

Table S1 The identified *StSOT* gene family members with Sulfotransferase domain (PF00685) from the *Solanum tuberosum* genome. The proteins post-translational phosphorylation changes have been investigated.

Gene symbol	Protein length (aa)	Phosphorylation sites ^a	Score
<i>StSOT01</i>	296	14 S TSRLSENYG	0.986
		41 S PKRESEYPF	0.979
		151 S LLPISILES	0.978
		186 S KAKLSTKVS	0.991
		222 S YWKASVERP	0.992
		257 S DKPLSKEEE	0.998
<i>StSOT02</i>	345	222 S YWKASVEKP	0.984
		257 S DKPFSKEEQ	0.998
<i>StSOT03</i>	337	24 S QETLSEEL	0.996
		190 S IRPESLGPL	0.988
		291 S KGAI SVFEN	0.991
		320 S FERLSNVMD	0.952
<i>StSOT04</i>	344	16 S EEEASSKFK	0.961
		64 S NFKSSWNDI	0.991
		69 Y WNDIYICSA	0.979
		117 S LEFDSPKHS	0.991
		150 S QSLDSTKMI	0.981
		191 S ELLISFEEG	0.995
		255 S GKPSRDEE	0.986
<i>StSOT05</i>	350	250 S EQPFSLEEQ	0.993
		309 S KNHLSEEMI	0.973
<i>StSOT06</i>	326	14 S IIDSSQSSE	0.960
		16 S DSSQSSEEK	0.997
		17 S SSQSSEEKD	0.995
		121 S SSIYSTKPT	0.988
		216 S YWSESQKRT	0.997
		264 S VWRCSLERL	0.992
<i>StSOT07</i>	101	80 S TVEMSEKLN	0.976
<i>StSOT08</i>	101	54 S NEKLSTGER	0.953
<i>StSOT09</i>	313	78 S IVNRSSKES	0.996
		79 S VNRSSKESL	0.997
		201 S FRKASLEKP	0.992
<i>StSOT10</i>	330	148 S SLPKSIKDS	0.998
		186 S KDIHSIEEI	0.991
		199 S CKGVSPYGP	0.975
		250 S ECPFSIEEE	0.959
<i>StSOT11</i>	335	7 S KSQTSPQIP	0.974
		77 T ILVTTPKSG	0.959
		142 S PRLSTHMP	0.967
		153 S SLPKSVQDS	0.996
		157 S SVQDSKTKL	0.972
		255 S ECPFSIEEE	0.959
		288 S DGKLSTGEE	0.964
<i>StSOT12</i>	335	8 S SQTSSPTPP	0.991
		77 T ILVTTPKSG	0.959
		153 S SLPKSVQDS	0.997
		157 S SVQDSRTKL	0.969
		191 S IDTNSIEEM	0.981
		255 S EFPFSIEEE	0.972
		288 S NGKLSTGEE	0.995

<i>StSOT13</i>	308	148 S SLPKSVKDS	0.998
		152 S SVKDSKTKL	0.979
		186 S KDIHSIEEI	0.991
		199 S CKGVSPYGP	0.975
		250 S ECPFSIEEE	0.959
<i>StSOT14</i>	329	15 S EDSLSEECK	0.981
		71 T ILVTTPKSG	0.959
		118 Y EHTLYVDGQ	0.963
		147 S SLPKSIMDS	0.997
		249 S ECPFSMEEE	0.972
		266 S LRMCSFENL	0.969
<i>StSOT15</i>	330	282 S NGKLSTGEG	0.994
		16 S QEGLSEECK	0.985
		36 Y WMESYIYNY	0.962
		148 S SLPKSVQDS	0.996
		152 S SVQDSKTKL	0.972
<i>StSOT16</i>	332	199 S CKGVSPYGP	0.975
		250 S ECPFSIEEE	0.959
		7 S TSQNSPPKY	0.976
		17 S QEDQSEECK	0.973
		73 S ILVTSPKSG	0.996
		149 S SLPKSVKNS	0.997
		217 S YWKESIENP	0.990
<i>StSOT17</i>	240	252 S ECPFSIEEE	0.959
		269 S LRMCSFENL	0.969
		42 T SSFTTPRLL	0.984
		58 S SLPKSAQDS	0.995
		62 S SAQDSKTKL	0.954
		96 S KDTNSIEEM	0.983
		160 S ECPFSIKEE	0.971
<i>StSOT18</i>	269	193 S TGKLSTGEE	0.991
		219 S TTEMSEKFN	0.972
		93 S VLLDSIKNS	0.995
<i>StSOT19</i>	268	161 S YWEEKSKRP	0.952
		247 T KNHMTPKME	0.966
		63 S EVMHSYSKT	0.990
<i>StSOT20</i>	209	93 S ILPNSIKNS	0.975
		130 S LEDLSPLEE	0.995
		4 Y -MDYYLKTP	0.953
<i>StSOT21</i>	359	33 S VLPDSIKNL	0.997
		71 S LEDLSPLEE	0.995
		10 Y SPPGYNNPT	0.969
		34 S LQDDSLSEE	0.960
		36 S DDSLSEECK	0.979
		133 S VLVPSPERT	0.993
<i>StSOT22</i>	226	168 S SLPKSVLDS	0.996
		272 S ECPFSIEEE	0.959
		8 S SQSSSPKYL	0.995
		11 Y SSPKYLQED	0.961
		17 S QEDLSEERK	0.993
		73 S ILVTSPKSG	0.996
		149 S SLPKSVQNS	0.973
		188 S KDTNSIEEM	0.983
		217 S YWKKSIENS	0.994
		221 S SIENSDKDF	0.997

<i>StSOT23</i>	118	-	-
<i>StSOT24</i>	316	140 S VLPDSFKNS 178 S LENPSPLEE 294 T KNHMTPKME	0.997 0.990 0.966
<i>StSOT25</i>	244	35 S INFTSLDDT 56 S CLPQSIIDS 127 S YRKASKDHH 164 S GKPFSEEEE	0.976 0.994 0.972 0.997
<i>StSOT26</i>	329	15 S EDNLSEECK 71 T ILVTTPKSG 147 S SLPKSVQDS 151 S SVQDSKTKL 185 S NDTNSIEEM 282 S NGKFSTGEA	0.956 0.959 0.996 0.972 0.980 0.996
<i>StSOT27</i>	161	17 S KDTNSIEEM 81 S ECPFSIEEE 114 S NGKFSTGEP	0.983 0.959 0.996
<i>StSOT28</i>	105	25 S ECPFSIEEG 58 S NGKFSTGEE	0.970 0.996
<i>StSOT29</i>	106	-	-

^a The phosphorylation regions as the post-transcriptional changes predicted in S: serine , T: threonine and Y: tyrosine residues from StSOT proteins (with the scores higher than 0.950)