

Accession ID	Protein name and pathway information	Peptide sequence	Precursor ion	Product m/z	Product ion
Traes_1A1_1DC9BD199.1	Ketol-acid reductoisomerase (NADP(+))	STVEGITGISK	602.8428++	788.48763	G - y8+
Traes_1A1_2EC98608D.2	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	MSPLVSELR	516.2813++	407.245078	P - y7++
Traes_1A1_2EC98608D.2	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	GDVNVVPIGAVPR	639.3824++	596.351471	P - y6+
Traes_1A1_2EC98608D.2	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	IQNAGTEVVEAK	629.8355++	1017.521115	N - y10+
Traes_1A1_52E56C8D3.1	ATP synthase subunit beta - mitochondrial electron transport / ATP synthesis.F1-ATPase	THDFLPIHR	379.2051+++	522.314692	P - y4+
Traes_1A1_52E56C8D3.1	ATP synthase subunit beta - mitochondrial electron transport / ATP synthesis.F1-ATPase	VDDLLAPQALR	587.3350++	652.293622	P - y4+
Traes_1A1_5738CCBF8.1	Pyruvate, phosphate dikinase - gluconeogenesis / glyoxylate cycle.pyruvate dikinase	VMANADTPGDALR	736.8617++	770.415528	P - y8+
Traes_1A1_5738CCBF8.1	Pyruvate, phosphate dikinase - gluconeogenesis / glyoxylate cycle.pyruvate dikinase	QMIMAPTVELR	644.8412++	714.414465	P - y6+
Traes_1A1_D2049E4A2.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	VLVVAANPANTNALIK	825.5011++	1054.625521	P - y10+
Traes_1A1_D2049E4A2.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	EFAPSIPEK	509.2662++	373.208161	P - y3+
Traes_1A1_DA0EE1337.2	Fructose-1,6-bisphosphatase class 1 - major CHO metabolism.synthesis.sucrose.FBPase	TDLMTITR	475.7524++	490.298373	T - y4+
Traes_1A1_DA0EE1337.2	Fructose-1,6-bisphosphatase class 1 - major CHO metabolism.synthesis.sucrose.FBPase	TDLMTITR	483.7499++	490.298373	T - y4+
Traes_1A1_EF31F706D.1	Tryptophan synthase alpha chain - amino acid metabolism.synthesis.aromatic aa.tryptophan.tryptophan synthase	TISGTFITNLK	541.2980++	867.457058	S - y8+
Traes_1A1_FBEE851D3.1	ATP synthase gamma chain - mitochondrial electron transport / ATP synthesis.F1-ATPase	YVILGK	411.2420++	559.344989	I - y5+
Traes_1A1_171AA28CA.1	Dihydroliopyl dehydrogenase - TCA / org transformation.TCA.pyruvate DH.E3	ASGVAYQVNGK	490.2640++	665.361701	A - y6+
Traes_1A1_682A666AE.1	Glucose-6-phosphate isomerase	TFTAETMLNAR	678.3348++	1107.546284	T - y10+
Traes_1A1_682A666AE.1	Glucose-6-phosphate isomerase	AILPYSOALEK	616.8479++	935.483273	P - y8+
Traes_1A1_80446C38C.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase - glycolysis.cytosolic branch.fructose-2,6-bisphosphatase (Fru2,6BisPase)	TATIWTSLQQR	639.3461++	891.468292	W - y7+
Traes_1A1_80446C38C.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase - glycolysis.cytosolic branch.fructose-2,6-bisphosphatase (Fru2,6BisPase)	TILTATPIVGFPK	679.4081++	1143.677222	L - y11+
Traes_2A1_141C6B5E4.1	ATP synthase subunit alpha - mitochondrial electron transport / ATP synthesis.F1-ATPase	AAELTTLLESR	602.3326++	819.457058	T - y7+
Traes_2A1_141C6B5E4.1	ATP synthase subunit alpha - mitochondrial electron transport / ATP synthesis.F1-ATPase	AVDSLVLPIGR	513.8007++	442.277243	P - y4+
Traes_2A1_141C6B5E4.1	ATP synthase subunit alpha - mitochondrial electron transport / ATP synthesis.F1-ATPase	TAIAIDITNLQK	650.8772++	1015.578236	A - y9+
Traes_2A1_2E2DFB904.1	Aminomethyltransferase - PS.photosynthesis.glycine cleavage.T subunit	MYFSDFK	469.2098++	643.308603	F - y5+
Traes_2A1_2E2DFB904.1	Aminomethyltransferase - PS.photosynthesis.glycine cleavage.T subunit	MPVPPTK	410.2253++	345.213246	P - y3+
Traes_2A1_3315250C9.2	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	TEFGSPQPK	569.2824++	907.467229	F - y8+
Traes_2A1_3315250C9.2	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	LVGSVEITTTGVK	660.3563++	1107.552809	G - y11+
Traes_2A1_3315250C9.2	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	LVGSVEITTTGVR	492.6070+++	632.330598	G - y12++
Traes_2A1_608FCB8C83.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	GGVIDEDALR	572.3039++	817.405023	P - y12++
Traes_2A1_79FAAA6E1.2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 - mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear	NPTLPLVLR	511.8215++	597.408258	P - y5+
Traes_2A1_7F64A38C7.2	Glucose-6-phosphate 1-dehydrogenase - OPP.oxidative PP.G6PD	LFLPLWNR	529.8109++	685.37802	P - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	IIFTNVGNPHGLQKPLTFPR	774.1023+++	816.952081	G - y15++
Traes_2A1_85FCE950B.1	Aminotransferase	HYLSLAPGLGAYSISR	588.6286+++	755.331858	G - y7+
Traes_2A1_85FCE950B.1	Aminotransferase	LLEATGISTVPSGFGQK	881.4727++	777.389979	F - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	IGSTMFLFK	586.8046++	683.376289	F - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	GLVVPVIR	426.7869++	484.324194	P - y4+
Traes_2A1_85FCE950B.1	Aminotransferase	IANQLYK	481.7871++	778.445765	N - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	IGPFAK	316.6919++	315.202681	P - y3+
Traes_2A1_85FCE950B.1	Aminotransferase	EIQAAFR	417.7271++	464.261593	A - y4+
Traes_2A1_85FCE950B.1	Aminotransferase	SIVQFPR	488.2665++	676.3413	F - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	GVPIMLSAGTAK	572.8234++	438.236395	P - y9++
Traes_2A1_85FCE950B.1	Aminotransferase	LILTMPTMSMER	755.3773++	938.407013	P - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	VAYALAQGLK	517.3057++	863.498529	F - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	EAGSTMAVVAEQTK	711.3507++	845.472708	F - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	APINATLTK	470.7949++	435.276378	P - y8++
Traes_2A1_85FCE950B.1	Aminotransferase	FASINVENVEDNRR	554.9447+++	722.860585	S - y12++
Traes_2A1_85FCE950B.1	Aminotransferase	ALGVDVTPVLVGPVSYLLSK	714.0924+++	1076.635023	G - y10+
Traes_2A1_85FCE950B.1	Aminotransferase	YFLGAVDGR	548.7929++	820.431178	F - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	EVEDLEAGGQIQVIEAALR	756.7288+++	915.489421	Q - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	ANVILPSSAASEK	681.8668++	852.409774	P - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	SIFPIGAK	481.2713++	372.224145	P - y4+
Traes_2A1_85FCE950B.1	Aminotransferase	VAEYFLPWK	576.8080++	430.244881	P - y3+
Traes_2A1_85FCE950B.1	Aminotransferase	ANNMFPDYK	551.2553++	310.176132	Y - y2+
Traes_2A1_85FCE950B.1	Aminotransferase	VAEFSFR	428.2216++	756.367515	A - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	TSLAPGSGVVK	508.2928++	643.377351	P - y7+
Traes_2A1_85FCE950B.1	Aminotransferase	GFPISYNNR	526.7798++	638.32565	S - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	SINQITGLR	501.2905++	801.457727	N - y7+
Traes_2A1_85FCE950B.1	Aminotransferase	FLANVDPVDVAR	658.3539++	656.3726	P - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	IMPEEYSR	577.2633++	455.201064	P - y7++
Traes_2A1_85FCE950B.1	Aminotransferase	DLNGAADHAPQQR	696.8344++	599.325985	A - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	LDLSDDAEVSGLK	667.3459++	905.457452	S - y9+
Traes_2A1_85FCE950B.1	Aminotransferase	SYSHLLR	330.1907+++	514.371144	L - y4+
Traes_2A1_85FCE950B.1	Aminotransferase	LGPDVK	314.6869++	515.282388	G - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	GAGVAVMPFSIR	602.8290++	750.396707	P - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	NIAMGYVK	448.2389++	668.343608	A - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	TVAINPPTTR	536.3115++	871.499592	A - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	DAVSEVR	437.7351++	589.330401	S - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	LLVSDSPFGNER	667.3410++	1008.438114	S - y9+
Traes_2A1_85FCE950B.1	Aminotransferase	LIDGVPETLDDLK	727.4167++	956.541122	P - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	LVFVTNNSTR	561.8113++	664.326044	T - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	VYVIGEEGILK	610.3503++	745.409046	G - y7+
Traes_2A1_85FCE950B.1	Aminotransferase	YLVSPVPIR	593.8452++	811.467229	S - y7+
Traes_2A1_85FCE950B.1	Aminotransferase	DAILSGK	352.2029++	404.25036	L - y4+
Traes_2A1_85FCE950B.1	Aminotransferase	AGQPMLDK	430.2207++	603.317059	P - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	IYSVNEGNAK	547.7775++	818.400272	S - y8+
Traes_2A1_85FCE950B.1	Aminotransferase	NWDPTTK	466.7272++	416.25036	P - y4+
Traes_2A1_85FCE950B.1	Aminotransferase	SPILFGSSDVEEIK	818.4092++	1078.489875	G - y10+
Traes_2A1_85FCE950B.1	Aminotransferase	VTEVMYDLK	549.2810++	669.327624	M - y5+
Traes_2A1_85FCE950B.1	Aminotransferase	GNINIEELR	529.2855++	773.415194	N - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	EYAAFPAAWLR	647.8326++	713.40932	P - y6+
Traes_2A1_85FCE950B.1	Aminotransferase	HDVVYPIR	499.7745++	746.455936	V - y6+

Traes_7AS_9DF135C9F.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	TALAFVTLR	496.3004++	706.424636 A - y6+
TRAES3BF050800360CFD_r1	Glutamate decarboxylase - amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase	ADGVLPLVAIR	505.8033++	668.445371 P - y6+
Traes_4AL_9BC837710.2	Glutamate decarboxylase - amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase	VHLEDALPSR	625.3486++	519.272355 P - y9++
new - TraesCS1A01G105600.1	Dihydroliopyl dehydrogenase - TCA / org transformation.TCA.pyruvate DH.E3	AVSGLTK	338.2054++	418.26601 G - y4+
new - TraesCS1A01G105600.1	Dihydroliopyl dehydrogenase - TCA / org transformation.TCA.pyruvate DH.E3	VGVGDTSGSGVK	552.7984++	906.452701 G - y10+
new - TraesCS1A01G105600.1	Dihydroliopyl dehydrogenase - TCA / org transformation.TCA.pyruvate DH.E3	FPLLANSR	459.2638++	560.315085 L - y5+
TraesCS1A01G155200.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	ALGOISER	437.2431++	689.357679 G - y6+
TraesCS1A01G155200.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	NAIIWGNHSSQYDPVNHATVK	813.3998+++	980.51597 P - y9+
TraesCS1A01G155200.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	TPSGEKPIVR	485.7694++	435.245609 P - y8++
TraesCS1A01G221000.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	NVSQADALK	508.7722++	402.271095 A - y4+
TraesCS1A01G221000.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	YVGSVLGK	461.2738++	659.408652 G - y7+
TraesCS1A01G221000.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	LAVQLVAGESGK	642.8797++	760.419945 Y - y8+
TraesCS1A01G273900.1	Fructose-1,6-bisphosphatase class 1 - major CHO metabolism.synthesis.sucrose.FBPase	FVASAVNK	418.2373++	589.330401 A - y6+
TraesCS1A01G273900.1	Fructose-1,6-bisphosphatase class 1 - major CHO metabolism.synthesis.sucrose.FBPase	TLLYGGIFLYPADK	785.9294++	400.229624 P - y4+
TraesCS1A01G273900.1	Fructose-1,6-bisphosphatase class 1 - major CHO metabolism.synthesis.sucrose.FBPase	ALEIVPEIHQR	734.4014++	942.479191 P - y7+
TraesCS1A01G348500.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	VAVLGAAGGIGQPLGLLIK	874.0456++	1165.73032 G - y12+
TraesCS1A01G348500.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	TRPSVTFDEETEELTK	661.6566+++	720.377411 T - y6+
TraesCS1A01G348500.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	ALEALKPELK	371.2289++	486.292225 P - y4+
TraesCS1A01G412900.1	Malate dehydrogenase - TCA / org transformation.TCA.malate DH	GFVGDQLGEALEGADLVIIIPAGVPR	870.1254+++	596.351471 P - y6+
TraesCS1A01G412900.1	Malate dehydrogenase - TCA / org transformation.TCA.malate DH	LFVGTLLDVVR	610.3559++	959.552021 G - y9+
TraesCS1A01G412900.1	Malate dehydrogenase - TCA / org transformation.TCA.malate DH	TQDGGTVEVEAK	617.3015++	1004.489481 D - y10+
TraesCS1A01G419600.1	Glucose-1-phosphate adenylyltransferase - major CHO metabolism.synthesis.starch.AGPase	VDTSLNFVAIDPPAK	826.9120++	315.202681 P - y3+
TraesCS1A01G428400.1	Tryptophan synthase alpha chain - amino acid metabolism.synthesis.aromatic aa tryptophan tryptophan synthase	GVANFMNSDD	526.2839++	895.4706 A - y8+
TraesCS1A01G428400.1	Tryptophan synthase alpha chain - amino acid metabolism.synthesis.aromatic aa tryptophan tryptophan synthase	EAGVHGLVVPDPLEETDILR	753.4057+++	543.295496 P - y9++
TraesCS1A01G428400.1	Tryptophan synthase alpha chain - amino acid metabolism.synthesis.aromatic aa tryptophan tryptophan synthase	AVAVGGFVSPTEQVK	744.9065++	1148.594615 G - y11+
TraesCS1D01G153900.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformatons.cyt MDH	TSSGKPIVR	480.7591++	772.431178 S - y7+
TraesCS1D01G274000.1	Fructose-1,6-bisphosphatase class 1 - major CHO metabolism.synthesis.sucrose.FBPase	ALEIVPEIHQR	464.5929+++	866.447891 P - y7+
TraesCS2A01G041100.1	Acetyltransferase component of pyruvate dehydrogenase complex - TCA / org transformation.TCA.2-oxoglutarate dehydrogenase	FIASEGDTVPTGTVIAVSK	1003.0462++	984.608808 P - y10+
TraesCS2A01G041100.1	Acetyltransferase component of pyruvate dehydrogenase complex - TCA / org transformation.TCA.2-oxoglutarate dehydrogenase	DADTMNFADIEK	685.3006++	836.414859 N - y7+
TraesCS2A01G041100.1	Acetyltransferase component of pyruvate dehydrogenase complex - TCA / org transformation.TCA.2-oxoglutarate dehydrogenase	EAVFYLR	449.2451++	598.334758 Y - y4+
TraesCS2A01G123800.1	4-alpha-glucanotransferase - major CHO metabolism.degradation.starch.D enzyme	HILLSDGLSR	555.8169++	860.483607 L - y8+
TraesCS2A01G123800.1	4-alpha-glucanotransferase - major CHO metabolism.degradation.starch.D enzyme	GDPLPIGVDR	471.2562++	656.3726 P - y6+
TraesCS2A01G123800.1	4-alpha-glucanotransferase - major CHO metabolism.degradation.starch.D enzyme	AWWEGDEGTR	603.7624++	949.401 W - y8+
TraesCS2A01G168200.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	SLGTLQALR	508.2984++	815.473377 G - y8+
TraesCS2A01G168200.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	ISQGLOR	429.7432++	530.304521 G - y5+
TraesCS2A01G261600.1	Aminotransferase	ALDYEELNENVK	718.8488++	1252.569188 D - y10+
TraesCS2A01G261600.1	Aminotransferase	EVQLSFTNVSK	694.3826++	805.420279 S - y7+
TraesCS2A01G261600.1	Aminotransferase	TVDEYK	434.2266++	667.329733 D - y5+
TraesCS2A01G272800.1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 - mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear	YDMGVER	435.1947++	591.291907 M - y5+
TraesCS2A01G272800.1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 - mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear	LDLGETAQIDK	601.8168++	804.409774 T - y7+
TraesCS2A01G292100.1	Histidinol dehydrogenase - amino acid metabolism.synthesis.histidine.histidinol dehydrogenase	VSDLPDAELDPAVK	734.8801++	1054.541516 P - y10+
TraesCS2A01G292100.1	Histidinol dehydrogenase - amino acid metabolism.synthesis.histidine.histidinol dehydrogenase	IFGPNQVTTAAK	683.3617++	553.285462 G - y11++
TraesCS2A01G292100.1	Histidinol dehydrogenase - amino acid metabolism.synthesis.histidine.histidinol dehydrogenase	YITVQSLTEGLR	754.9014++	1032.532014 Q - y9+
TraesCS2A01G489600.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	DLSQADFGR	504.7409++	565.272886 A - y5+
TraesCS2A01G489600.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	DSAAVFAWK	497.7533++	621.403172 A - y6+
TraesCS2A01G489600.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	ITKQPOTDR	536.3115++	716.304915 P - y6+
TraesCS2A01G489600.2	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	VAAHLGK	404.7556++	638.398421 A - y6+
TraesCS2A01G489600.2	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	AQSEYIPIPVMDGPYKPAAYR	742.3794+++	667.348594 P - y12++
TraesCS2A01G493600.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	LELDLAEVEMPEGLMACR	649.6510+++	804.38549 P - y7+
TraesCS2A01G493600.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	VPDPESTDNPKF	737.8385++	582.264393 P - y10++
TraesCS2A01G493600.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	TGIVLAEGR	514.8086++	644.3726 Y - y6+
TraesCS2A01G508900.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	NVAQADASLK	508.7722++	803.425758 A - y8+
TraesCS2A01G508900.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	TLAILGFQK	460.2842++	705.429387 A - y7+
TraesCS2A01G508900.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	VTYASAR	384.2060++	567.288536 Y - y5+
TraesCS2A01G588300.1	Beta-fructofuranosidase, insoluble protein - major CHO metabolism	GWSGVQTVPR	543.7882++	843.468292 S - y8+
TraesCS2B01G145700.1	4-alpha-glucanotransferase - major CHO metabolism.degradation.starch.D enzyme	NVIFSATDPAK	590.3039++	853.405023 F - y8+
TraesCS2B01G308600.1	Histidinol dehydrogenase - amino acid metabolism.synthesis.histidine.histidinol dehydrogenase	TVVILATPPSR	520.8086++	456.256508 P - y4+
TraesCS2B01G517500.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	AQSEYIPIVEGPKPAAYR	747.0513+++	674.356419 P - y12++
TraesCS2B01G521600.1	Adenosylhomocysteinase - amino acid metabolism.degradation.aspartate family.methionine	SQSDYIPIEGPKPAAYR	752.3829+++	811.364244 P - y12++
TraesCS2B01G594900.1	Beta-fructofuranosidase, insoluble protein	LYGASGPASSAVR	618.3226++	681.431906 S - y9+
TraesCS2D01G042300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	TIFHLPNSGR	571.3093++	643.352199 L - y6+
TraesCS2D01G042300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	IIDTYGGWGAHGGAFFSGK	655.3269+++	623.314751 G - y7+
TraesCS2D01G042300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	SIASGLAR	444.2691++	574.330736 A - y6+
TraesCS3A01G015500.1	Sucrose phosphate synthase - major CHO metabolism.synthesis.sucrose.SPS	ALGETPGVYR	531.7826++	591.324922 P - y5+
TraesCS3A01G015500.1	Sucrose phosphate synthase - major CHO metabolism.synthesis.sucrose.SPS	LNFPVLASR	565.3400++	642.393336 P - y6+
TraesCS3A01G087100.1	Cysteine synthase - amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	VDIFIGIGITGGTISGAGR	874.4705++	1160.601825 G - y14+
TraesCS3A01G087100.1	Cysteine synthase - amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	LIVVFPFSGER	681.8926++	692.336215 P - y6+
TraesCS3A01G087100.1	Cysteine synthase - amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	YLSVILFQISR	656.8666++	1036.578571 S - y9+
TraesCS3A01G146800.1	D-3-phosphoglycerate dehydrogenase - amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	VGNLIGER	429.2456++	361.183009 G - y3+
TraesCS3A01G195300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	ATVDYEK	413.2031++	554.245669 D - y4+
TraesCS3A01G195300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	NIGFSDDVGLDADR	803.8890++	1062.469808 S - y10+
TraesCS3A01G195300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	EHVIKPIPEK	430.2590+++	1072.281161 P - y3+
TraesCS3A01G400000.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	EALWPSLEEAR	650.8302++	801.410108 P - y7+
TraesCS3A01G400000.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	VQQVDTTGAGDAFIGSLLR	650.0093+++	545.340572 G - y5+
TraesCS3A01G400000.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	IVQDPSALQDK	607.3248++	758.404294 P - y7+
TraesCS3B01G397900.1	Alpha-1,4 glucan phosphorylase - major CHO metabolism.degradation.starch.starch phosphorylase	QLLNILGAYVR	630.3772++	678.393336 L - y6+
TraesCS3B01G433000.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	LMLVTLGDQGCK	667.8440++	878.403643 T - y8+
TraesCS3B01G433000.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	GTVPYSK	376.2029++	494.260925 P - y4+
TraesCS3D01G008400.1	Fructokinase-2 - major CHO metabolism.degradation.sucrose.fructokinase	TALAFVTLK	482.2973++	678.418488 A - y6+
TraesCS3D01G008400.1	Fructokinase-2 - major CHO metabolism.degradation.sucrose.fructokinase	DGIMSIVK	475.2442++	664.348694 M - y5+
TraesCS3D01G008400.1	Fructokinase-2 - major CHO metabolism.degradation.sucrose.fructokinase	NVLSLWFEEGLK	653.3637++	1092.608808 L - y9+

TraesCS3D01G394200.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	EALWPSLDEAR	643.8224++	787.394458 P - y7+
TraesCS4A01G225100.1	Sucrose-phosphate synthase - major CHO metabolism.synthesis.sucrose.SPS	SFDDQALHK	530.7565++	826.405357 D - y7+
TraesCS4A01G225100.1	Sucrose-phosphate synthase - major CHO metabolism.synthesis.sucrose.SPS	ALGFAPGR	394.7243++	400.230293 A - y4+
TraesCS4A01G243500.1	Acetyltransferase component of pyruvate dehydrogenase complex - TCA / org transformation.TCA.2-oxoglutarate dehydrogenase	FIASEGDVTPTGK	711.8592++	402.23471 P - y4+
TraesCS4A01G243500.1	Acetyltransferase component of pyruvate dehydrogenase complex - TCA / org transformation.TCA.2-oxoglutarate dehydrogenase	EAVLFR	424.2554++	435.27143 F - y3+
TraesCS4A01G298700.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	FALESFWDGK	600.2902++	981.467623 L - y8+
TraesCS4A01G298700.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	WFDTNYHFVPELSPATK	722.3616+++	842.461809 P - y8+
TraesCS4A01G298700.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	AAGASWIOFDEPTLVK	866.9489++	1076.562252 G - y9+
TraesCS4A01G446700.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	IGDLSAHPNELVAVFTR	642.6742+++	906.965582 G - y17++
TraesCS4A01G446700.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	FNIVSPGADMSYFPYSEQSR	803.3791+++	866.400272 P - y7+
TraesCS4A01G446700.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	NLTGLVLELYGK	603.8401++	979.545873 T - y9+
TraesCS4B01G172700.1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase - glycolysis.cytosolic branch.phosphoglycerate mutase	GWDAQVLGEAPHK	469.9054+++	638.32565 G - y6+
TraesCS4D01G012900.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	DGAYFAANAAQAQR	742.3499++	930.475168 A - y10+
TraesCS5A01G022200.1	Cysteine synthase - amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	DVTELGINTPLVVLNK	894.9907++	537.303124 Y - y4+
TraesCS5A01G022200.1	Cysteine synthase - amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	IDGLVSGITGGTITGTGK	852.4623++	1206.632457 G - y14+
TraesCS5A01G022200.1	Cysteine synthase - amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	YLSVLFHSIK	647.3637++	1017.572757 S - y9+
TraesCS5A01G024900.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	WFDTNYHFVPELAPSTK	722.3616+++	432.254275 P - y4+
TraesCS5A01G024900.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	SFSPLLLSLIPVYK	876.0031++	506.29731 P - y4+
TraesCS5A01G024900.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	VTNEEVQK	473.7456++	746.367909 N - y6+
TraesCS5A01G131300.1	2-isopropylmalate synthase - amino acid metabolism.synthesis.branched chain group.leucine specific.2-isopropylmalate synthase	IDDPNYVR	496.2458++	648.346386 P - y5+
TraesCS5A01G131300.1	2-isopropylmalate synthase - amino acid metabolism.synthesis.branched chain group.leucine specific.2-isopropylmalate synthase	IFDITTLR	433.2425++	605.325316 D - y5+
TraesCS5A01G131300.1	2-isopropylmalate synthase - amino acid metabolism.synthesis.branched chain group.leucine specific.2-isopropylmalate synthase	AVDQIQPITVLR	733.4405++	585.371872 P - y5+
TraesCS5A01G286200.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	APGGAPANVSIAR	675.8780++	997.578905 P - y10+
TraesCS5A01G286200.1	pfkB-like carbohydrate kinase family protein - major CHO metabolism.degradation.sucrose.fructokinase	EAGALLSYDPNPR	701.8517++	483.267407 P - y4+
TraesCS5A01G483900.1	Fructokinase-2 - major CHO metabolism.degradation.sucrose.fructokinase	GAIPALPTATALELSK	884.0168++	1244.709644 P - y12+
TraesCS5A01G505000.2	Aconitate hydratase - TCA / org transformation.TCA.aconitase	ILLESAIR	457.7871++	688.398815 L - y6+
TraesCS5A01G505000.2	Aconitate hydratase - TCA / org transformation.TCA.aconitase	ILDWENSATK	588.7984++	906.421401 D - y8+
TraesCS5B01G012400.1	Malate dehydrogenase - gluconeogenesis / glyoxylate cycle.Malate DH	LLGVTTLDVVR	593.3637++	803.462144 T - y7+
TraesCS5B01G012400.1	Malate dehydrogenase - gluconeogenesis / glyoxylate cycle.Malate DH	ANTFVGEVLDPDR	744.3963++	955.520721 G - y9+
TraesCS5B01G022800.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	DEAYFSANAAALASR	778.8706++	931.495569 S - y10+
TraesCS5B01G022800.1	5-methyltetrahydropteroyltriglutamate - homocysteine methyltransferase - amino acid metabolism.synthesis.aspartate family.methionine	LNLPLPITTTIGSPQTVELR	770.7738+++	842.473043 P - y7+
TraesCS5B01G133500.1	2-isopropylmalate synthase - amino acid metabolism.synthesis.branched chain group.leucine specific.2-isopropylmalate synthase	VVIAGDVSADKPALTSNSNR	672.0236+++	908.463403 I - y18+
TraesCS6A01G159100.1	Fumarylacetoacetase - amino acid metabolism.degradation.aromatic aa.tyrosine	ILSADEPLVR	556.8191++	886.462872 S - y8+
TraesCS6A01G159100.1	Fumarylacetoacetase - amino acid metabolism.degradation.aromatic aa.tyrosine	DIQAWETIPLGFLGK	892.9827++	828.497801 P - y8+
TraesCS6A01G169300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	ANVDYELK	419.7007++	429.218725 Y - y3+
TraesCS6A01G169300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	TQVTVVEYHNDNGAMVPIR	682.0021+++	858.412128 T - y15+
TraesCS6A01G169300.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	SGAYVAR	362.1928++	506.287808 Y - y4+
TraesCS6A01G247900.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	TQVTIEYLNLEGGAMVPPR	659.6752+++	786.429069 G - y8+
TraesCS6A01G247900.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	YLDENITFIHLNPSGR	888.4392++	416.225208 P - y4+
TraesCS6A01G247900.1	S-adenosylmethionine synthase - amino acid metabolism.synthesis.aspartate family.methionine.S-adenosylmethionine synthetase	DDADFTWEVVKPLK	554.9506+++	357.249632 P - y3+
TraesCS6A01G360700.1	Aspartate aminotransferase - amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	LNLGVGAYR	481.7745++	735.4148 L - y7+
TraesCS6A01G360700.1	Aspartate aminotransferase - amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	LAAAFIOR	445.2663++	634.367121 A - y5+
TraesCS6A01G360700.1	Aspartate aminotransferase - amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	NLGLYAR	468.2509++	708.367515 G - y6+
TraesCS6B01G393600.1	Aspartate aminotransferase - amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	LYDSLTEK	484.7504++	692.346111 D - y6+
TraesCS7A01G158900.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	YAPFDILR	562.2928++	445.242535 P - y7++
TraesCS7A01G158900.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	ESLYPLLFLK	668.8792++	844.529101 P - y7+
TraesCS7A01G158900.1	Sucrose synthase - major CHO metabolism.degradation.sucrose.Susy	GLQSLR	372.7218++	574.330736 Q - y5+
TraesCS7A01G263300.1	1-deoxy-D-xylulose 5-phosphate synthase 1 - TCA / org transformation.TCA.pyruvate DH.E1	SNYMSAGQSVPIVFR	884.9562++	631.392608 P - y5+
TraesCS7A01G263300.1	1-deoxy-D-xylulose 5-phosphate synthase 1 - TCA / org transformation.TCA.pyruvate DH.E1	AEVLDSSFSVPIGK	724.8852++	414.271095 P - y4+
TraesCS7A01G263300.1	1-deoxy-D-xylulose 5-phosphate synthase 1 - TCA / org transformation.TCA.pyruvate DH.E1	LAVPQVEDIVR	619.8588++	955.520721 P - y8+
TraesCS7A01G287400.1	Glucose-1-phosphate adenyltransferase - major CHO metabolism.synthesis.starch.AGPase	GGPIGIGK	406.2554++	584.376623 P - y6+
TraesCS7A01G386600.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformations.cyt MDH	ILPEASYK	460.7580++	694.340632 P - y6+
TraesCS7B01G219800.1	Fructokinase-2 - major CHO metabolism.degradation.sucrose.fructokinase	VSDDEVFALTQGDATDEK	970.4420++	1077.505859 L - y10+
TraesCS7B01G289400.1	Malate dehydrogenase - TCA / org transformation.other organic acid transformations.cyt MDH	TRPSVTFIDETEELTK	661.3286+++	719.393395 T - y6+

Accession ID	Protein name	Peptide sequence	Precursor ion	Product m/z	Product ion
Traes_1AL_1DC9BD199.1	Ketol-acid reductoisomerase (NADP(+))	STVEGITGIISK	602.8428++	788.48763	G - y8+
Traes_1AL_2EC98608D.2	Malate dehydrogenase	MSPLVSELRL	516.2813++	407.245078	P - y7++
Traes_1AL_2EC98608D.2	Malate dehydrogenase	GVDVVVPIAGVPR	639.3824++	596.351471	P - y6+
Traes_1AL_52E56C8D3.1	ATP synthase subunit beta	THDFLPIHR	379.2051+++	522.314692	P - y4+
Traes_1AL_52E56C8D3.1	ATP synthase subunit beta	VVDLLAPYQR	587.3350++	634.330736	A - y5+
Traes_1AL_5738CCBF8.1	Pyruvate, phosphate dikinase	VMANADTPGDALAAR	736.8617++	770.415528	P - y8+
Traes_1AL_5738CCBF8.1	Pyruvate, phosphate dikinase	QMIMAPTVELR	644.8412++	714.414465	P - y6+
Traes_1AL_D2049E4A2.1	Malate dehydrogenase	VLVVANPANTNALILK	825.5011++	1054.625521	P - y10+
Traes_1AL_D2049E4A2.1	Malate dehydrogenase	EFAPSIPEK	509.2662++	335.692147	P - y6++
Traes_1AL_DA0EE1337.2	Fructose-1,6-bisphosphatase class 1	TDLMTITR	483.7499++	490.298373	T - y4+
Traes_1AL_EF31F706D.1	Tryptophan synthase alpha chain	TISGTFNTLK	541.2980++	867.457058	S - y8+
Traes_1AL_FBE851D3.1	ATP synthase gamma chain	YVILGEK	411.2420++	559.344989	I - y5+
Traes_1AS_171AA28CA.1	Dihydropyridyl dehydrogenase	ASGVAYQVVK	490.2640++	665.361701	A - y6+
Traes_1AS_682A666AE.1	Glucose-6-phosphate isomerase	AILPYSQALEK	616.8479++	468.245275	P - y8++
Traes_1AS_80446C38C.1	Phosphofructokinase 2	TATIWTSTLQR	639.3461++	705.388979	T - y6+
Traes_1AS_80446C38C.1	Phosphofructokinase 2	TILTATPIVGFPK	679.4081++	1143.677222	L - y11+
Traes_2AL_141C6B5E4.1	ATP synthase subunit alpha	AAELTTLLSR	602.3326++	604.277637	L - y4+
Traes_2AL_141C6B5E4.1	ATP synthase subunit alpha	AVDSLVPIGR	513.8007++	442.277243	P - y4+
Traes_2AL_141C6B5E4.1	ATP synthase subunit alpha	TAIAIDTILNQK	650.8772++	1015.578236	A - y9+
Traes_2AL_2E2DFB904.1	Aminomethyltransferase	MYFSDFK	469.2098++	643.308603	F - y5+
Traes_2AL_2E2DFB904.1	Aminomethyltransferase	MPFVPTK	410.2253++	344.705057	P - y6++
Traes_2AL_3315250C9.2	Adenosylhomocysteinase	TEFGPSQPFK	569.2824++	907.467229	F - y8+
Traes_2AL_3315250C9.2	Adenosylhomocysteinase	LVGVSEITTTGVK	660.3563++	1107.552809	G - y11+
Traes_2AL_608FCBC83.1	D-3-phosphoglycerate dehydrogenase	GGVIDEDALVR	572.3039++	817.405023	D - y7+
Traes_2AL_783CF383F.1	Glyceraldehyde-3-phosphate dehydrogenase	AAALNIVPTSTGAAK	692.8934++	732.388644	P - y8+
Traes_2AL_783CF383F.1	Glyceraldehyde-3-phosphate dehydrogenase	AVLALVLPNLK	519.3395++	683.445037	V - y6+
Traes_2AL_79FAAA6E1.2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NPTLPLVILR	511.8215++	597.408258	P - y5+
Traes_2AL_7F64A38C7.2	glucose-6-phosphate dehydrogenase	LFLPLWNR	529.8109++	685.37802	P - y5+
Traes_2AL_85FCE950B.1	Aminotransferase	IIFTNVGNPHALGQKPLTFPR	774.1023+++	1047.565797	F - y19++
Traes_2AL_85FCE950B.1	Aminotransferase	HYLSLAPGGLGAYSDSR	588.6286+++	755.331858	G - y7+
Traes_2AL_85FCE950B.1	Aminotransferase	LLEATGISTVPGSGFGQK	881.4727++	777.388979	P - y8+
Traes_2AS_2B3603918.1	Ribulose biphosphate carboxylase small chain	FETLSYLPPLSTEALLK	641.3556+++	534.818607	P - y10++
Traes_2AS_2B3603918.1	Ribulose biphosphate carboxylase small chain	VGVFVR	362.7107++	625.345657	G - y5+
Traes_2AS_2B3603918.1	Ribulose biphosphate carboxylase small chain	EYPDAYVR	506.7404++	506.7404++	P - y6++
Traes_2AS_3BA916807.1	Succinate--CoA ligase [ADP-forming] subunit alpha	IGSTMFEFLK	586.8046++	1059.517944	G - y9+
Traes_2AS_84EA9C609.1	Ribose-5-phosphate isomerase A	FVVVVDTEK	518.2897++	789.43526	V - y7+
Traes_2AS_EF55AF9DD.1	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 1, mitochondrial	GLVVPVIR	426.7869++	484.324194	P - y4+
Traes_3AL_1953CF160.2	Transaldolase	IANQLYLK	481.7871++	778.445765	N - y6+
Traes_3AL_4F4132490.2	Carbonic anhydrase	IGFPAK	316.6919++	519.292559	G - y5+
Traes_3AL_681758236.2	Phosphoenolpyruvate carboxylase	EIQAAFR	417.7271++	464.261593	A - y4+
Traes_3AL_681758236.2	Phosphoenolpyruvate carboxylase	SIVFQEPK	488.2665++	775.409714	V - y6+
Traes_3AL_8512360E1.1	Glycine dehydrogenase decarboxylating protein	LGTVTVQELPYFDTVK	905.4853++	869.440346	P - y7+
Traes_3AS_2F7B3D3C1.1	Fructose-bisphosphate aldolase	TVVSIKPGTALAVK	756.9264++	1013.544828	P - y10+
Traes_3AS_2F7B3D3C1.1	Fructose-bisphosphate aldolase	EAAWGLAR	437.2325++	416.261593	G - y4+
Traes_3AS_5E5EA077A.1	Pyruvate kinase	GVIPMLSGTAK	572.8234++	438.236395	P - y9++
Traes_3AS_A3FC93C65.2	Cysteine synthase	LILTMPTSMSEK	755.3773++	938.407013	P - y8+
Traes_3AS_AE3D5013D.1	Triosephosphate isomerase	VAYALAQGLK	517.3057++	629.398087	L - y6+
Traes_3AS_AE3D5013D.1	Triosephosphate isomerase	EAGSTMVVAEQTK	711.3507++	675.367181	V - y6+
Traes_3AS_D41508CC4.1	Phosphate translocator	APINATLLK	470.7949++	435.276378	P - y8++
Traes_3BF107400010CFD_t1	Fructose-bisphosphate aldolase	FASINVENVEDNRR	554.9447+++	722.860585	S - y12++
Traes_4AL_8D0193195.2	5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase	ALGVDTVPVLVGPVSYLLSK	714.0924+++	1076.635023	G - y10+
Traes_4AL_8D0193195.2	5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase	YLFAGVVDGR	548.7929++	602.32565	G - y6+
Traes_4AL_A1D089370.1	NADH-ubiquinone oxidoreductase subunit	ANVILPSSAFSEK	681.8668++	852.409774	P - y8+
Traes_4AL_B9FA07247.2	Ferredoxin--NADP reductase	LVYTNDAGEVVK	654.3457++	1095.53168	Y - y10+
Traes_4AL_B9FA07247.2	Ferredoxin--NADP reductase	DPNATIIMLATGTGIAPFR	653.6838+++	660.382771	G - y6+
Traes_4AL_C3729F680.2	Fructose-bisphosphate aldolase	LASIGLENTEANR	694.3624++	1003.480313	G - y9+
Traes_4AL_C3729F680.2	Fructose-bisphosphate aldolase	EAAAYQQGAR	578.7727++	722.358013	Y - y6+
Traes_4AL_C3729F680.2	Fructose-bisphosphate aldolase	TWGGRPENVAQAQALLLR	684.7044+++	882.989391	G - y17++
Traes_4AS_91D4C5213.1	FBPase	YIGSLVGDFFHR	421.8875+++	631.294684	G - y5+
Traes_4AS_91D4C5213.1	FBPase	VPLYVGSVEEVEKVEK	601.9961+++	568.973332	P - y15+++
Traes_4AS_D605C5422.1	Aminotransferase	SIFEIPGAK	481.2713++	761.419216	F - y7+
Traes_4BL_13B3CC649.2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	VAEFLPWK	576.8080++	430.244881	P - y3+

Traes_4BL_F7AFF4D6C.1	Aconitate hydratase	VAEFSFR	428.2216++	685.330401 E - y5+
Traes_4BL_F7AFF4D6C.1	Aconitate hydratase	TSLAPGSGVVK	508.2928++	643.377351 P - y7+
EPITAEPO0000010007	Photosystem II CP43 reaction center protein	LGANVGSQAQPGTLGK	713.8861++	972.510885 G - y11+
EPITAEPO0000010007	Photosystem II CP43 reaction center protein	APWLEPLR	491.2795++	627.382437 L - y5+
EPITAEPO0000010007	Photosystem II CP43 reaction center protein	GPNGLDLSR	464.7460++	490.261987 D - y4+
EPITAEPO0000010009	Photosystem I iron-sulfur center	VYLGPEPTR	518.2771++	660.33113 G - y6+
EPITAEPO0000010015	Photosystem II CP47 reaction center protein	LAFDYIGNNPAK	743.3723++	600.31 G - y6+
EPITAEPO0000010015	Photosystem II CP47 reaction center protein	SQLGEIFELDR	653.8355++	1091.573151 L - y9+
EPITAEPO0000010030	Photosystem II D2 protein	AYDFVSEQIR	614.3039++	632.336215 S - y5+
EPITAEPO0000010030	Photosystem II D2 protein	AAEDPEFTFYTK	774.3487++	581.276772 P - y9++
EPITAEPO0000010030	Photosystem II D2 protein	NILLNEGIR	521.3062++	814.478128 L - y7+
EPITAEPO0000010041	Cytochrome b559 subunit alpha	QGIPLITDR	506.7929++	714.414465 P - y6+
EPITAEPO0000010041	Cytochrome b559 subunit alpha	FDSLQDLDFSR	743.3464++	1023.474165 E - y8+
EPITAEPO0000010044	Photosystem II protein D1	ETTENESANEQYK	736.3128++	768.352259 S - y7+
EPITAEPO0000010044	Photosystem II protein D1	VINTWADIINR	657.8619++	701.394064 A - y6+
EPITAEPO0000010044	Photosystem II protein D1	ANLGMVMHER	643.8026++	988.433897 G - y8+
EPITAEPO0000010047	Ribulose biphosphate carboxylase large chain	LTYYTPEYTK	704.3376++	766.361761 P - y6+
EPITAEPO0000010047	Ribulose biphosphate carboxylase large chain	DTDILAAFR	511.2693++	577.345657 L - y5+
EPITAEPO0000010047	Ribulose biphosphate carboxylase large chain	TFQGPPIHQVER	733.3810++	516.78289 P - y9++
EPITAEPO0000010047	Ribulose biphosphate carboxylase large chain	DNGLLLHIHR	594.3358++	675.404904 L - y5+
EPITAEPO0000010051	PS.lightreaction.cytochrome b6/f.apocytochrome f (CYF)	P5IYVGGNR	519.7720++	665.336549 Y - y6+
EPITAEPO0000010051	PS.lightreaction.cytochrome b6/f.apocytochrome f (CYF)	GQIYPDGSK	482.7404++	666.309331 Y - y6+
EPITAEPO0000010051	PS.lightreaction.cytochrome b6/f.apocytochrome f (CYF)	SNNTVYNATSTGIVR	798.9025++	1081.563649 Y - y10+
TRAES3BF052700140CFD_t1	6-phosphogluconate dehydrogenase, decarboxylating	GFPISVYNR	426.7798++	624.734877 P - y7++
EPITAEPO0000010066	Cytochrome b6	LEIQAIADDITSK	708.8827++	933.488752 A - y9+
EPITAEPO0000010066	Cytochrome b6	GSASVQGSLTR	582.3044++	762.410442 G - y7+
Traes_1AL_0F39673AF1.3	Chlorophyll a-b binding protein, chloroplastic	AKPVSSGSPWYGADR	526.5951+++	418.204472 G - y4+
Traes_1AL_0F39673AF1.3	Chlorophyll a-b binding protein, chloroplastic	FGEAVWFK	492.2529++	836.430115 G - y7+
Traes_1AL_7C91EF27D.1	Phosphoglycerate kinase	ELDYLDGAVSNPK	710.8514++	787.394458 D - y8+
Traes_1AL_7C91EF27D.1	Phosphoglycerate kinase	GVLLLLPSDVIIADK	770.4533++	957.525138 P - y9+
Traes_1AL_E5E41283E.1	Pyruvate, phosphate dikinase	SINQITGLR	501.2905++	801.457727 N - y7+
Traes_1AS_45DF41500.1	ATP synthase subunit beta	AHGGVSVFVGGVGER	664.8389++	1120.574548 G - y12+
Traes_1AS_45DF41500.1	ATP synthase subunit beta	ESGVINEK	438.2271++	503.282388 I - y4+
Traes_1AS_45DF41500.1	ATP synthase subunit beta	AITLEENK	523.7719++	862.415253 T - y7+
Traes_1BS_757804D58.2	Glucose-6-phosphate isomerase	FLANVDPVDVAR	658.3539++	656.3726 P - y6+
Traes_1DS_87CA06255.2	6-phosphofructo-2-kinase/fructose-2-, 6-bisphosphatase	IMPEEYSR	577.2633++	455.201064 P - y7++
Traes_2AL_0A039E562.1	Oxygen-evolving enhancer protein 2-1, chloroplastic	NTDFVAYSLEGFK	717.8304++	858.399209 A - y8+
Traes_2AL_0A039E562.1	Oxygen-evolving enhancer protein 2-1, chloroplastic	QYYSITVLR	622.3377++	589.366787 T - y5+
Traes_2AL_0A039E562.1	Oxygen-evolving enhancer protein 2-1, chloroplastic	HQLITATVADGK	627.3461++	988.567337 L - y10+
Traes_2AL_14B62F6C1.1	Photosystem I reaction center subunit psaK	FGLAPSANR	466.7511++	544.283785 P - y5+
Traes_2AL_264BF03F4.1	Oxygen-evolving enhancer protein 1	LTFDEIQSK	540.7822++	866.425424 F - y7+
Traes_2AL_264BF03F4.1	Oxygen-evolving enhancer protein 1	DGIDYAAVTVQLPgger	880.9443++	515.257236 P - y5+
Traes_2AL_44F435468.1	Photosystem II reaction center PsbP family protein	VLSTATAEYSGR	627.8199++	1042.479979 S - y10+
Traes_2AL_C51BB91CC.3	Peroxisomal (S)-2-hydroxy-acid oxidase	AIALTVDTPR	528.8060++	688.36243 T - y6+
Traes_2AL_C51BB91CC.3	Peroxisomal (S)-2-hydroxy-acid oxidase	GVITAEDSR	474.2433++	678.305309 T - y6+
Traes_2AL_C51BB91CC.3	Peroxisomal (S)-2-hydroxy-acid oxidase	GAGGQIPVFLDGGVR	721.8912++	959.530892 P - y9+
Traes_2AL_E7B360A43.1	Chlorophyll a-b binding protein, chloroplastic	TAENFANFTGEQYPPGK	944.4290++	358.208495 P - y4+
Traes_2AL_E7B360A43.1	Chlorophyll a-b binding protein, chloroplastic	FFDPLGLGGETK	640.8297++	717.488358 P - y9+
Traes_2AS_1475F8BDB.1	Cytochrome b6-f complex iron-sulfur subunit	LGNDILVDWKL	707.8825++	902.498196 L - y7+
Traes_2AS_1475F8BDB.1	Cytochrome b6-f complex iron-sulfur subunit	GDPTYLVVSDK	661.8274++	676.351196 V - y6+
Traes_2AS_1475F8BDB.1	Cytochrome b6-f complex iron-sulfur subunit	VVFPVWVETDFR	747.3930++	1049.505071 P - y8+
Traes_2AS_2E706E893.1	Glyceraldehyde-3-phosphate dehydrogenase	AGGPATPPGISDK	584.3039++	713.382831 P - y7+
Traes_2AS_64BCCA8B.1	Oxygen-evolving enhancer protein 3-2, chloroplastic	FYLQPLPAAEAAR	786.4327++	1020.583656 P - y10+
Traes_2AS_64BCCA8B.1	Oxygen-evolving enhancer protein 3-2, chloroplastic	TVLGDVLAK	458.2791++	715.434866 L - y7+
Traes_2AS_8169B126A.2	Chlorophyll a-b binding protein, chloroplastic	STFPQPYAEVFLQQR	870.4412++	1179.615684 P - y10+
Traes_2AS_84EA9C6091.1	Ribose-5-phosphate isomerase A	LSGIVGVPTSK	529.3162++	687.403566 V - y7+
Traes_2AS_A18A69CB0.2	Chlorophyll a-b binding protein, chloroplastic	ALEVIHGR	447.7614++	710.394398 E - y6+
Traes_2AS_C1EA81EC4.2	60 kDa chaperonin	TVQGLIEELER	643.8512++	675.330795 E - y5+
Traes_2AS_C1EA81EC4.2	60 kDa chaperonin	SIVFENAR	532.7722++	636.31 F - y5+
Traes_2AS_C1EA81EC4.2	60 kDa chaperonin	LGADIIQK	429.2582++	744.42503 G - y7+
Traes_2AS_C9B034A45.1	60 kDa chaperonin	AALQAQVEK	443.7533++	631.340966 Q - y6+
Traes_2AS_D26D32A7C.1	Photosystem I reaction center subunit N	AATSGANFAR	483.2436++	635.325985 G - y6+
Traes_2BL_197D53AD5.1	NAD(P)H-quinone oxidoreductase subunit M	GPAQSLPR	413.2325++	472.287808 S - y4+

Traes_2BL_D90CBBDD96.1	Aminomethyltransferase	NIAMGYVK	448.2389++	668.343608 A - y6+
Traes_2BS_8684E0E15.1	Aldehyde dehydrogenase	TVAVNPPTTR	536.3115++	871.499592 A - y8+
Traes_2BS_8684E0E15.1	Aldehyde dehydrogenase	DAVSEVVR	437.7351++	589.330401 S - y5+
Traes_2BS_8684E0E15.1	Aldehyde dehydrogenase	LLVSDSFPGNR	667.3410++	572.27877 T - y5+
Traes_2DL_04AA47AA7.1	Glyceraldehyde-3-phosphate dehydrogenase	VLITAPGK	399.7578++	586.355888 I - y6+
Traes_2DL_C795EACF1.1	Phosphoglycolate phosphatase	LIDGVPETLDDR	727.4167++	956.541122 P - y8+
Traes_2DL_C795EACF1.1	Phosphoglycolate phosphatase	LVFVTNNSTK	561.8113++	910.462872 F - y8+
Traes_2DL_C795EACF1.1	Phosphoglycolate phosphatase	VYVIGEEGILK	610.3503++	745.409046 G - y7+
Traes_2DS_489826DD0.2	NADH-cytochrome b5 reductase	FAEWESSGLK	577.2798++	935.446888 E - y8+
Traes_3AL_392D17B3C.2	Fructose-1,6-bisphosphatase class 1	IYSVNEGNAK	547.7775++	818.400272 S - y8+
Traes_3AL_392D17B3C.2	Fructose-1,6-bisphosphatase class 1	NWDTPATAK	466.7272++	632.324982 D - y6+
Traes_3AL_392D17B3C.2	Fructose-1,6-bisphosphatase class 1	SPIFLGSSDDVVEIK	818.4092++	1078.489875 G - y10+
Traes_3AL_585690EFD.1	Glycerate kinase	LQAEVAMR	459.2473++	676.344671 A - y6+
Traes_3AL_6771AB197.2	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	YLVSPPLIER	593.8452++	724.435201 P - y6+
Traes_3AL_6771AB197.2	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	AGQPMLDK	430.2207++	603.317059 P - y5+
Traes_3AL_B8ED39820.1	Fructose-1,6-bisphosphatase class 1	MFSPGNLR	461.2342++	643.352199 S - y6+
Traes_3AL_B8ED39820.1	Fructose-1,6-bisphosphatase class 1	ATFDNPDYDK	593.2566++	637.282782 P - y5+
Traes_3AL_B8ED39820.1	Fructose-1,6-bisphosphatase class 1	GIFTNVTSPATAK	618.3352++	604.330067 T - y6+
Traes_3AS_C082CDCFE.1	Hexose transporter	VTEVMYDLK	549.2810++	897.438631 E - y7+
Traes_3B_3793EBCBE.1	Photosystem I reaction center subunit XI	TAVSPLLR	428.7662++	585.371872 S - y5+
Traes_3DL_A6F32E158.1	Glycine dehydrogenase decarboxylating protein	GNINIEELR	529.2855++	546.288202 E - y4+
Traes_3DL_A6F32E158.1	Glycine dehydrogenase decarboxylating protein	IAILNANYMAK	611.3366++	811.3767 N - y7+
Traes_3DL_A6F32E158.1	Glycine dehydrogenase decarboxylating protein	EYAAFPAAWLR	647.8326++	713.40932 P - y6+
Traes_3DL_FFCCD5827.1	Alpha-1,4 glucan phosphorylase	AF3TYTNAK	493.7507++	768.388644 A - y7+
Traes_3DL_FFCCD5827.1	Alpha-1,4 glucan phosphorylase	ADQIAGLR	422.2378++	416.261593 A - y4+
Traes_3DS_116082A6F.1	Pyruvate kinase	EMGLCNAGESIVALHR	586.2872+++	312.177864 H - y2+
Traes_4AL_4C3BBE546.1	1-deoxy-D-xylulose-5-phosphate synthase, Transketolase	VTTTIGFGSPNK	611.3273++	706.351865 G - y7+
Traes_4AL_4C3BBE546.1	1-deoxy-D-xylulose-5-phosphate synthase, Transketolase	ISIEAGSTLGGWK	695.3723++	947.494506 A - y9+
Traes_4AL_4C3BBE546.1	1-deoxy-D-xylulose-5-phosphate synthase, Transketolase	EYGITAENVIKAAK	725.3288++	987.546936 T - y10+
Traes_4AL_A92657C6E.2	Phosphoglucosamine mutase	MQSSLDVNVK	554.7688++	849.431238 S - y8+
Traes_4AL_A92657C6E.2	Phosphoglucosamine mutase	YLFGDGSR	457.7220++	638.289265 T - y6+
Traes_4AL_A92657C6E.2	Phosphoglucosamine mutase	IYEQYEK	543.2793++	809.40396 I - y6+
Traes_4AL_A9E7CD7B8.2	PGR5-like protein 1A, chloroplastic	TIGEMEQEFLR	676.8294++	1138.519735 G - y9+
Traes_4AL_A9E7CD7B8.2	PGR5-like protein 1A, chloroplastic	ALQSFYYDQK	631.8062++	950.425424 S - y7+
Traes_4AL_A9E7CD7B8.2	PGR5-like protein 1A, chloroplastic	AINDVLLIK	556.3579++	927.557344 I - y8+
Traes_4AL_B128F1907.2	Ribulose biphosphate carboxylase/oxygenase activase	GLAYDISDDQQDITR	855.4025++	1077.480707 S - y9+
Traes_4AL_B128F1907.2	Ribulose biphosphate carboxylase/oxygenase activase	GIFQTDNVSDSVVK	819.4045++	763.383225 S - y7+
Traes_4AL_B128F1907.2	Ribulose biphosphate carboxylase/oxygenase activase	WWTSTGIENIK	652.8459++	1019.536765 T - y10+
Traes_4AL_CF0AB0643.2	60 kDa chaperonin	AIELADPMENAGAALIR	877.9589++	1142.598654 P - y11+
Traes_4AS_13C312D8E.1	Ribulose-phosphate 3-epimerase	SDIIVSPILSANFAK	831.4591++	1134.61535 S - y11+
Traes_4AS_13C312D8E.1	Ribulose-phosphate 3-epimerase	GVNPNVIEVDGGVSPK	777.4016++	642.335152 P - y12++
Traes_4AS_3D64BC0EF.1	PsbP family protein, expressed	NVQLQSVR	472.2696++	730.420613 Q - y6+
Traes_4AS_3D64BC0EF.1	PsbP family protein, expressed	VAFIPTQK	452.2686++	473.271824 P - y4+
Traes_4AS_71B1DAAE4.1	ATP synthase subunit b photosynthesis	ALDAQIVLSDEIVK	800.9433++	989.551353 V - y9+
Traes_4AS_DE6DD58CC.1	Photosynthetic NDH subcomplex B 2	FGTDATGAPTAELSVR	796.8994++	872.483607 P - y8+
Traes_4AS_DE6DD58CC.1	Photosynthetic NDH subcomplex B 2	VYAAPPEER	516.2615++	627.309666 P - y5+
Traes_4AS_DE6DD58CC.1	Photosynthetic NDH subcomplex B 2	FTTIDQSSGLGFR	714.8595++	966.463935 D - y9+
Traes_4BL_5F6926B56.1	Glyoxylate reductase/hydroxypyruvate reductase	VGIHGLGR	392.7556++	402.245943 G - y4+
Traes_4BL_5F6926B56.1	Glyoxylate reductase/hydroxypyruvate reductase	GVLINIGR	421.2663++	459.267407 N - y4+
Traes_4BL_A9FAA75A9.1	Glyceraldehyde-3-phosphate dehydrogenase	ENSPLEVIVINDSGGVR	899.4707++	1029.568734 I - y10+
Traes_4BL_A9FAA75A9.1	Glyceraldehyde-3-phosphate dehydrogenase	IVDNETISVDGK	645.3328++	1077.505859 D - y10+
Traes_4BL_A9FAA75A9.1	Glyceraldehyde-3-phosphate dehydrogenase	VIITAPAK	406.7656++	600.371538 I - y6+
Traes_4BL_B25B3CE48.1	Fructose-1,6-bisphosphatase class 1	TMLYGGIYGPSDQK	846.9005++	574.283117 P - y5+
Traes_4BL_B25B3CE48.1	Fructose-1,6-bisphosphatase class 1	VLDIMPTAVHQR	690.3768++	808.442411 P - y7+
Traes_4BL_B25B3CE48.1	Fructose-1,6-bisphosphatase class 1	VPLYVGSVEEVEK	724.3876++	876.430903 G - y8+
Traes_4BL_F32809B15.1	Glyceraldehyde-3-phosphate dehydrogenase	VVAWYDNEWGYSQR	886.9050++	390.209558 S - y3+
Traes_4BS_2966F5332.1	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	SPSRPPLPPLAEAK	487.2804+++	363.213246 P - y7++
Traes_4BS_2966F5332.1	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	TAEIIWDSR	545.7800++	676.3413 I - y5+
Traes_4BS_D4D9B5E3E.1	Sucrose-phosphate synthase	YFVEEVVR	520.7742++	730.40938 V - y6+
Traes_4DL_2A7895E16.1	Fructose-1,6-bisphosphatase class 1	VLDIMPTEVHQR	719.3796++	866.447891 P - y7+
Traes_4DL_4C587188B.1	Ribulose biphosphate carboxylase small chain	VGFIHR	369.7185++	639.361307 G - y5+
Traes_4DL_4C587188B.1	Ribulose biphosphate carboxylase small chain	EHNASPGGYDGR	455.8655+++	510.230687 Y - y4+
Traes_4DL_4C587188B.1	Ribulose biphosphate carboxylase small chain	YWMTMVK	457.7151++	565.28028 T - y4+

Traes_4DL_4C587188B.1	Ribulose biphosphate carboxylase small chain	YWTMWK	465.7126++	581.275195 T - y4+
Traes_4DL_599E286321.1	Photosystem II Psb27 protein	ILEEMDAVEK	588.7945++	950.413539 E - y8+
Traes_4DL_6FCD82E92.1	Ribulose biphosphate carboxylase small chain	IIGFDNMR	483.2473++	739.319185 G - y6+
Traes_4DL_6FCD82E92.1	Ribulose biphosphate carboxylase small chain	IIGFDNMR	491.2448++	755.3141 G - y6+
Traes_4DS_1C3F09598.1	Fructose-bisphosphate aldolase	LDSIGLENTEANR	716.3573++	1003.480313 G - y9+
Traes_4DS_35423C70B.1	Photosynthetic NDH subcomplex L 2	FFEPGLTTEEAAR	769.8779++	558.288202 P - y11++
Traes_4DS_38E8ECB52.1	Phosphoglycerate kinase	VILSTHLGRPK	407.5873+++	457.288142 G - y4+
Traes_4DS_4466EB786.1	Photosystem I reaction center subunit V	FVFFNFQR	552.7849++	858.425699 F - y6+
Traes_4DS_85CAB8497.1	Fructose-bisphosphate aldolase	ANSLAQLGK	451.2587++	516.314023 A - y5+
Traes_4DS_BD04D4260.1	Sucrose-phosphate synthase	DYSQEVAR	484.2276++	689.357679 S - y6+
Traes_4DS_CC9F9317E.2	Chlorophyll a-b binding protein, chloroplast	IYLPNGLLDR	587.3350++	784.431178 P - y7+
Traes_4DS_CC9F9317E.2	Chlorophyll a-b binding protein, chloroplast	YQAFELIHR	624.3302++	956.531226 A - y8+
Traes_4DS_CC9F9317E.2	Chlorophyll a-b binding protein, chloroplast	ITNGLEFDDK	576.2826++	937.426152 N - y8+
Traes_5AL_0B9E87942.1	1-deoxy-D-xylulose 5-phosphate synthase 1	IAGADVPMPYAANLR	844.4272++	1161.572105 P - y10+
Traes_5AL_3AF3E7C87.2	Chlorophyll a-b binding protein, chloroplast	QVASGSPWYGSDDR	705.3258++	880.394792 P - y7+
Traes_5AL_65FC8CBE2.1	Phosphoenolpyruvate carboxylase	TQPTPQDEMR	601.7771++	973.440756 P - y8+
Traes_5AL_65FC8CBE2.1	Phosphoenolpyruvate carboxylase	VVPLFEK	416.2524++	633.360639 P - y5+
Traes_5AL_65FC8CBE2.1	Phosphoenolpyruvate carboxylase	LATPTEYVGR	568.7828++	426.198324 P - y7++
Traes_5AL_E97939490.2	UTP--glucose-1-phosphate uridylyltransferase	GGTLISYVGR	526.7722++	611.278366 S - y5+
Traes_5AL_E97939490.2	UTP--glucose-1-phosphate uridylyltransferase	AIGINVPR	420.2585++	655.388585 G - y6+
Traes_5AL_E97939490.2	UTP--glucose-1-phosphate uridylyltransferase	VANFLAR	395.7321++	620.351471 N - y5+
Traes_5BL_29847C42C.1	Chlorophyll a-b binding protein, chloroplast	SAPQSIWYGDRPK	801.4072++	722.3726 P - y12++
Traes_5BL_29847C42C.1	Chlorophyll a-b binding protein, chloroplast	ELEVIHSR	328.1821+++	370.70612 E - y6++
Traes_5BL_3212A5875.1	Glucose-1-phosphate adenyllyltransferase	ASDFGLMK	434.7153++	710.354173 D - y6+
Traes_5BL_62C79EBEC.1	pfkB-like carbohydrate kinase family protein	LGGEAAVFGK	474.7611++	835.430844 G - y9+
Traes_5BL_7EDE873F5.1	Photosystem I reaction center subunit III	YAPDSAPALAIQATIEK	879.9673++	762.917038 P - y15++
Traes_5BL_7EDE873F5.1	Photosystem I reaction center subunit III	SYLIASVGEK	533.7926++	590.314417 A - y6+
Traes_5BL_7EDE873F5.1	Photosystem I reaction center subunit III	GFIWVPAAYR	590.3191++	676.377686 P - y6+
Traes_5BL_D70B77649.3	Peroxisomal (S)-2-hydroxy-acid oxidase (glycolate oxidase)	FVLPGLTLK	542.8419++	725.455602 P - y7+
Traes_5BL_D70B77649.3	Peroxisomal (S)-2-hydroxy-acid oxidase (glycolate oxidase)	GVITAEDAR	466.2458++	662.310394 T - y6+
Traes_5BL_D70B77649.3	Peroxisomal (S)-2-hydroxy-acid oxidase (glycolate oxidase)	IPVYLDGGVVR	544.8086++	779.404629 Y - y7+
Traes_5BL_DBC5D12AB.1	Chlorophyll a-b binding protein, chloroplast	AGLLNAPEWYDAGK	752.8752++	965.436323 P - y8+
Traes_5BL_E3BC16326.4	Chlorophyll a-b binding protein, chloroplast	VAASSPWWYGSDDR	691.8204++	880.394792 P - y7+
Traes_5BS_160B04E8D.1	Fructose-bisphosphate aldolase	ATPEQVADYTLK	668.3432++	582.300778 P - y10++
Traes_5BS_FF89E832D.1	glycolysis.plastid branch.enolase	HAGWGVMTSHR	413.5331+++	500.257571 T - y4+
Traes_5DL_0927957E4.1	Malate dehydrogenase	DDLFNK	376.1847++	408.224145 F - y3+
Traes_5DL_0927957E4.1	Malate dehydrogenase	ANTFVAEVLGVDPDR	744.3963++	543.288536 G - y5+
Traes_5DL_FAF23C705.1	glycolysis.cytosolic branch.pyruvate kinase (PK)	IVGTGLPK	392.7500++	572.340238 G - y6+
Traes_5DL_FAF23C705.1	glycolysis.cytosolic branch.pyruvate kinase (PK)	GLYPVETISTVGR	696.3801++	529.795663 P - y10++
Traes_6AL_CDC715B50.1	Glycine cleavage system h protein, putative	VKPSAPAELEGLDSAK	580.9841+++	703.398481 G - y7+
Traes_6AS_1A94E971B.1	Beta-fructofuranosidase, insoluble protein	IIWGWSR	459.2532++	691.33107 W - y5+
Traes_6AS_1A94E971B.1	Beta-fructofuranosidase, insoluble protein	SAVESFGGGGR	512.2463++	637.305249 S - y7+
Traes_6AS_27483C00F.1	D-glycerate dehydrogenase/hydroxypyruvate reductase	GQTVGVIGAGR	507.7882++	629.372935 G - y7+
Traes_6AS_27483C00F.1	D-glycerate dehydrogenase/hydroxypyruvate reductase	EAVLVNNSR	479.7694++	546.299435 V - y5+
Traes_6AS_27483C00F.1	D-glycerate dehydrogenase/hydroxypyruvate reductase	NAVVVPHIASASK	646.8697++	810.446828 P - y8+
Traes_6AS_C1BA35408.1	Phosphoenolpyruvate carboxylase	LADLEAAPAAVAR	634.3539++	584.351471 P - y6+
Traes_6BL_47379C27B.1	Aspartate aminotransferase	LADVIEEK	458.7529++	732.377411 D - y6+
Traes_6BL_B95E66E93.1	Glyceraldehyde-3-phosphate dehydrogenase	IGINGFGR	417.2350++	436.230293 G - y4+
Traes_6BL_B95E66E93.1	Glyceraldehyde-3-phosphate dehydrogenase	TLLFGEK	404.2342++	593.329339 L - y5+
Traes_6BL_B95E66E93.1	Glyceraldehyde-3-phosphate dehydrogenase	AGIALNDNFVK	581.3168++	920.483607 A - y8+
Traes_6DS_8D580A93D.2	Chlorophyll a-b binding protein, chloroplast	WLAYGEIFNGR	663.3355++	1026.50032 A - y9+
Traes_6DS_8D580A93D.2	Chlorophyll a-b binding protein, chloroplast	QYFLGLEK	499.2713++	446.260925 G - y4+
Traes_6DS_CDB16CE3F.1	Phosphoglycerate kinase	LASVADLYVNDAFGTAHR	640.6585+++	541.28412 G - y5+
Traes_6DS_CDB16CE3F.1	Phosphoglycerate kinase	TFEAALDTTK	548.7797++	848.435989 A - y8+
Traes_6DS_CDB16CE3F.1	Phosphoglycerate kinase	FAAGTDAIAK	482.7585++	746.404294 A - y8+
Traes_7AL_112C7294C.1	Photosystem II reaction center PsbP family protein	YSSAAPLSPDAR	617.8068++	755.404629 P - y7+
Traes_7AL_112C7294C.1	Photosystem II reaction center PsbP family protein	SAPEPNLFR	515.7694++	646.367121 P - y5+
Traes_7AL_AFA2C29C9.2	Photosystem II stability/assembly factor HCF136	AAVQETVSATLNR	680.3650++	661.362764 S - y6+
Traes_7AL_AFA2C29C9.2	Photosystem II stability/assembly factor HCF136	FGGILDVGYR	548.7929++	722.383165 L - y6+
Traes_7AS_089028EAD.1	Alanine:glyoxylate aminotransferase PS.photosynthesis.amino transferases peroxisomal	LVAWAWLK	464.7844++	645.371872 A - y6+
Traes_7AS_70ED86B15.1	Starch synthase, chloroplast/amyloplastic	MVVMVMPR	416.2326++	601.349028 V - y5+
Traes_7DL_1A847FDCC.1	Fructokinase-2	LLIVTDGKE	494.2897++	648.319896 V - y6+
Traes_7DL_85A6FC0F2.1	Post-illumination chlorophyll fluorescence increase protein	IFYNPGTTK	520.7742++	780.388644 Y - y7+

Traes_7DS_01A0AF589.1	Ferredoxin--NADP reductase	GIDEIMIPLASK	643.8549++	515.318774	P - y5+
Traes_7DS_01A0AF589.1	Ferredoxin--NADP reductase	EGIDWIDYR	583.7775++	338.18228	Y - y2+
Traes_7DS_02539EB3B.1	Glucose-1-phosphate adenyllyltransferase	ATAFGLMK	419.7282++	666.364344	A - y6+
Traes_7DS_02539EB3B.1	Glucose-1-phosphate adenyllyltransferase	SAPIYQPR	516.7773++	664.3413	Y - y5+
Traes_7DS_7254A96B4.1	60 kDa chaperonin	IVNDGVTVAR	522.2958++	831.431906	N - y8+
Traes_7DS_7254A96B4.1	60 kDa chaperonin	VIAAGANPQITR	655.3830++	713.43045	P - y6+
Traes_7DS_7254A96B4.1	60 kDa chaperonin	ADNTVLGTAAK	530.7853++	560.340238	L - y6+
Traes_7DS_7254A96B4.1	60 kDa chaperonin	VLSNDNFK	468.7429++	724.326044	S - y6+
TRAES3BF044000030CFD_t1	Fructose-bisphosphate aldolase	NAAYIGTPGK	496.2640++	301.187031	P - y3+
TRAES3BF044000030CFD_t1	Fructose-bisphosphate aldolase	AAFLVR	338.7107++	534.339844	F - y4+
TRAES3BF044200210CFD_t1	Photosystem II 22 kDa protein, chloroplastic	TEDGIFGTSGGIGFTK	793.8885++	1071.546936	F - y11+
TRAES3BF044200210CFD_t1	Photosystem II 22 kDa protein, chloroplastic	ENELFVGR	482.2483++	478.277243	F - y4+
TRAES3BF044200210CFD_t1	Photosystem II 22 kDa protein, chloroplastic	FVDEQPTTGLDK	675.3328++	731.393395	P - y7+
TRAES3BF079100070CFD_t1	Triosephosphate isomerase	SLMGESSEFVGEK	700.3241++	1068.484395	G - y10+
TRAES3BF079100070CFD_t1	Triosephosphate isomerase	EAGSTMEVVAEQTK	740.3534++	675.367181	V - y6+
TRAES3BF079100070CFD_t1	Triosephosphate isomerase	TNVSPVAASTR	616.3175++	830.436657	P - y8+
TRAES3BF117100180CFD_t1	Phosphoenolpyruvate carboxylase	EILAAFR	410.2398++	464.261593	A - y4+
TRAES3BF154700090CFD_t1	Photosystem II reaction center PsbP family protein	VQVVASPLIR	541.3400++	854.545814	V - y8+
Traes_4DL_8DBE42AE9.2	Malate dehydrogenase	LASGEVFGQDQPIALK	836.9489++	1116.604785	F - y10+
Traes_4DL_8DBE42AE9.2	Malate dehydrogenase	SSAASTAVSIVDAMR	733.3694++	791.408	S - y7+
Traes_4DS_1EDBCFF93.1	Phosphoglycerate kinase	FSLAPLVR	500.3029++	581.376957	P - y5+
Traes_4DS_5E720DFF7.1	Glyceraldehyde-3-phosphate dehydrogenase	AASFNIIPSSGAAK	717.8830++	831.457058	I - y9+
Traes_4DS_5E720DFF7.1	Glyceraldehyde-3-phosphate dehydrogenase	LTGMSFR	414.2076++	613.276258	G - y5+
Traes_4DS_5E720DFF7.1	Glyceraldehyde-3-phosphate dehydrogenase	VPTVDVSVVDLTVR	500.2874+++	603.346051	D - y5+
Traes_4DS_BA5F86673.1	Alanine:glyoxylate aminotransferase	SPAIPALTK	449.2738++	529.334424	P - y5+
Traes_4DS_BA5F86673.1	Alanine:glyoxylate aminotransferase	YNLSLGLGLNK	596.3402++	601.366787	G - y6+
Traes_4DS_D277993E3.1	Malate dehydrogenase	LLGVTTLDVAR	579.3481++	531.520721	G - y9+
Traes_5AL_3848A3E60.1	Aspartate-semialdehyde dehydrogenase	AAPGVITSDDR	551.2804++	480.243263	P - y9++
Traes_5AL_5A931BF50.1	2-isopropylmalate synthase	ANEFQIVL GK	524.2953++	586.392273	G - y6+
Traes_5AL_89F608111.1	Pyruvate kinase	LLPINFAGLAK	578.8581++	465.774002	P - y9++
Traes_5AL_89F608111.1	Pyruvate kinase	VDSMSTDNLRPTR	501.9243+++	653.314425	D - y11++
Traes_5AL_A33DF5E3A.1	Triosephosphate isomerase	KEDIDGFLVGGASLK	516.9471+++	532.308937	G - y6+
Traes_5AL_A33DF5E3A.1	Triosephosphate isomerase	EDIDGFLVGGASLK	710.8696++	532.308937	G - y6+
Traes_5AL_AE2EF1F20.1	Glucose-1-phosphate adenyllyltransferase	ASEGFHIR	458.7354++	629.351805	G - y5+
Traes_5AS_116663495.1	Enolase	AAVPSGASTGVYEALELR	895.9678++	775.396469	P - y15++
Traes_5AS_116663495.1	Enolase	VNQIGSVTESIEAVK	787.4252++	1119.589195	G - y11+
Traes_5AS_116663495.1	Enolase	IEEELGDAAVYAGLK	789.4065++	964.509822	G - y10+
Traes_5AS_EAE5D853B.1	Cysteine synthase	GFIVPGK	359.2183++	301.187031	P - y3+
Traes_5AS_EAE5D853B.1	Cysteine synthase	LVLTMPASMSMER	733.3642++	908.396449	P - y8+
Traes_5BL_BF98F80FD.1	Glucosamine-6-phosphate deaminase	LALDGFLSK	482.2791++	779.429781	L - y7+
Traes_5DL_CFFABFAA6.2	UTP--glucose-1-phosphate uridylyltransferase	IVTEDFLPLPSK	679.8819++	331.197596	P - y3+
Traes_5DL_CFFABFAA6.2	UTP--glucose-1-phosphate uridylyltransferase	VQLLEIAQVPDEHVNEFK	703.3723+++	1114.516364	P - y9+
Traes_6AL_0F8A39C3D.1	Aspartate aminotransferase	ISLAGLNLA	500.3135++	686.419551	A - y7+
Traes_6AL_727AEFCD4.1	Ornithine carbamoyltransferase	VLSGYNDIIMAR	676.3556++	1139.55137	S - y10+
Traes_6AL_7C6EE2D46.1	Phosphoribulokinase	ANDFDLMEYQVK	736.8399++	666.345717	Y - y5+
Traes_6AL_7C6EE2D46.1	Phosphoribulokinase	KPDFDAFIDPQK	474.2418+++	600.335152	I - y5+
Traes_6AL_871B47695.1	Acetolactate synthase	IVHIDIDPAEIGK	473.9329+++	307.679039	P - y6++
Traes_6AL_871B47695.1	Acetolactate synthase	GFNVPAVR	430.2429++	442.277243	P - y4+
Traes_6DL_A19C3ABDA.1	ATP synthase delta-subunit	IFAEIAIEFFDNPTVPR	689.3458+++	569.340572	P - y5+
Traes_6DL_A19C3ABDA.1	ATP synthase delta-subunit	TALIDEIAK	487.2819++	801.471646	L - y7+
Traes_6DL_A19C3ABDA.1	ATP synthase delta-subunit	SSELQPHTVNFLNVVIDNTR	761.7291+++	618.320565	I - y5+
Traes_7AL_5427988BA.1	Fructose-bisphosphate aldolase	VGAEVIAEYTVAAALR	521.2910+++	430.277243	A - y4+
Traes_7AL_5427988BA.1	Fructose-bisphosphate aldolase	ENVADAQATFLAR	703.3571++	1063.553084	A - y10+
Traes_7AS_9DF135C9F.1	pfkB-like carbohydrate kinase family protein	TALAFVTLR	496.3004++	635.387522	F - y5+
TRAES3BF021900080CFD_t1	Mitochondrial outer membrane protein porin	SILSLVDPQR	613.8588++	515.257236	P - y4+
Traes_1BL_22B15A022.1	Mitochondrial outer membrane porin	GVLSLFPFYQK	624.8530++	779.408652	P - y6+
Traes_1BL_22B15A022.1	Mitochondrial outer membrane porin	SLITLSTEVDTK	653.8587++	993.509882	T - y9+
Traes_4AS_620D02FAE.1	Outer mitochondrial membrane protein porin	FPDYNAGK	456.2165++	382.68231	P - y7++
Traes_4AS_620D02FAE.1	Outer mitochondrial membrane protein porin	ASAVAETFTR	476.2483++	623.314751	A - y5+