

## Matching the proteome to the genome

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Supplementary Table 6. Comparison of putative *P. chrysogenum* PTS proteins with those identified (in red) by Mass Spec analysis

ORF code	Description of putative <i>P. chrysogenum</i> ORF	Average transcript levels	Putative	Putative
		DS17690 + PAA	PTS1	PTS2
Pc21g21370	Acyl-coenzyme A:isopenicillin N acyltransferase	2648.55	nARL*	
Pc21g00970	Woronin body protein Hex1	2448.45	gSRL*	
Pc06g01600	Putative FAD-dependent L-sorbose dehydrogenase / GMC oxidoreductase	2223.13	yPRI*	
Pc21g03400	Triose-phosphate-isomerase TpiA	1813.75	nARI*	
Pc22g24860	Putative aldehyde dehydrogenase	1655.93	IPRL*	
Pc12g13740	Catalase/oxidase KatG	1637.98	rPRL*	
Pc21g17590	Putative acyl-CoA dehydrogenase	1248.65	kSHL*	
Pc22g19440	Aspartate transaminase Aat2	1212.05	sAKL*	9 / dRLsslssHIM
Pc20g03610	NADP-dependent isocitrate dehydrogenase IcdA	1200.78	kARL*	
Pc12g11190	Argininosuccinate synthase Arg1	1190.75	gERL*	
Pc13g05220	Putative cytochrome b5	1126.73	aAKL*	
Pc18g01220	Fructose-bisphosphate aldolase Fba1	1109.53	aGQL*	
Pc22g19490	Putative 2-nitropropane dioxygenase family oxidoreductase	956.15	vSKL*	
Pc22g13390	Putative Zn-dependent alcohol dehydrogenase	917.10	gSKL*	
Pc13g02710	Putative beta-oxidation protein/dehydratase	853.38	kSKL*	
Pc22g15030	Peroxisomal 2,4-dienoyl-CoA reductase Sps19	813.73	kSKL*	
Pc14g01270	Putative fumarylacetoacetate hydrolase family protein	806.98	sSKL*	
Pc13g03610	Putative YcaC-related amidohydrolase	524.75	fSKI*	
Pc16g08670	C-8 sterol isomerase Erg-1	515.40	qLKL*	
Pc20g04300	Putative flavin-containing monooxygenase	507.25	tARL*	
Pc21g16840	Putative NAD+-dependent 15-hydroxyprostaglandin dehydrogenase	507.20	IPKL*	
Pc18g03000	Aldose 1-epimerase	501.10	kSRL*	
Pc13g10320	Putative short chain dehydrogenase	484.23		5 / dRLtqvneHL
Pc20g03330	Glucose-6-phosphate 1-dehydrogenase GsdA	480.10	pNRL*	
Pc22g03680	Putative NADPH-dependent beta-ketoacyl reductase	460.73	sAKL*	
Pc22g20270	Phenylacetyl-CoA ligase PhIB	458.80	kAKL*	
Pc13g11580	Putative epoxide hydrolase	458.30	kARL*	
Pc13g12930	Putative 3-ketoacyl-CoA thiolase	442.33		4 / dRLsslIsHL
Pc13g12080	Putative protein with alpha/beta hydrolase fold	440.23	aARL*	
Pc21g16080	Putative HypA-like protein / oxidase required for aflatoxin biosynthesis	431.73	qAHI*	
Pc20g10840	Putative long-chain-fatty-acid-CoA ligase	425.08	aGKL*	
Pc22g01300	Lipid transfer protein Scp2	403.55	gAKL*	
Pc13g01890	Putative acyl-CoA synthetase	391.13		6 / sRLsgllgHF
Pc21g06860	Peroxisomal Lon protease	378.08	eSRL*	

Pc22g14900	Phenylacetyl-CoA ligase PclA	377.09	gSKI*	
Pc21g05590	Putative D-amino-acid oxidase	372.93	rAKL*	
Pc20g12470	Delta3-cis-delta2-trans-enoyl-CoA isomerase Eci1	360.75	rHKL*	
Pc12g08530	Putative long-chain acyl-CoA dehydrogenase	352.00	nAKI*	
Pc22g00060	Putative fructosyl amine oxidase	334.18	aAKL*	
Pc22g14270	Putative 2-nitropropane dioxygenase family oxidoreductase	333.53	sSKL*	
Pc13g05940	Trifunctional enzyme Fox-2	322.68	kAKL*	
Pc22g15180	Putative pyruvate carboxylase like protein	297.30	rGKL*	
Pc21g14590	Insulin-degrading enzyme / a factor processing peptidase Ste23	285.30	dAKL*	
Pc13g04370	Intraperoxisomal peroxin Pex8	273.85	eSKL*	
Pc16g14240	Putative amidase	272.30	sAKL*	
Pc15g00410	Putative 3-ketoacyl-CoA thiolase	271.45		6 / qRLnsvanQL
Pc22g11470	Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase	271.18	rARL*	
Pc12g05400	Citrate synthase CitA	266.80	gAKL*	
Pc22g16280	Conserved hypothetical protein	254.53	eGRL*	
Pc22g24780	Putative 4-coumarate-CoA ligase	252.33	kAKL*	
Pc21g21810	Putative levodione reductase / short chain dehydrogenase	241.25		7 / qRLqalskQL
Pc16g14230	Putative NADPH-dependent beta-ketoacyl reductase	241.13	kGRL*	
Pc22g17070	Putative sterol carrier protein-2	238.55	IARF*	
Pc22g02620	Monoglyceride lipase	238.30	kAKL*	
Pc21g01650	Putative thioesterase	237.35	eAKL*	
Pc18g03470	Lysine aminopeptidase ApsA	236.55	qSKL*	
Pc12g05520	Long-chain-fatty-acid-CoA ligase Faa2	235.20	kAKL*	
Pc22g10030	Betaine-aldehyde dehydrogenase	232.75	fAKL*	
Pc22g10020	Putative FAD-dependent alcohol dehydrogenase / GMC oxidoreductase	231.30	qPRL*	
Pc20g01800	Putative palmitoyl-CoA oxidase	230.88	kSKL*	
Pc20g13410	Putative aminotransferase	229.33	aWKL*	
Pc13g07430	Putative dioxygenase	226.33	aSKL*	
Pc20g13690	Putative CoA-binding protein	226.30	sQRL*	
Pc13g06300	Putative amidase	225.40	hSKI*	
Pc21g05490	Dihydroxyacetone phosphate acyltransferase	201.75	eAKL*	
Pc12g14280	Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase	195.83	kPKL*	
Pc13g15940	Putative copper amine oxidase	195.53	kSHI*	
Pc13g09740	Fructosyl peptide oxidase FpoxE	193.65	dAKL*	
Pc20g15010	Carnitine O-acetyltransferase	192.43	kPKL*	
Pc21g07210	Conserved hypothetical protein	190.35	rSKL*	
Pc21g23650	D-lactate dehydrogenase	189.88	pVRL*	
Pc22g25150	Putative very-long-chain acyl-CoA dehydrogenase	189.28	gSKL*	

Pc20g13550	Malate synthase AcuE	188.58	aAKL*	
Pc12g01170	Putative enoyl-CoA hydratase/isomerase family protein	187.33	kAKL*	
Pc13g02990	Protein phosphatase 2C Ptc5	179.30	kSKL*	
Pc18g02760	Putative aldehyde dehydrogenase	179.05	gTKL*	
Pc22g11520	Conserved hypothetical protein	176.13	kVRL*	
Pc21g14640	Putative dephospho-CoA kinase	175.88	kAKL*	
Pc22g12040	Putative nitroreductase	161.00	fGKL*	
Pc22g06820	3-ketoacyl-CoA thiolase Pthik	157.40		6 / qRLsqvssHF
Pc20g08300	Conserved hypothetical protein	150.13	eSKI*	
Pc20g13500	Isopenicillin N-CoA synthetase	143.70	sVRL*	
Pc16g07560	Putative long chain acyl-CoA dehydrogenase	143.08	gMKL*	
Pc22g22390	Putative enoyl-CoA hydratase/isomerase family protein	141.38	pSKL*	
Pc21g11670	Putative NADPH:quinone reductase / Zn-dependent oxidoreductase	139.55	kSKL*	
Pc13g12270	Putative 4-coumarate-CoA ligase	133.35	tAKL*	
Pc21g23730	Putative feruloyl-CoA synthetase	129.80		8 / qRLqqtIsHV
Pc21g19000	Putative acyl-CoA dehydrogenase	128.28	qSKV*	
Pc22g25570	Putative aminoglycoside phosphotransferase	124.23	eGKL*	
Pc13g01530	Putative aldo/keto reductase	123.28	dCKI*	
Pc21g20650	Putative 4-coumarate-CoA ligase	123.08	kARL*	
Pc20g15670	Glutathione-dependent formaldehyde-activating enzyme	119.10	fANL*	
Pc22g18190	Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase	113.65	sSKL*	
Pc13g11930	Putative very-long-chain acyl-CoA dehydrogenase	108.40	sSKL*	
Pc20g15660	Putative sterol carrier protein-2	107.70	kARI*	
Pc12g13480	Putative glycine/D-amino acid oxidase	104.65	nSKL*	
Pc21g02970	Putative 2-polyprenyl-6-methoxyphenol hydroxylase	104.65	qSRL*	
Pc18g05710	Putative long-chain fatty acid transporter /acyl CoA synthetase	101.30	qVRL*	
Pc22g15170	Putative propionyl-CoA carboxylase	100.65		19 / dRLhqvssHI
Pc21g08790	Putative NADP-dependent oxidoreductase	99.93	kAKL*	
Pc13g15840	Putative enoyl-CoA hydratase/isomerase family protein	97.50	fEKL*	
Pc22g05280	Putative histidine triad family hydrolase	97.18	rGKL*	
Pc22g20960	Urate oxidase Uaz	96.15	kAKL*	
Pc20g14920	Putative FAD dependent oxidoreductase	96.10	qARL*	
Pc14g00140	Putative acyl-CoA dehydrogenase	95.90	kARI*	
Pc22g07280	Putative peroxisomal acyl-CoA thioesterase	91.48	kVKL*	
Pc22g20380	Acetyltransferase SidF	90.15	nAKL*	
Pc22g00460	Protein with dehydrogenase domain of non-ribosomal peptide synthetases	87.93	kARI*	
Pc13g14420	Putative acyl-CoA synthetase	86.88	kARL*	
Pc20g01980	Putative 2-polyprenyl-6-methoxyphenol hydroxylase	79.53	gSRL*	

Pc20g06660	Putative D-amino-acid oxidase	79.48	kSRL*
Pc18g05540	Putative alcohol dehydrogenase, class IV	79.15	IANL*
Pc16g02530	Protein with pentatricopeptide repeat	76.13	kPKM*
Pc21g07490	Putative OHCU decarboxylase involved in purine catabolism	71.93	qSRI*
Pc21g16040	Conserved hypothetical protein	68.10	yANI*
<b>Pc21g04910</b>	<b>Conserved hypothetical protein</b>	<b>67.45</b>	<b>mEKL*</b>
Pc22g20320	Putative dehydrogenase	66.13	IARL*
Pc21g19510	Epoxide hydrolase	65.25	aGKL*
<b>Pc12g09740</b>	<b>Putative fructosyl amine oxidase</b>	<b>63.08</b>	<b>qAKL*</b>
Pc21g16710	Conserved protein with double-stranded beta helix domain	62.95	sARL*
<b>Pc13g05130</b>	<b>Putative acyl-CoA synthetase</b>	<b>56.75</b>	<b>kSKL*</b>
Pc21g17810	Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase	55.50	rPKL*
Pc21g23700	Long-chain-fatty-acid alcohol oxidase	55.33	iARL*
Pc13g09070	Putative esterase with alpha/beta hydrolase fold	54.45	tARL*
Pc14g00560	Conserved hypothetical protein	53.25	rAKL*
Pc22g23700	Putative FAD dependent oxidoreductase, partial	52.00	ISRL*
Pc21g12160	Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase	51.95	qVKL*
<b>Pc20g09430</b>	<b>Ureidoglycolate hydrolase Dal3</b>	<b>51.18</b>	<b>pAKL*</b>
Pc22g20370	Putative enoyl-CoA hydratase/isomerase family protein	43.33	nSKL*
Pc21g09780	Putative fructosyl amine oxidase	43.25	aSRL*
Pc22g16620	Protein weakly similar to ethanolamine utilization protein	42.08	tTKL*
Pc20g15650	Putative acetyl-CoA acetyltransferase, partial	41.18	tARL*
Pc22g25120	Putative enoyl-CoA hydratase/isomerase family protein	38.23	hSKL*
Pc15g01190	Putative catechol dioxygenase	37.83	qGKL*
Pc18g01590	Putative glycolate oxidase-like protein / FMN-dependent dehydrogenase	35.85	IARL*
<b>Pc22g21240</b>	<b>Catalase CatC</b>	<b>35.80</b>	<b>pARL*</b>
Pc21g22060	Conserved protein with DUF1446 domain of unknown function	34.98	rGKL*
Pc23g00390	Conserved hypothetical protein	34.03	kAKL*
Pc13g04510	NADP-dependent malate dehydrogenase MaeA	33.35	nAKL*
Pc21g11780	Putative 4-hydroxyphenylpyruvate dioxygenase	32.60	kSRI*
Pc18g03220	Putative FAD-dependent oxidoreductase	30.33	tIKL*
Pc13g04270	Dimethylglycine oxidase	30.08	mSRL*
Pc22g05640	Putative toxin biosynthesis protein / hydrolase	29.08	eSKL*
Pc16g11200	Putative copper amine oxidase	27.40	qVKL*
Pc16g03860	Acetylase / siderophore biosynthesis protein Sid3	24.78	sLKL*
Pc21g12260	Putative alcohol dehydrogenase, class V	23.20	qAKL*
Pc13g14430	Putative enoyl-CoA hydratase/isomerase family protein	22.55	kVKI*
Pc22g14860	Copper amine oxidase AMO	21.30	

Pc13g14410	Putative palmitoyl-CoA oxidase	20.60	ISKL*
Pc13g03350	Putative copper amine oxidase	18.93	cCRL*
Pc20g15250	Putative dehydrogenase	18.65	kAQL*
<b>Pc13g06370</b>	<b>Protein weakly similar to ethanolamine utilization protein</b>	<b>15.85</b>	<b>kAKL*</b>
Pc22g13680	Isopenicillin N-CoA epimerase	15.40	kSKI*
Pc16g11790	Putative fructosyl amine oxidase	14.30	gSKI*
Pc21g21120	Putative monoamine oxidase N	14.25	sSHL*
Pc16g10070	Putative 2-nitropropane dioxygenase family oxidoreductase	13.00	vSKL*
Pc21g22010	Putative 4-coumarate-CoA ligase	11.73	pSKL*
Pc22g17230	Putative aldehyde dehydrogenase	11.60	kSKL*
Pc13g01380	Putative fructosyl amine oxidase	11.18	ISKL*
Pc06g01220	Putative lipase / hydrolase	11.05	qSNL*
Pc13g02660	Protein with Cupin barrel domain	9.45	kAKL*
Pc15g00420	Putative bifunctional fatty acid transporter/acyl-CoA synthetase	8.35	kAKI*
Pc22g24630	Putative isopenicillin N-CoA epimerase, partial	7.00	aAKI*
Pc18g01860	Putative D-amino-acid oxidase	6.78	qSHL*
Pc16g07600	Putative FAD dependent oxidoreductase	6.60	rANL*
Pc16g11910	Putative FAD dependent oxidoreductase	6.00	gSKL*
Pc21g09480	3-hydroxy-3-methylglutaryl CoA lyase HlyA	5.33	kSKL*
Pc22g17240	Putative copper amine oxidase	5.15	kPRM*
Pc22g19300	Putative aldehyde dehydrogenase	4.95	gTRL*
Pc20g10700	Putative sarcosine oxidase / FAD-dependent oxidoreductase	4.43	sSKI*
Pc22g00300	Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase	4.35	nSKL*
Pc13g08330	3-dehydroshikimate dehydratase Qa-4	4.30	qHRL*
Pc21g09440	Putative acyl-CoA dehydrogenase	4.23	qSKL*
Pc20g09660	Putative toxin biosynthesis protein / hydrolase	3.63	kSRF*
Pc22g23350	Putative fructosyl amine oxidase	3.53	aAKL*
Pc14g00970	Putative D-amino-acid oxidase	3.03	pSKL*
<b>Pc16g07060</b>	<b>Putative catalase</b>	<b>2.88</b>	<b>sSRL*</b>
<b>Pc16g07070</b>	<b>Formate oxidase Fod1</b>	<b>2.75</b>	<b>sSKL*</b>
Pc12g09950	Alcohol oxidase Aox	2.73	ISRL*
Pc12g11930	2-methylcitrate dehydratase, involved in propionate catabolism	2.65	kARF*
Pc06g01160	Putative 4-coumarate-CoA ligase	2.63	qTKI*
Pc13g14580	Putative thioesterase	2.58	tAKL*
Pc20g10430	D-mandelate dehydrogenase	2.58	gSKL*
Pc12g13290	Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase	2.48	sVKL*
Pc21g22360	Vanillyl-alcohol oxidase VaoA	2.35	tTKL*
Pc22g07740	Putative acyl-CoA oxidase	2.33	rAKL*

Pc22g00860	Putative ascorbate-peroxidase	1.98	rARL*
Pc22g24590	Putative FAD binding domain protein	1.73	qGRL*
Pc16g05060	3-hydroxy-3-methylglutaryl coenzyme A reductase	1.68	aSKI*
Pc17g00720	Conserved hypothetical protein	1.58	eARL*
Pc14g01040	Putative aldehyde dehydrogenase	1.33	nARL*
Pc12g14790	Putative enoyl-CoA hydratase/isomerase family protein	1.18	kAKL*
Pc22g25190	Conserved hypothetical protein	1.18	aVKL*
Pc13g12580	Putative aminotransferase	0.90	kARL*
Pc22g15400	Putative toxin biosynthesis protein / hydrolase	0.58	rSKI*
Pc06g01180	Putative acyl-CoA dehydrogenase	0.48	sAKI*
Pc22g24620	Putative sugar phosphate isomerases/epimerase	0.43	kHKL*
Pc20g09670	Putative phosphotransferase	0.38	yYKL*
Pc21g09470	Putative feruloyl-CoA synthetase	0.33	rAKL*
Pc22g19270	Putative glycolate oxidase-like protein / FMN-dependent dehydrogenase	0.23	ISKL*