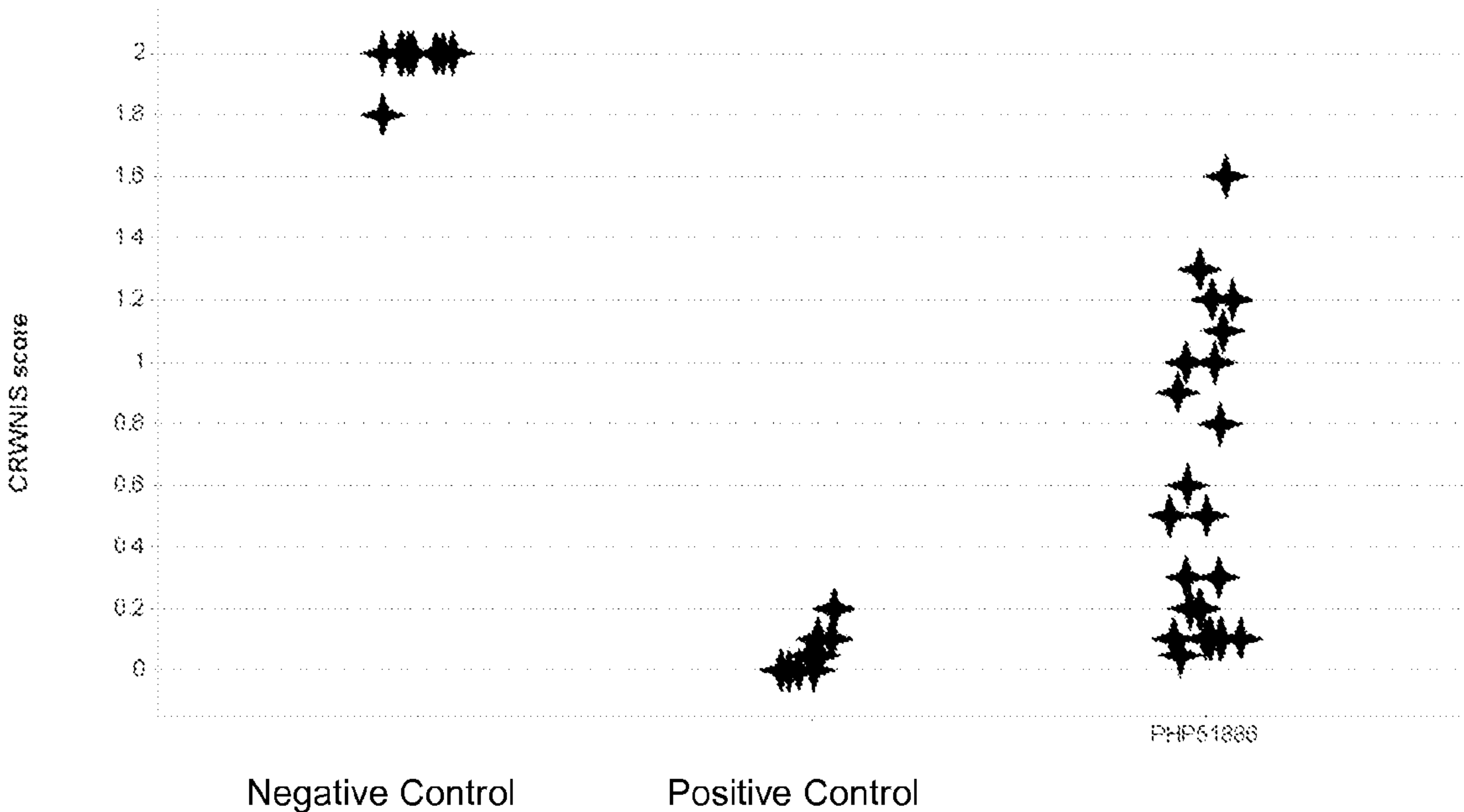




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(54) **Titre :** POLYPEPTIDES RECOMBINANTS D'ALCALIGENES FAECALIS ET LEURS METHODES D'UTILISATION
(54) **Title:** RECOMBINANT ALCALIGENES FAECALIS INSECTICIDAL POLYPEPTIDES AND METHODS FOR THEIR USE



(57) **Abrégé/Abstract:**
Compositions and methods for controlling pests are provided. The methods involve transforming organisms with a nucleic acid sequence encoding recombinant *Alcaligenes faecalis* insecticidal protein. In particular, the nucleic acid sequences are useful for preparing plants and microorganisms that possess insecticidal activity. Thus, transformed bacteria, plants, plant cells, plant tissues and seeds are provided. Compositions are insecticidal *Alcaligenes faecalis* nucleic acids and *Alcaligenes faecalis* proteins. The sequences find use in the construction of expression vectors for subsequent transformation into organisms of interest including plants, as probes for the isolation of other homologous (or partially homologous) genes. The *Alcaligenes faecalis* pesticidal proteins find use in controlling, inhibiting growth or killing Lepidopteran, Coleopteran, Dipteran, fungal, Hemipteran and nematode pest populations and for producing compositions with insecticidal activity.

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Recombinant *Alcaligenes faecalis* insecticidal polypeptides and methods for their use

ABSTRACT OF THE DISCLOSURE

Compositions and methods for controlling pests are provided. The methods involve transforming organisms with a nucleic acid sequence encoding recombinant *Alcaligenes faecalis* insecticidal protein. In particular, the nucleic acid sequences are useful for preparing plants and microorganisms that possess insecticidal activity. Thus, transformed bacteria, plants, plant cells, plant tissues and seeds are provided. Compositions are insecticidal *Alcaligenes faecalis* nucleic acids and *Alcaligenes faecalis* proteins. The sequences find use in the construction of expression vectors for subsequent transformation into organisms of interest including plants, as probes for the isolation of other homologous (or partially homologous) genes. The *Alcaligenes faecalis* pesticidal proteins find use in controlling, inhibiting growth or killing Lepidopteran, Coleopteran, Dipteran, fungal, Hemipteran and nematode pest populations and for producing compositions with insecticidal activity.

THAT WHICH IS CLAIMED:

1. A recombinant nucleic acid molecule encoding an *Alcaligenes faecalis* Insecticidal polypeptide-1A (AfIP-1A polypeptide) operably linked to a heterologous regulatory element, wherein the AfIP-1A polypeptide has at least 85% identity to the full length amino acid sequence of SEQ ID NO: 2.
2. The recombinant nucleic acid molecule of claim 1, wherein the AfIP-1A polypeptide comprises the amino acid sequence of SEQ ID NO: 257,
wherein
Xaa at position 6 is Ile, Thr, Leu, Met, Val or Ser;
Xaa at position 7 is Ala, Met, Val, Leu, Ile or Gly;
Xaa at position 8 is Thr, Asp, Ser or Glu;
Xaa at position 9 is Glu, Leu, Gly, Asp, Ala, Ile, Val or Met;
Xaa at position 10 is Glu, Asn, Asp or Gln;
Xaa at position 11 is Ser, Val, Thr, Ile, Leu or Met;
Xaa at position 12 is Lys, Glu, Arg or Asp;
Xaa at position 13 is Ile, Val, Leu or Met;
Xaa at position 14 is Arg, Gln, Lys or Asn;
Xaa at position 16 is Tyr, Gln, Trp, Phe or Asn;
Xaa at position 17 is Ala, Ser, Gly or Thr;
Xaa at position 19 is Trp, Glu, Phe, Ile, His, Asn or Tyr;
Xaa at position 20 is Ile, Val, Ala, Cys, Glu, Phe, Gly, Met, Asn, Gln, Arg, Ser or Thr;
Xaa at position 23 is Thr, Glu, Ala, Ser, Asp or Gly;
Xaa at position 24 is Ile, Leu, Val or Met;
Xaa at position 26 is Val, Ser, Ile, Leu, Met or Thr;
Xaa at position 27 is Val, Glu, Ile, Leu, Met or Asp;
Xaa at position 29 is Ser, Met, Thr, Ile, Leu or Val;
Xaa at position 30 is Asn, Asp, Ser, Glu, Gln or Thr;
Xaa at position 31 is Phe, Ile, Leu, Val or Met;
Xaa at position 32 is Lys, Glu, Arg or Asp;
Xaa at position 33 is Val, Ile, Leu or Met;
Xaa at position 34 is Glu, Lys, Asp or Arg;
Xaa at position 35 is Gly or Asn;
Xaa at position 36 is Ala, Gly, Asp, Glu, Phe, Gly, Ile, Leu, Pro, Gln, Arg, Ser, Thr, Val, Trp or Tyr;
Xaa at position 37 is Tyr, Ala, Cys, Asp, Glu, Gly, His, Ile, Lys, Leu, Met, Pro, Arg, Ser, Thr, Val or Trp;
Xaa at position 38 is Leu, Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Met, Gln, Arg, Ser, Thr, Val, Trp or Tyr;
Xaa at position 39 is Arg, Lys, Cys, Asp, Glu, Phe, Gly, Ile, Lys, Leu, Met, Asn, Pro, Ser, Thr, Val, Trp or Tyr;
Xaa at position 40 is Trp, Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val or Tyr;
Xaa at position 41 is Gly, Cys or Gln;
Xaa at position 42 is Lys, Cys, Glu, His, Leu, Met, Asn, Gln, Arg or Thr;
Xaa at position 43 is Phe, Tyr, Ala, Cys, Glu, Ile, Leu, Met, Gln, Ser, Val or Trp;

Xaa at position 44 is His, Ala, Asp, Glu, Gly, Lys, Leu, Met, Asn, Pro, Glu, Arg, Ser, Thr, Val, Trp;
 Xaa at position 45 is Val, Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Asn, Pro, Gln, Arg, Ser, Thr or Trp;
 Xaa at position 46 is Pro, Ala, Cys, Asp, Glu, Gly, His, Lys, Leu, Met, Gln, Arg, Ser, Thr, Val, Trp or Tyr;
 Xaa at position 47 is Gly, Leu or Phe;
 Xaa at position 48 is Asp, Asn, Glu, Gln, Leu or Phe;
 Xaa at position 50 is Asp, Ser, Glu, Thr, Leu or Phe;
 Xaa at position 51 is Lys, Asn, Arg, Gln, Leu or Phe;
 Xaa at position 52 is Glu, Leu or Phe;
 Xaa at position 53 is Ile, Leu or Phe;
 Xaa at position 54 is Ser, Thr, Leu or Phe;
 Xaa at position 55 is Pro, Ser, Thr, Leu or Phe;
 Xaa at position 56 is Ser, Asp, Thr, Glu or Leu;
 Xaa at position 57 is Gln, Thr, Glu, Asn, Ser, Asp, Leu or Phe;
 Xaa at position 58 is Ile, Val, Leu, Met or Phe;
 Xaa at position 60 is Gly, Lys, Ala or Arg;
 Xaa at position 61 is Thr, Ile or Phe;
 Xaa at position 62 is Ile, Lys, Val, Leu, Met, Arg or Phe;
 Xaa at position 64 is Lys, Ser, Glu, Arg, Thr, Asp, Leu or Phe;
 Xaa at position 65 is Asp, Ser, Glu, Thr, Leu or Phe;
 Xaa at position 66 is Glu, Gly, Asp or Ala;
 Xaa at position 67 is Asp, Thr, Glu or Ser;
 Xaa at position 68 is Ser, Lys, Thr or Arg;
 Xaa at position 69 is Tyr, Ser, Trp, Phe or Thr;
 Xaa at position 70 is Thr, Lys, Ser or Arg;
 Xaa at position 73 is Ser, Ala, Thr or Gly;
 Xaa at position 74 is Cys, Ala, Asp, Glu, Gly, His, Ile, Lys, Leu, Asn, Pro, Gln, Arg, Ser, Thr or Tyr;
 Xaa at position 76 is Arg, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Ser, Thr, Val, Trp or Tyr;
 Xaa at position 77 is Glu, Ala, Asp or Gly;
 Xaa at position 78 is Asn, Asp, Gln or Glu;
 Xaa at position 79 is Ala, Thr, Gly or Ser;
 Xaa at position 82 is Gly, Glu, Asn, Trp or Tyr;
 Xaa at position 86 is Gly, Lys, Ala or Arg;
 Xaa at position 88 is Ser, Glu, Thr or Asp;
 Xaa at position 89 is Leu, Ile, Val or Met;
 Xaa at position 91 is Asp, His or Glu;
 Xaa at position 92 is Gly, Asp, Ala or Glu;
 Xaa at position 95 is Leu, Trp, Ile, Val, Met, Phe or Tyr;
 Xaa at position 96 is Val, Leu, Ile or Met;
 Xaa at position 97 is Phe, Ala or Gly;
 Xaa at position 98 is Glu, Thr, Asp or Ser;
 Xaa at position 100 is Tyr, Lys, Trp or Arg;
 Xaa at position 101 is Trp, Phe or Tyr;
 Xaa at position 104 is Pro, Ala, Phe, Gly, His, Met, Gln, Arg or Val;
 Xaa at position 105 is Trp, Asp, Phe, Ile, Leu or Tyr;
 Xaa at position 106 is Ser, Ala, Thr or Gly;
 Xaa at position 111 is Asp, His, Asn, Glu or Gln;

Xaa at position 112 is Glu, Ser, Asp or Thr;
 Xaa at position 113 is Leu, Ser, Ile, Val, Met or Thr;
 Xaa at position 114 is Thr or Ser;
 Xaa at position 115 is Val, Ile, Val or Met;
 Xaa at position 116 is Lys, Thr, Glu, Arg, Ser or Asp;
 Xaa at position 117 is Asp or Glu;
 Xaa at position 118 is Lys, Asp, Arg or Glu;
 Xaa at position 119 is Glu, Asn, Asp or Gln;
 Xaa at position 120 is Asn, Lys, Asp or Arg;
 Xaa at position 121 is Tyr, Leu or Phe;
 Xaa at position 122 is Thr, Lys, Ser, Arg, Leu or Phe;
 Xaa at position 123 is Val, Ile, Leu, Met, Phe or Asn;
 Xaa at position 124 is Ile, Ser, Asp, Leu, Val Met, Thr, Glu or Phe;
 Xaa at position 125 is Lys, Leu, Phe or Met;
 Xaa at position 126 is Lys, Glu, Arg, Asp, Leu or Phe;
 Xaa at position 128 is Gly, Leu or Phe;
 Xaa at position 129 is Gly, Asn, Ala, Gln, Leu or Phe;
 Xaa at position 130 is Ser, Ile, Thr, Leu, Val, Met or Phe;
 Xaa at position 131 is Pro, Ser or Thr;
 Xaa at position 132 is Ser, Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Thr, Val, Trp or Tyr;
 Xaa at position 133 is Gly, Ala, Cys, Asp, Glu, Phe, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val or Trp;
 Xaa at position 134 is Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp or Tyr;
 Xaa at position 135 is Thr, Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Val, Trp or Tyr;
 Xaa at position 136 is Gly, Ala, Cys, Asp, Glu, Phe, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp or Tyr;
 Xaa at position 137 is Asn, Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Pro, Glu, Arg, Ser, Thr, Val, Trp or Tyr;
 Xaa at position 138 is Ile, Ala, Cys, Asp, Glu, Phe, Gly, His, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp or Tyr;
 Xaa at position 139 is Phe, Ala, Cys, Asp, Glu, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp or Tyr;
 Xaa at position 140 is Ile, Ala, Cys, Phe, His, Leu, Met, Asn, Gln, Thr, Val or Tyr;
 Xaa at position 142 is Val, Cys, Ile, Leu or Met;
 Xaa at position 143 is Val, Ile; Leu or Met;
 Xaa at position 145 is Lys, Val, Arg, Ile, Leu or Met; and
 Xaa at position 146 is Ser, Gly, Thr or Ala;

and wherein, 1 to 14 amino acids are optionally deleted from the N-terminus of the polypeptide.

3. The recombinant nucleic acid molecule of claim 2, wherein the AfIP-1A polypeptide comprises the amino acid motifs as represented by positions 15-26 of SEQ ID NO: 257, positions 33-53 of SEQ ID NO: 257, positions 71-84 of SEQ ID NO: 257, and positions 100-107 of SEQ ID NO: 257.

4. The recombinant nucleic acid molecule of claim 1, wherein the nucleic acid molecule encodes an AfIP-1A polypeptide comprising an amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 94.
5. A transgenic plant cell from a transgenic plant or transgenic progeny thereof, wherein the plant cell, plant and progeny comprise the recombinant nucleic acid molecule of claim 1.
6. A transgenic plant cell from a transgenic plant or transgenic progeny thereof, wherein the plant cell, plant and progeny are stably transformed with the recombinant nucleic acid molecule of claim 1.
7. The transgenic plant cell of claim 6, wherein the transgenic plant is a monocotyledon.
8. The transgenic plant cell of claim 6, wherein the plant cell, plant and progeny further comprise one or more additional transgenic traits.
9. An expression cassette, comprising the recombinant nucleic acid molecule of claim 1 and one or more regulatory sequences operably linked to and directing expression of the AfIP-1A polypeptide.
10. A transgenic plant cell from a transgenic plant, wherein the plant cell and the plant comprise the expression cassette of claim 9.
11. A seed cell, grain cell or cell from a processed product of the transgenic plant of claim 10 or the progeny of the plant, wherein the seed cell, grain cell or cell from the processed product comprise the recombinant nucleic acid molecule.
12. The seed cell of claim 11, wherein one or more seed treatment has been applied to a seed comprising said seed cell.
13. A transgenic plant cell from a transgenic plant, wherein the transgenic plant cell and transgenic plant are capable of expressing a recombinant polynucleotide encoding an AfIP-1A polypeptide having at least 85% identity to the full length amino acid sequence of SEQ ID NO: 2.
14. The transgenic plant cell of claim 13, wherein the transgenic plant is a monocotyledon.
15. The transgenic plant cell of claim 13, wherein the transgenic plant cell and the transgenic plant express one or more additional transgenic traits.
16. A recombinant nucleic acid molecule encoding an *Alcaligenes faecalis* Insecticidal polypeptide-1B (AfIP-1B polypeptide) operably linked to a heterologous regulatory element, wherein the AfIP-1B polypeptide has at least 95% identity to the full length amino acid sequence of SEQ ID NO: 4.
17. The recombinant nucleic acid molecule of claim 16, wherein the AfIP-1B polypeptide comprises the amino acid sequence of SEQ ID NO: 259,

wherein

Xaa at position 12 is Met, Leu, Ile or Val;
Xaa at position 34 is Ile or Leu;
Xaa at position 38 is Ile or Leu;
Xaa at position 42 is Glu or Asp;
Xaa at position 43 is Ile or Leu;
Xaa at position 53 is Tyr or Phe;
Xaa at position 55 is Tyr or Phe;
Xaa at position 71 is Gly, Cys or Ala;
Xaa at position 86 is Val or Leu;
Xaa at position 94 is Tyr or Phe;
Xaa at position 97 is Ile or Leu;
Xaa at position 101 is Tyr or Phe;
Xaa at position 103 is Ile, Leu, Gly, Val, Trp, Phe, Thr, Cys, Glu or Arg;
Xaa at position 105 is Met, Gly, Val, Leu, Trp, Phe, Pro, Thr, Cys, Asn, Gln or Arg;
Xaa at position 106 is Ile or Leu;
Xaa at position 108 is Gly, Ala, Leu, Val, Ile, Met, Trp, Phe, Ser, Thr, Cys, Tyr, Asn, Glu, Asp, Lys or His;
Xaa at position 109 is Ile, Leu, Ala, Val, Leu, Met, Trp, Phe, Pro, Cys, Asn or Glu;
Xaa at position 110 is Glu, Gly, Ala, Val, Leu, Met, Trp, Ser, Thr, Cys, Tyr, Asp, Arg or His;
Xaa at position 111 is Tyr, Gly, Ala, Val, Leu, Ile, Met, Trp, Ser, Thr, Cys, Asp, Glu, Lys, Arg or His;
Xaa at position 115 is Asp or Glu;
Xaa at position 119 is Val, Ala, Ile or Leu;
Xaa at position 134 is Ser or Leu;
Xaa at position 137 is Val, Phe, Ala, Leu, Trp, Pro, Ser, Cys, Asp, Glu or Arg;
Xaa at position 139 is Glu or Asp;
Xaa at position 141 is Phe, Val, Leu, Ile, Trp, Ser or Cys;
Xaa at position 144 is Ala, Val, Gly, Ile, Leu or Met;
Xaa at position 148 is Ser, Phe, Thr or Trp;
Xaa at position 152 is Ile, Thr, Leu, Val, Met or Ser;
Xaa at position 155 is Asp or Glu;
Xaa at position 179 is Gly, Val, Trp, Ser, Cys or Arg;
Xaa at position 181 is Ile, Val, Met or Leu;
Xaa at position 182 is Trp, Gly, Ala, Val, Leu, Met, Ser, Cys, Glu or Arg;
Xaa at position 188 is Val or Leu;
Xaa at position 196 is Lys or Glu;
Xaa at position 197 is Thr or Ser;
Xaa at position 201 is Trp, Cys, Tyr or Phe;
Xaa at position 202 is Lys, Asn or Arg;
Xaa at position 203 is Tyr or Phe;
Xaa at position 208 is Glu or Asp;
Xaa at position 214 is Ile or Leu;
Xaa at position 220 is Ile or Leu;
Xaa at position 224 is Tyr or Phe;
Xaa at position 234 is Glu or Asp;
Xaa at position 235 is Val or Leu;
Xaa at position 270 is Ile, Val, Leu or Met;
Xaa at position 296 is Lys or Glu;
Xaa at position 298 is Ala, Glu, Gly or Asp;

Xaa at position 299 is Glu, Gly, Asp or Ala;
 Xaa at position 300 is Ile, Val, Ile or Met;
 Xaa at position 305 is Asp or Glu;
 Xaa at position 317 is Ala, Ser, Gly or Thr;
 Xaa at position 323 is Glu or Asp;
 Xaa at position 335 is Glu or Asp;
 Xaa at position 352 is Glu or Asp;
 Xaa at position 359 is Glu, Gly, Ala, Val, Leu, Trp, Phe, Pro, Ser, Thr, Lys or Arg;
 Xaa at position 360 is Asn, Gly, Val, Leu, Ile, Met, Phe, Pro, Thr, Asn, Asp, Lys, Arg or His;
 Xaa at position 361 is Ser, Gly, Val, Leu or Glu;
 Xaa at position 363 is Asp, Gly, Leu, Ile, Trp or Ser;
 Xaa at position 364 is Val, Pro, Ser, Thr, Asn, Gln, Asp, Glu or Lys;
 Xaa at position 365 is Leu, Gly, Ala, Val, Ile, Trp, Phe, Pro, Ser, Thr, Cys, Tyr, Gln, Asp, Glu, Arg or His;
 Xaa at position 367 is Glu or Lys;
 Xaa at position 368 is Gly or Asp;
 Xaa at position 370 is Ile, Val, Leu or Met;
 Xaa at position 373 is Arg or Ser;
 Xaa at position 374 is Asn, Lys, Gln or Arg;
 Xaa at position 377 is Leu, Ile, Val or Met;
 Xaa at position 384 is Thr, Ala, Ser or Gly;
 Xaa at position 385 is Ile, Ser, Leu, Val, Met or Thr;
 Xaa at position 388 is Asp or Glu;
 Xaa at position 393 is Tyr, Phe or Trp;
 Xaa at position 398 is Ala or Val;
 Xaa at position 414 is Tyr or Phe;
 Xaa at position 418 is Ile or Leu;
 Xaa at position 419 is Ser, Asn, Thr or Gln;
 Xaa at position 423 is Val or Leu;
 Xaa at position 425 is Glu or Val;
 Xaa at position 427 is Ile or Val;
 Xaa at position 434 is Met or Thr;
 Xaa at position 481 is Glu or Asp;
 Xaa at position 495 is Asp or Glu;
 Xaa at position 509 is Phe, Gly, Ala, Val, Leu, Ile, Met, Trp, Ser, Cys, Tyr, Asn, Asp, Glu or Arg;
 Xaa at position 512 is Asn, Ser, Gly, Ala, Leu, Met, Trp, Phe, Ser, Thr, Cys, Gln or Arg;
 Xaa at position 514 is Glu, Gly, Ile, Asp or Arg;
 Xaa at position 516 is Gly, Ala, Val, Met, Pro, Thr, Asn, Gln, Asp, Glu or Lys;
 Xaa at position 519 is Leu, Gly, Ala, Val, Met, Phe, Pro, Tyr, Gln, Asp, Lys or Arg;
 Xaa at position 526 is Val or Leu;
 Xaa at position 530 is Ile or Leu;
 Xaa at position 533 is Val or Ala;
 Xaa at position 536 is Ile or Leu;
 Xaa at position 538 is Tyr, Phe or Trp;
 Xaa at position 543 is Tyr or Phe;
 Xaa at position 544 is Lys or Arg;
 Xaa at position 547 is Tyr or Phe;
 Xaa at position 550 is Tyr, Phe or Trp;

Xaa at position 552 is Asn, Ser, Gln or Thr;
 Xaa at position 558 is Phe or Leu;
 Xaa at position 600 is Met or Val;
 Xaa at position 602 is Met, Ile, Leu or Val;
 Xaa at position 607 is Asp or Gly;
 Xaa at position 610 is Thr, Lys, Ser or Arg;
 Xaa at position 612 is Ile or Thr;
 Xaa at position 613 is Leu or Pro;
 Xaa at position 615 is Asn or Asp;
 Xaa at position 619 is Lys or Arg;
 Xaa at position 625 is Tyr, Phe or Trp;
 Xaa at position 631 is Ile, Val, Leu or Met;
 Xaa at position 633 is Trp or Phe;
 Xaa at position 646 is Gln or Arg;
 Xaa at position 661 is Asn or Ser;
 Xaa at position 683 is Thr, Ala, Ser or Gly; and
 Xaa at position 696 is Glu or Asp;
 Xaa at position 700 is Ser or Gly; and
 Xaa at position 702 is Phe or Ser;

and wherein, 1 to 25 amino acids are optionally deleted from the C-terminus of the polypeptide.

18. The recombinant nucleic acid molecule of claim 17, wherein the AfIP-1B polypeptide comprises the amino acid motifs as represented by positions 105-115 of SEQ ID NO: 259, positions 133-144 of SEQ ID NO: 259, positions 177-184 of SEQ ID NO: 259, positions 358-365 of SEQ ID NO: 259, and positions 511-520 of SEQ ID NO: 259.
19. The recombinant nucleic acid molecule of claim 16, wherein the nucleic acid molecule encodes an AfIP-1B polypeptide comprises an amino acid sequence of SEQ ID NO: 4 or SEQ ID NO: 76.
20. A transgenic plant cell from a transgenic plant or transgenic progeny thereof, wherein the plant cell, plant and progeny comprise the recombinant nucleic acid molecule of claim 16.
21. A transgenic plant cell from a transgenic plant or transgenic progeny thereof, wherein the plant cell, plant and progeny are stably transformed with the recombinant nucleic acid molecule of claim 16.
22. The transgenic plant cell of claim 21, wherein the transgenic plant is a monocotyledon.
23. The transgenic plant cell of claim 21, wherein the plant cell, plant and progeny further comprise one or more additional transgenic traits.
24. An expression cassette, comprising the recombinant nucleic acid molecule of claim 16 operably linked to one or more regulatory sequences directing expression of the AfIP-1B polypeptide.

25. A transgenic plant cell from a transgenic plant, wherein the plant cell and plant comprise the expression cassette of claim 24.
26. A seed cell, grain cell or cell from a processed product of the transgenic plant of claim 25 or a progeny of the plant thereof, wherein the seed cell, grain cell or cell from the processed product comprise the recombinant nucleic acid molecule.
27. The seed cell of claim 26, wherein one or more seed treatment has been applied to a seed comprising said seed cell.
28. A transgenic plant cell from a transgenic plant, wherein the transgenic plant and the transgenic plant cell are capable of expressing a recombinant polynucleotide encoding an AfIP-1B polypeptide having at least 95% identity to the full length amino acid sequence of SEQ ID NO: 4.
29. The transgenic plant cell of claim 28, wherein the transgenic plant is a monocotyledon.
30. The transgenic plant cell of claim 28, wherein the transgenic plant cell and transgenic plant express one or more additional transgenic traits.
31. A transgenic plant cell from a transgenic plant or transgenic progeny thereof, wherein the plant cell, plant and progeny comprise the recombinant nucleic acid molecule of claim 1 and the recombinant nucleic acid molecule of claim 16.
32. A transgenic plant cell from a transgenic plant or transgenic progeny thereof, wherein the plant cell, plant and progeny are stably transformed with the recombinant nucleic acid molecule of claim 1 and the recombinant nucleic acid molecule of claim 16.
33. The transgenic plant cell of claim 32, wherein the transgenic plant is a monocotyledon.
34. The transgenic plant cell of claim 32, wherein the plant is selected from barley, corn, oat, rice, rye, sorghum, turf grass, sugarcane, wheat, alfalfa, banana, broccoli, bean, cabbage, canola, carrot, cassava, cauliflower, celery, citrus, cotton, a cucurbit, eucalyptus, flax, garlic, grape, onion, lettuce, pea, peanut, pepper, potato, poplar, pine, sunflower, safflower, soybean, strawberry, sugar beet, sweet potato, tobacco, tomato ornamental, shrub, nut, chickpea, pigeon pea, millets, hops and pasture grasses.
35. The transgenic plant cell of claim 32, wherein the plant cell, plant and progeny further comprise one or more additional transgenic traits.
36. The transgenic plant cell of claim 35, wherein the one or more additional transgenic trait is selected from insect resistance, herbicide resistance, fungal resistance, viral resistance, stress tolerance, disease resistance, male sterility, stalk strength, increased yield, modified starches, improved oil profile, balanced amino acids, high lysine or methionine, increased digestibility, improved fiber quality, flowering, ear and seed development,

enhancement of nitrogen utilization efficiency, altered nitrogen responsiveness, drought resistance or tolerance, cold resistance or tolerance, salt resistance or tolerance and increased yield under stress.

37. A seed cell, grain cell or cell from a processed product of the transgenic plant of claim 32, or the progeny of the plant thereof wherein the seed cell, grain cell, or cell from the processed product comprise the recombinant nucleic acid molecule of claim 1 and the recombinant nucleic acid molecule of claim 16.
38. An expression cassette, comprising the recombinant nucleic acid molecule of claim 1 operably linked to one or more regulatory sequences directing expression of an AfIP-1A polypeptide and the recombinant nucleic acid molecule of claim 16 operably linked to one or more regulatory sequences directing expression of an AfIP-1B polypeptide.
39. A transgenic plant cell from a transgenic plant, wherein the plant cell and the plant comprise the expression cassette of claim 38.
40. A seed cell, grain cell or cell from a processed product of the transgenic plant of claim 39 or the progeny of the plant thereof, wherein the seed cell, grain cell, or cell from the processed product comprise the recombinant nucleic acid molecule of claim 1 and the recombinant nucleic acid molecule of claim 16.
41. The seed cell of claim 40, wherein one or more seed treatment has been applied to a seed comprising said seed cell.
42. A method for expressing in a plant a polynucleotide encoding an insecticidal protein, comprising
 - (a) inserting into a plant cell the recombinant nucleic acid molecule of claim 1 encoding an AfIP-1A polypeptide; and
the recombinant nucleic acid molecule of claim 16 encoding an AfIP-1B polypeptide;
 - (b) obtaining a transformed plant cell comprising the nucleic acid sequence of step (a); and
 - (c) generating from the transformed plant cell a plant capable of expressing the nucleic acid molecules encoding an AfIP-1A polypeptide and an AfIP-1B polypeptide.
43. A method for protecting a plant from an insect pest, comprising expressing in the plant or cell thereof, an insecticidally-effective amount of an AfIP-1A polypeptide having at least 85% identity to the full length amino acid sequence of SEQ ID NO: 2 and an AfIP-1B

polypeptide having at least 95% identity to the full length amino acid sequence of SEQ ID NO: 24.

44. A fusion protein comprising a recombinant AfIP-1A polypeptide having at least 85% identity to the full length amino acid sequence of SEQ ID NO: 2.
45. A fusion protein comprising a recombinant AfIP-1B polypeptide having at least 95% identity to the full length amino acid sequence of SEQ ID NO: 4.
46. A fusion protein comprising a recombinant AfIP-1A polypeptide having at least 85% identity to the full length amino acid sequence of SEQ ID NO: 2 and a recombinant AfIP-1B polypeptide having at least 95% identity to the full length amino acid sequence of SEQ ID NO: 4.

		1		50
		HHHHHHHHHHHHHHHHHHHHHBBBBBBB	TT TTTTT TT T	
AfIP-1A-31	(1)	MTAKDIATEESKIRAYAQWIEITIFVVNSNFKVEGAYLRWGKFHVPGDKD		
AfIP-1A_49677	(1)	MTAKDIATVESKVRAYAQWIEITIFVVNSNFKVEGAYLKWGKFHVPGNKD		
AfIP-1A_27066	(1)	MTAKDIATEESKIRAYAQWIEITIFVVNSNFKVEGAYLKWGKFHVPGDKD		
AfIP-1A_19209	(1)	MTAKDIATEESKVRAYAQWIEITIFVVNSNFKVEGAYLKWGKFHVPGDKD		
AfIP-1A-33585	(1)	MTAKDIATEESKVRAYAQWIEITIFVVNSNFKVEGAYLKWGKFHVPGDKD		
SLIN6118	(1)	-----MAYSEWVEIRIYSENMEIKIKNIKLNWGKFYE ~~GPNQD~~		
FGTW-51	(1)	-----MDLNVEVQAQSQWVEIEIFSENMDIEIKKAELLWGKFHKPGNKS		
		51		100
		TT BBBBT	TTTTT TTT TTT TTTT BBBBT	
AfIP-1A-31	(51)	KEISPSQINGTI IKDEDSYTIASCGRENASSGTEGGFSLYDGDKLVFEYY		
AfIP-1A_49677	(51)	KEISPSQINGTI IKDEDSYTIASCGRENASSGTEGGFSLYDGDKLVFEYY		
AfIP-1A_27066	(51)	KEITPSQINGTI IKDEDSYTIASCGRENASSGTEGGFSLYDGDKLVFEYY		
AfIP-1A_19209	(51)	REITPSQINGTI IKDEDSYTIASCGRENASSGTEGGFSLYDGDKLVFEYY		
AfIP-1A_33585	(51)	KEITPSQINGTI IKDEDSYTIASCGRENASSGTEGGFSLYDGDKLVFEYY		
SLIN6118	(38)	IEITAPVLSDAVIKSGEKYT ~~VWSCGRDGASSGTEGSFELYDGD~~ TQVARFG		
FGTW-51	(45)	NEISSDTVNKT ~~KISSGTKSKIASCGRADTSSGTEGKFEIYHDD~~ KWLATYK		
		101		148
		TT TT HHHHHHHHH HBBBTTT	BBBBBBBT	
AfIP-1A-31	(101)	WDCPWSGSNSDELTVKDKEN--YTVIKKGGGSPSGATGNIFITVVKKS		
AfIP-1A_49677	(101)	WDCPWSGSNSDELTVKDKEN--YTVS ~~KKGGGSPSGATGNIFITVVKKS~~		
AfIP-1A_27066	(101)	WDCPWSGSNSDELTVKDKEN--YTVS ~~KKGGGSPSGATGNIFITVVKKS~~		
AfIP-1A_19209	(101)	WDCPWSGSNSDELTVKDKEN--YTVS ~~KKGGGSPSGATGNIFITVVKKS~~		
AfIP-1A_33585	(101)	WDCPWSGSNSDELTVKDKEN--YTVS ~~KKGGGSPSGATGNIFITVVKKS~~		
SLIN6118	(88)	WICPWSGANS ~~CSLI~~ PGEQENKLYKTARQWSGLTSGPLGTITLSCV ~~KLL~~		
FGTW-51	(95)	WDCPWAGSN ~~SHSLSV~~ TQDND--YKIDKEGGNISD ~~GALGNIRITCI~~ KVG		
AfIP-1A-31	SEQ ID NO:	2		
AfIP-1A_49677	SEQ ID NO:	786		
AfIP-1A_27066	SEQ ID NO:	32		
AfIP-1A_19209	SEQ ID NO:	778		
AfIP-1A_33585	SEQ ID NO:	36		
SLIN6118	SEQ ID NO:	14		
FGTW-51	SEO ID NO:	18		

Fig. 2A

	1	50
AfIP-1B_49677	(1) ---MGIEAKSINPLLLGITVGSTVLGN--DFKPSVLIN-----PITRM	
AfIP-1B_19209	(1) ---MGIEAKSINPLLLGITVGSTVLGN--DFKPSVLIN-----PITRM	
AfIP-1B_43161	(1) ---MDIEAKSINPLMGITVGSTVLGN--DFKPSVLIN-----PITRM	
AfIP-1B_27066	(1) ---MDIEAKSINPLLLGITVGSTVLGN--DFKPSVLIN-----PITRM	
AfIP-1B_33585	(1) ---MDIEAKSINPLLLGITVGSTVLGN--DFKPSVLIN-----PITRM	
AfIP-1B-32	(1) ---MDIEAKSINPLMGITVGSTVLGN--DFKPSVLIN-----PITRM	
Slin6117	(1) MSKTASTELRYNPFYAVRVGSTIDGNTSQFFPTVIADTDASDKPVAITTL	
FGTW-52	(1) ---MKTQIEIVNPFAGVKIGSYVSGN--QFSPSVITG-----DITRM	
	51	100
AfIP-1B_49677	(38) ITQKEIEMGMSGKSQYVYTDSLNEGTIGFSGAYGPSGIAKFTSAVAVSVS	
AfIP-1B_19209	(38) ITQKEIEMGMSGKSQYVYTDSLNEGTIGFSGAYGPSGIAKFTSAMAVSVS	
AfIP-1B_43161	(38) ITQKEIEMGMSGKSQYVYTDSLNEGTIGFSGAYGPSGIAKFTSAVAVSVS	
AfIP-1B_27066	(38) ITQKEIEMGMSGKSQYVYTDSLNEGTIGFSGAYGPSGIAKFTSAVAVSVS	
AfIP-1B_33585	(38) ITQKEIEMGMSGKSQYVYTDSLNEGTIGFSGAYGPSGIAKFTSAVAVSVS	
AfIP-1B-32	(38) ITQKEIEMGMSGKSQYVYTDSLNEGTIGFSGAYGPSGIAKFTSAVAVSVS	
Slin6117	(51) SAEKDMRTSMTGESSYVYNDQMNQGS LGVAGSYGVSGVSKVSAAVSVYAG	
FGTW-52	(38) EEVLEVQKYISGRSNYVYSDKLNEAS LGVSGAYGVTGVSKLTSSVSAHAG	
	101	150
AfIP-1B_49677	(88) NATASEYKSIKVSYNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSLKV	
AfIP-1B_19209	(88) NATASEYKSIKVSYNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSLKV	
AfIP-1B_43161	(88) NATASEYKSIKVSYNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSLKV	
AfIP-1B_27066	(88) NATASEYKSIKVSYNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSLKV	
AfIP-1B_33585	(88) NATASEYKSIKVSYNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSLKV	
AfIP-1B-32	(88) NATASEYKSIKVSYNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSLKV	
Slin6117	(101) KSSASSSSSINLNYNVQLLAGVEYIDFDRLSPETLLNALKNGPRYRALAA	
FGTW-52	(88) NATASADKSIKLSYNISMISGIEYIDFDSLTAEDILNSLKPGPKSLVVDV	
	151	200
AfIP-1B_49677	(138) LEKFIAARDCTGSS-----TEKDELMKEWVKSLQNFISSYG	
AfIP-1B_19209	(138) LEKFIAARDCTGSS-----TEKDELMKEWVKSLQNFISSYG	
AfIP-1B_43161	(138) LEKFIAVRDCFGSS-----TEKDELMKEWVKSLQNFISSYG	
AfIP-1B_27066	(138) LEKFIAARDCSGSS-----TEKDELMKEWVKSLQNFISSYG	
AfIP-1B_33585	(138) LEKFIAARDCTGSS-----TEKDELMKEWVKSLQNFISSYG	
AfIP-1B-32	(138) LEKFIAARDCSGSS-----IEKDELMKEWVKSLQNFISSYG	
Slin6117	(151) LTKFLDVKKAIQNRN--LVEALKDPAQKEEIERVLAGWHNARENFFKQDG	
FGTW-52	(138) LDKFNTLRDYQQENNLSLFDNNMSFIQDARQDELVDWLKALNYFYQTYA	
	201	250
AfIP-1B_49677	(174) DGLVVGAIWGGMGSVSTEMTSKKSEDSWKYGETAEFSYSGIGSSVSIAQT	
AfIP-1B_19209	(174) DGLVVGAIWGGMGSVSTEMTSKKSEDSWKYGETAEFSYSGIGSSVSIAQT	
AfIP-1B_43161	(174) DGLVVGAIWGGMGSVSTEMTSKKTEDSWKYGETAEFSYSGIGSSVSIAQT	
AfIP-1B_27066	(174) DGLVVGAIWGGMGSVSTEMTSKKSEDSWKYGETAEFSYSGIGSSVSIAQT	
AfIP-1B_33585	(174) DGLVVGAIWGGMGSVSTEMTSKKSEDSWKYGETAEFSYSGIGSSVSIAQT	
AfIP-1B-32	(174) DGLVVGAIWGGMGSVSTEMTSKKTEDSWKYGETAEFSYSGIGSSVSIAQT	
Slin6117	(199) DGLVVGVMWGGLGTVSLQIDNTSGQSNWKYGGRGNF SYAGINGSVSVEAA	
FGTW-52	(188) DGMVVGVIWGGIGGVSMDIGRSSYEKNWTYGGQADFTYSGTGAAVSVAAT	

Fig. 2B

		251	300
AfIP-1B_49677	(224)	YNGSQKQDSSEVEVSCALASGGCVESQVNSWFDVVANKSFAEISGISLL	
AfIP-1B_19209	(224)	YNGSQKQDSSEVEVSCALASGGCVESQVNSWFDVVANKSFAEISGISLL	
AfIP-1B_43161	(224)	YNGSQKQDSSEVEVSCALASGGCVESQVNSWFDVVANKSFAEISGISLL	
AfIP-1B_27066	(224)	YNGSQKQDSSEVEVSCALASGGCVESQVNSWFDVVANKSFAEISGISLL	
AfIP-1B_33585	(224)	YNGSQKQDSSEVEVSCALASGGCVESQVNSWFDVVANKSFAEISGISLL	
AfIP-1B-32	(224)	YNGSQKQDSSEVEVSCALASGGCVESQVNSWFDVVANKSFAEISGISLL	
Slin6117	(249)	<u>YDGSQQRKNTDVKVSCSSVAMGGCISQQIADWEKKFTNLGFDKLADAKLL</u>	
FGTW-52	(238)	<u>YNGKQSDKGTSDVDVSCSSFSSGTCVNVQVNEWFKVVENKAYSEITDLKLL</u>	
		301	350
AfIP-1B_49677	(274)	DKAPMQSSVSPPPKIPDFLKPEKNEEVTEKLDTIKKLGDSEEFSLASGYE	
AfIP-1B_19209	(274)	DKAPMQSSVSPPPKIPDFLKPEKNEEVTEKLDTIKKLGDSEEFSLASGYE	
AfIP-1B_43161	(274)	DKAPMQSSVSPPPKIPDFLKPEKNAEITEKLDTIKKLGDSEEFALASGYE	
AfIP-1B_27066	(274)	DKAPMQSSVSPPPKIPDFLKPEKNEGVTEKLDTIKKLGDSEEFSLASGYE	
AfIP-1B_33585	(274)	DKAPMQSSVSPPPKIPDFLKPEKNEEVTEKLDTIKNLGNSEEFSLASGYE	
AfIP-1B-32	(274)	DKAPMQSSVSPPPKIPDFLKPEKNAEITEKLDTIKKLGDSEEFALASGYE	
Slin6117	(299)	<u>DSAPGIDTLNTTPTAPAFVEPTKDKGIAARIEAIRDLNGLEAFAIASAYD</u>	
FGTW-52	(288)	<u>DSAPAQGGVKPPPPLPPFVVPKKDPAIEHKLAKIGRLGNTTEELSIMGYD</u>	
		351	400
AfIP-1B_49677	(324)	EAKKTNP--LTFFEFKSTVREKNNIDGLNDLASKVQENSLDVLAEGSVS	
AfIP-1B_19209	(324)	EAKKTNP--LTFFEFKSTVRDKNNIDGLNDLASKVQENSLDVLAEGSVS	
AfIP-1B_43161	(324)	EAKKTNP--LTFFEFKSTVRDKNNIDGLNELASKVQENSLDVLAEGSIS	
AfIP-1B_27066	(324)	EAKKTNP--LTFFEFKSTVRDKNNIDGLNDLASKVQENSLDVLAEGSVS	
AfIP-1B_33585	(324)	EAKKTNP--LTFFEFKSTVRDKNNIDGLNDLASKVQENSLDVLAEGSVS	
AfIP-1B-32	(324)	EAKKTNP--LTFFEFKSTVRDKNNIDGLNELASKVQENSLDVLAEGSIS	
Slin6117	(349)	<u>KASKDPKNKDLTLAQFIDQTKKPADTRAVDELTSNAANNDIDVLTTSGL</u>	
FGTW-52	(338)	<u>KAKKDDSS--MTPEKFEKTRQRNSLDKLTELEIKLKNQLDVLLDINKV</u>	
		401	450
AfIP-1B_49677	(372)	RRKKNI----SLQGVRASSLDSSSDYAVLGAWIANWSDIFPWMSMGYMNE	
AfIP-1B_19209	(372)	RRKKNI----SLQGVRASSLDSSSDYAVLGAWIANWSDIFPWMSMGYMNE	
AfIP-1B_43161	(372)	RRNKNI----SLQGVRTISLDSSSDYAVLGAWIANWSDIFPWMSMGYMNE	
AfIP-1B_27066	(372)	RRKKNI----SLQGVRASSLDSSSDYAVLGAWIANWSDIFPWMSMGYMNE	
AfIP-1B_33585	(372)	RRKKNI----SLQGVRASSLDSSSDYAVLGAWIANWSDIFPWMSMGYMNE	
AfIP-1B-32	(372)	RRNKNI----SLQGVRTISLDSSSDYAVLGAWIANWSDIFPWMSMGYMNE	
Slin6117	(399)	<u>AGLEEESLLPPDDISEPALTRTADDFTVLGVWIANWADLFPWLATGYLNE</u>	
FGTW-52	(386)	<u>ISVE-----SPSFEPIAMADNHSGFVPLGVWIVNWADIFPWLSTGYLND</u>	
		451	500
AfIP-1B_49677	(418)	INDAEVAEYILKIRCMMQDLSTLNTIYNTFNACNIKLDLC-HLNSASQVA	
AfIP-1B_19209	(418)	INDAEVAEYILKIRCMMQDLSTLNTIYNTFNACNIKLDLC-HLNSASQVA	
AfIP-1B_43161	(418)	INDAEVAEYILKIRCMMQDLSTLNTIYNTFNACNIKLDLC-HLNSASQVA	
AfIP-1B_27066	(418)	INDAEVAEYILKIRCMMQDLSTLNTIYNTFNACNIKLDLC-HLNSASQVA	
AfIP-1B_33585	(418)	INDAEVAEYILKIRCMMQDLSTLNTIYNTFNACNIKLDLC-HLNSASQVA	
AfIP-1B-32	(418)	ISDAEVAEYILKIRCMMQDLSTLNTIYNTFNACNIKLDLC-HLNSASQVA	
Slin6117	(449)	<u>VSTVEAAQQILAKQCMIQDLLTLRLYRTLASTGLKYEQLGITAPFDQIA</u>	
FGTW-52	(430)	<u>ISDTAAAEALAKKRCMMQDFCTLSSIYNTFHSSGIKMEG--KLDAPDQIA</u>	

Fig. 2C

	501	550
AfIP-1B_49677	(467)	DSFKIAQGVLSDNVESDDAVEIAFNSLSDEAKKIYTAWNEIGFLRNAELG
AfIP-1B_19209	(467)	DSFKIAQGVLSDNVESDDAVEIAFNSLSDEAKKIYTAWNEIGFLRNAELG
AfIP-1B_43161	(467)	DSFKIAQGVLSDNVESDDAVEIAFNSLSDEAKKIYTAWNEIGFLRNAELG
AfIP-1B_27066	(467)	DSFKIAQGVLSDNVESDDAVEIAFNSLSDEAKKIYTAWNEIGFLRNAELG
AfIP-1B_33585	(467)	DSFKIAQGVLSDNVESDDAVEIAFNSLSDEAKKIYTAWNEIGFLRNAELG
AfIP-1B-32	(467)	DSFKIAQGVLSDNVESDDAVEIAFNSLSDEAKKIYTAWNEIGFLRNAELG
Slin6117	(499)	NSFSQEYSWLKDNLDKNNAVRQSYGQLGIQARAIYGFWNTYGFLRGAELG
FGTW-52	(478)	NAFSNALTILKDNQDQDNVIQQAYDRLGSDAQGIYKIWNHNGFLRNAELG
	551	600
AfIP-1B_49677	(517)	LGLLIG-DQSVSSEIIDVKPIPYPEVITYKAAYCSYG---SNNPTAFSSFI
AfIP-1B_19209	(517)	LGLLIG-DQSVSSEIIDVKPIPYPEVITYKAAYCSYG---SNNPTAFSSFI
AfIP-1B_43161	(517)	LGLLIG-DQSVSSEIIDVKPIPYPEVITYKAAYCSYG---NNNPTAFSSFI
AfIP-1B_27066	(517)	LGLLIG-DQSVSSEIIDVKPIPYPEVITYKAAYCSYG---SNNPTAFSSFI
AfIP-1B_33585	(517)	LGLLIG-DQSVSSEIIDVKPIPYPEVITYKAAYCSYG---SNNPTAFSSFI
AfIP-1B-32	(517)	LGLLIG-DQSVSSEIIDVKPIPYPEVITYKAAYCSYG---NNNPTAFSSFI
Slin6117	(549)	LGLMLDDKSLTTTISKQEVADDFICQTYTLESCTFVTDKTNYSGFASF
FGTW-52	(528)	FGLMFDTNRSISSTVDRVKGVPHPEVVYKSEYCSFD---KVNYHAFKSM
	601	650
AfIP-1B_49677	(563)	KMLPFIDTNGDIYAFGPSIMLLRKALPEKMIFTKGGEMAMKLTADKDKGI
AfIP-1B_19209	(563)	KMLPFIDTNGDIYAFGPSIMLLRKALPEKMIFTKGGEMAMKLTADKDKGI
AfIP-1B_43161	(563)	KMLPFIDTNGDIYAFGPSIMLLRKALPEKMIFTKGGEMAMKLTADKDTGI
AfIP-1B_27066	(563)	KMLPFIDTNGDIYAFGPSIMLLRKALPEKMIFTKGGEMAMKLTADKDKGI
AfIP-1B_33585	(563)	KMLPFIDTNGDIYAFGPSIMLLRKALPEKMIFTKGGEMAMKLTADKDKGI
AfIP-1B-32	(563)	KMLPFIDTNGDIYAFGPSIMLLRKALPEKMIFTKGGEMAMKLTADKDTGI
Slin6117	(599)	KLLPFITPDGKVYVFGPANMLVSEVTDEGIVLSKNPAKAMAFTADTTNKL
FGTW-52	(575)	KVLPIIDLGGNVYAFGPSAMLLKNTINNEVTFTKSVLTAMRFEIDKDNKI
	651	700
AfIP-1B_49677	(613)	LTNDSVRLIPIPYSAAGV-QWRGQGQGRSLASSQSLQDQFAALEKELGN
AfIP-1B_19209	(613)	LTNDSVRLIPIPYSAANGV-QWRGQGQGRSLASSQSLQDQFAALEKELGN
AfIP-1B_43161	(613)	LTNDSVKLIPIPYSAAGI-QWRGQGQGRSLASSQSLQDQFAALEKELGN
AfIP-1B_27066	(613)	LTNDSVRLIPIPYSAAGV-QWRGQGQGRSLASSQSLQDQFAALEKELGN
AfIP-1B_33585	(613)	LTNDSVRLIPIPYSAAGV-QWRGQGQGRSLASSQSLQDQFAALEKELGN
AfIP-1B-32	(613)	LTNDSVKLIPIPYSAAGI-QWRGQGQGRSLASSQSLQDQFAALEKELGN
Slin6117	(649)	LTNGNLKLYPIPFSGAEGVREWMGQSVSTNLASSITLKKRLNNVKDQLTE
FGTW-52	(625)	LKNSTTKLYPIPCSAAGINDWKGPVGINLSSSKSLSDQLEALRNELLK
	701	747
AfIP-1B_49677	(662)	LNICTLSSDSWSKDWTYTVPYTLRKISTTYIGTVEKINSIFG-----
AfIP-1B_19209	(662)	LNICTLSSDSWSKDWTYTVPYTLRKISTTYIGTVEKINSIFG-----
AfIP-1B_43161	(662)	LNICTLSSDSWSKDWTYTVPYTLRKISTTYIGTVQKINSIFG-----
AfIP-1B_27066	(662)	LNICTLSSDSWSKDWTYTVPYT-----
AfIP-1B_33585	(662)	LNICTLSSDSWSKDWTYTVPYTLRKISTTY-----
AfIP-1B-32	(662)	LNICTLSSDSWSKDWTYTVPYTLRKISTTYIGTVEKINSIFG-----
Slin6117	(699)	LSTYSFSSDNWNNDANAQAPYSIRLIKTOYVGLMEAAQSVFNGKPHP
FGTW-52	(675)	LNSCSVSSDKWNPVWQYTDPYHLKEMGTSYIGLVNKTAKTIFP----

Fig. 3A

	1	50
GI_115390458_A_terreus	(1)	-----MDDSQVSIHERD
GI_67522192_A_nidulans	(1)	-----
GI_145256342_A_niger	(1)	-----MPAAGPMDQVVSFHERD
GI_169785219_A_oryzae	(1)	-----MDTDLNKYNSWVEFHERD
GI_119487614_N_fischeri	(1)	-----MASTTGQYLDIEIKD
GI_121709507_A_clavatus	(1)	-----MAPTSAHQYLDMEIKD
GI_169772307_A_oryzae	(1)	-----MPADAYGQYVDIKIED
GI_169777319_A_oryzae	(1)	-----MALCLCQQSKISGAQ
GI_152985646_P_aeruginosa	(1)	-----MKVVVSN
GI_15595320_P_aeruginosa	(1)	-----MAYAEWIAVKVVSK
GI_2292820_C_bifermentans	(1)	-----MNNNCEVNCENTEENKSNRAYRWVKFHIEA
GI_2292821_C_bifermentans	(1)	-----MNNNCEVNCENTEENKSNRAYRWVKFHIEA
AfIP-1A-31	(1)	-----MTAKDIATEESKIRAYAQWIEITIFV
AfIP-1A-15554	(1)	-----MTAKDIATEESKIRAYAQWIEITIFV
AfIP-1A-27066	(1)	-----MTAKDIATEESKIRAYAQWIEITIFV
AfIP-1A-33585	(1)	-----MTAKDIATEESKVRAYAQWIEITIFV
SLIN6118	(1)	-----MAYSWVEIRIYS
FGTW-51	(1)	-----MDLNVEVQAQSQWVEIEIFS
GI_186897694_H_annosum	(1)	-----MAYAQWVILIIHN
GI_54312022_P_ostreatus_p	(1)	-----MAYAQWVILIIHN
GI_60461919_P_ostretus_o	(1)	-----AYAQWVILIIHN
GI_238581050_M_perniciosa	(1)	-----MAYAQWVIVLHN
GI_24636240_A_aegerita_A	(1)	-----MDSNKDERAYAQWVILIIHN
GI_90639437_T_versicolor	(1)	MNFELAHPSRPIAEGICVTEDVRTSEDFVVDNDDRHRAYAQWVSIETIN
GI_145230219_A_niger	(1)	-----MAERAQWVHIRVFN
GI_70985747_A_funigatus_h	(1)	-----MASVQAYAQWVTVHLIN
GI_158524422_R_australe	(1)	-----
GI_26112720_B_vulgaris	(1)	-----MAYAQWVVHIIHN
GI_46507636_L_multiflorum	(1)	-----MAYAQWVVIHIIHN
	51	100
GI_115390458_A_terreus	(14)	RLAQGNITIRSFYDCSRSGPLLLFRGQFSPEDKKALTEDDIDQLII
GI_67522192_A_nidulans	(1)	-----MTI
GI_145256342_A_niger	(19)	HLEKGEITVRHTVIEGG-----EFEDPNNRQSLTEDEIDEITII
GI_169785219_A_oryzae	(20)	HLKDGEISVRHTVIEDG-----EFQDPNNRQSLIHEDVIDEIVII
GI_119487614_N_fischeri	(17)	DMKYD-IRIENAHIESG-----EFYREGDQNDTLLTDDIEDMII
GI_121709507_A_clavatus	(17)	DMQYD-IRIENARIDSG-----EFHSASDENDTLLTDDVEDLMI
GI_169772307_A_oryzae	(17)	GMKYD-IRIENAHLD SG-----QFYRQGDQGDIMTADDIDDMII
GI_169777319_A_oryzae	(16)	ELIRLLFDIDLLHLLIDLNIR-----SRKI PKGNMERTKKYASQVNGKEI
GI_152985646_P_aeruginosa	(8)	SIGT--AGIRMATLQWG-----MECRCSNRDELSAEKDSSMNV
GI_15595320_P_aeruginosa	(16)	SIGT--VGIRMATLQWG-----KPYRYTNKDEISTEEVSSMNV
GI_2292820_C_bif	(32)	VNEG--LKIRNASLKWG-----KPEDPNNKDIPI SPEDISKINI
GI_2292821_C_bif	(32)	VHSN--LKIRNASL TWG-----KPEDPYNE DIPI SPEDISKINI
AfIP-1A-31	(27)	VNSN--FKVEGAYLRWG-----KPHVPGDKDKKEITPSQINGTII
AfIP-1A-15554	(27)	VNSN--FKVEGAYLRWG-----KPHVPGDKDKKEITPSQINGTII
AfIP-1A-27066	(27)	VNSN--FKVEGAYLRWG-----KPHVPGDKDKKEITPSQINGTII
AfIP-1A-33585	(27)	VNSN--FKVEGAYLRWG-----KPHVPGDKDKKEITPSQINGTII
SLIN6118	(14)	ENME--IKIKNIKLNWG-----KPYEGPNQDIETAPVLSDAVI
FGTW-51	(21)	ENMD--IEIKKAE LLWG-----KPEKPNESNEISSDTVNKTKI
GI_186897694_H_annosum	(14)	VGA AK-FSIRKLNPSWG-----KLHAEGDKTEVANKSTIEGKVV
GI_54312022_P_ostreatus	(14)	VGSKD-VKIKNLKPSWG-----KLHAEQDKTEVASKYEGTVI
GI_60461919_P_ostretus	(13)	VGQON-VKIKNLNASWG-----KLHAEQDKTEVASKYEGTVI
GI_238581050_M_per	(14)	VGN SP-MKVKKVSLDWG-----KEHV DGNKKKEIGKDQIEGKVI
GI_24636240_A_aegerita	(21)	VGSSP-FKIANLGLSWG-----KLHAEQDKTEVASKYEGTVI
GI_90639437_T_ver	(51)	YGPRP-VKIKNVYRSWG-----KLHAEQDKTEVASKYEGTVI
GI_145230219_A_niger	(17)	SLSFDTL SVRTWLWG-----KPEKENNESAEIPVSDINAIIRA
GI_70985747_A_funigatus_h	(18)	SMSSETLSIQNASLSWG-----KWKDGDKDAEITSEDVQOKTA
GI_158524422_R_australe	(1)	-----KDEEISANEVNOIRI
GI_26112720_B_vulgaris	(14)	SFRNGTISIKDAKAFWG-----KPYKNGNEDDELIANEVNOIRI
GI_46507636_L_multiflorum	(14)	SFRNGSISIKDAEAMWG-----KPEKNGNKKAEICAGEVNMKSV

Fig. 3B

	101	150
GI_115390458_A_terreus	(64)	PS-EGIGEVCAHGR---GSEGRIDLEFDG---EKKICELHNDNRTRPS
GI_67522192_A_nidulans	(4)	PA-EGLGEVCATGR---GSEGRIDLEFDG---EKKICELHNDNRAERRW
GI_145256342_A_niger	(58)	PS-YGIGEVCAHGR---GSEGRIDLEFDG---EKKICELHNDNRQGNPV
GI_169785219_A_oryzae	(59)	PS-DGIGEVCAHGR---GSEGRIDLEFDG---NDKICELHNDNRDGRRE
GI_119487614_N_fischeri	(55)	RHNGGLRHVCSSGEEGFGGLQCTIDLDVVK-DARICTLANNAFMEFGK
GI_121709507_A_clavatus	(55)	RHNGGTRHVCSSGEEGFGGLQCTIDLDVVR-DARICTLANNAFMEFGK
GI_169772307_A_oryzae	(55)	RHNGGIREVCSSGETDSMSGTQCTIDLDVVK-DTRICTLANNAFMEFGK
GI_169777319_A_oryzae	(61)	IP-GTSQLEETGESSAASGTGCTLELDK---TQTRICKLYWDCPWGSKV
GI_152985646_P_aerugin	(45)	QA-GSPQWIASCGRENASSGTGCTGCDCHDG---NTKMGTFSSWDDPRKSGA
GI_15595320_P_aeruginosa	(53)	QA-GSPQWIASCGRENASSGTGCTGCDCHDG---NTKMGTFSSWDDPWKSGA
GI_2292820_C_bif	(69)	EK-HDTAIIASSCKENTASGTGCTGVFYICDEN---EDKIAAIIYWDGCPWGSN
GI_2292821_C_bif	(69)	GI-GRIEIIASSCKENTASGTGCTGVFYICDEN---EKKIVTVYWDGCPWGSN
AfIP-1A-31	(64)	KD-EDSYTIIASSCKENASSGTGCTGGSFYIDG---DKLVFEYYWDGCPWGSN
AfIP-1A-15554	(64)	KD-EDSYTIIASSCKENASSGTGCTGGSFYIDG---DKLVFEYYWDGCPWGSN
AfIP-1A-27066	(64)	KD-EDSYTIIASSCKENASSGTGCTGGSFYIDG---DKLVFEYYWDGCPWGSN
AfIP-1A-33585	(64)	KD-EDSYTIIASSCKENASSGTGCTGGSFYIDG---DKLVFEYYWDGCPWGSN
SLIN6118	(51)	KS-GEKYTVWSGCRDGAASGTGCTGGSFYIDG---DTQVARFGWICPWGSN
FGTW-51	(58)	SS-GTKSKIASSCGRADTSSGTGCTGGSFYIDG---DKWLATYKWDGCPWGSN
GI_186897694_H_annosum	(52)	EA-DQQLRINACGRSDAAAGTTGCTGSDLVVAT-QQVIRHVYWDGCPWGSKR
GI_54312022_P_ostreatus	(52)	KP-DEKLQINACGRSDAAAGTTGCTGSDLVVAT-QQVIRHVYWDGCPWGSKT
GI_60461919_P_ostretus	(51)	AP-GDQVQINACGRSDAAAGTTGCTGSDLVVAT-QQVIRHVYWDGCPWGSKA
GI_238581050_M_pern	(52)	GP-DEKFQINACGRSDAASGTGCTGSDLVVAT-QQVIRHVYWDGCPWGSKT
GI_24636240_A_aegerita	(59)	GP-DEKIQINACGRSDAASGTGCTGSDLVVAT-QQVIRHVYWDGCPWGSKR
GI_90639437_T_versicolor	(89)	NP-NGTLTIIAGGGSNASSGTGCTGSDLVVAT-QQVIRHVYWDGCPWGSKT
GI_145230219_A_niger	(56)	AP-GGSFNVFACGRAHSPSGTGGTGFVYNG---DVRVAYIYWDGCPWGSKR
GI_70985747_A_funigatus	(57)	PP-GGSVNVSNGCRSDAASGTGCTGSDLVVAT-QQVIRHVYWDGCPWGSKT
GI_158524422_R_australe	(16)	PA-GSDGDIASSGSDSASGTGCTGQVYVYD---DTRVCTLYWDCPWGSKA
GI_26112720_B_vulgaris	(53)	PA-GSDGDIASSGSDSASGTGCTGQVYVYD---DTRVCTLYWDCPWGSKA
GI_46507636_L_multiflo	(53)	GA-GSSEKYSSGCRSDSASGTGCTGQVYVYD---DTRVCTLYWDCPWGSKS
	151	200
GI_115390458_A_terreus	(106)	N-EFEVIDGDKD-YKIECSGWSPOAG-PLGHVYFDISAAKKKAAAAAAK
GI_67522192_A_nidulans	(46)	N-DFEVLPEDEG-YRVECSGWSER-GPLGHVYFDVSARKEELRREKEL
GI_145256342_A_niger	(100)	N-IVEMLDNSK-YRVEHGGWSPEAG-PLGHVYFDILEQQKKKNSK----
GI_169785219_A_oryzae	(101)	N-LVEMLDSDK-YRVEHGGWSPEANGPLGHVYFDVWAKDKSK-----
GI_119487614_N_fischeri	(104)	R-NTFMLRDQDPRYNINIGKWNESG--ILGRVPYTISDE-----
GI_121709507_A_clavatus	(104)	R-NLLMMHHHDPOYNVEIGKWNESG--VMGTVPYTISNQ-----
GI_169772307_A_oryzae	(104)	K-NRFSMLNHDPRYKVEIGKWOESG--TMGTVPYVAIKDE-----
GI_169777319_A_oryzae	(107)	K-KFKVQEKYKT-YRVEVGPWNSYG-GALGNVDVEISRKRA-----
GI_152985646_P_aerug	(91)	TQTRHFTPASQN-YAGISSGGNATG-AASARSP-----
GI_15595320_P_aerugin	(99)	TNTHSFTPASAD-YAGITSGGNATG-TDICEVTETLGRFS-----
GI_2292820_C_bif	(116)	--KLTDKYNTK-FAIEQSPTMISSSGAIGDYNLKVSKIWA-----
GI_2292821_C_bif	(116)	--KFEERDKNPN-FIIEPTYPTMISSSGAIGDYNIRVFRF-----
AfIP-1A-31	(110)	SDELTVKDKEN--YTVIKKGGGSPS-GATENIFTTVVKKS-----
AfIP-1A-15554	(110)	SDELTVKDKEN--YTVIKKGGGSPS-GATENIFTTVVKKS-----
AfIP-1A-27066	(110)	SDELTVKDKEN--YTVSKKGGGSPS-GATENIFTTVVKKS-----
AfIP-1A-33585	(110)	SDELTVKDKEN--YTVSKKGGGSPS-GATENIFTTVVKKS-----
SLIN6118	(97)	SCSLIPGEQENKLYKTARQWSGLTS-GPLGTITLSCVKLL-----
FGTW-51	(104)	SHSLSVTQDND--YKIDKEGGSNID-GALGNIRETCIKVG-----
GI_186897694_H_annosum	(100)	N-TFTVSGSNSK-NMIEYSGQNLDS-GALGTISV-----
GI_54312022_P_ostreatus	(101)	N-TWTVSGSNTK-NMIEYSGQNLDS-GALGTITVDTLKGKN-----
GI_60461919_P_ostretus	(100)	N-SNVVGGSNSK-NMIEYTGQNLDS-GALGTITVNTLKGKN-----
GI_238581050_M_pern	(101)	N-TWTVSGSNSK-NMVEHQGANLYG-GALGTITVDAMKGKN-----
GI_24636240_A_aegerita	(108)	N-TWTPSGSNTK-NMVEWSSQNLDS-GALGTITVDVLRKGKN-----
GI_90639437_T_versicolor	(138)	N-KNSVSGSLSG-WDVYDKGANIDS-GALGNITETTVYKG-----
GI_145230219_A_niger	(102)	N-QFRYDRIADD-YWVETGYWQSG-GAIGSVTVEIGRRDRAIRSSL---
GI_70985747_A_funigatus	(103)	N-DFDVGERNKN-YWVIGTWNKYG-GAIGTVDVVEVGRKR-----
GI_158524422_R_australe	(62)	N-DFQIRNINRD-YGITLGOWNRDS-GALGKYVDVDFSLWLEDVLGKKLW
GI_26112720_B_vulgaris	(99)	N-NFHIRNINKD-YGITPSOWNRDS-GALGRVNDI-----
GI_46507636_L_multiflo	(99)	N-NFQIQNRNKD-YGITLGOWNRDS-GALGEVDVDISRKG-----

Fig. 3C

	201	244
GI_115390458_A_terreus (153)	-----	-----
GI_67522192_A_nidulans (93)	GGLRVFEGPGVGEKSVDVDVAEEVPVLGGLGGIGGNITMGGFIS	-----
GI_145256342_A_niger (143)	-----	-----
GI_169785219_A_oryzae (142)	-----	-----
GI_119487614_N_fischeri (140)	-----	-----
GI_121709507_A_clavatus (140)	-----	-----
GI_169772307_A_oryzae (140)	-----	-----
GI_169777319_A_oryzae (145)	-----	-----
GI_152985646_P_aer (122)	-----	-----
GI_15595320_P_aer (137)	-----	-----
GI_2292820_C_bif s (154)	-----	-----
GI_2292821_C_bif (153)	-----	-----
AfIP-1A-31 (147)	-----	-----
AfIP-1A-15554 (147)	-----	-----
AfIP-1A-27066 (147)	-----	-----
AfIP-1A-33585 (147)	-----	-----
SLIN6118 (136)	-----	-----
FGTW-51 (141)	-----	-----
GI_186897694_H_annosum (131)	-----	-----
GI_54312022_P_ostreatus (139)	-----	-----
GI_60461919_P_ostretus (138)	-----	-----
GI_238581050_M_pern (139)	-----	-----
GI_24636240_A_aegerita (146)	-----	-----
GI_90639437_T_vers (175)	-----	-----
GI_145230219_A_niger (146)	-----	-----
GI_70985747_A_funigatus (140)	-----	-----
GI_158524422_R_australe (109)	LQSRSKLT-----	-----
GI_26112720_B_vulgaris (132)	-----	-----
GI_46507636_L_multi (136)	-----	-----

Fig. 4

		1		50
AfIP-1B-32	(1)	MDIEAKSINPLMGITVGSTVLGNDFKPSVLINPITRMITQKEIEMGMSGK		
FGTW-52	(1)	MKTQIEIVNPFAGVKIGSYVSGNQFSPSVITGDITRMEEVLEVQKYISGR		
		51		100
AfIP-1B-32	(51)	SQYVYTDSLNEGTFIGFSGAYGPSGIKFTSAVAVSVSNATASEYKSIKVS		
FGTW-52	(51)	SNYVYSDKLNEASLGVSAYGVTVGSKLTSSVSAHAGNATASADKSIKLS		
		101		150
AfIP-1B-32	(101)	YNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSIKVLEKFIAARDCSGS		
FGTW-52	(101)	YNISMISGIEYIDFDSLTAEDILNSLKPGPKSLVVDVLEKENTLRDYQQE		
		151		200
AfIP-1B-32	(151)	S-----IEKDELMKEWYKSLONFISSYGDGLVVGAIWGGMG		
FGTW-52	(151)	NNLSLFDNNMSFIQDARQDELVDWLKALNYFYQTYADGMVVGVIWGGIG		
		201		250
AfIP-1B-32	(187)	SVSTEMTSKKTEDSWKYGETAEFSYSGIGSSVSTIAQTYNGSQKDQSSEVE		
FGTW-52	(201)	GVSMDIGRSSYEKNWTYGGQADFTYSGTGAAVSVAATYNGKQSDKGTSD		
		251		300
AfIP-1B-32	(237)	VSCKALASGGCVESQVNSWFDVVANKSFAEISGISLLDKAPMQSSVSPPP		
FGTW-52	(251)	VSCSSFSSGTCVVNQVNEWFKVVENKAYSEITDLKLLDSAPAQGGVKPPP		
		301		350
AfIP-1B-32	(287)	KIPDFIKPEKNAEITEKLDTIKKLGDSEEFALASGYEEAKKTNPNITFEE		
FGTW-52	(301)	PLPPFVVPKKDPAIEHKLAKIGRLGNTTEELSMSGYDKAKKDDSSMTPEK		
		351		400
AfIP-1B-32	(337)	FKSTVRDKNNIDGLNELASKVQENSIDVLAEGSISRKNKNSLQGVRTIS		
FGTW-52	(351)	FKEKTRQNSLDKLTELEIKLGNQLDVLLDINKVISVE--SPSFEPAM		
		401		450
AfIP-1B-32	(387)	LDSSSDYAVLGAWIANWSDIFPWSMGYMNESDAEVAEYILKIRCMMD		
FGTW-52	(399)	ADNHSGFVPLGVWIVNWADIFPWLSTGYLNDISDTAAAEALKKRCMMD		
		451		500
AfIP-1B-32	(437)	LSTLNTIYNTFNACNIKIDFCHLNSASQVADSFKIAQGVLSDNVESDDAY		
FGTW-52	(449)	FCTLSSIYNTFHSSGIKMEG-KLDAPDQIANAFSNALTILKDNQDQDNT		
		501		550
AfIP-1B-32	(487)	EIAFNSLSDEAKKIYTAWNEIGFLRNAELGLGLIG-DQSVSSEIIVDKP		
FGTW-52	(498)	QQAYDRLGSDAQGIYKIWNHNGFLRNAELGFGLMFDTNRSISSTYDRVKG		
		551		600
AfIP-1B-32	(536)	IPYPEVTYKAAYSYGNNTAFSSFIKMLPFIDTNGDIYAFGPSIMLLR		
FGTW-52	(548)	VPHPEVVYKSEYCSFDKVNYHAFKSMKVLPIIDLGNVYAFGPSAMLLK		
		601		650
AfIP-1B-32	(586)	KALPEKMIFTKGEMAMKLTADKDTGILTNDVVKLIPIPYSAAKGI-QWR		
FGTW-52	(598)	NTINNEVTFTKSVLTAMRFEIDKDNKILKNSTTKLYPIPCSAAKGINDWK		
		651		700
AfIP-1B-32	(635)	GQGQGRSLASSQSLQDQFAALEKELGNLNICLSSDSWSKDWTYTVPYTL		
FGTW-52	(648)	GPGVGINLSSSKSLSDQLEALRNELLKLNCSVSSDKWNPVWQYTDPYHL		
		701		720
AfIP-1B-32	(685)	RKISTTYIGTVEKINSIFG-		
FGTW-52	(698)	KEMGTSYIGLVNKTAKTIFP		

Fig. 5

		101		150
GI_49175503_Bt_Cry34A_	(1)	-----	INNKRHTLQL	
Cry34Aa2_AAK64560	(1)	-----	MSAREVHIEINNKRHTLQL	
Cry34Ba1_AAK64566	(101)	IIENNNGKILTAGTGQSLGLLYLTDEIPEDSNQQWNLTSIQTISLPSQPI		
AfIP-1A-31	(1)	-----	MTAKDIATEESKIRAYAQWIEITIFVNSNFK	
SLIN6118	(1)	-----	MAYSEWVEIRIYSENMEIK	
FGTW-51	(1)	-----	MDLNVEVOAQSQWVEIEIFSENMDIE	
Cry34Ac2_AAK64562	(1)	-----	MSAREVHINVNNKTGHTLQL	
Cry34Ac1_AAG50118	(1)	-----	MSAREVHIDVNNKTGHTLQL	
Cry34Ab1_AAG41671	(1)	-----	MSAREVHIDVNNKTGHTLQL	
		151		200
GI_49175503_Bt_Cry34A	(12)	EDKTKLTSGRWRTSPTN	-----	VARDTIKTFVAES-
Cry34Aa2_AAK64560	(21)	EDKTKLSGGRWRTSPTN	-----	VARDTIKTFVAES-
Cry34Ba1_AAK64566	(151)	IDTTLVDYPKYSTTGSIYNGTALQLMGWTLIPCIMVYDKTIASTHTQIT		
AfIP-1A-31	(33)	VEGAYLRWGKFHVPDGDKE	-----	ISPSQINGTIKDE
SLIN6118	(20)	IKNIKLNWGKFYEGPNQDIE	-----	ITAPVLSDAVIKSG
FGTW-51	(27)	IKKAELLWGKFHKPGNKSNE	-----	ISSDTVNKTKISSG
Cry34Ac2_AAK64562	(21)	EDKTKLDGGRWRTSPTN	-----	VANDQIKTFVAES-
Cry34Ac1_AAG50118	(21)	EDKTKLDGGRWRTSPTN	-----	VANDQIKTFVAES-
Cry34Ab1_AAG41671	(21)	EDKTKLDGGRWRTSPTN	-----	VANDQIKTFVAES-
		201		250
GI_49175503_Bt_Cry34A	(42)	-----	HGFMTGIEGIIYFSVNGEAEISLHFDNPYVGSN	---KYDG
Cry34Aa2_AAK64560	(51)	-----	HGFMTGVEGIIYFSVNGDAEISLHFDNPYIGSN	---KCDG
Cry34Ba1_AAK64566	(201)	TTPYYILKKYQRWVLTGSGLSVPAHVKSTFEYENGTDTDQKTSVINTLG		
AfIP-1A-31	(67)	DSYTIASCGRENASSGTEGGFSLYDGDCLVFEYYWDCPWSGSNSDELTVK		
SLIN6118	(54)	EKYTVWSCGRDGASSGTEGSFELYDGDQVARFGWICPWSGANSCLIPG		
FGTW-51	(61)	TKSKIASCGRADTSSGTEGKFEIYHDDKWLATYKNDCPWAGSNSHSLSVT		
Cry34Ac2_AAK64562	(51)	-----	HGFMTGTEGHIYYSINGEAEISLYFDNPYSGSN	---KYDG
Cry34Ac1_AAG50118	(51)	-----	HGFMTGTEGTIYYSINGEAEISLYFDNPYSGSN	---KYDG
Cry34Ab1_AAG41671	(51)	-----	NGFMTGTEGTIYYSINGEAEISLYFDNPYSGSN	---KYDG
		251		300
GI_49175503_Bt_Cry34A	(79)	SSDKAAAYEVIAQGG	---SGDIS	-----
Cry34Aa2_AAK64560	(88)	SSDKPEYEVITQSG	---SGDKSHVTYTIQTVSLRL	-----
Cry34Ba1_AAK64566	(251)	FQINTDTKLKATVPEVGGGTDIRTQITEELKVEYSSSENKEMRKYKQSF		
AfIP-1A-31	(117)	DKEN--YTVIKKGGGSPSGATGNIFITVVKKS	-----	
SLIN6118	(104)	EQENKLYKTARQWSGLTSGPLGTITLSCVKLL	-----	
FGTW-51	(111)	QDND--YKIDKEGGNISDGALGNIRITCIKVG	-----	
Cry34Ac2_AAK64562	(88)	HSNKPQYEVTTQGG	---SGNQSHVTYTIQTASSRYGNNS	-----
Cry34Ac1_AAG50118	(88)	HSNKNQYEVITQGG	---SGNQSHVTYTIQTVSSRYGNNS	-----
Cry34Ab1_AAG41671	(88)	HSNKSQYEIITQGG	---SGNQSHVTYTIQTTSSRYGHKS	-----

Fig. 6

		451		500
AfIP-1A-31	(1)	-----MTAKDIATEESKIRAYAQWIEITIFV		
FGTW-51	(1)	-----MDLNVEVOAQSQWVEIEIFS		
SLIN6118	(1)	-----MAYSEWVEIRIYS		
Cry3A	(451)	DSIDQLPPETTDEPLEKGYSHQLNYVMCFMQSGRGTI PVLTWTHKSVDF		
		501		550
AfIP-1A-31	(27)	VNSNFKVEGAYLRWGKEHVPGDKDKEISPSQINGTI IKDED-----		
FGTW-51	(21)	ENMDIEIKKAELLWGKEFKPGNKSNEISSDTVNKTKISSGT-----		
SLIN6118	(14)	ENMEIKIKNIKLNWGKEYEGPNQDIEITAPVISDAVIKSGE-----		
Cry3A	(501)	FNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIIY		
		551		600
AfIP-1A-31	(68)	-----SYTIASCGRENASSGTEGGFSLYDGDKL VFEYYWDCPWSGSNSDE		
FGTW-51	(62)	-----KSKIASCGRADTSSGTEGKFEIYHDDKWLATYKWDCPWAGSNHS		
SLIN6118	(55)	-----KYTVWSCGRDGASSGTEGSFELYDGD TQVARFGWICPWSGANSCS		
Cry3A	(551)	VTPDVSYSQYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT		
		601		644
AfIP-1A-31	(113)	LTVKDKEN--YTVIKKGGGSPSGATGNIFTIVVKKS-----		
FGTW-51	(107)	LSVTQDND--YKIDKEGGNISDGALGNIRITCIKVG-----		
SLIN6118	(100)	LIPGEQENKLYKTARQWSGLTSGPLGTITLSCVKLL-----		
Cry3A	(601)	YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN		

Fig. 7

		1	50
AfIP-1B-32	(1)	MDIEAKSINPLMGITVGSTVLGN--DFKPSVLINPITRMITQKEIEMGMS	
Cry3A	(1)	MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDENYKEFLRMTA	
		51	100
AfIP-1B-32	(49)	GKSQYVYTDSLNEGTFSGAYGPSGIAKFTSAVAVSVSNATASEYKSIK	
Cry3A	(51)	DNN----TEALDSSTTKDVIQKGISVVGDLLGVVGFPPFGALVSFYTNFL	
		101	150
AfIP-1B-32	(99)	VSYNISMISGIEYIDFDNLTVEDVLNSLSAGPKNLSLKVLEKFTIAARDCS	
Cry3A	(97)	NTIWPSQDPWKAFMEQVEALMDQKIADYAKNKALAELOGLQNNVEDYVSA	
		151	200
AfIP-1B-32	(149)	GSSIEKDELMKEWVKS-----LQNFISSYGDGLVVGAIWGGMGSVSTE	
Cry3A	(147)	LSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLFLT	
		201	250
AfIP-1B-32	(192)	MTSKKTEDSWKYGETAETSYSGIGSSVSIAQTYNGSQKDQSSSEVEVSCKA	
Cry3A	(197)	YAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKR-QLKLTQEYTDHCVK	
		251	300
AfIP-1B-32	(242)	LASGGCVESQVNSWFDVVANKSTAEISGISLLDKAPMQSSVSPPPPIP	
Cry3A	(246)	WYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR-----L	
		301	350
AfIP-1B-32	(292)	LKPEKNAETTEKEDTIKKLGDSEEFALASGYEEAKKTNPNTTFEEFKSTV	
Cry3A	(291)	YPKEVKTELTRDVLTDPIVGVNNLRGYGT-----TFSNIENYI	
		351	400
AfIP-1B-32	(342)	RDKNNIDGLNELASKVQENSLDVLAEGSISRKNLSLQGVRTISLDSSS	
Cry3A	(329)	RKPHLFDYLHRIQFHTR-----FQPGYYGNDSFNYWSGNYVSTRPSIGS	
		401	450
AfIP-1B-32	(392)	DYAVLGAWIANWSDIFPWMSMGYMNEISDAEVAEYILKIRCMMQDLSTLN	
Cry3A	(373)	NDIITSPFYGNKS-SEPVQNLEFNGEKVYRAVAN-----TNLA	
		451	500
AfIP-1B-32	(442)	TIYNTFNACNIKLEDFCHLNSASQVADSFKIAQGVLSDNVESDDAVEIAFN	
Cry3A	(410)	VWPSAVYSGVTKVEFSQYNDQTEASTQTYDSKRNVGAVSWDSIDQIPPE	
		501	550
AfIP-1B-32	(492)	SLSDEAKKIYTAWNEIGFLRNAELGLGLLIGDQSVSSEIIDVKPIPYPEV	
Cry3A	(460)	TTDEPLEKGYSHQLNYVMCFLMQSGRGTIPVLTWTHKSVDFNMIIDSKKI	
		551	600
AfIP-1B-32	(542)	TYKAAYCSYGNNNPTAFSSFIKMLPFIDTNGDIYAFGPSLMLLRKALPEK	
Cry3A	(510)	TQLPLVKAYKLOS-----GASVVAGPRETGGDIIOCTENGSAAT	
		601	650
AfIP-1B-32	(592)	MIFTKGGEMAMKLTADKDTGILINDSVKLIPIPYSAAKGIQWRGQGGGRS	
Cry3A	(549)	IYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDT	
		651	700
AfIP-1B-32	(642)	LAS-SQSLQDQFAALEKELGNLNICTLSSDSWSKDNTYTVPTLRKISTT	
Cry3A	(599)	LTYNSEFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN----	
		701	713
AfIP-1B-32	(691)	YIGTVEKINSIFG	
Cry3A	(645)	-----	

Fig. 8

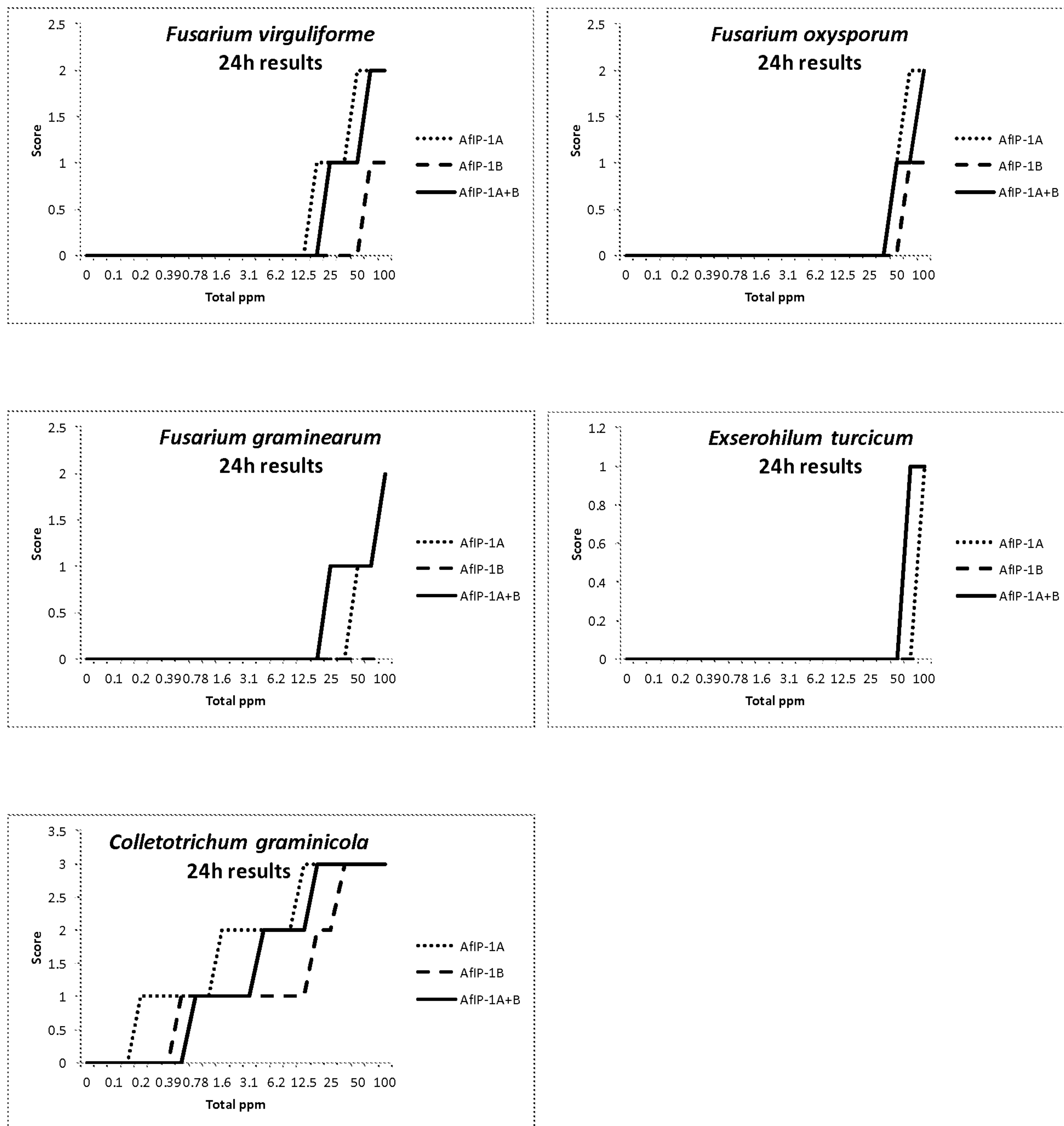


Fig. 10

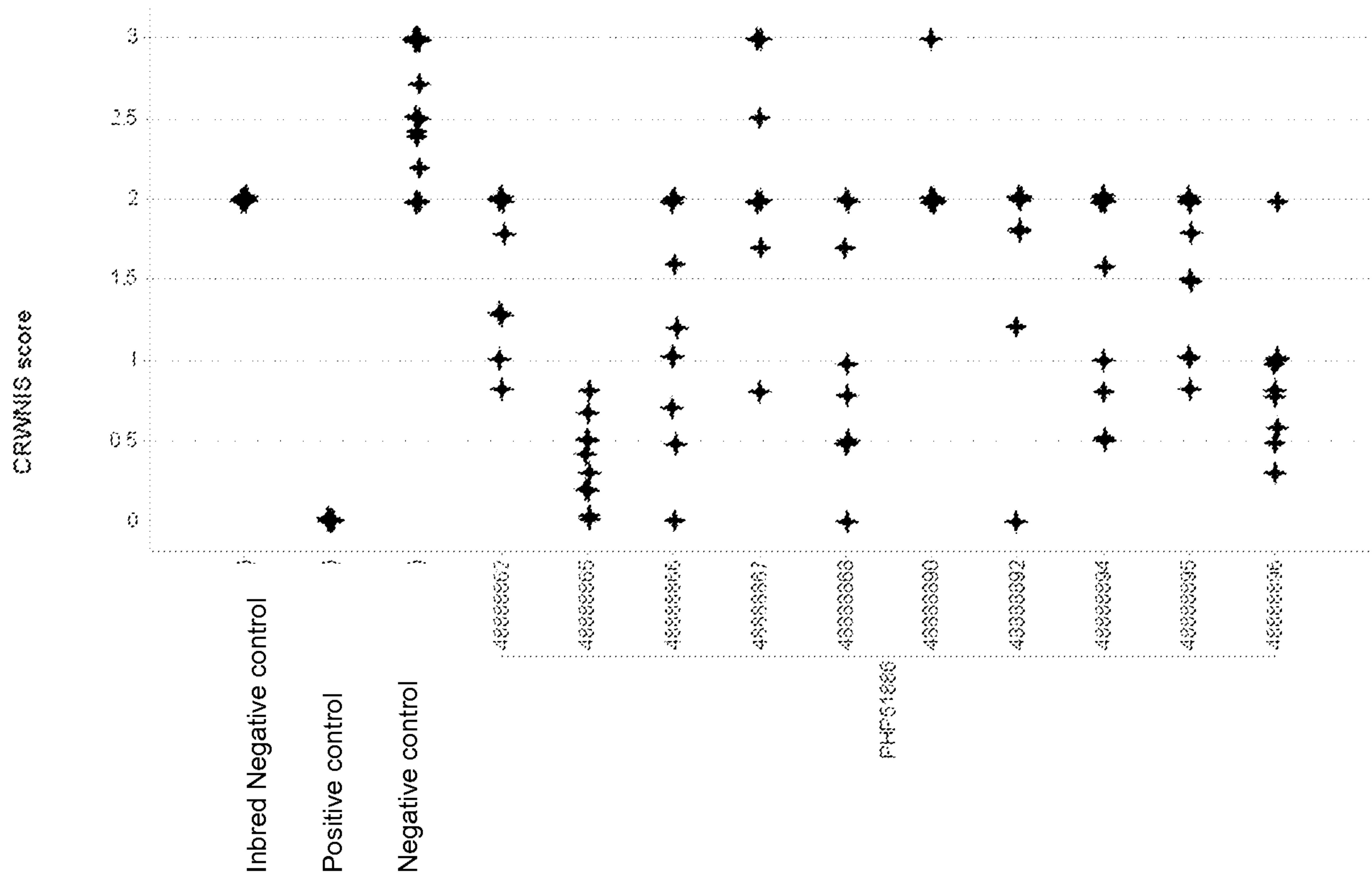


Fig. 11

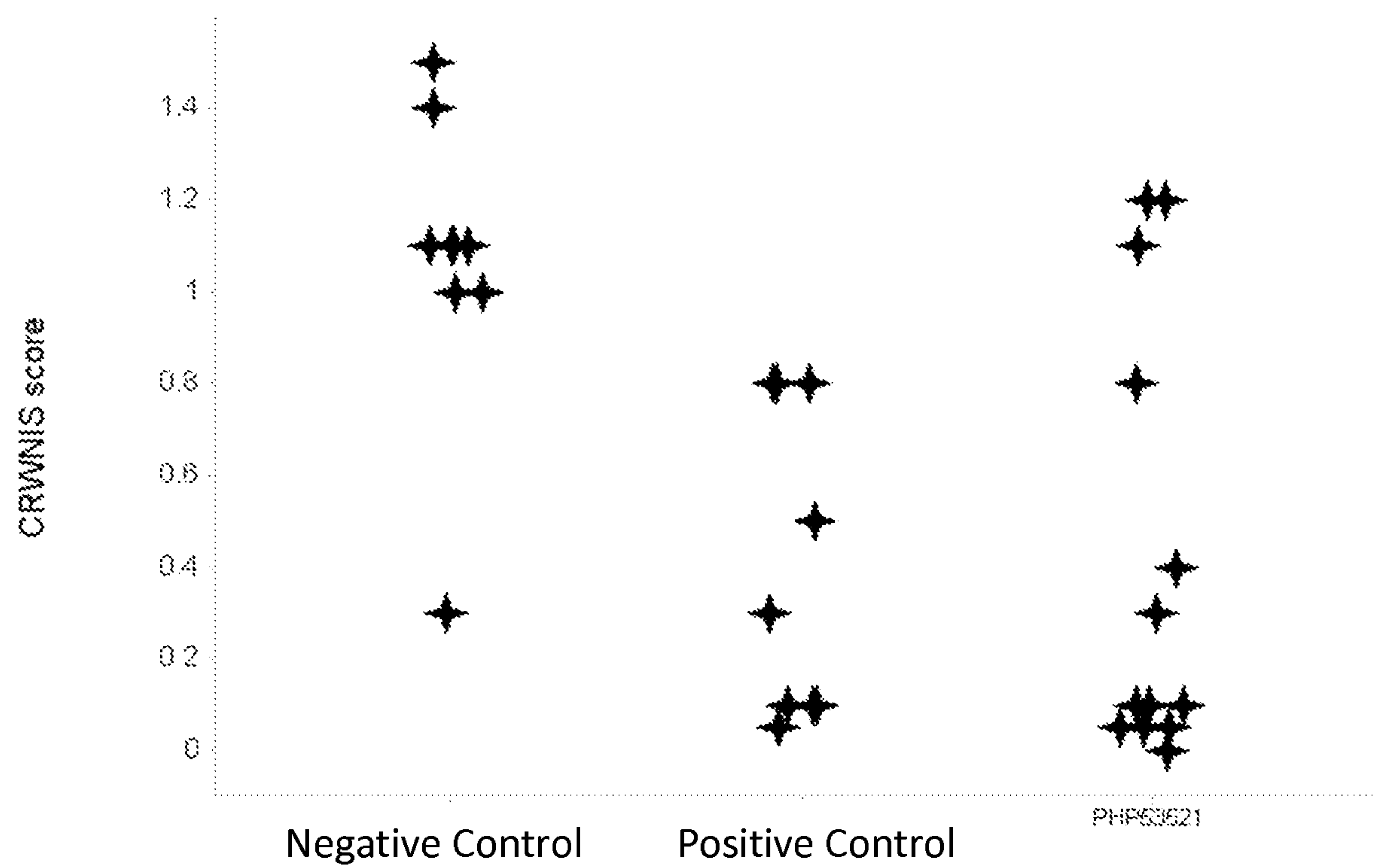


Fig. 12

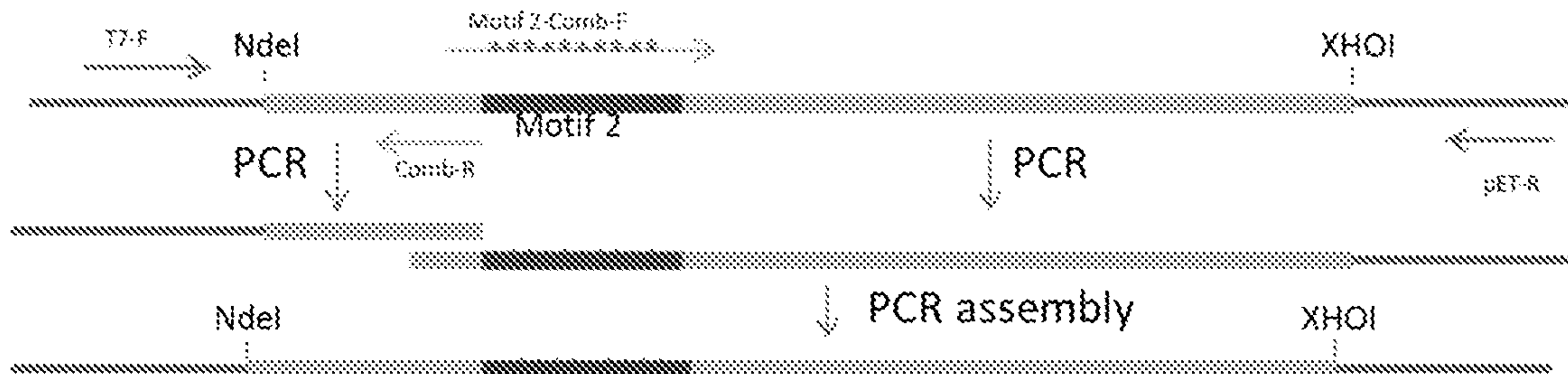
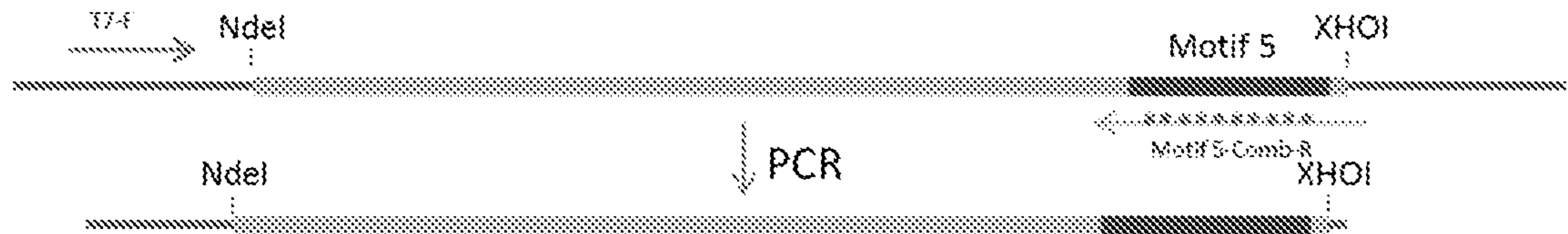
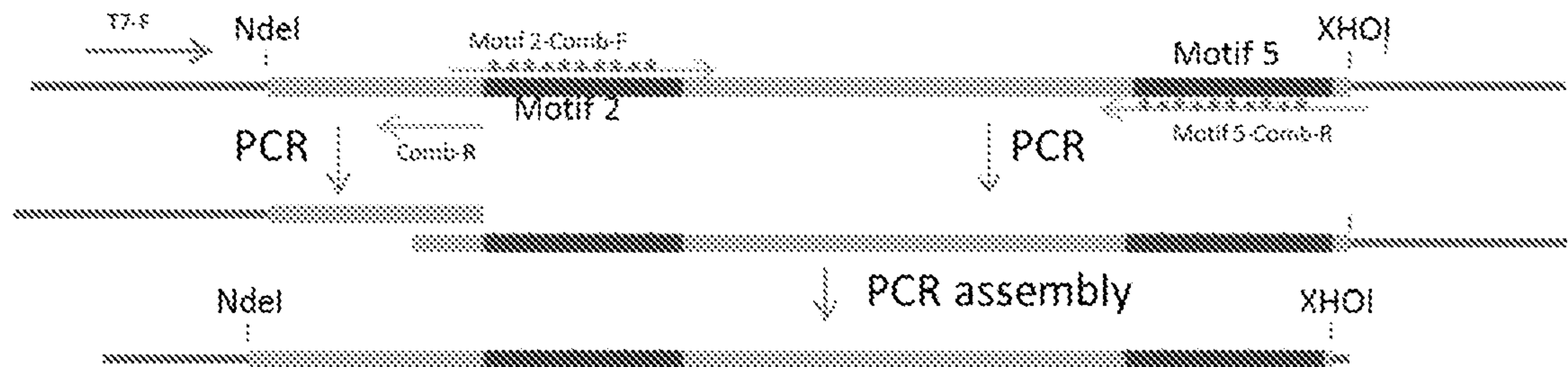
Motif 2 combinatory mutagenesisMotif 5 combinatory mutagenesisMotif 2+5 combinatory mutagenesis

Fig. 13

Motif 5 Cloning strategy

