

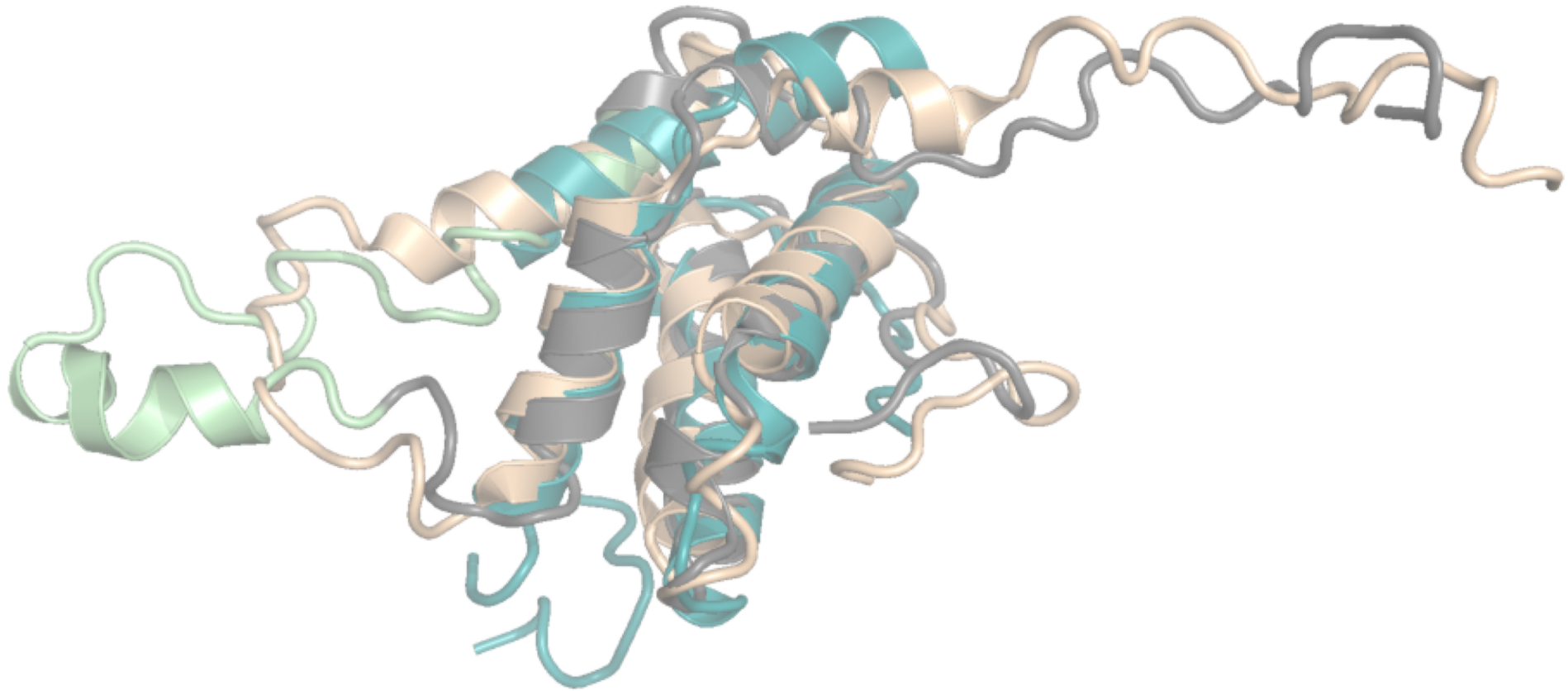
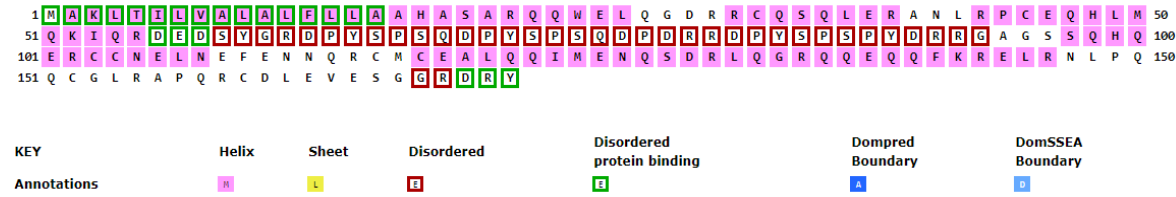


Figure S3A. Structural overlay of *A. hypogaea* 2.02 Ara h 2 homology model (dark grey), Ara h 2 NMR structure (PDB ID: 3OB4) with MBP removed for clarity (deep teal), and Ara h 6 NMR structure (PDB ID: 1W2Q , tan). Structures are shown as cartoon. The loop region that contains epitope 6, 7, and 7b in the homology model is shown as light green to denote it being missing from the Ara h 2 NMR structure.

A.



B.

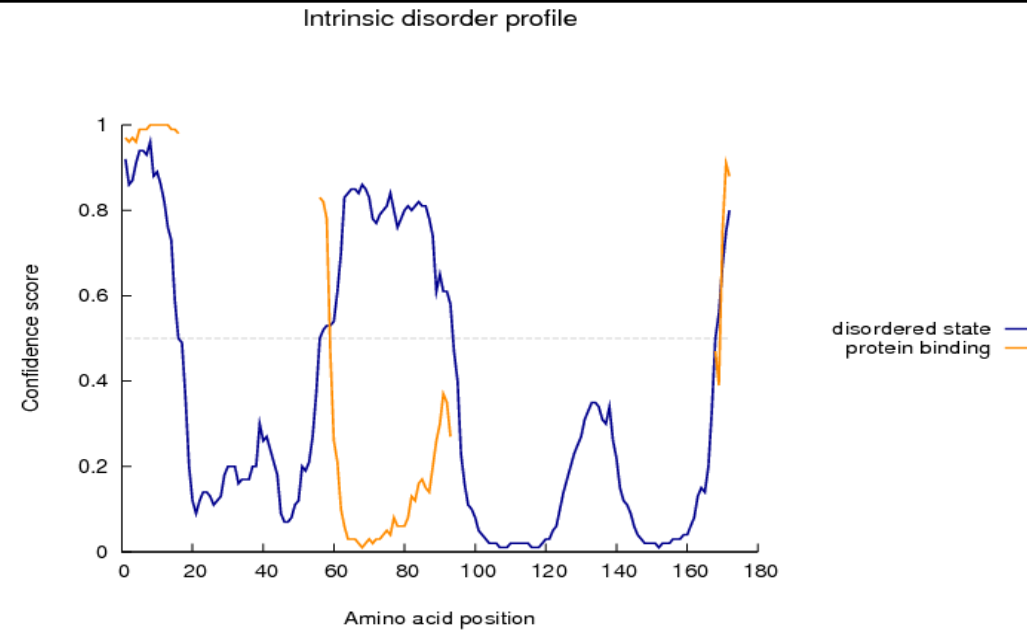


Figure S3B. PSIPRED sequence based disordered and disordered protein binding results for *A. ipaensis* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. , See figure legends for coloring descriptions.

A.

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1  M A K L T I L V A L A L F L L A A H A S A R Q Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
51 Q K I Q R D E D S Y E R D P Y S P S Q D P Y S P S P Y D R R G A G S S Q H Q E R C C N E L N E F E N 100
101 N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R A P Q R C D L 150
151 D V E S G G R D R Y

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KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
Annotations	M	L	E	G	A	O

B.

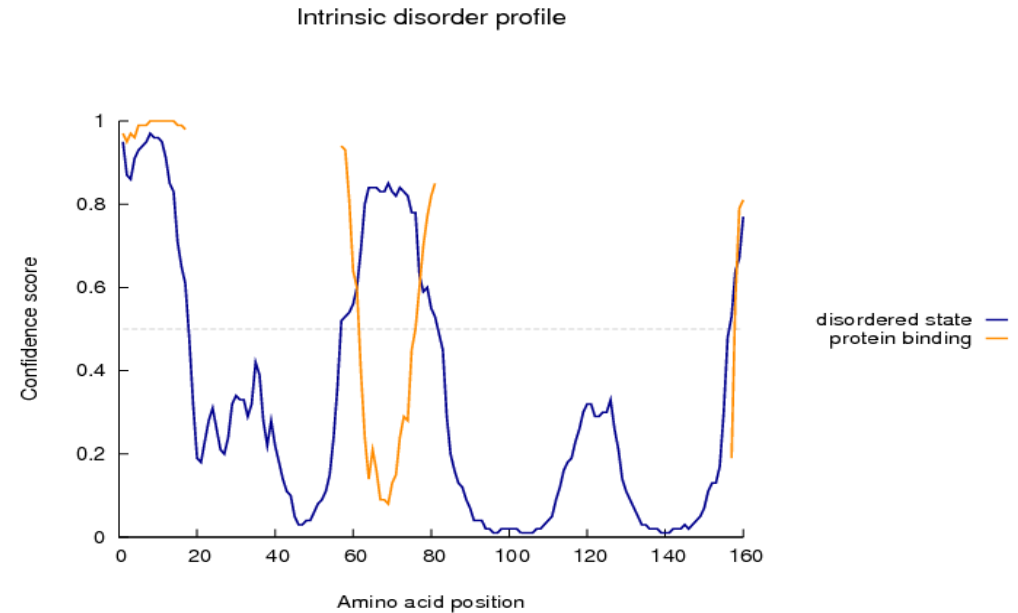


Figure S3C. PSIPRED sequence based disordered and disordered protein binding results for *A. duranensis* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. , See figure legends for coloring descriptions.

A.

1 M A K L T I L V A L A L F L L A H A S A R Q Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
 51 Q K I Q R D E D S Y E R D P Y S P S Q D P Y S P S P Y D R R G A G S S Q H Q E R C C N E L N E F E N 100
 101 N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R A P Q R C D L 150
 151 D V E S G G R D R Y

KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
Annotations	H	L	E	B	A	D

B.

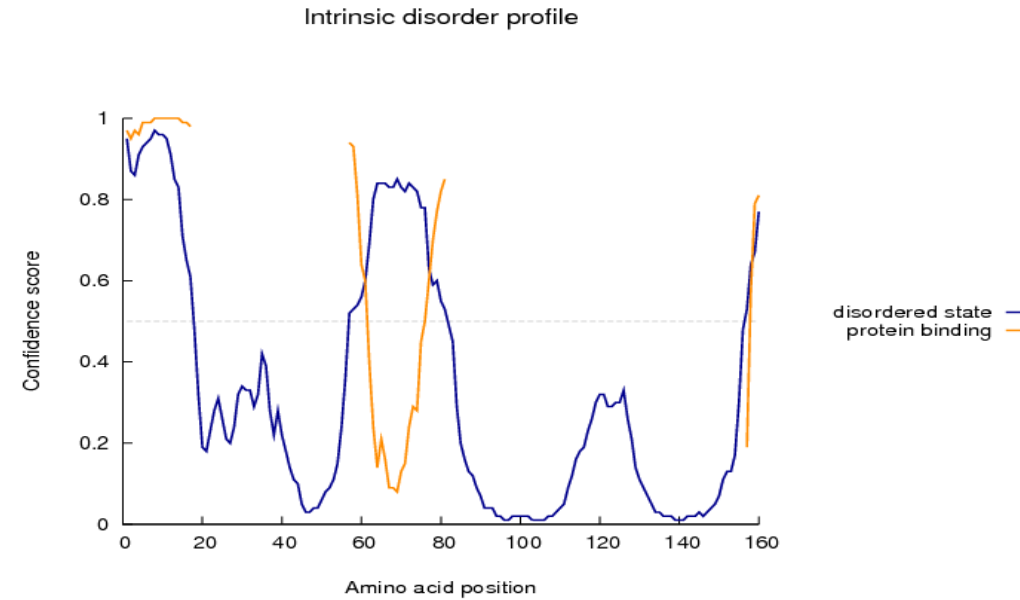
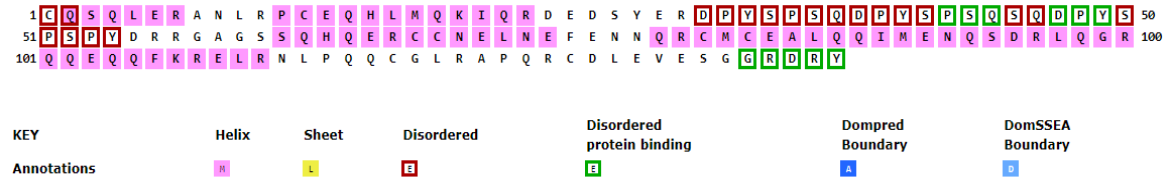


Figure S3D. PSIPRED sequence based disordered and disordered protein binding results for *A. hypogaea* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. , See figure legends for coloring descriptions.

A.



B.

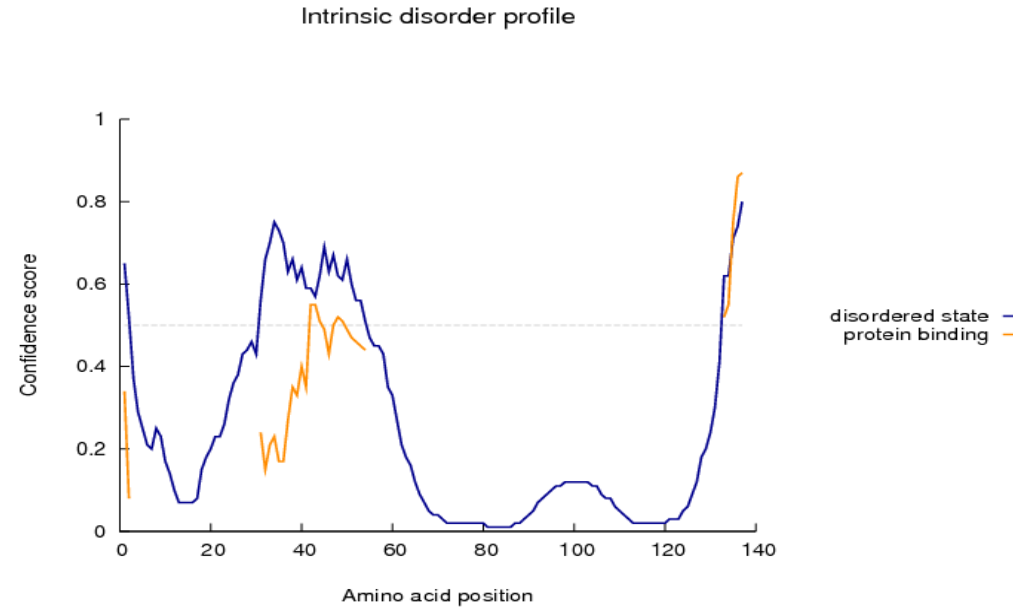


Figure S3E. PSIPRED sequence based disordered and disordered protein binding results for *A. monticola* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

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1  M A K L T I L V A L A L L L L A A H A S A R Q Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
51  Q K I Q R D Q S P Y S Q D P Y R Q E P Y E Y E S H D R R R A G S S Q H Q E R C C N E L N E F E N N Q 100
101 R C M C Q A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G F R A P Q R C D L E I 150
151 E S G G R D R Y

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KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
Annotations	R	L	D	E	A	B

B.

Intrinsic disorder profile

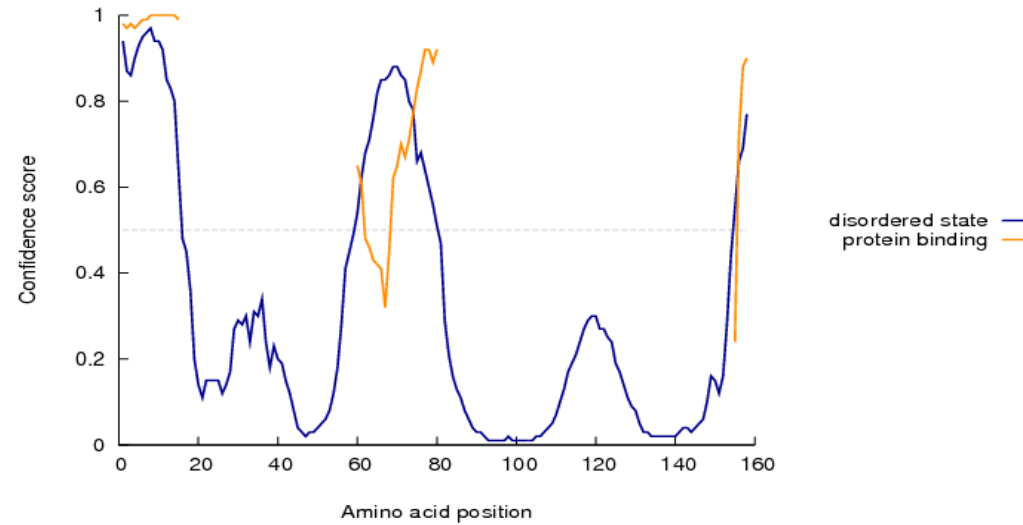
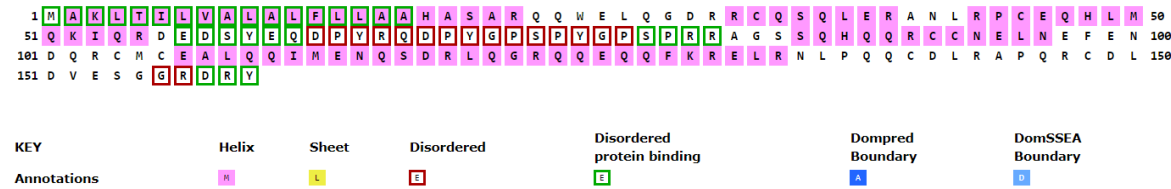


Figure S3F. PSIPRED sequence based disordered and disordered protein binding results for *A. triseminiata* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.



B.

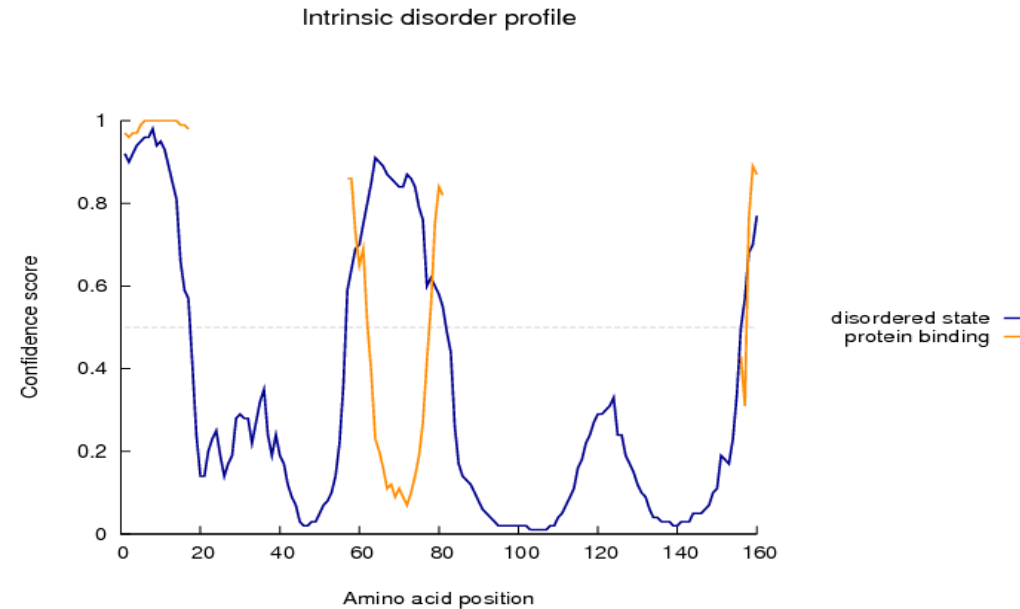
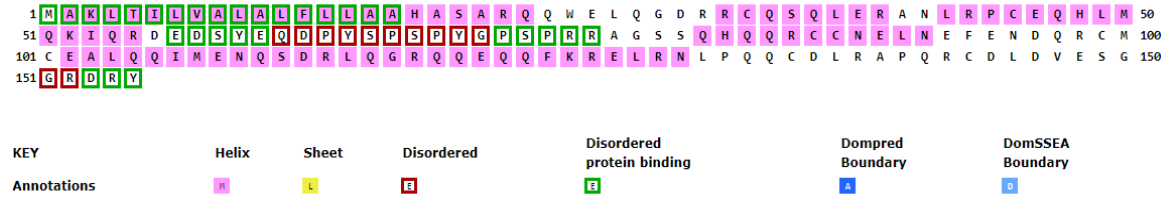


Figure S3G. PSIPRED sequence based disorder and disorder protein binding results for *A. guaranitica* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disorder profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.



B.

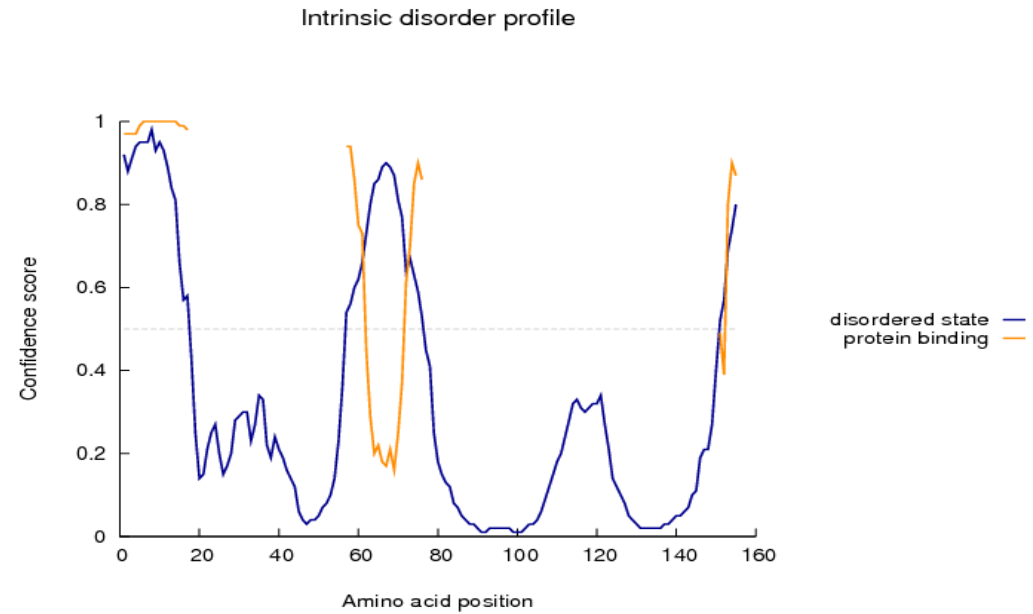


Figure S3H. PSIPRED sequence based disordered and disordered protein binding results for *A. rigonii* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

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1  M A K L T I L V A L A L F L L A A H A S A R Q Q W E L Q G D R R C Q Q S Q L E R A N L R P C E Q H L M 50
51 Q K I Q R D E D S Y E Q D P Y G P S P Y G P S P R R A G S S Q H Q R C C N E L N E F E N D Q R C M 100
101 C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C D L R A P Q R C D L D V E S G 150
151 G R D R Y
  
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KEY

Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
M	L	E	G	A	D

Annotations

B.

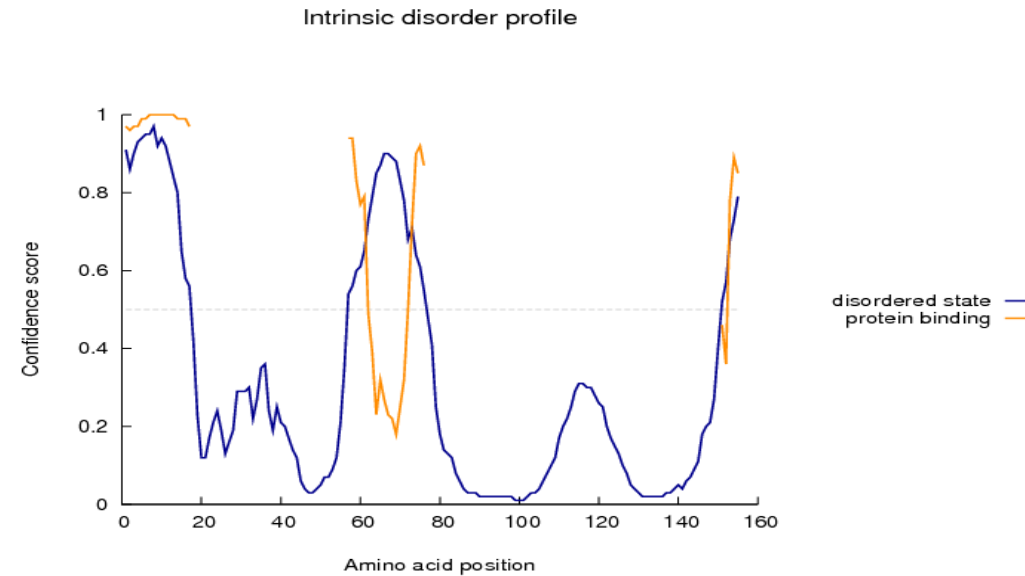


Figure S3I. PSIPRED sequence based disordered and disordered protein binding results for *A. appressipila* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

1 M S K F T E L V A L A L F L L A A H A S A R Q Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
 51 Q K I Q R D E D S Y E Q D P Y G P S P Y G P S P R R A G S S Q H Q Q R C C N E L N E F E N D Q R C M 100
 101 C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C D L R A P Q R C D L D V E S G 150
 151 G R D R Y

KEY Helix Sheet Disordered Disordered protein binding Dompred Boundary DomSSEA Boundary
 Annotations R L D E A D

B.

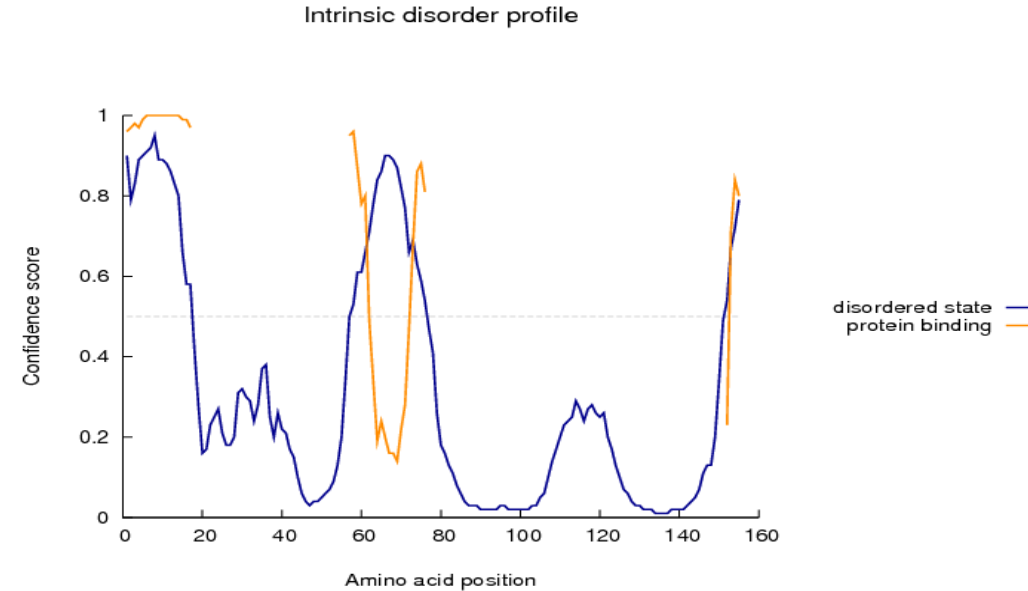
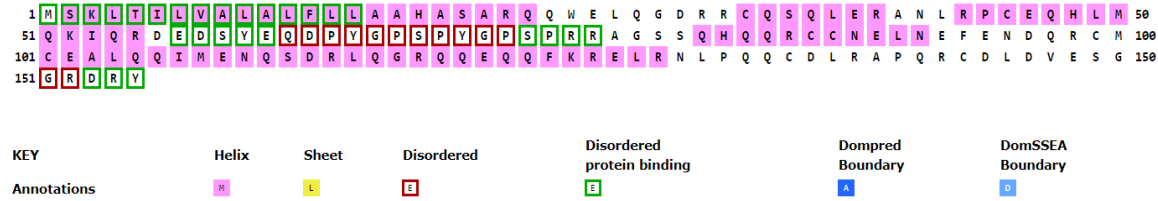


Figure S3J. PSIPRED sequence based disordered and disordered protein binding results for *A. paraguariensis* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.



B.

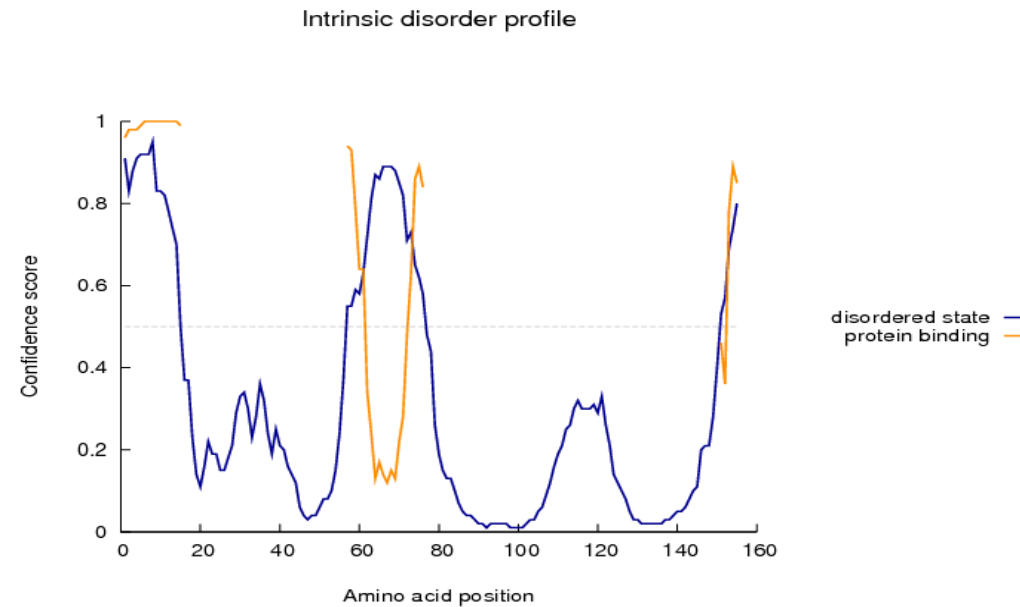
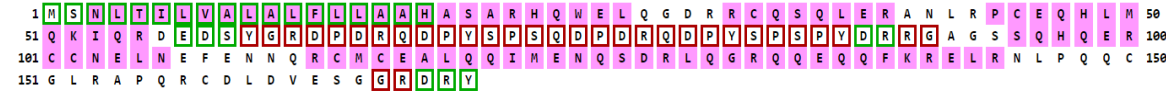


Figure S3J. PSIPRED sequence based disordered and disordered protein binding results for *A. dardani* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.



B.

Intrinsic disorder profile

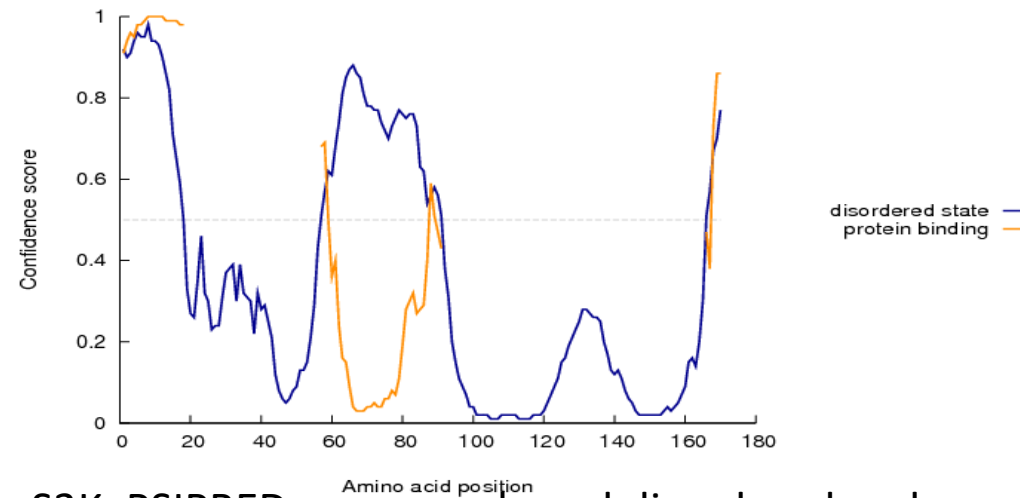


Figure S3K. PSIPRED sequence based disordered and disordered protein binding results for *A. glandulifera* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.



B.

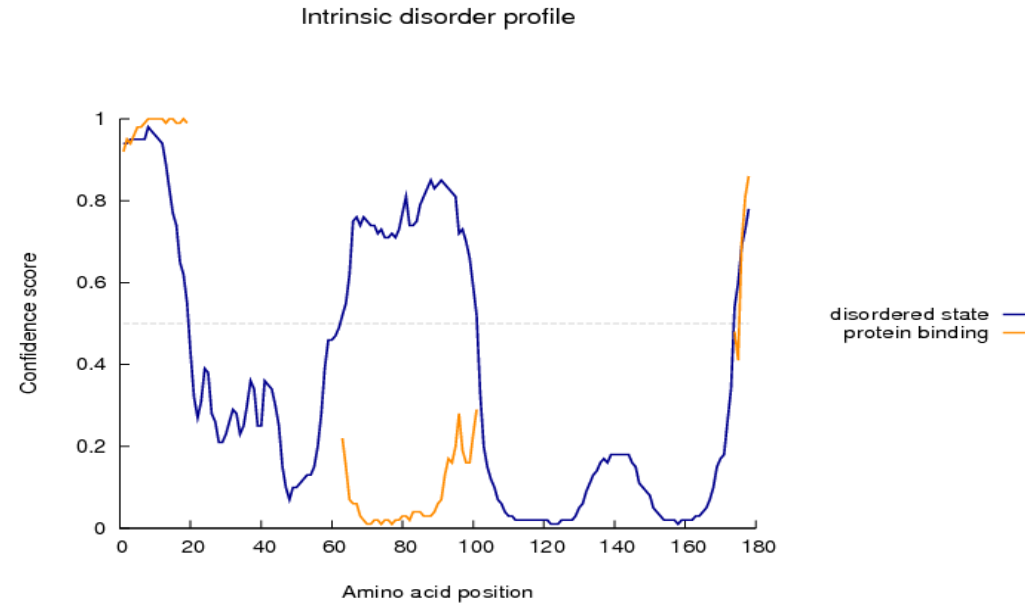


Figure S3L. PSIPRED sequence based disordered and disordered protein binding results for *A. praecox* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

1 M A K L T I L V A L A L F L L A A H A S A R Q Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
 51 Q K I Q R D E D S S Y G R D P D R E D P Y S P S Q D P D R E D P Y S P S P Y G P S P Y A R R R A G S 100
 101 S Q H Q E R C C N E L N E F E N N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R 150
 151 N L P Q Q C G L R A P Q R C D L D V E S G G R D R Y

KEY Helix Sheet Disordered Disordered protein binding Dompred Boundary DomSSEA Boundary
 Annotations H L R E A B D

B.

Intrinsic disorder profile

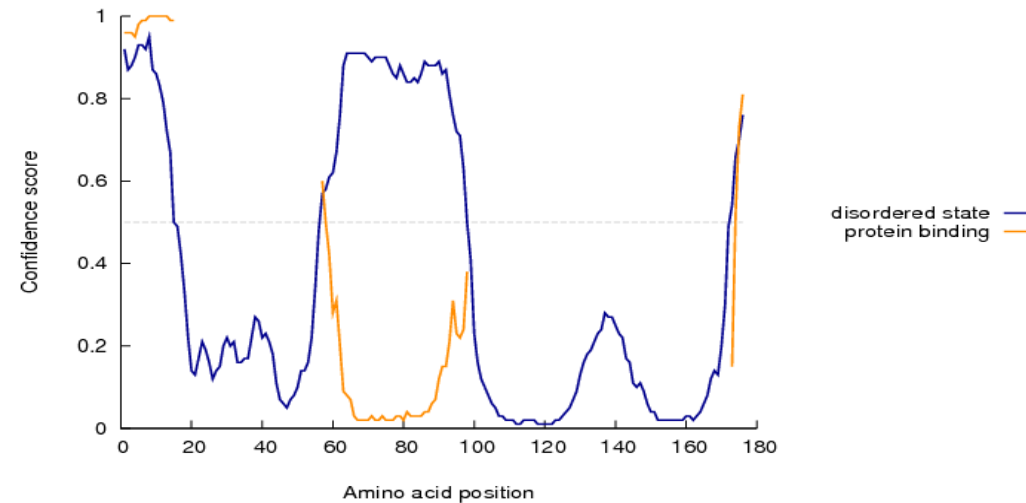


Figure S3M. PSIPRED sequence based disordered and disordered protein binding results for *A. palustris* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

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1  M S K L T I L V A L A L F L L A A H A S A R Q Q W E L R G D R R C Q S Q L E R A N L R P C E Q H L M 50
51 Q K I Q R E E D Q Y E Q D P Y S P S P Y G P S P Y D R R H A G S S Q H Q Q R C C N E L N E F E N N Q 100
101 R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R S P Q R C D L D V 150
151 E S G G R D R Y
  
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KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
Annotations	H	L	E	E	A	B

B.

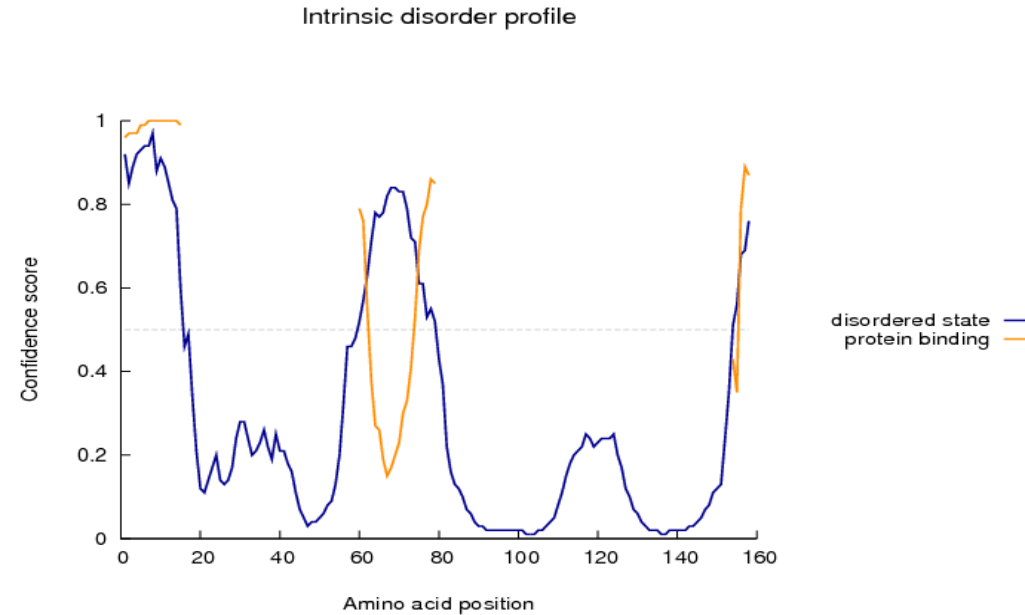


Figure S3N. PSIPRED sequence based disordered and disordered protein binding results for *A. pinto* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

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1  H S K L T F L V A L A L F L L A A H A S A R H Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
51 Q K I Q R D E D S Y G R D P Y S P S Q D P Y K Q D P Y T P S P Y D E R R A G S S Q H Q E R C C N E L 100
101 N E F E N N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R A P 150
151 Q R C D L D V E S G G R D R Y
  
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KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
Annotations	H	L	E	E	A	D

B.

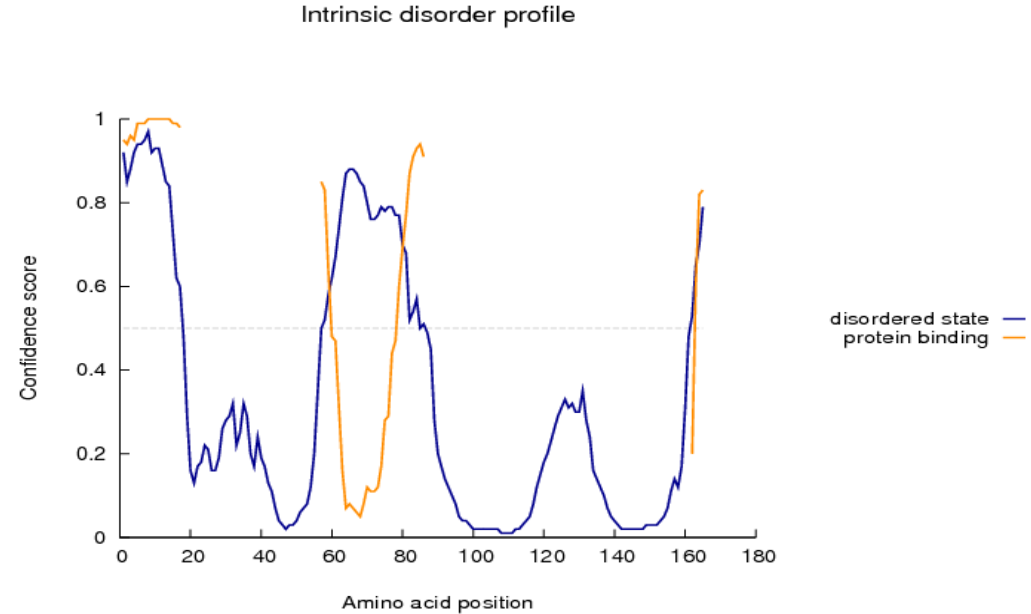


Figure S3O. PSIPRED sequence based disordered and disordered protein binding results for *A. glabrata* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. , See figure legends for coloring descriptions.

A.

1 M P M A K L T I L V A L A L F L L A A H A S A R Q Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H 50
 51 L M Q K I Q R D E D S Y E R D P Y S P S Q D P Y R Q D P Y T P S P Y D R G A G S S Q H Q E R C C N 100
 101 E L N E F E N N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R 150
 151 A P Q R C D L D V E S G G R D R Y

KEY Helix Sheet Disordered Disordered protein binding Domprmed Boundary DomSSEA Boundary
 Annotations H L E G A D

B.

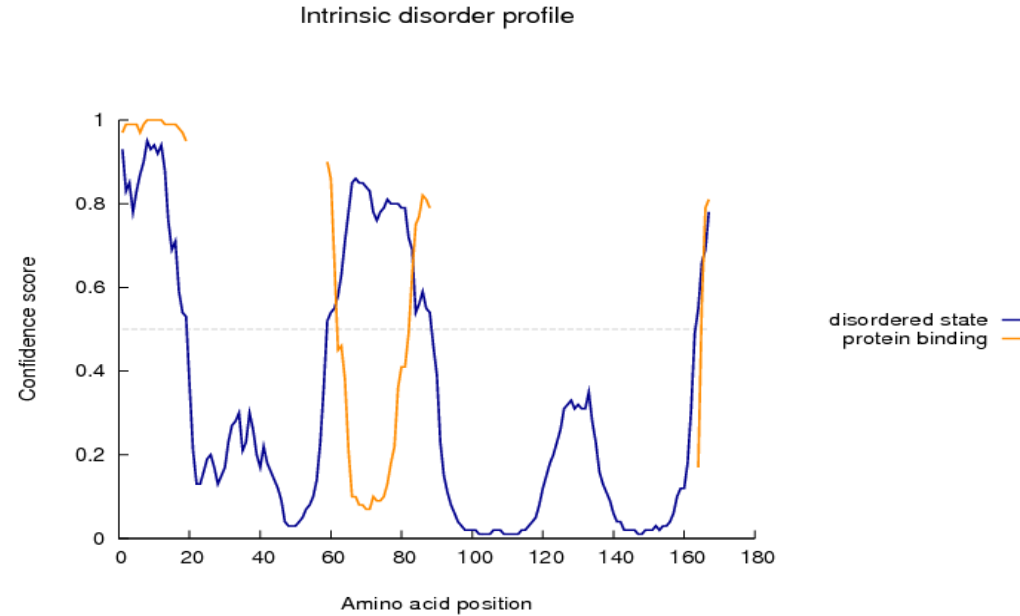
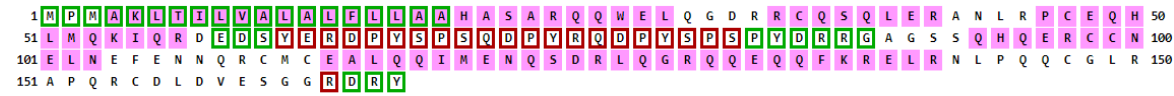


Figure S3P. PSIPRED sequence based disordered and disordered protein binding results for *A. hoehnei* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. , See figure legends for coloring descriptions.

A.



B.

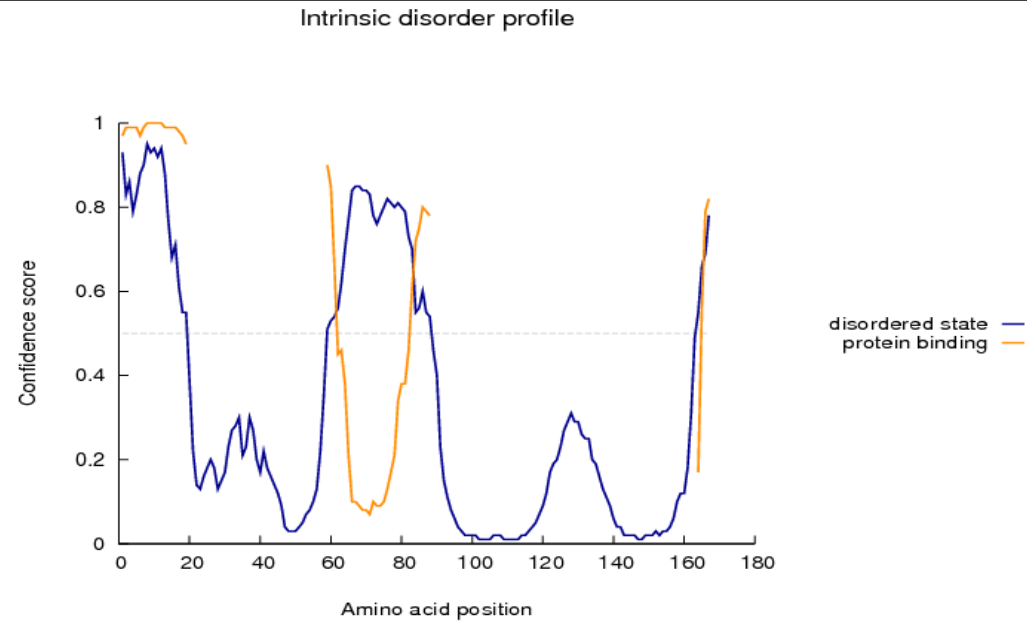
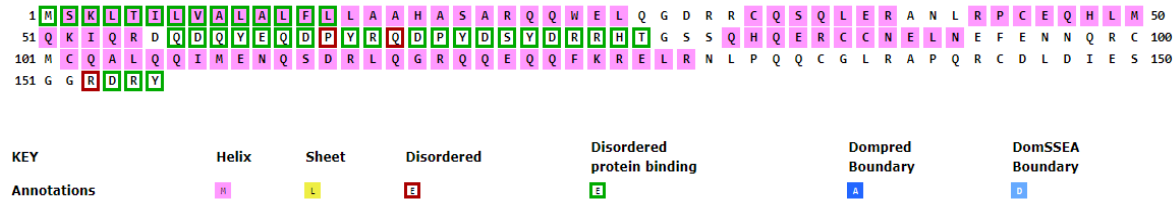


Figure S3Q. PSIPRED sequence based disordered and disordered protein binding results for *A. kretschmeri* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.



B.

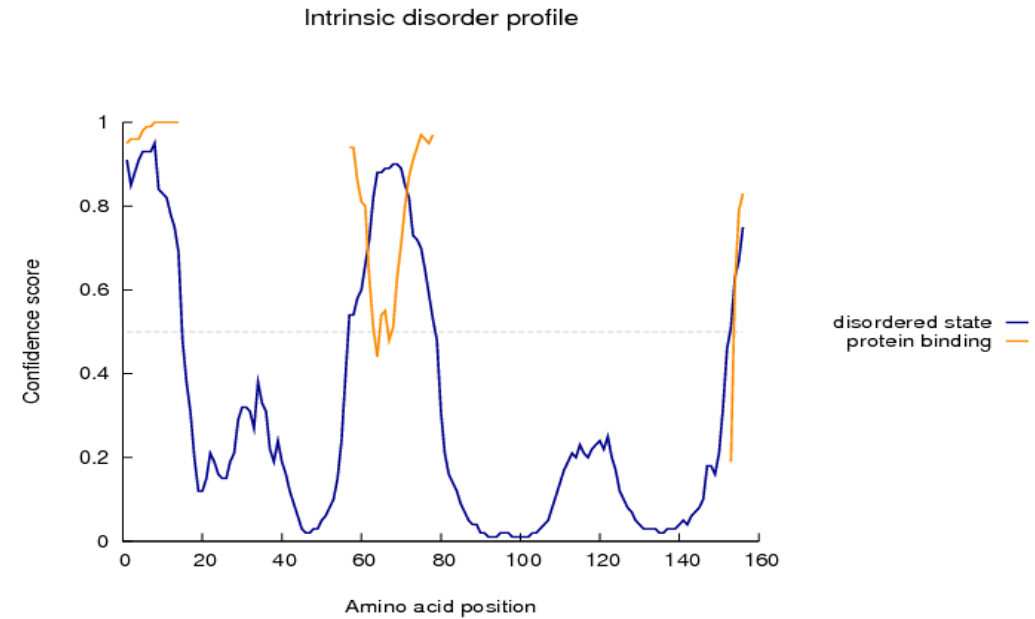


Figure S3R. PSIPRED sequence based disorder and disordered protein binding results for *A. macedo* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disorder profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

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1  M S K L T T L V A L A L F L L A A H A S A R H Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
51 Q K I Q R D E D S Y G R D P Y S P S Q D P Y K Q D P Y T P S P Y D E R R A G S S Q H Q E R C C N E L 100
101 N E F E N N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R A P 150
151 Q R C D L D V E S G G R D R Y

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KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
Annotations	R	L	E	E	A	D

B.

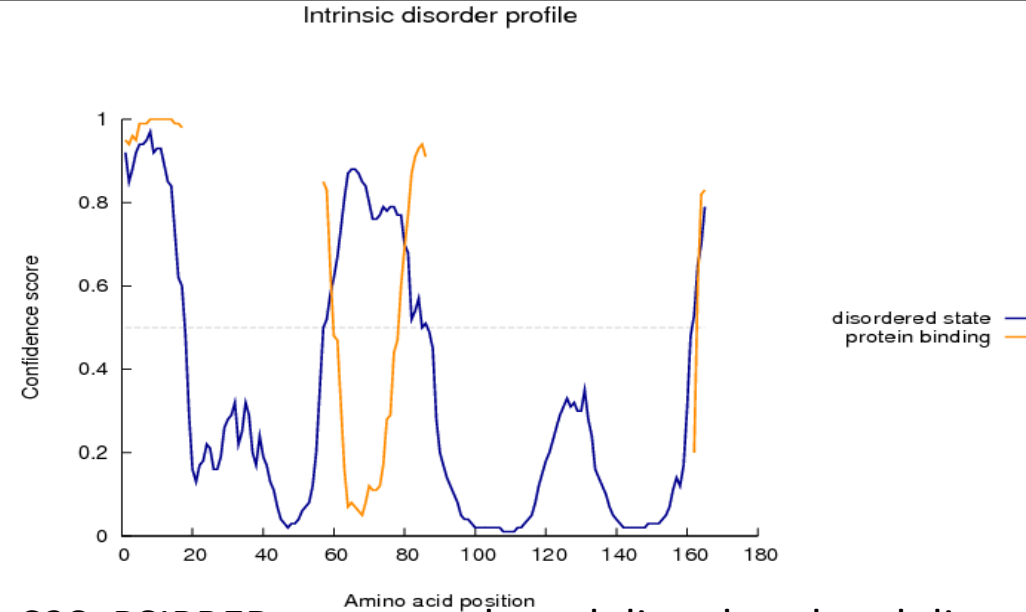


Figure S3S. PSIPRED sequence based disordered and disordered protein binding results for *A. batizocoi* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

1 M A K L T I L V A L A L F L L A A H A S A R H Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
 51 Q K I Q R D E D S Y E R D P Y S P S Q D P Y R Q D P Y S P S P Y D R R G A G S S Q H Q E R C C N E L 100
 101 N E F E N N Q R R M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R A P 150
 151 Q R C D L D V E S G G R D R Y

KEY Helix Sheet Disordered Disordered protein binding Dompred Boundary DomSSEA Boundary
 Annotations H L D G A B

B.

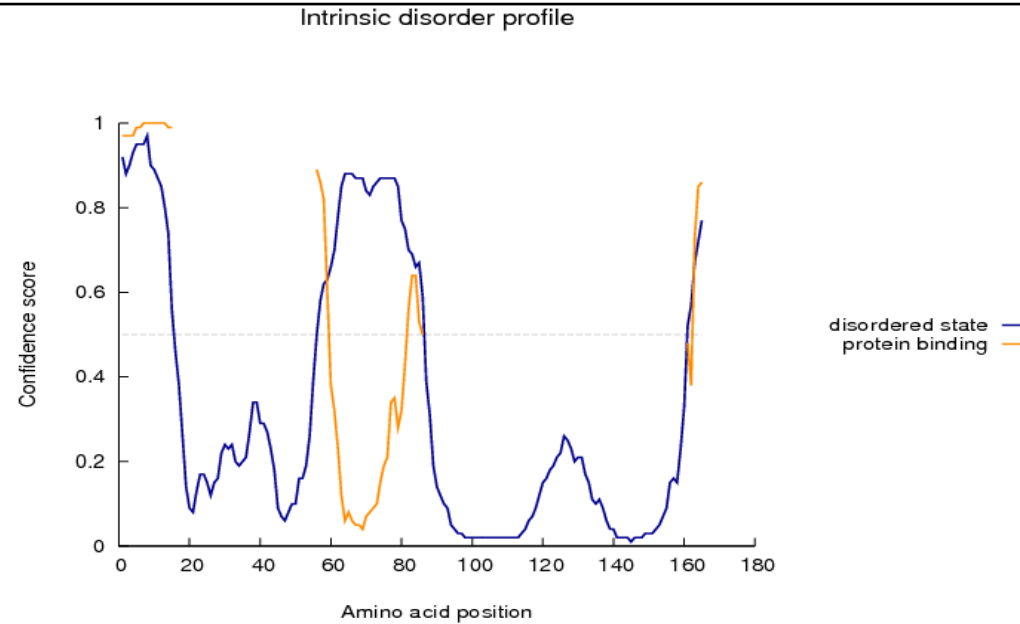


Figure S3T. PSIPRED sequence based disordered and disordered protein binding results for *A. lutescens* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. ,See figure legends for coloring descriptions.

A.

1 M A K L T I L V A L A L F L L A A H A S A R Q Q W E L Q G D R R C Q S Q L E R A N L R P C E Q H L M 50
 51 Q K I Q R D E D S Y E R D P Y S P S Q D P Y S P S P Y D R R G A G S S Q H Q E R C C N E L N E F E N 100
 101 N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E Q Q F K R E L R N L P Q Q C G L R A P Q R C D L 150
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KEY Helix Sheet Disordered Disordered protein binding Dompred Boundary DomSSEA Boundary
 Annotations R L R R G A B

B.

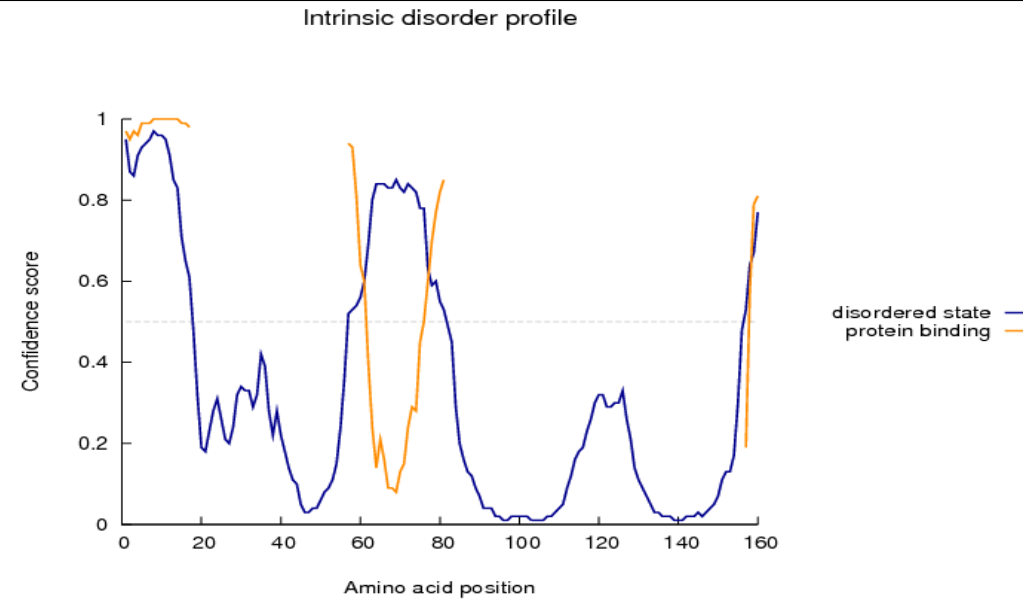


Figure S3U. PSIPRED sequence based disordered and disordered protein binding results for *A. villosulicarpa* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.

1 C Q S Q L E R A N L R P C Q H L M Q K I Q R D E D S Y E R D P Y S P S Q D P Y S P S Q D P Y S P S P 50
 51 Y D R R G A G S S Q H Q E R C C N E L N E F E N N Q R C M C E A L Q Q I M E N Q S D R L Q G R Q Q E 100
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KEY Helix Sheet Disordered Disordered protein binding Dompred Boundary DomSSEA Boundary
 Annotations H L E G A D

B.

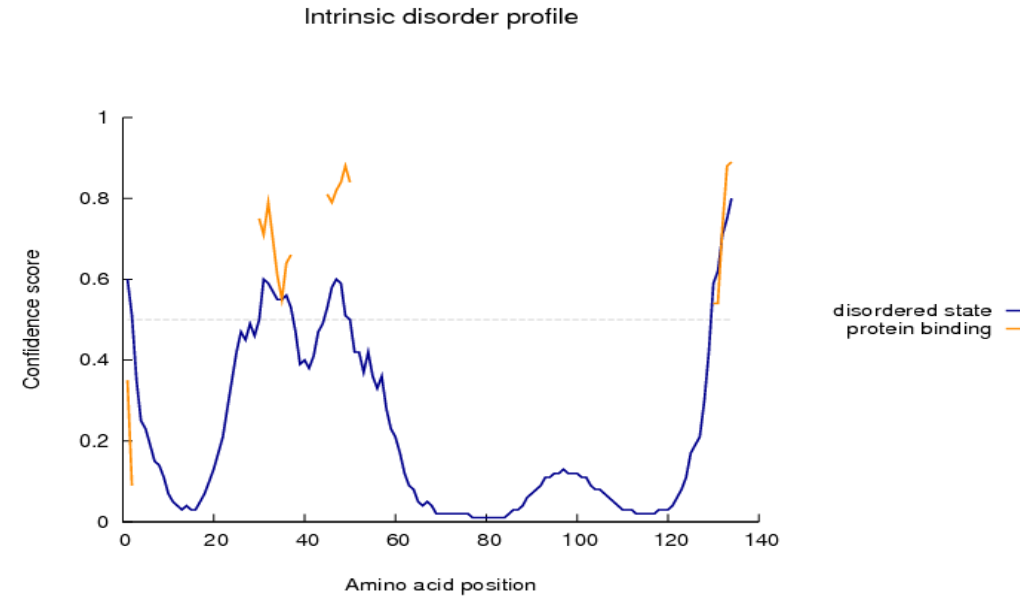
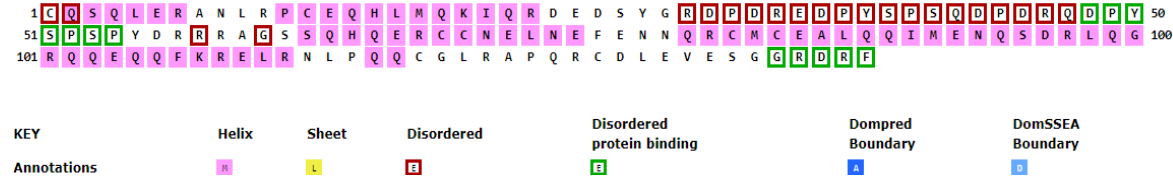


Figure S3V. PSIPRED sequence based disordered and disordered protein binding results for *A. helodes* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.

A.



B.

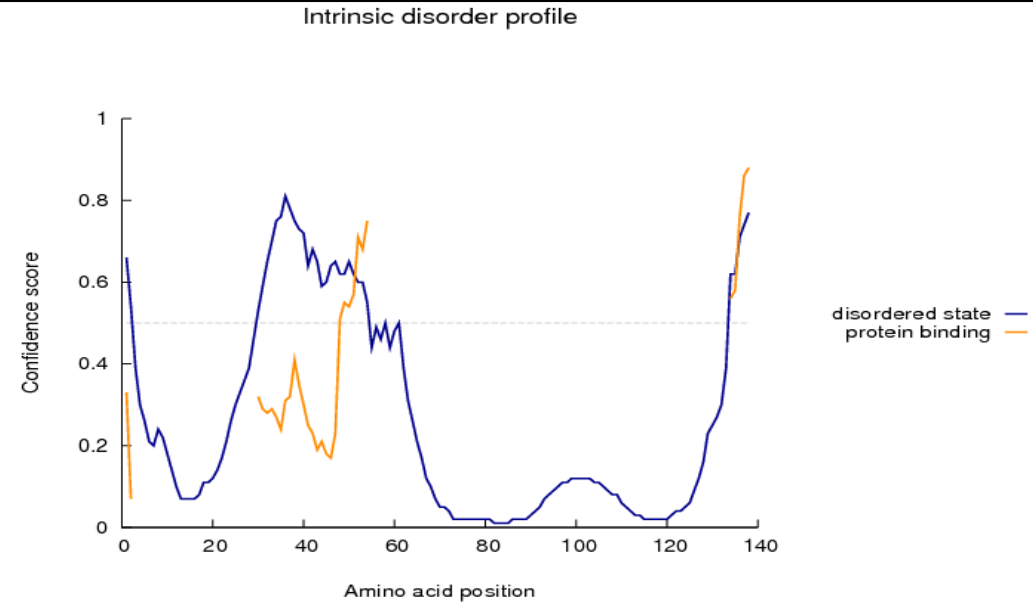


Figure S3W. PSIPRED sequence based disordered and disordered protein binding results for *A. trinitensis* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align with key epitope regions of Ara h 2. See figure legends for coloring descriptions.