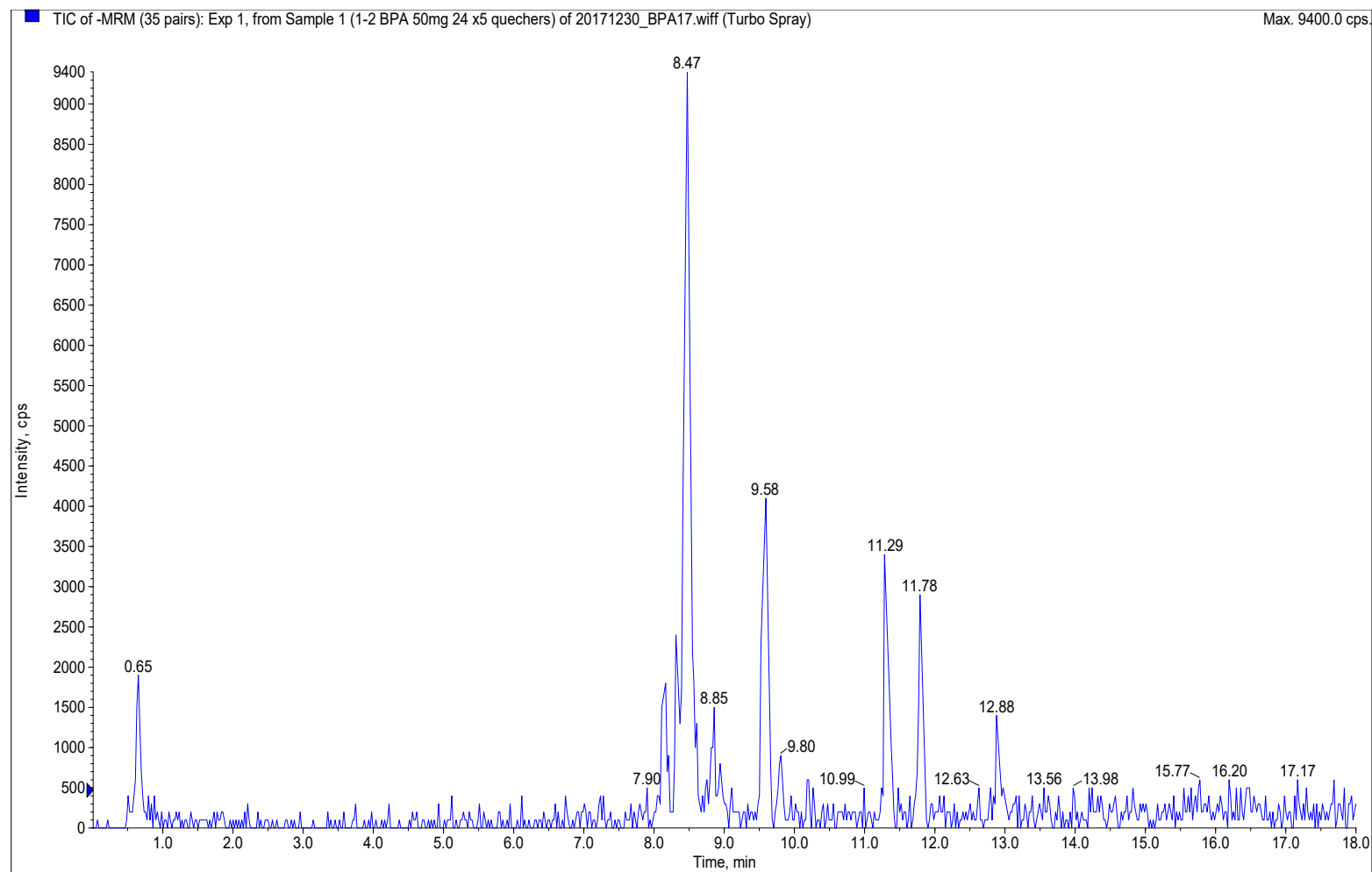
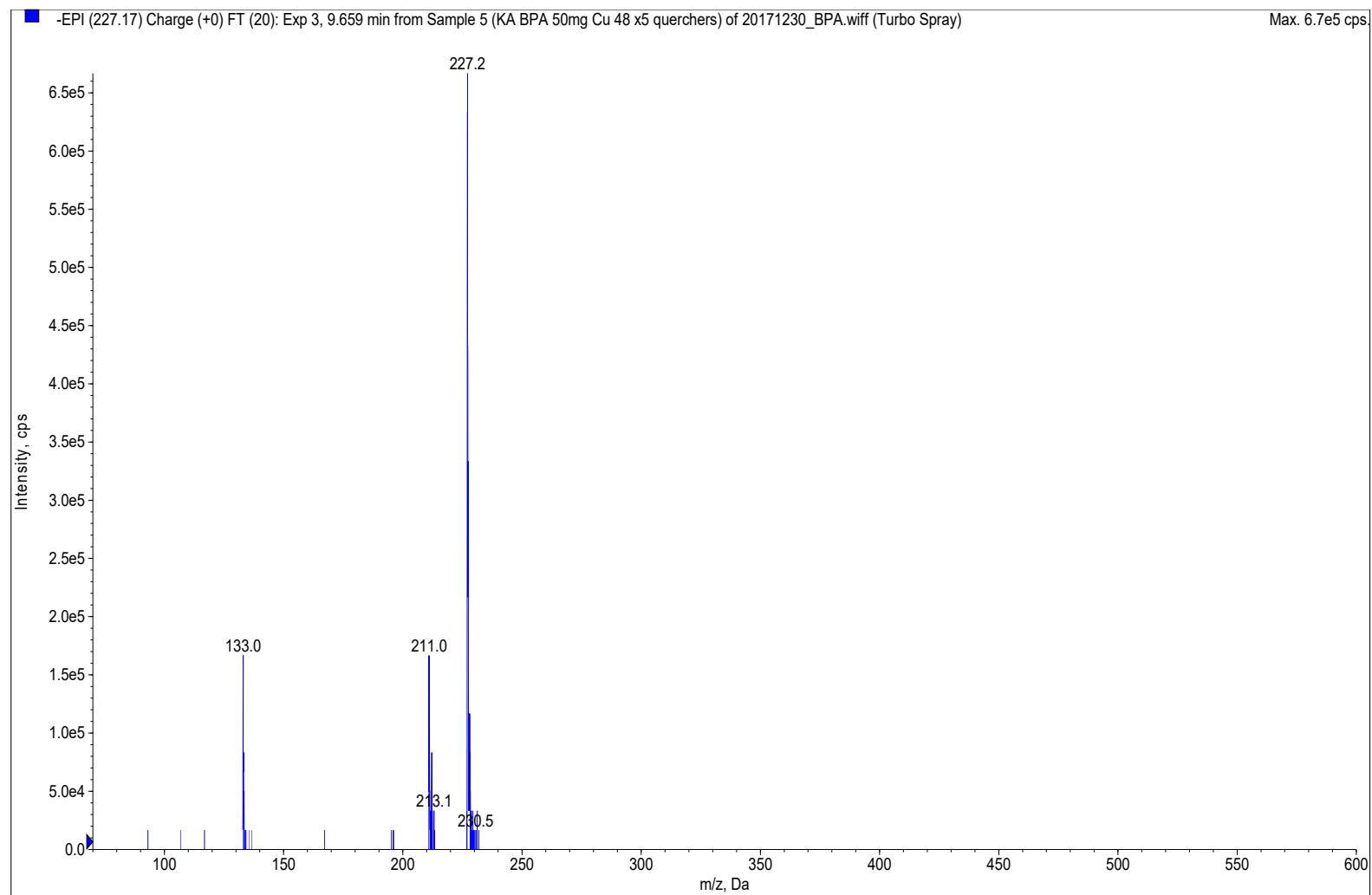


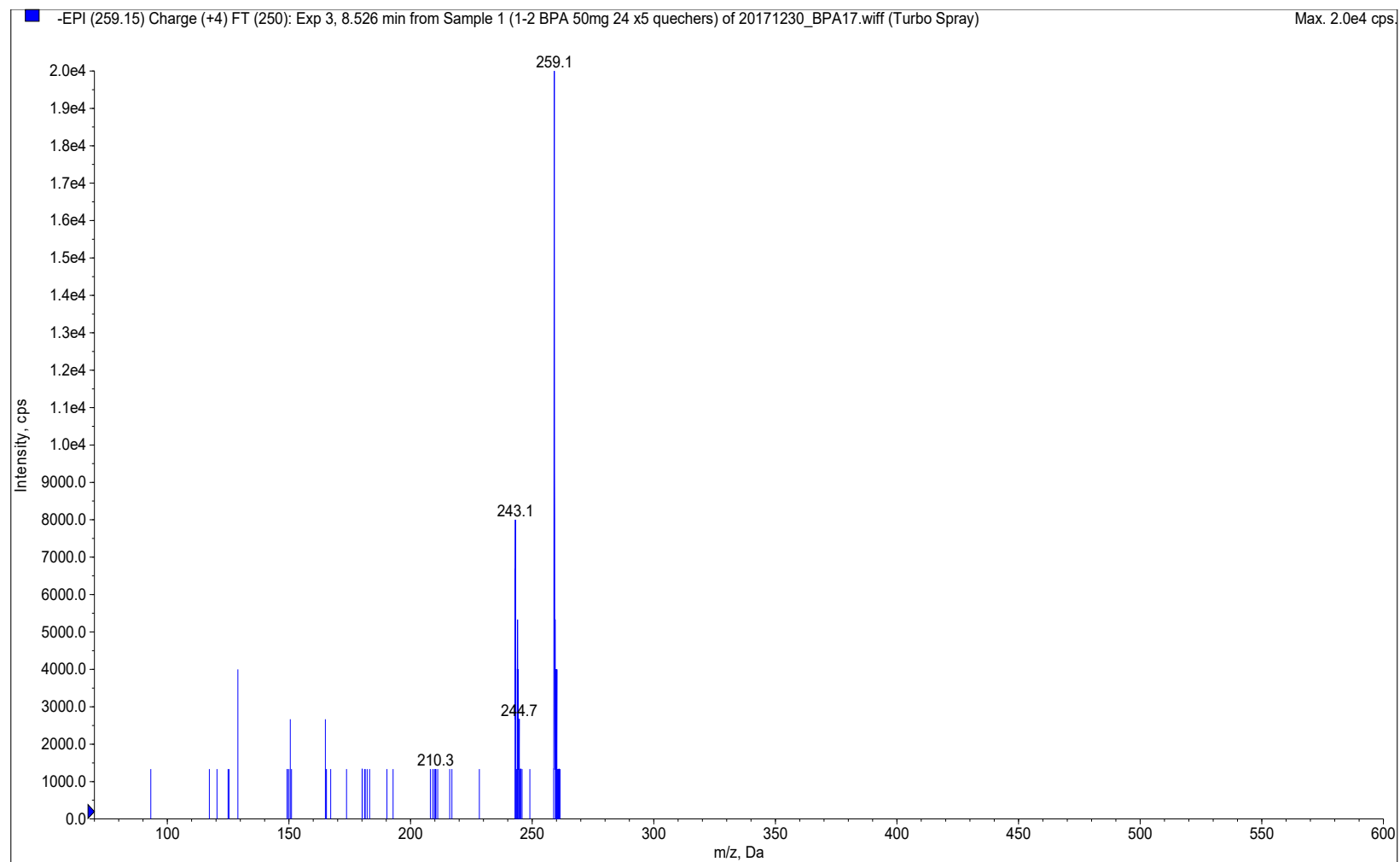
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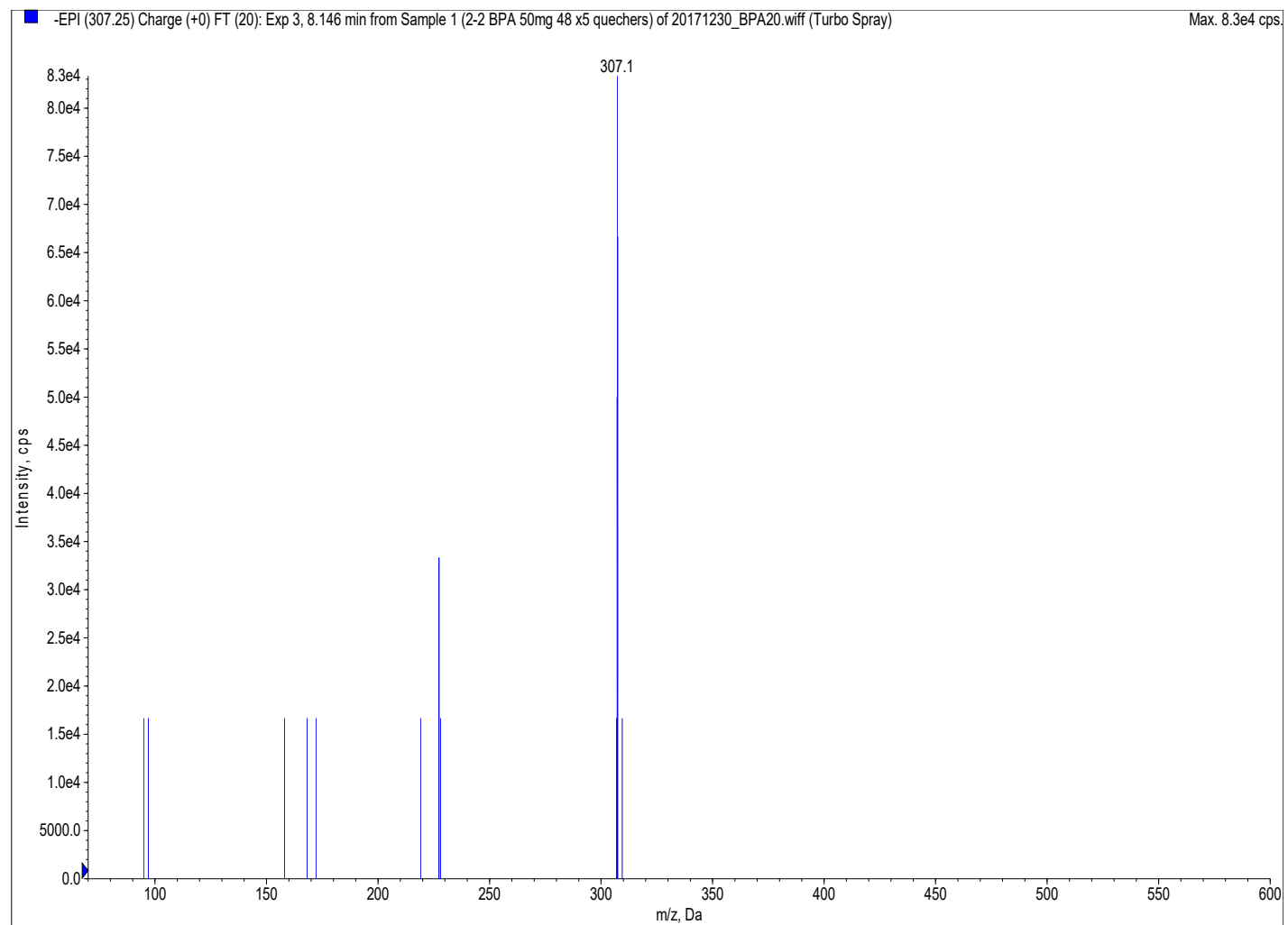
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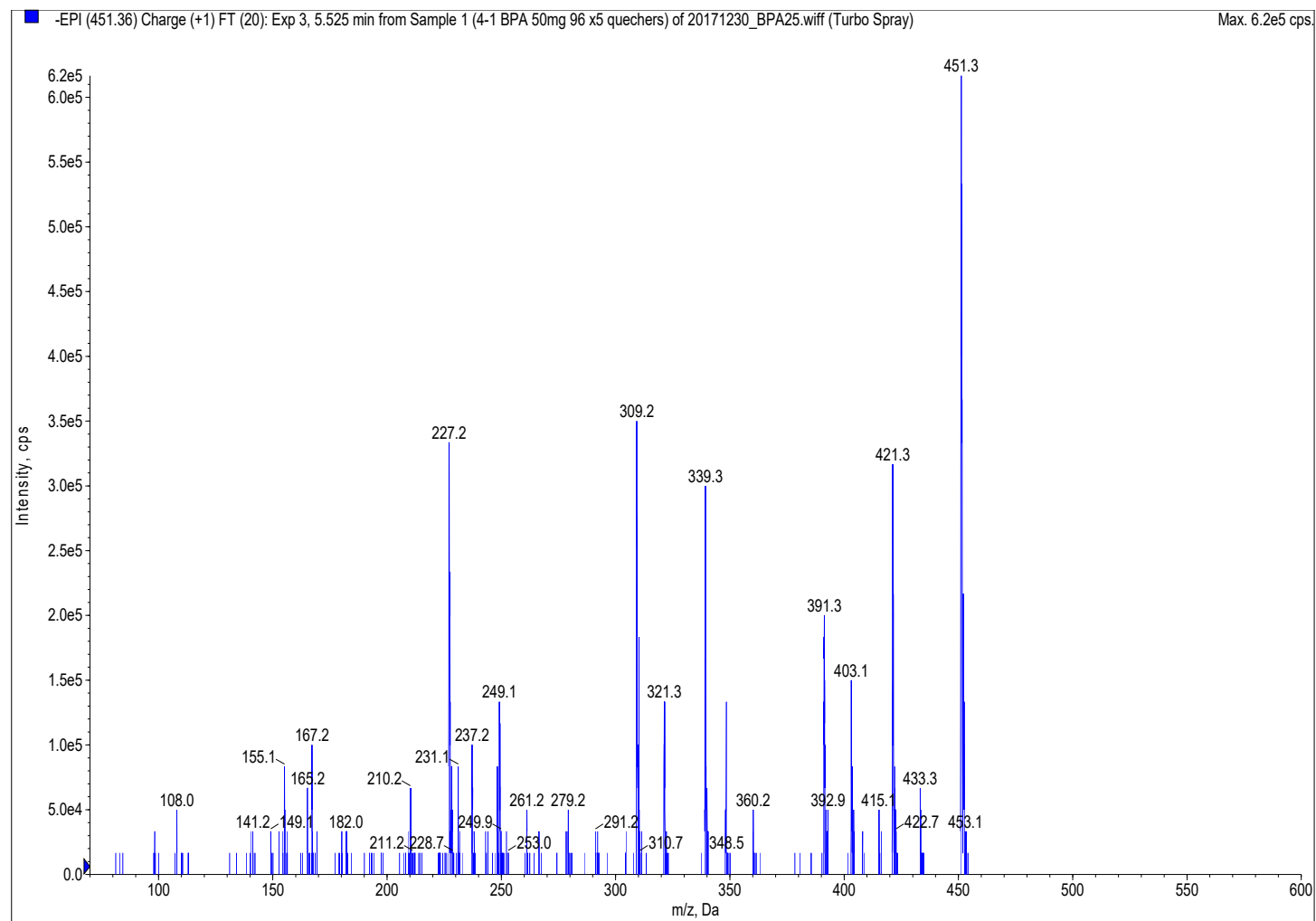
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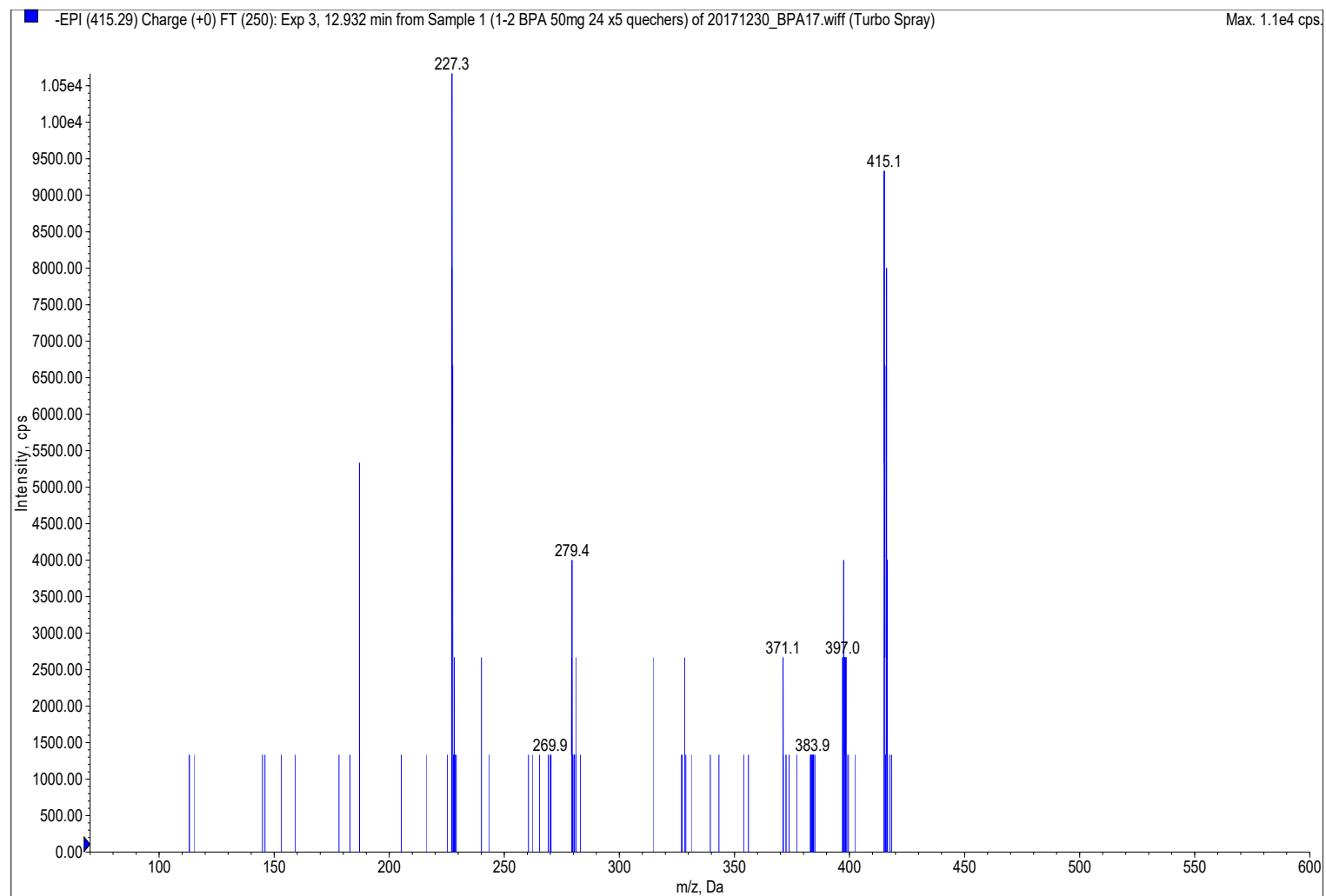
D



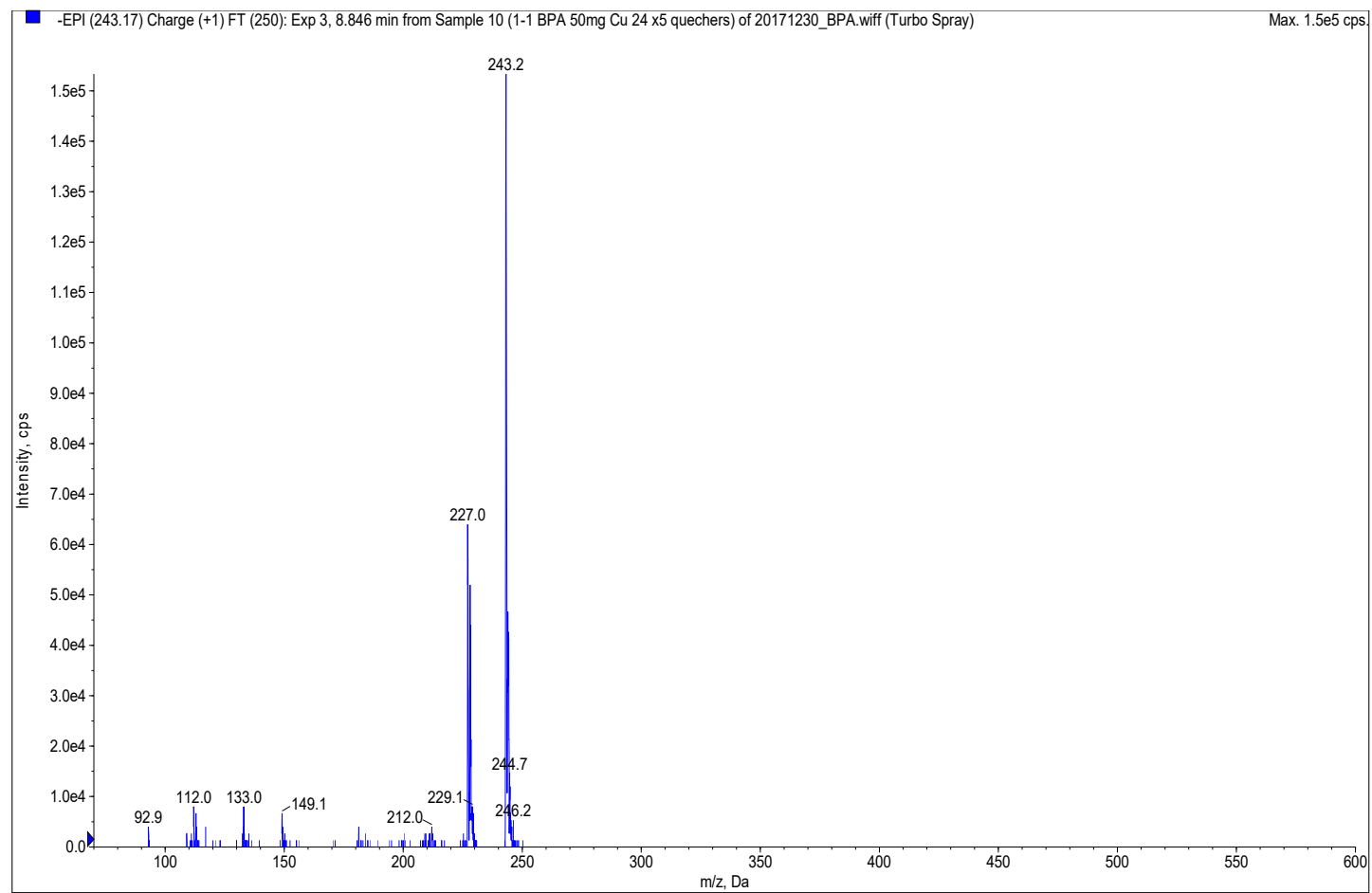
E



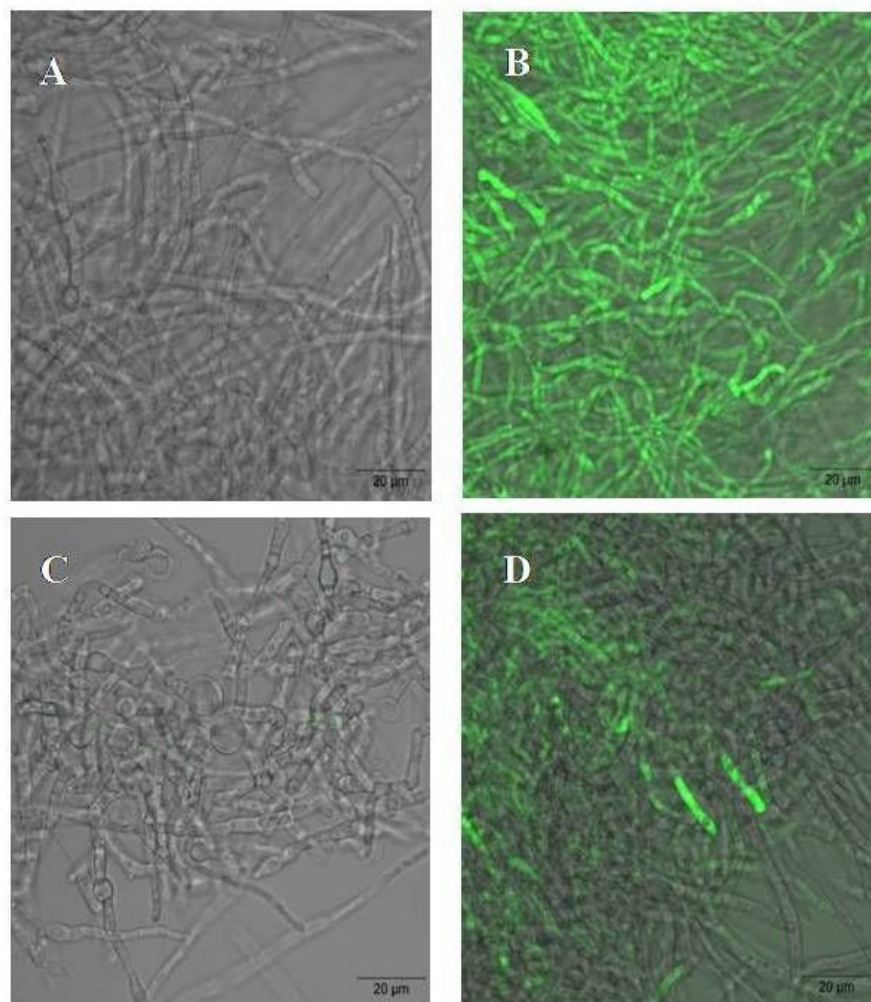
F



G



**Figure S1.** Chromatogram obtained after extraction of *M. roridum* cultures cultivated in Czapek-Dox medium supplemented with 50 mg l<sup>-1</sup> BPA (A) and mass spectra of BPA (B) and its metabolites: M1 (C), M2 (D), M3 (E), M4 (F), M5 (G) formed in fungal cultures.



**Figure S2.** ROS generation in the *M. roridum* cultures. Control without BPA after 24 h (A) and 72 h (C); cultures supplemented with BPA after 24 h (B) and 72 h (D). The hyphal fluorescence indicates ROS generation.





**Tabela S1.** Summary identification of *M. roridum* IM 6482 proteins isolated from control cultures (without BPA).

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
2	PQK16867.1	11454	148	hypothetical protein BB8028_0007g00680	<i>Beauveria bassiana</i>
5	OAA81287.1	19600	121	peptidyl-prolyl cis-trans isomerase	<i>Cordyceps confragosa</i> RCEF 1005
10	EEU44844.1	16912	91	predicted protein	<i>Nectria haematococcamp</i> VI 77-13-4
19	PTD04586.1	28552	79	40S ribosomal protein S3	<i>Fusarium culmorum</i>
22	XP_018656864.2	34018	199	malate dehydrogenase, partial	<i>Trichoderma gamsii</i>
29	XP_018180540.1	59623	92	ATP synthase alpha chain, mitochondrial precursor	<i>Purpureocillium lilacinum</i>
32	PTB35940.1	78531	84	hypothetical protein M441DRAFT_152105	<i>Trichoderma asperellum</i> CBS 433.97
55	KOS18933.1	54440	155	ATP synthase subunit beta	<i>Escovopsis weberi</i>
57	XP_016588082.1	69320	103	heat shock 70kDa protein 1/8	<i>Sporothrix schenckii</i> 1099-18
59	PTB80850.1	47299	80	phosphopyruvate hydratase	<i>Trichoderma longibrachiatum</i> ATCC 18648 0.1
60	ODA79096.1	42721	95	hypothetical protein RJ55_04687	<i>Drechmeria coniospora</i>

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
66	KIL95357.1	77769	155	hypothetical protein FAVG1_00093	<i>Fusariumavenaceum</i>
67	GAO16225.1	72752	103	hypothetical protein UVI_02000080	<i>Ustilagoideavirens</i>
68	PTB80850.1	47299	155	phosphopyruvatehydratase	<i>Trichodermalongibrachiatum</i> ATCC 18648
69	PTB80850.1	47299	146	phosphopyruvatehydratase	<i>Trichodermalongibrachiatum</i> ATCC 18648
70	PTB80850.1	47299	138	phosphopyruvatehydratase	<i>Trichodermalongibrachiatum</i> ATCC 18648
71	ODA77078.1	26963	100	hypothetical protein RJ55_07596	<i>Drechmeriaconiospora</i>
74	POR33248.1	62028	97	Inorganicpyrophosphatase	<i>Tolypocladiumparadoxum</i>
78	XP_018139774.1	31537	174	coatomersubunit epsilon	<i>Pochoniachlamydosporia</i> 170
81	ORY66301.1	43858	128	S-adenosylmethioninesynthetase	<i>Pseudomassariellavexata</i>
86	PTB35940.1	78531	78	hypothetical protein M441DRAFT_152105	<i>Trichodermaasperellum</i> CBS 433.97
88	AID48697.1	37452	200	actin, partial	<i>Neotyphodium</i> sp. NI_201306

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
90	PQK13047.1	30402	84	hypothetical protein BB8028_0003g16610	<i>Beauveria bassiana</i>
91	POR33248.1	62028	98	Inorganic pyrophosphatase	<i>Tolypocladium paradoxum</i>
92	OTA68683.1	25460	149	mitochondrial peroxiredoxin PRX1	<i>Hypoxylon</i> sp. EC38
96	XP_009260797.1	17927	119	hypothetical protein FPSE_09405	<i>Fusarium pseudograminearum</i> CS3096
97	PHH82764.1	18833	78	hypothetical protein CDD82_4929	<i>Ophiocordyceps australis</i>
98	PNY28828.1	26923	125	Actin cross-linking	<i>Tolypocladium capitatum</i>
99	PNY25025.1	13598	201	Profilin	<i>Tolypocladium capitatum</i>
100	XP_018160338.1	17955	156	Cytochrome c oxidase subunit Va	<i>Colletotrichum higginsianum</i> IMI 349063
101	CCE28255.1	16874	90	related to cofilin	<i>Claviceps purpurea</i> 20.1
105	EQL03272.1	36308	110	outer mitochondrial membrane protein porin	<i>Ophiocordyceps sinensis</i> CO18
106	PTD05987.1	16456	112	Nascent polypeptide-associated complex subunit beta	<i>Fusarium culmorum</i>
107	KIL96612.1	10977	75	hypothetical protein FAVG1_01356	<i>Fusarium avenaceum</i>

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
108	AGY49501.1	12583	137	calmodulin, partial	<i>Fusariumandiyazi</i>
109	PTD11202.1	31749	78	14-3-3 protein	<i>Fusariumculmorum</i>
110	PNY29201.1	10793	117	60S acidic ribosomal protein P2	<i>Tolypocladiumcapitatum</i>
111	PTB69803.1	30245	96	14-3-3-like protein	<i>Trichodermacitrinoviride</i>
112	PTB69803.1	30245	96	14-3-3-like protein	<i>Trichodermacitrinoviride</i>

**Tabela S2.** Summary identification of *M. roridum* IM 6482 proteins isolated from cultures containing 50 mg L<sup>-1</sup> BPA.

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
115	PQK15291.1	22856	144	hypothetical protein BB8028_0005g08050	<i>Beauveria bassiana</i>
116	ABQ42572.1	36234	224	glyceraldehyde-3-phosphate dehydrogenase	<i>Myrothecium gramineum</i>
117	PSR79323.1	11114	136	peptidyl-prolyl cis-trans isomerase fkr-3	<i>Coniella lustricola</i>
118	EEU44844.1	16912	173	predicted protein	<i>Nectria haematococcamp</i> VI 77-13-4
119	EEU44844.1	16912	150	predicted protein	<i>Nectria haematococcamp</i> VI 77-13-4
120	OAA81287.1	19600	284	peptidyl-prolyl cis-trans isomerase	<i>Cordyceps confragosa</i> RCEF 1005
121	EEU44844.1	16912	115	predicted protein	<i>Nectria haematococcamp</i> VI 77-13-4
122	PQK16867.1	11454	91	hypothetical protein BB8028_0007g00680	<i>Beauveria bassiana</i>
123	EEU45443.1	37541	475	predicted protein	<i>Nectria haematococcamp</i> VI 77-13-4
124	KFH42761.1	49928	30	Elongation factor 1-alpha-like protein	<i>Acremonium chrysogenum</i> ATCC 11550
125	PQK15291.1	22856	128	hypothetical protein BB8028_0005g08050	<i>Beauveria bassiana</i>

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
131	EEU42998.1	23091	131	predicted protein	<i>Nectria haematococcamp</i> VI 77-13-4
133	POR36939.1	15791	91	Superoxide dismutase [Cu-Zn]	<i>Tolypocladium paradoxum</i>
142	PNY25025.1	13598	79	Profilin	<i>Tolypocladium capitatum</i>
144	XP_018177206.1	36217	219	glyceraldehyde-3-phosphate dehydrogenase	<i>Purpureocillium lilacinum</i>
145	XP_024404531.1	52336	130	adenylyl-sulfate kinase	<i>Trichoderma gamsii</i>
146	POR37810.1	55242	322	ATP synthase subunit beta	<i>Tolypocladium paradoxum</i>
147	POR37810.1	55242	262	ATP synthase subunit beta	<i>Tolypocladium paradoxum</i>
148	POR35368.1	52948	344	Enolase, partial	<i>Tolypocladium paradoxum</i>
149	EMT70814.1	35277	407	Malate dehydrogenase, mitochondrial	<i>Fusarium oxysporum f. sp. cubense</i> race 4
150	OAR02581.1	38327	509	hypothetical protein LLEC1_00332, partial	<i>Cordyceps confragosa</i>
151	KZZ90744.1	34989	521	malate dehydrogenase precursor	<i>Moelleriella libera</i> RCEF 2490
152	XP_018136472.1	40886	159	acetyl-CoA C-acetyltransferase	<i>Pochonia chlamydosporia</i> 170

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
153	XP_022284686.1	58260	419	6-phosphogluconate dehydrogenase	<i>Pochoniachlamydosporia</i> 170
154	EEU44203.1	77244	85	hypothetical protein NECHADRAFT_65315	<i>Nectria haematococcamp</i> VI 77-13-4
155	KIL87093.1	81262	202	catalase-peroxidase	<i>Fusarium avenaceum</i>
156	EFY93483.1	73112	508	heat shock 70 kDa protein precursor	<i>Metarhizium acridum</i> CQMa 102
157	PQK16496.1	PQK16496.1	141	hypothetical protein BB8028_0006g08160	<i>Beauveria bassiana</i>
158	ABQ42572.1	ABQ42572.1	548	glyceraldehyde-3-phosphate dehydrogenase	<i>Myrothecium gramineum</i>
159	XP_013944143.1	36069	284	UDP-glucose 4-epimerase Gal10	<i>Trichoderma atroviride</i> IMI 206040
162	IQCR2_NEUCR	40553	75	Ubiquinol-cytochrome-c reductase complex core protein	<i>Neurospora crassa</i> OR74A
163	GAO18194.1	36533	452	hypothetical protein UVI_02036930	<i>Ustilago idaeae</i> virens
164	KFA79660.1	46953	380	hypothetical protein S40288_04082	<i>Stachybotrys chartarum</i> IBT 40288
165	XP_018235168.1	19005	178	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	<i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> 4287
166	KFA60529.1	56642	101	hypothetical protein S40285_07587	<i>Stachybotrys chlorohalonata</i> IBT 40285



Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
167	PQK16496.1	36069	126	hypothetical protein BB8028_0006g08160	<i>Beauveria bassiana</i>
168	PTB77983.1	24242	106	HSP20-like chaperone	<i>Trichoderma longibrachiatum</i> ATCC 18648
169	KFA78328.1	79469	239	hypothetical protein S40288_05032	<i>Stachybotrys chartarum</i> IBT 40288
170	KFA79660.1	47482	430	hypothetical protein S40288_04082	<i>Stachybotrys chartarum</i> IBT 40288
171	KZZ94886.1	65977	1050	ATP synthase beta chain precursor	<i>Moelleriella libera</i> RCEF 2490]
172	KND89290.1	42624	170	Vacuolar protease A	<i>Tolypocladium ophioglossoides</i> CBS 100239
173	PQK09468.1	55548	156	hypothetical protein BB8028_0001g1538	<i>Beauveria bassiana</i>
174	XP_018655921.1	59487	146	ATP synthase subunit alpha, mitochondrial	<i>Trichoderma gamsii</i>
175	XP_018658099.1	31900	212	40S ribosomal protein S0	<i>Trichoderma gamsii</i>
176	XP_018656673.1	54863	254	ATP synthase subunit beta	<i>Trichoderma gamsii</i>
178	PTB36680.1	38397	142	hypothetical protein M441DRAFT_176232	<i>Trichoderma asperellum</i> CBS 433.97
179	AQX77513.1	40124	437	actin gamma, partial	<i>Gliocladium</i> sp.

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
180	CCE27930.1	30012	248	probable 14-3-3-like protein	<i>Clavicepspurpurea</i> 20.1
181	KFA76311.1	17815	339	hypothetical protein S40288_02977	<i>Stachybotryschartarum</i> IBT 40288
182	CEI40789.1	72567	81	unnamed protein product	<i>Fusariumvenenatum</i> ]
183	XP_018183267.1	17532	225	translationelongationfactor, IF5A	<i>Purpureocilliumlilacinum</i>
184	KFA79660.1	47482	241	hypothetical protein S40288_04082	<i>Stachybotryschartarum</i> IBT 40288
185	XP_018656887.1	23353	236	hypothetical protein TGAM01_v209462	<i>Trichodermagamsii</i>
186	OAA44345.1	141716	99	1,4-alpha-glucan branchingenzyme	<i>Metarhiziumrileyi</i> RCEF 4871
189	KDB12143.1	33116	109	proteasome regulatory subunit 12	<i>Ustilaginoideavirens</i>
190	AQX77513.1	40124	437	actin gamma, partial	<i>Gliocladium</i> sp.
191	EFY92780.1	45159	246	TH14-3-3 like protein	<i>Metarhiziumacridum</i> CQMa 102
192	KIL96612.1	10977	82	hypothetical protein FAVG1_01356	<i>Fusariumavenaceum</i>
194	XP_018160338.1	17955	346	Cytochrome c oxidase subunit Va	<i>Colletotrichumhigginsianum</i> IMI 349063
195	PQK16496.1	36069	98	hypothetical protein BB8028_0006g08160	<i>Beauveriabassiana</i>

Spot no.	Best Protein Accession	Best Protein Mass	Best Protein Score	Best Protein Description	Organism
196	XP_018181948.1	27661	149	RanBP1 domain-containing protein	<i>Purpureocilliumlilacinum</i>
197	KFH44584.1	36904	114	hypothetical protein ACRE_046720	<i>Acremoniumchrysogenum</i> ATCC 11550
198	XP_023424735.1	70964	212	probable heat shock protein 70 (hsp70)	<i>Fusariumfujikuroi</i> IMI 58289]
199	EJP67331.1	72459	177	hsp70-like protein	Beauveriabassiana ARSEF 2860
201	KLO87050.1	15126	98	putative ribosomal protein S19.e, cytosolic	<i>Fusariumfujikuroi</i>
203	AID48698.1	37472	88	actin, partial	<i>Neotyphodium</i> sp. NI_201308]