

**Table S14:** The distribution of *Fusarium circinatum*-specific proteins, determined through BLASTp analyses, amongst the Sordariomycetes genomes included in JGI's MycoCosm database.

Query Gene	Species	Protein Name	Location and Position (bp)	E-Value	Alignment Length <sup>a</sup>	Identity (%) <sup>a</sup>	Positives <sup>a</sup>
FCIRG_04559	<i>Nectria haematococca</i>	Necha2_85516	Scaffold 82: 321 452-323 813	0	631	53,41	337
	<i>Colletotrichum graminicola</i>	Colgr1_8656	Supercontig_50: 180 011-182 343	6,10E-140	514	51,95	267
	<i>C. somersetensis</i>	Colso1_562257	Scaffold_5: 5 546-7 862	4,87E-140	529	50,85	269
	<i>C. zoysiae</i>	Colzo1_662029	Scaffold 36: 116 255-118 577	2,43E-139	529	50,66	268
	<i>Glomerella cingulata</i>	Gloci1_06755	Scaffold_3: 3 858 958-3 861 286	6,66E-157	570	50,53	288
	<i>C. falcatum</i>	Colfa1_579345	Scaffold 159: 77 191-79 537	3,12E-145	542	50,37	273
	<i>G. acutata</i>	Gloac1_1604846	Scaffold_5: 349 856-352 862	8,50E-158	562	50,36	283
	<i>G. cingulata</i>	Gloci1_1888518	Scaffold_5: 2 203 672-2 206 213	1,52E-128	512	50,2	257
	<i>C. higginsianum</i>	Colhi1_4201	Supercontig_2 356: 957-3 348	1,62E-128	508	50,2	255
	<i>G. acutata</i>	Gloac1_1649532	Scaffold_50: 2 434-5 397	3,24E-122	506	50	253
	<i>C. somersetensis</i>	Colso1_359207	Scaffold_36: 98 497-99 622	3,15E-123	498	50	249
	<i>C. eremochloae</i>	Coler1_633355	Scaffold_183: 7 254-9 630	7,50E-129	512	49,8	255
	<i>C. sublineola</i>	Colsu1_566281	Scaffold_7: 181 246-183 629	8,36E-130	516	49,61	256
	<i>Ilyonectria sp.</i>	Ilysp1_1670160	Scaffold_11: 451 054-453 831	4,24E-145	560	49,11	275
	<i>C. falcatum</i>	Colfa1_184145	Scaffold_237: 61 036-63 721	5,44E-129	542	48,71	264
	<i>Fusarium graminearum</i>	Fusgr1_02825	Supercontig 3.2: 5 277 911-5 280 156	1,21E-114	532	47,37	252
	<i>Verticillium dahliae</i>	VDAG_07234	Supercontig_1.16: 153 242-155 530	1,50E-126	520	46,54	242
	<i>F. verticillioides</i>	FVEG_13162	Supercontig_2.4: 2 087 517-2 088 685	1,23E-128	550	46,36	255
	<i>Trichoderma asperellum</i>	Trias1_6221256	Scaffold_16: 192 146-194 524	9,42E-118	533	76	247
	<i>F. oxysporum</i> f. sp. lycopersici	FOXG_1517	Supercontig_2.29: 296 837-299 006	1,07E-133	533	46,34	247
<i>F. fujikuroi</i> IMI 58289	Fusfu1_05520	Chromosome 06 : 472 080-474 225	8,35E-129	572	45,8	262	
FCIRG_04558	<i>Trichoderma harzianum</i>	Triha1_82923	Scaffold_5: 1 567 355-1 568 758	5,62E-76	352	40,34	142
	<i>T. virens</i> Gv29-8	TriviGv29_8_2_3_7668	Scaffold_5: 1 353 185-1 354 507	1,00E-75	336	41,67	140
	<i>T. longibrachiatum</i>	Trilo3_65536	Scaffold_5:1 232 601-1 234 007	9,93E-72	336	41,18	136
	<i>T. asperellum</i> CBS 433.97	Trias1_132357	Scaffold_3: 1 656 338-1 657 741	1,77E-75	335	41,49	139
	<i>T. reesei</i> RUT C-30	TrireRUTC30_1_77797	Scaffold_7: 69 152-70 558	2,54E-71	336	40,18	135
	<i>Fusarium oxysporum</i> 4287	FOXG_13046.3	Supercontig 17: 1 278 078-1 279 412	0	407	40,2	231
	<i>F. graminearum</i> PH-1	FGSG_04832.3	Supercontig 3: 400 164-401 498	0	407	40,2	233
FCIRG_04557	<i>Phaeoacremonium aleophilum</i>	Phaal1_778	Scaffold_154: 162 296-163 690	0	389	77,12	300
	<i>Trichoderma asperellum</i>	Trias1_132357	Scaffold_3:1 656 338-1 657 741	0	399	75,69	302
	<i>T. virens</i>	TriviGv29_8_2_37668	Scaffold_5: 1 353 182-1 354 585	0	392	75,51	296
	<i>Metarhizium robertsii</i>	Metan1_2313	Scaffold_002: 2 663 647-2 665 053	0	394	74,62	294
	<i>Niesslia exilis</i>	Nieex1_798650	Scaffold_2: 522 055-523 455	0	412	74,51	307
	<i>T. reesei</i>	TrireRUTC30_1_77797	Scaffold_7: 69 152-70 558	0	401	74,31	298
	<i>T. reesei</i>	Trire2_107172	Scaffold_8: 1 336 705-1 338 111	0	401	74,31	298
	<i>T. harzianum</i>	Triha1_82923	Scaffold_5: 1 567 355-1 568 758	0	399	74,19	296
	<i>T. longibrachiatum</i>	Trilo3_65536	Scaffold_5: 1 232 601-1 234 007	0	401	72,82	292
	<i>M. inundatum</i>	Myrin1_38252	Scaffold_1: 4 180 495-4 182 177	0	407	74,2	302
	<i>T. atroviride</i>	Triat2_223009	Contig_25: 1 334 207-1 335 837	0	399	74,19	296
	<i>Ilyonectria sp.</i>	Ilysp1_1664978	Scaffold_10: 962 471-964 399	0	412	71,84	296
	<i>Ophiostoma piceae</i>	Ophpc1_6776	Scaffold_17: 104 917-106 287	0	378	71,43	270
	<i>Eucalypta lata</i>	Eutla1_1479	Scaffold_1294: 9719-11 119	0	412	68,2	281
	<i>Beauveria bassiana</i>	Beaba1_3102	Scaffold_00006: 1 079 862-1 081 274	1,52E-135	423	66,67	282
	<i>F. oxysporum</i> f. sp. lycopersici	Fusox1_14897	Supercontig_2.52: 93 747-95 379	1,37E-152	365	64,93	237
	<i>Thozetella sp.</i> PMI_491	ThoPMI491_1_631583	Scaffold_1: 1 449 042-1 450 367	7,11E-123	367	53,95	198
	<i>F. graminearum</i>	Fusgr1_5624	Supercontig_3.3: 400 164-401 498	7,65E-118	369	52,85	195
	<i>Ilyonectria sp.</i>	Ilysp1_1522559	Scaffold_5: 663 621-664 931	4,15E-121	366	52,73	193
	<i>F. solani</i>	Necha2_84411	Chromosome 9: Scaffold 27: 269 225-270 547	1,03E-122	373	52,01	194
<i>F. oxysporum</i> f. sp. lycopersici	Fusox1_6035	Supercontig_2.17: 1 278 078-1 279 412	7,64E-116	371	51,48	191	

FCIRG_04556	<i>Fusarium solani</i> v2.0	Necha2_51514	Chromosome 11: 117 201-118 955	0	524	58,78	308
	<i>F. oxysporum</i> v1.0	FOXG1_1091	Supercontig 2.14: 288 749-291 052	0	552	53,99	298
FCIRG_04555	<i>Hypoxyton</i> sp. EC38	HypEC38_1_385672	Scaffold_19: 346 386-348 063	4,94E-162	365	61,92	226
	<i>Hypoxyton</i> sp. CO27-5	HypCO275_1_391925	Scaffold_4: 285 371-286 943	9,50E-162	366	61,48	225
	<i>Hypoxyton</i> sp. CI-4A	HypCI4A_1_51722	Scaffold_3: 990 218-991 612	2,86E-156	364	60,44	220
	<i>Trichoderma longibrachiatum</i>	Trilo3_1392130	Scaffold_8: 280 933-282 444	1,47E-134	363	55,1	200
	<i>T. harzianum</i>	Triha1_490835	Scaffold_2: 2 158 760-2 160 237	1,15E-137	370	54,86	203
	<i>Niesslia exilis</i>	Nieex1_803415	Scaffold_18: 572 636-573 993	3,39E-75	331	42,9	142
	<i>Metarhizium undatum</i>	Myrin1_512013	Scaffold_1: 3 666 365-3 667 773	5,38E-151	369	57,72	213

<sup>a</sup>Given in amino acids.