

spot	GenBank accession ^a	Description ^a	organism ^b	predicted MW ^c	peptide hits MS blast ^d	MS BLAST score ^e
1	ACL36977.1	putative ecdysone oxidase	<i>Helicoverpa zea</i>	63,8	3	181
2	EDV38464.1	GF19436	<i>Drosophila ananassae</i>	132,8	8	431
3	ACC94296.1	glucose oxidase-like enzyme	<i>Helicoverpa armigera</i>	66,9	19	1152
4	BAI49425.1	neuroglian	<i>Mythimna separata</i>	140	7	375
5	XP_001603338.1	PREDICTED: hypothetical protein	<i>Nasonia vitripennis</i>	76,1	1	67
6	XP_001946039.1	PREDICTED: similar to AGAP008350-PA	<i>Acyrtosiphon pisum</i>	154,1	7	297
7	XP_311557.4	AGAP010390-PA	<i>Anopheles gambiae str. PEST</i>	81,9	3	276
8	XP_002031106.1	GM24208	<i>Drosophila sechellia</i>	71	13	884
9	ABU98615.1	fructosidase	<i>H. armigera</i>	54	10	712
10	ACI32835.1	serine proteinase-like protein 1	<i>H. armigera</i>	46,5	5	388
11	ABU98615.1	Fructosidase	<i>H. armigera</i>	54	11	693
12	ABU98617.1	unknown	<i>H. armigera</i>	29,9	6	391
13	ABV74209.1	serpin-6	<i>Bombyx mori</i>	46,4	5	323
14	ABW03226.1	beta actin	<i>Xestia c-nigrum</i>	41,8	7	442
15	EAL40833.3	AGAP002826-PA	<i>A. gambiae str. PEST</i>	23,2	1	67
16	ACT80221.1	ATP synthase FO subunit 6	<i>Mayetiola destructor</i>	25,8	3	126
17	AAK52495.1	AF361483_1 chymotrypsin inhibitor Cl-8A	<i>B. mori</i>	43,8	5	292
18	BAG38534.1	14-3-3 epsilon	<i>B. mori</i>	29,6	6	398
19	AAA68242.1	juvenile hormone binding protein	<i>Heliothis virescens</i>	26,8	4	224
20	EDS42418.1	conserved hypothetical protein	<i>D. erecta</i>	16,8	9	301
21	ACR07788.1	14-3-3 zeta	<i>H. virescens</i>	28	12	796
22	XP_973769.1	PREDICTED: similar to Elongation factor 1 beta CG6341-PA	<i>Tribolium castaneum</i>	29,2	4	221
23	XP_973117.1	PREDICTED: similar to proteasome zeta subunit	<i>T. castaneum</i>	26,4	2	198
24	XP_002429704.1	glucose dehydrogenase, putative	<i>Pediculus humanus corporis</i>	73,7	2	121
25	XP_001943976.1	PREDICTED: similar to viral A-type	<i>A. pisum</i>	199,8	4	179
26	XP_395299.2	PREDICTED: similar to Translationally controlled tumor protein CG4800-PA isoform 1	<i>Apis mellifera</i>	19,7	4	339
27	AAB32409.1	18 kda serine proteinase inhibitor	<i>H. zea</i>	3	1	63
28	EAT44854.1	initiation factor 5a	<i>Aedes aegypti</i>	17,5	2	115
29	EDW67351.1	GJ23129	<i>Drosophila virilis</i>	110,4	1	68
30	ABU98615.2	Fructosidase	<i>H. armigera</i>	54	1	68
31	P82171.1	CU095_LOCM1 RecName: Full=Cuticle protein 9.5;	<i>Locusta migratoria</i>	9,5	5	187
32	ABB04499.1	SUMO	<i>B. mori</i>	10,3	2	112
33	ABC96694.1	yellow-d	<i>B. mori</i>	50,3	4	503
34	XP_001649322.1	proacrosin, putative	<i>A. aegypti</i>	42	4	212
35	ABX57148.1	arginine kinase	<i>Archicaris parthenias</i>	22,6	16	822
36	ABX57154.1	arginine kinase	<i>Macrosoma tipulata</i>	22,6	7	445
37	ACI32835.1	serine proteinase-like protein 1	<i>H. armigera</i>	46,5	9	725
38	CAC88582.1	unnamed protein product	<i>H. virescens</i>	32	8	562
39	C1JE15.1	SCLXB_HELVI RecName: Full=Scolexin B; Flags:	<i>H. virescens</i>	30,5	6	306
40	EDW90053.1	GE13058	<i>Drosophila yakuba</i>	62	2	113
41	NP_001155191.1	silk gland derived serine protease	<i>B. mori</i>	42	6	276
42	ABM90638.1	6-phosphogluconolactonase	<i>B. mori</i>	25,9	3	182
43	XP_002007655.1	G112260	<i>Drosophila mojavensis</i>	29	3	148
44	XP_002093710.1	GE20611	<i>D. yakuba</i>	43,8	6	265
45	XP_968982.1	PREDICTED: similar to AGAP001957-PA	<i>T. castaneum</i>	31,3	6	311
46	CAA72953.1	diverged serine protease	<i>H. armigera</i>	27,3	2	171
47	ACV89326.1	triosephosphate isomerase	<i>Nigroria sp.</i>	17,5	2	121
48	ABW96360.1	thioredoxin peroxidase	<i>H. armigera</i>	21,9	6	521
49	XP_001866830.1	conserved hypothetical protein	<i>Culex pipiens</i>	19	5	279
50	AAR09835.1	similar to Drosophila melanogaster tsr	<i>D. yakuba</i>	17,1	7	443
51	XP_001985637.1	GH17180	<i>Drosophila grimshawi</i>	207,9	2	160
52	NP_001093087.1	mobility group protein 1B	<i>B. mori</i>	13,3	1	95
53	XP_394370.1	PREDICTED: similar to CG5255-PA	<i>Apis mellifera</i>	28	2	113
54	AAM53644.1	abnormal wing disc-like protein	<i>Choristoneura parallela</i>	17	8	574
55	EDV53781.1	GG11332	<i>Drosophila erecta</i>	63,2	1	86
56	CAB55605.1	arylphorin subunit	<i>Spodoptera litura</i>	84,1	6	355
57	CAB55605.1	arylphorin subunit	<i>S. litura</i>	84,1	7	416
58	BAD12426.1	fructose 1,6-bisphosphate aldolase	<i>Antheraea yamamai</i>	39,7	10	660
59	ABU98615.1	fructosidase	<i>H. armigera</i>	54	4	270
60	AAU95199.1	putative glyceraldehyde-3-phosphate dehydrogenase	<i>Oncometopia nigricans</i>	35,6	7	399
61	ABV60323.1	putative glyceraldehyde-3-phosphate dehydrogenase	<i>Lutzomyia longipalpis</i>	35,2	7	485
62	XP_002423913.1	GTP-binding nuclear protein RAN1, putative	<i>Pediculus humanus corporis</i>	49,7	5	351
63	ABK29488.1	promoting protein	<i>H. armigera</i>	8,4	2	146
64	XP_001119897.1	PREDICTED: similar to Cyclophilin 1	<i>A. mellifera</i>	17,8	6	305
65	ACD69576.1	peptidyl-prolyl isomerase-1	<i>Gryllus pennsylvanicus</i>	17,9	3	149