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Supporting Information

# Rationally Designed Novel Antimicrobial Peptides Targeting Chitin Synthase for Combating Soybean Phytophthora Blight

Yue Ran, Kiran Shehzadi, Jian-Hua Liang \* and Ming-Jia Yu \*

School of Chemistry and Chemical Engineering, Beijing Institute of Technology, Beijing 100081, China

\* Correspondence: ljhbit@bit.edu.cn (J.-H.L.); mjyu@bit.edu.cn (M.-J.Y.)

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**Table S1.** Library of antimicrobial peptides with inhibitory activity against *Phytophthora*.

Serial number	Amino acid sequence	Plant pathogen	Inhibition efficacy	Reference
01	NH <sub>2</sub> -GIGKFLHSAKKFGKAF VGEIMNS-COOH	<i>Phytophthora infestans</i>	MIC=40 (µg/ml)	1
02	NH <sub>2</sub> -GLWGTLGGLFGWLGA AGKTTGSARAKQRLKLMAG -COOH	<i>Phytophthora infestans</i>	MIC=20 (µg/ml)	1
03	NH <sub>2</sub> -KWKVFKKIEKMGRNIR NGIVKAGPAIAVLGEAKAL- COOH	<i>Phytophthora infestans</i>	MIC=20 (µg/ml)	1
04	NH <sub>2</sub> -EWKLLKKIGAVLKLKLV-C OOH	<i>Phytophthora infestans</i>	MIC=15 (µM)	2
05	NH <sub>2</sub> -KWKLFFKKILKVL-COO H	<i>Phytophthora infestans</i>	MIC=15 (µM)	2
06	NH <sub>2</sub> -WKLFKKILKVL-COOH	<i>Phytophthora infestans</i>	MIC=15 (µM)	2
07	NH <sub>2</sub> -KWKLFFKKIGIGAVLKV LTTGLPALIS-COOH	<i>Phytophthora infestans</i>	MIC=40 (µM)	2
08	NH <sub>2</sub> -GIFSKLAGKKLKNLLIS GL-COOH	<i>Phytophthora nicotianae</i>	MIC=12 (µM)	3
09	NH <sub>2</sub> -GIFSKLAGKKLKNLLIS GLKNVGKEVGLDVVRTGIDI AGCKIKGEC-COOH	<i>Phytophthora nicotianae</i>	MIC=75 (µM)	3
10	NH <sub>2</sub> -EGPVGLADPDGPASAP LGAP-COOH	<i>Phytophthora capsici</i>	EC <sub>50</sub> =3.14 (µg/ml)	4
11	NH <sub>2</sub> -FRLKFH-COOH	<i>Phytophthora infestans</i>	IC <sub>50</sub> =56 (µM)	5
12	NH <sub>2</sub> -RLARLAR-COOH	<i>Phytophthora infestans</i>	IC <sub>50</sub> =910 (µM)	5
13	NH <sub>2</sub> -WKLFKKILKVL-COOH	<i>Phytophthora infestans</i>	IC <sub>50</sub> =17 (µM)	5
14	NH <sub>2</sub> -MASRAARLAARLARLA LRAL-COOH	<i>Phytophthora infestans</i>	IC <sub>50</sub> =14 (µM)	5
15	NH <sub>2</sub> -YSYKKIDCGGACAARO RLSSRPRLCNRACGTCCARC NCVPPGTSGNTETCPCYASL TTHGNKRKCP-COOH	<i>Phytophthora cucumerina</i>	EC <sub>50</sub> =10 (µM)	6
16	NH <sub>2</sub> -GSNFCDSKCKLRCSKA	<i>Phytophthora cucumerina</i>	EC <sub>50</sub> =10 (µM)	6

GLADRCLKYCGICOECKVV

PSGTYGNKHECPCYRDKN

SKGKSKCP-COOH

**Table S2.** The interaction of hydrogen bonds between AMP\_04 and chitin synthase.

Antimicrobial peptide	Receptor residue	Ligand residue	Hydrogen bond [Å]	Hydrogen bond angle [°]
AMP_04	r:SER534	l:ASP8	2.4064	131.532
	r:ASP382	l:ALA13	2.2816	149.906
	r:PRO454	l:SER14	1.9174	173.496
	r:ASP440	l:GLY18	2.5774	119.957
	r:LYS355	l:GLY2	1.9231	143.658
	r:SER436	l:PRO16	2.1238	157.535
	r:SER436	l:LEU17	2.3747	100.13
	r:SER451	l:PRO20	2.5826	160.587
	r:ARG497	l:PRO20	2.0833	129.641
	r:LYS537	l:LEU6	2.4322	135.489
	r:ARG538	l:GLU1	2.7702	118.131
	r:ARG538	l:PRO9	2.5881	130.017
	r:ARG538	l:PRO3	2.299	116.71
	r:TRP539	l:ALA13	2.9607	106.998
	r:TYR492	l:PRO3	2.4986	140.745
	r:ASP524	l:PRO12	3.0166	128.342
	r:ASP382	l:PRO12	2.623	143.675
	r:PRO454	l:ALA13	2.6924	130.504
	r:ARG538	l:ASP8	3.0407	118.905

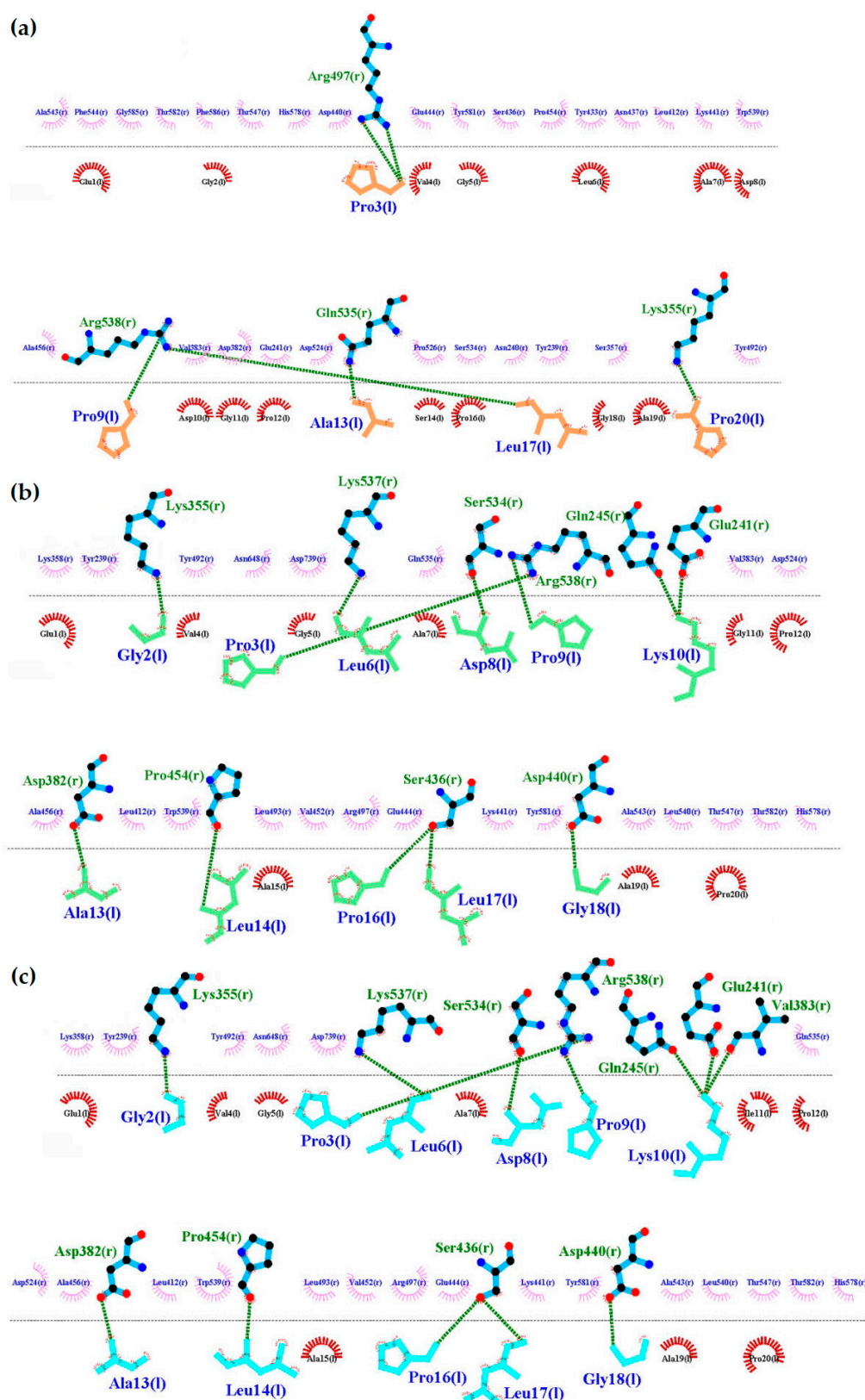
**Table S3.** The interaction of hydrogen bonds between DP and chitin synthase.

Antimicrobial peptide	Receptor residue	Ligand residue	Hydrogen bond [Å]	Hydrogen bond angle [°]
AMP_04_D10k_S14L (DP)	r:SER534	l:ASP8	2.4061	131.554
	r:VAL383	l:LYS10	2.7573	125.104
	r:GLU241	l:LYS10	2.2056	153.118
	r:GLN245	l:LYS10	2.0885	120.851
	r:ASP382	l:ALA13	2.2695	149.456
	r:PRO454	l:LEU14	1.9228	170.018
	r:ASP440	l:GLY18	2.5774	119.957
	r:LYS355	l:GLY2	1.9236	143.631
	r:SER436	l:PRO16	2.1215	157.315
	r:SER436	l:LEU17	2.3509	101.574
	r:SER451	l:PRO20	2.5726	160.775

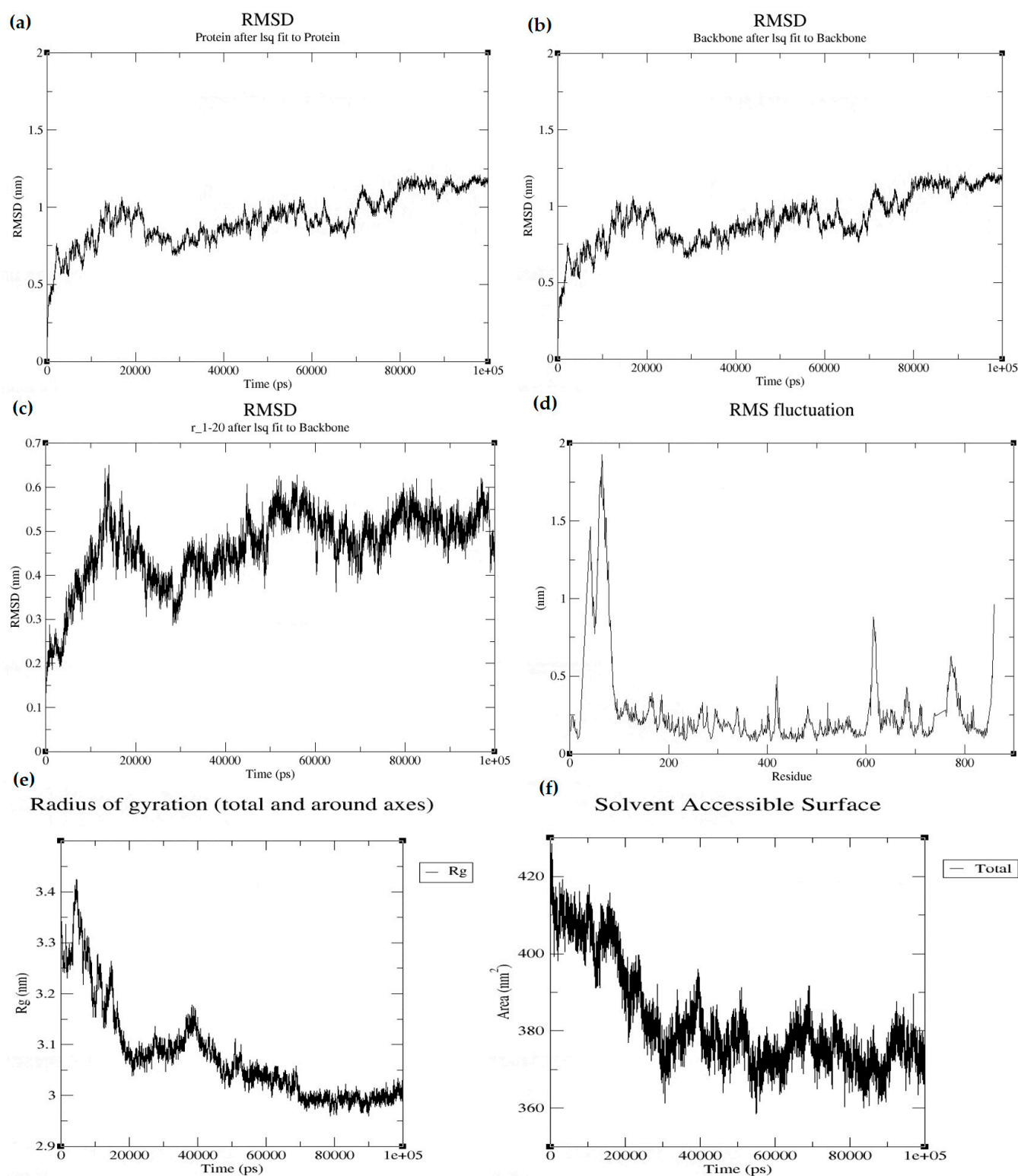
r:ARG497	l:PRO20	2.0696	129.543
r:ARG497	l:ALA19	2.8065	164.996
r:LYS537	l:LEU6	2.4322	135.489
r:ARG538	l:GLU1	2.8071	116.936
r:ARG538	l:PRO9	2.5597	131.470
r:ARG538	l:PRO3	2.3190	117.634

**Table S4.** The interaction of hydrogen bonds between TP and chitin synthase.

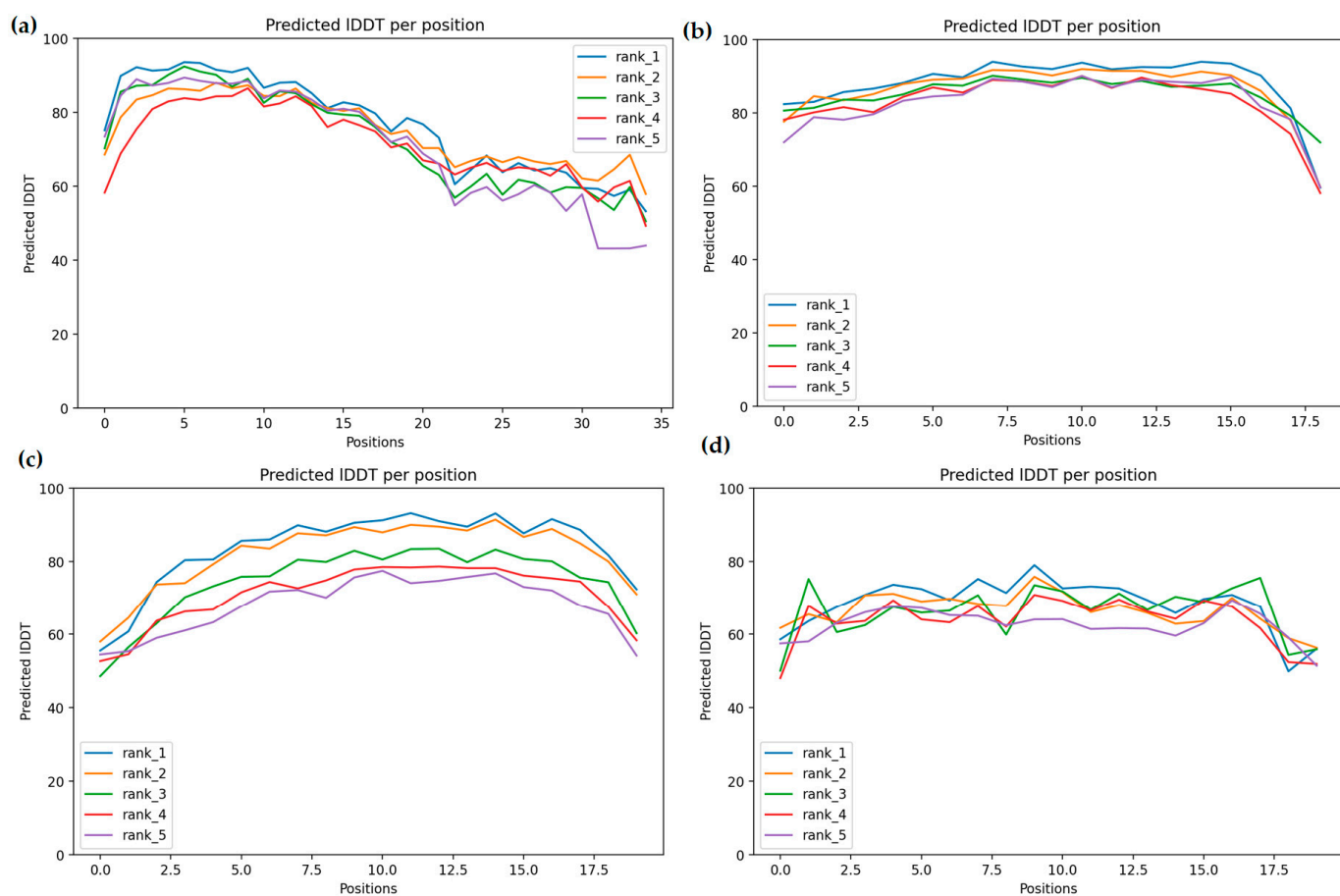
Antimicrobial peptide	Receptor residue	Ligand residue	Hydrogen bond [Å]	Hydrogen bond angle [°]
AMP_04_D10K_G11I_S14L (TP)	r:SER534	l:ASP8	2.4062	131.540
	r:VAL383	l:LYS10	2.3032	140.361
	r:GLU241	l:LYS10	2.0644	149.860
	r:GLN245	l:LYS10	2.2089	124.333
	r:ASP382	l:ALA13	2.2670	148.960
	r:PRO454	l:LEU14	1.9229	169.958
	r:ASP440	l:GLY18	2.5774	119.957
	r:LYS355	l:GLY2	1.9236	143.620
	r:SER436	l:PRO16	2.1211	157.251
	r:SER436	l:LEU17	2.3506	101.568
	r:SER451	l:PRO20	2.5739	160.843
	r:ARG497	l:PRO20	2.0620	130.102
	r:ARG497	l:A19	2.8067	165.384
	r:LYS537	l:LEU6	2.4301	135.709
	r:ARG538	l:GLU1	2.9462	114.847
	r:ARG538	l:PRO9	2.4624	134.716
	r:ARG538	l:PRO3	2.4198	118.125
	r:ARG538	l:GLU1	3.0346	114.473
	r:TRP539	l:ALA13	2.8935	116.991



**Figure S1.** The interaction between the receptor (in deep blue) and the ligand displayed by LigPlot+. (a) The 2D interaction map between the receptor and AMP\_04, with AMP\_04 depicted in orange. (b) The 2D interaction map between the receptor and the double mutant DP, with DP represented in green. (c) The 2D interaction map between the receptor and the triple mutant TP, with TP shown in sky blue.



**Figure S2** Molecular dynamics simulation results between TP and chitin synthase. (a) Overall RMSD plot of the receptor-lig and protein. (b) RMSD plot of the receptor-ligand backbone. (c) RMSD plot of the antimicrobial peptide TP. (d) RMSF plot of the overall receptor-ligand protein. (e) Gyration radius plot of the overall receptor-ligand protein. (f) Solvent accessible s urface area plot of the overall receptor-ligand protein.



**Figure S3** Predicting pLDDT plots of four antimicrobial peptides using alphafold2. (a) AMP\_01. (b) AMP\_02. (c) AMP\_03. (d) AMP\_04.

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