

**Supplement Figure S1:** Multiple sequence alignment between TRPS from *Melampsora larici*, *Puccinia striiformis*, *Puccinia sorghi*, *Puccinia graminis*, *Puccinia triticina* and the *Hemileia vastatrix* protein contig\_208623\_14257. The alignment was built by Muscle.

\* (asterisk) indicates positions which have a single, fully conserved residue.

: (colon) indicates conservation between groups of strongly similar properties - scoring > 0.5 in the Gonnet PAM 250 matrix.

. (period) indicates conservation between groups of weakly similar properties - scoring =< 0.5 in the Gonnet PAM 250 matrix.

```

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
MATHIRQVFANKAAQNLPVLTFTAGTFPHKQYVPLLLALEAGGADILELGIPTSDPLA
MAELRHVFSEKAAQNLPVLTFTAGTFPNPDATVPLMLAMEAGGADILELGVPTDPLA
MAVQLRNVFTEKARNLPVFTFTITAGTFPNQSTVPLMLAMEAGGADILELGVPTDPLA
MAAQLRDVFAQKASRELPLVFTFTITAGTFPNPESTVPLMLAMEAGGADILELGVPTDPLA
MAVQLRNVFTEKAARDLPVFTFTITAGTFPNPEATVPLMLAMEAGGADILELGVPTDPLA

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
DGVVIESNNIALSHNVNNTTCLGYVKEARKQGLKAPVILMGYYNPLMSYGEQLAVSEAK
DGAAIQESNNVALSHNVDPCLKFVSDARSQGLKAPVILMGYYNPLMAHGEQASVNDK
DGPATQESNNVALSHNVDPCLKFVSEARQGLKTPVILMGYYNPLMAHGEQASVNDK
DGPATQESNNVALSHNVDPCLKFVSEARSQGLKTPVILMGYYNPLMAHGEQASIDDAK
DGPATQESNNVALSHNVDPCLKFVSEARSQGLKAPVILMGYYNPLMAHGEQASIDAK

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
EAGANGFIVDLPPESAIFKIKCTSSGLSYVPLIAPSTSDSRITFLTSIADSFVYVVS
QAGANGFIVDLPPESAIFKIKCTSSGLSYVPLIAPSTSDSRITFLTSIADSFVYVVS
QAGANGFIVDLPPESAIFKIKCTSSGLSYVPLIAPSTSDSRITFLTSIADSFVYVVS
QAGANGFIVDLPPESAIFKIKCTSSGLSYVPLIAPSTSDSRITFLTSIADSFVYVVS

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
MGTGASNAVESLPLQVSRIRSLATAS- AEGPVPLAVGFGVSTPAHFDVGVAVGVV
LGTGTAQVETSLPDLIARIRKFSHTG- GDSIPLAVGFGISTADHFDHVGGLADGVV
LGTGTAQVETSLPDLIARIRKFSHTG- GDSIPLAVGFGISTADHFDHVGGLADGVV
LGTGTAQVETSLPDLIARIRKFSHTG- GDSIPLAVGFGISTADHFDHVGGLADGVV
LGTGTAQVETSLPDLIARIRKFSHTG- GDSIPLAVGFGISTADHFDHVGGLADGVV

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
GSKLLTFLEKEGGDQVINAATSFCEIICGGKSGRKRMESTSTVPT- -TWGN-
GSKIIIEIKLNQGEAGTKAQVEFCSEGLCGGKAGRPKKEKNGIMNGLVSKVSNLVTNGT
GSKIIIEIKLNQGEAGTKAQVEFCSEGLCGGKAGRPKKEKNGIMNGLVSKVSNLVTNGT
GSKIIIEIKLNQGEAGTKAQVEFCSEGLCGGKAGRPKKEKNGIMNGLVSKVSNLVTNGT
GSKIIIEIKLNQGEAGTKAQVEFCSEGLCGGKAGRPKKEKNGIMNGLVSKVSNLVTNGT

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
-----QTSNGTITTH-----SDTQNSSDYRFGFEGGOY
-----TAHPPTNGISKHE-----PTSETSLPYRFGFEGGOY
HPLTNGTSHVATNGNSHASTNASHPTNGTNGTSHSTKNGTSELPTPATSLPYRFGFEGGOY
-----NGTNGVNGIARPPVNGTSKQ-----PTPETSLPYRFGFEGGOY
-----AHPTNGTSKQ-----PTPDNSLPYRFGFEGGOY

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
VPESLVDCLLELEACHKAAKADPSFQAEFQSYGYMNRPSGLYAKRLTEKIGGAKIWF
VPEALVNCLELETCHEAMADPKFAEPKSYGYMNRPSGLYPAQLRTEHIGGAKIWF
VPEALVNCLELETCHEAMADPKFAEPKSYGYMNRPSGLYPAQLRTEHIGGAKIWF
VPEALVNCLELETCHEAMADPKFAEPKSYGYMNRPSGLYPAQLRTEHIGGAKIWF
VPEALVNCLELETCHEAMADPKFAEPKSYGYMNRPSGLYPAQLRTEHIGGAKIWF

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
REDLNHTGSHKINNVAQQLLALRLGKRIIAETGAGQHGAVATVCAKFGLECVVYMG
REDLNHTGSHKINNVAQQLLALRLGKRIIAETGAGQHGAVATVCAKFGLECVVYMG
REDLNHTGSHKINNVAQQLLALRLGKRIIAETGAGQHGAVATVCAKFGLECVVYMG
REDLNHTGSHKINNVAQQLLALRLGKRIIAETGAGQHGAVATVCAKFGLECVVYMG
REDLNHTGSHKINNVAQQLLALRLGKRIIAETGAGQHGAVATVCAKFGLECVVYMG

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
EDARRQALNVFRMKMLGAQVVAVTSGSOTLKDAINEAMRDWNTVSTTHYLVGSAIGPH
EDARRQALNVFRMKMLGAQVVAVTSGSOTLKDAINEAMRDWNTVSTTHYLVGSAIGPH
EDARRQALNVFRMKMLGAQVVAVTSGSOTLKDAINEAMRDWNTVSTTHYLVGSAIGPH
EDARRQALNVFRMKMLGAQVVAVTSGSOTLKDAINEAMRDWNTVSTTHYLVGSAIGPH
EDARRQALNVFRMKMLGAQVVAVTSGSOTLKDAINEAMRDWNTVSTTHYLVGSAIGPH

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
FPTIVRDFQSVIGREIKDQLFHSKLLPDAVACVGGGSNAIGTFHFFINETSVRMIGVE
FPTIVRDFQSVIGREIKDQLFHSKLLPDAVACVGGGSNAIGTFHFFINETSVRMIGVE
FPTIVRDFQSVIGREIKDQLFHSKLLPDAVACVGGGSNAIGTFHFFINETSVRMIGVE
FPTIVRDFQSVIGREIKDQLFHSKLLPDAVACVGGGSNAIGTFHFFINETSVRMIGVE
FPTIVRDFQSVIGREIKDQLFHSKLLPDAVACVGGGSNAIGTFHFFINETSVRMIGVE

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
AGGTGA---LHSATLTNGTKGLVHGVTYILQSSSGQVNTHTSISAGLDYAGVGPEHSYL
AGGSOTDTHSATLSKGTGKVLHGVLTYILQSSSGQVNTHTSISAGLDYAGVGPEHSYL
AGGSOTDTHSATLSKGTGKVLHGVLTYILQSSSGQVNTHTSISAGLDYAGVGPEHSYL
AGGSOTDTHSATLSKGTGKVLHGVLTYILQSSSGQVNTHTSISAGLDYAGVGPEHSYL
AGGSOTDTHSATLSKGTGKVLHGVLTYILQSSSGQVNTHTSISAGLDYAGVGPEHSYL

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
KDSGRAEYRVATDLEALKGFKDCVLEGLIIPALETAHAWGASQALAKLPGKDIVICF
KDSGRAEYRVATDLEALKGFKDCVLEGLIIPALETAHAWGASQALAKLPGKDIVICF
KDSGRAEYRVATDLEALKGFKDCVLEGLIIPALETAHAWGASQALAKLPGKDIVICF
KDSGRAEYRVATDLEALKGFKDCVLEGLIIPALETAHAWGASQALAKLPGKDIVICF
KDSGRAEYRVATDLEALKGFKDCVLEGLIIPALETAHAWGASQALAKLPGKDIVICF

contig_208623_14257
TrpS_Melampsora_larici
TrpS_Puccinia_striiformis
TrpS_Puccinia_sorghi
TrpS_Puccinia_graminis
TrpS_Puccinia_triticina
F-----
SGRGDKDVEQIAQQLPKFADALDWHIAP
SGRGDKDVEQIAQQLPKFADALDWHIAP
SGRGDKDVEQIAQQLPKFADALDWHIAP
SGRGDKDVEQIAQQLPKFADALDWHIAP
SGRGDKDVEQIAQQLPKFADALDWHIAP

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**Supplement Figure S2:** Multiple sequence alignment between TRPS from *Melampsora larici*, *Puccinia striiformis*, *Puccinia sorghi*, *Puccinia graminis*, *Puccinia triticina* and the newly annotated *Hemileia vastatrix* Tryptophan synthase. The alignment was built by Muscle.

\* indicates positions which have a single, fully conserved residue.  
: indicates conservation between groups of strongly similar properties - scoring > 0.5 in the Gonnet PAM 250 matrix.  
. indicates conservation between groups of weakly similar properties - scoring ≤ 0.5 in the Gonnet PAM 250 matrix.

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TrpS_Hemileia_vastatrix      MSADIKRVFATNSQLNIPVFISFVTAGFFPHDPLTVPIILLALQAAGSHIIELGIPFTDPLA
TrpS_Melampsora_larici      MATHIRGVFANKAQNLPVLVTLTAGFFPHKVTVPVLLALEAGGADIIELGIPFSDPLA
TrpS_Puccinia_striiformis   MAEELRHVFSEKAAQNLPFVFTFITAGYPNPDDATVPLMLAMEAGGADIELGVPFTDPLA
TrpS_Puccinia_sorghi        MAVQLRNVFTEKEARNLPVFVFTFITAGYPNPSTVPLMLAMEAGGADIELGVPFTDPLA
TrpS_Puccinia_graminis      MAQQLRDVFAQKASRELVPFVFTFITAGYPNPSTVPLMLAMEAGGADIELGVPFTDPLA
TrpS_Puccinia_triticina     MAVQLRNVFTEKAARDLPFVFTFITAGYPNPATVPLMLAMEAGGADIELGVPFTDPLA
*.:.:.:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      DGPAIQSANNVALKHNVSFKDITLNLLSLARQRLSPVVPVLMGYNPNFLAHGEAQAVVDAK
TrpS_Melampsora_larici      DGAAIQSSNNVALSHNVVDYRCLKFVSEARSQGLKAPVILMGYYNPLMSYGEQLAVSEAK
TrpS_Puccinia_striiformis   DGPALQSSNNVALSHNVDPQCLKFVSEARSQGLKTPVILMGYYNPLMAHGEQASVNDK
TrpS_Puccinia_sorghi        DGPALQSSNNVALSHNVDRKCLQFVSEARSQGLKTPVILMGYYNPLMAHGEQASIDDAK
TrpS_Puccinia_graminis      DGPALQSSNNVALSHNVDRKCLKFVSEARSQGLKAPVILMGYYNPLMAHGEQASIDDAK
TrpS_Puccinia_triticina     DGAIPQSSNNVALSHNVDRKCLKFVSEARSQGLKAPVILMGYYNPLMAHGEQASIDDAK
**.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      KARANGFIIVDLPPEEATTFRQYCTDHQMSYIPLIAPSTPDHRIEFIKSIADSFYVVVSK
TrpS_Melampsora_larici      EAGANGFIIVDLPPEEAKFRKICTSSGLSVPLIAPSTSDSRITFLTISIADSFYVVVSK
TrpS_Puccinia_striiformis   QAGANGFIIVDLPPEEAVKFRITLCTGAGLSYVPLIAPTTTGSRTITFLSSIADSFYVVVSK
TrpS_Puccinia_sorghi        QAGANGFIIVDLPPEEAVKFRITLCTGAGLSYVPLIAPTTTGSRTITFLSSIADSFYVVVSK
TrpS_Puccinia_graminis      QAGANGFIIVDLPPEEAVKFRITLCTGAGLSYVPLIAPTTTGSRTITFLSSIADSFYVVVSK
TrpS_Puccinia_triticina     QAGANGFIIVDLPPEEAVKFRITLCTGAGLSYVPLIAPTTTGSRTITFLSSIADSFYVVVSK
.*.*****.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      MGVTGASALLEEYLPNLLQKIK---SSGSKSPHLAVGFGISTPSHFDHVASLAEGVVV
TrpS_Melampsora_larici      MGTGTGASNAVESSLPOLVSRIRSLAT-ASAEQVPLAVGFGVSTPAHFDEVGAVANGVVI
TrpS_Puccinia_striiformis   LGTTGATAQVETSLPDLIARIRKFSH-ASGHPPIPLAVGFGISTADHFDHVGGLADGVVV
TrpS_Puccinia_sorghi        LGTTGASEKVATSLPDLIARIRKFSH-TGGDNSIPLAVGFGISTADHFDHVGGMADGVVV
TrpS_Puccinia_graminis      LGTTGATEKVATSLPDLISIRIRKFSHTTDANKSIPLAVGFGISTADHFDHVGGLADGVVV
TrpS_Puccinia_triticina     LGTTGTSEKVATSLPDLISIRIRKFSH-AGTDNSIPLAVGFGISTADHFDHVGGLADGVVV
*.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      GSKLSEFFNDAP--KFDQLIQFCKTLTNSNN-KPRTSPSLSDL-----
TrpS_Melampsora_larici      GSKLLTFLKEQEGDQVINAATSFCEIICGGKSGRKRMESTVPT-----TNGN-
TrpS_Puccinia_striiformis   GSKIIIEVLKNOGEAGTKAVQEFCEGLCGGKAGRPKEKEKENGIMGLVSKNLSNLTNGT-
TrpS_Puccinia_sorghi        GSKIIIEVLKNOGEAGTKAVQEFCEGLCGGKAGRPKEKPLKTAMSHLTSQLSNLVTNGTS
TrpS_Puccinia_graminis      GSKIIIEVLKNOGEAGTKAVQEFCEGLCGGKAGRPKEKGINIATNLVSQLSTLMTNGT-
TrpS_Puccinia_triticina     GSKIIIEVLKNOGEAGTKAVQEFCEGLCGGKAGRPKEKAPVKNAINGLVSQLSTLMTNGH-
**.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      -----PKLDSLNPT-----MPQTSSSSLSKISTGRFG
TrpS_Melampsora_larici      -----QTSNGTITT-----HSDTQNSDY-----RFG
TrpS_Puccinia_striiformis   -----TAHPPTNGISKH-----EPTSETSLPY-----RFG
TrpS_Puccinia_sorghi        HPLTNGTSHVATNGNSHASTNASSHPSTNGTSKNGTSELPTPATSLPY-----RFG
TrpS_Puccinia_graminis      -----NGTNGVNGIARPPVNGTSK-----QPTPETSLPY-----RFG
TrpS_Puccinia_triticina     -----AHPPTNGTSK-----OPTDNLSPY-----RFG
*.:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      SFGGQYVPEIIWQCLVELEAAHYNAMHDPVFLDEFKSYGYGMNRPFSQLYHATRLTQAWGG
TrpS_Melampsora_larici      EFGGQYVPEALVNCLELETCHREAMADPKFQAEFKSYGYGMNRPFSGLYFAERLTEHVGG
TrpS_Puccinia_striiformis   EFGGQYVPEALVNCLELETCHREAMADPKFQAEFKSYGYGMNRPFSGLYFAERLTDHIGG
TrpS_Puccinia_sorghi        EFGGQYVPEALVDCLELETCHREAMADPKFQAEFKSYGYGMNRPFSGLYFAERLTEHVGG
TrpS_Puccinia_graminis      EFGGQYVPEALVDCLELETCHREAMADPKFQAEFKSYGYGMNRPFSGLYFAERLTEHVGG
TrpS_Puccinia_triticina     EFGGQYVPEALVDCLELETCHREAMADPKFQAEFKSYGYGMNRPFSGLYFAERLTEHVGG
.******:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      ANIWLKREDLNHTGSHKINNNAVQILLAKRLGKSRIIAETGAGQHGVTATVCARFGMEC
TrpS_Melampsora_larici      AKIWFKREDLNHTGSHKINNNAVQILLAKRLGKSRIIAETGAGQHGVTATVCARFGLEC
TrpS_Puccinia_striiformis   AKIWFKREDLNHTGSHKINNNAVQILLAKRLGKTRIIAETGAGQHGVTATVCARFGLEC
TrpS_Puccinia_sorghi        AKIWFKREDLNHTGSHKINNNAVQILLAKRLGKTRIIAETGAGQHGVTATVCARFGMEC
TrpS_Puccinia_graminis      AKIWFKREDLNHTGSHKINNNAVQILLAKRLGKTRIIAETGAGQHGVTATVCARFGMEC
TrpS_Puccinia_triticina     AKIWFKREDLNHTGSHKINNNAVQILLAKRLGKTRIIAETGAGQHGVTATVCARFGMEC
*:*:*****.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      VVYMGEDARRQALNVFRMRMLGAKVVCVAGSGRTLKDAISFVDEAMRDWATNLSVTHYL
TrpS_Melampsora_larici      VVYMGAEADARRQALNVFRMRMLGAKVVAVTSGSQTLKDAI--NEAMRDWVTNLTSTHYL
TrpS_Puccinia_striiformis   VVYMGAEADARRQSLNVFRMRMLGAKVVAVTSGSQTLKDAI--NEAMRDWVANVHTHYL
TrpS_Puccinia_sorghi        VVYMGAEADARRQSLNVFRMRMLGAKVVAVTSGSQTLKDAI--NEAMRDWVTNVSTHYL
TrpS_Puccinia_graminis      VVYMGAEADARRQSLNVFRMRMLGAKVVAVTSGSQTLKDAI--NEAMRDWVTNVSTHYL
TrpS_Puccinia_triticina     VVYMGAEADARRQSLNVFRMRMLGAKVVAVTSGSQTLKDAI--NEAMRDWVTNVSTHYL
*****.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      VGSAIGHPFPPTIVRDFQSVIGKEIKDQLFHSKKLDPDAVVACVGGGSNAIGAFAPFVEE
TrpS_Melampsora_larici      VGSAIGHPFPPTIVRDFQSVIGNEIKEQMQAQIIGGLPDAVIACVGGGSNAIGTFYSFLPD
TrpS_Puccinia_striiformis   VGSAIGHPFPPTIVRDFQSVIGREIKEIMSEVGLPDAVIACVGGGSNAIGTFHFPIDD
TrpS_Puccinia_sorghi        VGSAIGHPFPPTIVRDFQSVIGREIREQLMSEIGKLPDAVIACVGGGSNAIGTFHFPINE
TrpS_Puccinia_graminis      VGSAIGHPFPPTIVRDFQSVIGREIKDQLLAIEIGKLPDAVIACVGGGSNAIGTFHFPINE
TrpS_Puccinia_triticina     VGSAIGHPFPPTIVRDFQSVIGREIKEQLLAIEIGKLPDAVIACVGGGSNAIGTFHFPINE
*****.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      KSVRLGVGEAGGTGA--LHSATLTNGTKVGLHGVMTYILQSSSGQVENVTHSISAGLDYA
TrpS_Melampsora_larici      KSVRLIGVEAGSGTSGHEHSATLSKGTGKVLHGVLTLYILQSSSDGQISETHSISAGLDYP
TrpS_Puccinia_striiformis   KSVRMIGVEAGSGGLDGDQHSATLSKSGSKVLHGVLTLYILQSSSQISETHSISAGLDYP
TrpS_Puccinia_sorghi        TSVRMIGVEAGSGTDTDRHSATLSKGTGKVLHGVLTLYILQSSPGQISETHSISAGLDYP
TrpS_Puccinia_graminis      KSVRMIGVEAGSGTDTDRHSATLSKGTGKVLHGVLTLYILQSSSGQISETHSISAGLDYP
TrpS_Puccinia_triticina     KSVRMIGVEAGSGTDTDRHSATLAKGTGKVLHGVLTLYILQSSPGQIATHSISAGLDYP
*:*:*****.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      GVGPESYLYKDSGRAEYRVATDLEALKGFKDCVLEGIIPALETAAHAWGASQALAKLGP
TrpS_Melampsora_larici      GVGPESHAYLKDAGRAEYRVATDVEALKGFKMCVEQEGIIPALETAAHAIWSTADVAREVGK
TrpS_Puccinia_striiformis   GVGPESHFLKDAGRAEYRVATDLEALKGFRLCVQYEGIIPALETAAHAIWSTAEVARELGR
TrpS_Puccinia_sorghi        GVGPESHFLKDAGRAEYRVATDLEALKGFRLCVQYEGIIPALETAAHAIWSTAEVARELGR
TrpS_Puccinia_graminis      GVGPESHFLKDAGRAEYRVATDLEALKGFRLCVQYEGIIPALETAAHAIWSTAEVARELGR
TrpS_Puccinia_triticina     GVGPESHFLKDAGRAEYRVATDLEALKGFRLCVQYEGIIPALETAAHAIWSTAEVARELGR
*****.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

TrpS_Hemileia_vastatrix      GKDIVISFSGRGDKDVEEVSRRLPPEFAKELNWHIAPEKISHGNSAS
TrpS_Melampsora_larici      DANIVMCLSGRGDKDVEQIAQQLPKFADALDWHIAP-----
TrpS_Puccinia_striiformis   DANIVMCLSGRGDKDVEQIAQQLPKFADALDWHIAP-----
TrpS_Puccinia_sorghi        GANIVMCLSGRGDKDVEQIAQQLPKFADALDWHISS-----
TrpS_Puccinia_graminis      DANIVMCLSGRGDKDVEQIAQQLPKFADALDWHISP-----
TrpS_Puccinia_triticina     DANIVMCLSGRGDKDVEQIAQQLPKFADALDWHIAP-----
*.:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:.*:

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**Supplementary Figure S3:** Structural superposition of 3D models for TRPS. In blue the AlphaFold result for *H. Vastatrix* Tryptophan synthase. In green the Modeller 3D0 proposed structure for *H. Vastatrix* Tryptophan synthase. RMSD between pruned atoms was 1.018 Angstroms.

