-AARSLYVSSVF
WSZ2A	ERHIPRQKVALRQFKLPKFKISFGIEASDLLKHLGLQLPFSDEADLSEMVDSP-MPQGLRISSVF
<div> <div>P15</div> <div>→</div> <div>P1-P1'</div> </div>	
TcSERPIN	HKSFIEVNEEG <sup>48</sup> TEAAAASAGVIRLRGV <sup>49</sup> LVE-EKIDFVADHPFLFLIRE <sup>50</sup> DVTGVVLFIGHVLNP
AtSerp1	HKACIEVNEEG <sup>51</sup> TEAAAASAGVIKLRGLLMEEDEIDFVADHPFLLVVTENITGVVLFIGQVVD <sup>52</sup> P
CmPS-1	HKAFIEVDEEG <sup>53</sup> TKAAASSAVTVGIVS--LPINRIDFIANRPFLYLIRE <sup>54</sup> DKSGTLLFIGQVLNP
ZXA	HKSFVEVNEEG <sup>55</sup> TEAAAATAAVITLRSAP---IAEDFVADHPFLFLIQEDMTGVVLFVGHV <sup>56</sup> VNP
BSZx	HKSFVEVNEEG <sup>57</sup> TEAAARTARVVTLRSLPVEPVKVDFVADHPFLFLIRE <sup>58</sup> DLTGVVLFVGHVFN <sup>59</sup> P
WSZ2A	HKT <sup>60</sup> FVEVNET <sup>61</sup> GTEAAAATIAKAVLLS-ASPPSDMDFIADHPFLFLIRE <sup>62</sup> DTSGVVLFIGHV <sup>63</sup> VNP

**Supplementary Figure 2.** Analysis of the primary structure of the TcSERPIN protein. Sequence alignment of amino acid residues of the domain of *Theobroma cacao* (TcSERPIN, Tc02v2\_p008580.1), *Arabidopsis thaliana* (AtSerp1, NP\_190108.1), *Curcubita maxima* (CmPS-1, AAG02411.1), *Oryza sativa* (ZXA, XP\_015632921.2), *Hordeum vulgare* (BSZx, Q40066.1), and *Triticum aestivum* (SPZ2A, Q9ST57.1). Conserved regions are highlighted in gray and gap regions are indicated by (-). The P<sub>15</sub> – P<sub>1'</sub> region of the RCL is underlined. Phosphorylation and glycosylation sites are marked by rectangles and circles, respectively.