Supplementary Figure S1. Multiple sequence alignment of full-length Sl-TPL proteins. Conserved domains are underlined. The red line represents LisH domain. The blue line represents CTLH domain. The light green line represents the WD40-repeat 1 domain, the dark green line represents WD40-repeat 2 domain.

WD40-repeat 1

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                                                              WD40-repeat 1
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At-tpl   -PDDLPKTVARTLSQGSS------------------PMSMDFHPIKQTLLLVGTNVGDIGLWEVGSRERLVQKTFKVWDLSKCSMPLQAALVKEPVVSVNRVIWSPDGSLFGVAYSRHIVQLYSYHGGEDMRQ-HLEIDAHVGGVNDIS   480
At-tpr1  -PDDLPKTVARTLSQGSS------------------PMSMDFHPIKQTLLLVGTNVGDIGLWEVGSRERLVQKTFKVWDLSKCSMPLQAALVKEPVVSVNRVIWSPDGSLFGVAYSRHIVQLYSYHGGEDMRQ-HLEIDAHVGGVNDIA   479
Sl-tpl1  -PDDLPKTVARTLNQGSS------------------PMSMDFHPSQQTLLLVGTNVGDIALWEVGSRERLVLRNFKVWDLSACSMPLQTALVKDPGVSVNRVIWSPDGSLFGVAYSRHIVQIYSYHGNDDIRQ-HVEIDAHVGGVNDLA   478
At-tpr4  -TDDLPKNVSRILSQGSA------------------IKSMDFHPVQQTMLLVGTNLGDIAIWEVGSREKLVSRSFKVWDLATCTVNLQASLASEYTAAVNRVVWSPDGDGLLGVAYSKHIVHIYSYHGGEDLRN-HLEIDAHGNVSDLA   482
Sl-tpl4  -SDDLPKTVVVNLNQGSA------------------VKSMDFHPVQQTLLLVGTNIGDIAIWEIGGRERLAFKNFKVWEIGNCSMTLQASLANEYTATVNRVMWSPDGNLLGVAYSKHIVHLYSYHGGDDLRN-HLEIDAHVGNVSDLA   480
Sl-tpl5  -SDDLPKAFVMTLNQGSS------------------VKSMDFHPVQQILLLVGTGTGEVMLWELGSRERIANRNFKIWDLSQCSVALQASMASEYSAAVNRVMWSPDGTLFGVAFSKHLVHVYSYHGGDDLRN-HLEIEAHSGSVNDLA   485
At-tpr3  --EDLPTKAALALHQGST------------------VTSMEFYPMQNTLLLVGSATGEITLWELAARERLVSRPFKIWDMSNCSHQFQALIAKETPISVTRVAWSPDGNFIGVAFTKHLIQLYAFSGPNDLRQ-HTEIDAHVGAVNDLA   470
Sl-tpl3  --DDLPRTVAFTLPQGSS------------------VTSMDFHPSHHTYLLVGSTNGEITLWEVATREKLVAKAFKIWDVQACTLTFQASASKDAPFSSRVAWSPDGTFVGVAFSKHLVHLYATVGTNDLRQ-HLEMDAHAGSVNDLA   472
At-tpr2  -DDLPRNVVSTIRQGSV------------------VISMDFHPSHHTTLAVGCSSGEVTLWEVGSREKVVTEPFKIWNMAACSVIFQGSIVKEPSISVTRVAWSPDGNLLGVSFTKHLIHVYAYQG-SDLRQ-HLEIDAHAGGVNDIA   471
Sl-tpl2  --DDLPKTVVVRNLSQGSN------------------VMSMDFHPQQQTVLLVGTNVGDISIWEVGSRERLAHKSFKVWDISACSMPFQSALVKDATVSVNRCVWGPDGSILGVAFSKHIVQIYTYSPAGELRQ-HLEIDAHAGGVNDIA   470
Sl-tpl6  LSDDFPKTVERVLTIGNPPTASDYPTIRSIYPTVNYYPTTMDFHPVQQTLLIVGDGGGSVELWDVSSGKMLFRRTLMWEVEVFSPDFLKSMGEDPRISVNRVLWNPDGSLFGVASSKNIVQLYSYHNNDNHAENHLEIEAHFGSINDLA   599
         .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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          *: **.*: : ***:*  :***:  .* : .  ****.*****:*** **  ::**::*: :*:****:*:.  *.  *.*:**.   *  *.*:* *******.*:*:*.:*****::*  :  **:  :  *  ***:**   :*.::.*:.
At-tpl   FSTPNKQLCVITCGDDKTIKVWDAATGVKRHTFEGHEAPVYSVCPHYKENIQFIFSTALDGKIKAWLYDNMGSRVDYDAPGRWCTTMAYSADGTRLFSCGTSKDGESFIVEWNESEGAVKRTYQGFHKRSLGVVQFDTTKNRYLAAGDDF   630
At-tpr1  FSTPNKQLCVTTCGDDKTIKVWDAATGVKRYTFEGHEAPVYSICPHYKENIQFIFSTALDGKIKAWLYDNMGSRVDYEAPGRWCTTMAYSADGTRLFSCGTSKDGESFIVEWNESEGAVKRTYQGFHKRSLGVVQFDTTKNRYLAAGDDF   629
Sl-tpl1  FSHPNKQLSVITCGDDKTIKVWDATSGARQYTFEGHEAPVYSVCPHHKFTIQFIFSTALDGKIKAWLYDNLGSRVDYEAPGRWCTTMAYSADGTRLFSCGTSKDGESHIVEWNESEGAVKRTYQGFRKRSLGVVQFDTTKNRFLAAGDDF   628
At-tpr4  FSQPNQQLCVVTCGEDKTIKVWDAVTGNKLHTFEGHEAPVYSVCPHQKENIQFIFSTAVDGKIKAWLYDNMGSRVDYDAPGRLCTTMSYSADGTRLFSCGTSKEGESFIVEWNESEGAVKRTYLGLGKRSVGVVQFDTMKNKFLVAGDEF   632
Sl-tpl4  FSHPNKQLCIITCGEDKAIKVWDAATGSKLYTFEGHEAPVYSVCPHHKESIQFIFATAVDGKIKAWLYDNMGSRVDYDAPGHSCTTMAYSADGARLFSCGTSKDGESYLVEWNESEGAVKRTYVGLGKRSVGVVQFDTTKNRFLAAGDEF   630
Sl-tpl5  FSYPNKQICIVTCGDDRLIKVWDAATGAKQYTFEGHEAPVYSVCPHHKESIQFIFSTAIDGKIKAWLYDNVGSRVDYDAPGHSSTTMAYSADGTRLFSCGTNKEGESYLVEWNESEGAVKRTFSGLGKRAGGVVQFDTTKNRFLAAGDEF   635
At-tpr3  FANPNRQLCVITCGDDKLIKVWD-VSGRKHFTFEGHDAPVYSICPHYKENIQFIFSTAIDGKIKAWLYDNLGSRVDYDAPGKWCTRMLYSADGTRLFSCGTSKDGDSFLVEWNESEGSIKRTYKEFQKKLAGVVQFDTSKNHFLAVGEDG   619
Sl-tpl3  FAYPNKQLCIVTCGDDKLIKVWD-ITGRKLFNFEGHEAPVYSICPHQKESIQFIFSTAIDGKIKAWLYDNMGSRVDYDAPGHWCTTMLYSADGTRLFSCGTGKEGDSFLVEWNESEGAIKRTYSGFRKKSAGVVQFDTTQNHFLAVGEDS   621
At-tpr2  FAHPNKQMCVVTCGDDKLIKVWD-LSGKKLFTFEGHEAPVYSICPHQKENIQFIFSTALDGKIKAWLYDNVGSRVDYDAPGQWCTTMLYSADGSRLFSCGTSKEGDSFLVEWNESEGALKRTYLGFRKKSAGVVQFDTTRNRFLAVGEDN   620
Sl-tpl2  FSHPNKQLCVVTCGEDKLIKVWDAVSGRREHMFEGHEAPVYSICPHQKEDVHFILSTSTNGEIKAWIYENSGPCVSYEAPSKCCMRMLYSANGKRLFSCGTNKDGDSHLVEWNETDGFIVRTYLGLGKCSSGVVEFDISRNNYVAAGDSH   620
Sl-tpl6  FSKPNNQLLVITCGEDMLVKVWNANNGAKQYTFEGHKAPVYSLCPHEKEDVHFILSTSTNGEIKAWIYENSGPCVSYEAPSKCCMRMLYSANGKRLFSCGTNKDGDSHLVEWNETDGFIVRTYLGLGKCSSGVVEFDISRNNYVAAGDSH   749
         .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
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          :****::: :   :*:   .  *.*  *  :*:.*:* ****:  .* .*::.* *  ::  : *                                                             *                       .   .
At-tpl   SIKFWDMDAVQLLTAIDGDGGLQASPRIRFNKEGSLLAVSGNENVIKIMANSDGLRLLH-TFENIS------SESSKPAINSIAAA----------AAAAATSAGHADRSANVVSIQGMNG-----DSRNMVDVKPVITEESNDKSKIWKL   765
At-tpr1  SIKFWDMDTIQLLTAIDADGGLQASPRIRFNKEGSLLAVSANDNMIKVMANSDGLRLLH-TVENLS------SESSKPAINSIP----------------MVERPASVVSIPGMNG-----DSRNMVDVKPVITEESNDKSKVWKL   753
Sl-tpl1  SIKFWDMDHVPLLTSIDADGGLPASPRIRFNKDGSLLAVSANENGIKILANNDGIRLIR-TFENLAYDASRASETTKPTVNPI-----------SVASANNSGFADRVASVVGISGMNG-----DARNPVDVKPRINEEPNDKSKIWKL   766
At-tpr4  QVKFWDMDSVDLLSSTAAEGGLPSSPCLRINKEGTLLAVSTTDNGIKILANAEGSRILH-SMANRG------LDSSRAPPGSVAKGPIVGTFGTPNSSTGMSLSMGERSGPVASVTGLNG-----DNRSLPDVKPIADD-AEKSKIWKL   775
Sl-tpl4  IIKFWDMDNTNLLTTADADGGLPASPCIRFSKEGTLLAVSTSENGVKILANADGVRLIR-ALESRA------LDPSRGPPGAVAKAPMISTYGASSSTAGTSISIADRTAPVTAIVQLNG-----DNRNLQDTKPRIPDE-LEKSKIWKL   773
Sl-tpl5  MIKFWEMDSVNLLTTTDADGGLPASPCLRFNKEGMLLAVSTSDNGLKILANADGVRLLR-SMENRP------FDASRVSSASAVKPSTVGSFGPP--STSVAASFVDRAVPMTS---MNG-----ESRNLGDARPRAAEEPVDKSKIWKP   774
At-tpr3  QIKFWDMNNINIVLTSTDAEGGLPALPHLRFNKDGNLLAVTTADNGFKILANPAGFRSLR-AMETPA------SETMRTP---VDFKAVP-----GAPVAS-VNCKVERGSPVRHSQMLNG-----VDPSKSRIDDS------TDKPKSWQL   749
Sl-tpl3  QIKFWDMDNINILTTIDADGGLPSLPRLRFNKEGNLLAVTTADNGIKILGNPAGMRSLR-TVEAPP------FEALRSP---IEAAAIKQGSGSVNATPVNCKVERSSPIRPSPILNG-----VDSVPRSMEKPRILEEVSDKAKPWQL   763
At-tpr2  QIKFWNMDNTNLLTVVEAEGGLPNLPRLRFNKDGNLLAVTTADNGIKILANTDGLRTLR-AFEARS------FEASKAS---IDMKVSTSAMASSISPAIGKIEHMDAGSPARPTPIPNG----IBAMSRTMEKPRNLDS-VDKSKPLEL   761
Sl-tpl2  QIKFWDMDNTNMLTATDGDGGLPASPRLRFNKEGSLLAVTTSDNGIKVLANTDGQRMLR-MLESRA------FEGSRALS-DVNVKPPIAGSLGPIPNISGSAPQIIERSDRTQQSMSIGNLATMESSRGPDVKPRIAEN-MDKIKSWKF   767
Sl-tpl6  VIKFWNVNDAQLLTVVDAGGDLPASPYVRFNKNGTLLAVSVDHNSVKILANDGGRILLQTSLDAST------YLSTRELAG------------------------NSLSGPANSSSIDG-----IVPPEMTAENLAKMEHHKILGNPST   869
         .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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WD40-repeat 2

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At-tp1    TEVSEPSQCRSLRLPEN-LRVAKISRLIFTNSGNAILALASNAIHLLWKWQRNERNATGKATASLPPQQWQPASGILMTNDVAE-TNPEEAVPCFALSKNDSYVMSASGGKISLFNMMTFKTMATFMPPPPAATFLAFHPQDNNIIAIGM    913
At-tpr1   TEVGEPSQCRSLRLPEN-MRVTKISRLIFTNSGNAILALASNAIHLLWKWQRNDRNATGKATASLPPQQWQPASGILMTNDVAE-TNPEEAVPCFALSKNDSYVMSASGGKISLFNMMTFKTMATFMPPPPAATFLAFHPQDNNIIAIGM    901
Sl-tpl1   TEISESSQCRSLKLPEN-LRVTKISRLIYTNSGNAVLALASNAIHILWKWQRNERNTSGKATASVSPQLWQPSSGILMTNDVHE-PNHEEAVSCFALSKNDSYVMSASGGKISLFNMMTFKTMTTFMPPPPAATFLAFHPQDNNIIAIGM    914
At-tpr4   TEISERSQLRTLRLPDT-LLPARVVKLIYTNSGGAILALAENAAHKLWKWQKSERNLLGKANSNVPPQLWQPSSGVLMTNDTRE-GNKEDVVPCFALSKNDSYVMSASGGKISLFNMMTFKTMTTFMAPPPAATSLAFHPQDNNIIAIGM    923
Sl-tp14   TEISEPAQVRSSRLPDN-QLSVRIIRLMYTNSGGAILALAYNAVHKLWKWQRNERNVTGKASTAVPPQLWQPSSGILMTNDISD-TNPEEAVPCFALSKNDSYVMSASGGKISLFNMMTFKTMTTFMPPPPAATFLAFHPQDNNIIAIGM    921
Sl-tp15   TEINEPSQCRFLKLPDS-ATTPRVTRLIYTNSGYAILALAANAVHKLWKWPRNDRHPTGKANASIVPQLWQPASGTLMTNDTND-TNPEEVVPCFALSKNDSYVMSASGGKISLFNMMTFKTMTTFMPAPPAATFLAFHPQDNNIIAIGM    922
At-tpr3   AEILDPSQCFQATLPDTAGSSTKVVQLLYTNSGAGILALGSNGIQRLWKWVPNEQNPSGKATATVVPQHWQPNSGLLMTNDVSG-VNLENAAPCIALSKNDSYVMSAAGGKVSLFNMMTFKVMTTFMPPPPASTFLAFHPQDNNVIAIGM    898
Sl-tp13   TEILDQAQCRLVTMPESSDSNNKVARLLYTNSGVGILALGSNGTQKLWKWTRNEQNPSGKATANVVPQYWQPNSGLLMTNDIVG-INLEEAVPCIALSKNDSYVMSAAGGKVSLFNMMTFKVMTTFMPPPPASTFLAFHPQDNNIIAIGM    912
At-tpr2   TEIVDPTQCRQVTMPDSKDSVSKVARLLYTNSGVGVLALGSNGVQRLWKWIRNEQNPTGKATASVTPQHWQPNSGLLMANDVP--ENPEGSVPCIALSKNDSYVMSACGGKVSLFNMMTFKVMTTFMPPPPASTFLAFHPQDNNIIAIGM    909
Sl-tp12   SDIADSSQLKTLKLPDP-LSASKVLRLLYTNSGLSVLALSSNAIHKLWKWQRNERNPSGKSSAAVVPQLWQPTNGALMSNDVGDAKSAEDAAACIALSKNDSYVMSASGGKVSLFNMMTFKVMTTFMPPPPAATYLAFHPQDNNVIAVGM    916
Sl-tp16   SKVVQISRCQSLRLPSE-VKTNKVCRLAYAQAGNILVALVTGGIHLIWKWSESDSNLTGQTTPKCTPQLWQPRSGVVPENSLLS-SDAGAVSPCIALTNNGFYALSASGGAVSIFNINLYKIMKSITPPKPAATCIACHPTNNNVIAVGM    1017
          ......910......920......930......940......950......960......970......980......990......1000......1010......1020......1030......1040......1050
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At-tp1    DDSTIQIYNVRVDEVKSKLKGHSKRITGLAFSNVLNVLVSSGADAQLCVWNTDGWEKQRSKVLPLPQGRPNSAPSDTRVQFHQDQAHFLVVHETQLAIYETTKLECMKQWAVRE-SLAPITHATFSCDSQLVYASFMDATVCVFSSANLR    1062
At-tpr1   DDSTIQIYNVRVDEVKSKLKGHSKRITGLAFSNVLNVLVSSGADAQLCVWNTDGWEKQKSKVLQIPQGRSTSSLSDTRVQFHQDQVHFLVVHETQLAIYETTKLECMKQWPVRE-SAAPITHATFSCDSQLIYTSFMDATICVFSSANLR    1050
Sl-tpl1   DDSTIQIYNVRVDEVKSKLKGHSKRITGLAFSHVLNVLVSSGADSQLCVWSTDGWEKQRARTLQLP-GRSTSQ-SDTRVQFHQDQTHFLAVHEAQIAIFETTKLECLKQWPVRE-SAAPISHATFSCDSQLIYASFLDATVCVFTAGHLH    1061
At-tpr4   DDSTIQIYNVRVDEVKSKLKGHQKRVTGLAFSNVLNVLVSSGADSQLCVWSMDGWEKQASKQIQIPSGHSPNPLAHTRVQFHQDQIHVLVVHASQLAIYEAPKLENMKQWIPKE-SSGSVTDAVYSCDSQSIYAAFDDGSVSILTATTLQ    1072
Sl-tp14   EDSSIQIYNVRVDEVKSKLKGHQKRVTGLAFSSVLNVLVSSGADAQLCVWSMDGWEKKASKFLQIPSGRAINPLAQTRVQFHQDQTHLLVVHETQIAIYEASKLECVKQWVS---PNFAVTDATYSCDSQSIFASFDDGSVSIFTAAALK    1068
Sl-tp15   DDSSIQIYNVRVDEVKTKLKGHQKRITGLAFSNSLNLISAGADSQLCVWSSDTWEKQTSKYLQIPAGRAAAPQADTRVQFHQDQTQLLVVHETQIAIFEAPKLECLKQWPRE-VTGPITHATYSCDSQSIFVSFEDASVGVLSAYTLR    1071
At-tpr3   EDSTIHIYNVRVDEVKSKLKGHQKRITGLAFSTALNILVSSGADAQICFWSIDTWEKRKSVAIQMPAGKAA--NGDTRVQFHVDQLRILVVHETQLAVFDASKMECIRQWIPQDSLSAPISSAVYACNSQLIYTTFRDGNIGVFDADSLR    1046
Sl-tp13   EDSTIHIYNVRVDEVKSKLKGHQKRITGLAFSTNLNILVSSGADAQLCLWSIDSWDKRKSVPIQLPAGKAP--SGDTRVQFHADQVRLLVSHETQLAIYDASKMERIRQWVPQDALSAPITYAAYSCNSQLVYASFSDGNIGVFDADTLR    1060
At-tpr2   EDSSIHIYNVRVDEVKTKLKGHQKHLTGLAFSTALNILVSSGADAQLFFWTADSWEKKKSSAIQLPPGKAP--VGDTRVQFHNDQIQLLVSHETQLAIYDASKMECIHKWVPQEALSSPITSASYSCNSQLVYASFADGNIAVFDAESLR    1057
Sl-tp12   EDSTIQIYNVRVDEVKIKLKGHQKRITGLAFSQSLNVLVSSGADSQLCIWSVDGWEKKKARPIQVPPGHQAPLVGETRVQFHNDQSHILVVHESQIGIYDI-QLECQRSWYPRDSLSAPISSAIYSCDGLLIFTGFCDGAIGIFDADSLR    1065
Sl-tp16   DDLTIIVYSVRTEELISRLNGHSKRITGLAFSNTMNVLVSSGADSQIVVWNSTNWEREGSTMLQTSADWLPTEVSETSVBFQRDEKCFLVVHETQIAIYEPTKLECVKQWIIKN-FCARISHATFSCDSEWIYAVMKDGIVLILSASDLS    1166
          ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160......1170......1180......1190......1200
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          : .: * :::.          * .::***.:.   *:*:.** * ::**   . :*                              :
At-tp1    LRCRVNPSAYLPA--SLSNSNVHPLVIAAHPQEPNMFAVGLSDGGVHIFEPLESEGKWGVAPPAEN----GSASGAPTAPSVGASASDQPQR    1148
At-tpr1   LRCRVNPSAYLPA--SLSNSNVHPLVIAAHPQESNMFAVGLSDGGVHIFEPLESEGKWGVAPPPEN----GSASAVTAIPSVGASASDQPQR    1136
Sl-tpl1   MRCRIIPSAYLSP--SISNSNIHPVVVAAHPQDPNQFALGLSDGSVHVFEPLESEGKWGVPPPLEN----GSTNGMPTAPSIGASGSDQAPR    1147
At-tpr4   LKCRIGPNSYLPS--NPS-SRVYPATVAAHPSEPNQFAVGLTDGGVHVIEPPGPEGKWGISAPPEN----GAG----PSVSSAP-GSDQQPR    1152
Sl-tp14   LRCRVNPAAYLPS--NPS-SRVYPLVVAAHPSESNQCAVGLTDGGVYVLEPLESEGKWGTPPPNEN----GVA----PGMSSAATGLDQASR    1149
Sl-tp15   WRCRINPTSYLPA--NPS-ARVHPLVIAAHPSDPNQFALGLNDGAVIVLEPLEAEGKWGMLPPADN----GNG----PSTSGAA-NSDQPQR    1151
At-tpr3   LRCRISPSAYLPQ----GNQGLSPLVVAAHPQDPNQFAVGLNDGSVKMMEPTEGEGKWGMIPPSE------------AINSPSTTSNQTPEQLQR    1125
Sl-tp13   LRCRVAPSAYLSQAVLTGSQSVYPLVVAAHPQEPSQFAVGLTDGTVKVIEPSESEGKWGVSPPVDN---GMLNGRVASSSTANNHAADQVQR    1149
At-tpr2   LRCRIAPSAYMPQPTP-NSAPIFPQVITAHPQEPNQLAVGLSDGSVKVIEPSELSRRWGVGVAAGSDKAGTENGRPSSSSAANNSSSDQIQR    1148
Sl-tp12   LRCRIAPSAYLSSIGS-GSGAAFPVVIAAHPSDSHQFALGMSDGTVHVIEPSDAEPKWGGSSSQEN----GAMPSIPSSSALNSQPSETPSR    1152
Sl-tp16   PKYEIDPSTFLTS-DLSCSAHVFPVVVAAHPENPNQLALGLNDGGVVVIEPSESDGKWCEPPNATT----------------LTNEQPI-    1238
          ......1210......1220......1230......1240......1250......1260......1270......1280......1290..
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Supplementary Table 1 : NLS prediction scores computed with cNLS Mapper (Kosugi et al, 2009)

SI-TPL	Score	Position	NLS sequence	Structure
SI-TPL1	6	588	RTYQGFRKRSLGVVQFDTTKNRFL	Bipartite
SI-TPL2	5	304	HLMKRMRAG	Monopartite
SI-TPL3	5.8	283	ILKRPLTPPATLGMLDYQSADHEQLMKRL	Bipartite
SI-TPL4	5.3/ 5	74	FEIRKQKYLEALDRHDQAKAVEILVKDLKV	Bipartite
		163	FPSLKNSRLRTLINQSLNWQHQLCKNPKP	
SI-TPL5	5.2/5.7	-37	FEIRKQKYLEALDRNDRPKAVEILVKDLKV	Bipartite
		-249	MLKRPRTPTNNSAVDYQTADSEHMLKRSRP	
SI-TPL6	4.1/ 4.2	-139	RNRIMKILRVVIETNPQLNGKLHFPELTKSRL	Bipartite
		-271	MPKPSKAISAATPAQLVKQMPGPSKAISA	