

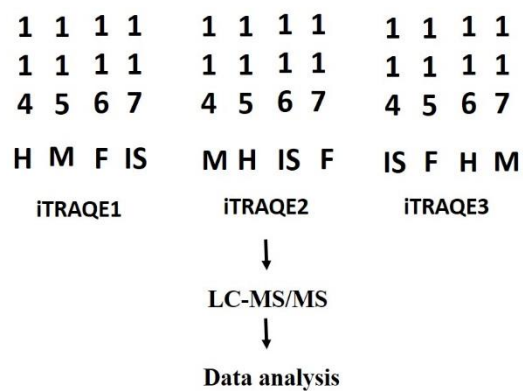


Fig. 1. Suppl. A schematic representation of the experimental design for isobaric tags for relative and absolute quantitation (iTRAQ) proteomic analysis. H - hybrid line RS5322, F - female parent RS 53, M - male parent SN22, IS - internal standard.

Table 1 Suppl. The *Kyoto encyclopedia of genes and genomes* list of differentially abundant proteins (DAPs) between hybrid RS 5322 and its parental lines RS53 and SN22.

Pathway	DAP with pathway annotation	Percentage	P value	Pathway ID
Metabolic pathways	122	15.12	0.04938	ko01100
Biosynthesis of secondary metabolites	59	7.31	0.730973	ko01110
Ribosome	19	2.35	0.089727	ko03010
Protein processing in endoplasmic reticulum	16	1.98	0.067121	ko04141
Spliceosome	13	1.61	0.371996	ko03040
Glyoxylate and dicarboxylate metabolism	12	1.49	0.002617	ko00630
Starch and sucrose metabolism	12	1.49	0.483409	ko00500
Phagosome	10	1.24	0.020409	ko04145
Peroxisome	10	1.24	0.039202	ko04146
Oxidative phosphorylation	10	1.24	0.123473	ko00190
Cysteine and methionine metabolism	9	1.12	0.017098	ko00270
Glutathione metabolism	8	0.99	0.105794	ko00480
Galactose metabolism	8	0.99	0.18022	ko00052
Glycolysis / Gluconeogenesis	8	0.99	0.824468	ko00010
RNA transport	8	0.99	0.849754	ko03013
Phenylpropanoid biosynthesis	8	0.99	0.867828	ko00940
Fatty acid metabolism	7	0.87	0.158212	ko00071
Glycine, serine and threonine metabolism	7	0.87	0.233695	ko00260
Fructose and mannose metabolism	7	0.87	0.254231	ko00051
Carbon fixation in photosynthetic organisms	7	0.87	0.463634	ko00710
Amino sugar and nucleotide sugar metabolism	7	0.87	0.639263	ko00520
alpha-Linolenic acid metabolism	6	0.74	0.090846	ko00592
Pentose phosphate pathway	6	0.74	0.098311	ko00030
Proteasome	6	0.74	0.159013	ko03050
Photosynthesis	6	0.74	0.210233	ko00195
Arginine and proline metabolism	6	0.74	0.289812	ko00330
Phenylalanine metabolism	6	0.74	0.586369	ko00360
mRNA surveillance pathway	6	0.74	0.730663	ko03015
Purine metabolism	6	0.74	0.871863	ko00230
Plant-pathogen interaction	6	0.74	0.962452	ko04626
Nitrogen metabolism	5	0.62	0.073093	ko00910
Propanoate metabolism	5	0.62	0.319244	ko00640
Valine, leucine and isoleucine degradation	5	0.62	0.332748	ko00280
Citrate cycle (TCA cycle)	5	0.62	0.359891	ko00020
Flavonoid biosynthesis	5	0.62	0.660545	ko00941

Pathway	DAP with pathway annotation	Percentage	<i>P</i> value	Pathway ID
Plant hormone signal transduction	5	0.62	0.942414	ko04075
Biosynthesis of plant hormones	4	0.50	0.365789	ko01070
Selenocompound metabolism	4	0.50	0.040542	ko00450
Alanine, aspartate and glutamate metabolism	4	0.50	0.477473	ko00250
Ascorbate and aldarate metabolism	4	0.50	0.506898	ko00053
Pentose and glucuronate interconversions	4	0.50	0.506898	ko00040
Ribosome biogenesis in eukaryotes	4	0.50	0.687493	ko03008
Aminoacyl-tRNA biosynthesis	4	0.50	0.729572	ko00970
Pyruvate metabolism	4	0.50	0.948228	ko00620
Steroid biosynthesis	3	0.37	0.196174	ko00100
N-Glycan biosynthesis	3	0.37	0.306092	ko00510
Biosynthesis of unsaturated fatty acids	3	0.37	0.381079	ko01040
Phenylalanine, tyrosine and tryptophan biosynthesis	3	0.37	0.418005	ko00400
DNA replication	3	0.37	0.436203	ko03030
Cutin, suberine and wax biosynthesis	3	0.37	0.673034	ko00073
Cyanoamino acid metabolism	3	0.37	0.722307	ko00460
Glycerophospholipid metabolism	3	0.37	0.744689	ko00564
Pyrimidine metabolism	3	0.37	0.975565	ko00240
Benzoxazinoid biosynthesis	2	0.25	0.189287	ko00402
Vitamin B6 metabolism	2	0.25	0.239732	ko00750
Glycosaminoglycan degradation	2	0.25	0.438288	ko00531
Valine, leucine and isoleucine biosynthesis	2	0.25	0.527046	ko00290
Fatty acid biosynthesis	2	0.25	0.567741	ko00061
Lysine degradation	2	0.25	0.623936	ko00310
Terpenoid backbone biosynthesis	2	0.25	0.623936	ko00900
Inositol phosphate metabolism	2	0.25	0.719097	ko00562
beta-Alanine metabolism	2	0.25	0.719097	ko00410
Tryptophan metabolism	2	0.25	0.758587	ko00380
Glycerolipid metabolism	2	0.25	0.841209	ko00561
Other glycan degradation	2	0.25	0.885391	ko00511
Endocytosis	2	0.25	0.938259	ko04144
Ubiquitin mediated proteolysis	2	0.25	0.965467	ko04120

Table 2 Suppl. Some pathways and its differentially abundant proteins (DAPs) between hybrid RS5322 and its parental lines.

Pathway	Protein
Protein processing in endoplasmic reticulum	gi 475560782 gb EMT13638.1 , gi 473843006 gb EMS47358.1 , gi 326523407 dbj BAJ88744.1 , gi 473886821 gb EMS48186.1 , gi 475501687 gb EMT04348.1 , gi 475614856 gb EMT29218.1 , gi 475585010 gb EMT19943.1 , gi 474200923 gb EMS58484.1 , gi 525333932 gb AGR45906.1 , gi 475613767 gb EMT28866.1 , gi 299469372 emb CBG91904.1 , gi 475474990 gb EMT02551.1 , gi 474188500 gb EMS58004.1 , gi 475507214 gb EMT04916.1 , gi 296524366 emb CBM36838.1 , gi 475502924 gb EMT04480.1
Oxidative phosphorylation	gi 556927207 ref YP_008758164.1 , gi 475602936 gb EMT25261.1 , gi 291498617 gb ADE08091.1 , gi 326496134 dbj BAJ90688.1 , gi 227303166 emb CAY05799.1 , gi 285014508 gb ADC33136.1 , gi 475609344 gb EMT27349.1 , gi 326510121 dbj BAJ87277.1 , gi 474365424 gb EMS63441.1 , gi 326508923 dbj BAJ86854.1
Cysteine and methionine metabolism	gi 68655456 emb CAJ01706.1 , gi 14522834 dbj BAB61039.1 , gi 122220777 sp Q4LB22.1 METK3_HORVU, gi 326500176 dbj BAJ90922.1 , gi 326507468 dbj BAK03127.1 , gi 326512178 dbj BAJ96070.1 , gi 300592971 emb CBV31787.1 , gi 326498609 dbj BAK02290.1 , gi 473842616 gb EMS47328.1
Starch and sucrose metabolism	gi 475477580 gb EMT02687.1 , gi 189096679 gb ABY56824.3 , gi 18076790 emb CAC85913.1 , gi 475536281 gb EMT08894.1 , gi 18025340 gb AAK38481.1 , gi 433359116 dbj BAM74037.1 , gi 26986190 emb CAD58960.1 , gi 474340105 gb EMS62631.1 , gi 326496208 dbj BAJ94566.1 , gi 475537000 gb EMT09010.1 , gi 269316344 gb ACZ37249.1 , gi 326533776 dbj BAK05419.1
Glycolysis/gluconeogenesis	gi 326509025 dbj BAJ86905.1 , gi 475611094 gb EMT27967.1 , gi 18076790 emb CAC85913.1 , gi 475596279 gb EMT23312.1 , gi 474069723 gb EMS54289.1 , gi 474213532 gb EMS58952.1 , gi 326499908 dbj BAJ90789.1 , gi 326513996 dbj BAJ92148.1
Proteasome	gi 474394962 gb EMS65641.1 , gi 474135678 gb EMS56329.1 , gi 326509597 dbj BAJ87014.1 , gi 474358967 gb EMS63228.1 , gi 473990592 gb EMS51868.1 , gi 475615536 gb EMT29474.1
Glycine, serine and threonine metabolism	gi 475611952 gb EMT28261.1 , gi 296514046 emb CBM39882.1 , gi 326490820 dbj BAJ90077.1 , gi 326500176 dbj BAJ90922.1 , gi 475582311 gb EMT19090.1 , gi 326507214 dbj BAJ95684.1 , gi 408689025 gb AFU81119.1
Arginine and proline metabolism	gi 326509025 dbj BAJ86905.1 , gi 473888366 gb EMS48337.1 , gi 475578811 gb EMT18195.1 , gi 326495404 dbj BAJ85798.1 , gi 300592971 emb CBV31787.1 , gi 60686892 gb AAX35536.1
Citrate cycle (TCA cycle)	gi 475611094 gb EMT27967.1 , gi 473887274 gb EMS48231.1 , gi 474057746 gb EMS53891.1 , gi 475561313 gb EMT13756.1 , gi 326495330 dbj BAJ85761.1
Plant hormone signal transduction	gi 475618002 gb EMT30308.1 , gi 326504274 dbj BAJ90969.1 , gi 473755236 gb EMS45715.1 , gi 475615731 gb EMT29542.1 , gi 326526535 dbj BAJ97284.1
Biosynthesis of plant hormones	gi 82907865 dbj ABB93126.1 , gi 431812563 dbj AGA84060.1 , gi 1032288430 sp OAP02757.1 , gi 326499558 dbj BAJ86090.1
Pyruvate metabolism	gi 326509025 dbj BAJ86905.1 , gi 475611094 gb EMT27967.1 , gi 474023061 gb EMS52969.1 , gi 326495330 dbj BAJ85761.1
Ubiquitin mediated proteolysis	gi 475577091 gb EMT17712.1 , gi 326526535 dbj BAJ97284.1

Table 3 Suppl. Primer sequences of different abundant proteins (DAPs) encoding genes used for real time quantitative PCR.
H - hybrid, P - parents.

Uniprot ID	Protein name	Primer (5'-3')	Expression change in H vs. P
B5LEC3	thioredoxin RT-F	TCCTTCCTGTCGTCCTTG TG	down
	thioredoxin RT-R	GTGTTCCCTCCCAGTGCTTG T	
B6ECP0	6-fructosyltransferase RT-F	CACAGAAGCAACGACA ACTC	down
	6-fructosyltransferase RT-R	AGAACGAGGTGGACGCATA	
B6T7B2	40S ribosomal protein S9 RT-F	GTATCTTTGAGGGTGAGGCG	down
	40S ribosomal protein S9 RT-R	GACAAGTGTTTGAAGCCGC	
C0KWE8	glucose-1-phosphate adenylyltransferase RT-F	GGGTGCCAACTACAGGCTTA	down
	glucose-1-phosphate adenylyltransferase RT-F	AGGGTTATCTGGGCTCTGCT	
Q281E8	NDHF, NAD(P)H-quinone oxidoreductase subunit 5 RT-F	CAGCACCGTAAATCCACTTGA	down
	NDHF, NAD(P)H-quinone oxidoreductase subunit 5 RT-R	GGCATTCTGTTGAGACCTGA	
F6LAX4	protein phosphatase 2A structural subunit RT-F	TCCGAGACAAAGCAGTTGAG	down
	protein phosphatase 2A structural subunit RT-R	GGTGGCACTTGATAGGCTA	
G0Z6F1	26s proteasome non-ATPase regulatory subunit RT-F	TTGCTGGCTATCGGGTGTT	down
	26s proteasome non-ATPase regulatory subunit RT-R	GATGGCTTATTCAGGTGCCC	
Q0WVG8	triticain alpha RT-F	AGGTCTGATGGACTATGCGT	up
	triticain alpha RT-R	TTCTCACTGTTACGGGCA	
Q1XIR9	beta-glucosidase RT-F	ACCCACCCATCTTCATCACT	up
	beta-glucosidase RT-R	CCCAGGCTCCATTCAAAGTT	
Q401N7	aspartic proteinase RT-F	CTTCATTGCTTGCTGGTCCC	up
	aspartic proteinase RT-R	CACGAGTCCCATCAAAGGTG	
Q41534	ATP synthase subunit beta RT-F	AACCAACTCTTGCCACCGAT	up
	ATP synthase subunit beta RT-R	AACAGCAGGGTAAATGCCCA	
D8L9B0	putative PDI-like protein RT-F	ATCACCACCCCTCACACAGGA	up
	putative PDI-like protein RT-R	TCACGCTCCACAAAGACAAA	

Table 4 Suppl. A part of significant differently abundant proteins (DAPs) in hybrid RS5322 compared with its parental lines. More DAPs and their detailed information could be found at the research laboratory homepage: (http://www.538hybridwheatsd.cn/Blog/html/blog_github.html).

Group ID	Accession	Description	Score	Mass
136	gi 475609344 gb EMT27349.1	ATP synthase subunit O, mitochondrial [<i>Aegilops tauschii</i>]	158	32912
95	gi 475558941 gb EMT13223.1	hypothetical protein F775_42463 [<i>Aegilops tauschii</i>]	188	13259
77	gi 326526193 dbj BAJ93273.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	241	37059
35	gi 475611952 gb EMT28261.1	hypothetical protein F775_27222 [<i>Aegilops tauschii</i>]	237	31519
129	gi 213509661 emb CAS92352.1	unnamed protein product [<i>Triticum aestivum</i>]	82	45494
50	gi 119390311 pdb 2IWT A	Chain A, Thioredoxin H2 (Hvtrhx2) In A Mixed Disulfide Complex With The Target Protein Basi	136	16825
37	gi 14522834 dbj BAB61039.1	IDI1 [<i>Hordeum vulgare</i>]	117	28183
159	gi 475585498 gb EMT20069.1	hypothetical protein F775_52645 [<i>Aegilops tauschii</i>]	43	39294
30	gi 475563300 gb EMT14246.1	Aspartic proteinase nepenthesin-2 [<i>Aegilops tauschii</i>]	92	47681
51	gi 326506068 dbj BAJ91273.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	76	49487
109	gi 355525033 gb AET05487.1	26S proteasome non-ATPase regulatory subunit 1 homolog, OS= <i>Medicago truncatula</i> (Barrel medic) (<i>Medicago tribuloides</i>)	502	76441
45	gi 326510869 dbj BAJ91782.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326488323 dbj BAJ93830.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	181	48406
72	gi 326525759 dbj BAJ88926.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326500054 dbj BAJ90862.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	88	23066
126	gi 326488085 dbj BAJ89881.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	334	32733
86	gi 475559891 gb EMT13441.1	Phosphatase yidA [<i>Aegilops tauschii</i>]	164	69528
102	gi 473865714 gb EMS47652.1	T-complex protein 1 subunit gamma [<i>Triticum urartu</i>]	406	76608
179	gi 475537000 gb EMT09010.1	6(G)-fructosyltransferase [<i>Aegilops tauschii</i>]	2228	66361
207	gi 326495324 dbj BAJ85758.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	89	88226

Group ID	Accession	Description	Score	Mass
20	gi 475560782 gb EMT13638.1	hypothetical protein F775_28551 [<i>Aegilops tauschii</i>]	198	55436
60	gi 474145957 gb EMS56757.1	Peroxiredoxin-2C [<i>Triticum urartu</i>]	773	21329
131	gi 474188572 gb EMS58008.1	hypothetical protein TRIUR3_09624 [<i>Triticum urartu</i>]	109	2E+05
201	gi 475584115 gb EMT19676.1	Chalcone--flavonone isomerase [<i>Aegilops tauschii</i>]	421	23902
183	gi 475514396 gb EMT05713.1	putative Lichenase-2 [<i>Aegilops tauschii</i>]	121	36596
68	gi 189096679 gb ABY56824.3	starch synthase IIb precursor [<i>Triticum aestivum</i>]	170	82422
154	gi 474403036 gb EMS66221.1	Pre-mRNA-splicing factor SYF1 [<i>Triticum urartu</i>]	195	1E+05
163	gi 475615536 gb EMT29474.1	Proteasome subunit beta type-2 [<i>Aegilops tauschii</i>]	586	27613
9	gi 475618002 gb EMT30308.1	Putative serine/threonine-protein kinase [<i>Aegilops tauschii</i>]	79	57547
164	gi 326496134 dbj BAJ90688.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326492994 dbj BAJ84958.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	583	61331
59	gi 257626285 emb CBD24261.1	unnamed protein product [<i>Triticum aestivum</i>]	146	41182
160	gi 475612040 gb EMT28285.1	Putative serine/threonine-protein kinase [<i>Aegilops tauschii</i>]	61	87560
194	gi 474240143 gb EMS59767.1	Peroxisomal fatty acid beta-oxidation multifunctional protein [<i>Triticum urartu</i>]	480	97618
115	gi 475602383 gb EMT25116.1	ADP,ATP carrier protein 1, chloroplastic [<i>Aegilops tauschii</i>]	244	85308
69	gi 474060815 gb EMS53996.1	Cysteine proteinase 1 [<i>Triticum urartu</i>]	66	52014
32	gi 213509663 emb CAS92353.1	unnamed protein product [<i>Triticum aestivum</i>]	102	48923
62	gi 474140076 gb EMS56522.1	Formation of crista junctions protein 1 [<i>Triticum urartu</i>]	171	88547
27	gi 474019416 gb EMS52793.1	Photosystem I reaction center subunit III, chloroplastic [<i>Triticum urartu</i>]	485	35153
65	gi 388890585 gb AFK80346.1	cysteine endopeptidase EP alpha [<i>Secale cereale</i> x <i>Triticum durum</i>] >gi 111073715 dbj BAF02546.1 triticain alpha [<i>Triticum aestivum</i>]	768	58569
1	gi 474415713 gb EMS67155.1	hypothetical protein TRIUR3_35361 [<i>Triticum urartu</i>]	253	56757

Group ID	Accession	Description	Score	Mass
112	gi 257741606 emb CBC56521.1	unnamed protein product [Triticum aestivum] >gi 257298603 emb CBC19272.1 unnamed protein product [Triticum aestivum] >gi 219800275 emb CAW50356.1 unnamed protein product [Triticum aestivum] >gi 219768479 emb CAW68999.1 unnamed protein product [Tr	65	86162
53	gi 474225619 gb EMS59460.1	Isopenicillin N epimerase [Triticum urartu]	269	67161
3	gi 50659030 gb AAT80328.1	UDP-D-glucuronate decarboxylase [Hordeum vulgare]	1013	48327
36	gi 474207793 gb EMS58764.1	Beta-adaptin-like protein C [Triticum urartu]	768	1E+05
169	gi 326520097 dbj BAK03973.1	predicted protein [Hordeum vulgare subsp. vulgare]	718	32198
130	gi 474394962 gb EMS65641.1	putative 26S proteasome non-ATPase regulatory subunit 7 [Triticum urartu]	246	43650
94	gi 474139210 gb EMS56443.1	Eukaryotic translation initiation factor 3 subunit H [Triticum urartu]	168	43639
5	gi 300592971 emb CBV31787.1	unnamed protein product [Triticum aestivum] >gi 259665562 emb CBG18432.1 unnamed protein product [Triticum aestivum] >gi 227468359 emb CAY35068.1 unnamed protein product [Triticum aestivum]	167	54349
209	gi 326495040 dbj BAJ85616.1	predicted protein [Hordeum vulgare subsp. vulgare]	446	59596
138	gi 326525118 dbj BAK07829.1	predicted protein [Hordeum vulgare subsp. vulgare] >gi 326501688 dbj BAK02633.1 predicted protein [Hordeum vulgare subsp. vulgare]	258	18530
70	gi 475576617 gb EMT17593.1	Transcription-associated protein 1 [Aegilops tauschii]	264	5E+05
193	gi 326505920 dbj BAJ91199.1	predicted protein [Hordeum vulgare subsp. vulgare] >gi 326503086 dbj BAJ99168.1 predicted protein [Hordeum vulgare subsp. vulgare]	267	33768
178	gi 326499686 dbj BAJ86154.1	predicted protein [Hordeum vulgare subsp. vulgare]	639	38428

Group ID	Accession	Description	Score	Mass
14	gi 86169677 gb ABC87082.1	1,4-beta-D-mannan endohydrolase precursor [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	85	47090
92	gi 475596279 gb EMT23312.1	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic [<i>Aegilops tauschii</i>] >gi 253783729 emb CAZ76054.1 glyceraldehyde-3-phosphate dehydrogenase [<i>Triticum aestivum</i>]	3408	46049
189	gi 474202683 sp EMS58583.1	26S proteasome non-ATPase regulatory subunit 1 homolog, OS= <i>Hordeum vulgare</i> subsp. <i>vulgare</i> (Domesticated barley)	942	30644
75	gi 326500842 dbj BAJ95087.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	86	89433
103	gi 475549225 gb EMT11221.1	Prohibitin-1, mitochondrial [<i>Aegilops tauschii</i>]	258	28720
93	gi 326512146 dbj BAJ96054.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	71	1E+05
206	gi 285014508 gb ADC33136.1	ATP synthase subunit [<i>Triticum aestivum</i>]	1073	46096
158	gi 474433632 gb EMS68077.1	Nuclear cap-binding protein subunit 1 [<i>Triticum urartu</i>]	452	1E+05
180	gi 326531822 dbj BAJ97915.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326489045 dbj BAK01506.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	153	58244
110	gi 473938861 gb EMS50224.1	hypothetical protein TRIUR3_26641 [<i>Triticum urartu</i>]	206	17045
156	gi 326529313 dbj BAK01050.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	148	34261
4	gi 326495308 dbj BAJ85750.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	69	20865
28	gi 326507370 dbj BAK03078.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326494084 dbj BAJ85504.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	70	16010
48	gi 474276985 gb EMS61093.1	Nucleosome assembly protein 1-like 1 [<i>Triticum urartu</i>]	701	55681
192	gi 475621735 gb EMT31601.1	hypothetical protein F775_07603 [<i>Aegilops tauschii</i>]	188	163208

Group ID	Accession	Description	Score	Mass
126	gi 475626301 gb EMT33287.1	Eukaryotic translation initiation factor 3 subunit C [Aegilops tauschii]	675	125127
14	gi 82780752 gb ABB90545.1	lipid transfer protein [Triticum aestivum]	92	22611
31	gi 472904168 gb EMS35737.1	hypothetical protein TRIUR3_33418 [Triticum urartu]	142	16609
87	gi 326534196 dbj BAJ89448.1	predicted protein [Hordeum vulgare subsp. vulgare] >gi 326488909 dbj BAJ98066.1 predicted protein [Hordeum vulgare subsp. vulgare]	88	58125
145	gi 326500968 dbj BAJ95150.1	predicted protein [Hordeum vulgare subsp. vulgare]	102	38309
161	gi 474440426 gb EMS68368.1	Methyl-CpG-binding domain-containing protein [Triticum urartu]	11 585	78020
74	gi 475533405 gb EMT08381.1	Peroxidase 1 [Aegilops tauschii]	330	46600
104	gi 475557235 gb EMT12797.1	hypothetical protein F775_30117 [Aegilops tauschii]	310	15322
186	gi 474124792 gb EMS56163.1	60S ribosomal protein L34 [Triticum urartu]	224	22448
144	gi 475585010 gb EMT19943.1	Calreticulin [Aegilops tauschii]	325	67890
91	gi 26986190 emb CAD58960.1	apoplastic invertase 1 [Hordeum vulgare subsp. vulgare]	725	74823
70	gi 475557449 gb EMT12851.1	hypothetical protein F775_28068 [Aegilops tauschii]	104	41175
103	gi 326497903 dbj BAJ94814.1	predicted protein [Hordeum vulgare subsp. vulgare]	1089	61459
107	gi 207080698 gb ACI22694.1	chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Secale cereale]	955	10024
160	gi 473849801 gb EMS47466.1	hypothetical protein TRIUR3_28031 [Triticum urartu]	766	35778
129	gi 475474990 gb EMT02551.1	Calreticulin [Aegilops tauschii]	1510	60259
84	gi 1657845 gb AAB18202.1	cold acclimation protein WCOR410c [Triticum aestivum]	341	39792
127	gi 326511861 dbj BAJ92075.1	predicted protein [Hordeum vulgare subsp. vulgare]	279	47150
191	gi 433359116 dbj BAM74037.1	cell wall invertase [Triticum aestivum]	787	76325
206	gi 475523982 gb EMT06961.1	hypothetical protein F775_32078 [Aegilops tauschii]	643	57441

Group ID	Accession	Description	Score	Mass
90	gi 475555504 gb EMT12442.1	hypothetical protein F775_07994 [<i>Aegilops tauschii</i>]	935	63764
173	gi 326512178 dbj BAJ96070.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 257676135 emb CBD28039.1 unnamed protein product [<i>Hordeum vulgare</i>] >gi 68655500 emb CAJ01714.1 methionine synthase 2 enzyme [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	6623	100536
201	gi 475616307 gb EMT29716.1	Heparanase-like protein 3 [<i>Aegilops tauschii</i>]	149	60479
207	gi 315113283 pdb 3IZR II	Chain i, Localization Of The Large Subunit Ribosomal Proteins Into A 5.5 A Cryo-Em Map Of <i>Triticum aestivum</i> Translating 80s Ribosome >gi 57471712 gb AAW50987.1 ribosomal protein l34 [<i>Triticum aestivum</i>]	151	19602
108	gi 194339241 gb ACF49504.1	cyclophilin B-D, partial [<i>Triticum durum</i>] >gi 194339239 gb ACF49503.1 cyclophilin B-A, partial [<i>Triticum durum</i>] >gi 194339235 gb ACF49501.1 cyclophilin B-A [<i>Triticum aestivum</i>]	945	28151
98	gi 475612487 gb EMT28429.1	Galactokinase [<i>Aegilops tauschii</i>]	404	114489
88	gi 475552515 gb EMT11805.1	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha [<i>Aegilops tauschii</i>]	219	20722
50	gi 475538478 gb EMT09254.1	Putative chromo domain-containing protein LHP1 [<i>Aegilops tauschii</i>]	164	42506
195	gi 475533715 gb EMT08444.1	hypothetical protein F775_29168 [<i>Aegilops tauschii</i>]	156	105672
158	gi 474015310 gb EMS52665.1	Heat shock 70 kDa protein 4L [<i>Triticum urartu</i>]	2651	168229
99	gi 109716218 gb ABG43091.1	histone deacetylase HDAC2 [<i>Triticum aestivum</i>]	251	47543
159	gi 475561280 gb EMT13748.1	Mitochondrial carnitine/acylcarnitine carrier-like protein [<i>Aegilops tauschii</i>]	310	36541
168	gi 296517433 emb CBM35165.1	unnamed protein product [<i>Triticum aestivum</i>]	205	21053

Group ID	Accession	Description	Score	Mass
25	gi 347954127 gb AEP33646.1	RNA-binding Ras-GAP SH3 binding protein [<i>Triticum aestivum</i>] >gi 347954125 gb AEP33645.1 RNA-binding Ras-GAP SH3 binding protein [<i>Triticum aestivum</i>]	495	53348
8	gi 475625278 gb EMT32909.1	Zinc finger CCCH domain-containing protein 44 [<i>Aegilops tauschii</i>]	73	224258
152	gi 326496895 dbj BAJ98474.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	99	27453
58	gi 431812563 dbj AGA84060.1	NCED2-3, 9-cis-epoxycarotenoid dioxygenase, OS= <i>Triticum aestivum</i>	1242	46865
122	gi 326503624 dbj BAJ86318.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	136	75708
76	gi 474299793 gb EMS61594.1	40S ribosomal protein S11 [<i>Triticum urartu</i>]	157	24264
140	gi 475542713 gb EMT10023.1	Plastocyanin, chloroplasic [<i>Aegilops tauschii</i>]	913	11985
75	gi 32351008 gb AAP76508.1	cyclophilin, partial [<i>Triticum aestivum</i>] >gi 32401384 gb AAP80861.1 cyclophilin [<i>Triticum aestivum</i>]	942	30644
194	gi 114145394 dbj BAF30986.1	glycine-rich RNA-binding protein [<i>Triticum aestivum</i>]	1093	16956
185	gi 525333932 gb AGR45906.1	DnaJ protein 2-like protein [<i>Triticum aestivum</i>]	394	58742
68	gi 475609023 gb EMT27233.1	Actin-2 [<i>Aegilops tauschii</i>] >gi 474372381 gb EMS63944.1 Actin-2 [<i>Triticum urartu</i>] >gi 326495636 dbj BAJ85914.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	4648	47947
39	gi 326511543 dbj BAJ91916.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326494746 dbj BAJ94492.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	894	45045
143	gi 475617700 gb EMT30219.1	Nucleoside-triphosphatase [<i>Aegilops tauschii</i>]	134	59843
109	gi 326499005 dbj BAK05993.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	760	24030
175	gi 269316344 gb ACZ37249.1	alpha-glucosidase [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>]	449	101798

Group ID	Accession	Description	Score	Mass
62	gi 326531758 dbj BAJ97883.1	predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326527311 dbj BAK04597.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326518336 dbj BAJ88197.1 predicted protein [<i>Hordeum vulgare</i> subsp. <i>vulgare</i>] >gi 326516004 dbj BAJ88025.1	539	58158
204	gi 296524366 emb CBM36838.1	unnamed protein product [<i>Triticum aestivum</i>] >gi 257693190 emb CBC96507.1 unnamed protein product [<i>Triticum aestivum</i>] >gi 257676499 emb CBD30051.1 unnamed protein product [<i>Triticum aestivum</i>] >gi 257664356 emb CBD03971.1	1129	77204
164	gi 474150924 gb EMS56954.1	hypothetical protein TRIUR3_15970 [<i>Triticum urartu</i>]	220	179313