

Table 1. Yeast mutations with increased sensitivity to pyocyanin.

Disrupted cellular pathway	Yeast genes	Mammalian orthologs*	% Identity/ % similarity ⁺	Gene function
Vacuolar ATPase biosynthesis, vesicle transports, and protein sorting	VMA6	ATP6V ₀ D1	44/62	Subunit “d” of the vacuolar ATPase V ₀ proton pore complex
	VMA7	ATP6V ₁ F	53/66	Subunit “F” of the vacuolar ATPase V ₁ catalytic complex
	VMA8	ATP6V ₁ D	54/73	Subunit “D” of the vacuolar ATPase V ₁ catalytic complex
	VMA21	Unknown	Unknown	Vacuolar ATPase assembly integral membrane protein
	YPT6	RAB6B	60/75	GTP-binding protein, participates in post-Golgi transport
	SEC16	FLJ00305	23/37	Vesicle trafficking protein
	SEC22	SEC22b	37/56	Vesicle trafficking protein
	SEC28	COPE	26/42	COPI-mediated membrane traffic
	VPS4	VPS4B/	58/70	Vacuolar protein sorting
	VPS20	FLJ11749	30/60	Vacuolar protein sorting
	VPS28	VPS28	30/53	Vacuolar protein sorting
Electron transport, oxidative stress, and apoptosis	YSA1	NUDT5	43/60	Type motif 5, ADP-sugar pyrophosphatase
	BNA2	IDO	31/49	Indoleamine-pyrrole 2,3 dioxygenase
	COQ1	TPT	37/56	Trans-prenyltransferase
	YDL119C	FLJ20551	31/43	Calcium-binding mitochondrial carrier protein
	BSD2	Unknown	Unknown	Metal homeostasis regulator
	EGR4	LBR	28/43	Lamin B receptor/ C-24 sterol reductase
	ELO2	LCE	29/43	Long-chain fatty-acyl elongase
	OSH2	OSBPL2	31/47	Oxysterol-binding protein
Cell cycle progression	CDC50	FLJ10856	35/49	Regulate cell cycle START event
	CLN2	CCNA3	23/43	Control the G ₁ /S(START) and the G ₂ /M (MITOSIS) transitions
	SSD1	DIS3	25/42	Regulation of mitosis
	HRS1	Unknown	Unknown	Global transcriptional activation/repression co-factor
	SIR4	Unknown	Unknown	Regulates gene silencing at telomeres
	PSP1	Unknown	Unknown	Multicopy suppressor of cdc17 DNA Polymerase- α mutations
Unknown	YJL048C	AAH00902	26/46	Contain ubiquitin regulatory protein domain
	FYV3	Unknown	Unknown	Function required for yeast viability on toxin exposure
	FIG2	Unknown	Unknown	Membrane protein required for efficient mating and cell fusion
	GAS1	Unknown	Unknown	Acidic PH tolerance
	YER083C	Unknown	Unknown	Unknown
	YPL066W	Unknown	Unknown	Unknown
	YLR428C	Unknown	Unknown	Unknown
	YGL024W	Unknown	Unknown	Unknown
	YOL070C	Unknown	Unknown	Unknown

*Similarities are to proteins or hypothetical proteins from human.

⁺At the amino acid level over the entire ORF.

COPI=Coatamer complex I.