

Table S1. Results table of an example of CCD1 protein detection by LCMS, *Petunia x hybrida* PhCCD1 with MW 61.3 kDa, line 6731

#	Checked	Master	Accession	Description	Cove#	Pes#	PSI#	Un#	AA	MW	calc.	Score#	Pes Biological	Cellular C	Molecular Pfam IDs	Entrez Ge	Ensembl	C Gene Sym	Chro	KEGG Pat	WikiPathw	Reactome #	Pro Foun	Pro	
6470	FALSE	Master Pn	Q03558	NADPH dehydrogenase 2 OS=Saccharomyces cerevisiae (stra	34	11	17	11	400	45	6.57	476	11	cell death	cytoplasm catalytic	a PF00724	856584	YHR179W OYE2	VIII				0 High	1	
6491	FALSE	Master Pn	P38693	Acid phosphatase PHO12 OS=Saccharomyces cerevisiae (str	20	10	20	8	467	52.7	5.16	476	10	metabolic vacuole	catalytic	a PF00328	856625	YHR215W PHO12	VIII	Metabolic			2 High	1	
6515	FALSE	Master Pn	P07262	NADP-specific glutamate dehydrogenase 1 OS=Saccharomyc	32	11	15	7	454	49.5	5.69	457	11	metabolic cytoplasm	catalytic	a PF02008, F854557	YOR375C GDH1	XV	Arginine b Superpath Amino aci				12 High	1	
6534	FALSE	Master Pn	P14126	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (stra	40	15	17	15	387	43.7	10.3	456	15	cell organi	cytoplasm nucleotide	a PF00297	854229	YOR063W RPL3	XV	Ribosome Cytoplasm Formator			14 High	1	
6555	FALSE	Master Pn	C7GVZ9	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (st	42	12	14	2	255	28.8	10.1	456	12	metabolic cytoplasm	structural	a PF01015							0 High	1	
6573	FALSE	Master Pn	P46955	Beta-glucosidase-like protein NCA3, mitochondrial OS=Sacch	21	7	14	6	337	35.4	4.46	456	7	cell organi	cell surfac	a PF03856	853326	YIL116C NCA3	X				0 High	1	
6591	FALSE	Master Pn	P41939	Isocitrate dehydrogenase [NAD(P)] cytoplasmic OS=Saccharon	25	9	14	8	412	46.5	6.19	454	9	metabolic cytoplasm	catalytic	a PF00180	850871	YLR174W IDP2	XII	Carbon m Principle F Citric acid			26 High	1	
6609	FALSE	Master Pn	P31539	Heat shock protein 104 OS=Saccharomyces cerevisiae (strain	18	13	14	13	908	102	5.45	448	13	cell organi	cytoplasm catalytic	a PF00004, F850633	YLL026W HSP104	XII	Longevity				1 High	1	
6627	FALSE	Master Pn	B3RHW0	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (st	42	12	14	2	255	28.7	9.99	445	12	metabolic cytoplasm	structural	a PF01015		SCRG_043					0 High	1	
6645	FALSE	Master Pn	P19097	Fatty acid synthase subunit alpha OS=Saccharomyces cerevis	11	18	18	18	1887	207	5.44	442	18	metabolic cytoplasm	catalytic	a PF00106, F855845	YPL231W FAS2	XVI	Fatty acid Fatty Acid				6 High	1	
6667	FALSE	Master Pn	PDCX82	60S ribosomal protein L19-A OS=Saccharomyces cerevisiae (	26	7	11	7	189	21.7	11.4	430	7	cell organi	cytoplasm RNA bindi	a PF01280	852254; 8	YBL027W; RPL19B; R II		Ribosome Cytoplasm Formator			14 High	1	
6682	FALSE	Master Pn	P60010	Actin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2	30	9	15	3	375	41.7	5.68	425	9	cell organi	cytoplasm catalytic	a PF00022	850504	YFL039C ACT1	VI	Phagosome			RHO GTPa	10 High	1
6701	FALSE	Master Pn	P47143	Adenosine kinase OS=Saccharomyces cerevisiae (strain ATCC	40	9	13	9	340	36.4	5.16	425	9	metabolic cytoplasm	catalytic	a PF00294	853569	YIR105W ADO1	X	Metabolic			Purine sal	6 High	1
6718	FALSE	Master Pn	P36110	Protein PRY2 OS=Saccharomyces cerevisiae (strain ATCC 204	13	3	9	3	329	33.8	4.6	420	3	transport	endoplasm	a PF00188	853882	YKR013W PRY2	XI					0 High	1
6731	FALSE	Master Pn	JT_Ph_CCD1	Petunia x hybrida carotenoid cleavage dioxygenase 1 (CCD1)	24	10	12	10	546	61.3	6.27	420	10										0 High	1	
6747	FALSE	Master Pn	P54070	Mannosyltransferase KTR6 OS=Saccharomyces cerevisiae (st	28	11	13	11	446	52.1	5.5	417	11	cell organi	Golgi;men catalytic	a PF01793	856054	YPL053C KTR6	XVI	Metabolic				2 High	1
6764	FALSE	Master Pn	P23254	Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 2	22	13	17	13	680	73.8	7.01	413	13	metabolic cytoplasm	catalytic	a PF00456, F856188	YMR074C TKL1	XVI	Pentose p Principle F Pentose p					18 High	1
6785	FALSE	Master Pn	P00729	Carboxypeptidase Y OS=Saccharomyces cerevisiae (strain AT	20	10	15	10	532	59.8	4.73	412	10	metabolic cytoplasm	catalytic	a PF00450, F855343	YMR297W PC1	XIII					Neutrophil	3 High	1
6804	FALSE	Master Pn	P37291	Serine hydroxymethyltransferase, cytosolic OS=Saccharomyc	32	14	14	13	469	52.2	7.43	386	14	metabolic cytoplasm	catalytic	a PF00155, F850747	YLR058C SHM2	XII	Cyanoami Pathways				Carnitine :	22 High	1
6822	FALSE	Master Pn	P13130	Sporelation-specific wall maturation protein OS=Saccharomyl	14	3	6	3	326	34.2	5.41	385	3	cell differe	catalytic	a PF00710	856541	YHR139C SPS100	VIII					0 High	1
6832	FALSE	Master Pn	P38887	Uncharacterized protein YHR202W OS=Saccharomyces cerev	22	13	18	13	602	69	6.23	381	13	metabolic cytosol;va	catalytic	a PF00149	856609	YHR202W YHR202W	VIII					0 High	1
6854	FALSE	Master Pn	P15992	Heat shock protein 26 OS=Saccharomyces cerevisiae (strain	58	9	13	9	214	23.9	5.53	378	9	metabolic cytoplasm	protein bli	a PF00011	852364	YBR072W HSP26	II	Protein pr				1 High	1
6871	FALSE	Master Pn	P38109	Putative serine carboxypeptidase YBR139W OS=Saccharomyc	20	9	15	9	508	57.6	5.31	376	9	metabolic vacuole	catalytic	a PF00450	852436	YBR139W YBR139W	II				Neutrophil	3 High	1
6890	FALSE	Master Pn	P53090	Aromatic/aminoadipate aminotransferase 1 OS=Saccharomyc	24	11	12	11	500	56.1	6.01	373	11	metabolic cytoplasm	catalytic	a PF00155, F856272	YGL201W ARO8	VII	Lysine bio; Phenylala; Lysine cati				23 High	1	
6906	FALSE	Master Pn	P00817	Inorganic pyrophosphatase OS=Saccharomyces cerevisiae (st	48	9	13	9	287	32.3	5.58	372	9	metabolic cytoplasm	catalytic	a PF00719	852296	YBR011C IPP1	II	Oxidative UDP-Glucx Cytosolic i				9 High	1
6923	FALSE	Master Pn	Q08271	1,3-beta-glucanosyltransferase GAS4 OS=Saccharomyces cer	18	7	12	7	471	53.8	4.89	370	7	cell organi	membran catalytic	a PF00150, F853988	YOL132W GAS4	XV					0 High	1	
6939	FALSE	Master Pn	P06168	Ketol-acyl reductoisomerase, mitochondrial OS=Saccharomyc	30	9	12	9	395	44.3	9.04	368	9	cell organi	mitochondri catalytic	a PF01450, F851069	YLR355C ILV5	XII	Metabolic Isoleucine					10 High	1
6955	FALSE	Master Pn	P36105	60S ribosomal protein L14-A OS=Saccharomyces cerevisiae (	52	10	12	10	138	15.2	10.9	365	10	cell comm cytoplasm	nucleotide	a PF01929	853864	YKL006W RPL14A	XI	Ribosome Cytoplasm				2 High	1

Table S2. Results table indicating no detection by LCMS of any CCD1 protein secreted from the empty plasmid (p\_Empty) between the range of CCD1 sizes used: MW 61.1 kDa – 62.4 kDa

#	Checked	Master	Accession	Description	Cover	Per #	PSI #	Un #	AA	MW	calc.	score	Per Biological	Cellular C	Molecular P	Path IDs	Entrez Ge	Ensembl	C Gene	Sym	Chro	KEGG	Path	WikiPath	Reactome	#	Pro	Four	#	Pro	
12170	FALSE	Master Pri	P33734	Imidazole glycerol phosphate synthase hisHf OS=Saccharo	9	5	6	5	552	61.3	5.49	126	5	metabolic	cytoplasm	catalytic	a Pf00117, i852550	YBR248C	HIS7	II				Histidine r	Histidine f	5	High	1			
12176	FALSE	Master Pri	Q08224	Hydroxymethylpyrimidine/phosphomethylpyrimidine kina	3	2	2	2	551	61.2	6.16	59	2	metabolic	cytosol	catalytic	a Pf05048, i854099	YOL055C	THI20	XV				Metabolic		2	High	1			
12181	FALSE	Master Pri	P12709	Glucose-6-phosphate isomerase OS=Saccharomyces cerev	57	26	61	26	554	61.3	6.46	1868	26	metabolic	cytoplasm	catalytic	a Pf00342, i852495	YBR196C	PGI1	II	Glucoseo			Pentose p	Principle f	25	High	1			
12186	FALSE	Master Pri	P06169	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces ceri	54	24	77	21	563	61.5	6.19	2776	24	metabolic	cytoplasm	catalytic	a Pf00205, i850733	YLR044C	PDG1	XII				Glycolysis	Principle f	9	High				
12193	FALSE	Master Pri	P26263	Pyruvate decarboxylase isozyme 3 OS=Saccharomyces ceri	12	4	22	1	563	61.5	6.19	771	4	metabolic	cytoplasm	catalytic	a Pf00205, i852978	YGR087C	PCDC	VII				Glycolysis	Principle f	9	High	1			
12199	FALSE	Master Pri	P47079	T-complex protein 1 subunit theta OS=Saccharomyces cere	7	4	4	4	568	61.6	5.72	70	4	metabolic	cytoplasm	nucleotide	Pf00118, i853447	YJL008C	CCT8	X	Cooperati					8	High	1			
12204	FALSE	Master Pri	P43590	Uncharacterized peptidase YFR006W OS=Saccharomyces c	3	2	2	2	535	61.7	6.16	51	2	metabolic	cytoplasm	catalytic	a Pf00557, i850556	YFR006W	YFR006W	VI						0	High	1			
12209	FALSE	Master Pri	P53966	Probable mannosyltransferase KTR5 OS=Saccharomyces ce	2	1	2	1	522	61.7	5.73	23	1	metabolic	cytoplasm	catalytic	a Pf01793, i855703	YNL029C	KTR5	XIV						0	High	1			
12214	FALSE	Master Pri	P40413	T-complex protein 1 subunit epsilon OS=Saccharomyces ce	4	2	2	2	562	61.9	5.53	58	2	metabolic	cytoplasm	nucleotide	Pf00118, i853527	YJL064W	CCT5	X	Cooperati					5	High	1			
12221	FALSE	Master Pri	P23292	Casein kinase I homolog 2 OS=Saccharomyces cerevisiae (	8	3	3	3	546	62.0	9.07	129	3	cell organi	cytoplasm	catalytic	a Pf00069, i855568	YNL154C	YCK2	XIV				Hippo sign		2	High	1			
12227	FALSE	Master Pri	P38628	Phosphocatalyticglucosamine mutase OS=Saccharomyces ce	2	1	1	1	557	62.2	5.91	38	1	cell organi	cytoplasm	catalytic	a Pf00408, i856652	YEL058W	PCM1	V	Synthesis			Amino sug	UDP-N-Ac	10	High	1			
12232	FALSE	Master Pri	P35527	SWISS-PROT:P35527 Tax_id=9606 Gene_Symbol=KRT9 Ker	43	21	50	21	623	62.1	5.3	1826	21	cell death,	cytosol;	mi structural	Pf00038, i3857		KRT9	17							0	High			
12237	FALSE	Master Pri	B3LJRO	Folylpolyglutamate synthase OS=Saccharomyces cerevisia	2	1	1	1	548	62.1	8.82	28	1	metabolic	cytoplasm	catalytic	a Pf02875		SCRG_016								0	High	1		
12243	FALSE	Master Pri	P54838	Dihydroxyacetone kinase 1 OS=Saccharomyces cerevisiae (	20	10	12	11	584	62.2	5.41	367	11	metabolic	cytoplasm	catalytic	a Pf02733, i854932	YML070W	DAK1	XIII	Fructose c	Carbon m	Xylulose-n			10	High	1			
12249	FALSE	Master Pri	P38707	Asparagine-tRNA ligase, cytoplasmic OS=Saccharomyces c	22	10	12	10	554	62.2	5.85	288	10	metabolic	cytoplasm	catalytic	a Pf00152, i856412	YHR019C	DEB1	VIII				Aminoacy	Cytoplasm r	2	High	1			
12254	FALSE	Master Pri	P13647	SWISS-PROT:P13647 Tax_id=9606 Gene_Symbol=KRT5 Ker	23	15	23	7	590	62.3	7.74	729	15	cell death,	cytoplasm	catalytic	a Pf00038, i3852	ENS0000C	KRT5	12	Formation			</td>							
12259	FALSE	Master Pri	P21264	Phosphoribosylaminoimidazole carboxylase OS=Saccharor	15	8	10	8	571	62.3	7.33	215	8	metabolic	cytoplasm	catalytic	a Pf00731, i854295	YJR028C	ADE2	XV				Metabolic De	Novo E	5	High	1			
12264	FALSE	Master Pri	Q06336	ADP-ribosylation factor-binding protein GGA1 OS=Sacchar	10	4	4	4	557	62.3	5.62	77	4	transport	cytosol;	Gc protein bi	Pf00790, i851960	YDR3558W	GGA1	IV	TBC/RAB					4	High	1			
12270	FALSE	Master Pri	P28240	Isocitrate lyase OS=Saccharomyces cerevisiae (strain ATCC	58	28	66	28	557	62.4	6.42	2107	28	metabolic	cytoplasm	catalytic	a Pf00463, i856794	YER065C	ICL1	V				Carbon m	Principle f	7	High	1			
12276	FALSE	Master Pri	Q08977	Cu(2+) suppressing and bleomycin sensitive protein 1 OS=	5	3	3	3	551	62.7	5.12	77	3		cytoplasm		Pf10303, i855867	YPL263W	YPL260W	XVI						0	High	1			
12282	FALSE	Master Pri	P30952	Malate synthase 1 OS=Saccharomyces cerevisiae (strain AI	49	29	58	29	554	62.8	7.18	1337	29	metabolic	cytoplasm	catalytic	a Pf01274, i855606	YNL117W	MLS1	XVI				Carbon m	Principle f	7	High	1			
12287	FALSE	Master Pri	P39522	Dihydroxy-acid dehydratase, mitochondrial OS=Saccharom	8	3	3	3	585	62.8	7.83	62	3	metabolic	mitochondr	catalytic	a Pf00920, i853473	YJL016C	ILV3	X				Metabolic	isoleucine	11	High	1			
12292	FALSE	Master Pri	P37012	Phosphoglucumutase 2 OS=Saccharomyces cerevisiae (str	31	16	32	14	569	63	6.62	1001	16	cellular hc	cytoplasm	catalytic	a Pf00408, i855131	YMR105C	PGM2	XIII	Galactose			Pentose p	Starch anc	24	High	1			
12297	FALSE	Master Pri	Q04636	FACT complex subunit POB3 OS=Saccharomyces cerevisiae	3	3	3	3	552	63	4.86	63	3	cell organi	chromoso	DNA bindi	Pf00531, i854933	YML069W	POB3	XIII	TP53 Regu					8	High	1			
12302	FALSE	Master Pri	P23287	Serine/threonine-protein phosphatase 2B catalytic subuni	2	1	1	1	553	63	6.67	31	1	cell divisio	cytoplasm	catalytic	a Pf00149, i851153	YLR433C	CNA1	XII						0	High				