

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.**

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

KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSEA Boundary
Annotations	H	L	D	D	A	D

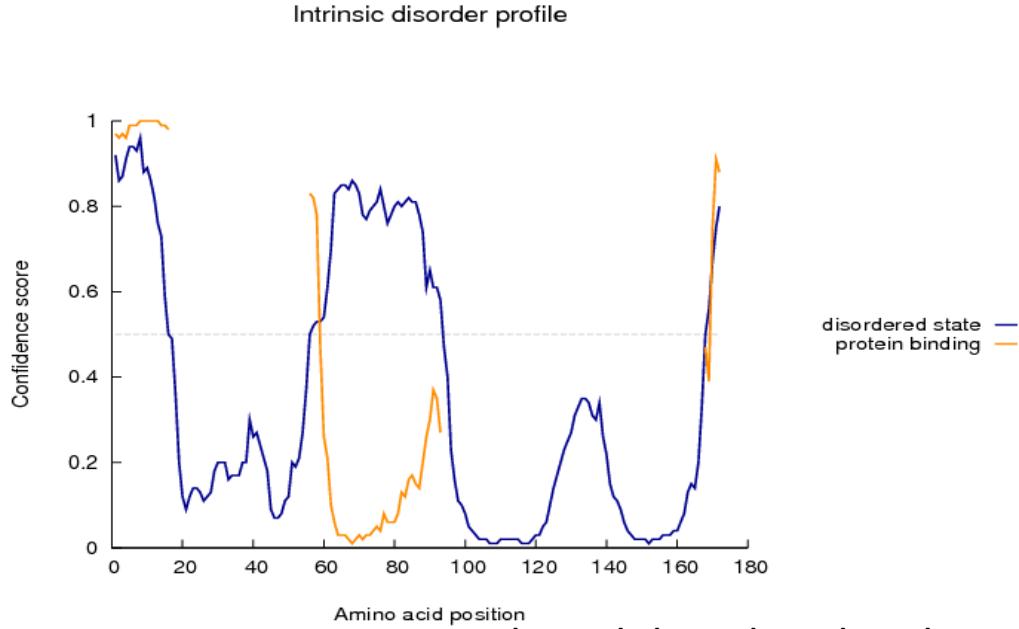
**B.**

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.**

1 H A K L T I L V A L A L F A 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 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	DomSEA Boundary
Annotations	R	L	B	G	A	D

**B.**

Intrinsic disorder profile

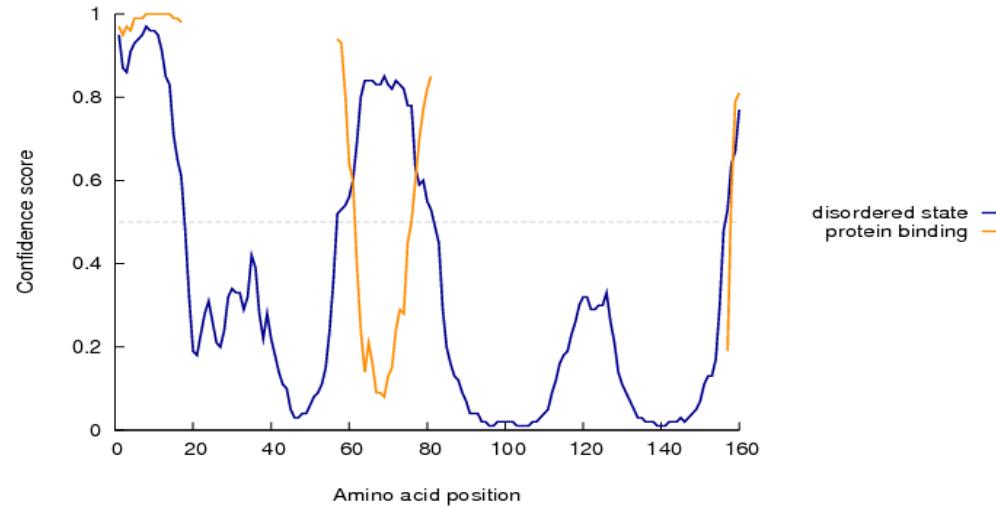
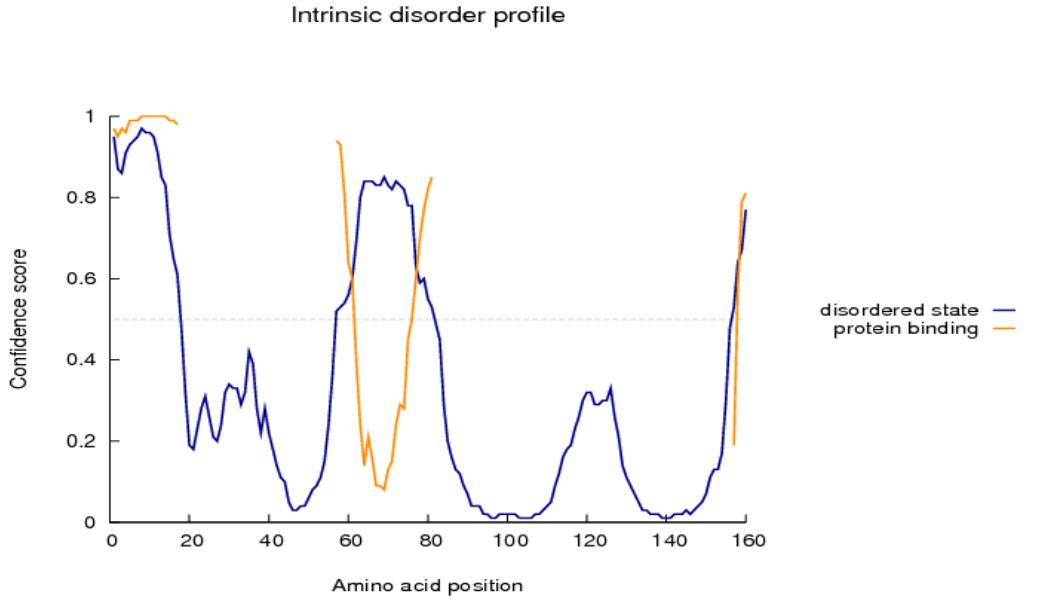


Figure S3C. PSIPRED sequence based disordered and disordered protein binding results for *A. duranensis* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that 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 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	DomSEA Boundary
Annotations	H	L	E	E	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.

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

KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSSEA Boundary
Annotations						

B.

Intrinsic disorder profile

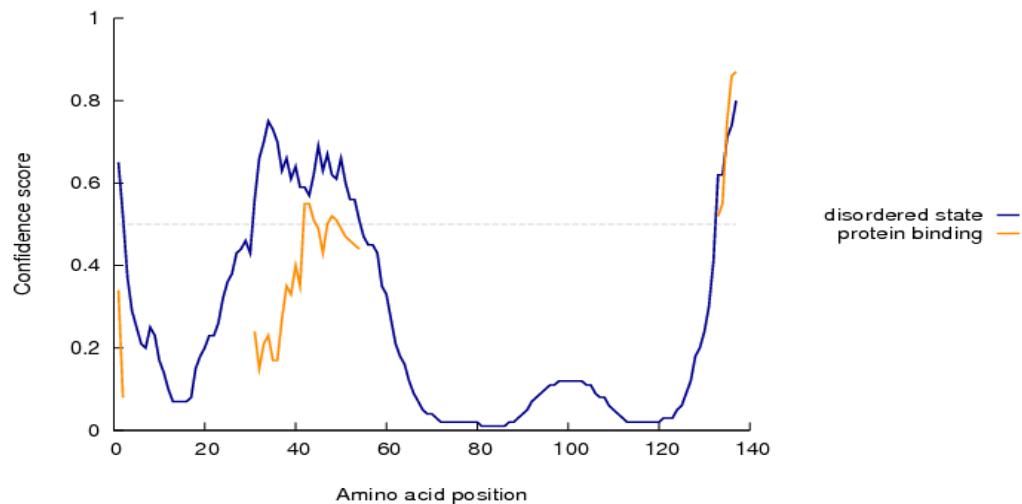


Figure S3E. PSIPRED sequence based disordered and disordered protein binding results for *A. monticola* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that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

**A.**

1 H A K K T I L V A N A A N E L L U 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 V S Q D P Y R Q E P Y E V 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 V

KEY	Helix	Sheet	Disordered	Disordered protein binding	Dompred Boundary	DomSEA Boundary
Annotations	R	L	B	H	A	I

**B.**

Intrinsic disorder profile

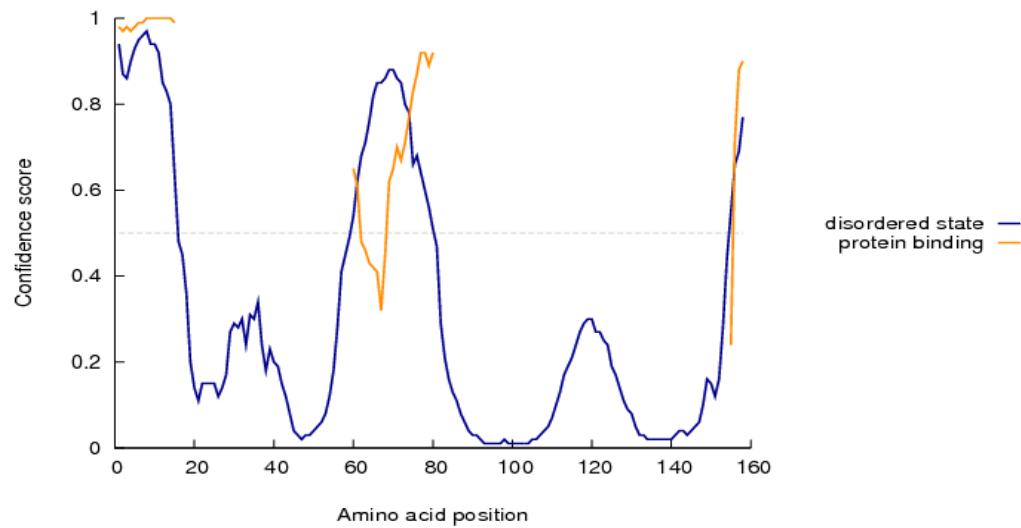


Figure S3F. PSIPRED sequence based disordered and disordered protein binding results for *A. triseminiata* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that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

A.

1 M A K E 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 Q D P Y R Q D P Y G P S P Y G D S P R R A G S S Q H Q Q R C C N E L N E F E N 100  
101 D 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 D 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	DomSEA Boundary
Annotations	H	L	E	E	A	B

B.

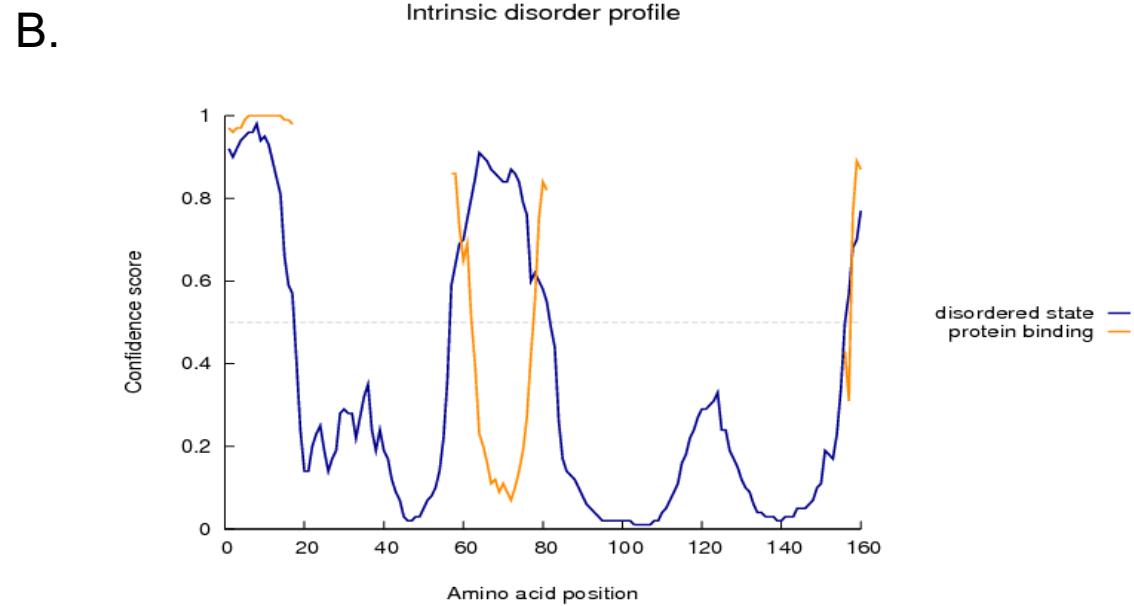


Figure S3G. PSIPRED sequence based disordered and disordered protein binding results for *A. guaranitica* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that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

**A.**

1 H 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 Q D P Y S 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	G	A	B

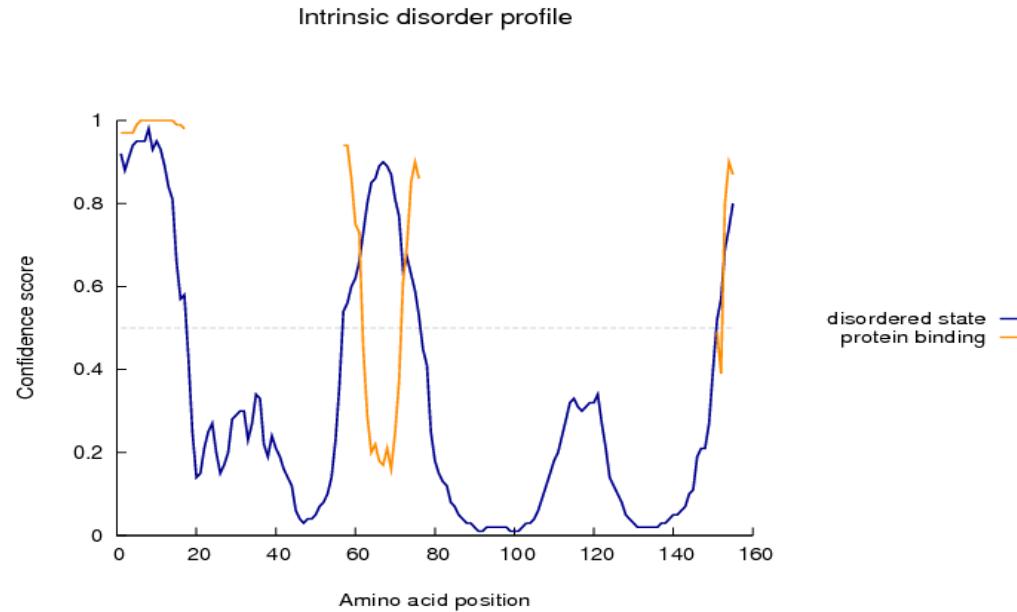
**B.**

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.**

1 H A K L T I L V A U 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 H 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	Domped Boundary	DomSSEA Boundary
Annotations	H	L	E	E	A	D

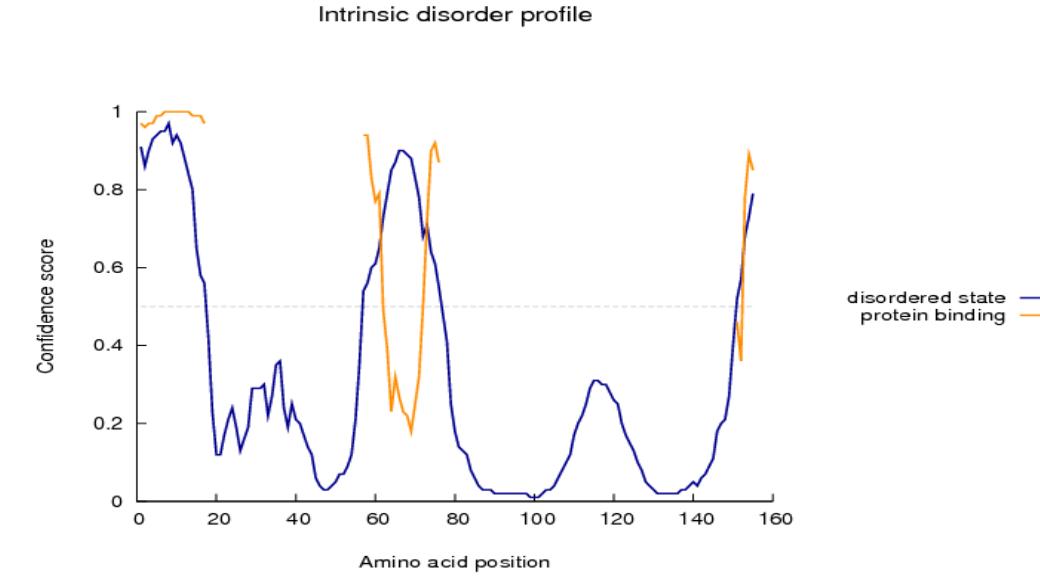
**B.**

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 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 Q D P V G P S P Y G H 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 O 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	Domained Boundary	DomSEA Boundary
Annotations						

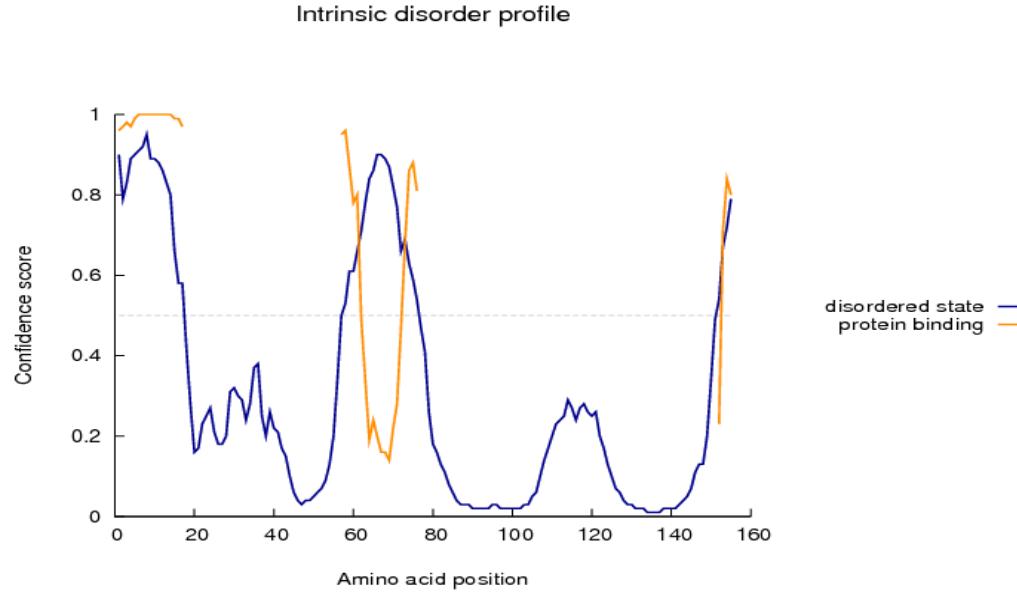
**B.**

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.**

1 H S K L T I L V A L A L F L L A A H A S A R 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 V G D S D 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	H	L	E	E	A	D

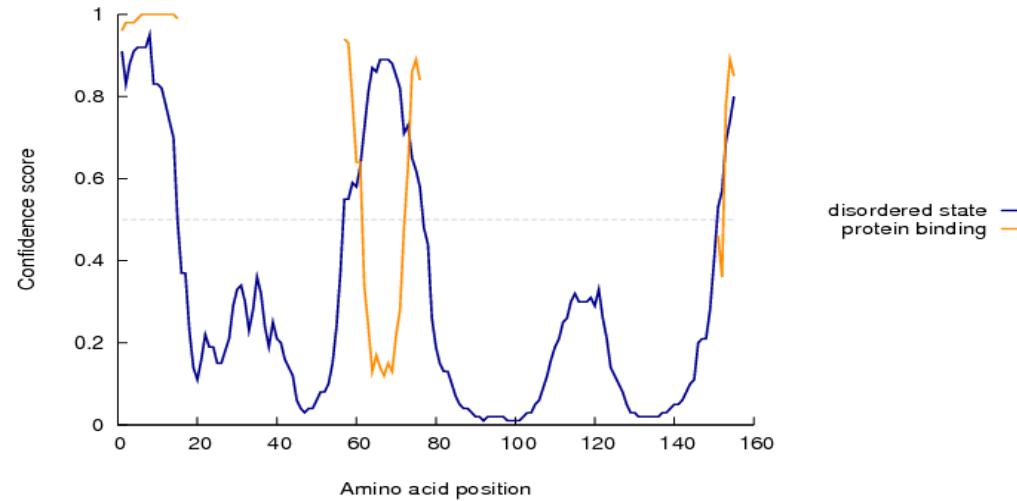
**B.****Intrinsic disorder profile**

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.

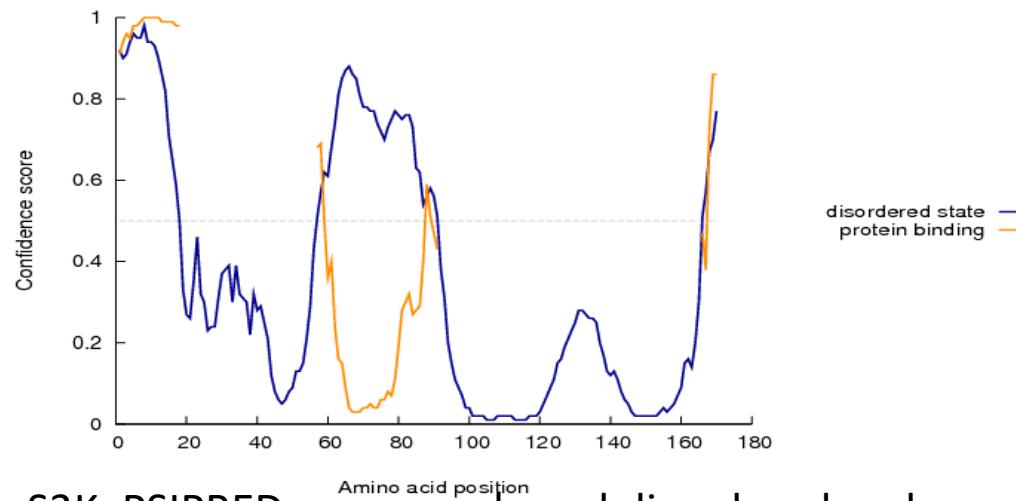
A.



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

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.**

1 H D I P 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 50  
51 L M Q K I Q R D E D S S Y G R D P D R E D 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 100  
101 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 Q Q F K R E 150  
151 L R 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	Domained Boundary	DomSSEA Boundary
Annotations	H	L	E	E	A	D

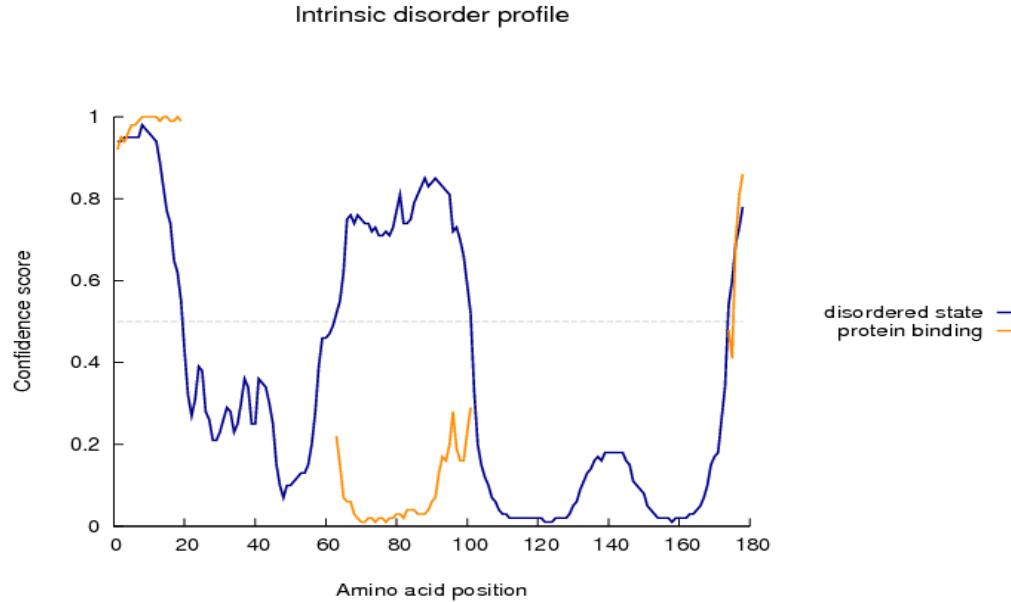
**B.**

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 A A 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 O S S Y V G R D P D R E D P Y S P S Q D P D H 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	E	E	A	B

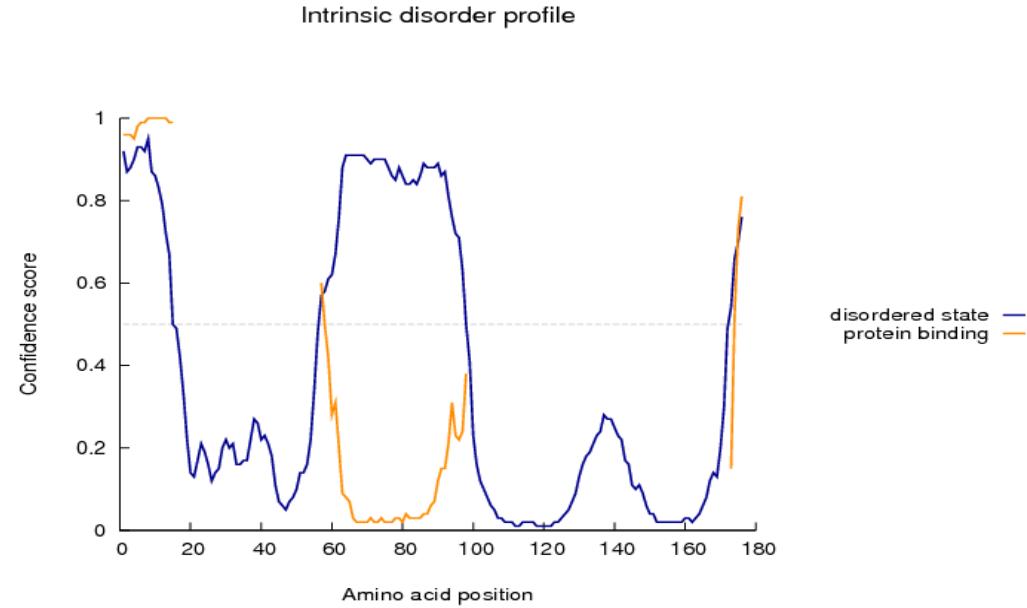
**B.**

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.**

1 H S K L T I L V A L A L F I L L A A H A S A R Q Q N 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 V 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 N Q 100  
101 R C M C E A L Q Q I M E N Q S D R L Q Q 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

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

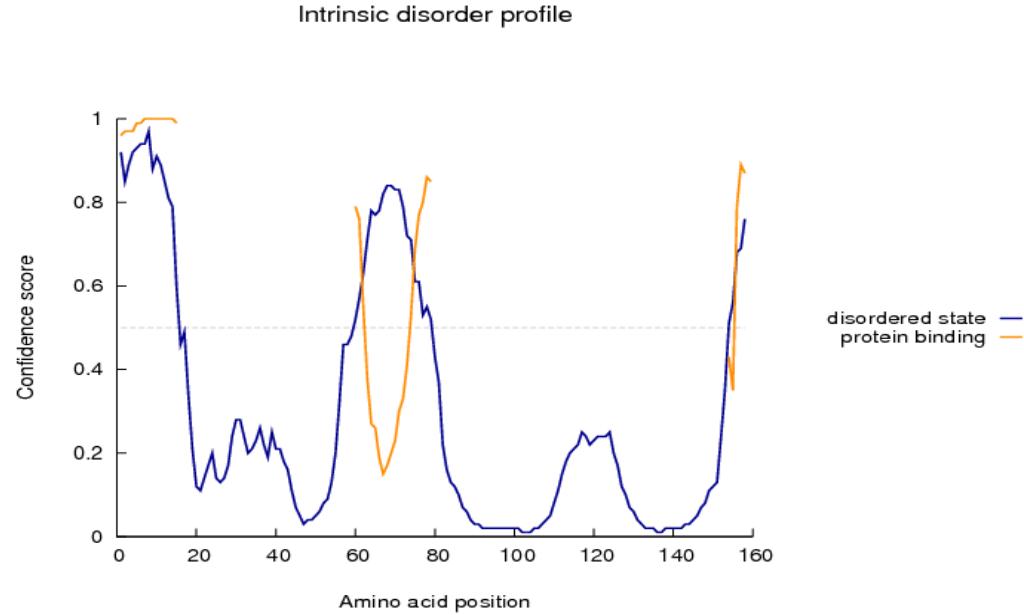
**B.**

Figure S3N. PSIPRED sequence based disordered and disordered protein binding results for *A. pintoi* 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 H S 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 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 H 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	DomSEA Boundary
Annotations	H	L	E	S	A	D

Intrinsic disorder profile  
**B.**

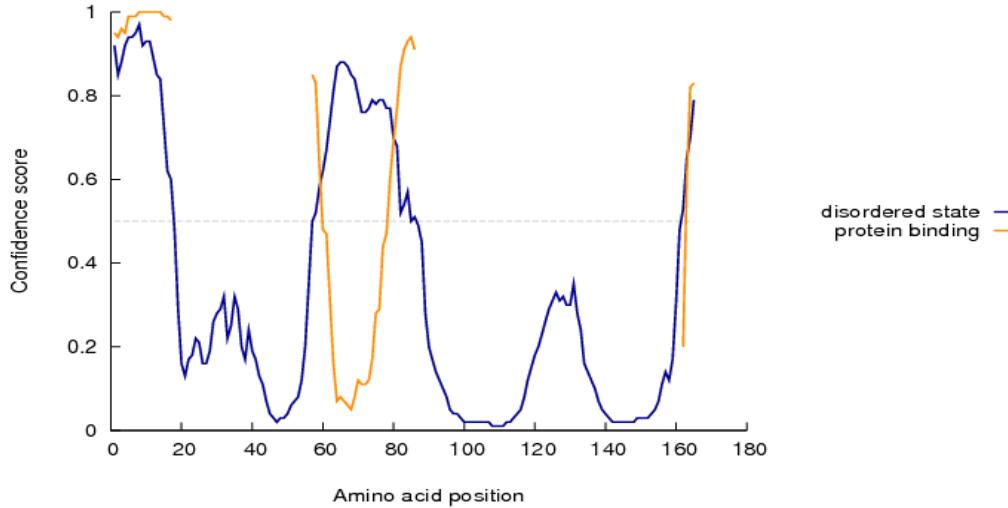


Figure S3O. PSIPRED sequence based disordered and disordered protein binding results for *A. glabrat*a Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that align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

**A.**

1 H P H 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 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 R G A G S S Q H Q E R C C N 100  
101 E L N E F D 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	Dompred Boundary	DomSSEA Boundary
Annotations	H	L	E	E	A	D

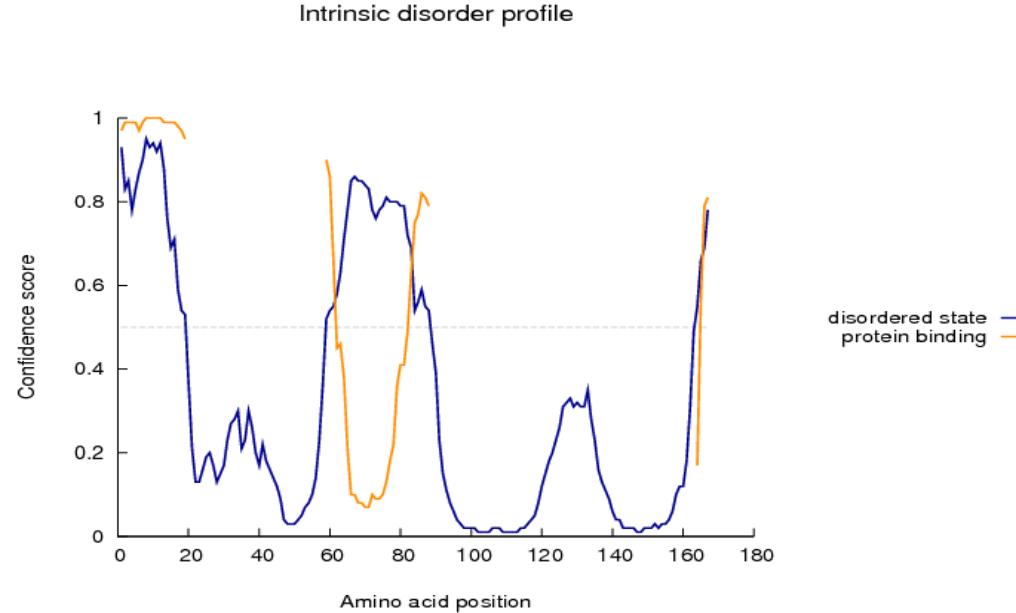
**B.**

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.**

1 H P H 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 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 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	DomPRED Boundary	DomSSEA Boundary
Annotations	R	L	E	E	A	D

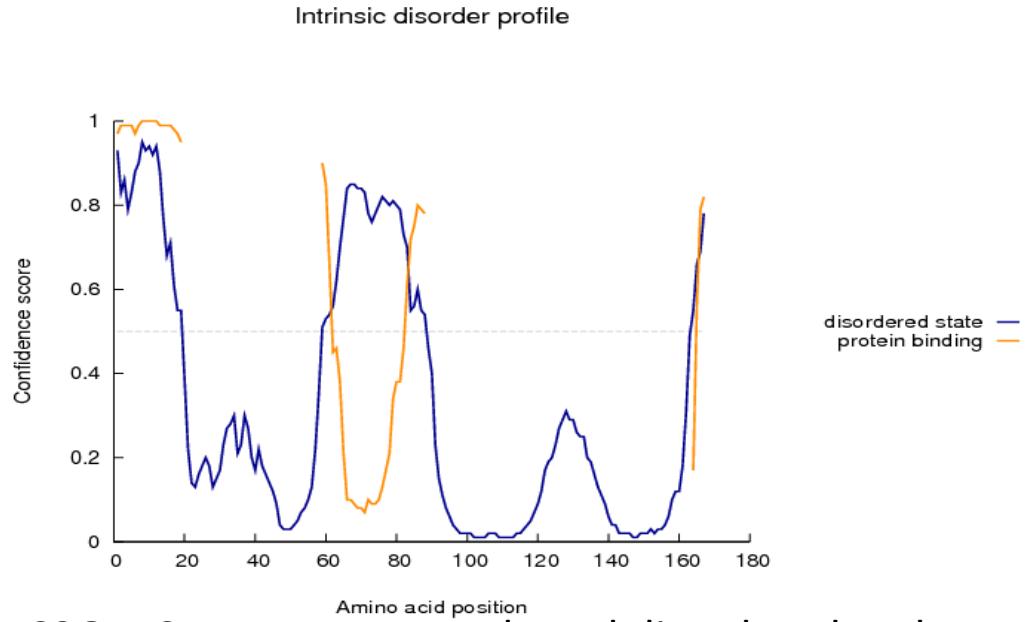
**B.**

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.**

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

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

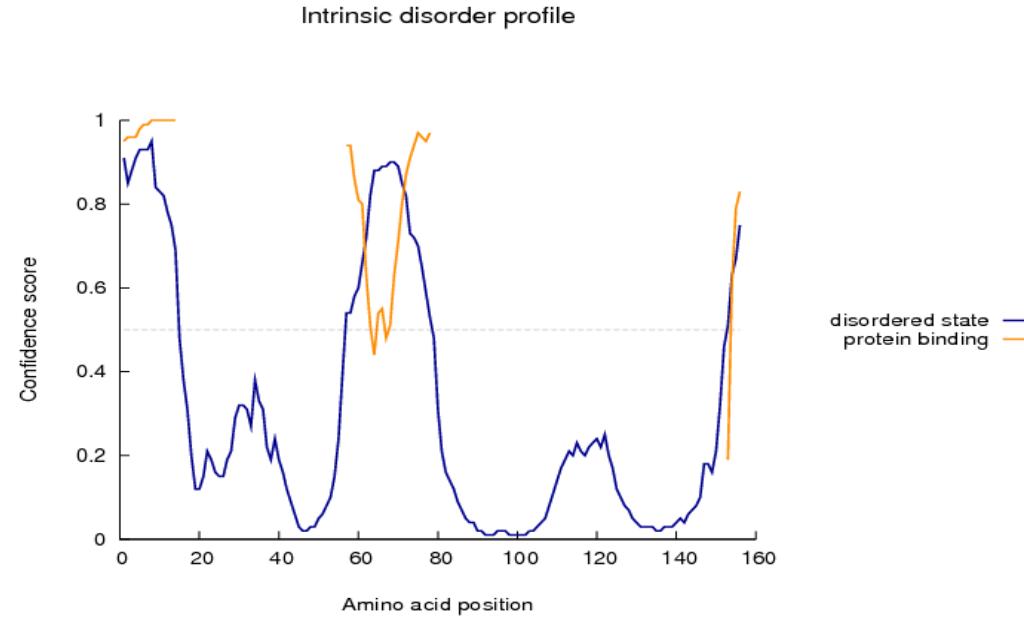
**B.**

Figure S3R. PSIPRED sequence based disordered 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 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 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 G R D P V S P S Q D P V K Q D P V T D 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

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

B.

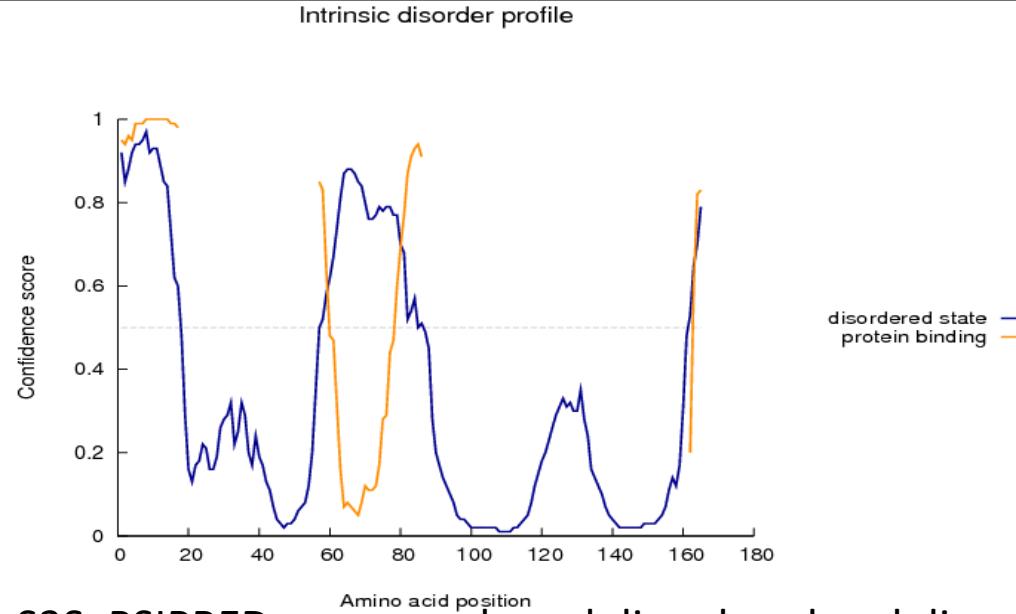


Figure S3S. PSIPRED sequence based disordered and disordered protein binding results for *A. batizocoi* Ara h 2. (A) shows the residues predicted to be disordered, involved in a helix, and to bind other proteins (e.g. IgE). (B) highlights the intrinsic disordered profile per amino acid position that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

**A.**

1 H A K L T I L V A I A L F L L A A H A S A R H Q W E L Q G D R R C O 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 V E R D P Y S P S O 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	DomSEA Boundary
Annotations	H	L	D	G	A	B

Intrinsic disorder profile

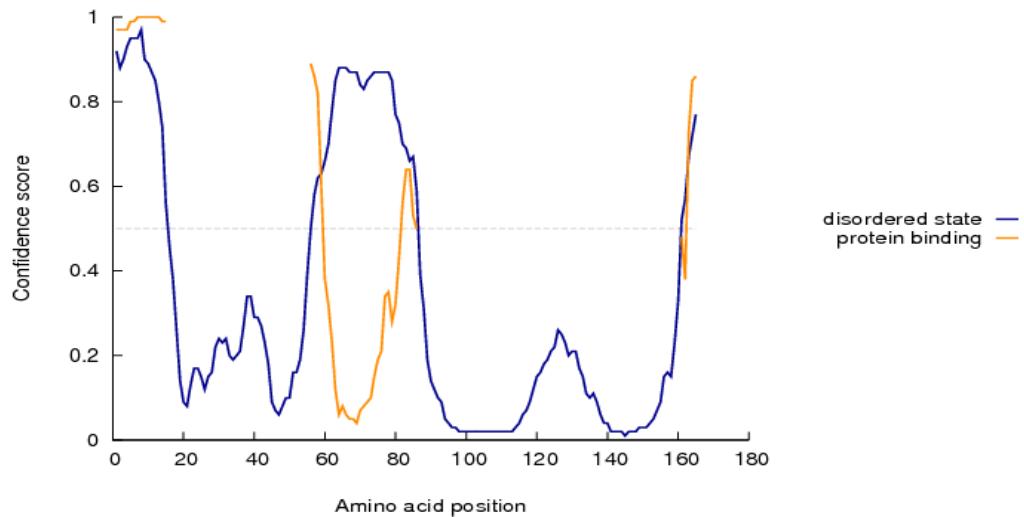
**B.**

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 V S P S Q D P Y S P S P Y D R N 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 I 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	DomSEA Boundary
Annotations	H	L	E	E	A	D

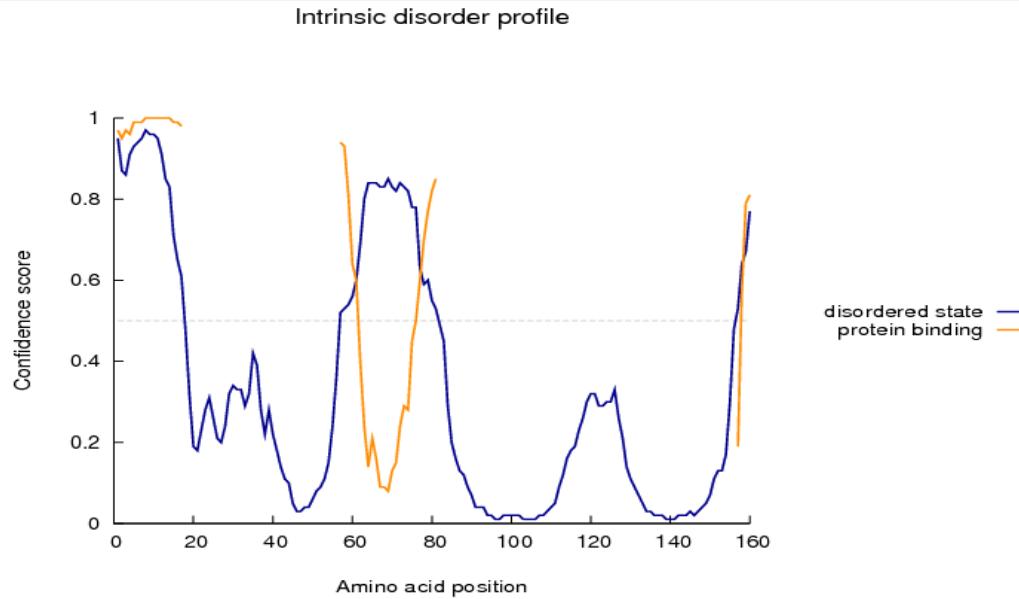
**B.**

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 O 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 E N 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  
101 Q Q F K R E L R 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	D	E	A	B

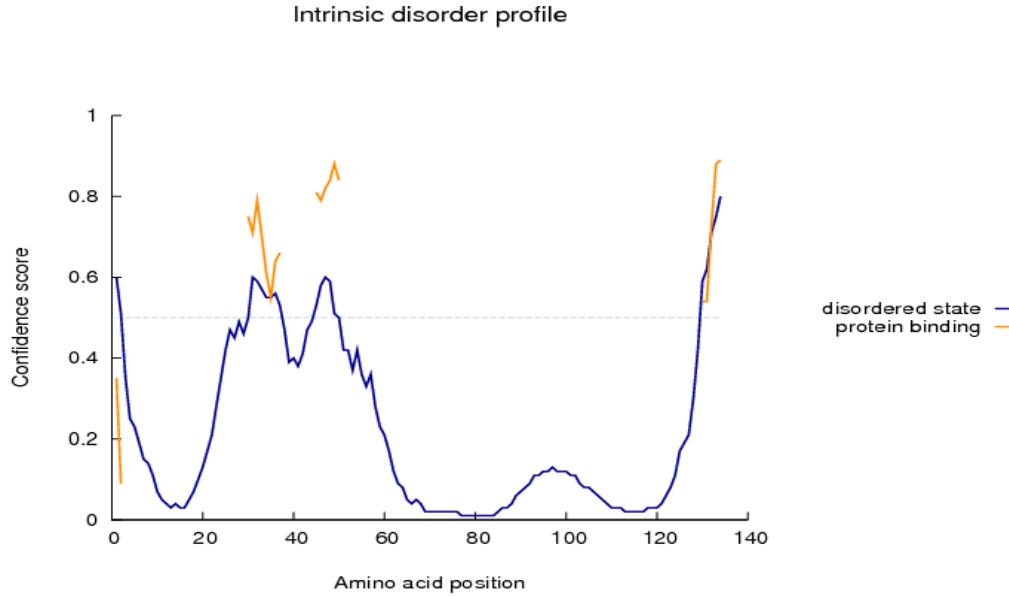
**B.**

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.**

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

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

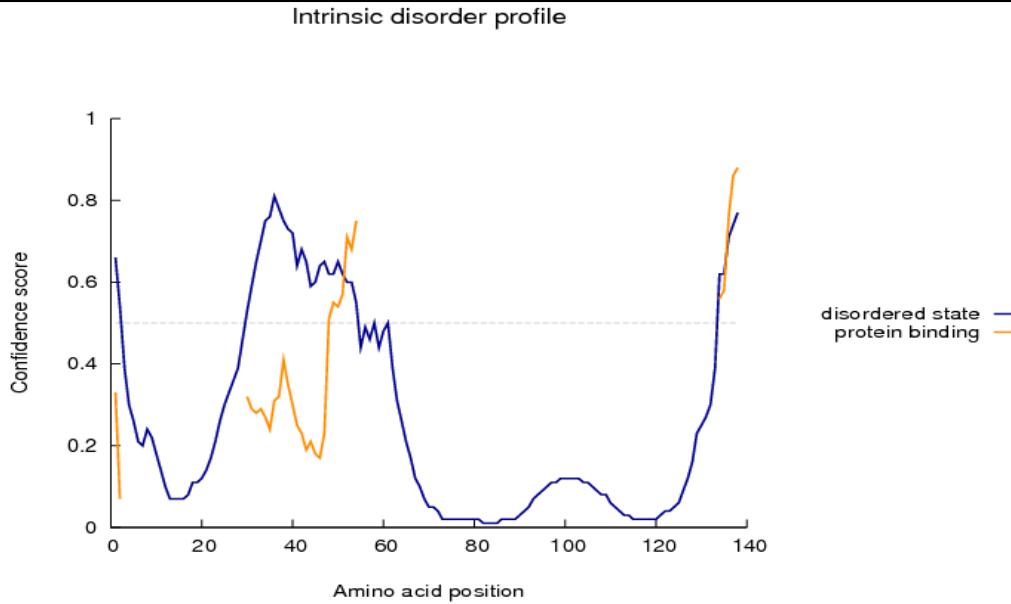
**B.**

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.