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**Proteomic analysis of axillary buds of sugarcane at different cutting stages: evidence for alterations in axillary bud gene expression**

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**Supplementary Table S1. Total and differential proteome of the plant cane axillary buds of the RB867515 sugarcane cultivar.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
1/CLH1_ORYSJ/ SwissProt	Clathrin heavy chain 1	4/4	219	3	194.534	<i>Oryza sativa</i> Japonica Group
2/KHG02463.1/ NCBIprot	Splicing factor 3B subunit 3	1/1	70	1	136.932	<i>Gossypium arboreum</i>
3/NM18365.1/ NCBIprot	*Acetyl-CoA carboxylase 2	1/1	49	1	135.515	<i>Zea mays</i>
4/EMT08767.1/ NCBIprot	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	1/1	51	1	119.941	<i>Egilopsis tauschii</i>
5/UBE11_WHEAT/ SwissProt	Ubiquitin-activating enzyme E1	1/1	55	1	117.846	<i>Triticum aestivum</i>
6/ACOC_ORYSJ/ NCBIprot	Putative aconitate hydratase, cytoplasmic (Aconitase)	1/1	54	2	98.591	<i>Oryza sativa</i> Japonica Group
7/ONM08081.1/ NCBIprot	Lipoxygenase	1/1	81	1	96.845	<i>Zea mays</i>
8/PHSH_SOLTU/ Swissprot	*Alpha-glucan phosphorylase, H isozyme	1/1	66	1	95.451	<i>Solanum tuberosum</i>
9/OEL20031.1/ NCBIprot	Elongation factor 2	7/7	336	10	94.808	<i>Dichantherium oligosanthes</i>
10/OEL17456.1/ NCBIprot	Heat shock 70 kDa protein 14	1/1	60	1	94.240	<i>Dichantherium oligosanthes</i>
11/ENPL_ARATH/ SwissProt	*Endoplasmic homolog (Protein SHEPHERD)	1/1	57	1	94.203	<i>Arabidopsis thaliana</i>
12/AGI56230.1/ NCBIprot	Sucrose synthase	8/7	526	16	93.492	<i>Saccharum officinarum</i>
13/PLDA1_BRAOC/ SwissProt	Phospholipase D alpha 1	1/1	67	1	92.236	<i>Brassica oleracea</i> var. capitata

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>14</b> /CD48A_ARATH/ SwissProt	Cell division control protein 48 homolog	2/2	124	3	90.079	<i>Arabidopsis thaliana</i>
<b>15</b> /AQK52792.1/ NCBIprot	<sup>a</sup> TUDOR-SN protein 1 (Ribonuclease TUDOR 1-like)	1/1	70	1	84.747	<i>Zea mays</i>
<b>16</b> /KXG24059.1/ NCBIprot	Hypothetical protein (5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase – UniProtKB)	12/4	864	21	84.696	<i>Sorghum bicolor</i>
<b>17</b> /AGC60019.1/ NCBIprot	Heat shock protein 90	4/0	239	7	80.355	<i>Saccharum</i> hybrid cultivar SP80-3280
<b>18</b> /MFP_ORYSJ/ SwissProt	Peroxisomal fatty acid beta-oxidation multifunctional protein (Enoyl-CoA hydratase)	1/1	58	1	79.038	<i>Oryza sativa</i> Japonica Group
<b>19</b> /BAD01242.1/ NCBIprot	Putative glycyl-tRNA synthetase	1/1	55	1	77.653	<i>Oryza sativa</i> Japonica Group
<b>20</b> /AQL02798.1/ NCBIprot	Peroxisomal acyl-coenzyme A oxidase	1/1	62	1	74.843	<i>Zea mays</i>
<b>21</b> /TKTC_MAIZE/ SwissProt	Transketolase, chloroplastic	1/1	57	1	73.347	<i>Zea mays</i>
<b>22</b> /HSP7J_ARATH/ SwissProt	Heat shock 70 kDa protein 10, mitochondrial	1/1	56	1	73.174	<i>Arabidopsis thaliana</i>
<b>23</b> /ONM09254.1/ NCBIprot	<sup>a</sup> Exhydrolase II	1/1	56	2	72.774	<i>Zea mays</i>
<b>24</b> /AQK53726.1/ NCBIprot	Phenylalanine ammonia lyase	7/0	414	13	72.130	<i>Zea mays</i>
<b>25</b> /NP_001306686.1/ NCBIprot	Probable mediator of RNA polymerase II transcription subunit 37 (Heat Shock Protein 70)	10/0	686	27	71.517	<i>Zea mays</i>
<b>26</b> /SDHA_ORYSJ/ SwissProt	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (Flavoprotein subunit of complex II)	2/2	168	4	69.494	<i>Oryza sativa</i> Japonica Group
<b>27</b> /VATA_ARATH/ SwissProt	V-type proton ATPase catalytic subunit A	2/1	140	4	69.111	<i>Arabidopsis thaliana</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>28</b> /XP_016551170.1/NCBIprot	<sup>a</sup> Predicted: methylenetetrahydrofolate reductase 2-like	1/1	53	1	68.077	<i>Capsicum annuum</i>
<b>29</b> /AAB94293.1/NCBIprot	Polyphenol oxidase	4/4	264	9	67.709	<i>Saccharum</i> hybrid cultivar
<b>30</b> /AFO64345.1/NCBIprot	Putative ATP citrate lyase	5/2	276	8	66.539	<i>Saccharum</i> hybrid cultivar GT28
<b>31</b> /RH52C_ORYSJ/SwissProt	<sup>a</sup> DEAD-box ATP-dependent RNA helicase 52C	1/1	60	2	66.232	<i>Oryza sativa</i> Japonica Group
<b>32</b> /OEL22530.1/NCBIprot	T-complex protein 1 subunit eta	2/2	137	6	66.202	<i>Dichantheium oligosanthes</i>
<b>33</b> /NP_001146890.1/NCBIprot	RuBisCO large subunit-binding protein subunit beta;	2/1	141	3	64.511	<i>Zea mays</i>
<b>34</b> /AAC49177.1/NCBIprot	<sup>a</sup> Dhurrinase (Cyanogenic beta-glucosidase dhurrinase)	2/2	106	3	64.195	<i>Sorghum bicolor</i>
<b>35</b> /ACG25573.1/NCBIprot	D-3-phosphoglycerate dehydrogenase	2/2	149	5	64.112	<i>Zea mays</i>
<b>36</b> /AQK46517.1/NCBIprot	<sup>a</sup> Beta-D-xylosidase 4	1/1	52	1	64.089	<i>Zea mays</i>
<b>37</b> /ONL98792.1/NCBIprot	Nucleoredoxin 1-1	1/1	68	2	64.030	<i>Zea mays</i>
<b>38</b> /NP_001170508.1/NCBIprot	<sup>a</sup> Dihydroxy-acid dehydratase chloroplastic	1/1	112	3	63.848	<i>Zea mays</i>
<b>39</b> /AQK54720.1/NCBIprot	Ppi-phosphofructokinase subunit alpha (Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit alpha)	1/1	92	2	63.745	<i>Zea mays</i>
<b>40</b> /AGT16432.1/NCBIprot	Phosphoglucomutase	2/2	125	8	63.202	<i>Saccharum</i> hybrid cultivar R570
<b>41</b> /XP_002454700.1/NCBIprot	Hypothetical protein (Leucine aminopeptidase family protein – UniProtKB)	4/4	250	14	62.121	<i>Sorghum bicolor</i>
<b>42</b> /NP_001168412.1/NCBIprot	Ppi-phosphofructokinase subunit beta (Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta)	2/2	116	4	61.640	<i>Zea mays</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
43/ONM41488.1/NCBIprot	<sup>a</sup> Ubiquitin carboxyl-terminal hydrolase	1/1	162	4	61.607	<i>Zea mays</i>
44/OEL25462.1/NCBIprot	RuBisCO large subunit-binding protein subunit alpha, chloroplastic;	4/4	261	10	61.586	<i>Dichantheium oligosanthes</i>
45/CDPKF_ORYSJ/SwissProt	<sup>a</sup> Calcium-dependent protein kinase (OsCDPK)	1/1	57	2	61.563	<i>Oryza sativa Japonica Group</i>
46/CH61_MAIZE/SwissProt	Chaperonin CPN60-1, mitochondrial; HSP60-1	1/1	69	2	61.458	<i>Zea mays</i>
47/AQK42951.1/NCBIprot	<sup>a</sup> Translation elongation factor EF1A/initiation factor IF2gamma family protein	1/1	54	1	61.326	<i>Zea mays</i>
48/ACG36897.1/NCBIprot	Aspartyl-tRNA synthetase	1/1	71	2	61.283	<i>Zea mays</i>
49/ONM26494.1/NCBIprot	<sup>a</sup> Protein disulfide isomerase	1/1	53	3	61.141	<i>Zea mays</i>
50/KHN24460.1/NCBIprot	<sup>a</sup> T-complex protein 1 subunit gamma	1/1	61	1	60.781	<i>Glycine soja</i>
51/KQL26130.1/NCBIprot	Hypothetical protein (Beta-amylase – UniProtKB)	2/2	109	6	60.452	<i>Setaria italica</i>
52/AFF18772.2/NCBIprot	Glutathione reductase	1/1	50	2	60.433	<i>Dimocarpus longan</i>
53/KXG33615.1/NCBIprot	Hypothetical protein (2,3-bisphosphoglycerate-independent phosphoglycerate mutase – UniProtKB)	2/2	81	3	60.384	<i>Sorghum bicolor</i>
54/EMS60932.1/NCBIprot	T-complex protein 1 subunit beta	2/2	97	4	59.628	<i>Triticum urartu</i>
55/ACG40009.1/NCBIprot	<sup>a</sup> T-complex protein 1 subunit épsilon	1/1	55	5	59.585	<i>Zea mays</i>
56/AQK54532.1/NCBIprot	Selenium-binding protein	1/1	50	2	59.467	<i>Zea mays</i>
57/EMT24003.1/NCBIprot	<sup>a</sup> RuvB-like protein 1 (49-kDa TATA box-binding protein-interacting protein)	1/1	58	2	58.973	<i>Aegilops tauschii</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>58</b> /KXG23127.1/ NCBIprot	<sup>a</sup> Hypothetical protein (Pyruvate dehydrogenase complex component E2–UniProtKB)	1/1	63	2	58.231	<i>Sorghum bicolor</i>
<b>59</b> /IMA1A_ORYSJ/ SwissProt	<sup>a</sup> Importin subunit alpha	2/2	132	6	58.162	<i>Oryza sativa</i> Japonica Group
<b>60</b> /XP_006647227.1/ NCBIprot	Predicted: T-complex protein 1 subunit delta	1/1	88	4	58.060	<i>Oryza brachyntha</i>
<b>61</b> /KPYC1_ORYSI/ SwissProt	Pyruvate kinase 1, cytosolic	1/1	88	4	57.740	<i>Oryza sativa</i> Indica Group
<b>62</b> /3FR7_A/ NCBIprot	Chain A, Ketol-Acid Reductoisomerase (Kari) In Complex With Mg2+	2/2	143	5	57.566	<i>Oryza sativa</i> Japonica Group
<b>63</b> /AHZ13843.1/ NCBIprot	Catalase	3/2	187	9	56.820	<i>Saccharum</i> hybrid cultivar Yacheng05-179
<b>64</b> /ADP02192.1/ NCBIprot	Putative non-cyanogenic beta-glucosidase	1/1	90	3	56.692	<i>Triticum aestivum</i>
<b>65</b> /XP_006649652.1/ NCBIprot	Predicted: Glucan endo-1,3-beta-glucosidase 3	1/1	52	2	56.571	<i>Oryza brachyantha</i>
<b>66</b> /UAP1_ARATH/ SwissProt	<sup>a</sup> UDP-N-acetylglucosamine diphosphorylase 1	1/1	56	2	56.548	<i>Arabidopsis thaliana</i>
<b>67</b> /YP_009295487.1/ NCBIprot	ATPase subunit 1,mitochondrion (ATP synthase F1, alpha subunit)	2/2	165	6	55.435	<i>Saccharum officinarum</i>
<b>68</b> /VATB1_ARATH/ SwissProt	V-type proton ATPase subunit B1	5/2	302	15	54.188	<i>Arabidopsis thaliana</i>
<b>69</b> /AGT16642.1/ NCBIprot	Adenosylhomocysteinase	5/4	294	14	53.888	<i>Saccharum</i> hybrid cultivar R570
<b>70</b> /XP_004968669.1/ NCBIprot	<sup>a</sup> Predicted: Dihydrolipoyl dehydrogenase, mitochondrial-like	1/1	54	3	53.609	<i>Setaria italica</i>
<b>71</b> /OEL22996.1/ NCBIprot	Putative elongation fator 1-gamma	1/1	55	4	53.467	<i>Dichantheium oligosanthes</i>
<b>72</b> /JAU25398.1/ NCBIprot	<sup>a</sup> 26S proteasome regulatory subunit 4 - like protein A, partial	1/1	58	2	53.430	<i>Noccaea caerulea</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>73</b> /XP_002444986.1/NCBIprot	Hypothetical protein (Glycosyltransferase – UniProtKB)	2/2	119	5	53.225	<i>Sorghum bicolor</i>
<b>74</b> /UGDH4_ORYSJ/SwissProt	UDP-glucose 6-dehydrogenase	4/0	341	14	53.391	<i>Oryza sativa</i> Japonica Group
<b>75</b> /KQJ84715.1/NCBIprot	<sup>a</sup> Hypothetical protein (Polyadenylate-binding protein RBP45-Like – UniProtKB)	1/1	65	1	53.263	<i>Brachypodium distachyon</i>
<b>76</b> /ACL80329.1/NCBIprot	UDP-glucose pyrophosphorylase	5/3	341	13	52.431	<i>Saccharum officinarum</i>
<b>77</b> /AGT15905.1/NCBIprot	Serine hydroxymethyltransferase	2/2	157	9	52.087	<i>Saccharum</i> hybrid cultivar R570
<b>78</b> /HISX_ORYSJ/SwissProt	<sup>a</sup> Histidinol dehydrogenase, chloroplastic	1/1	55	3	50.990	<i>Oryza sativa</i> Japonica Group
<b>79</b> /TBB1_MAIZE/SwissProt	Tubulin beta-1 chain	3/2	157	9	50.614	<i>Zea mays</i>
<b>80</b> /TBA1_ELEIN/NCBIprot	Tubulin alpha-1 chain	5/3	426	17	50.384	<i>Eleusine indica</i>
<b>81</b> /CAA75477.1/NCBIprot	ATP synthase subunit beta	6/5	378	18	49.219	<i>Sorghum bicolor</i>
<b>82</b> /OMO98074.1/NCBIprot	<sup>a</sup> Peptide chain release factor eRF1/aRF1	1/1	48	2	49.100	<i>Corchorus capsularis</i>
<b>83</b> /OEL38116.1/NCBIprot	<sup>a</sup> BAHD acyltransferase DCR	1/1	53	3	48.885	<i>Dichantheium oligosanthes</i>
<b>84</b> /EMT27516.1/NCBIprot	<sup>a</sup> Citrate synthase	1/1	57	3	48.396	<i>Aegilops tauschii</i>
<b>85</b> /ENO_ORYSJ/SwissProt	2-phospho-D-glycerate hydro-lyase (Enolase)	4/3	256	12	48.285	<i>Oryza sativa</i> Japonica Group
<b>86</b> /PRS8A_ARATH/SwissProt	<sup>a</sup> 26S protease regulatory subunit 8	1/1	53	3	47.389	<i>Arabidopsis thaliana</i>
<b>87</b> /IF4A_MAIZE/SwissProt	Eukaryotic initiation factor 4A	1/1	60	6	46.849	<i>Zea mays</i>
<b>88</b> /NP_001150503.1/NCBIprot	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase	1/1	47	2	46.584	<i>Zea mays</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>89</b> /BAD45460.1/ NCBIprot	Putative pectinesterase	2/1	110	5	46.405	<i>Oryza sativa</i> Japonica Group
<b>90</b> /NP_001150674.1/ NCBIprot	Transaldolase	2/2	132	6	46.274	<i>Zea mays</i>
<b>91</b> /ICDHC_ARATH/ SwissProt	Cytosolic isocitrate dehydrogenase [NADP]	1/1	65	4	46.059	<i>Arabidopsis thaliana</i>
<b>92</b> /AQK40926.1/ NCBIprot	Obg-like ATPase 1	1/1	73	4	46.058	<i>Zea mays</i>
<b>93</b> /PRS6B_ARATH/ SwissProt	<sup>a</sup> 26S protease regulatory subunit 6B homolog	1/1	89	4	45.984	<i>Arabidopsis thaliana</i>
<b>94</b> /PS10A_ARATH/ SwissProt	<sup>a</sup> 26S protease regulatory subunit 10B homolog A	1/1	76	5	44.960	<i>Arabidopsis thaliana</i>
<b>95</b> /AXS_ORYSJ/ SwissProt	<sup>a</sup> UDP-D-apiose/UDP-D-xylose synthase	1/1	67	2	44.818	<i>Oryza sativa</i> Japonica Group
<b>96</b> /NP_001147047.1/ NCBIprot	<sup>a</sup> 60S ribosomal protein L4	3/3	102	8	44.528	<i>Zea mays</i>
<b>97</b> /XP_002447121.1/ NCBIprot	Hypothetical protein (Aminomethyltransferase – UniProtKB)	1/1	53	2	44.388	<i>Sorghum bicolor</i>
<b>98</b> /AGT16628.1/ NCBIprot	<sup>a</sup> Elongation factor 1 alpha	3/1	154	13	44.302	<i>Saccharum</i> hybrid cultivar R570
<b>99</b> /ONM10543.1/ NCBIprot	<sup>a</sup> Hypothetical protein (DNA-directed RNA polymerase subunit beta – UniProtKB)	2/2	121	9	44.043	<i>Zea mays</i>
<b>100</b> /KXG33418.1/ NCBIprot	<sup>a</sup> Hypothetical protein (Aspartate aminotransferase – UniProtKB)	1/1	50	2	43.956	<i>Sorghum bicolor</i>
<b>101</b> /OPR7_ORYSJ/ SwissProt	12-oxophytodienoate reductase	1/1	52	2	43.878	<i>Oryza sativa</i> Japonica Group
<b>102</b> /EOY27737.1/ NCBIprot	<sup>a</sup> 3-ketoacyl-acyl carrier protein synthase I	1/1	63	3	43.735	<i>Theobroma cacao</i>
<b>103</b> /XP_008800626.1/ NCBIprot	Predicted: probable LL-diaminopimelate aminotransferase	1/1	55	3	43.613	<i>Phoenix dactylifera</i>



**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>104</b> /XP_020101537.1/NCBIprot	<sup>a</sup> S-adenosylmethionine synthase 5	1/1	83	3	43.510	<i>Ananas comosus</i>
<b>105</b> /B0LDU6.1/NCBIprot	<sup>a</sup> Chalcone synthase	1/1	54	3	43.203	<i>Rubus idaeus</i>
<b>106</b> /GME1_ORYSI/SwissProt	<sup>a</sup> GDP-mannose 3,5-epimerase 1	1/1	60	4	43.180	<i>Oryza sativa</i> Indica Group
<b>107</b> /ONM15574.1/NCBIprot	Isopropylmalate dehydrogenase 2	2/2	116	9	43.132	<i>Zea mays</i>
<b>108</b> /ACG35066.1/NCBIprot	Pyruvate dehydrogenase E1 component alpha subunit	1/1	67	3	43.105	<i>Zea mays</i>
<b>109</b> /NP_001142404.1/NCBIprot	Phosphoglycerate kinase	6/2	313	19	42.470	<i>Zea mays</i>
<b>110</b> /AQK96567.1/NCBIprot	<sup>a</sup> UBPI-associated protein 2C (Heterogeneous nuclear ribonucleoprotein 1)	1/1	67	5	42.200	<i>Zea mays</i>
<b>111</b> /ACT3_PEA/SwissProt	<sup>a</sup> Actin	2/1	98	10	41.836	<i>Pisum sativum</i>
<b>112</b> /CBB36460.1/NCBIprot	<sup>a</sup> Alcohol dehydrogenase	1/1	75	5	41.685	<i>Saccharum</i> hybrid cultivar R570
<b>113</b> /KXG39210.1/NCBIprot	Hypothetical protein (Putative acetyl-CoA acetyltransferase cytosolic – UniProtKB)	3/1	153	13	41.564	<i>Sorghum bicolor</i>
<b>114</b> /OEL24402.1/NCBIprot	3-hydroxyisobutyryl-CoA hydrolase-like protein 5, partial	1/1	51	1	41.366	<i>Dichantheium oligosanthes</i>
<b>115</b> /XP_012854067.1/NCBIprot	<sup>a</sup> Predicted: UDP-arabinopyranose mutase 3	1/1	50	5	41.204	<i>Erythranthe guttata</i>
<b>116</b> /OQU78658.1/NCBIprot	Hypothetical protein (Nucleoside-triphosphatase; Apyrase – UniProtKB)	1/1	60	3	40.969	<i>Sorghum bicolor</i>
<b>117</b> /XP_002466246.1/N8BIprot	Hypothetical protein (Imidazolonepropionase-UniProtKB)	2/2	134	6	40.544	<i>Sorghum bicolor</i>
<b>118</b> /OEL24262.1/NCBIprot	<sup>a</sup> Hypothetical protein (Activator of 90 kDa heat shock protein ATPase – UniProtKB)	1/1	64	5	40.041	<i>Dichantheium oligosanthes</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>119</b> /ONM22945.1/ NCBIprot	P-loop containing nucleoside triphosphate hydrolase superfamily protein	1/1	101	4	39.908	<i>Zea mays</i>
<b>120</b> /AAQ67347.1/ NCBIprot	Caffeic acid 3-O-methyltransferase	3/3	156	9	39.824	<i>Saccharum</i> hybrid cultivar
<b>121</b> /XP_002454890.1 /NCBIprot	<sup>a</sup> Uncharacterized protein (Vegetative storage protein PNI288 – UniProtKB)	1/1	81	6	39.730	<i>Sorghum bicolor</i>
<b>122</b> /KQK91059.1/ NCBIprot	Hypothetical protein (Ricin B-like lectin R40G2 – UniProtKB)	1/1	92	5	39.274	<i>Setaria italica</i>
<b>123</b> /AQK89688.1/ NCBIprot	2-alkenal reductase (NADP(+)-dependent (Putative alcohol dehydrogenase superfamily protein))	1/1	71	3	39.196	<i>Zea mays</i>
<b>124</b> /BAI59775.1/ NCBIprot	Fructose-bisphosphate aldolase cytoplasmic isozyme (Aldolase C-2)	4/4	230	10	39.170	<i>Phyllostachys edulis</i>
<b>125</b> /LDH_MAIZE/ SwissProt	<sup>a</sup> L-lactate dehydrogenase	1/1	69	3	38.698	<i>Zea mays</i>
<b>126</b> /XP_002440480.1/ NCBIprot	<sup>a</sup> Hypothetical protein (13S globulin seed storage protein – UniProtKB)	1/1	59	3	38.091	<i>Sorghum bicolor</i>
<b>127</b> /OEL25000.1/ NCBIprot	Ribokinase	1/1	69	3	37.603	<i>Dichantheium oligoanthes</i>
<b>128</b> /XP_008645951.2/ NCBIprot	Adenosine kinase 2	3/2	195	14	37.539	<i>Zea mays</i>
<b>129</b> /OEL22313.1/ NCBIprot	Peroxidase	2/2	119	11	36.793	<i>Dichantheium oligoanthes</i>
<b>130</b> /GBLPA_ORYSJ/ =SwissProt	Guanine nucleotide-binding protein subunit beta-like protein A (Receptor for activated C kinase)	3/3	159	10	36.665	<i>Oryza sativa</i> Japonica Group
<b>131</b> /OEL20760.1/ NCBIprot	<sup>a</sup> Putative voltage-gated potassium channel subunit beta	1/1	59	4	36.625	<i>Dichantheium oligoanthes</i>
<b>132</b> /KXG20851.1/ NCBIprot	Hypothetical protein (Glyceraldehyde-3-phosphate dehydrogenase – UniProtKB)	5/4	350	24	36.618	<i>Sorghum bicolor</i>
<b>133</b> /KXG24253.1/ NCBIprot	Hypothetical protein (Fructokinase – UniProtKB)	8/6	520	29	35.831	<i>Sorghum bicolor</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>134</b> /NP_001130539.1 /NCBIprot	Late embryogenesis abundant protein group 2	3/2	167	14	35.309	<i>Zea mays</i>
<b>135</b> /XP_002454396.1 /NCBIprot	Hypothetical protein (Thioredoxin reductase – UniProtKB)	1/1	71	6	35.006	<i>Sorghum bicolor</i>
<b>136</b> /SPDE_COFAR/ SwissProt	Spermidine synthase (Putrescine aminopropyltransferase)	1/1	72	4	34.878	<i>Coffea arabica</i>
<b>137</b> /OQU90839.1/ NCBIprot	<sup>a</sup> Hypothetical protein (Glutamate dehydrogenase – UniProtKB)	1/1	60	7	34.859	<i>Sorghum bicolor</i>
<b>138</b> /RL51_ORYSI/ SwissProt	<sup>a</sup> 60S ribosomal protein L5-1	1/1	55	2	34.791	<i>Oryza sativa</i> Indica Group
<b>139</b> /AQK39735.1/ NCBIprot	Putative oxidoreductase, aldo/keto reductase family protein	1/1	64	6	34.649	<i>Zea mays</i>
<b>140</b> /RLA0_MAIZE/ SwissProt	60S acidic ribosomal protein P0	1/1	92	10	34.597	<i>Zea mays</i>
<b>141</b> /ONM12595.1/ NCBIprot	26S proteasome non-ATPase regulatory subunit 7 homolog	1/1	48	3	34.543	<i>Zea mays</i>
<b>142</b> /XP_006650879.1/ NCBIprot	<sup>a</sup> Uncharacterized protein (Late embryogenesis abundant protein Lea14-A – Uniprot)	1/1	59	7	34.533	<i>Oryza brachyantha</i>
<b>143</b> /OEL25171.1/ NCBIprot	<sup>a</sup> NADH-cytochrome b5 reductase-like protein	1/1	60	3	34.201	<i>Dichantherium olihosanthes</i>
<b>144</b> /ONM42211.1/ NCBIprot	V-type proton ATPase subunit C	1/1	79	5	34.106	<i>Zea mays</i>
<b>145</b> /ABA99939.2/ NCBIprot	Malate dehydrogenase, glyoxysomal precursor, putative, expressed	1/1	52	3	34.009	<i>Oryza sativa</i> Japonica Group
<b>146</b> /KXG24064.1/ NCBIprot	Hypothetical protein (Cysteine synthase-like – UniProtKB)	1/1	67	5	34.280	<i>Sorghum bicolor</i>
<b>147</b> /MD36A_ARATH/ SwissProt	<sup>a</sup> Mediator of RNA polymerase II transcription subunit 36a	1/1	49	3	33.803	<i>Arabidopsis thaliana</i>
<b>148</b> /OEL19650.1 / NCBIprot	<sup>a</sup> 40S ribosomal protein SA	1/1	65	3	33.698	<i>Dichantherium oligosanthes</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>149</b> /OEL18647.1/ NCBIprot	Malate dehydrogenase, cytoplasmic	4/3	282	22	33.656	<i>Dichantheium oligosanthes</i>
<b>150</b> /ACG31861.1/ NCBIprot	Succinyl-CoA ligase alpha-chain 2	1/1	66	3	33.517	<i>Zea mays</i>
<b>151</b> /EMS52981.1/ NCBIprot	Legumin-like protein (Glutelin type-A1)	2/2	100	8	33.443	<i>Triticum urartu</i>
<b>152</b> /AHF18211.1/ NCBIprot	Glyoxylase 1 (Lactoylglutathione lyase)	1/1	77	3	33.005	<i>Saccharum</i> Hybrid cultivar
<b>153</b> /IFRH_MAIZE/ SwissProt	Isoflavone reductase homolog IRL	1/1	57	3	32.831	<i>Zea mays</i>
<b>154</b> /ABB47824.1/ NCBIprot	<sup>a</sup> Protochlorophyllide reductase B, chloroplast precursor, putative, expressed	1/1	55	4	31.585	<i>Oryza sativa</i> Japonica Group
<b>155</b> /AAS86422.1/ NCBIprot	Glutathione S-transferase GSTF14, partial	1/1	51	5	30.766	<i>Oryza sativa</i> Japonica Group
<b>156</b> /OMP08788.1/ NCBIprot	<sup>a</sup> Ribosomal protein S5	1/1	61	5	29.701	<i>Corchorus olitorius</i>
<b>157</b> /OEL25577.1/ NCBIprot	Proteasome subunit beta type 1	2/2	140	7	29.394	<i>Dichantheium oligosanthes</i>
<b>158</b> /AQL01982.1/ NCBIprot	Aspartic proteinase A1	1/1	63	8	28.998	<i>Zea mays</i>
<b>159</b> /ACG36992.1/ NCBIprot	<sup>a</sup> 60S ribosomal protein L2; 60S ribosomal protein L8	1/1	71	4	28.354	<i>Zea mays</i>
<b>160</b> /AGO97076.1/ NCBIprot	Ascorbate peroxidase	4/3	324	26	27.556	<i>Saccharum</i> hybrid cultivar GT28
<b>161</b> /XP_020184931.1/ NCBIprot	Stress-response A/B barrel domain-containing protein DABB1-like	1/1	53	4	27.325	<i>Aegilops tauschii</i> subsp. <i>tauschii</i>
<b>162</b> /ACG24648.1/ NCBIprot	Triosephosphate isomerase, cytosolic	7/0	560	41	27.278	<i>Zea mays</i>
<b>163</b> /AGT17219.1/ NCBIprot	Proteasome alpha subunit D2	2/2	118	10	27.087	<i>Saccharum</i> hybrid cultivar R570
<b>164</b> /EMT10898.1/ NCBIprot	Ras-related protein ARA-3	1/1	66	5	27.044	<i>Aegilops tauschii</i>

**S-1, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>165</b> /XP_010493182.1/NCBIprot	<sup>a</sup> Predicted: 20 kDa chaperonin, chloroplastic (CPN21)	1/1	72	10	26.829	<i>Camelia sativa</i>
<b>166</b> /EMS48502.1/NCBIprot	<sup>a</sup> 40S ribosomal protein S3	1/1	59	5	25.515	<i>Triticum urartu</i>
<b>167</b> /RL10_MAIZE/SwissProt	<sup>a</sup> 60S ribosomal protein L10	1/1	70	5	25.359	<i>Zea mays</i>
<b>168</b> /RS8_MAIZE/SwissProt	<sup>a</sup> 40S ribosomal protein S8	2/1	149	13	25.155	<i>Zea mays</i>
<b>169</b> /EF1D1_ORYSJ/SwissProt	<sup>a</sup> Elongation factor 1-delta 1	1/1	55	3	24.904	<i>Oryza sativa</i> Japonica Group
<b>170</b> /GSTF1_MAIZE/SwissProt	Glutathione S-transferase 1	2/2	106	13	24.034	<i>Zea mays</i>
<b>171</b> /RABD1_ARATH/SwissProt	<sup>a</sup> Ras-related protein RABD1	1/1	73	7	22.995	<i>Arabidopsis thaliana</i>
<b>172</b> /AGT16630.1/NCBIprot	<sup>a</sup> GTP-binding nuclear protein	1/1	70	5	22.851	<i>Saccharum</i> hybrid cultivar R570
<b>173</b> /RIC1_ORYSJ/SwissProt	<sup>a</sup> Ras-related protein RIC1	1/1	73	7	22.690	<i>Oryza sativa</i> Japonica Group
<b>174</b> /CDI66516.1/NCBIprot	<sup>a</sup> CBS domain-containing protein	1/1	54	5	22.531	<i>Saccharum</i> hybrid cultivar R570
<b>175</b> /NACA_PINTA/SwissProt	<sup>a</sup> Nascent polypeptide-associated complex subunit alpha-like protein	1/1	80	8	22.452	<i>Pinus taeda</i>
<b>176</b> /GL814_ORYSJ/SwissProt	<sup>a</sup> Germin-like protein 8-14 (Auxin-binding protein)	1/1	50	10	22.018	<i>Oryza sativa</i> Japonica Group
<b>177</b> /KMZ64823.1/NCBIprot	<sup>a</sup> Ribosomal protein 5B	1/1	56	6	21.967	<i>Zostera marina</i>
<b>178</b> /KHN19077.1/NCBIprot	Flavoprotein wrbA (NAD(P)H dehydrogenase(quinone) FQR1)	1/1	59	5	21.113	<i>Glycine soja</i>
<b>179</b> /ACG31637.1/NCBIprot	<sup>a</sup> 60S ribosomal protein L11	1/1	53	7	20.865	<i>Zea mays</i>
<b>180</b> /AQK53244.1/NCBIprot	60S ribosomal protein L6;	1/1	60	8	18.857	<i>Zea mays</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>181</b> /AGT16090.1/ NCBIprot	Cyclophilin (Peptidyl-prolyl cis-trans isomerase-like)	2/2	143	18	18.610	<i>Saccharum</i> hybrid cultivar R570
<b>182</b> /AGT16537.1/ NCBIprot	60S ribosomal protein L12	1/1	76	9	17.807	<i>Saccharum</i> hybrid cultivar R570
<b>183</b> /NP_001146919.1/ NCBIprot	<sup>a</sup> OB-fold nucleic acid binding domain containing protein	1/1	58	6	15.544	<i>Zea mays</i>

<sup>a</sup> – Proteins found only in plant cane

**Supplementary Table S2. Total and differential proteome of forth ratoon axillary buds of the RB867515 sugarcane cultivar.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
1/CLH1_ORYSJ/SwissProt	Clathrin heavy chain 1	5/2	319	4	194.534	<i>Oryza sativa</i> Japonica Group
2/OEL24502.1/NCBIprot	Splicing factor 3B subunit 3	1/1	56	1	137.265	<i>Dichantherium oligosanthes</i>
3/EMT08767.1/NCBIprot	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	1/1	58	1	119.941	<i>Aegilops tauschii</i>
4/UBE11_WHEAT/SwissProt	Ubiquitin-activating enzyme E1 1	1/1	74	1	117.846	<i>Triticum aestivum</i>
5/AEK76075.1/NCBIprot	<sup>b</sup> Heat shock protein 101 (Hsp101; Chaperone protein ClpB1)	1/1	84	1	101.101	<i>Saccharum</i> hybrid cultivar SP80-3280
6/ONM35737.1/NCBIprot	Lipoxygenase	2/2	141	2	99.495	<i>Zea mays</i>
7/AQK70569.1/NCBIprot	<sup>b</sup> Aminopeptidase M1	1/1	52	1	99.279	<i>Zea mays</i>
8/AQK50311.1/NCBIprot	Aconitate hydratase, mitochondrial (Aconitase)	3/2	200	6	96.324	<i>Zea mays</i>
9/OEL20031.1/NCBIprot	Elongation factor 2	7/2	404	12	94.808	<i>Dichantherium oligosanthes</i>
10/OEL17456.1/NCBIprot	Heat shock 70 kDa protein 14	2/2	101	3	94.240	<i>Dichantherium oligosanthes</i>
11/AGI56230.1/NCBIprot	Sucrose synthase	5/5	348	7	93.492	<i>Saccharum officinarum</i>
12/PLDA1_BRAOC/SwissProt	Phospholipase D	1/1	70	1	92.236	<i>Brassica oleracea</i> var. <i>capitata</i>
13/AEI01159.1/NCBIprot	Cell division cycle protein 48, partial	1/1	74	1	86.499	<i>Zea mays</i>
14/OEL32117.1/NCBIprot	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase 2	7/0	497	16	83.709	<i>Dichantherium oligosanthes</i>
15/AGC60019.1/NCBIprot	Heat shock protein 90	1/1	66	1	80.355	<i>Saccharum</i> hybrid cultivar SP80-3280

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>16</b> /EMS45026.1 / NCBIprot	<sup>b</sup> Eukaryotic translation initiation factor 3 subunit B	1/1	66	1	79.818	<i>Triticum urartu</i>
<b>17</b> /AGF69114.1/ NCBIprot	Phenylalanine ammonia lyase	6/0	386	12	76.007	<i>Saccharum</i> hybrid cultivar ROC22
<b>18</b> /OEL36924.1/ NCBIprot	Glycine--tRNA ligase, mitochondrial 1	1/1	50	1	75.960	<i>Dichantheium oligosanthes</i>
<b>19</b> /ACOX1_ARATH/ SwissProt	Peroxisomal acyl-coenzyme A oxidase	1/1	78	1	74.996	<i>Arabidopsis thaliana</i>
<b>20</b> /AQK72170.1/ NCBIprot	<sup>b</sup> Glycerophosphodiester phosphodiesterase GDPDL3	1/1	58	1	74.087	<i>Zea mays</i>
<b>21</b> /XP_019200429.1 /NCBIprot	<sup>b</sup> Predicted: Luminal-binding protein (Heat shock 70 kDa protein BIP1)	4/1	261	6	73.880	<i>Ipomoea nil</i>
<b>22</b> /JAT41108.1/ NCBIprot	<sup>b</sup> Pentatricopeptide repeat-containing protein At2g15630, mitochondrial, partial (Mitochondrial small ribosomal subunit protein mS39)	1/1	51	1	73.554	<i>Anthurium amnicola</i>
<b>23</b> /TKTC_MAIZE/ SwissProt	Transketolase, chloroplastic	1/1	52	1	73.347	<i>Zea mays</i>
<b>24</b> /HSP7J_ARATH /SwissProt	Heat shock 70 kDa protein 10, mitochondrial	1/1	57	1	73.174	<i>Arabidopsis thaliana</i>
<b>25</b> /AAK21879.1/ NCBIprot	<sup>b</sup> Arabinoxylan arabinofuranohydrolase isoenzyme AXAH-I	1/1	70	2	72.557	<i>Hordeum vulgare</i>
<b>26</b> /NP_001306686.1 /NCBIprot	Probable mediator of RNA polymerase II transcription subunit 37 (Heat shock protein 70)	9/1	599	23	71.517	<i>Zea mays</i>
<b>27</b> /AQK91457.1/ NCBIprot	Enoyl-CoA hydratase 1 (Peroxisomal fatty acid beta-oxidation multifunctional protein)	2/2	62	4	71.334	<i>Zea mays</i>
<b>28</b> /SDHA_ORYSJ/ SwissProt	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	1/1	105	2	69.494	<i>Oryza sativa</i> Japonica Group
<b>29</b> /AAB94293.1/ NCBIprot	Polyphenol oxidase	4/4	252	10	67.709	<i>Saccharum</i> hybrid cultivar
<b>30</b> /EMT13737.1/ NCBIprot	<sup>b</sup> Glucose-6-phosphate isomerase	1/1	59	1	67.675	<i>Aegilops tauschii</i>



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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>31</b> /ACX50497.1/ NCBIprot	<sup>b</sup> NADP-dependent malic enzyme	1/1	58	3	67.635	<i>Zea mays</i>
<b>32</b> /AFO64345.1/ NCBIprot	Putative ATP citrate lyase; ATP-citrate synthase	3/1	236	5	66.539	<i>Saccharum</i> hybrid cultivar GT28
<b>33</b> /PDC2_ORYSI/ SwissProt	<sup>b</sup> Pyruvate decarboxylase	3/3	208	8	65.889	<i>Oryza sativa</i> Indica Group
<b>34</b> /ACG25573.1/ NCBIprot	D-3-phosphoglycerate dehydrogenase	2/2	110	5	64.112	<i>Zea mays</i>
<b>35</b> /NRX11_ORYSJ/ SwissProt	Probable nucleoredoxin 1-1	1/1	53	2	64.047	<i>Oryza sativa</i> Japonica Group
<b>36</b> /AQK54720.1/ NCBIprot	Ppi-phosphofructokinase subunit alpha (Pyrophosphate--fructose 6-phosphate 1- phosphotransferase subunit alpha)	1/1	67	2	63.745	<i>Zea mays</i>
<b>37</b> /AQL00827.1/ NCBIprot	Ppi-phosphofructokinase subunit beta (Pyrophosphate--fructose 6-phosphate 1- phosphotransferase subunit beta)	1/1	51	2	63.451	<i>Zea mays</i>
<b>38</b> /AQK92331.1/ NCBIprot	Ketol-acid reductoisomerase, chloroplastic	3/1	231	7	63.213	<i>Zea mays</i>
<b>39</b> /AGT16432.1/ NCBIprot	Phosphoglucomutase	3/2	172	11	63.202	<i>Saccharum</i> hybrid cultivar R570
<b>40</b> /VATA_MAIZE/ SwissProt	V-type proton ATPase catalytic subunit A	1/1	93	4	62.198	<i>Arabidopsis</i> <i>thaliana</i>
<b>41</b> /KHM98926.1 /NCBIprot	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	1/1	74	2	61.724	<i>Glycine soja</i>
<b>42</b> /XP_002528805.1/ NCBIprot	Predicted: T-complex protein 1 subunit eta	2/1	133	5	61.160	<i>Ricinus communis</i>
<b>43</b> /KXG33615.1/ NCBIprot	Hypothetical protein (2,3-bisphosphoglycerate- independent phosphoglycerate mutase – UniProtKB)	1/1	103	3	60.384	<i>Sorghum bicolor</i>
<b>44</b> /EMS60932.1/ NCBIprot	T-complex protein 1 subunit beta	1/1	95	4	59.628	<i>Triticum urartu</i>

**S-2, Cont.**

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>45</b> /XP_006652614.1/NCBIprot	<sup>b</sup> Predicted: T-complex protein 1 subunit alpha	1/1	60	5	59.571	<i>Oryza Brachyantha</i>
<b>46</b> /BAB92019.1/NCBIprot	<sup>b</sup> Mitochondrial aldehyde dehydrogenase	1/1	63	2	59.521	<i>Sorghum bicolor</i>
<b>47</b> /AQK54532.1/NCBIprot	Selenium-binding protein	1/1	49	2	59.467	<i>Zea mays</i>
<b>48</b> /ATPBM_MAIZE/SwissProt	ATP synthase subunit beta, mitochondrial	8/5	374	16	59.181	<i>Zea mays</i>
<b>49</b> /NP_001167830.1/NCBIprot	Putative TCP-1/cpn60 chaperonin family protein	4/3	366	21	58.096	<i>Zea mays</i>
<b>50</b> /XP_004986000.1/NCBIprot	Predicted: T-complex protein 1 subunit delta	4/3	396	18	57.946	<i>Setaria italica</i>
<b>51</b> /AIY34491.1/NCBIprot	<sup>b</sup> Glucose-6-phosphate dehydrogenase	1/1	55	2	57.923	<i>Saccharum</i> hybrid cultivar Yacheng05-179
<b>52</b> /KPYC1_ORYSI/SwissProt	Pyruvate kinase 1, cytosolic	1/1	55	4	57.740	<i>Oryza sativa</i> Indica Group
<b>53</b> /AHZ13843.1/NCBIprot	Catalase	2/2	146	6	56.820	<i>Saccharum</i> hybrid cultivar Yacheng05-179
<b>54</b> /ADP02192.1/NCBIprot	Putative non-cyanogenic beta-glucosidase	1/1	124	3	56.692	<i>Triticum aestivum</i>
<b>55</b> /OEL32960.1/NCBIprot	Leucine aminopeptidase 2, chloroplastic	3/3	178	8	55.748	<i>Dichantheium oligosanthos</i>
<b>56</b> /AGZ15751.1/NCBIprot	<sup>b</sup> Betaine-aldehyde dehydrogenase 2	2/1	180	8	55.590	<i>Sorghum bicolor</i>
<b>57</b> /AMYB_MAIZE/SwissProt	Beta-amylase	1/1	85	3	55.487	<i>Zea mays</i>
<b>58</b> /YP_009295487.1/NCBIprot	ATP synthase subunit alpha, mitochondrial	1/1	64	4	55.435	<i>Saccharum officinarum</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>59</b> /VATB1_GOSHI /SwissProt	V-type proton ATPase subunit B1	5/2	320	15	54.286	<i>Gossypium hirsutum</i>
<b>60</b> /AGT16642.1/ NCBIprot	Adenosylhomocysteinase	3/2	176	9	53.888	<i>Saccharum hybrid cultivar R570</i>
<b>61</b> /GSHRC_ORYSJ /SwissProt	Glutathione reductase, cytosolic	1/1	52	4	53.873	<i>Oryza sativa Japonica Group</i>
<b>62</b> /UGDH5_ORYSJ /SwissProt	UDP-glucose 6-dehydrogenase	4/4	212	15	53.455	<i>Oryza sativa Japonica Group</i>
<b>63</b> /ACL80329.1/ NCBIprot	UDP--glucose pyrophosphorylase	8/3	552	26	52.431	<i>Saccharum officinarum</i>
<b>64</b> /ACG28578.1/ NCBIprot	<sup>b</sup> Cytochrome P450 CYP74A19	1/1	50	3	53.357	<i>Zea mays</i>
<b>65</b> /KVH40997.1/ NCBIprot	<sup>b</sup> Aldehyde dehydrogenase, conserved site-containing protein	1/1	49	3	52.352	<i>Cynara cardunculus var. scolymys</i>
<b>66</b> /XP_002444986.1/ NCBIprot	Hypothetical protein (Glycosyltransferase – UniProtKB)	1/1	106	2	53.225	<i>Sorghum bicolor</i>
<b>67</b> /XP_002442053.1/ NCBIprot	<sup>b</sup> Hypothetical protein (Argininosuccinate synthase – UniProtKB)	1/1	62	3	53.100	<i>Sorghum bicolor</i>
<b>68</b> /LCYD1_ORYSJ /SwissProt	<sup>b</sup> Putative L-cysteine desulhydrase 1; Isopenicillin N epimerase -like	1/1	102	5	52.430	<i>Oryza sativa Japonica Group</i>
<b>69</b> /AGT15905.1/ NCBIprot	Serine hydroxymethyltransferase	2/2	131	6	52.087	<i>Saccharum hybrid cultivar R570</i>
<b>70</b> /GDI_ARATH/ SwissProt	<sup>b</sup> Guanosine nucleotide diphosphate dissociation inhibitor At5g09550 (Rab GDP dissociation inhibitor alpha-like)	1/1	70	5	49.974	<i>Arabidopsis thaliana</i>
<b>71</b> /ENO_ORYSJ/ SwissProt	2-phospho-D-glycerate hydro-lyase (Enolase)	4/0	259	12	48.285	<i>Oryza sativa Japonica Group</i>
<b>72</b> /KXG22883.1/ NCBIprot	Hypothetical protein (Nucleoside-triphosphatase; Apyrase – UniProtKB)	2/2	112	6	48.195	<i>Sorghum bicolor</i>
<b>73</b> /IF4A_MAIZE/ SwissProt	Eukaryotic initiation factor 4A	2/1	114	9	46.849	<i>Zea mays</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
74/OEL34186.1/NCBIprot	Transaldolase	3/1	193	10	46.320	<i>Dichantheium oligosanthos</i>
75/EMT04083.1/NCBIprot	LL-diaminopimelate aminotransferase, chloroplastic	1/1	60	4	46.306	<i>Aegilops tauschii</i>
76/ICDHC_ARATH/SwissProt	Cytosolic isocitrate dehydrogenase [NADP]	1/1	89	4	46.059	<i>Arabidopsis thaliana</i>
77/AQK40926.1/NCBIprot	Obg-like ATPase 1	1/1	69	4	46.058	<i>Zea mays</i>
78/OEL32119.1/NCBIprot	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase	1/1	67	2	46.047	<i>Dichantheium oligosanthos</i>
79/NP_001151172.1/NCBIprot	<sup>b</sup> 10-deacetylbaocatin III 10-O-acetyltransferase (10-DBAT)	1/1	50	5	45.911	<i>Zea mays</i>
80/XP_008665881.1/NCBIprot	<sup>b</sup> Predicted: uncharacterized protein (Topless-related protein – UniProtKB)	1/1	51	3	45.605	<i>Zea mays</i>
81/XP_002447121.1/NCBIprot	Hypothetical protein (Aminomethyltransferase - UniProtKB)	2/2	121	7	44.388	<i>Sorghum bicolor</i>
82/OPR7_ORYSJ/SwissProt	12-oxophytodienoate reductase	1/1	64	2	43.878	<i>Oryza sativa Japonica Group</i>
83/OEL37569.1/NCBIprot	RuBisCO large subunit-binding protein subunit beta, chloroplastic, partial	2/1	111	5	43.488	<i>Dichantheium oligosanthos</i>
84/ONM15574.1/NCBIprot	Isopropylmalate dehydrogenase 2	1/1	64	3	43.132	<i>Zea mays</i>
85/NP_001150259.1 /NCBIprot	Pyruvate dehydrogenase E1 component alpha subunit	1/1	67	3	43.002	<i>Zea mays</i>
86/ONM20737.1/NCBIprot	<sup>b</sup> Polyadenylate-binding protein 2, partial	1/1	64	4	42.897	<i>Zea mays</i>
87/KMZ65420.1 /NCBIprot	V-type proton ATPase subunit C	1/1	63	4	42.641	<i>Zostera marina</i>
88/NP_001142404.1/NCBIprot	Phosphoglycerate kinase	4/4	284	16	42.470	<i>Zea mays</i>
89/KHG03650.1/NCBIprot	<sup>b</sup> Putative fructose-bisphosphate aldolase 3, chloroplastic	1/1	92	3	41.943	<i>Gossypium arboreum</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>90</b> /KXG39210.1/NCBIprot	Hypothetical protein (Acetyl-CoA acyltransferase - UniProtKB)	2/2	132	6	41.564	<i>Sorghum bicolor</i>
<b>91</b> /OEL24402.1/NCBIprot	3-hydroxyisobutyryl-CoA hydrolase-like protein 5, partial	1/1	54	3	41.366	<i>Dichantheium oligosanthes</i>
<b>92</b> /AGI97002.1/NCBIprot	Cysteine synthase	1/1	50	3	41.361	<i>Triticum turgidum</i> subsp. <i>durum</i>
<b>93</b> /XP_002466246.1/NCBIprot	Hypothetical protein (Imidazolonepropionase - UniProtKB)	2/2	135	6	40.544	<i>Sorghum bicolor</i>
<b>94</b> /ONM22945.1/NCBIprot	P-loop containing nucleoside triphosphate hydrolase superfamily protein	1/1	66	4	39.908	<i>Zea mays</i>
<b>95</b> /COMT1_SACOF/SwissProt	Caffeic acid 3-O-methyltransferase;	3/3	126	8	39.838	<i>Saccharum officinarum</i>
<b>96</b> /XP_002465329.1/NCBIprot	Hypothetical protein (Ricin B-like lecithin R40G2 – UniProtKB)	1/1	79	5	39.718	<i>Sorghum bicolor</i>
<b>97</b> /ONM13950.1 /NCBIprot	<sup>b</sup> Adenosylmethionine aminotransferase 1	1/1	63	3	39.635	<i>Zea mays</i>
<b>98</b> /AAW21273.1/NCBIprot	<sup>b</sup> Glutamine synthetase	3/2	166	14	39.387	<i>Saccharum Officinarum</i>
<b>99</b> /ALF_MAIZE/SwissProt	Aldolase C (Fructose-bisphosphate aldolase cytoplasmic)	3/2	216	13	39.036	<i>Zea mays</i>
<b>100</b> /XP_004960754/NCBIprot	Predicted: 2-alkenal reductase (NADP(+)-dependent)-like	1/1	55	3	38.880	<i>Setaria italica</i>
<b>101</b> /ACG36544.1/NCBIprot	Legumin-like protein (Glutelin type-A1)	2/0	125	8	38.077	<i>Zea mays</i>
<b>102</b> /EMS53569.1/NCBIprot	Adenosine kinase 2	3/1	178	12	37.680	<i>Triticum urartu</i>
<b>103</b> /OEL25000.1/NCBIprot	Ribokinase	2/2	118	6	37.603	<i>Dichantheium oligosanthes</i>
<b>104</b> /OEL22313.1/NCBIprot	Peroxidase	3/3	149	13	36.793	<i>Dichantheium oligosanthes</i>
<b>105</b> /NP_001136800.1/NCBIprot	Guanine nucleotide-binding protein subunit beta-like protein A (Receptor for activated C kinase 1A)	5/1	313	13	36.670	<i>Zea mays</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>106</b> /KXG20851.1/ NCBIprot	Hypothetical protein (Glyceraldehyde-3-phosphate dehydrogenase – UniProtKB)	3/3	226	16	36.618	<i>Sorghum bicolor</i>
<b>107</b> /AEA11483.1/ NCBIprot	Beta-1,3-glucanase (Glucan endo-1,3-beta-glucosidase, basic vacuolar isoform)	1/1	143	10	35.987	<i>Zea mays</i>
<b>108</b> /MDHC_BETVU/ SwissProt	Malate dehydrogenase, cytoplasmic	2/1	155	10	35.810	<i>Beta vulgaris</i>
<b>109</b> /NP_001142100.1/ NCBIprot	Malate dehydrogenase, mitochondrial	4/2	344	26	35.492	<i>Zea mays</i>
<b>110</b> /NP_001130539.1/ NCBIprot	Late embryogenesis abundant protein group 2	2/2	127	7	35.309	<i>Zea mays</i>
<b>111</b> /AQL07637.1/ NCBIprot	<sup>b</sup> UDP-glucuronic acid decarboxylase	1/1	49	3	35.007	<i>Zea mays</i>
<b>112</b> /SPDE_COFAR /SwissProt	Spermidine synthase	1/1	53	4	34.878	<i>Coffea arabica</i>
<b>113</b> /APF31922.1/ NCBIprot	Putative fructokinase 1	3/2	225	13	34.865	<i>Saccharum spontaneum</i>
<b>114</b> /XP_015612215.1/ NCBIprot	<sup>b</sup> Predicted: nitrile-specifier protein 5	1/1	53	3	34.746	<i>Oryza sativa Japonica Group</i>
<b>115</b> /XP_020108004.1/ NCBIprot	<sup>b</sup> Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	1/1	50	7	34.672	<i>Ananas comosus</i>
<b>116</b> /AQK39735.1/ NCBIprot	Putative oxidoreductase, aldo/keto reductase family protein	1/1	77	6	34.649	<i>Zea mays</i>
<b>117</b> /ONM12595.1/ NCBIprot	26S proteasome non-ATPase regulatory subunit 7 homolog A	1/1	52	3	34.543	<i>Zea mays</i>
<b>118</b> /NP_001144369.1/ NCBIprot	<sup>b</sup> Uncharacterized protein (2,3-dimethylmalate lyase-like - UniProtKB)	2/2	128	9	33.588	<i>Zea mays</i>
<b>119</b> /ACG31861.1/ NCBIprot	Succinyl-CoA ligase alpha-chain 2	1/1	70	6	33.517	<i>Zea mays</i>
<b>120</b> /AHF18211.1/ NCBIprot	Glyoxylase 1(Lactoylglutathione lyase)	1/1	59	4	33.005	<i>Sccharum hybrid cultivar</i>
<b>121</b> /IFRH_MAIZE/ SwissProt	Isoflavone reductase homolog IRL	1/1	54	3	32.831	<i>Zea mays</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>122</b> /AQQ46679.1/NCBIprot	<sup>b</sup> Cysteine protease 1	1/1	64	5	32.811	<i>Zea mays</i>
<b>123</b> /KDSA_PEA/SwissProt	<sup>b</sup> 2-dehydro-3-deoxyphosphooctonate aldolase	1/1	58	4	32.045	<i>Pisum sativum</i>
<b>124</b> /OEL27074.1/NCBIprot	60S acidic ribosomal protein P0	2/2	98	15	31.928	<i>Dichantheium oligosanthos</i>
<b>125</b> /ABR25574.1/NCBIprot	Tubulin alpha-3 chain, partial	2/1	116	12	31.592	<i>Oryza sativa Japonica Group</i>
<b>126</b> /AQL00963.1/NCBIprot	<sup>b</sup> Putative carboxylesterase 2 (gibberellin receptor GID1L2)	1/1	51	3	31.561	<i>Zea mays</i>
<b>127</b> /EMT30183.1/NCBIprot	<sup>b</sup> Putative oxidoreductase GLYR1(Succinic semialdehyde/glyoxylate reductase)	1/1	49	7	31.284	<i>Aegilops tauschii</i>
<b>128</b> /XP_020197734.1/NCBIprot	<sup>b</sup> Stem 28 kDa glycoprotein-like	1/1	54	5	30.561	<i>Aegilops tauschii</i> subsp. <i>tauschii</i>
<b>129</b> /AQL04115.1/NCBIprot	Elongation factor 1-gamma 3	1/1	68	7	29.369	<i>Zea mays</i>
<b>130</b> /XP_015901239.1/NCBIprot	Predicted: Pectinesterase 3, partial	1/1	52	3	29.318	<i>Ziziphus jujuba</i>
<b>131</b> /XP_002465318.1/NCBIprot	<sup>b</sup> Hypothetical protein (Hydroxyacylglutathione hydrolase, putative, expressed; Glyoxalase II – UniProtKB)	1/1	54	4	29.012	<i>Sorghum bicolor</i>
<b>132</b> /AAP48904.1/NCBIprot	<sup>b</sup> 14-3-3-like protein	1/1	50	11	28.978	<i>Saccharum hybrid cultivar CP65-357</i>
<b>133</b> /ACN33806.1/NCBIprot	<sup>b</sup> Unknown (6-phosphogluconolactonase – UniProtKB)	1/1	65	6	28.956	<i>Zea mays</i>
<b>134</b> /AQL04284.1/NCBIprot	<sup>b</sup> Transducin/WD40 repeat-like superfamily protein	1/1	53	4	28.752	<i>Zea mays</i>
<b>135</b> /PMM_ORYSI/SwissProt	<sup>b</sup> Phosphomannomutase	1/1	55	7	28.403	<i>Oryza sativa Indica Group</i>
<b>136</b> /EES06920.2/NCBIprot	<sup>b</sup> Hypothetical protein (2-cys peroxiredoxin BAS1 – UniProtKB)	1/1	49	5	28.236	<i>Sorghum bicolor</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>137</b> /AGO97076.1/NCBIprot	Ascorbate peroxidase	3/1	213	19	27.556	<i>Saccharum</i> hybrid cultivar GT28
<b>138</b> /XP_020184931.1/NCBIprot	Stress-response A/B barrel domain-containing protein DABB1-like	1/1	71	4	27.325	<i>Aegilops tauschii</i> subsp. <i>tauschii</i>
<b>139</b> /ALP06207.1/NCBIprot	Triosephosphate isomerase	4/4	254	26	27.181	<i>Saccharum officinaum</i>
<b>140</b> /AGT17219.1/NCBIprot	Proteasome alpha subunit D2 (Proteasome alpha-type)	1/1	96	5	27.087	<i>Saccharum</i> hybrid cultivar R570
<b>141</b> /EXPA1_ARATH/SwissProt	<sup>b</sup> Expansin-A1	1/1	51	3	26.957	<i>Arabidopsis thaliana</i>
<b>142</b> /XP_008652895.1/NCBIprot	Predicted: Proteasome subunit beta type-1	3/2	217	19	26.502	<i>Zea mays</i>
<b>143</b> /AOC_ORYSI/SwissProt	<sup>b</sup> Allene oxide cyclase, chloroplastic	1/1	57	3	26.206	<i>Oryza sativa</i> Indica Group
<b>144</b> /NP_001148765.1/NCBIprot	<sup>b</sup> Endo-1,3-1,4-beta-D-glucanase	1/1	83	7	25.930	<i>Zea mays</i>
<b>145</b> /ONM05978.1/NCBIprot	Aspartic proteinase A1	3/3	204	20	25.606	<i>Zea mays</i>
<b>146</b> /ACT53877.1/NCBIprot	<sup>b</sup> Superoxide dismutase [Mn]	3/3	180	14	25.327	<i>Saccharum officinarum</i>
<b>147</b> /JAU71746.1/NCBIprot	ATP-citrate synthase beta chain protein 1	1/1	59	5	25.076	<i>Noccaea caerulescens</i>
<b>148</b> /GSTF1_MAIZE/SwissProt	Glutathione S-transferase 1	1/1	54	9	24.034	<i>Zea mays</i>
<b>149</b> /CFIS2_ARATH/SwissProt	<sup>b</sup> Pre-mRNA cleavage factor Im 25 kDa subunit 2	1/1	77	7	23.043	<i>Arabidopsis thaliana</i>
<b>150</b> /XP_018721988.1/NCBIprot	Predicted: Aspartate--tRNA ligase 2, cytoplasmic-like (Aspartyl-tRNA synthetase, cytoplasmic)	1/1	64	6	22.889	<i>Eucalyptus grandis</i>
<b>151</b> /XP_006644813.1/NCBIprot	Predicted: NAD(P)H dehydrogenase (quinone) FQR1-like (Flavoprotein wrbA)	2/1	136	17	21.702	<i>Oryza brachyantha</i>
<b>152</b> /EMT08544.1/NCBIprot	Ras-related protein ARA-3	2/1	132	13	21.365	<i>Aegilops tauschii</i>



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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
<b>153</b> /OEL13196.1/ NCBIprot	<sup>b</sup> Cyclic phosphodiesterase	1/1	52	6	21.039	<i>Dichantheium oligosanthes</i>
<b>154</b> /ARF_MAIZE/ SwissProt	<sup>b</sup> ADP-ribosylation factor	1/1	65	7	20.705	<i>Zea mays</i>
<b>155</b> /KQL13994.1/ NCBIprot	<sup>b</sup> Hypothetical protein (DEAD-box ATP-dependent RNA helicase 56 – UniProtKB)	1/1	84	12	20.625	<i>Setaria italica</i>
<b>156</b> /AID15806.1/ NCBIprot	Beta-tubulin, partial	1/1	55	5	19.345	<i>Hypericum perforatum</i>
<b>157</b> /AQK53244.1/ NCBIprot	60S ribosomal protein L6	1/1	57	8	18.857	<i>Zea mays</i>
<b>158</b> /AGT16090.1/ NCBIprot	Cyclophilin (Peptidyl-prolyl cis-trans isomerase)	2/1	132	16	18.160	<i>Saccharum hybrid cultivar R570</i>
<b>159</b> /AGT16537.1/ NCBIprot	60S ribosomal protein L12	2/1	116	14	17.807	<i>Saccharum hybrid cultivar R570</i>
<b>160</b> /AHX42566.1/ NCBIprot	<sup>b</sup> Translation initiation factor5A	1/1	58	7	17.671	<i>Saccharum hybrid cultivar ROC22</i>
<b>161</b> /ACG31943.1/ NCBIprot	<sup>b</sup> Hypothetical protein – Peptide: STGFVWLR (DUF538 family protein -UniProtKB)	1/1	55	4	17.568	<i>Zea mays</i>
<b>162</b> /XP_002446634.1/ NCBIprot	<sup>b</sup> Hypothetical protein (Major latex protein – UniProtKB)	1/1	52	10	17.385	<i>Sorghum bicolor</i>
<b>163</b> /ABA41463.1/ NCBIprot	<sup>b</sup> Chitinase, partial (Endochitinase)	1/1	54	10	16.919	<i>Sorghum halepense</i>
<b>164</b> /EMT30334.1/ NCBIprot	Thioredoxin reductase (Peroxisomal antioxidant enzyme)	1/1	72	20	9.219	<i>Zea mays</i>

<sup>b</sup> – Proteins found only in fourth raton