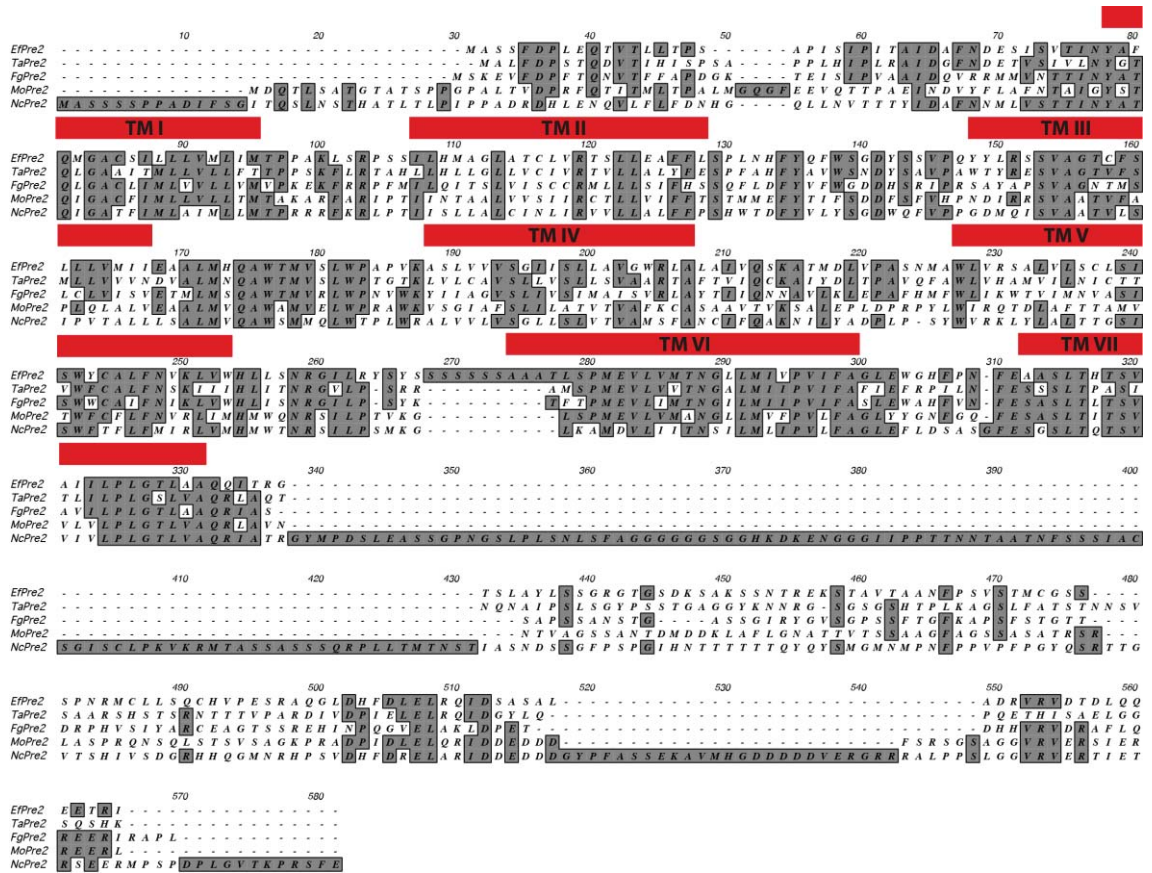


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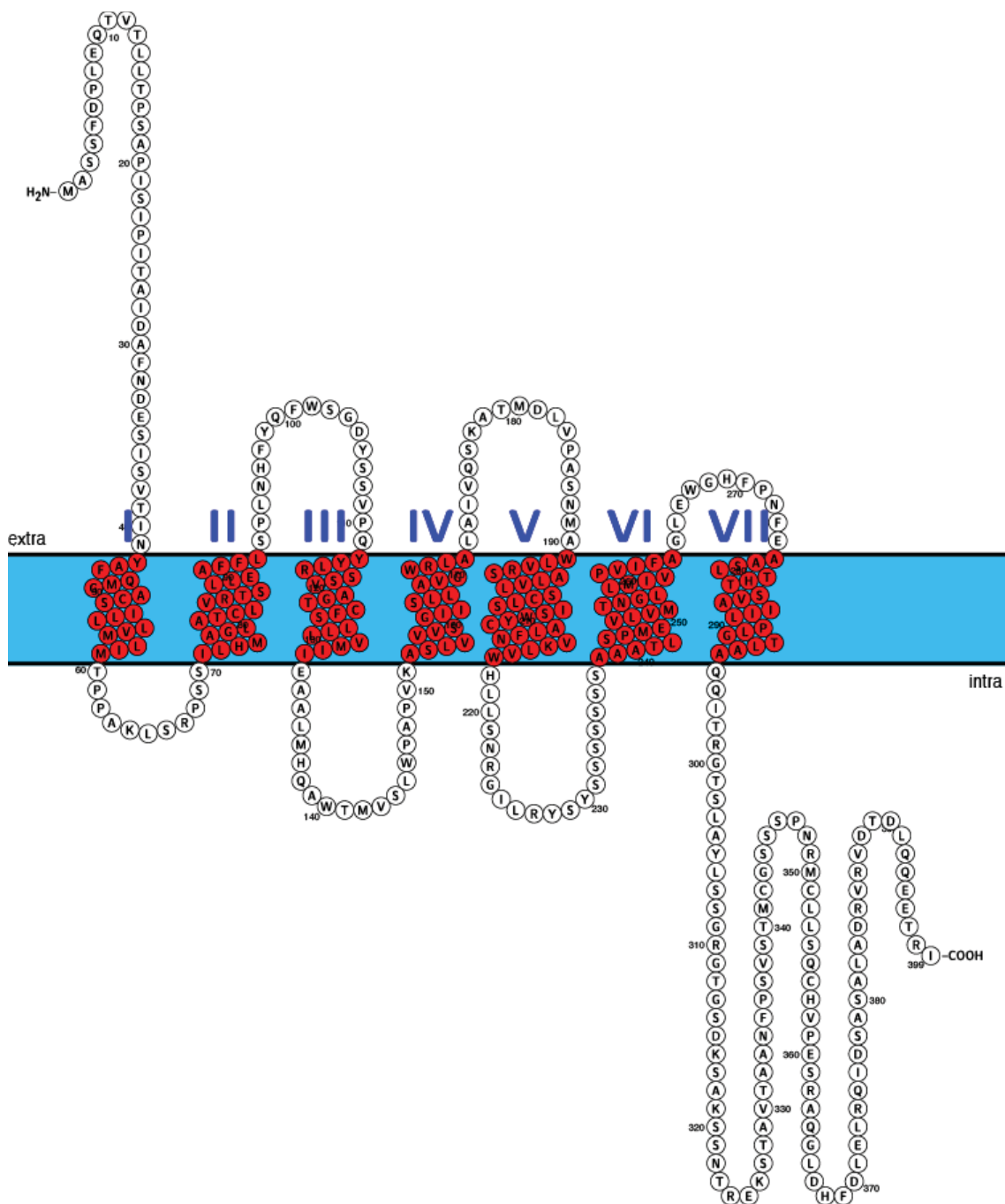
Supplementary data

Supplementary 1: Multiple sequence alignment of *E. festucae* Pre2 homologues



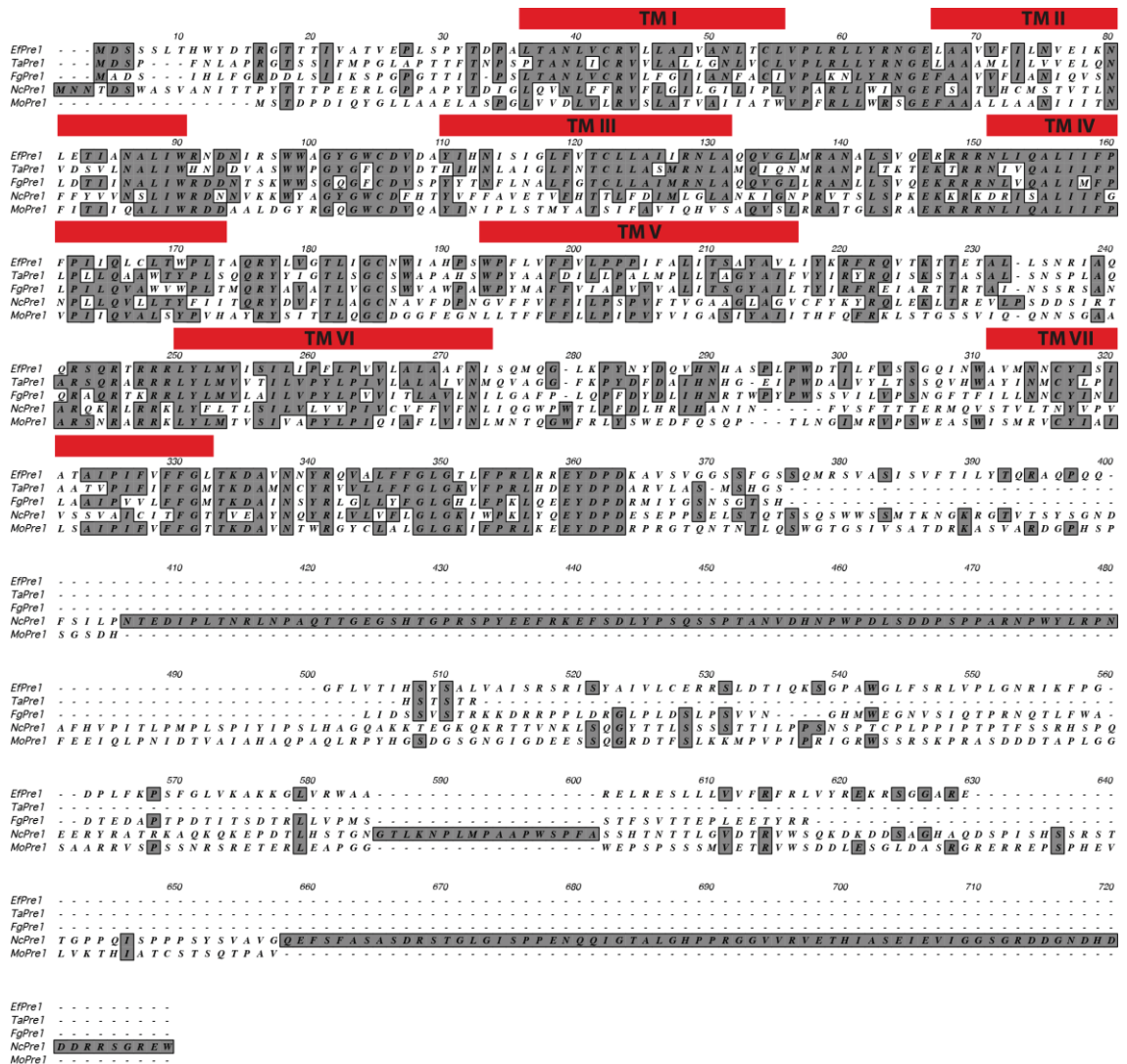
The predicted amino acid sequence of *E. festucae* Pre2 (EfPre2, Efm3. 072620) is aligned with the corresponding homologues in *N. crassa* NcPre2 (NCU05758), *F. graminearum* FgPre2 (FGSG_02655), *M. oryzae* MoPre2 (Ste2; MGG_04711) and *T. atroviride* TaPre2 (TRIATDRAFT_36032). *E. festucae* Pre2 displays 25.1% amino acid identity to *N. crassa* Pre2, 42.9% identity to the *F. graminearum* homologue, 33.5% identity to the *M. oryzae* homologue and 39.5% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 2: Predicted protein topology of *E. festucae* Pre2

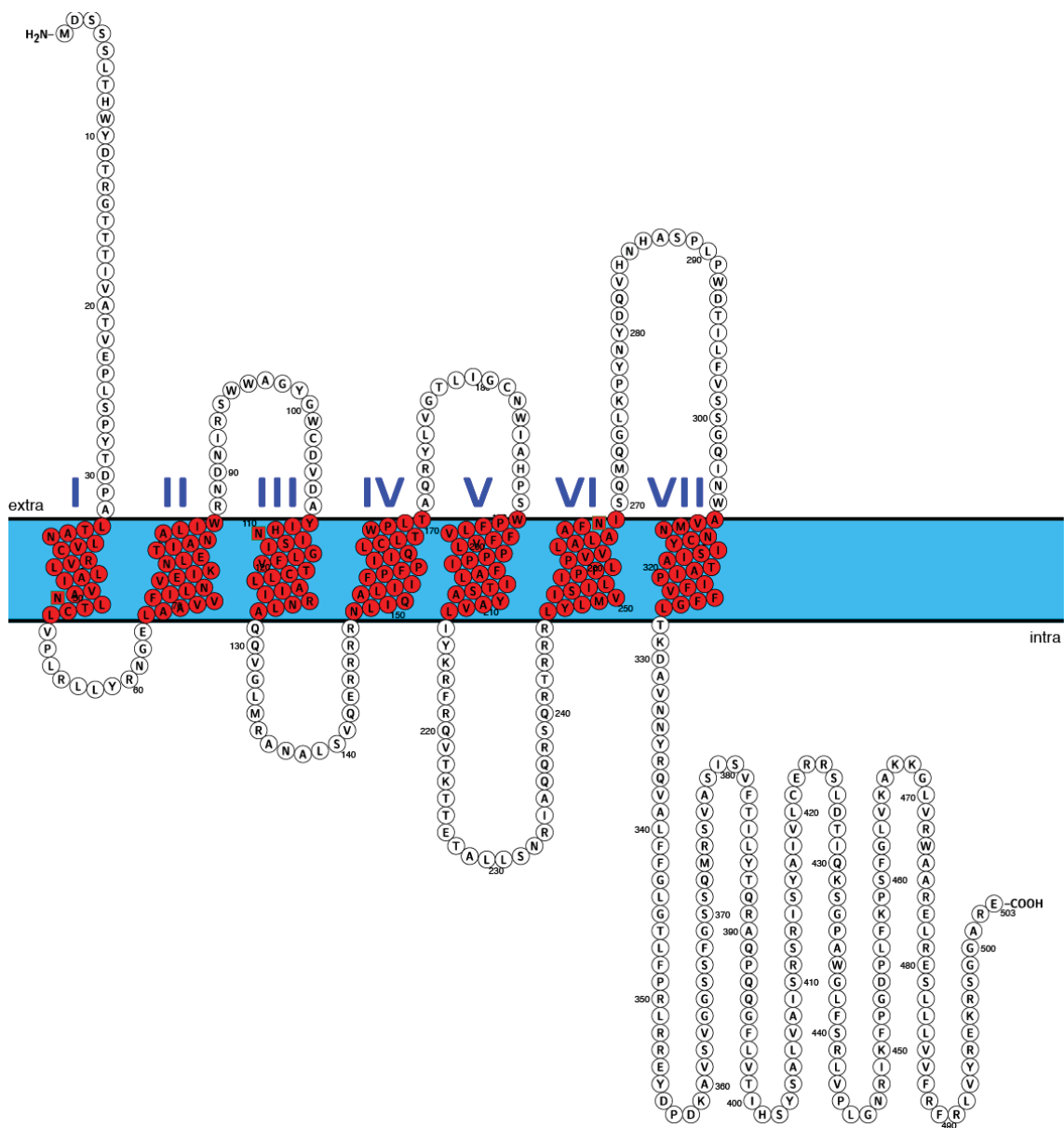


The predicted Pre2 polypeptide is 399 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 3: Multiple sequence alignment of *E. festucae* Pre1 homologues

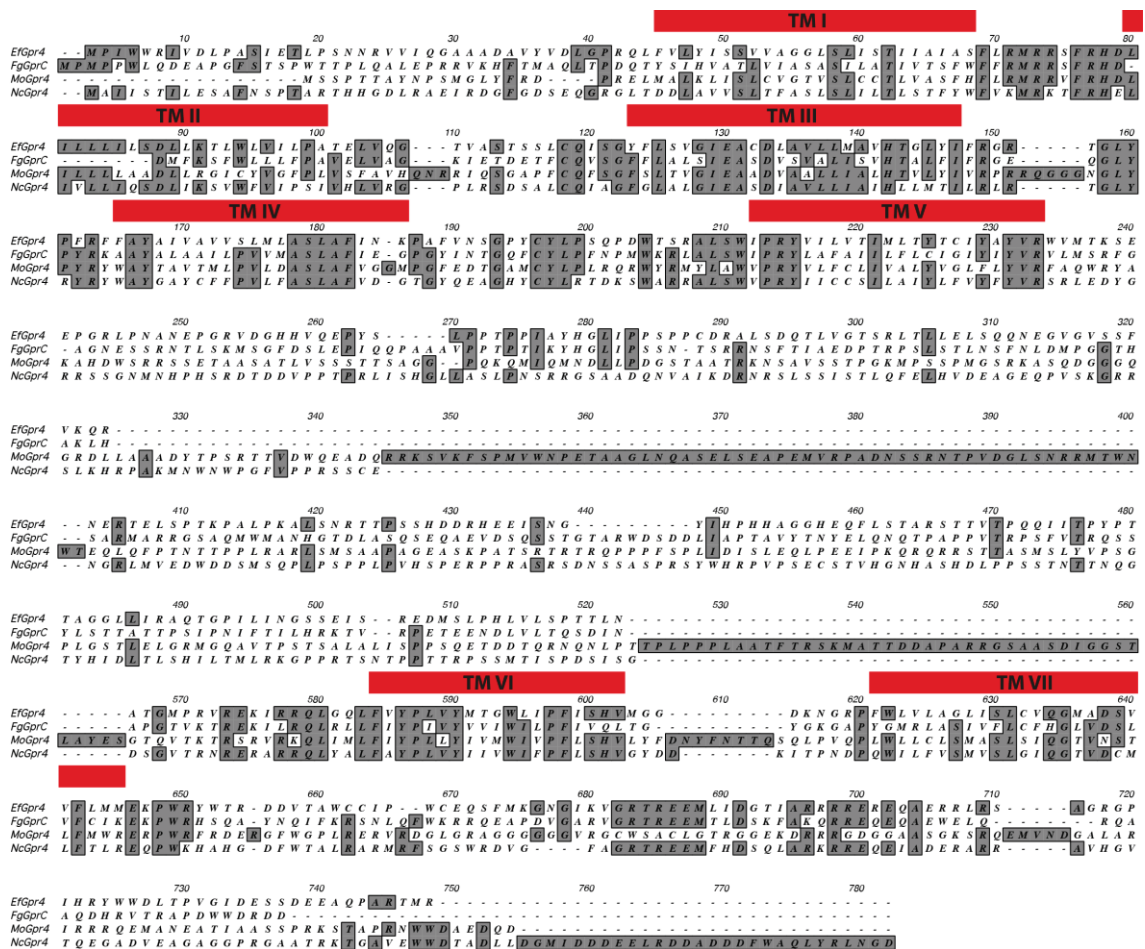


Supplementary 4: Predicted protein topology of *E. festucae* Pre1



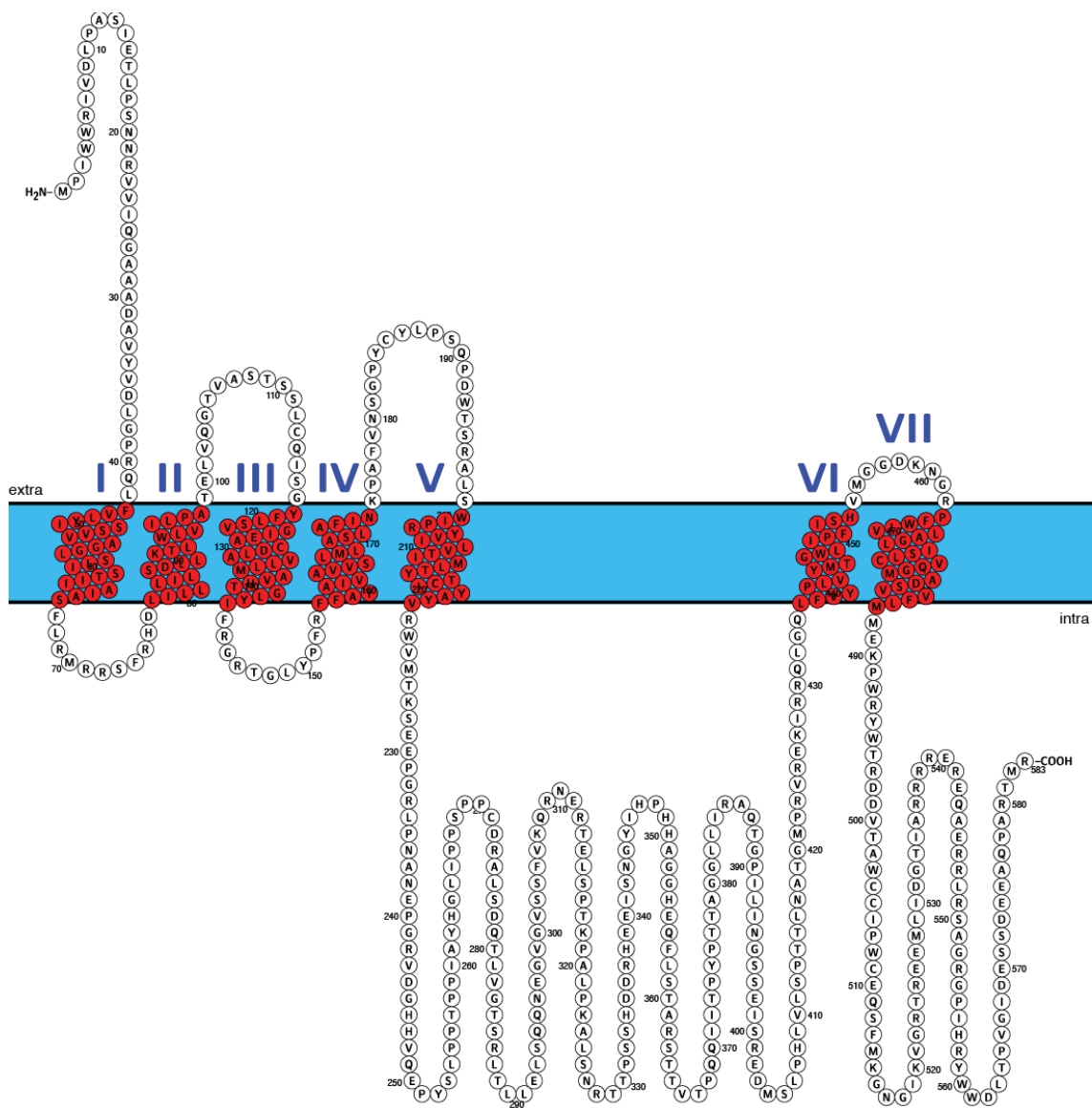
The predicted Pre1 polypeptide is 503 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 5: Multiple sequence alignment of *E. festucae* Gpr4 homologues



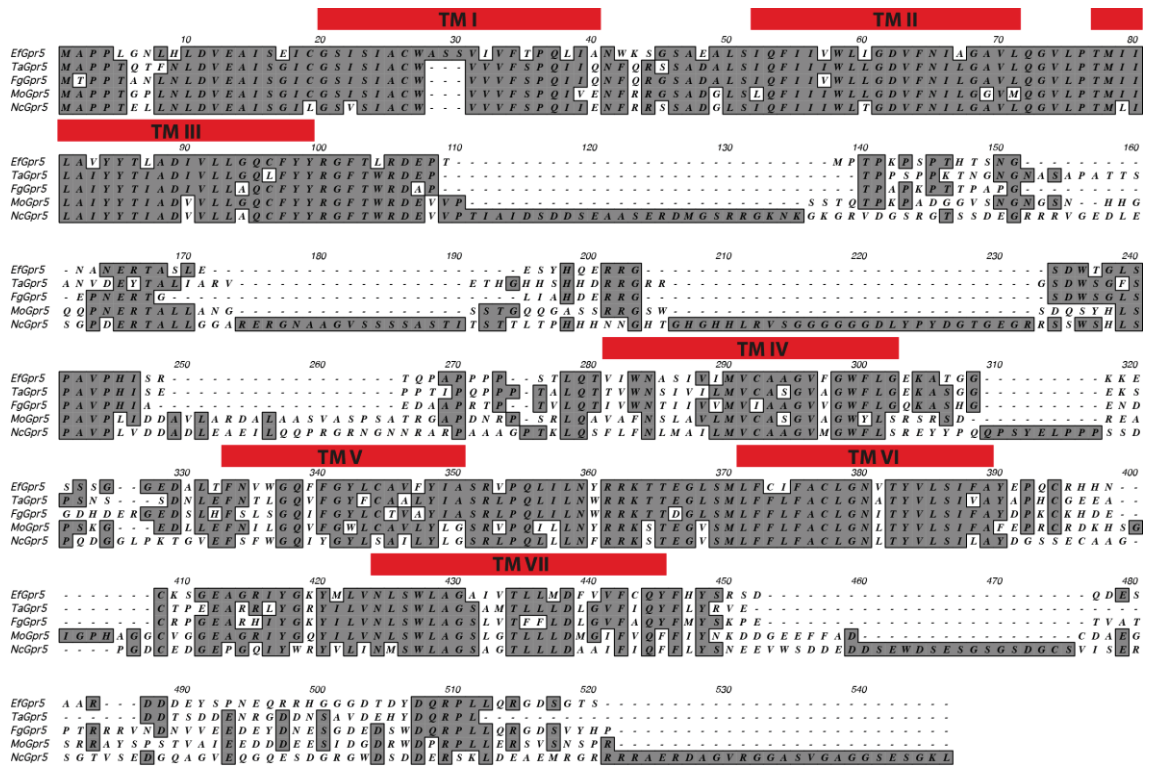
The predicted amino acid sequence of *E. festucae* Gpr4 (EfGpr4, EfM3. 044840) is aligned with the corresponding homologues in *N. crassa* NcGpr4 (NCU06312), *F. graminearum* FgGprC (FGSG_05006) and *M. oryzae* MoGpr4 (MGG_08803). *E. festucae* Gpr4 displays 26.3% amino acid identity to *N. crassa* Gpr-4, 30.6% identity to the *F. graminearum* homologue and 19.6% identity to the *M. oryzae* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 6: Predicted protein topology of *E. festucae* Gpr4



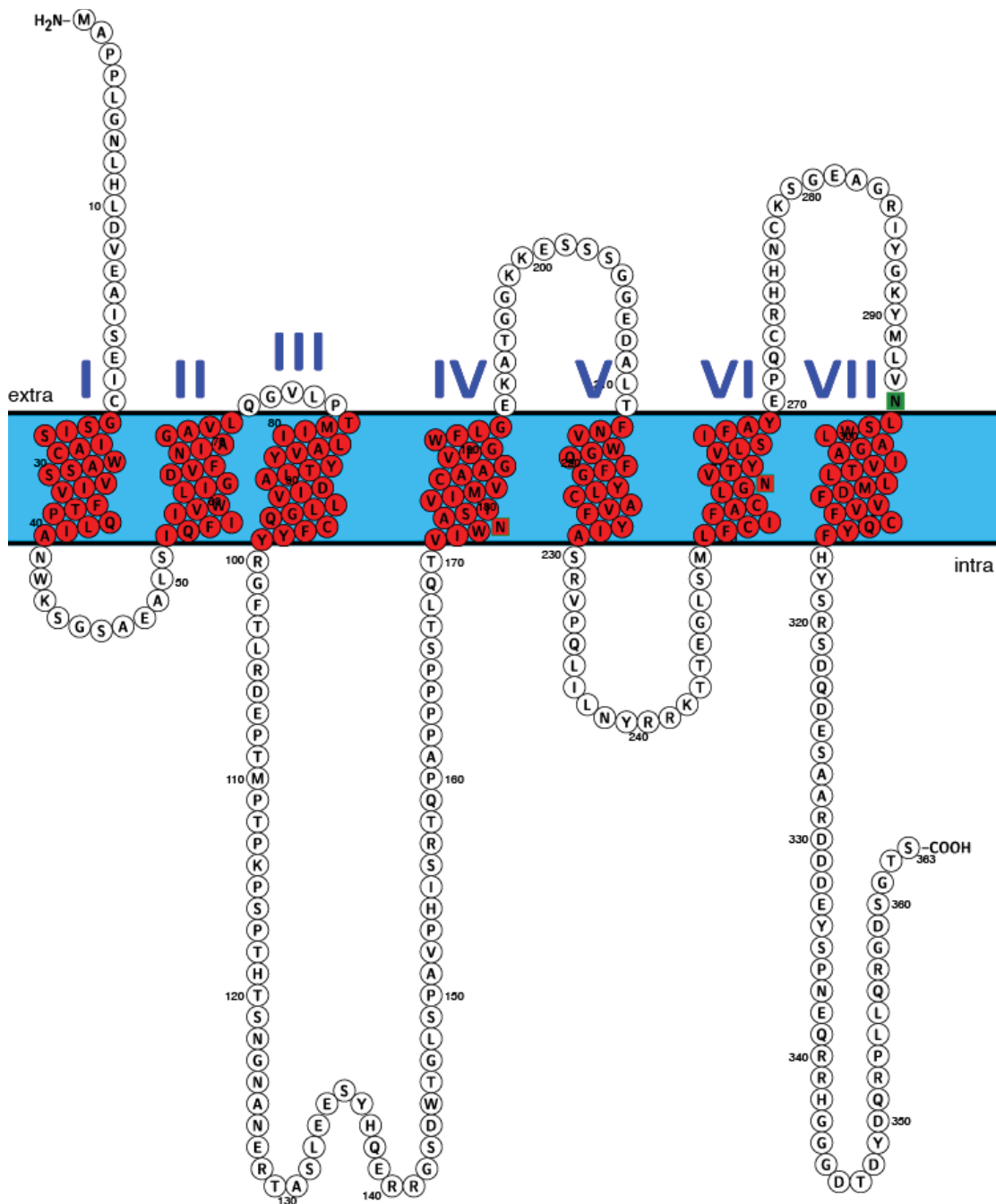
The predicted Gpr4 polypeptide is 583 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and an intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with long ICL3. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 7: Multiple sequence alignment of *E. festucae* Gpr5 homologues



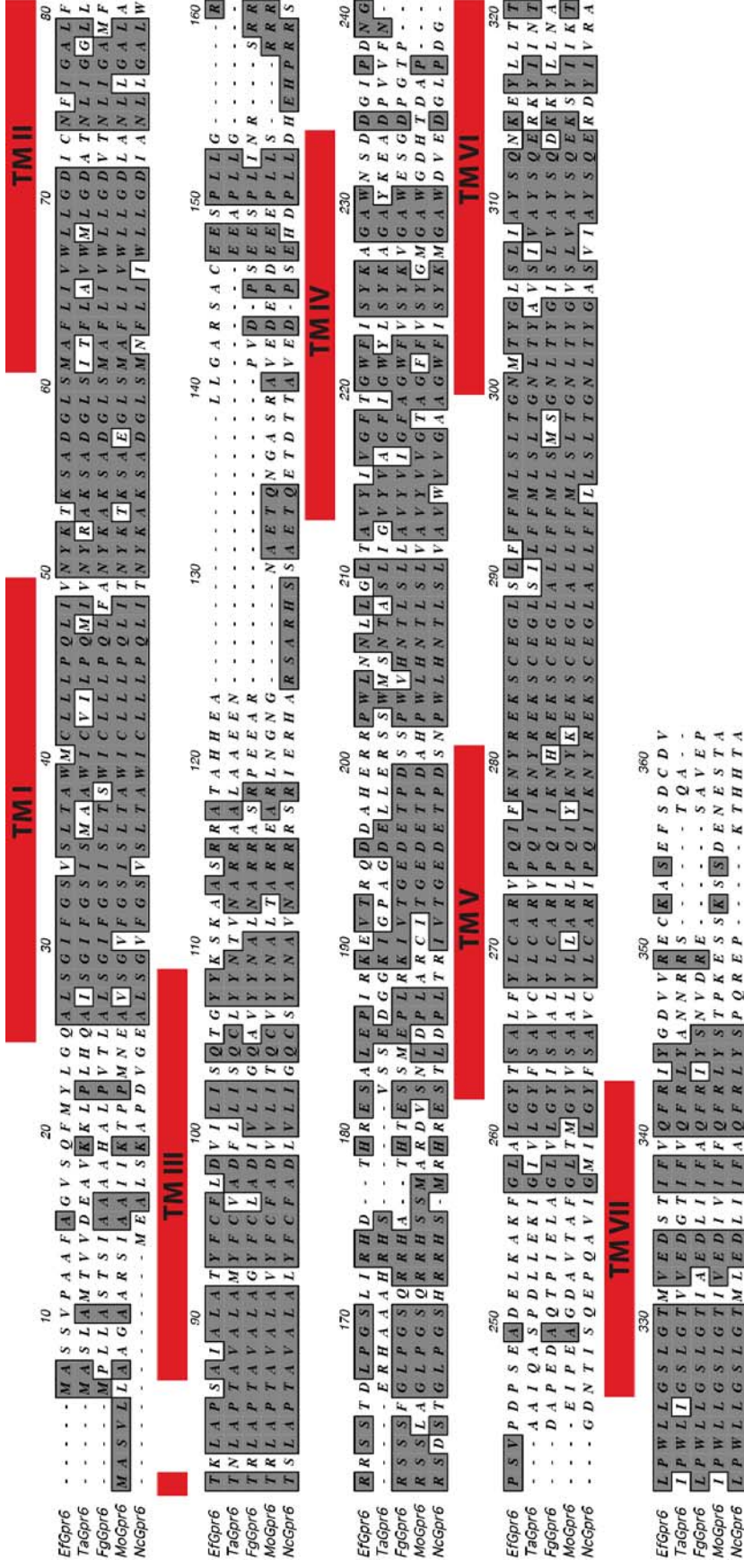
The predicted amino acid sequence of *E. festucae* Gpr5 (EfGpr5, Efm3.042760) is aligned with the corresponding homologues in *N. crassa* NcGpr5 (NCU00300), *F. graminearum* FgGpr5 (FGSG_05579), *M. oryzae* MoGpr5 (MGG_04698) and *T. atroviride* TaGpr5 (TRIATDRAFT_238619). *E. festucae* Gpr5 displays 35.1% amino acid identity to *N. crassa* Gpr-5, 63% identity to the *F. graminearum* homologue, 50.1% identity to the *M. oryzae* homologue and 60.2% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 8: Predicted protein topology of *E. festucae* Gpr5



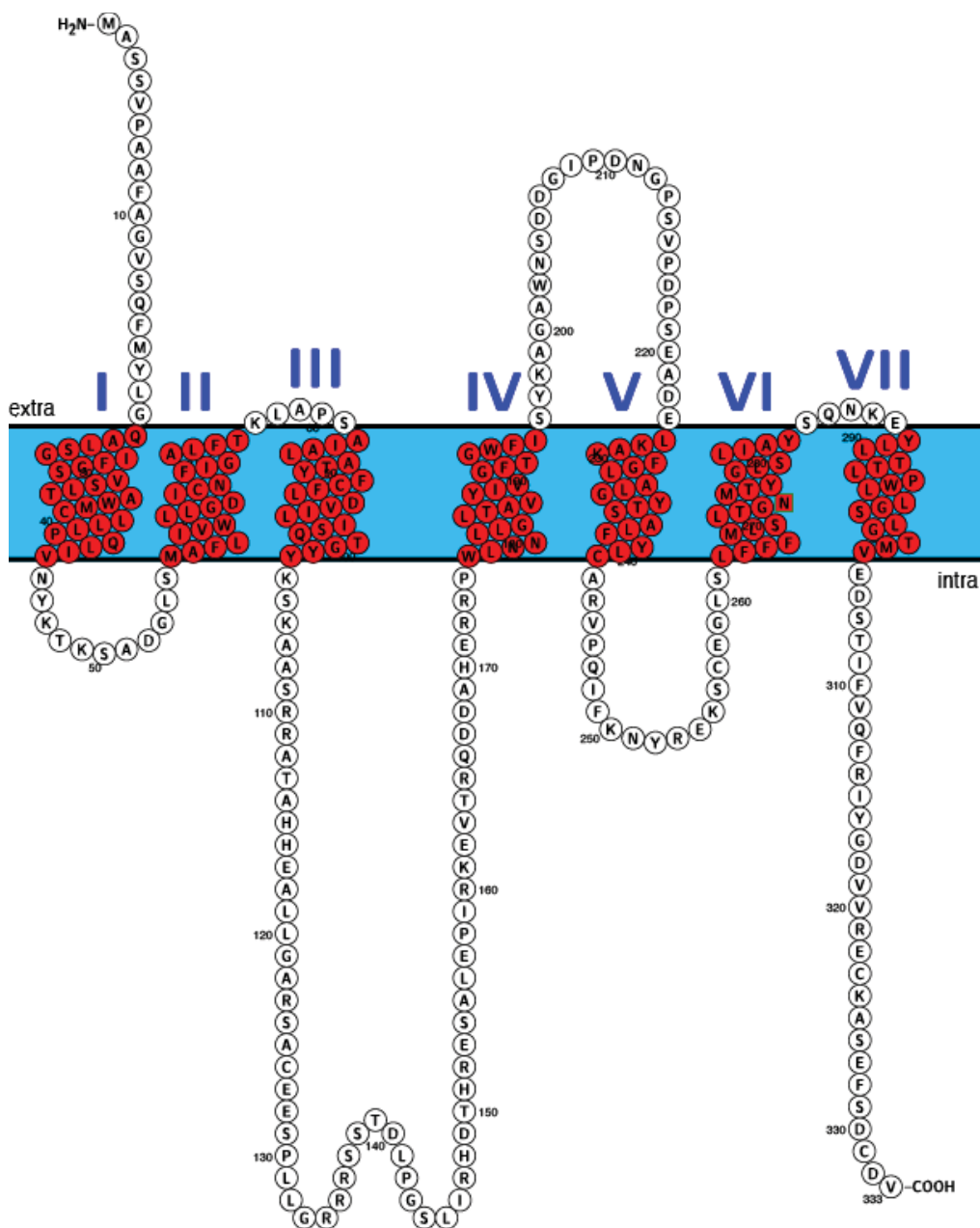
The predicted Gpr5 polypeptide is 363 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and an intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with long ICL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 9: Multiple sequence alignment of *E. festucae* Gpr6 homologues



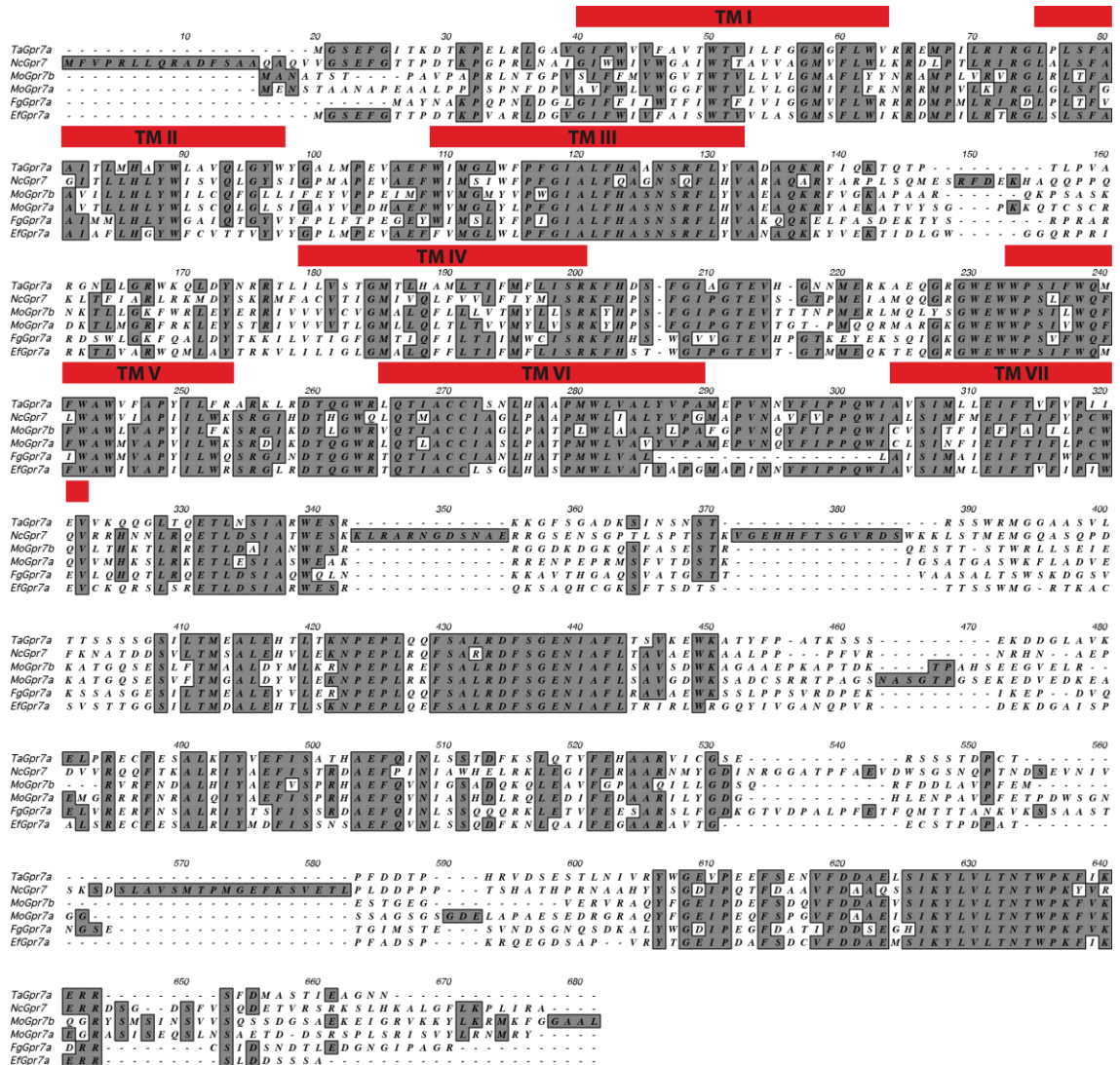
The predicted amino acid sequence of *E. festucae* Gpr6 (EfGpr6, EfM3.019030) is aligned with the corresponding homologues in *N. crassa* NcGpr6 (NCU09195), *F. graminearum* FgGpr6 (FGSG_08496), *M. oryzae* MoGpr6 (MGG_03051) and *T. atroviride* TaGpr6 (TRIATDRAFT_300620). *E. festucae* Gpr6 displays 54.6% amino acid identity to *N. crassa* Gpr-6, 57% identity to the *F. graminearum* homologue, 53.1% identity to the *M. oryzae* homologue and 47.3% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 10: Predicted protein topology of *E. festucae* Gpr6



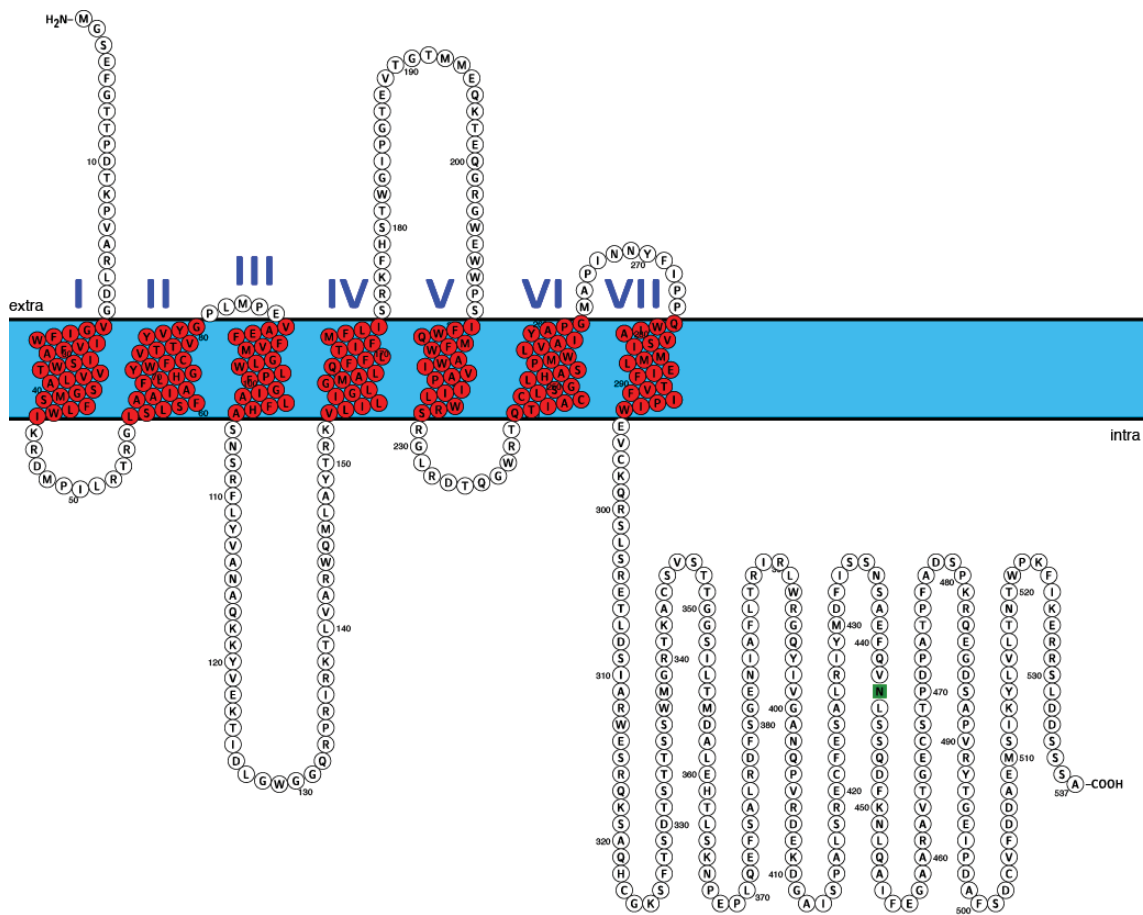
The predicted Gpr6 polypeptide is 333 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and an intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with long ICL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 11: Multiple sequence alignment of *E. festucae* Gpr7a homologues



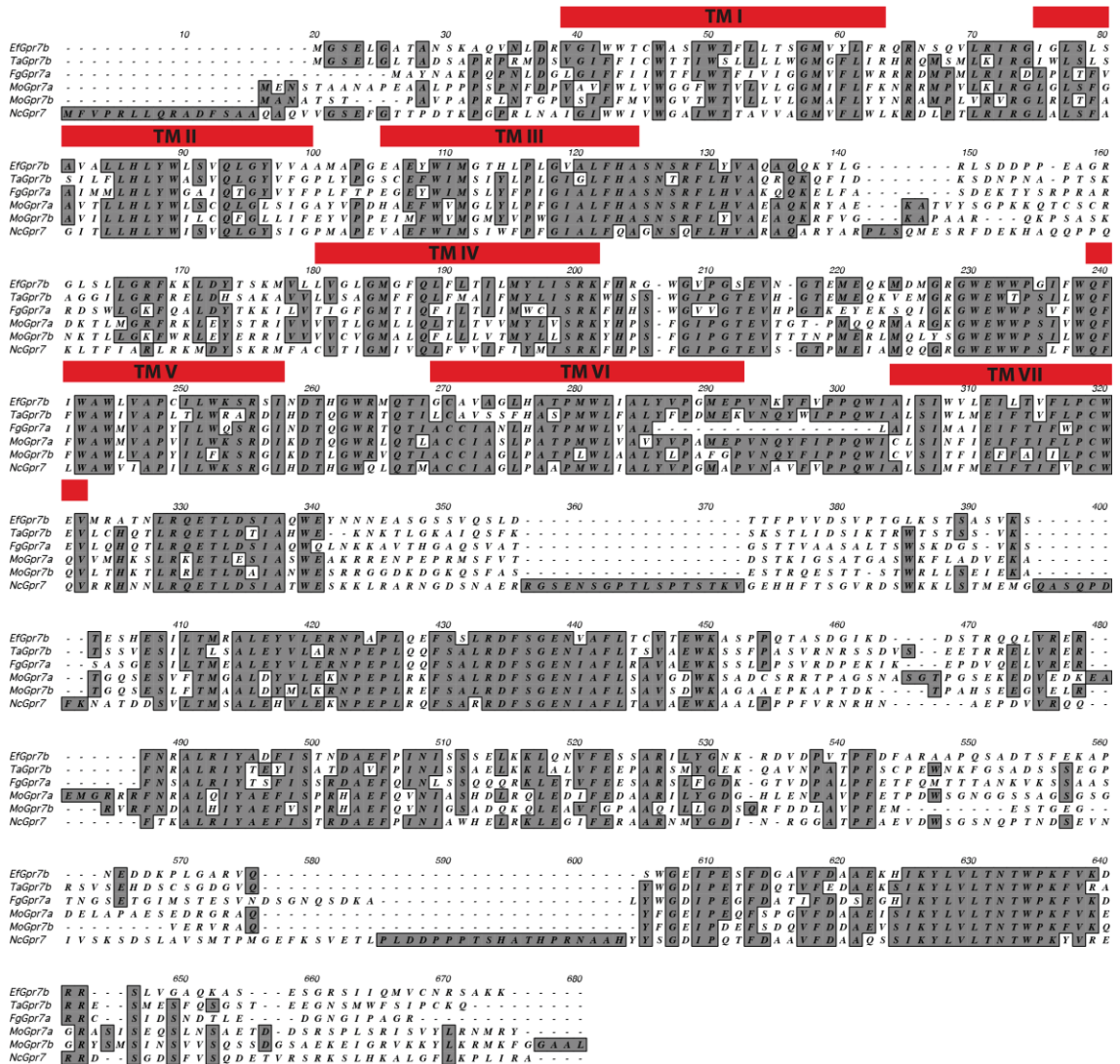
The predicted amino acid sequence of *E. festucae* Gpr7a (EfGpr7a, Efm3. 007810) is aligned with the corresponding homologues in *N. crassa* NcGpr7 (NCU09883), *F. graminearum* FgGpr7a (FGSG_04628), *M. oryzae* MoGpr7a (MGG_13926) and MoGpr7b (MGG_11693) and *T. atroviride* TaGpr7a (TRIATDRAFT_40423). *E. festucae* Gpr7a displays 43.6% amino acid identity to *N. crassa* Gpr-7, 46.1% identity to the *F. graminearum* homologue, 45.5% identity to the *M. oryzae* homologue and 63% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 12: Predicted protein topology of *E. festucae* Gpr7a



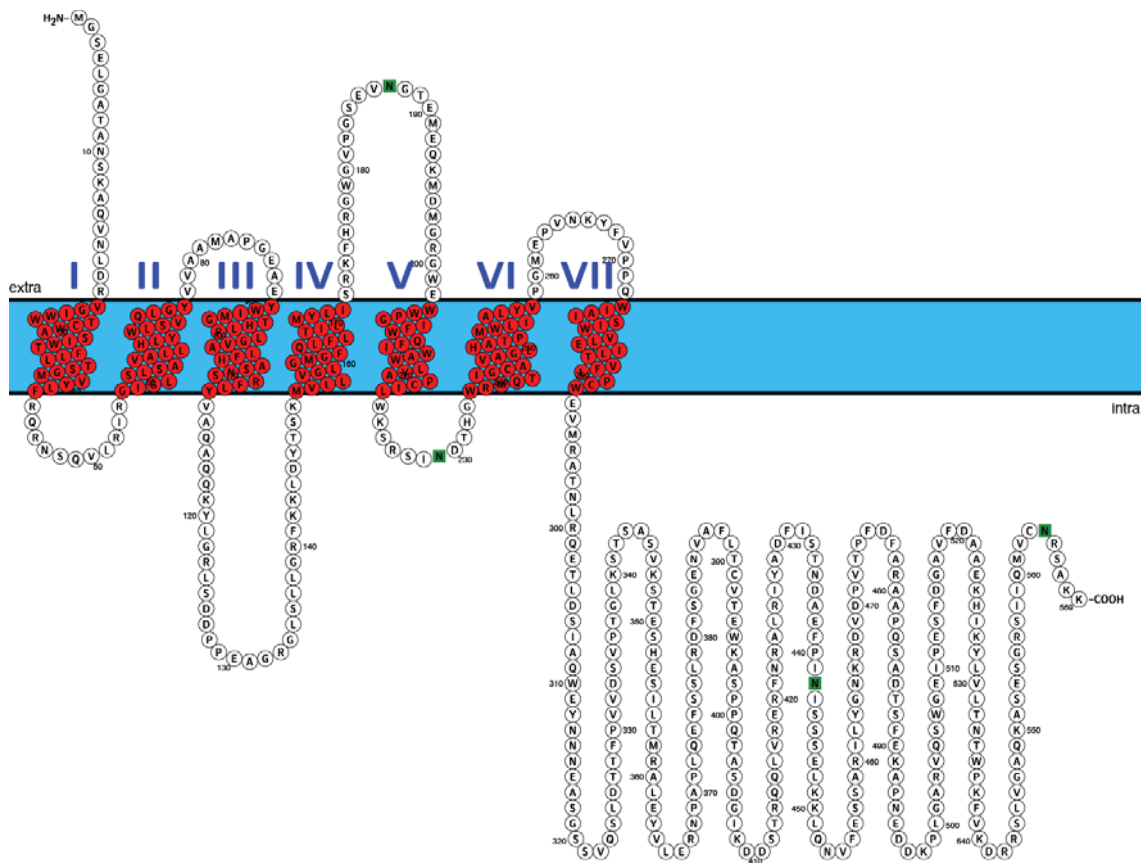
The predicted Gpr7a polypeptide is 537 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with longer ICL2 and ECL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 13: Multiple sequence alignment of *E. festucae* Gpr7b homologues



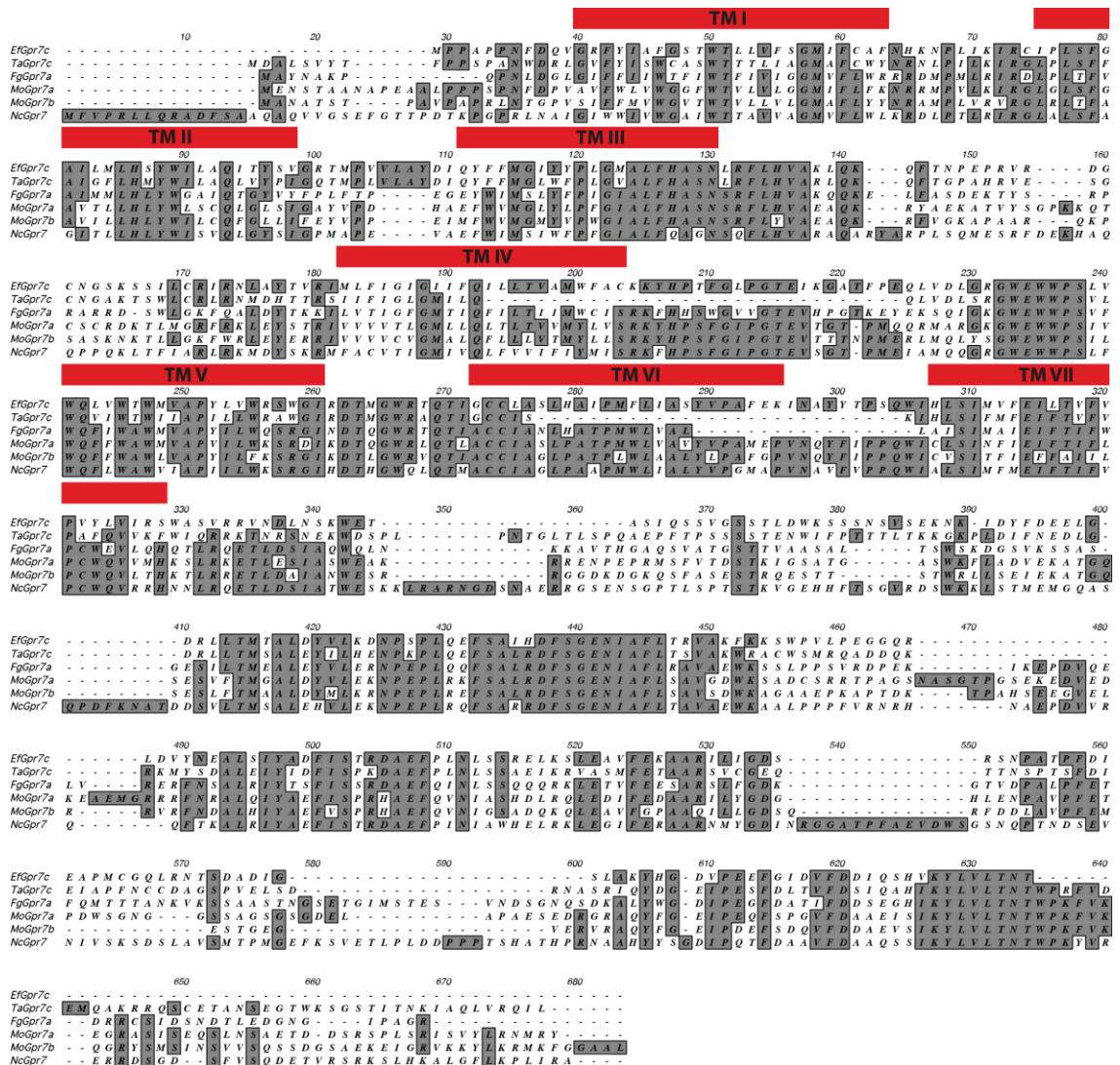
The predicted amino acid sequence of *E. festucae* Gpr7b (EfGpr7b, EfM3. 040610) is aligned with the corresponding homologues in *N. crassa* NcGpr7 (NCU09883), *F. graminearum* FgGpr7a (FGSG_04628), *M. oryzae* MoGpr7a (MGG_13926) and MoGpr7b (MGG_11693) and *T. atroviride* TaGpr7b (TRIATDRAFT_293686). *E. festucae* Gpr7b displays 44.7% amino acid identity to *N. crassa* Gpr-7, 50% identity to the *F. graminearum* homologue, 46.3% identity to the *M. oryzae* homologue and 54.2% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 14: Predicted protein topology of *E. festucae* Gpr7b



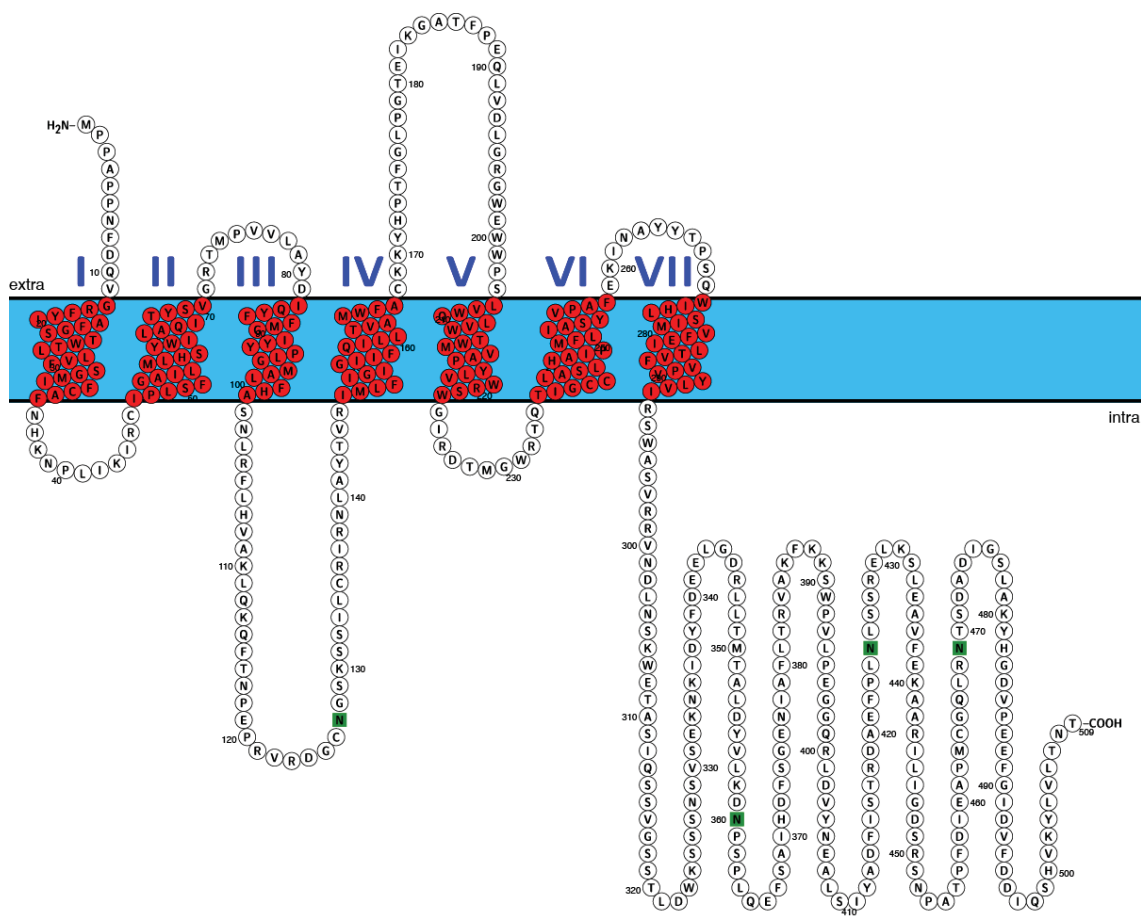
The predicted Gpr7b polypeptide is 569 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with longer ICL2 and ECL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 15: Multiple sequence alignment of *E. festucae* Gpr7c homologues



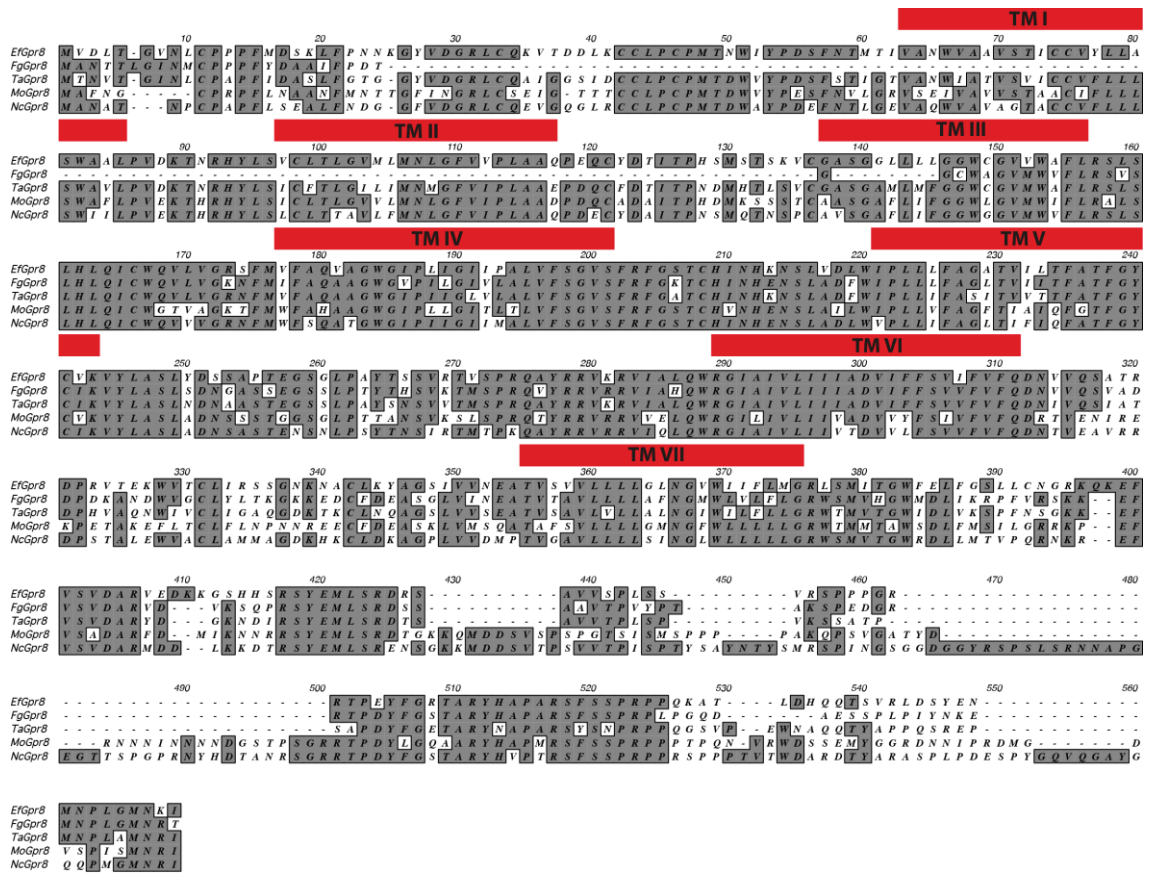
The predicted amino acid sequence of *E. festucae* Gpr7c (EfGpr7c, Efm3. 059600) is aligned with the corresponding homologues in *N. crassa* NcGpr7 (NCU09883), *F. graminearum* FgGpr7a (FGSG_04628) and *M. oryzae* MoGpr7a (MGG_13926) and MoGpr7b (MGG_11693) and *T. atroviride* TaGpr7c (TRIATDRAFT_210761). *E. festucae* Gpr7c displays 34.5% amino acid identity to *N. crassa* Gpr-7, 38.7% identity to the *F. graminearum* homologue, 39.1% identity to the *M. oryzae* homologue and 49.3% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 16: Predicted protein topology of *E. festucae* Gpr7c



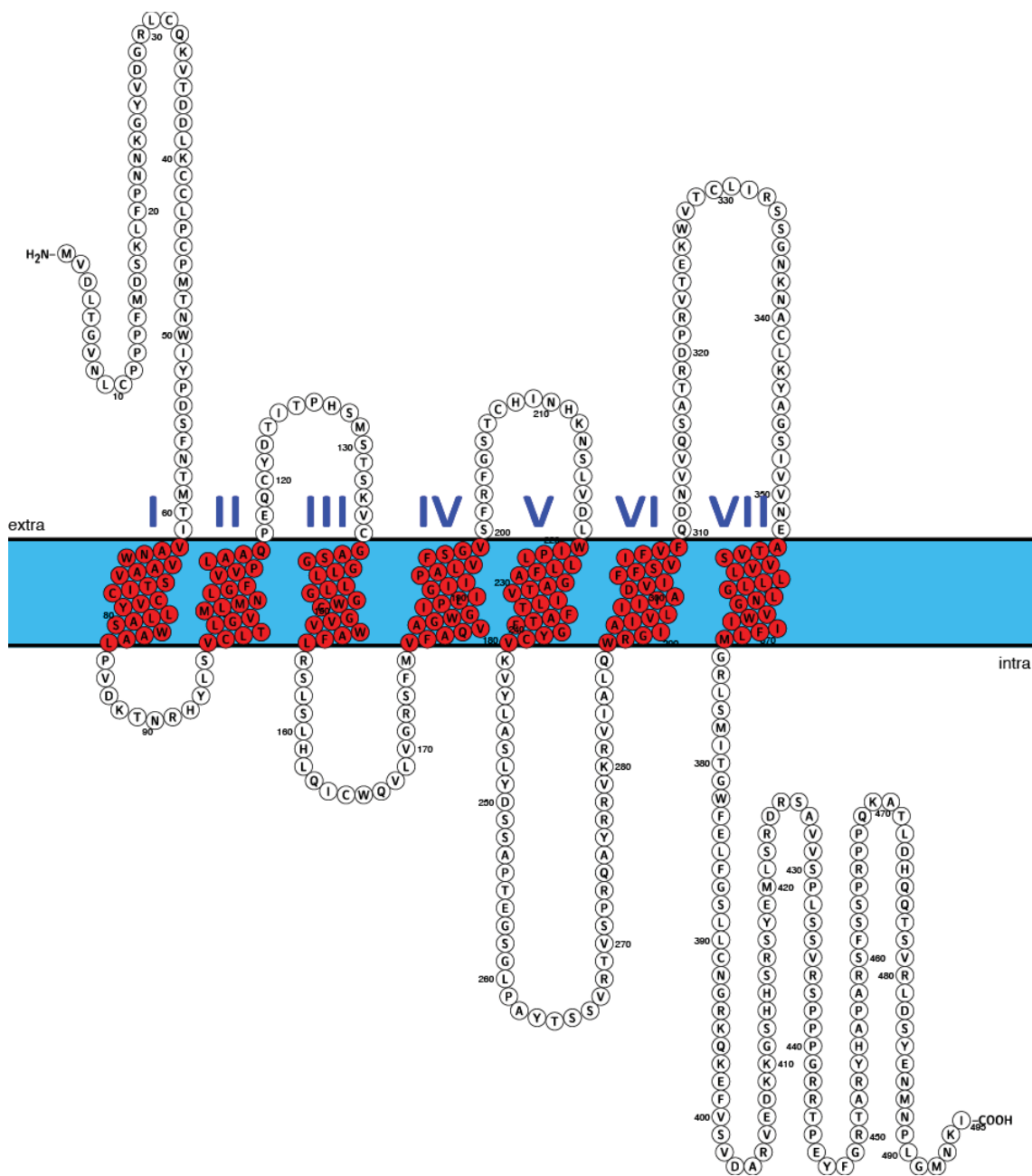
The predicted Gpr7c polypeptide is 509 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with longer ICL2 and ECL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 17: Multiple sequence alignment of *E. festucae* Gpr8 homologues



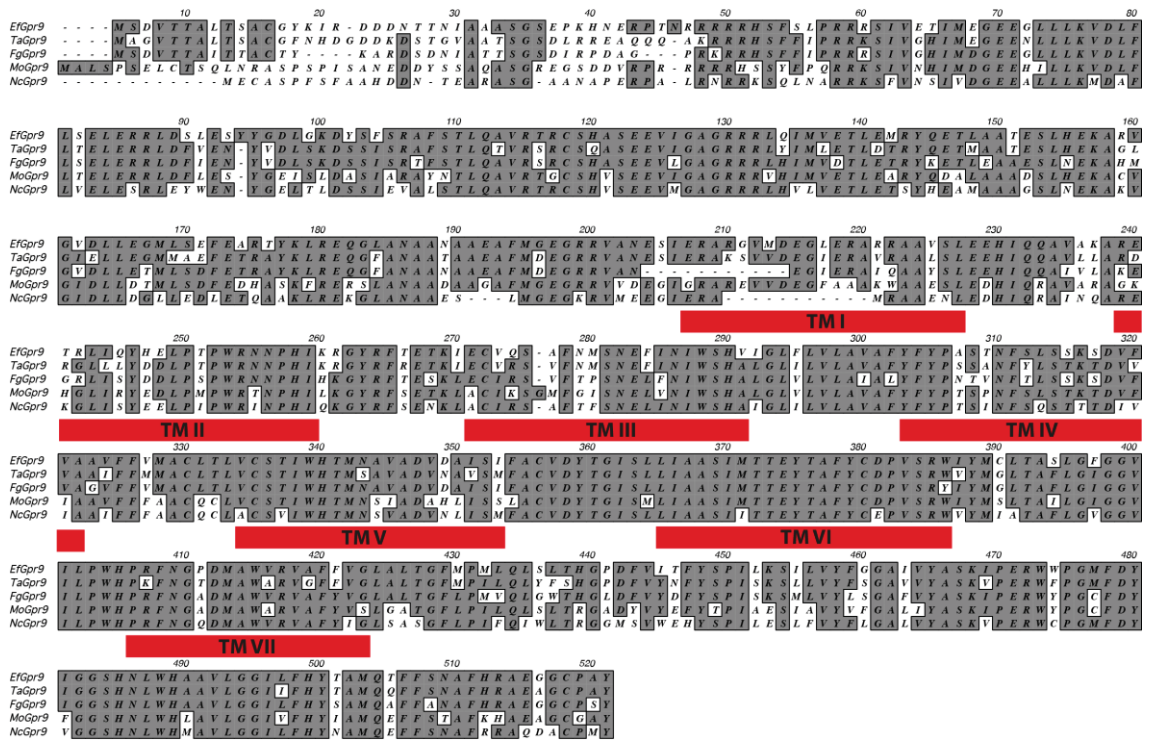
The predicted amino acid sequence of *E. festucae* Gpr8 (EfGpr8, EFM3.118420) is aligned with the corresponding homologues in *N. crassa* NcGpr8 (NCU03253), *F. graminearum* FgGpr8 (FGSG_00527), *M. oryzae* MoGpr8 (MGG_00532) and *T. atroviride* TaGpr8 (TRIATDRAFT_133045). *E. festucae* Gpr8 displays 53.7% amino acid identity to *N. crassa* Gpr-8, 47.5% identity to the *F. graminearum* homologue, 51.3% identity to the *M. oryzae* homologue and 68% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 18: Predicted protein topology of *E. festucae* Gpr8



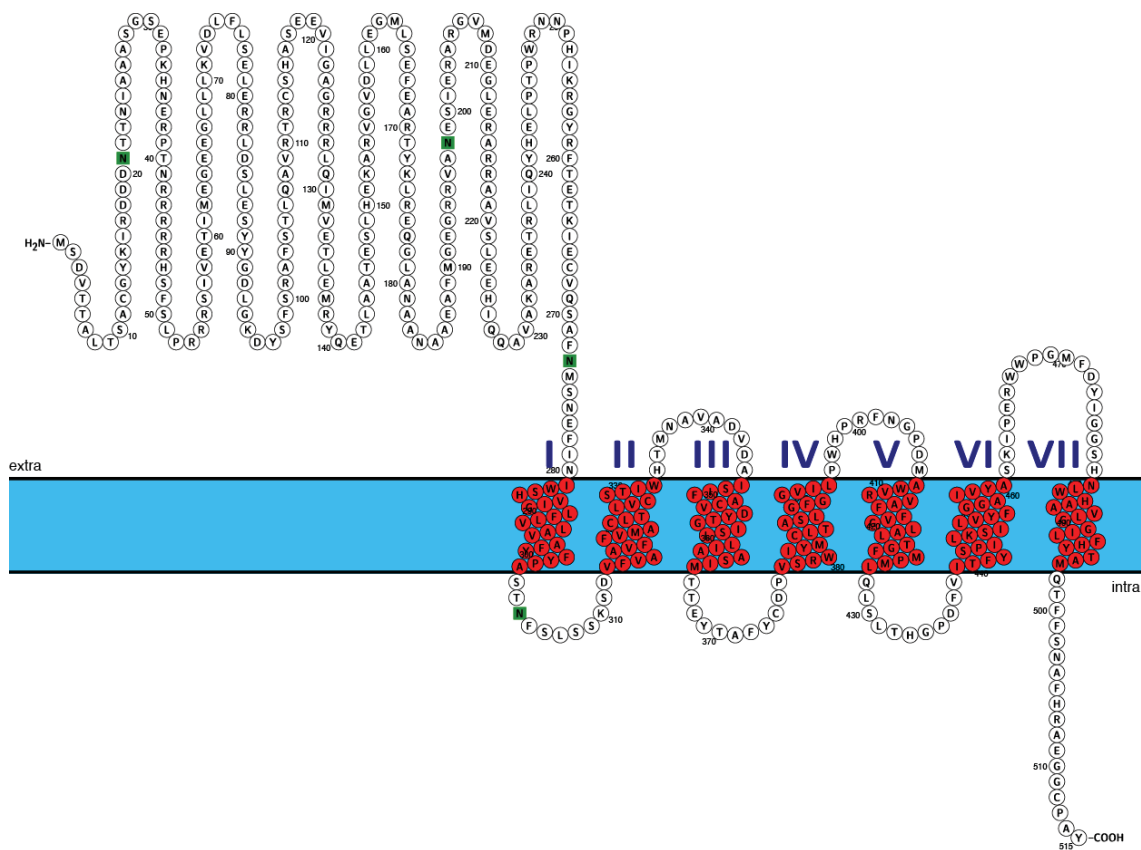
The predicted Gpr8 polypeptide is 495 amino acids in length and is predicted to contain seven transmembrane domains (TM), a longer extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with longer ICL3 and ECL3. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 19: Multiple sequence alignment of *E. festucae* Gpr9 homologues



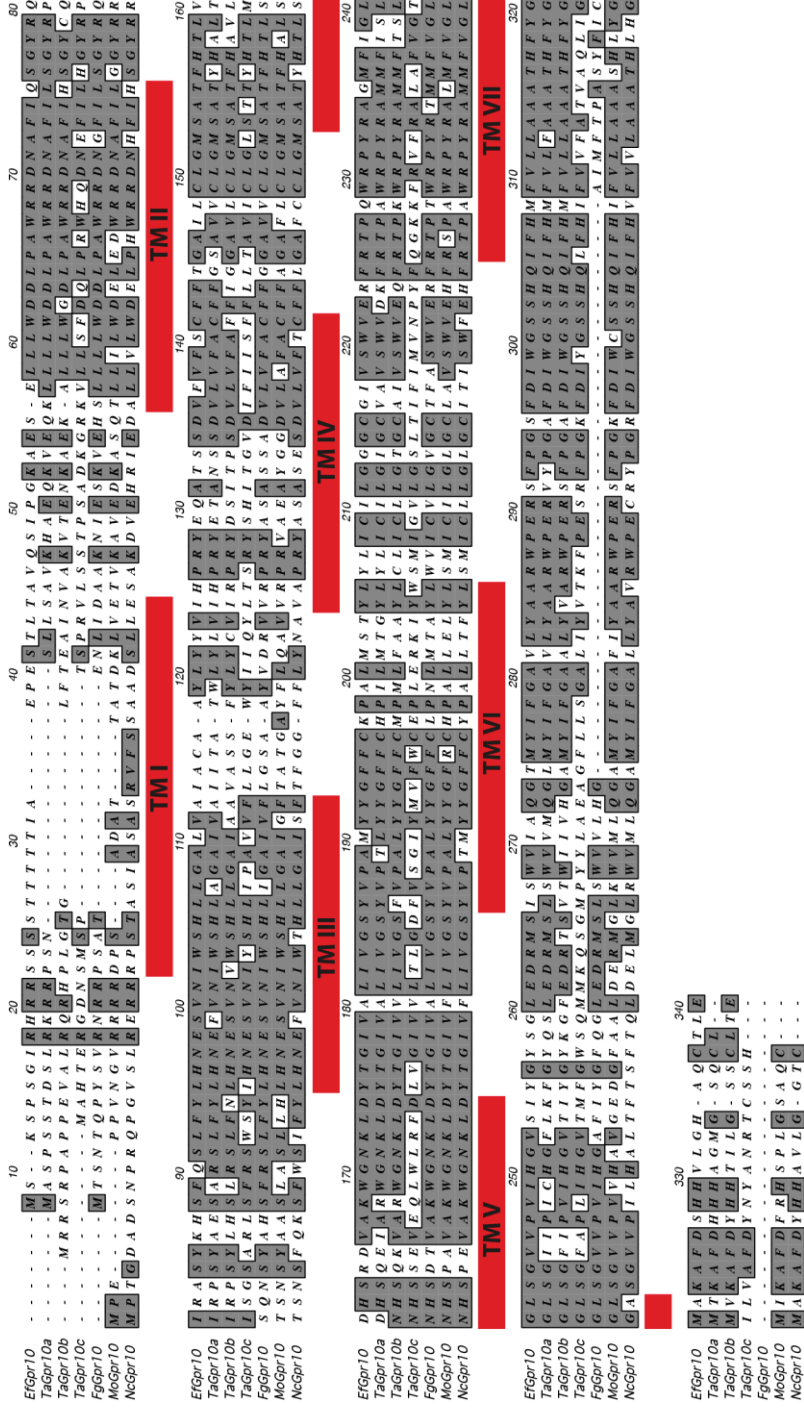
The predicted amino acid sequence of *E. festucae* Gpr9 (EfGpr9, Efm3.063600) is aligned with the corresponding homologues in *N. crassa* NcGpr9 (NCU03238), *F. graminearum* FgGpr9 (FGSG_01064), *M. oryzae* MoGpr9 (MGG_04679) and *T. atroviride* TaGpr9 (TRIATDRAFT_136196). *E. festucae* Gpr9 displays 63.1% amino acid identity to *N. crassa* Gpr-9, 67.9% identity to the *F. graminearum* homologue, 66.4% identity to the *M. oryzae* homologue and 77.5% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 20: Predicted protein topology of *E. festucae* Gpr9



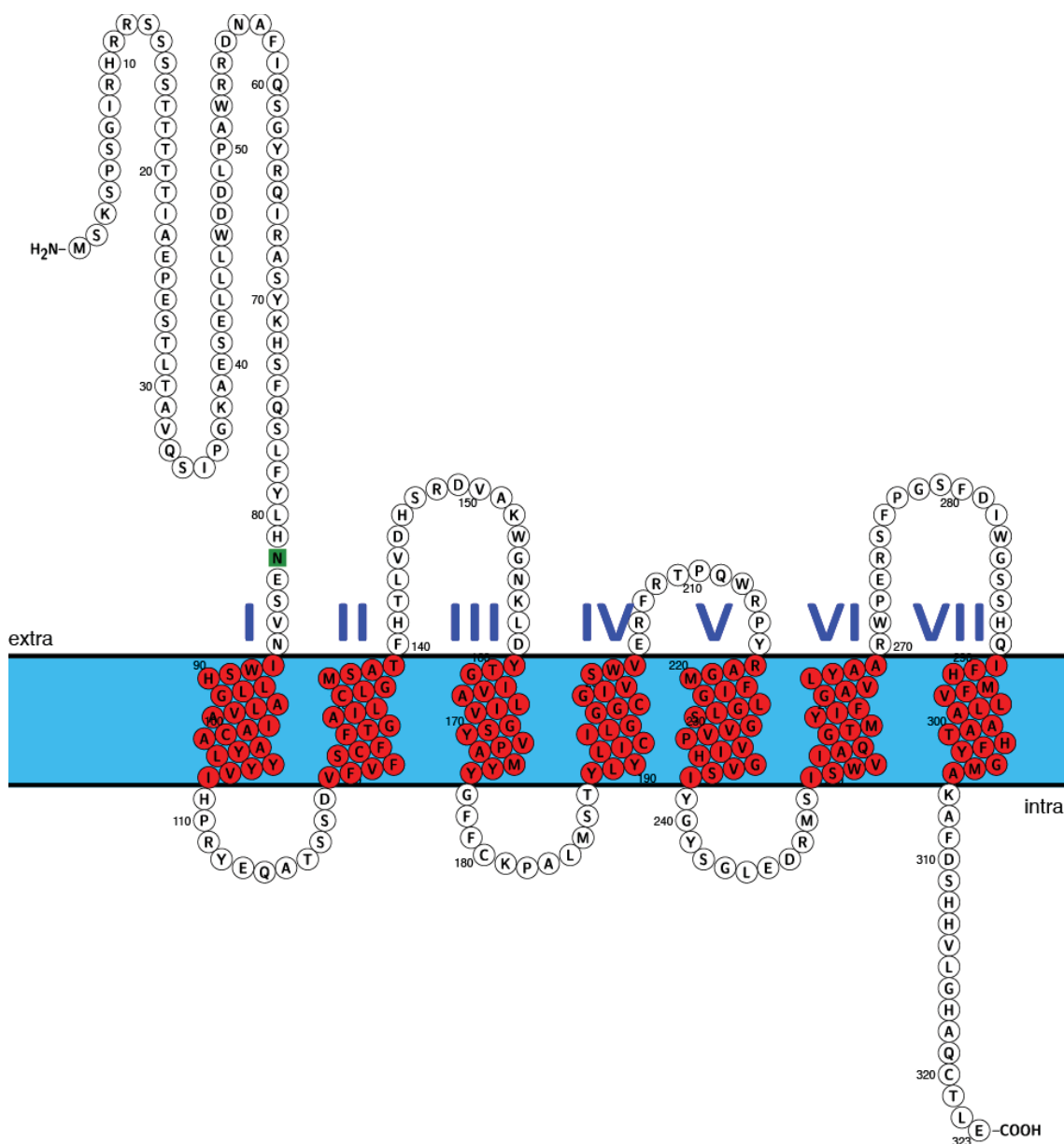
The predicted Gpr9 polypeptide is 515 amino acids in length and is predicted to contain seven transmembrane domains (TM), a long extracellular amino-terminal (N₂H) and a short intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 21: Multiple sequence alignment of *E. festucae* Gpr10 homologues



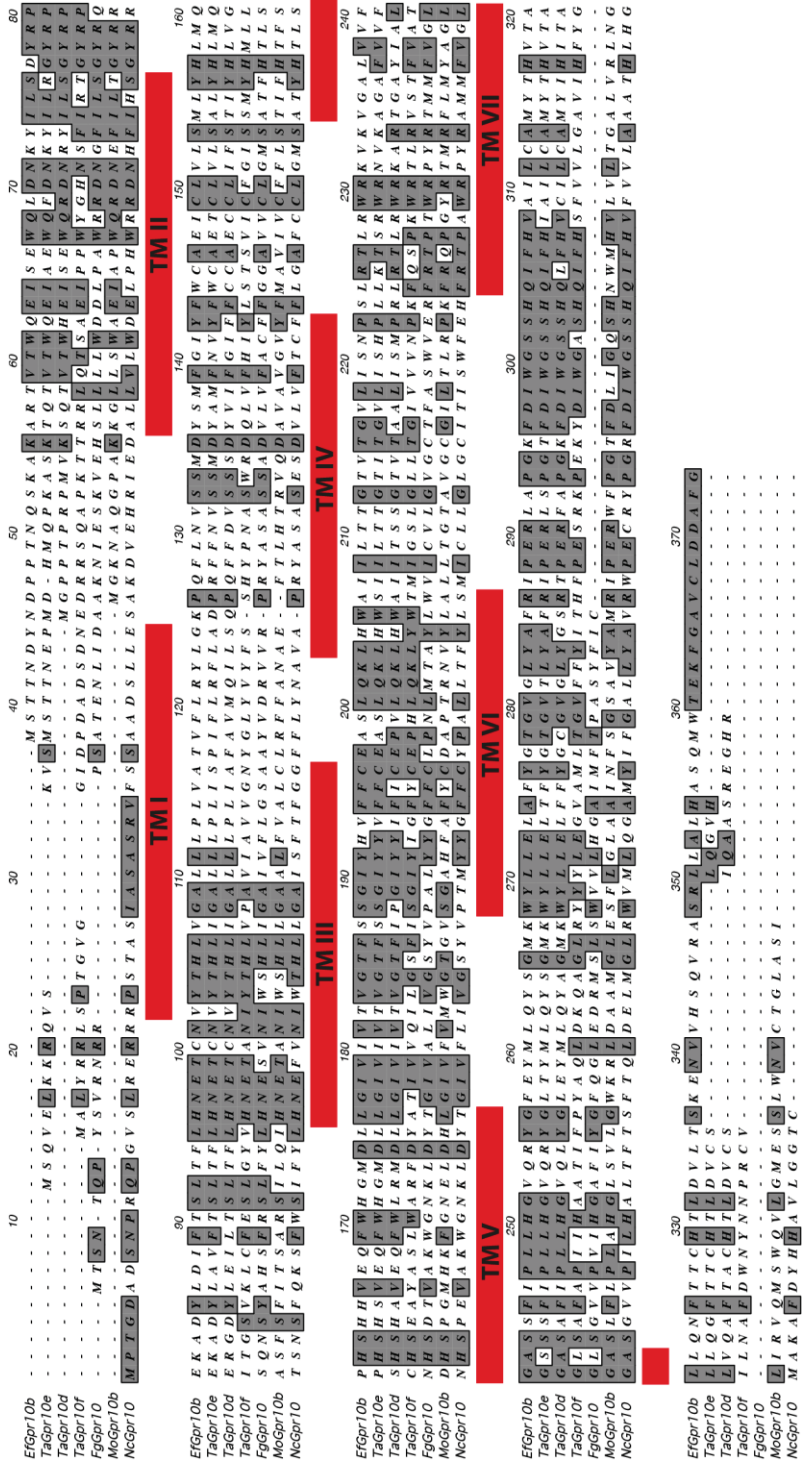
The predicted amino acid sequence of *E. festucae* Gpr10 (EfGpr10, EF3. 029580) is aligned with the corresponding homologues in *N. crassa* Nc_Gpr10 (NCU04986), *F. graminearum* FgGpr10 (FGSG_04051), *M. oryzae* MoGpr10 (MGG_16855) and *T. atroviride* TaGpr10a (TRIATDRAFT_290047; 68), TaGpr10b (TRIATDRAFT_210209; 65) and TaGpr10c (TRIATDRAFT_152366; 33.2). *E. festucae* Gpr10 displays 57.1% amino acid identity to *N. crassa* Gpr-10, 63.7% identity to the *F. graminearum* homologue, 60.1% identity to the *M. oryzae* homologue and 68%, 65% and 33.2% identity to the *T. atroviride* homologues TaGpr10a, TaGpr10b and TaGpr10c respectively. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 22: Predicted protein topology of *E. festucae* Gpr10



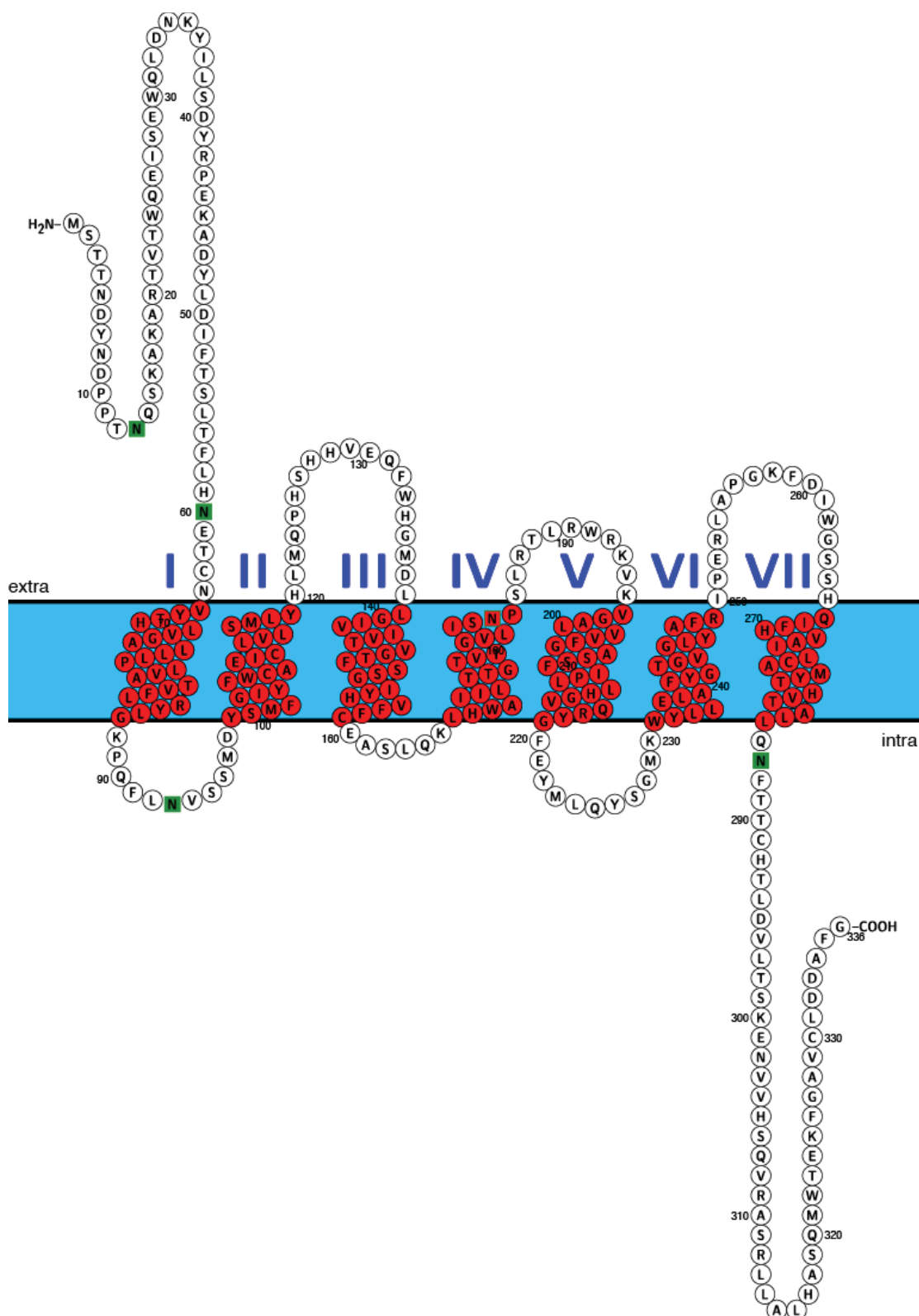
The predicted Gpr10 polypeptide is 323 amino acids in length and is predicted to contain seven transmembrane domains (TM), a long extracellular amino-terminal (N₂H) and a short intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 23: Multiple sequence alignment of *E. festucae* Gpr10b homologues



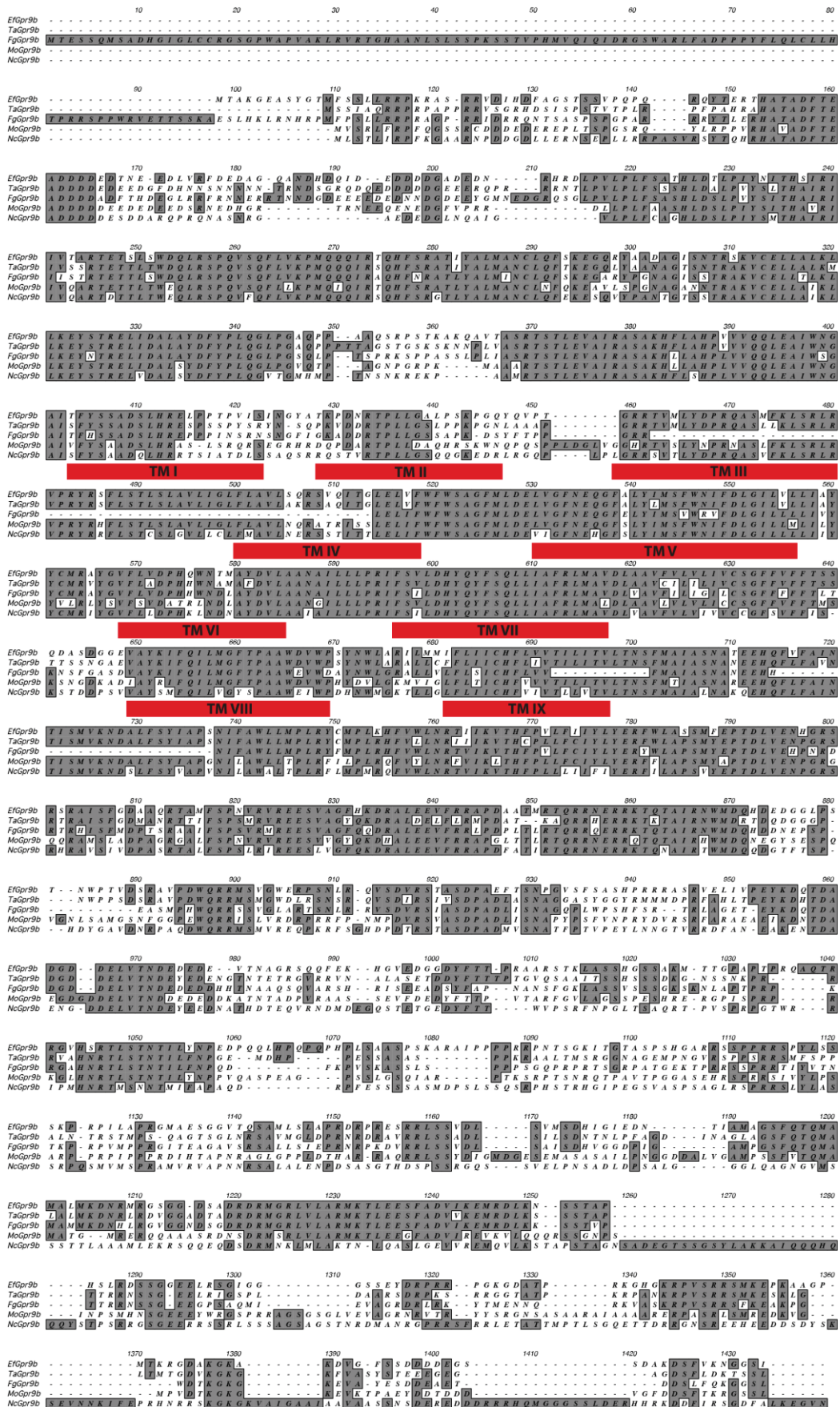
The predicted amino acid sequence of *E. festucae* Gpr10b (EfGpr10b, EF3.021530) is aligned with *N. crassa* Nc_Gpr10 (NCU04986) and *M. oryzae* MoGpr10b (MGG_09091) and *T. atroviride* Ta_Gpr10d (TRIATDRAFT_142946, 79.9), Ta_Gpr10e (TRIATDRAFT_046847, 68.4) and Ta_Gpr10f (TRIATDRAFT_142943, 36). *E. festucae* Gpr10b displays 32.4% amino acid identity to *N. crassa* Gpr-10, 30.8% identity to the *M. oryzae* homologue, 79.9%, 68.4 and 36% identity to the *T. atroviride* TaGpr10d, TaGpr10e and TaGpr10f respectively. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 24: Predicted protein topology of *E. festucae* Gpr10b



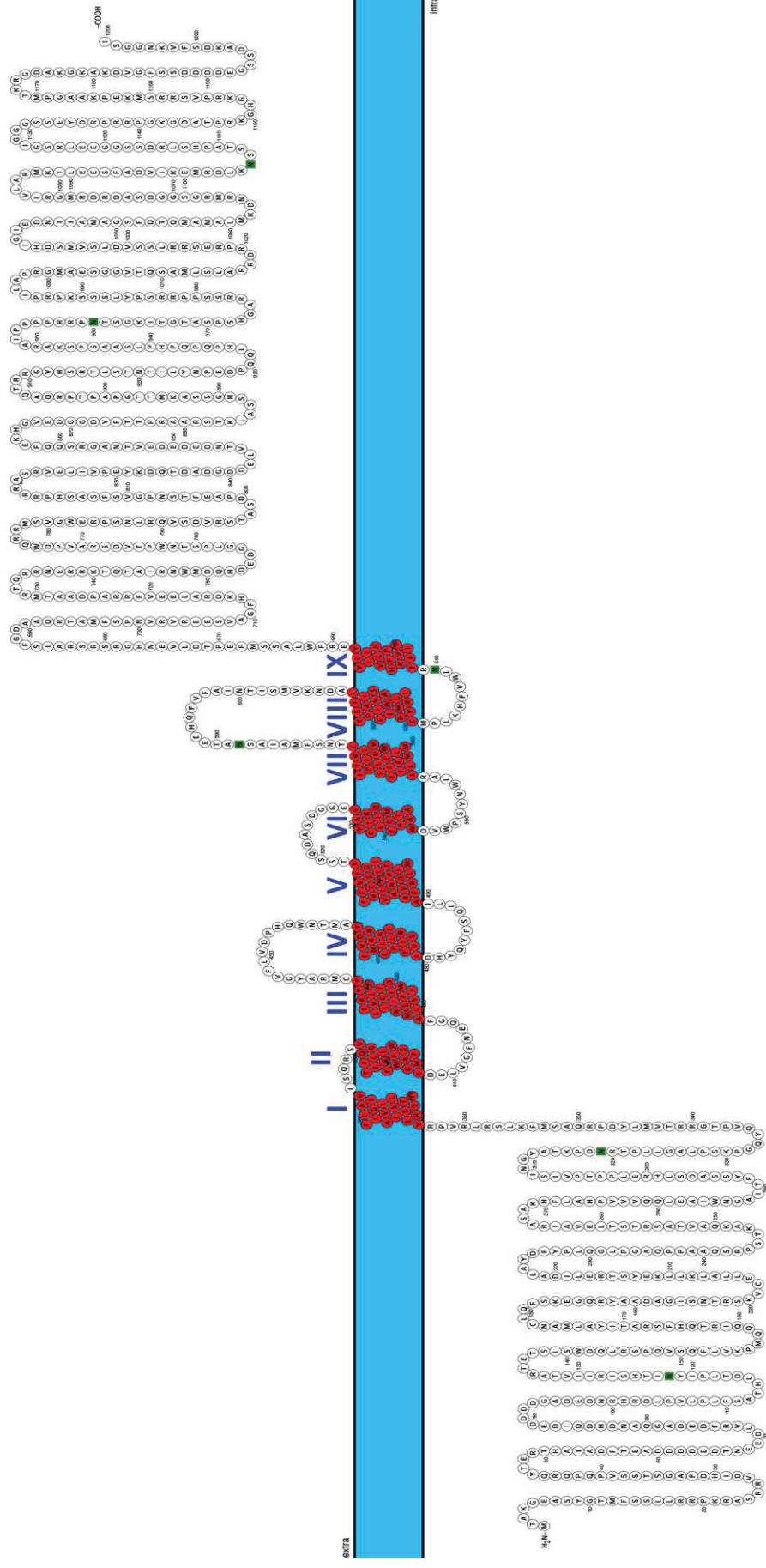
The predicted Gpr10b polypeptide is 336 amino acids in length and is predicted to contain seven transmembrane domains (TM), a longer extracellular amino-terminal (N₂H) and a shorter intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 25: Multiple sequence alignment of *E. festucae* Gpr9b homologues



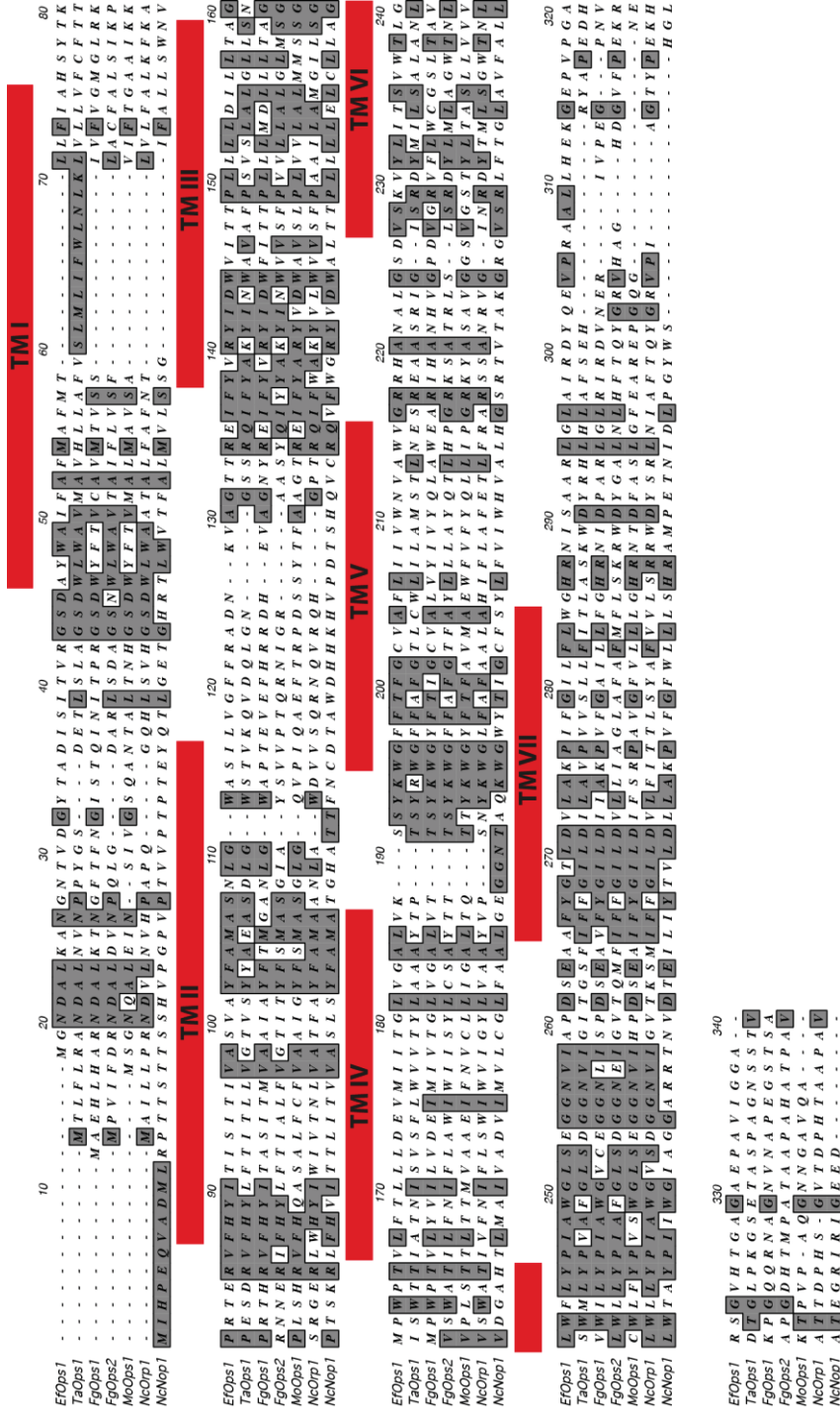
The predicted amino acid sequence of *E. festucae* Gpr9b (EfGpr9b, EfM3.080640) is aligned with the corresponding homologues *N. crassa* Nc_Gpr9b (NCU08283), *F. graminearum* FgGpr9b (FGSG09798), *M. oryzae* MoGpr9b (MGG_01538) and *T. atroviride* TaGpr9b (TRIATDRAFT_161784). *E. festucae* Gpr9b displays 46.2% amino acid identity to *N. crassa* Gpr-1, 53.1% identity to the *F. graminearum* homologue, 52.5% identity to the *M. oryzae* homologue and 65.9% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 26: Predicted protein topology of *E. festucae* Gpr9b



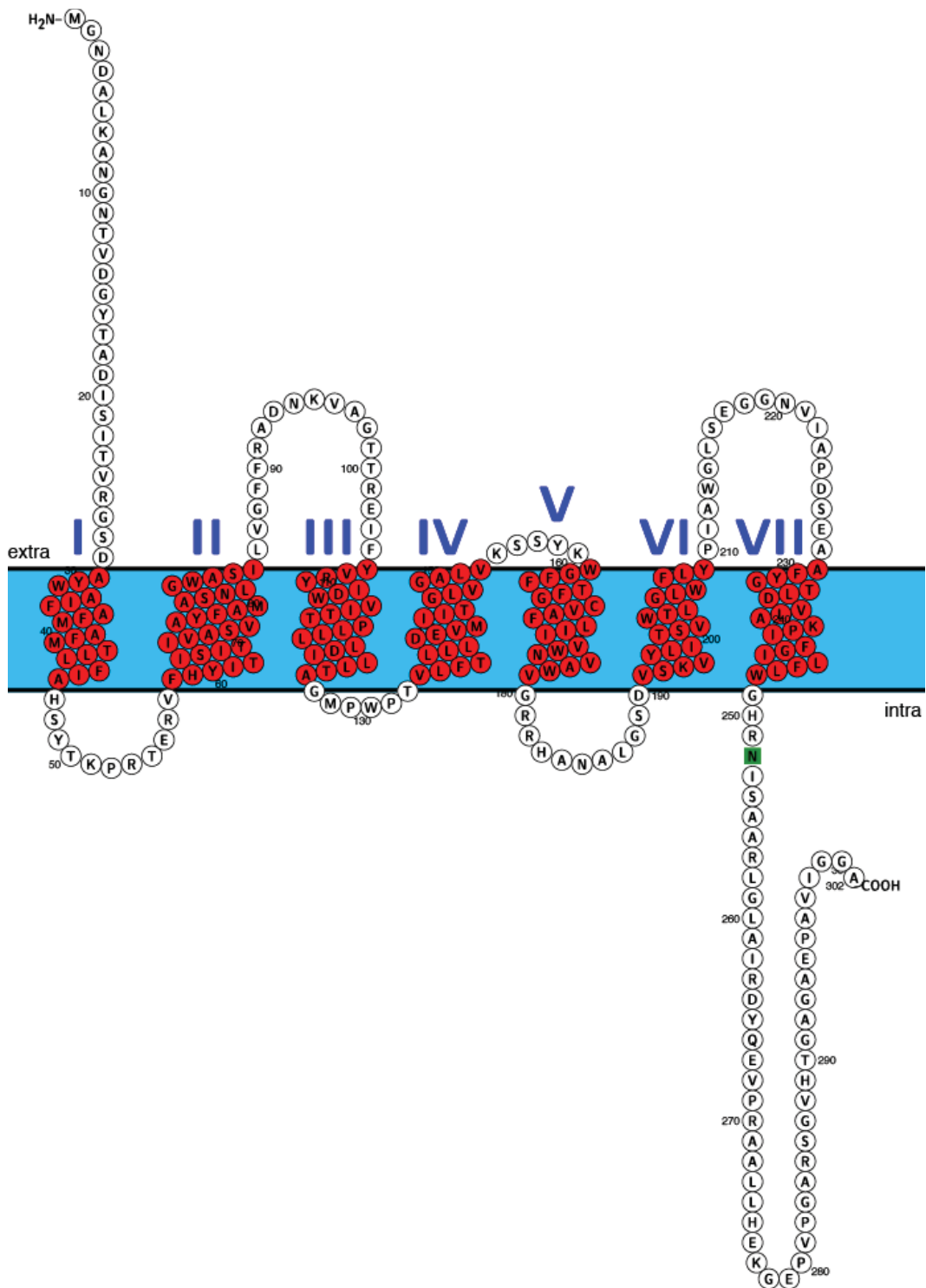
The predicted Gpr9b polypeptide is 1208 amino acids in length and is predicted to contain GPCR-atypical nine transmembrane domains (TM), a long intracellular amino-terminal (N₂H) and a long extracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 27: Multiple sequence alignment of *E. festucae* Ops1 homologues



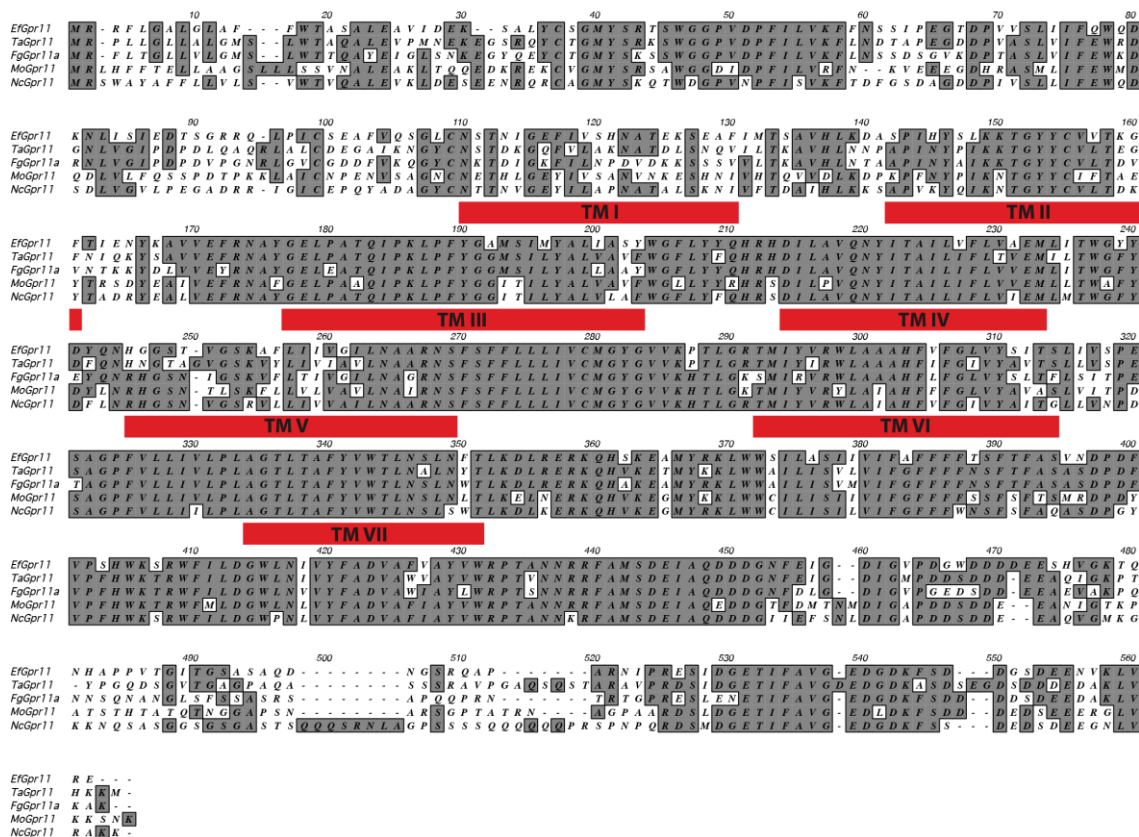
The predicted amino acid sequence of *E. festucae* Ops1 (EF0ps1, EFM3.031650) is aligned with the corresponding homologues *N. crassa* NcOrp1 (NCU01735) and *NcNo p* (NCU10055), *F. graminearum* FgOps1 (FGSG_03064) and FgOps2 (FGSG_01440), *M. oryzae* MoOps1 (MGG_09015) and *T. atroviride* Ta_Ops1 (TRIATDRAFT_210598). *E. festucae* Ops1 displays 33.3% amino acid identity to *N. crassa* Ops-1 and 31.4% to Nop-1, 56.6% identity to the *F. graminearum* homologues Ops1 and 33% to Ops2, 37% identity to the *M. oryzae* homologues and 29% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I - TM VII) in *E. festucae*.

Supplementary 28: Predicted protein topology of *E. festucae* Ops1



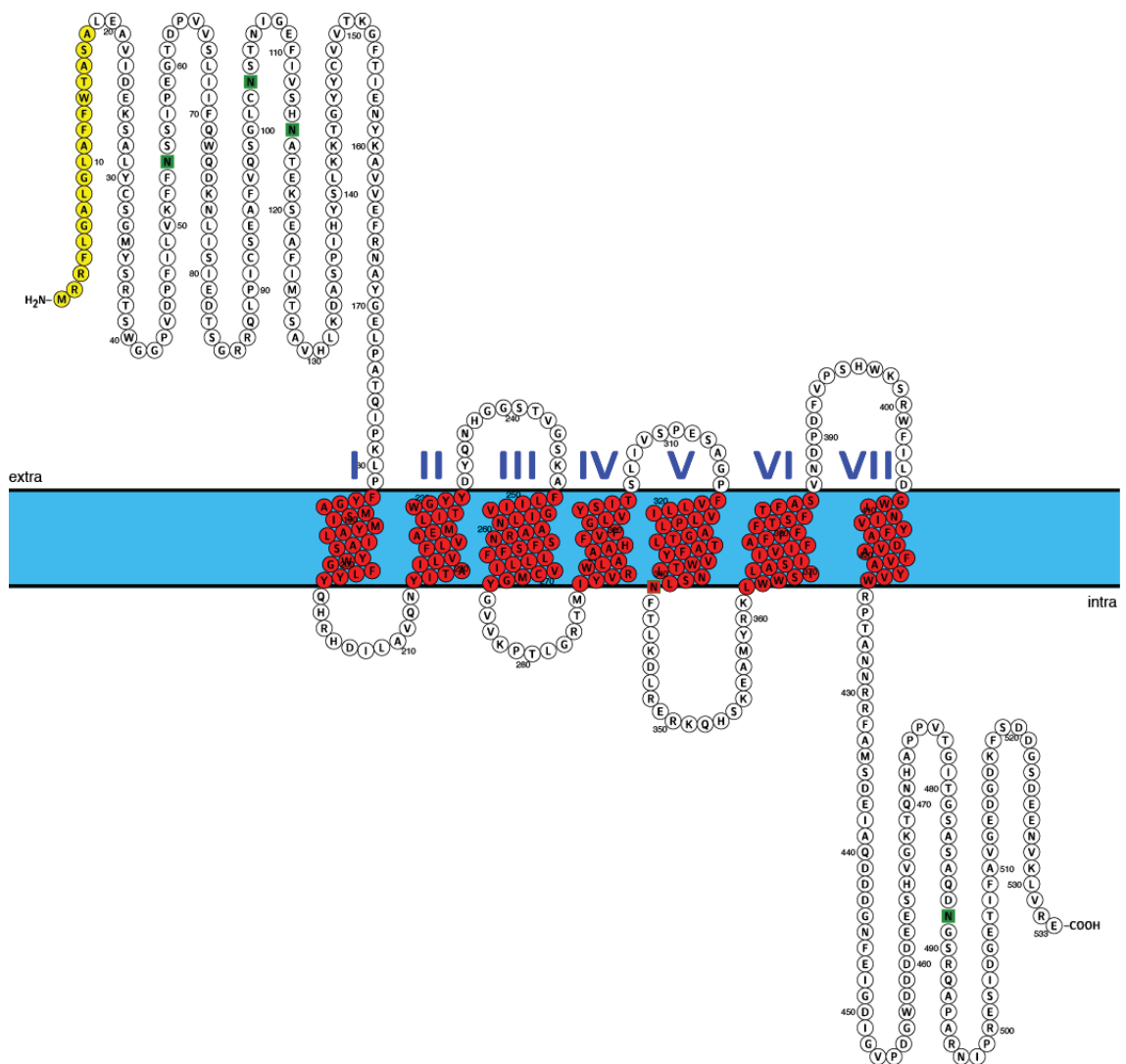
The predicted Ops1 polypeptide is 302 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and an intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 29: Multiple sequence alignment of *E. festucae* Gpr11 homologues



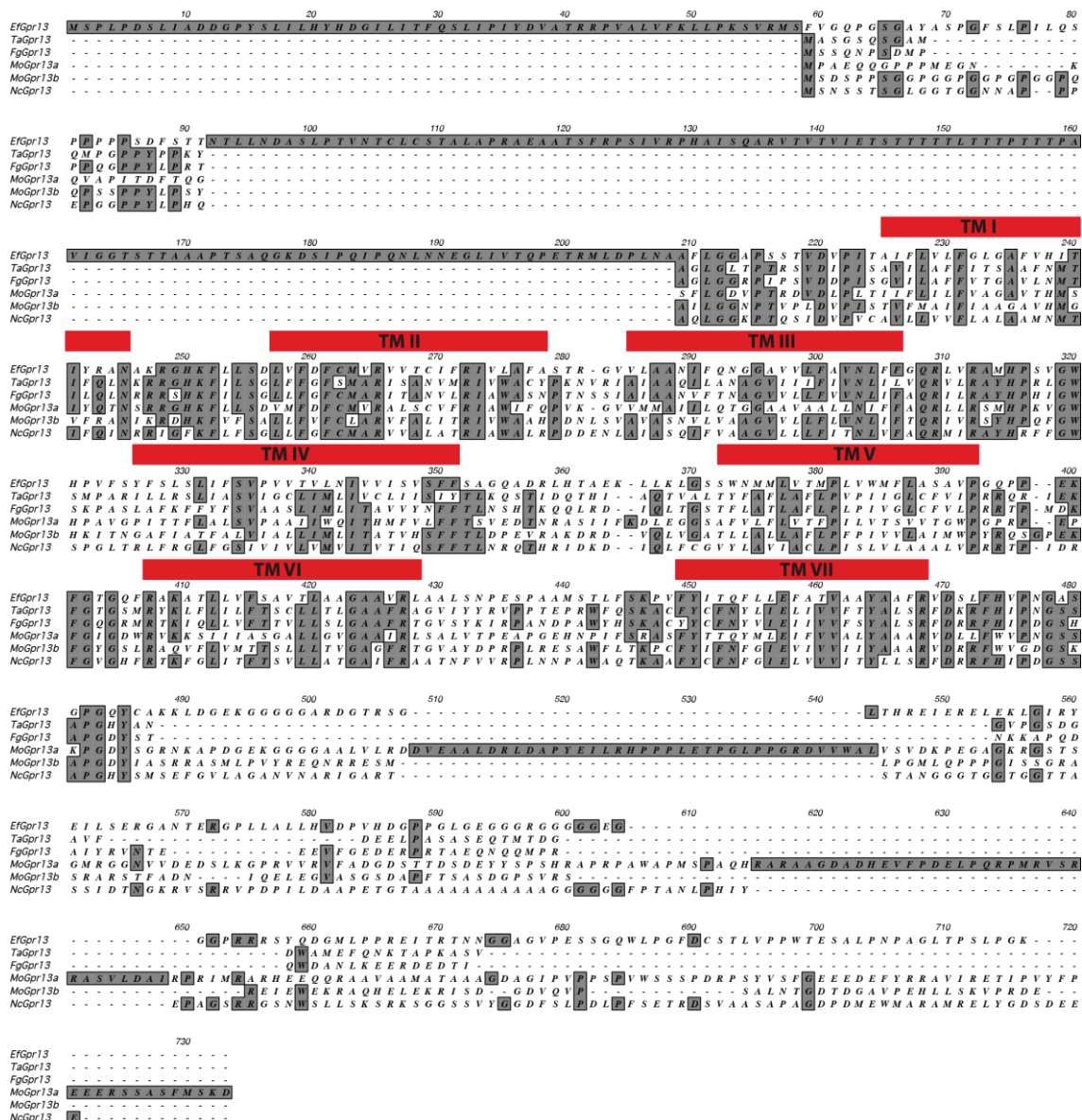
The predicted amino acid sequence of *E. festucae* Gpr11 (EfGpr11, EfM3.071470) is aligned with the corresponding homologues *N. crassa* NcGpr11 (NCU00182), *F. graminearum* FgGpr11 (FGSG_05404), *M. oryzae* Mo_Gpr11 (MGG_06418) and *T. atroviride* TaGpr11 (TRIATDRAFT_210445). *E. festucae* Gpr11 displays 60.3% amino acid identity to *N. crassa* Gpr-11, 67.7% identity to the *F. graminearum* homologue, 58.9% identity to the *M. oryzae* homologue and 68.3% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 30: Predicted protein topology of *E. festucae* Gpr11



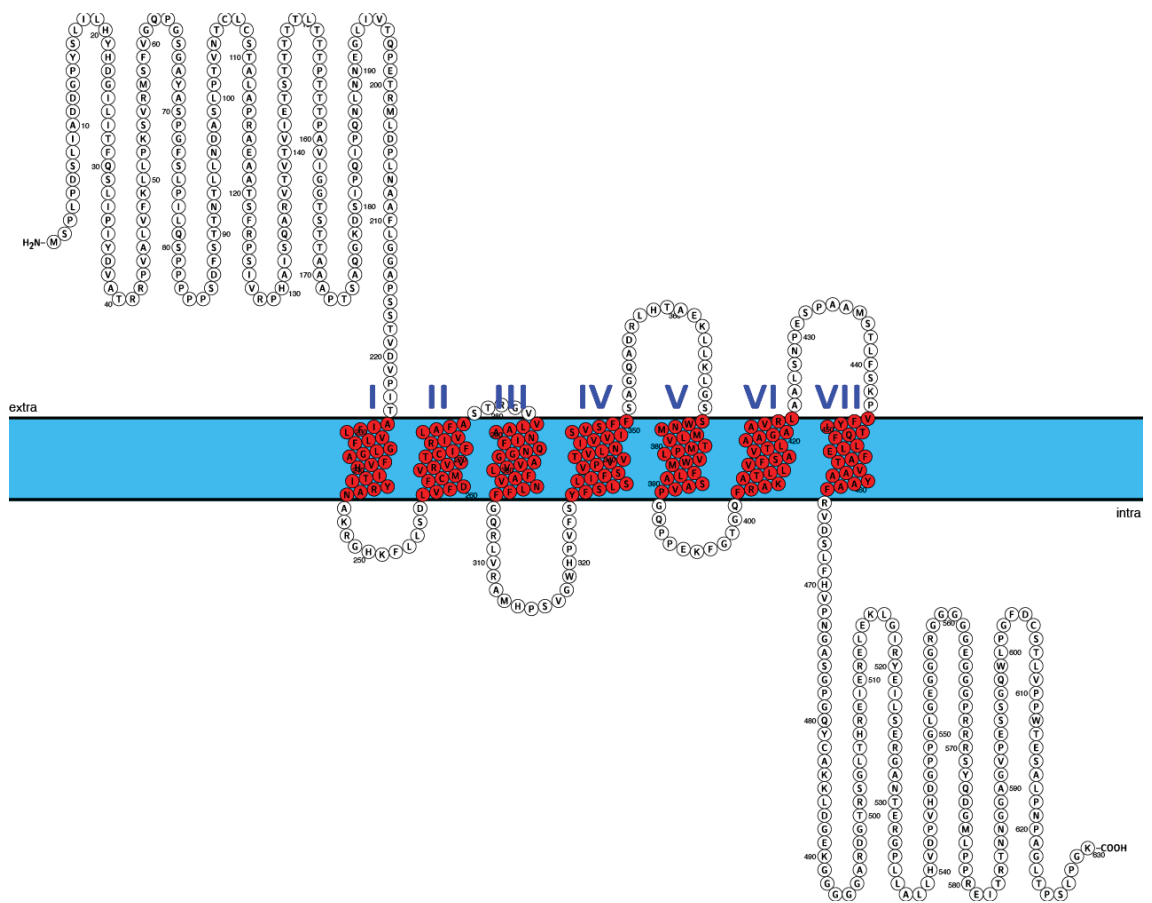
The predicted Gpr11 polypeptide is 533 amino acids in length and is predicted to contain seven transmembrane domains (TM), a long extracellular amino-terminal (N₂H) and an intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). The N-terminus contains a signal peptide domain (yellow). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 31: Multiple sequence alignment of *E. festucae* Gpr13 homologues



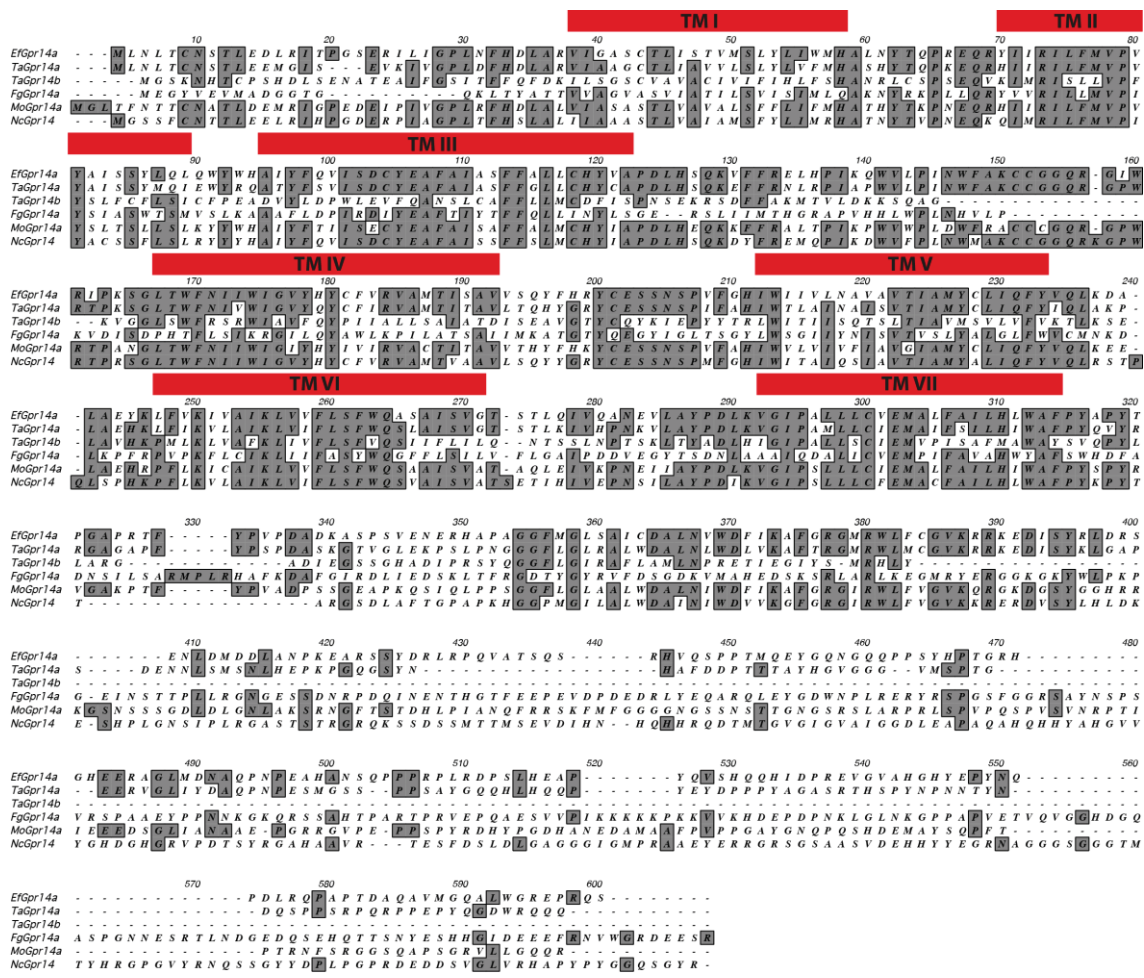
The predicted amino acid sequence of *E. festucae* Gpr13 (EfGpr13, EfM3.038560) is aligned with the corresponding homologues *N. crassa* NcGpr13 (NCU06629), *F. graminearum* FgGpr13 (FGSG_09814), *M. oryzae* MoGpr13a (MGG_07414), MoGpr13b (MGG_06103) and *T. atroviride* Ta_Gpr3 (TRIATDRAFT_83166). *E. festucae* Gpr13 displays 23.1% amino acid identity to *N. crassa* Gpr-13, 28.8% identity to the *F. graminearum* homologue, 32.4% identity to the *M. oryzae* Gpr13a and 22.2% Gpr13b and 25% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 32: Predicted protein topology of *E. festucae* Gpr13



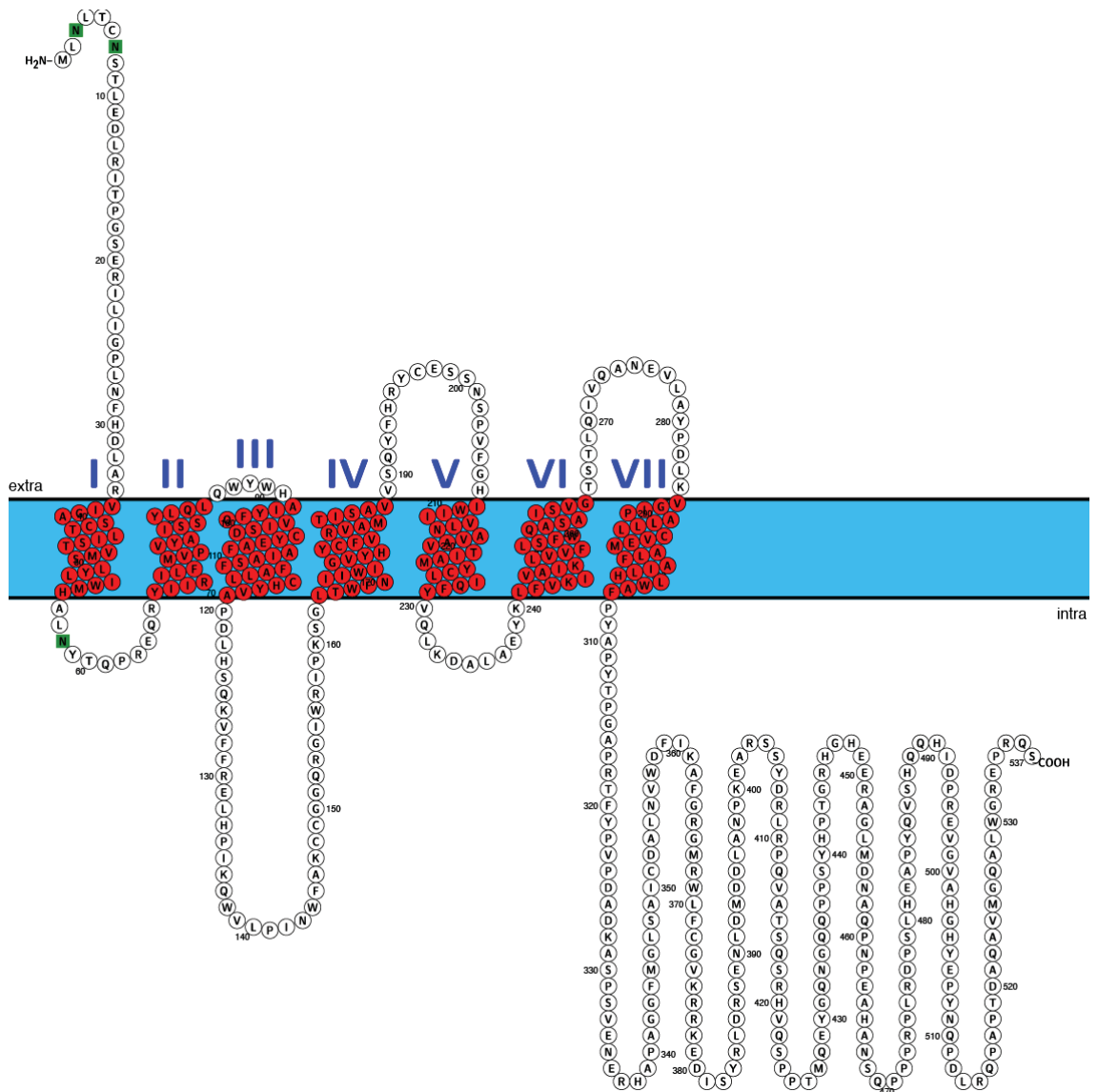
The predicted Gpr13 polypeptide is 630 amino acids in length and is predicted to contain seven transmembrane domains (TM), a long extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 33: Multiple sequence alignment of *E. festucae* Gpr14a homologues



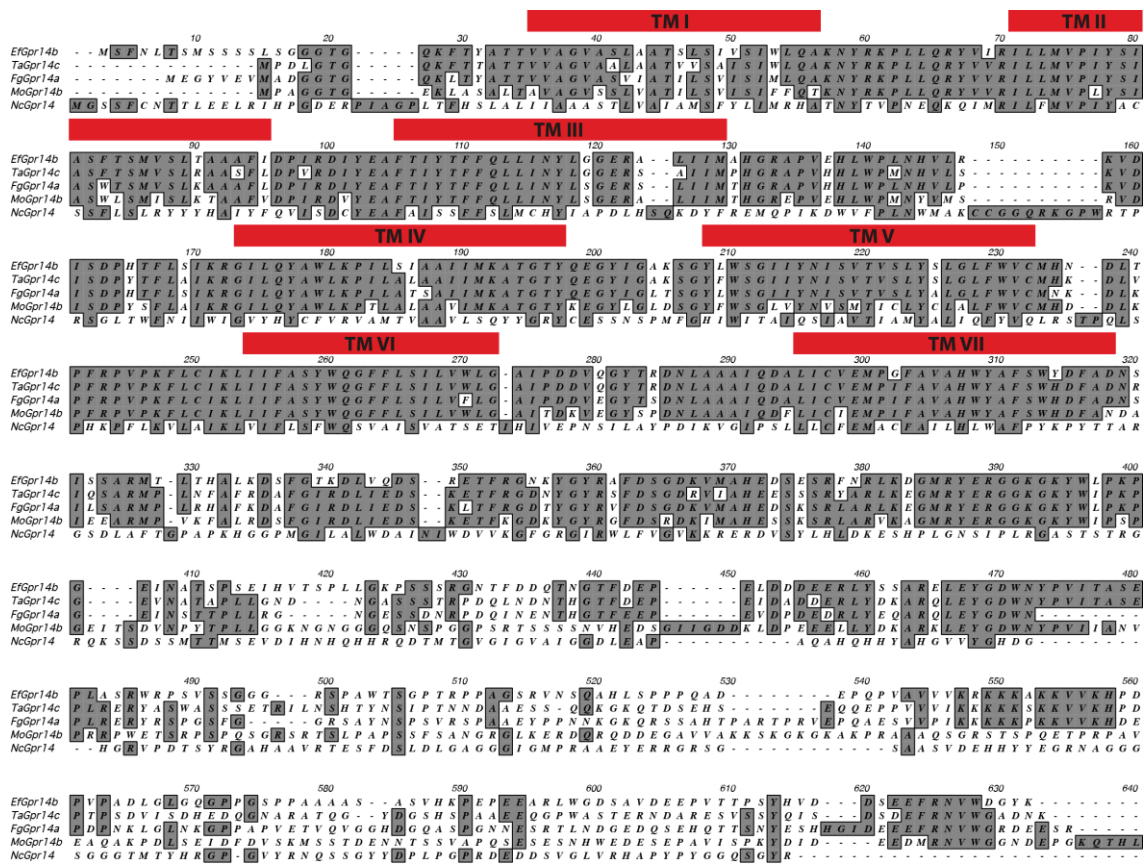
The predicted amino acid sequence of *E. festucae* Gpr14a (EfGpr14a, Efm3.040570) is aligned with the corresponding homologues *N. crassa* NcGpr14 (NCU06987), *F. graminearum* FgGpr14a (FGSG_09576), *M. oryzae* MoGpr14a (MGG_01467), the *T. atroviride* homologues TaGpr14a (TRIATDRAFT_152316) and TaGpr14b (TRIATDRAFT_296436). *E. festucae* Gpr14a displays 44.1% amino acid identity to *N. crassa* Gpr-14, 23% identity to the *F. graminearum* homologue, 50.9% identity to the *M. oryzae* homologue and 59.7% identity to the *T. atroviride* homologue. *E. festucae* Gpr14a shares 23.5% identity to *T. atroviride* TaGpr14b. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 34: Predicted protein topology of *E. festucae* Gpr14a



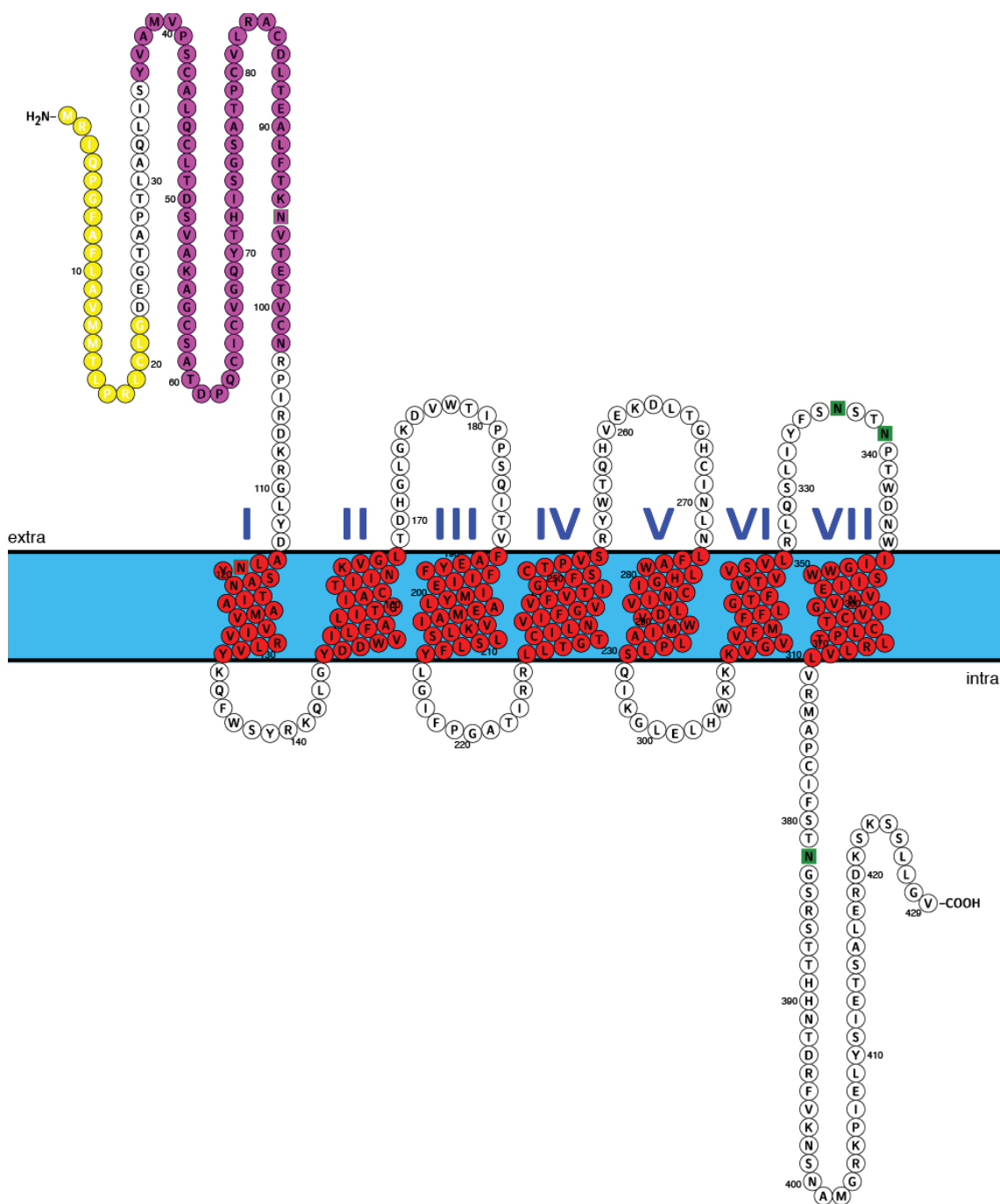
The predicted Gpr14a polypeptide is 537 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with longer ECL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 35: Multiple sequence alignment of *E. festucae* Gpr14b homologues



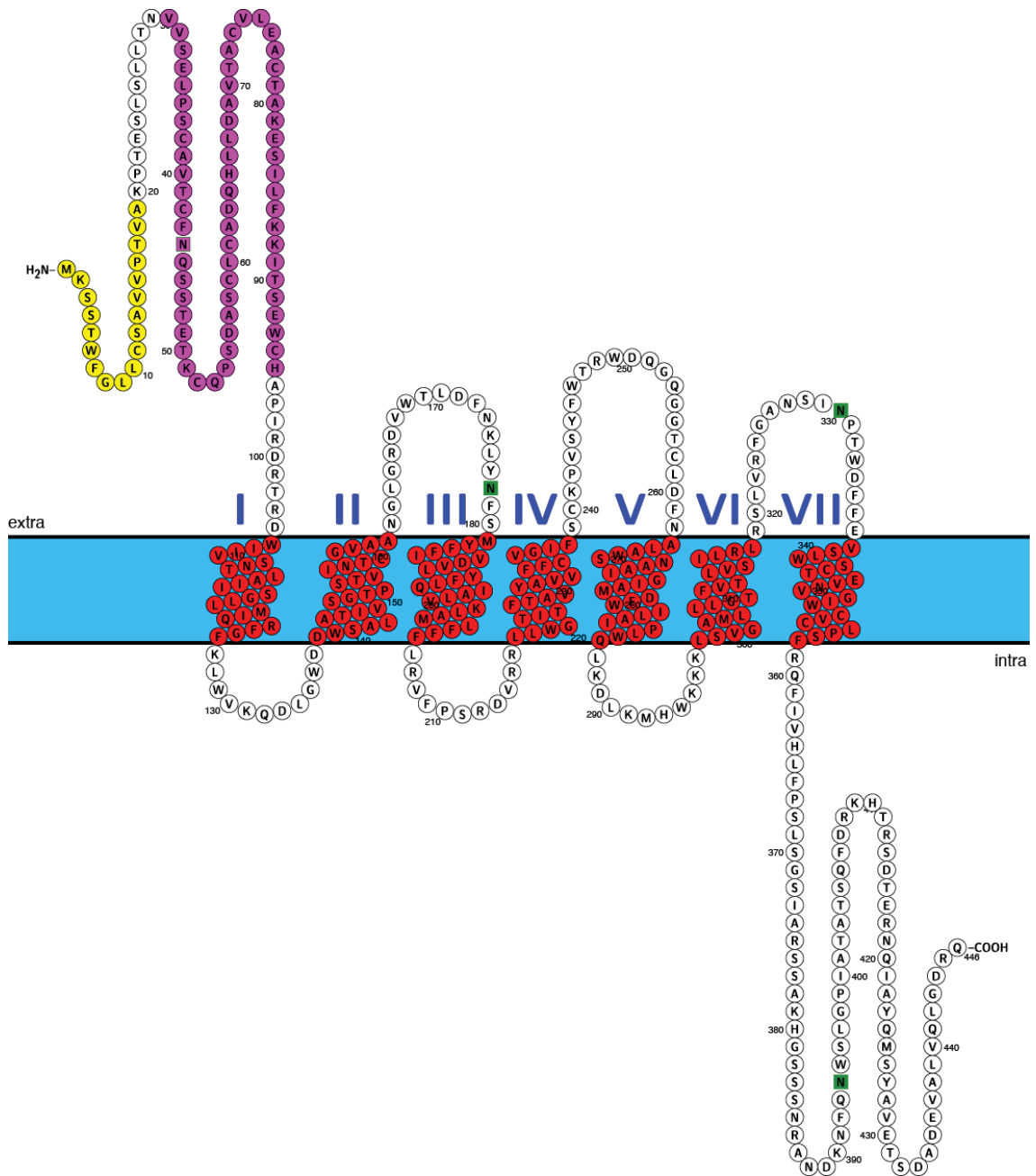
The predicted amino acid sequence of *E. festucae* Gpr14b (EfGpr14b, EfM3. 021230) is aligned with the corresponding homologues *N. crassa* NcGpr14 (NCU06987), *F. graminearum* FgGpr14b (FGSG_03059), *M. oryzae* MoGpr14b (MGG_15321) and *T. atroviride* TaGpr14c (TRIATDRAFT_136442). *E. festucae* Gpr14b displays 16.6% amino acid identity to *N. crassa* Gpr-14, 67.7% identity to the *F. graminearum* homologue, 54.3% identity to the *M. oryzae* homologue and 69.4% identity to the *T. atroviride* homologue. ClustalW was used to align GPCR sequences, with conserved residues are shaded in grey. Red bars above the sequence mark the predicted seven transmembrane domains (TM I – TM VII) in *E. festucae*.

Supplementary 37: Predicted protein topology of *E. festucae* Pth11-1



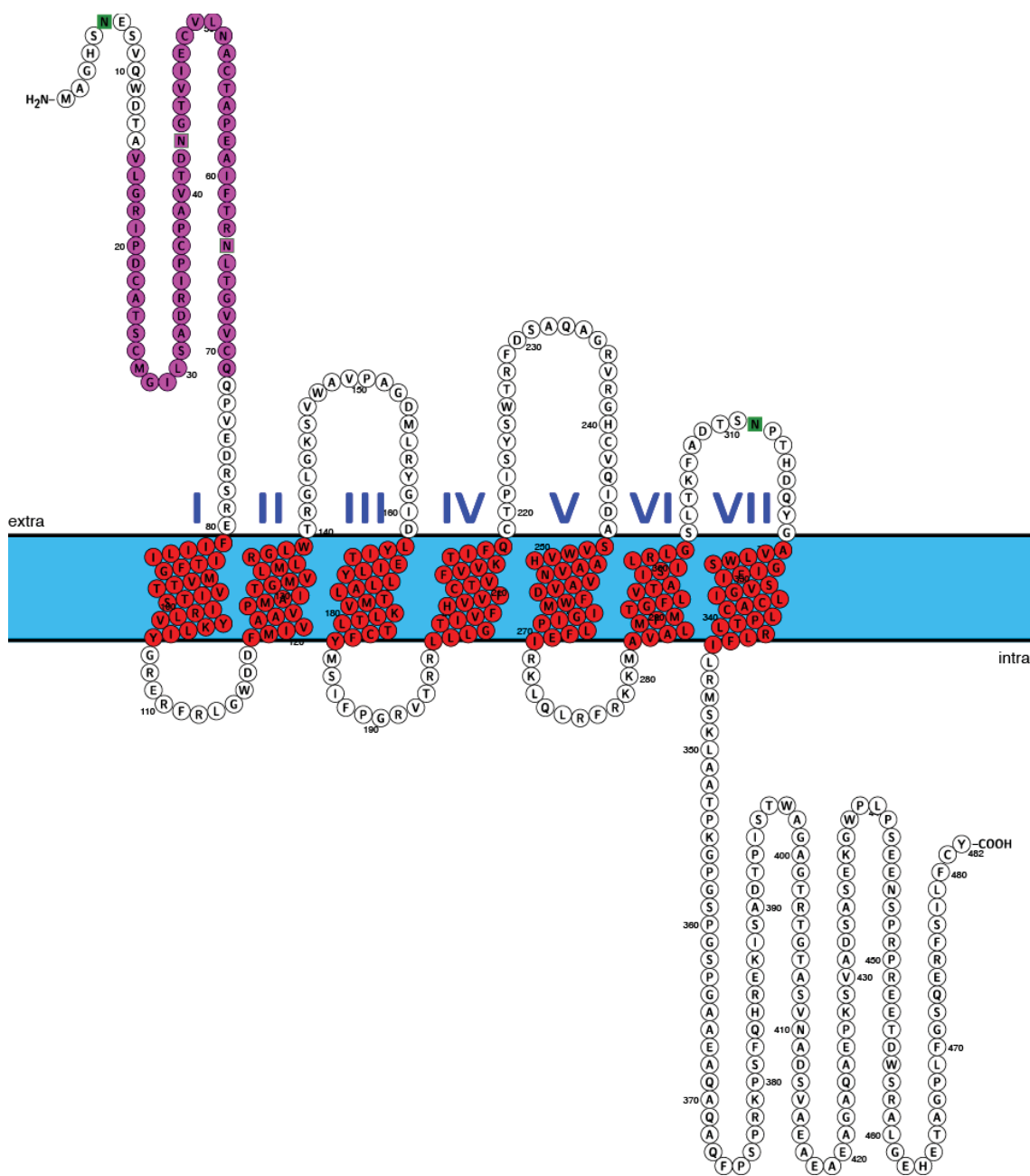
The predicted Pth11-1 polypeptide is 429 amino acids in length and is predicted to contain seven transmembrane domains (TM), a long extracellular amino-terminal (N₂H) and an intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). The N-terminus contains a signal peptide domain and a CFEM domain (magenta). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 38: Predicted protein topology of *E. festucae* Pth11-2



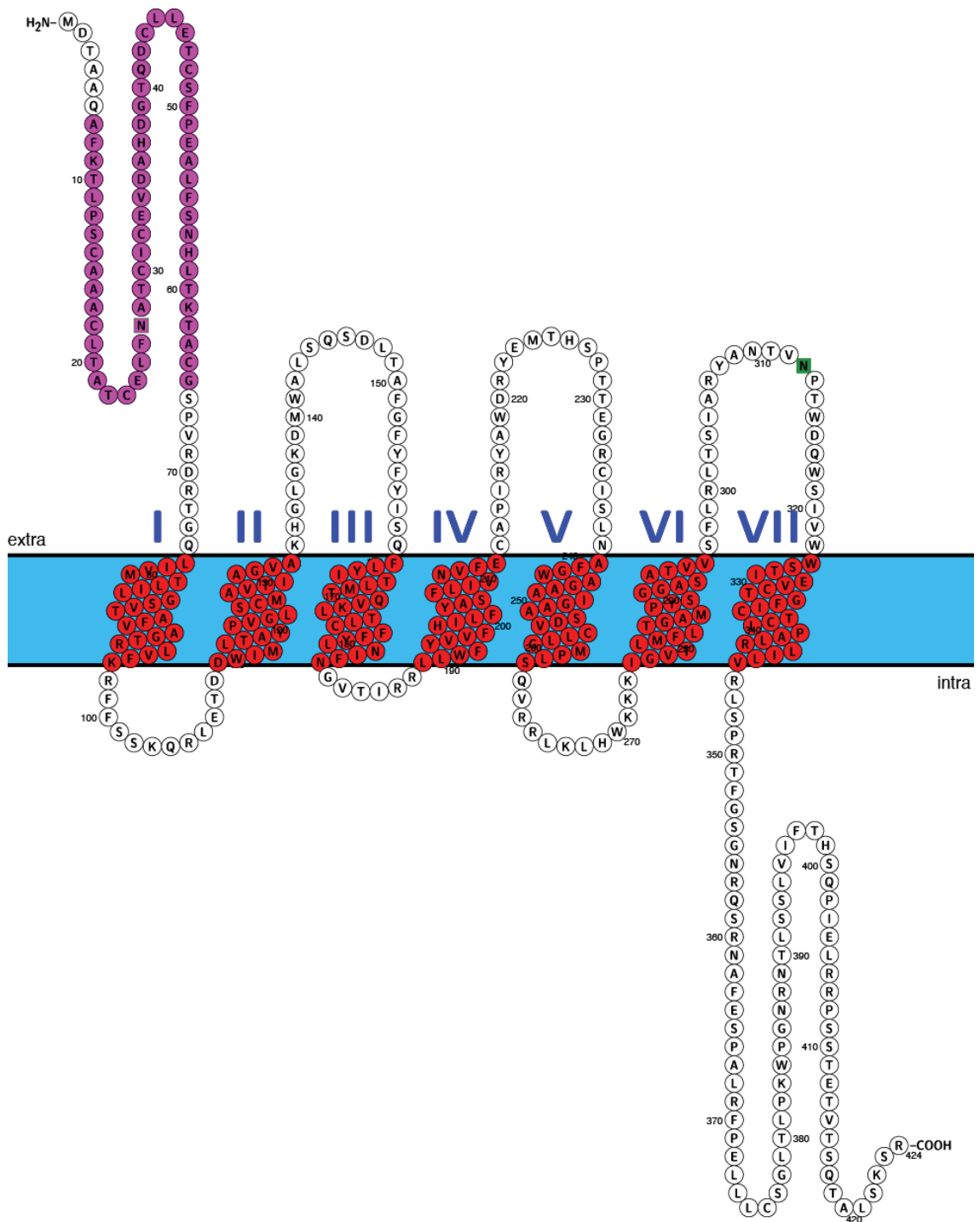
The predicted Pth11-1 polypeptide is 446 amino acids in length and is predicted to contain seven transmembrane domains (TM), a long extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). The N-terminus contains a signal peptide domain and a CFEM domain (magenta). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 39: Predicted protein topology of *E. festucae* Pth11-3



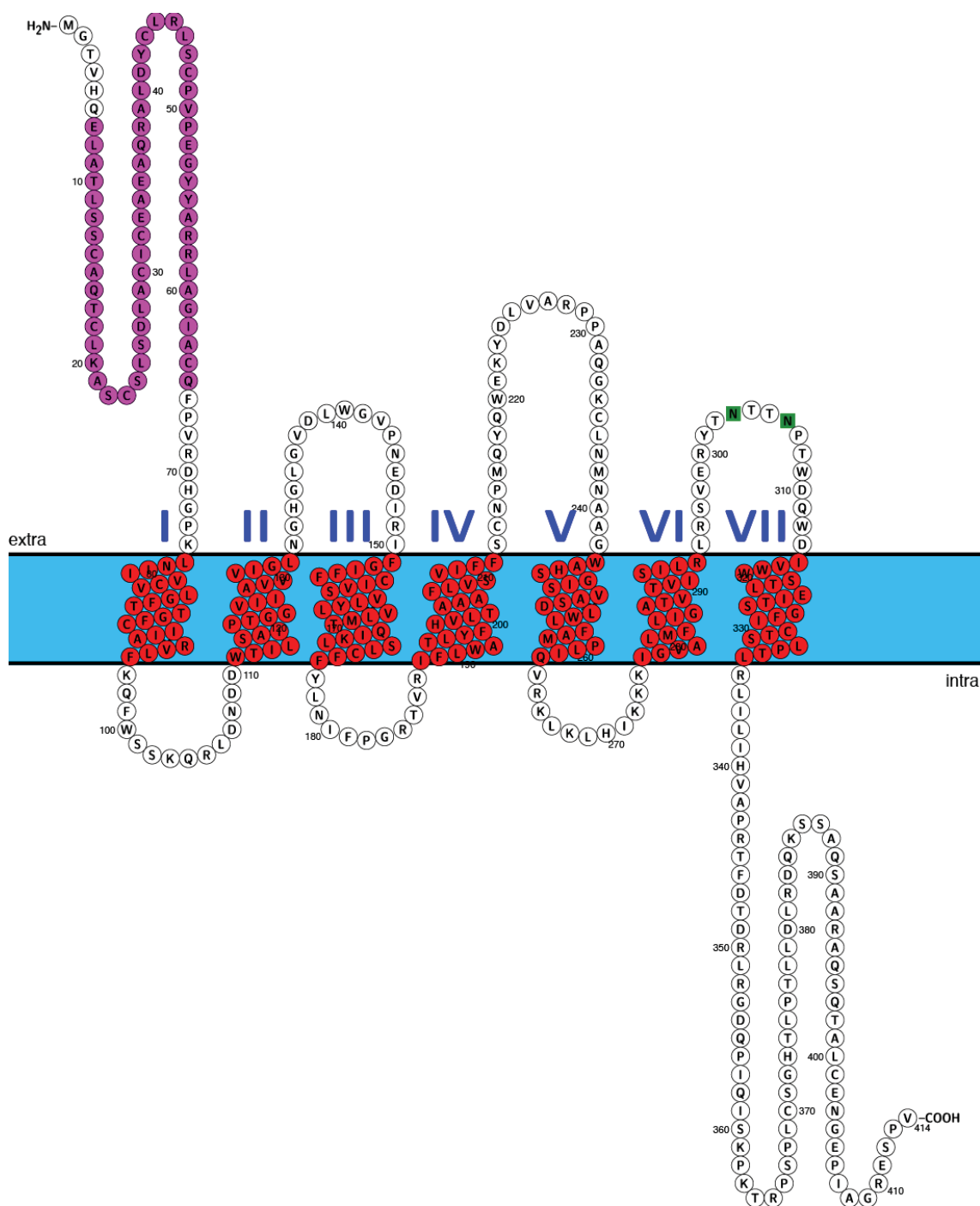
The predicted Pth11-3 polypeptide is 482 amino acids in length and is predicted to contain seven transmembrane domains (TM), a longer extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). The N-terminus contains a CFEM domain (magenta). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 40: Predicted protein topology of *E. festucae* Pth11-4



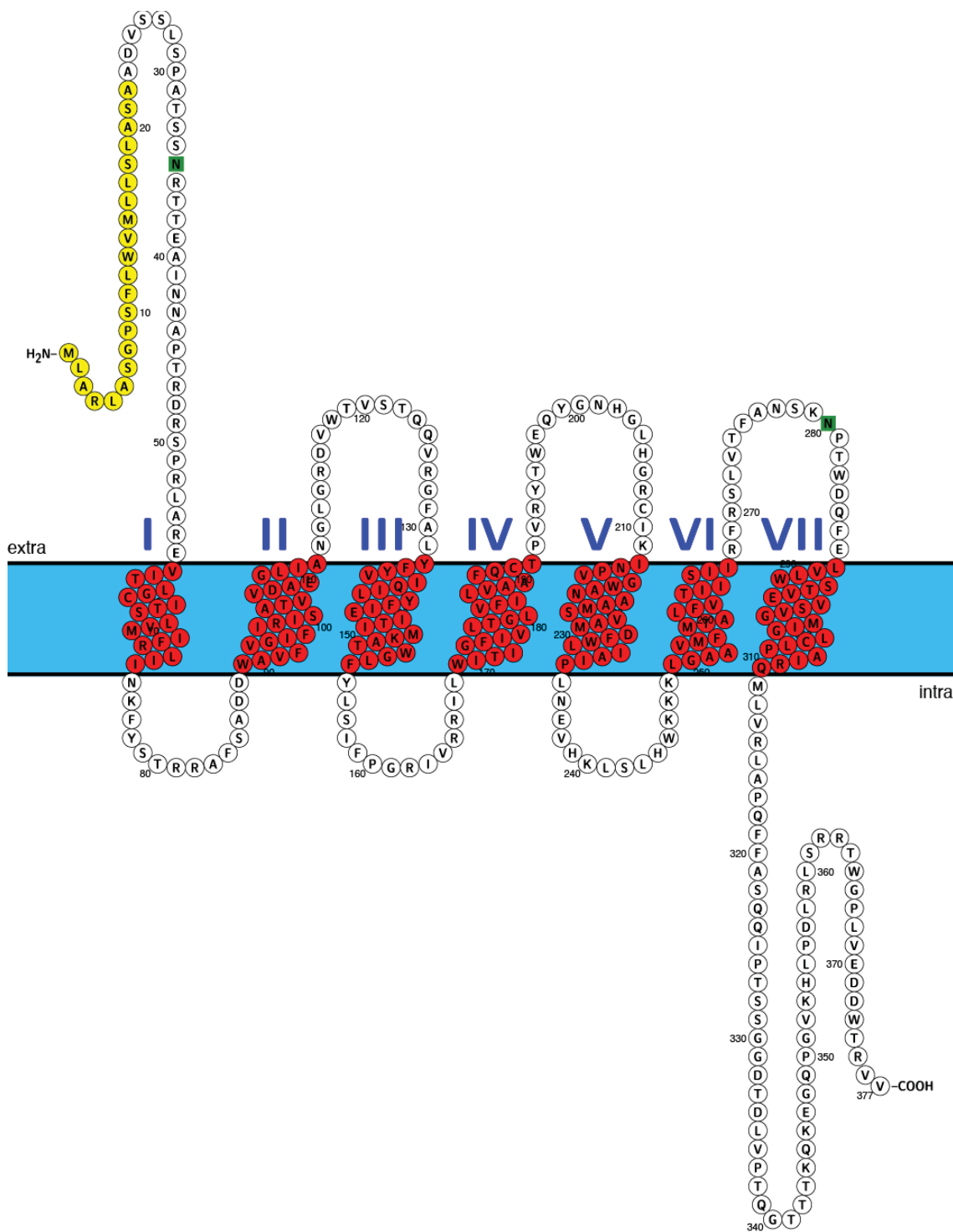
The predicted Pth11-4 polypeptide is 424 amino acids in length and is predicted to contain seven transmembrane domains (TM), a longer extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). The N-terminus contains a CFEM domain (magenta). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 41: Predicted protein topology of *E. festucae* Pth11-5



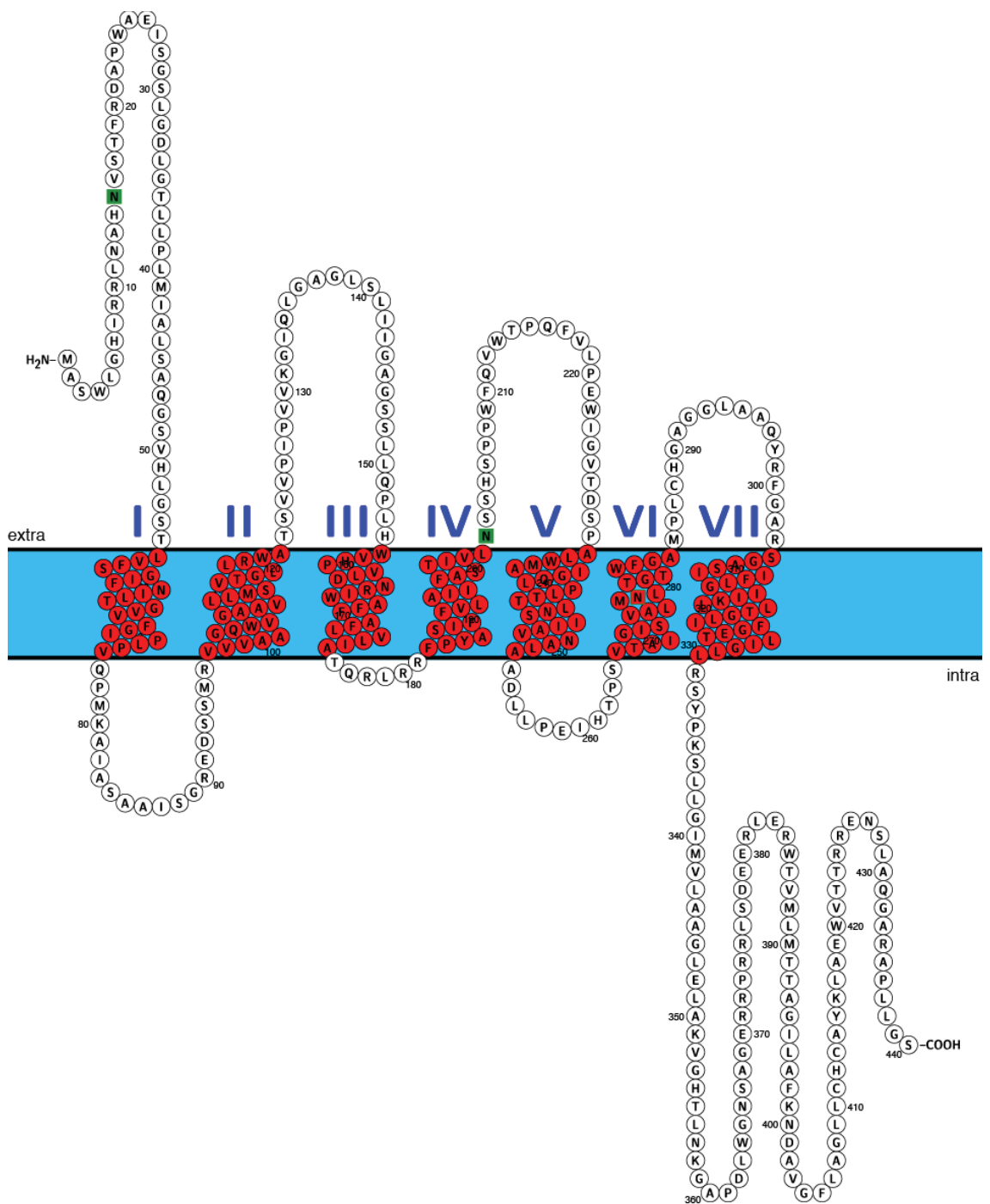
The predicted Pth11-5 polypeptide is 414 amino acids in length and is predicted to contain seven transmembrane domains (TM), a longer extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). The N-terminus contains a CFEM domain (magenta). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 43: Predicted protein topology of *E. festucae* Pth11-7



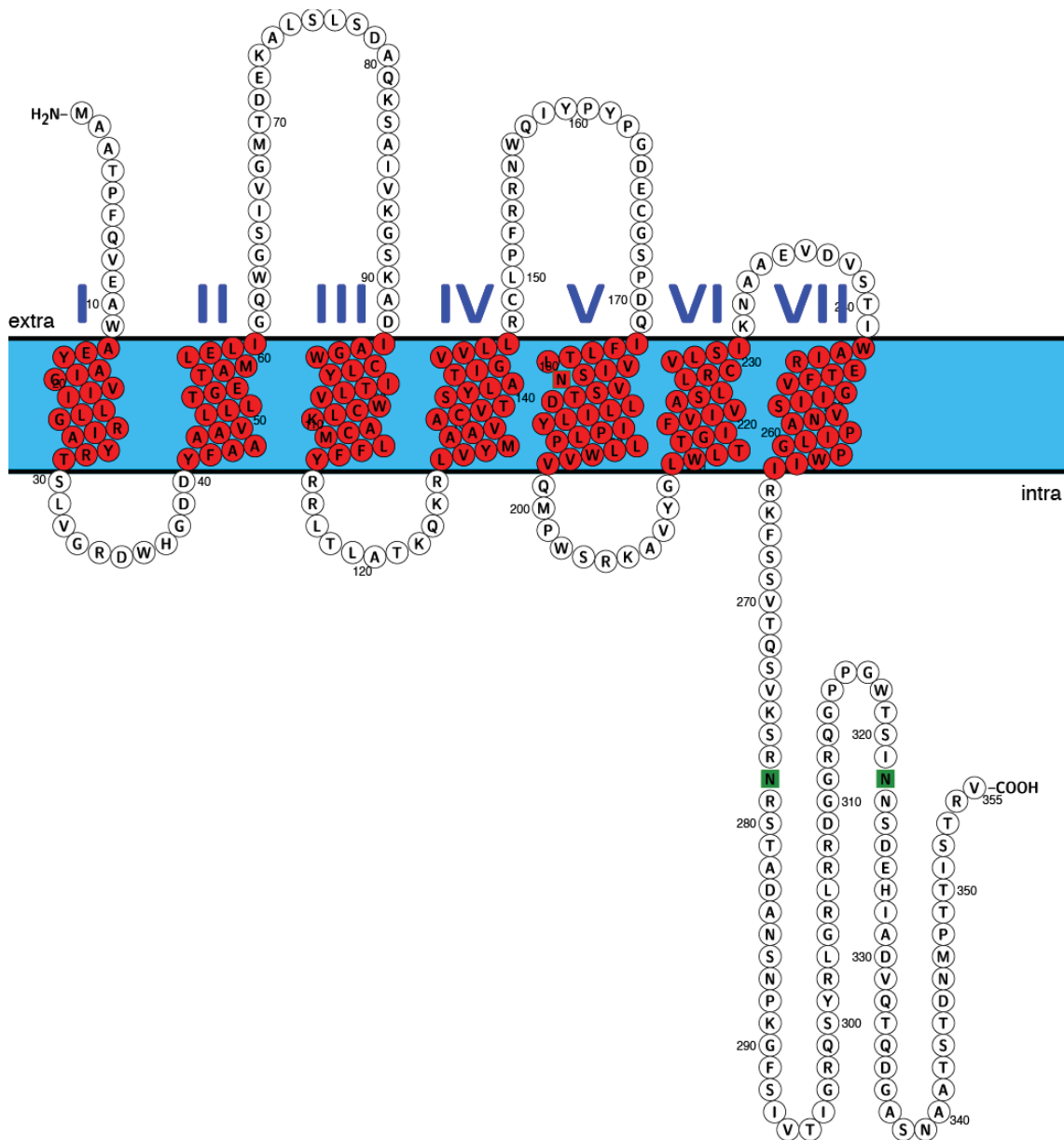
The predicted Pth11-7 polypeptide is 377 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and an intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). The N-terminus contains a signal peptide domain (yellow). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 44: Predicted protein topology of *E. festucae* Pth11-8



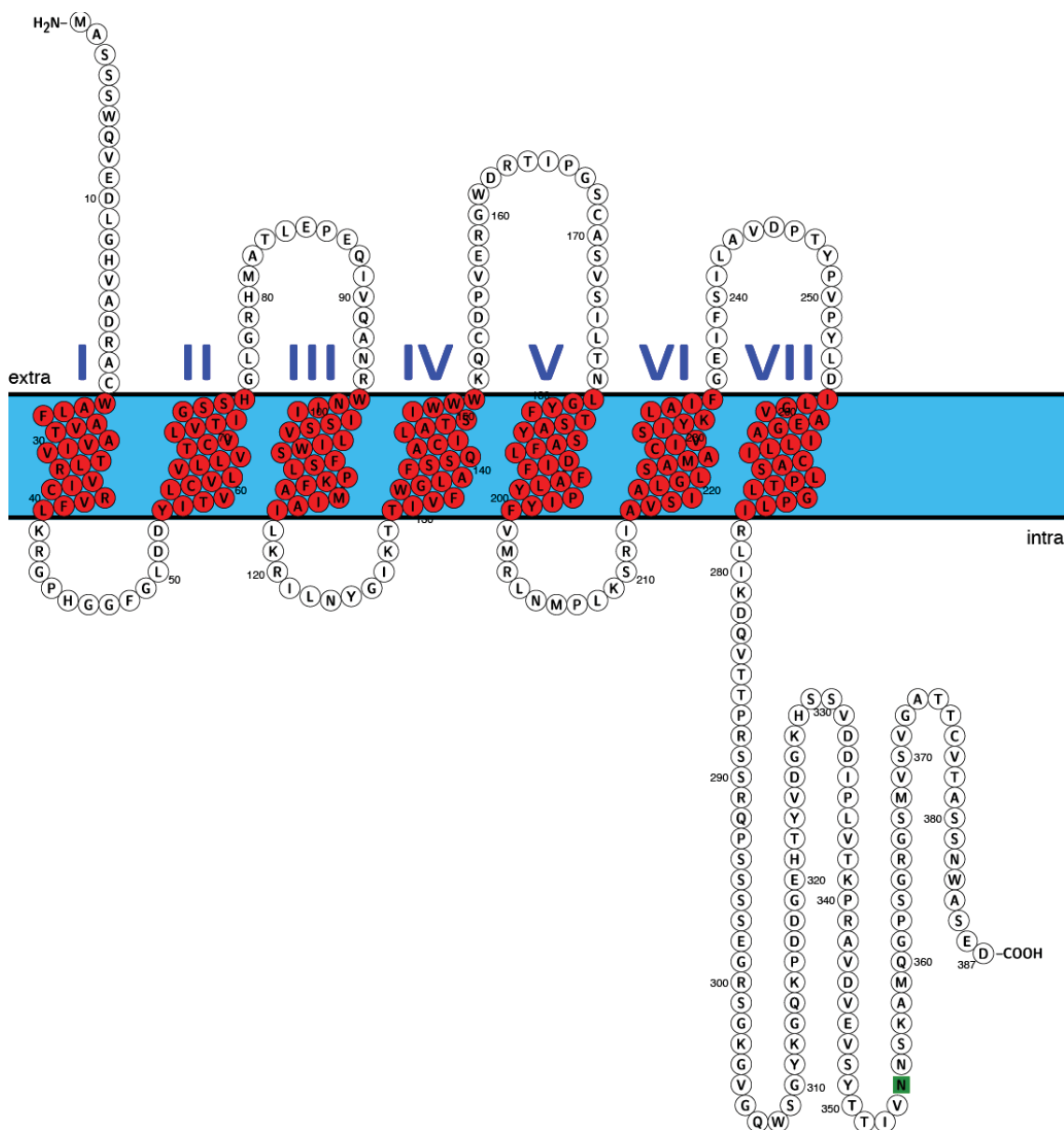
The predicted Pth11-8 polypeptide is 440 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 45: Predicted protein topology of *E. festucae* Pth11-9



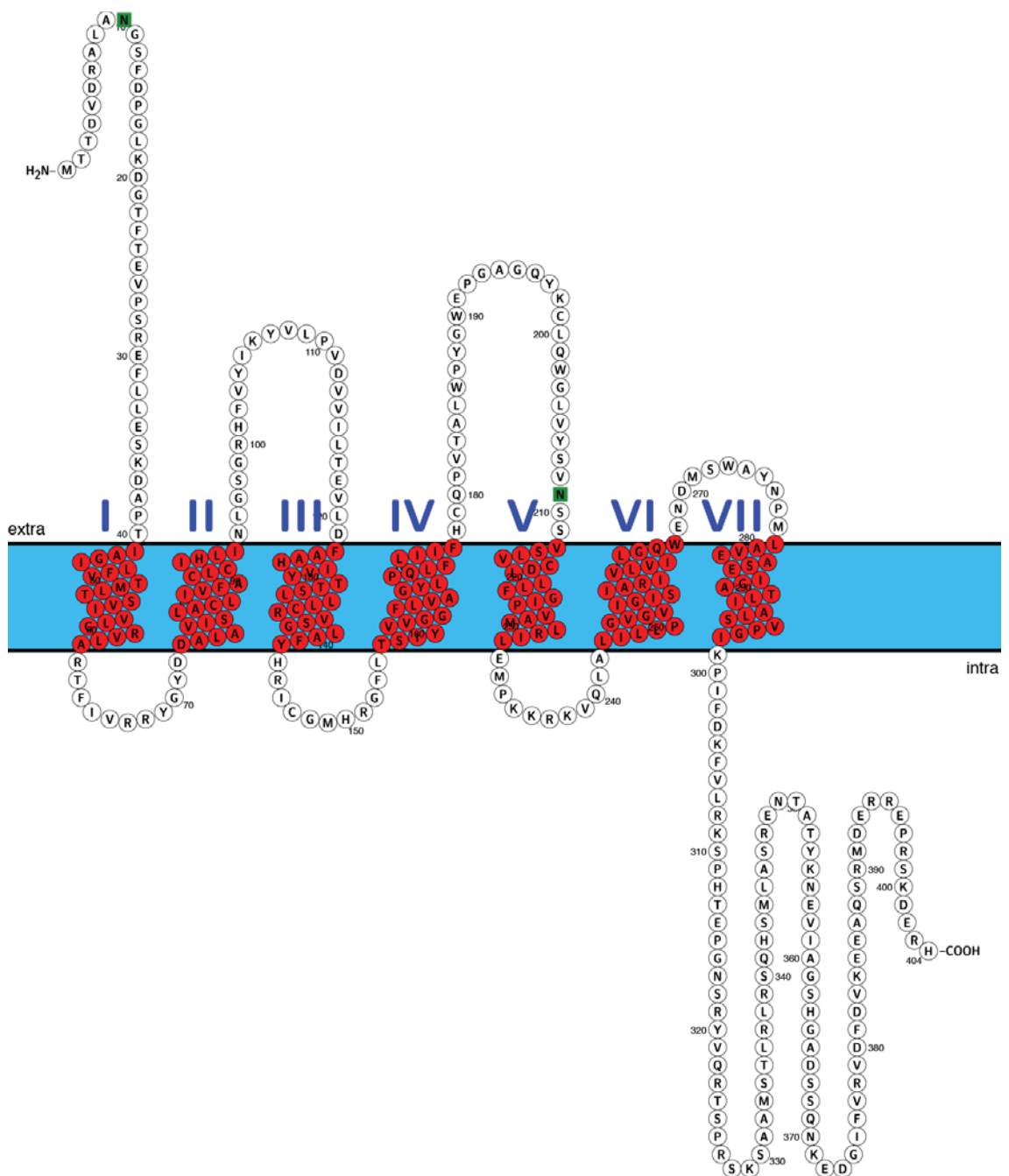
The predicted Pth11-9 polypeptide is 355 amino acids in length and is predicted to contain seven transmembrane domains (TM), a short extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 47: Predicted protein topology of *E. festucae* Pth11-11



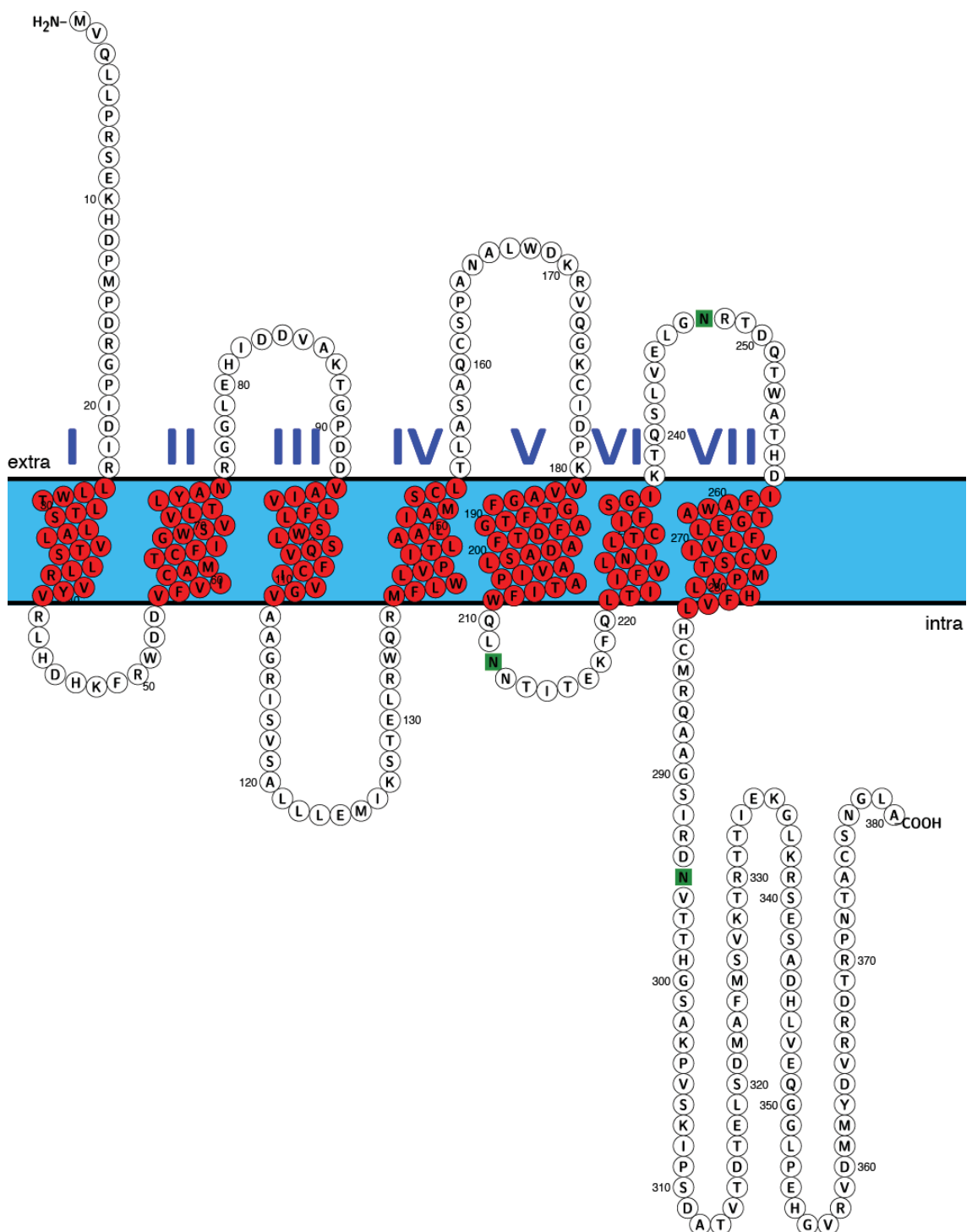
The predicted Pth11-11 polypeptide is 387 amino acids in length and is predicted to contain seven transmembrane domains (TM), a short extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 48: Predicted protein topology of *E. festucae* Pth11-12



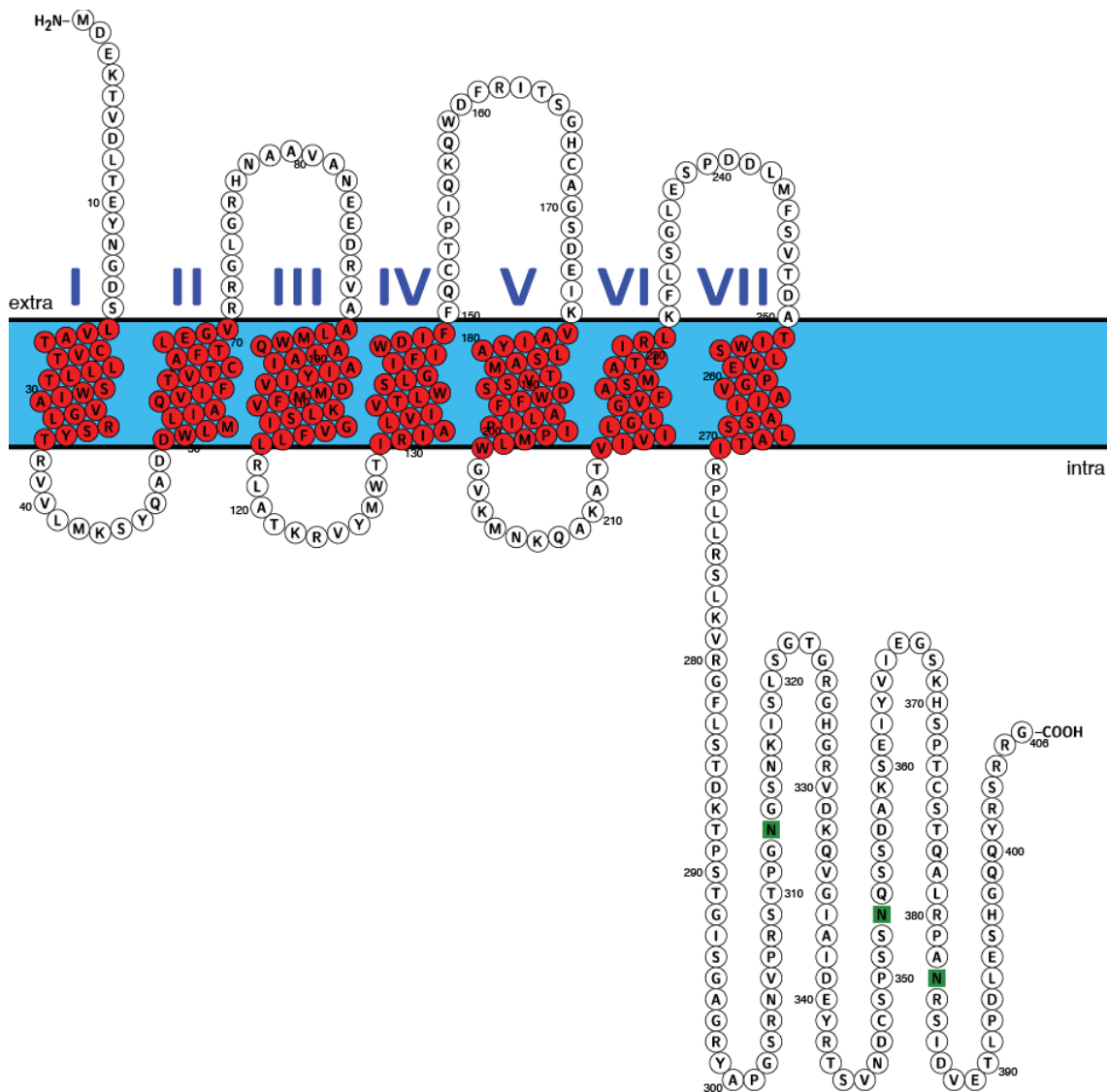
The predicted Pth11-12 polypeptide is 404 amino acids in length and is predicted to contain seven transmembrane domains (TM), a short extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 50: Predicted protein topology of *E. festucae* Pth11-14



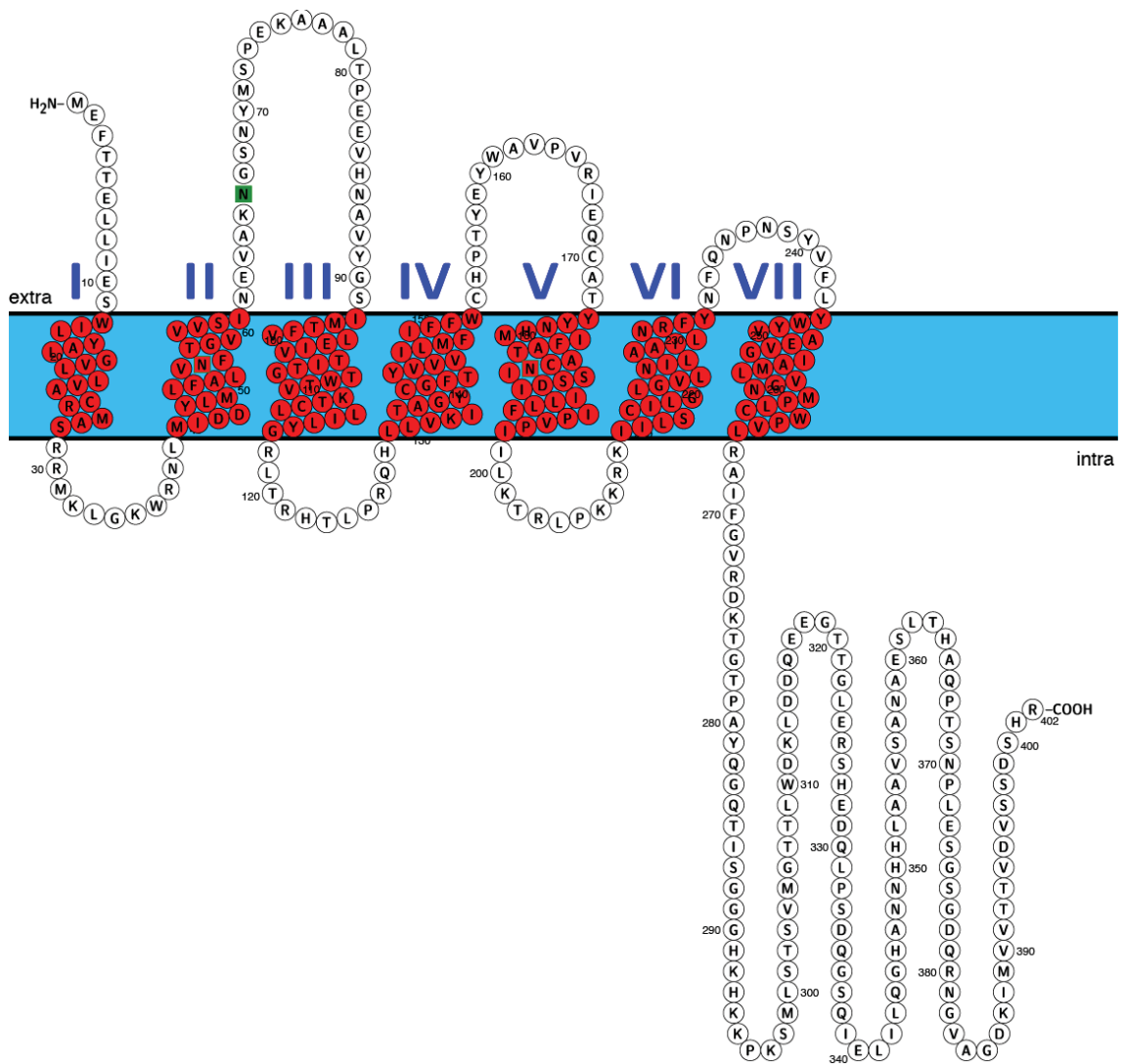
The predicted Pth11-14 polypeptide is 380 amino acids in length and is predicted to contain seven transmembrane domains (TM), a short extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 51: Predicted protein topology of *E. festucae* Pth11-15



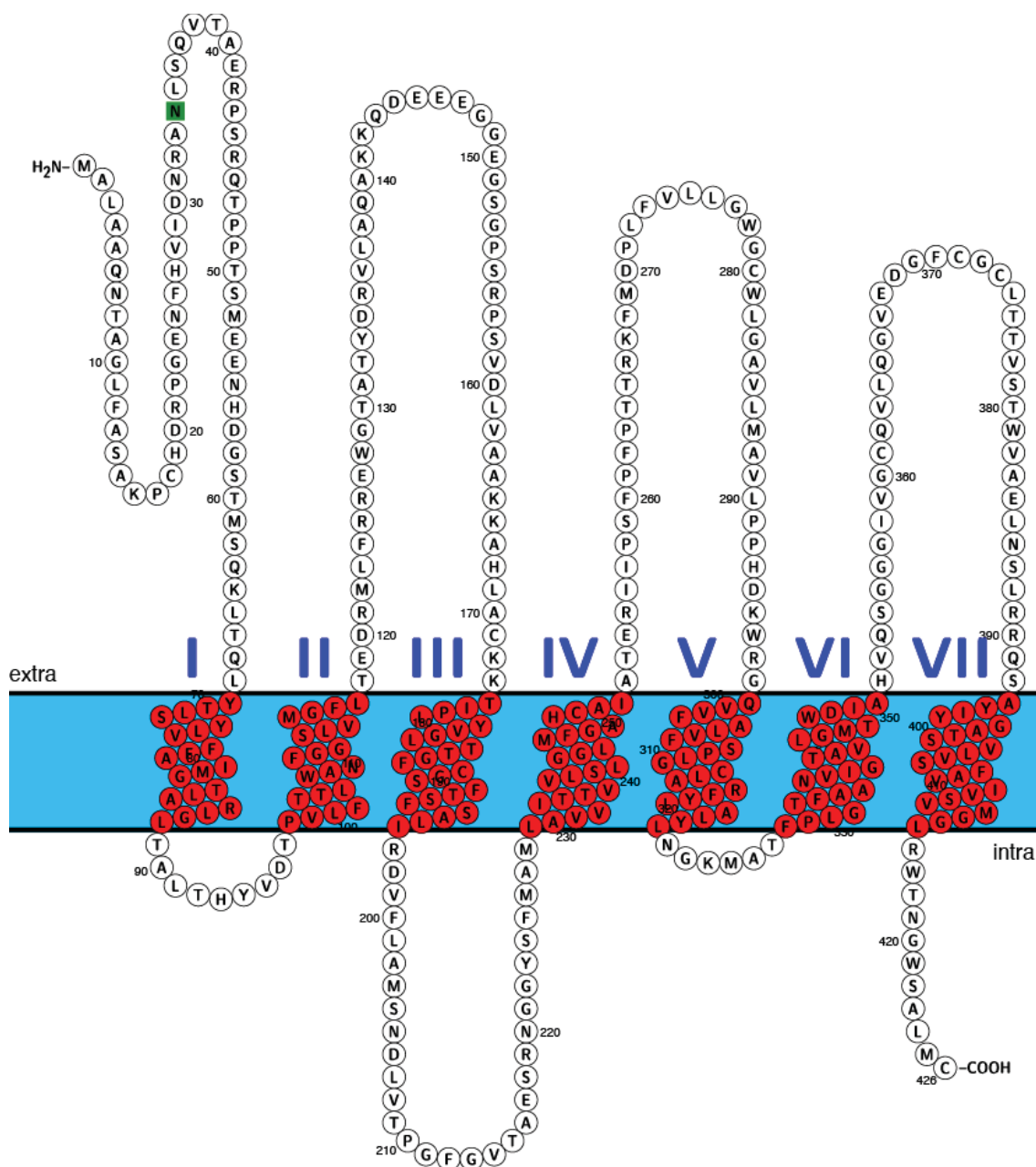
The predicted Pth11-15 polypeptide is 406 amino acids in length and is predicted to contain seven transmembrane domains (TM), a short extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 52: Predicted protein topology of *E. festucae* Pth11-16



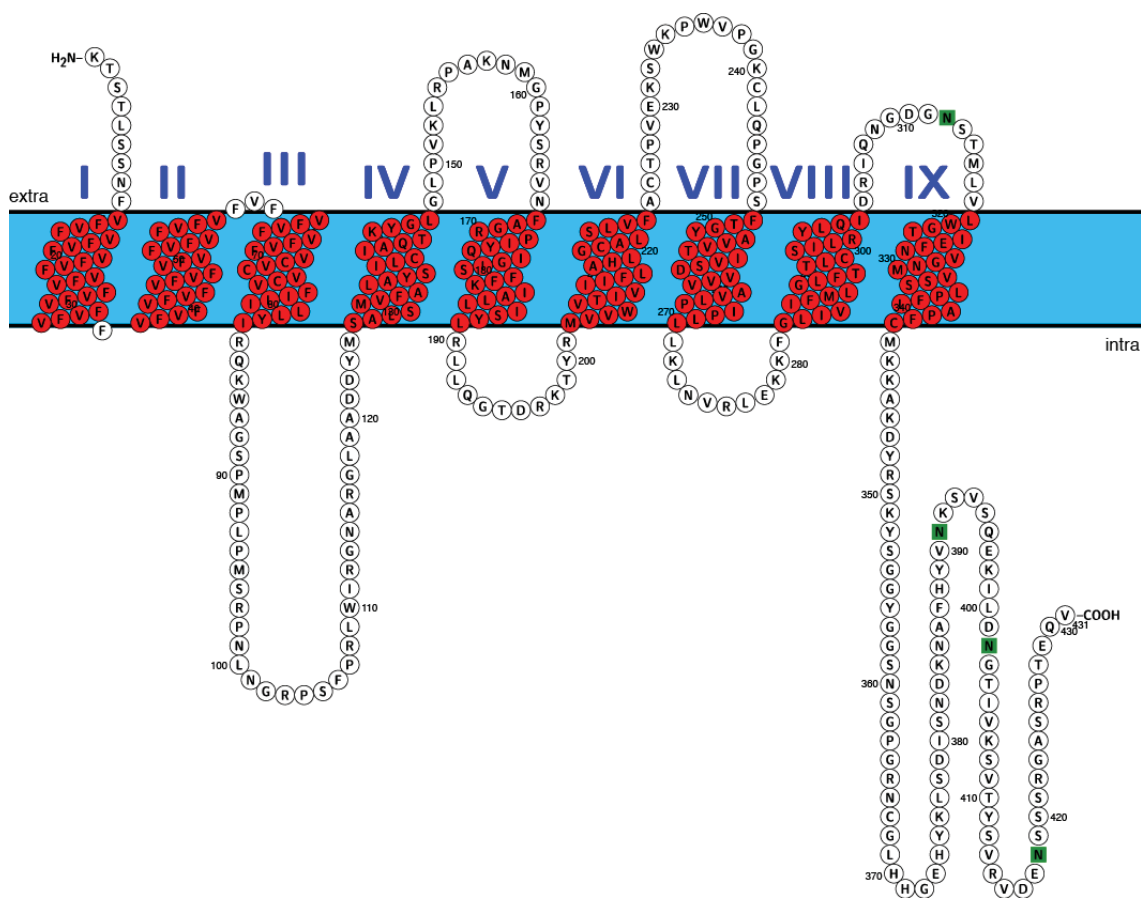
The predicted Pth11-16 polypeptide is 402 amino acids in length and is predicted to contain seven transmembrane domains (TM), a short extracellular amino-terminal (N₂H) and a long intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL). Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 53: Predicted protein topology of *E. festucae* Pth11-17



The predicted Pth11-17 polypeptide is 426 amino acids in length and is predicted to contain seven transmembrane domains (TM), an extracellular amino-terminal (N₂H) and a short intracellular carboxy-terminal (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with long ECL1-3 and long ICL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 55: Predicted protein topology of *E. festucae* Pth11-19



The predicted Pth11-19 polypeptide is 431 amino acids in length and is predicted to contain GPCR atypical nine transmembrane domains (TM), a short extracellular amino-terminal (N₂H) and a longer intracellular carboxy-terminal domain (COOH) as well as intracellular (ICL) and extracellular loop domains (ECL) with short ICL1 and ECL1 and longer ICL2. Topology was predicted by TMHMM v2.0 and visualised using Protter v1.0 with predicted transmembrane helices (red) in cell membrane (blue).

Supplementary 56: Multiple sequence alignment of *E. festucae* Gpa1 homologues

	10	20	30	40	50	60	70	80																																																																										
<i>EfGpa1</i>	M	G	C	G	M	S	T	E	E	K	E	G	K	A	R	N	E	E	E	E	E	N	Q	L	K	R	D	K	M	M	Q	R	N	E	I	K	M	L	L	L	G	A	G	E	S	G	K	S	T	I	L	K	Q	M	K	L	I	H	E	G	G	Y	S	R	D	E	R	E	S	F	K	E	I	I	F	S	N	T	V	Q	S	
<i>FgGpa1</i>	M	G	C	G	M	S	T	E	E	K	E	G	K	A	R	N	E	E	E	E	E	E	N	Q	L	K	R	D	K	M	M	Q	R	N	E	I	K	M	L	L	L	G	A	G	E	S	G	K	S	T	I	L	K	Q	M	K	L	I	H	E	G	G	Y	S	R	D	E	R	E	S	F	K	E	I	I	F	S	N	T	V	Q	S
<i>MoMagA</i>	M	G	C	G	M	S	T	E	E	K	E	G	K	A	R	N	E	E	E	E	E	E	N	Q	L	K	R	D	R	L	Q	Q	R	N	E	I	K	M	L	L	L	G	A	G	E	S	G	K	S	T	I	L	K	Q	M	K	L	I	H	E	G	G	Y	S	R	D	E	R	E	S	F	K	E	I	I	F	S	N	T	V	Q	S
<i>NcGna1</i>	M	G	C	G	M	S	T	E	E	K	E	G	K	A	R	N	E	E	E	E	E	E	N	Q	L	K	R	D	R	M	Q	Q	R	N	E	I	K	M	L	L	L	G	A	G	E	S	G	K	S	T	I	L	K	Q	M	K	L	I	H	E	G	G	Y	S	R	D	E	R	E	S	F	K	E	I	I	F	S	N	T	V	Q	S
	80	90	100	110	120	130	140	150	160																																																																									
<i>EfGpa1</i>	M	R	V	I	L	E	A	M	E	S	L	E	L	P	L	E	D	Q	R	M	E	Y	H	V	Q	T	I	F	M	Q	P	A	Q	I	E	G	E	V	L	P	P	E	V	G	G	S	A	I	E	A	L	W	K	D	R	G	V	Q	E	C	F	K	R	S	R	E	Y	Q	L	N	D	S	A	R	Y	Y	F	F	D	N	I	A
<i>FgGpa1</i>	M	R	V	I	L	E	A	M	E	S	L	E	L	P	L	E	D	Q	R	M	E	Y	H	V	Q	T	I	F	M	Q	P	A	Q	I	E	G	E	V	L	P	P	E	V	G	G	S	A	I	E	A	L	W	K	D	R	G	V	Q	E	C	F	K	R	S	R	E	Y	Q	L	N	D	S	A	R	Y	Y	F	F	D	N	I	A
<i>MoMagA</i>	M	R	V	I	L	E	A	M	E	S	L	E	L	P	L	E	D	Q	R	M	E	Y	H	V	Q	T	I	F	M	Q	P	A	Q	I	E	G	E	V	L	P	P	E	V	G	G	N	A	I	E	A	L	W	K	D	R	G	V	Q	E	C	F	K	R	S	R	E	Y	Q	L	N	D	S	A	R	Y	Y	F	F	D	N	I	A
<i>NcGna1</i>	M	R	V	I	L	E	A	M	E	S	L	E	L	P	L	E	D	Q	R	M	E	Y	H	V	Q	T	I	F	M	Q	P	A	Q	I	E	G	E	V	L	P	P	E	V	G	G	N	A	I	E	A	L	W	R	D	A	G	V	Q	S	C	F	K	R	S	R	E	Y	Q	L	N	D	S	A	R	Y	Y	F	F	D	N	I	A
	160	170	180	190	200	210	220	230	240																																																																									
<i>EfGpa1</i>	R	I	A	A	P	D	Y	M	P	N	D	Q	D	V	L	R	S	R	V	K	T	T	G	I	T	E	T	T	F	I	I	G	D	L	T	Y	R	M	F	D	V	G	G	Q	R	S	E	R	K	K	W	I	H	C	F	E	N	V	T	T	I	L	F	L	V	A	I	S	E	Y	D	Q	L	L	F	E	D	E	T	V		
<i>FgGpa1</i>	R	I	A	A	P	D	Y	M	P	N	D	Q	D	V	L	R	S	R	V	K	T	T	G	I	T	E	T	T	F	I	I	G	D	L	T	Y	R	M	F	D	V	G	G	Q	R	S	E	R	K	K	W	I	H	C	F	E	N	V	T	T	I	L	F	L	V	A	I	S	E	Y	D	Q	L	L	F	E	D	E	T	V		
<i>MoMagA</i>	R	I	A	A	P	D	Y	M	P	N	D	Q	D	V	L	R	S	R	V	K	T	T	G	I	T	E	T	T	F	I	I	G	D	L	T	Y	R	M	F	D	V	G	G	Q	R	S	E	R	K	K	W	I	H	C	F	E	N	V	T	T	I	L	F	L	V	A	I	S	E	Y	D	Q	L	L	F	E	D	E	T	V		
<i>NcGna1</i>	R	I	A	A	P	D	Y	M	P	N	D	Q	D	V	L	R	S	R	V	K	T	T	G	I	T	E	T	T	F	I	I	G	D	L	T	Y	R	M	F	D	V	G	G	Q	R	S	E	R	K	K	W	I	H	C	F	E	N	V	T	T	I	L	F	L	V	A	I	S	E	Y	D	Q	L	L	F	E	D	E	T	V		
	240	250	260	270	280	290	300	310	320																																																																									
<i>EfGpa1</i>	N	R	M	Q	E	A	L	T	L	F	D	S	I	C	N	S	R	W	F	I	K	T	S	I	I	L	F	L	N	K	I	D	R	F	K	E	K	L	P	V	S	P	M	K	N	Y	F	F	P	D	Y	E	G	G	D	D	Y	A	A	C	D	Y	I	L	N	R	F	V	S	L	N	Q	H	E	T	K	Q	I	Y	T		
<i>FgGpa1</i>	N	R	M	Q	E	A	L	T	L	F	D	S	I	C	N	S	R	W	F	I	K	T	S	I	I	L	F	L	N	K	I	D	R	F	K	E	K	L	P	V	S	P	M	K	N	Y	F	F	P	D	Y	E	G	G	D	D	Y	A	A	C	D	Y	I	L	N	R	F	V	S	L	N	Q	H	E	T	K	Q	I	Y	T		
<i>MoMagA</i>	N	R	M	Q	E	A	L	T	L	F	D	S	I	C	N	S	R	W	F	I	K	T	S	I	I	L	F	L	N	K	I	D	R	F	K	E	K	L	P	V	S	P	M	K	N	Y	F	F	P	D	Y	E	G	G	D	D	Y	A	A	C	D	Y	I	L	N	R	F	V	S	L	N	Q	H	E	T	K	Q	I	Y	T		
<i>NcGna1</i>	N	R	M	Q	E	A	L	T	L	F	D	S	I	C	N	S	R	W	F	I	K	T	S	I	I	L	F	L	N	K	I	D	R	F	K	E	K	L	P	V	S	P	M	K	N	Y	F	F	P	D	Y	E	G	G	D	D	Y	A	A	C	D	Y	I	L	N	R	F	V	S	L	N	Q	H	E	T	K	Q	I	Y	T		
	320	330	340	350																																																																														
<i>EfGpa1</i>	H	F	T	C	A	T	D	T	T	Q	I	R	F	V	M	A	A	V	N	D	I	I	I	Q	E	N	L	R	L	C	G	L	I																																																	
<i>FgGpa1</i>	H	F	T	C	A	T	D	T	T	Q	I	R	F	V	M	A	A	V	N	D	I	I	I	Q	E	N	L	R	L	C	G	L	I																																																	
<i>MoMagA</i>	H	F	T	C	A	T	D	T	T	Q	I	R	F	V	M	A	A	V	N	D	I	I	I	Q	E	N	L	R	L	C	G	L	I																																																	
<i>NcGna1</i>	H	F	T	C	A	T	D	T	T	Q	I	R	F	V	M	A	A	V	N	D	I	I	I	Q	E	N	L	R	L	C	G	L	I																																																	

The predicted amino acid sequence of *E. festucae* Gga1 (EfGpa1, EfM3_062630) is aligned with the corresponding homologues *N. crassa* NcGna-1 (NCU06493), *F. graminearum* FgGpa1 (Fga1; FGSG_05535) and *M. oryzae* MoMagA (MGG_00365). *E. festucae* Gpa1 displays 98.9% amino acid identity to *N. crassa* Gna-1, 99.2% identity to the *F. graminearum* homologue and 99.7% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 57: Multiple sequence alignment of *E. festucae* Gpa2 homologues

EfGpa2	10	20	30	40	50	60	70	80
FgGpa2								
MoMagB								
NcGna2								
EfGpa2	90	100	110	120	130	140	150	160
FgGpa2								
MoMagB								
NcGna2								
EfGpa2	170	180	190	200	210	220	230	240
FgGpa2								
MoMagB								
NcGna2								
EfGpa2	250	260	270	280	290	300	310	320
FgGpa2								
MoMagB								
NcGna2								
EfGpa2	330	340	350					
FgGpa2								
MoMagB								
NcGna2								

The predicted amino acid sequence of *E. festucae* Gpa2 (EfGpr2, EFM3.045200) is aligned with the corresponding homologues *N. crassa* NcGna-2 (NCU06729), *F. graminearum* FgGpa2 (Fgs2; FGSG_05239) and *M. oryzae* MoMagB (MGG_04204). *E. festucae* Gpa2 displays 87.9% amino acid identity to *N. crassa* Gna-2, 80.8% identity to the *F. graminearum* homologue, 87.9% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 58: Multiple sequence alignment of *E. festucae* Gpa3 homologues

EfGpa3	- - - M G I G C M S S S S E E A E Q K K K S Q A I D R V I E E D S R R L R K E C K I L L L G S G E S G K S T I V K Q M K I I H L K G Y S E D E L Y N Y R P T V F K	10	20	30	40	50	60	70	80
FgGpa3	- - - M G A C M S S S N E E V D I Q K K K S Q A I D K I L E E D S K R L R K E C K I L L L G S G E S G K S T I V K Q M K I I H L K G Y S D E L F N Y R P T V F K								
MoMagC	- - - M G A C M S A S E E S E Q K K R S Q K I D R D L E E D S K R L R K E C K I L L L G S G E S G K S T I V K Q M K I I H L K G Y S D E L L Y N Y R P T V F K								
NcGna3	M I K M G A C M S K N D E E T E Q K K R S Q K I D R D L E E D S K R L R K E C K I L L L G S G E S G K S T I V K Q M K I I H L K G Y S D E F E L Y N Y R P T V Y K								
EfGpa3	N L V E C A K A V I T A M Q Q F E I E P P Q R K E N R T Y V D Y L L S Y Q A E S G P Q A Q - I D P I Q V G V A V Q S L W A I D P A R D R L M E H H Q T E F Y L M D S A E	90	100	110	120	130	140	150	160
FgGpa3	N L V E C A K A V I M A M Q Q F D I E P Q N E E N K A H A E F L L E Y Q A E S G P Q A H - I D A I K V G A A V Q A L W N D P A K D L L M E H H Q T E F Y L M D S A E								
MoMagC	N L I E C A K A V I S A M R Q F F D I E P Q L E G N K E L C D Y L L D Y M V E S G P Q A E - I D P K V G Q A V Q S I W N D P A R E Q L M E D R R Q T E F Y L M D S A E								
NcGna3	N L I E C A K A V I V A M H Q F D I Q P A D P S L R P Y V F F L Q Q D P I P G Q S I D P K V G T A T Q A L W N D P A K E Q L M E R R Q T E F Y L M D S A E								
EfGpa3	Y F F Q E V M R I V A T D Y L P N E M D V L R A R T K T T G I Y E T R F Q M G Q L S I H M F D V G G Q R S E R K K W I H C F F E N V T S I I F C V A L S E Y D Q V	170	180	190	200	210	220	230	240
FgGpa3	Y F F Q E V M R I V A T D Y L P N E M D V L R A R T K T T G I Y E T R F Q M G Q L S I H M F D V G G Q R S E R K K W I H C F F E N V T S I I F C V A L S E Y D Q V								
MoMagC	Y F F Q E V M R I V A S P D Y L P N E M D V L R A R T K T T G I Y E T R F Q M G Q L S I H M F D V G G Q R S E R K K W I H C F F E N V T S I I F C V A L S E Y D Q V								
NcGna3	Y F F T E V M R I V A E D Y R P N E M D V L R A R T K T T G I Y E T R F K M G Q L S I H M F D V G G Q R S E R K K W I H C F F E N V T S I I F C V A L S E Y D Q V								
EfGpa3	L L E E S S Q N R R M M E S L L L F D S V V N S R W F M R T S I I L F L N K K V D I F K Q K L T R S P L G N Y F P D Y S G G N D V N K A A K Y L L W R F N Q V N R A	250	260	270	280	290	300	310	320
FgGpa3	L L E E S S Q N R R M M E S L L L F D S V V N S R W F M R T S I I L F L N K K V D I F K Q K L S R S P L G N Y F P D Y S G G N D V N K A A K Y L L W R F N Q V N R A								
MoMagC	L L E E S S Q N R R M M E S L L L F D S V V N S R W F M R T S I I L F L N K K V D I F K Q K L G R S P L G N Y F P D Y S G G N D V N K A A K Y L L W R F N Q V N R A								
NcGna3	L L E E S S Q N R R M M E S L L L F D S V V N S R W F M R T S I I L F L N K K V D I F K Q K L G R S P L G N Y F P D Y S G G N D V N K A A K Y L L W R F N Q V N R A								
EfGpa3	H L N L Y P H L T Q A T D T S N I R L V F A A V K E T I L N N A L K D S G I L	330	340	350					
FgGpa3	H L N L Y P H L T Q A T D T S N I R L V F A A V K E T I L N N A L K D S G I L								
MoMagC	H L N L Y P H L T Q A T D T S N I R L V F A A V K E T I L N N A L K D S G I L								
NcGna3	H L N L Y P H L T Q A T D T S N I R L V F A A V K E T I L N N A L K D S G I L								

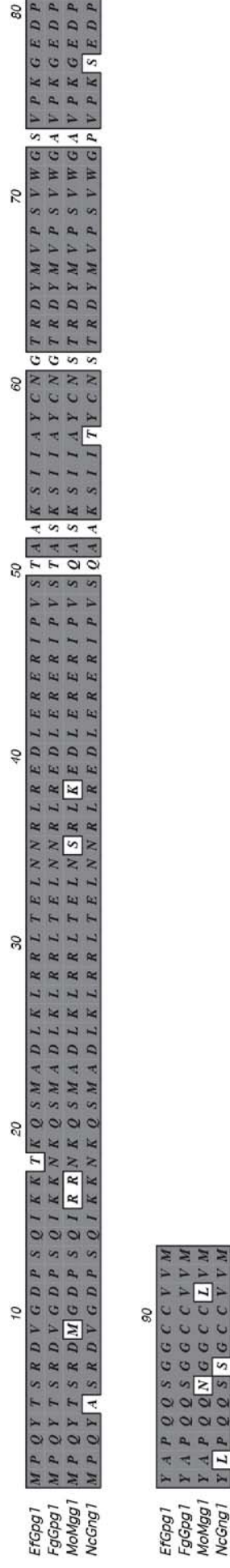
The predicted amino acid sequence of *E. festucae* Gpa3 (EfGpa3, EfM3.073950) is aligned with the corresponding homologues *N. crassa* NcGna-3 (NCU05206), *F. graminearum* FgGpa3 (Fgs3; FGSG_09614) and *M. oryzae* MoMagC (MGG_01818). *E. festucae* Gpa3 displays 91.6% amino acid identity to *N. crassa* Gna-3, 91.6% identity to the *F. graminearum* homologue and 95.2% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 59: Multiple sequence alignment of *E. festucae* Gpb1 homologues

EfGpb1	10	20	30	40	50	60	70	80
FgGpb1	MNSHG	NDVSP	PEAMQ	QARIQ	QARRR	EAE	TLKDR	IKRKK
MoMgb1	MNSQG	NDVSP	PEAMQ	QARIQ	QARRR	EAE	TLKDR	IKRKK
NcGnb1	MDSR	S	DVSP	PEAMQ	QARIQ	QARRR	EAE	TLKDR
EfGpb1	90	100	110	120	130	140	150	160
FgGpb1	TDRRHL	VSASQ	DGKLI	IWDAY	T	TNKV	HAI	PLRSS
MoMgb1	TDRRHL	VSASQ	DGKLI	IWDAY	T	TNKV	HAI	PLRSS
NcGnb1	TDRRHL	VSASQ	DGKLI	IWDAY	T	TNKV	HAI	PLRSS
EfGpb1	170	180	190	200	210	220	230	240
FgGpb1	GYLSC	CRFIN	DRSIL	TSSG	DMT	CMK	KWDI	IE
MoMgb1	GYLSC	CRFIN	DRSIL	TSSG	DMT	CMK	KWDI	IE
NcGnb1	GYLSC	CRFIN	DRSIL	TSSG	DMT	CMK	KWDI	IE
EfGpb1	250	260	270	280	290	300	310	320
FgGpb1	AGHES	DINA	IQ	FFPD	GHSF	V	TG	SDDA
MoMgb1	AGHES	DINA	IQ	FFPD	GHSF	V	TG	SDDA
NcGnb1	AGHES	DINA	IQ	FFPD	GHSF	V	TG	SDDA
EfGpb1	330	340	350					
FgGpb1	EKVGS	L	VGHEN	R	V	S	C	L
MoMgb1	EKVGS	L	VGHEN	R	V	S	C	L
NcGnb1	EKVGS	L	VGHEN	R	V	S	C	L

The predicted amino acid sequence of *E. festucae* Gpb1 (EfGpb1, EFM3_013730) is aligned with the corresponding homologues *N. crassa* NcGnb-1 (NCU00440), *F. graminearum* FgGpb1 (Fgb1; FGSG_04104) and *M. oryzae* MoMgb1 (MGG_05201). *E. festucae* Gpb1 displays 98.9% amino acid identity to *N. crassa* Gnb-1, 97.5% identity to the *F. graminearum* homologue and 95.5% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 60: Multiple sequence alignment of *E. festucae* Gpg1 homologues



The predicted amino acid sequence of *E. festucae* Gpg1 (EfGpg1, EFM3_015250) is aligned with the corresponding homologues *N. crassa* NcGng-1 (NCU00041), *F. graminearum* FgGpg1 (Fgg1; FGSG_07235) and *M. oryzae* MoMgg1 (MGG_10193). *E. festucae* Gpg1 displays 93.5% amino acid identity to *N. crassa* Gng-1, 96.8% identity to the *F. graminearum* homologue and 95.7% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 61: Multiple sequence alignment of *E. festucae* Ric8 homologues

<i>E</i> Ric8	10	20	30	40	50	60	70	80
<i>F</i> gRic8	M A T L P P A A G T A T G P A K L K A V T D L V N K L S D D L E N I S L L P K D R N N D A L E E L K I Y G R D P P K N A D P I F T A N V V R R S T A S F S T S L Y L T I							
<i>M</i> oRic8	M A T L P P A A G T A T G P A K L K A V T D L V N K L S D D L E N I S L L P K D R N N D A L E E L K I Y G R D P P K N A D P I F T A N V V R R S T A S F S T S L Y L T I							
<i>N</i> cRic8	M A T L P P A A G T A T G P A K L K A V T D L V N K L S D D L E N I S L L P K D R N N D A L E E L K I Y G R D P P K N A D P I F T A N V V R R S T A S F S T S L Y L T I							
<i>E</i> Ric8	90	100	110	120	130	140	150	160
<i>F</i> gRic8	V A K G I T M L L R R Y A F H T T S S E T A R A L R Y I A N A M L I L K P E T R Q M F V S K G Y P A Q A C E K L K T D N W D D E F L F S R I L F L S T Y G T I D I D							
<i>M</i> oRic8	V A K G I T M L L R R Y A F H T T S S E T A R A L R Y I A N A M L I L K P E T R Q M F V S K G Y P A Q A C E K L K T D N W D D E F L F S R I L F L S T Y G T I D I D							
<i>N</i> cRic8	V A K G I T M L L R R Y A F H T T S S E T A R A L R Y I A N A M L I L K P E T R Q M F V S K G Y P A Q A C E K L K T D N W D D E F L F S R I L F L S T Y G T I D I D							
<i>E</i> Ric8	170	180	190	200	210	220	230	240
<i>F</i> gRic8	L K A L I E D C Q L A E H I V N N L E R H I N L P S D - - K Q K Q K L D P M E E M A L G E T L K L M F N V T H F C K T K V S A F T I P A V S H I Y S L L W K Q D S							
<i>M</i> oRic8	L K A L I E D C Q L A E H I V N N L E R H I N L P S D - - K Q K Q K L D P M E E M A L G E T L K L M F N V T H F C K T K V S A F T I P A V S H I Y S L L W K Q D S							
<i>N</i> cRic8	L K A L I E D C Q L A E H I V N N L E R H I N L P S D - - K Q K Q K L D P M E E M A L G E T L K L M F N V T H F C K T K V S A F T I P A V S H I Y S L L W K Q D S							
<i>E</i> Ric8	250	260	270	280	290	300	310	320
<i>F</i> gRic8	S D A K - - P L E P P P F S P L V N S L I N L D L Q A D Q S Q L S L Y P Q D D P N K V T S R I L H L L D C G V R A Y S G S D L E T - V V T P V V S L I S K L Y E							
<i>M</i> oRic8	S D A K - - P L E P P P F S P L V N S L I N L D L Q A D Q S Q L S L Y P Q D D P N K V T S R I L H L L D C G V R A Y S G S D L E T - V V T P V V S L I S K L Y E							
<i>N</i> cRic8	S D A K - - P L E P P P F S P L V N S L I N L D L Q A D Q S Q L S L Y P Q D D P N K V T S R I L H L L D C G V R A Y S G S D L E T - V V T P V V S L I S K L Y E							
<i>E</i> Ric8	330	340	350	360	370	380	390	400
<i>F</i> gRic8	N A P R E V - - R Q K M K E S L L P T G E D R Q A V L G R G D S L P S V L K N S T N P T A L A L R D A I S H L L E D L S D K D A S K F V E N V Y G Y G F A S G F							
<i>M</i> oRic8	N A P R E V - - R Q K M K E S L L P T G E D R Q A V L G R G D S L P S V L K N S T N P T A L A L R D A I S H L L E D L S D K D A S K F V E N V Y G Y G F A S G F							
<i>N</i> cRic8	N A P R E V - - R Q K M K E S L L P T G E D R Q A V L G R G D S L P S V L K N S T N P T A L A L R D A I S H L L E D L S D K D A S K F V E N V Y G Y G F A S G F							
<i>E</i> Ric8	410	420	430	440	450	460	470	480
<i>F</i> gRic8	L F Q N N I P V P P S L S S L S T G D A - - - S G N Q K P V N P I T G Q F L D K Q K F A N A P E M T I E E K E R E A E R L F V L F E R L K K T G V I N I Q N							
<i>M</i> oRic8	L F Q N N I P V P P S L S S L S T G D A - - - S G N Q K P V N P I T G Q F L D K Q K F A N A P E M T I E E K E R E A E R L F V L F E R L K K T G V I N I Q N							
<i>N</i> cRic8	L F Q N N I P V P P S L S S L S T G D A - - - S G N Q K P V N P I T G Q F L D K Q K F A N A P E M T I E E K E R E A E R L F V L F E R L K K T G V I N I Q N							
<i>E</i> Ric8	490	500	510					
<i>F</i> gRic8	P V E K A V I Q E G R F E L S D D Y V E L D - - - - -							
<i>M</i> oRic8	P V E K A V I Q E G R F E L S D D Y V E L D - - - - -							
<i>N</i> cRic8	P V E K A V I Q E G R F E L S D D Y V E L D - - - - -							

The predicted amino acid sequence of *E. festucae* Ric8 (Efric8, EfM3, 064840) is aligned with the corresponding homologues *N. crassa* NcRic8 (NCU02788), *F. graminearum* FgRic8 (FGSG_01511) and *M. oryzae* MoRic8 (MGG_14008). *E. festucae* Ric8 displays 71.4% amino acid identity to *N. crassa* Ric8, 50.4% identity to the *F. graminearum* homologue, 61.2% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 62: Multiple sequence alignment of *E. festucae* AcyA homologues

The predicted amino acid sequence of *E. festucae* AcyA (EfAcyA, EfM3.022460) is aligned with the corresponding homologues *N. crassa* NcCr-1 (NCU08377), *F. graminearum* Fgac1 (FGSG_01234) and *M. oryzae* MoMac1 (MGG_09898). *E. festucae* AcyA displays 71.4% amino acid identity to *N. crassa* Cr-1, 70.2% identity to the *F. graminearum* homologue and 72.6% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 63: Multiple sequence alignment of *E. festucae* Pkac1 homologues



The predicted amino acid sequence of *E. festucae* Pkac1 (EfpKac1, Efm3.015410) is aligned with the corresponding homologues *N. crassa* NcPkc-1 (NCU06240), *F. graminearum* FgPkc1 (FGSG_07251) and *M. oryzae* MoPkc1 (MGG_06368). *E. festucae* Pkac1 displays 73.9% amino acid identity to *N. crassa* Pkac-1, 68.1% identity to the *F. graminearum* homologue and 71.7% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.

Supplementary 64: Multiple sequence alignment of *E. festucae* Pkar1 homologues

EfPkar1	- M S V P F S S P F G A N A N P F G D - - - R S Q N V M H S L A E E D E - N D G G T A P N - - - A T G I D S G T G L S - - F P G S L G G - D A H T D A P P	20	30	40	50	60	70	80
FgPkar1	- M S G P F S S P F G E N S N P F G T D R - G K R T N A I H R V V E E E E E N D T I T S P T N A R F G A S M F S G P F G G F F G G - D S S A E A P P							
MoSum1	M S A S G F T S P F G A N S N P F G S P E E R R G V A G S I Q P V L E E E E E - A D G I G S E P - - - S P G F R A P F F G G D A N S E G P P							
NcMcb	M S T G F T S P F G - N A N P F G S S - - G R S E S G P M H R L V E E D E - N D T I T S P T - - - T P H F G V K N N A A P A F W N G F G G - D A P S D M P -							
EfPkar1	T L R G P P N P D S Y P A Q Y N F S R R R T S V S A E S L K P S A D S Y D N W S P P F H E K S A E Q I E R L K K A I E G N F L F S H L D D E Q T A Q I L G A L V E	80	110	120	130	140	150	160
FgPkar1	A S R N V P N P D S Y P A Q Y N F G R R T S V S A E S L K P S A D S Y D N W S P P F H E K T P D Q I E R L K H A I E G N F L F S H L D D E Q S A Q I L G A L V E							
MoSum1	S S R P Q N - P D G Y P A Q Y N F A R R T S V S A E S L K P I A D S Y D N W T I P P F H P K S A E Q L D R L K K A I Q G N F L F S H L D D E Q S A Q I L G A L V E							
NcMcb	- V R R Q - - P D D F P A H Y N L G R R T S V S A E S L K P V T D N S D N W S P P V H P K T A E Q L E R L K K A I S G N F L F N H L E D Q S A Q V L G A L V E							
EfPkar1	K P I P A K G I K V I S Q G D A G D F F Y V V E I G S F D V H V N P S G T I Q P G L D G L G E K V G N I Q A G G S F G E L A L M Y N A P R A A T V I S V E A G C	170	180	190	200	210	220	230
FgPkar1	K P I P A K G I K V I S Q G D A G D Y F Y V V E K G S F D V Y V N P S G S L Q P G P D G M G N Q V G N I Q A G G S F G E L A L M Y N A P R A A T V I S A E P G C							
MoSum1	K P I P A K G I K V I V Q G D A G D Y F Y V V E K G K F S V H V N S S G V M Q A G T Q L G D H V G T I E A G G S F G E L A L M Y N A P R A A T V M S A E P N C							
NcMcb	K P V P A K G I K V I T Q G D A G D Y F Y V V E K G R F E V Y V N S T G A L Q P G P D G M Q K V G E I A E G G S F G E L A L M Y N A P R A A T V Y S A E P Q C							
EfPkar1	T I W A L D R I T F R R I L M E S T F A R R R M Y E T F L E E V P L L S L T P Y E R S K I A D A L E T R K A Q G E I I I K E G D P G D S F Y L L E S G E A D	250	260	270	280	290	300	310
FgPkar1	T V W A L D R V T F R R I L M E S T F A R R R M Y E S F L E E V P L L S T L T N P Y E R S K I A D A L E T Q K F A P G E I I I N E G D P G H A F Y L L E S G E A D							
MoSum1	V L W A L D R V T F R R I L M E S T F S R R R M Y E N F L E E V P I L S T L T A Y E R S K I A D A L E T O K Y P P G T V I I K E G D P G E D F Y L L E C G E A E							
NcMcb	T L W A L D R V T F R R I L M E S T F S R R R M Y E S F L E E V P I L K T L T P Y E R S K I A D A L E S Q K Y P A G H E I I I K E G D P G H S F F L L E A G E A A							
EfPkar1	A F K G D E S N K V L H Y K K G D Y F G E L A L L N D Q P R A A S V M A S S D V K V A T L G K N A F Q R L L G P V G G I L R R T R Y E G V A T G V E E M D P L H	330	340	350	360	370	380	390
FgPkar1	A Y I G Q P D N K V R H Y K K G D Y F G E L A L L N D A P R A A S T V A A S P V K V G S L G K N A F Q R L L G P V E G I L R R T R Y Q G V A T G V E E M D P L H							
MoSum1	A F K A G I D Q P P V K L Y K K G D F F G E L A L L N D A P R A A S V I V S K T E V K V A A L G K S A F Q R L L G P V E P I M R R T R Y D A I K T G V E E M D P L Q							
NcMcb	A F K R G N D S P V K N Y K K G D F F G E L A L L N D A P R A A S V I S Q T E V K V A R L G K N A F Q R L L G P T E S I L R R T R Y - - - V E A E E V D P L Q							

EfPkar1 R E
FgPkar1 T G
MoSum1 A A
NcMcb V S

The predicted amino acid sequence of *E. festucae* Pkar1 (EfPkar1, Efm3.071930) is aligned with the corresponding homologues *N. crassa* NcMcb1 (NCU01166), *F. graminearum* FgPkar1 (FGSG_09908) and *M. oryzae* MoSum1 (MGG_07335). *E. festucae* Pkar1 displays 77% amino acid identity to *N. crassa* Mcb-1, 74.7% identity to the *F. graminearum* homologue and 79.1% identity to the *M. oryzae* homologue. ClustalW was used to sequences, with conserved residues are shaded in grey.