

**Table S4. Predicted aromatic peripheral pathways in *C. metallidurans* CH34**

Central pathway	Peripheral pathway	Gene	ORF (aa)	CDS	Function	Organism	Id (%)	Cov (%)	UniProtKB Accession (aa)
Catechol	Toluene-Benzene (T2MO)	<i>tomA0</i>	RMET_RS06715 (74)	TomA0	Toluene-benzene-2-monooxygenase, component P0	<i>B. vietnamensis</i> G4	99	75	Q9ANX5 (97)
		<i>tomA1</i>	RMET_RS06710 (331)	TomA1	Toluene-benzene-2-monooxygenase, component P1	<i>B. vietnamensis</i> G4	99	99	Q9ANX4 (331)
		<i>tomA2</i>	RMET_RS06705 (89)	TomA2	Toluene-benzene-2-monooxygenase, component P2	<i>B. vietnamensis</i> G4	97	98	Q9ANX3 (89)
		<i>tomA3</i>	RMET_RS06700 (519)	TomA3	Toluene-benzene-2-monooxygenase, component P3	<i>B. vietnamensis</i> G4	99	100	Q9ANX2 (519)
		<i>tomA4</i>	RMET_RS06695 (118)	TomA4	Toluene-benzene-2-monooxygenase, component P4	<i>B. vietnamensis</i> G4	100	100	Q9ANX1 (118)
		<i>tomA5</i>	RMET_RS06690 (354)	TomA5	Toluene-benzene-2-monooxygenase, component P5	<i>B. vietnamensis</i> G4	98	100	Q9ANX0 (354)
		<i>fer2</i>	RMET_RS06685 (118)	Fer2	Ferredoxin	<i>Pseudomonas</i> sp. CF600	46	68	P23103 (112)
	Toluene (TMO)	<i>tmoA</i>	RMET_RS06640 (500)	TmoA	Toluene-4-monooxygenase system protein A	<i>P. mendocina</i> KR1	69	69	Q00456 (500)
		<i>tmoB</i>	RMET_RS06635 (88)	TmoB	Toluene-4-monooxygenase system protein B	<i>P. mendocina</i> KR1	49	95	Q00457 (84)
		<i>tmoC</i>	RMET_RS06630 (111)	TmoC	Toluene-4-monooxygenase system protein C	<i>P. mendocina</i> KR1	53	100	Q00458 (112)
		<i>tmoD</i>	RMET_RS06625 (104)	TmoD	Toluene-4-monooxygenase system protein D	<i>P. mendocina</i> KR1	60	91	Q00459 (103)
		<i>tmoE</i>	RMET_RS06620 (328)	TmoE	Toluene-4-monooxygenase system protein E	<i>P. mendocina</i> KR1	60	91	Q00460 (327)
		<i>tmoF</i>	RMET_RS06615 (340)	TmoF	Ferredoxin--NAD(+) reductase	<i>P. mendocina</i> KR1	43	99	Q8GI14 (329)
		<i>tmoX</i>	RMET_RS06590 (464)	TmoX	Aromatic hydrocarbon TbuX/Fad membrane transport protein	<i>P. mendocina</i> KR1	47	87	Q8KT43 (456)
	Phenol (PH)	<i>phyR</i>	RMET_RS08955 (542)	PhyR	Transcriptional activator of aromatic catabolism	<i>Ralstonia</i> sp. KN1	52	98	Q9RAG0 (446)
		<i>phyZ</i>	RMET_RS31735 (65)	PhyZ	Phenol hydroxylase P0 protein	<i>Ralstonia</i> sp. KN1	46	98	P19729 (72)
		<i>phyA</i>	RMET_RS08945 (331)	PhyA	Phenol hydroxylase P1 protein	<i>Ralstonia</i> sp. KN1	54	99	Q9RAF8 (331)
		<i>phyB</i>	RMET_RS08940 (90)	PhyB	Phenol hydroxylase P2 protein	<i>Ralstonia</i> sp. KN1	62	96	Q9RAF7 (90)
		<i>phyC</i>	RMET_RS08935 (515)	PhyC	Phenol hydroxylase P3 protein	<i>Ralstonia</i> sp. KN1	74	96	Q9RAF6 (504)
		<i>phyD</i>	RMET_RS08930 (120)	PhyD	Phenol hydroxylase P4 protein	<i>Ralstonia</i> sp. KN1	55	92	Q9RAF5 (119)
		<i>phyE</i>	RMET_RS08925 (356)	PhyE	Phenol hydroxylase P5 protein	<i>Ralstonia</i> sp. KN1	62	100	Q9RAF4 (356)
	Benzoate (BDO)	<i>benA</i>	RMET_RS25050 (464)	BenA	Benzoate 1,2-dioxygenase subunit alpha	<i>A. baylyi</i> ADP1	73	96	P07769 (461)
		<i>benB</i>	RMET_RS25055 (164)	BenB	Benzoate 1,2-dioxygenase subunit beta	<i>A. baylyi</i> ADP1	70	98	P07770 (169)
		<i>benC</i>	RMET_RS25060 (339)	BenC	Benzoate 1,2-dioxygenase electron transfer component	<i>A. baylyi</i> ADP1	65	98	P07771 (348)
		<i>benD</i>	RMET_RS25065 (264)	BenD	DHB dehydrogenase	<i>A. baylyi</i> ADP1	62	100	P07772 (261)
Protocatechuate	Ferulic acid	<i>fcs</i>	RMET_RS25745 (631)	Fcs	Feruloyl-CoA synthase	<i>S. stellata</i> E-37	39	86	A3K467 (610)
	Feruloyl-CoA	<i>ech</i>	RMET_RS11875 (289)	Ech	Crotonase/enoyl-CoA hydratase	<i>S. stellata</i> E-37	45	96	A3K472 (261)
	Conyferal alcohol	<i>calA</i>	RMET_RS05500 (342)	CalA	Coniferyl alcohol dehydrogenase	<i>P. putida</i> KT2440	43	98	Q88G86 (336)
	Conyferal aldehyde	<i>calB</i>	RMET_RS00805 (476)	CalB	Coniferyl aldehyde dehydrogenase	<i>P. putida</i> KT2440	52	99	Q88CR0 (476)
	Vanillin	<i>vdh</i>	RMET_RS25355 (482)	Vdh	Vanillin dehydrogenase	<i>Pseudomonas</i> sp. HR199	37	99	O05619 (481)
	Vanillate	<i>ivaA</i>	RMET_RS28335 (347)	IvaA	Isovanillate O-demethylase	<i>C. testosteroni</i> BR6020	41	97	Q2KQ79 (347)
		<i>ivaB</i>	RMET_RS28190 (331)	IvaB	Isovanillate O-demethylase oxidoreductase	<i>C. testosteroni</i> BR6020	45	97	Q2KQ78 (331)
	4-hydroxybenzoate	<i>pobA1</i>	RMET_RS20795 (398)	PobA1	4-hydroxybenzoate-3-monooxygenase	<i>A. baylyi</i> ADP1	64	98	Q03298 (404)
		<i>pobA2</i>	RMET_RS28050 (392)	PobA2	4-hydroxybenzoate-3-monooxygenase	<i>Paenibacillus</i> sp. JJ-1b	65	98	C4TP09 (394)
Homogentisate	Tyrosine	<i>tyrB1</i>	RMET_RS05120 (398)	TyrB1	Tyrosine aminotransferase	<i>P. aeruginosa</i> PAO1	75	99	P72173 (398)

Homogentisate		<i>tyrB2</i>	RMET_RS25280 (398) TyrB2	Tyrosine aminotransferase	<i>K. pneumoniae</i> ATCC 13883	57	99	O85746 (397)
	Phenylalanine	<i>phhA</i>	RMET_RS17750 (310) PhhA	Phenylalanine 4-monooxygenase	<i>R. solanacearum</i> GMI1000	80	99	Q8XU39 (313)
		<i>phhB</i>	RMET_RS17755 (99) PhhB	4 $\alpha$ -carbinolamine dehydratase	<i>C. pinatubonensis</i> JMP134	82	97	Q46VT8 (100)
	4-HPP	<i>hpdD</i>	RMET_RS25270 (357) HpdD	4-hydroxyphenylpyruvate dioxygenase	<i>Pseudomonas</i> sp. P.J. 874	78	99	P80064 (357)
	2-HPA	<i>ohpA</i>	RMET_RS25305 (780) OhpA	Cytochrome P450 CYP116B (2-HPA hydroxylase)	<i>C. pinatubonensis</i> JMP134			AAZ64624 (783)
Phenylacetyl-CoA	Phenylacetate	<i>paaK</i>	RMET_RS15870 (434) PaaK	Phenylacetate-CoA ligase	<i>B. cenocepacia</i> J2315	79	97	B4E7B5 (432)
Benzoyl-CoA	Benzoate (Bcl)	<i>bclA</i>	RMET_RS06180 (549) BclA	Benzoate--CoA ligase	<i>T. aromatica</i> K172	62	93	Q8GQN9 (527)
Aminobenzoyl-CoA	Tryptophan	<i>kynB</i>	RMET_RS13315 (-) KynB	Arylformamidase	PSEUDOGEN	-	-	-
		<i>kynU1</i>	RMET_RS13320 (418) KynU1	Kynureninase	<i>P. fluorescens</i>	72	99	P83788 (414)
		<i>kynA</i>	RMET_RS13325 (299) KynA	Tryptophan 2,3-dioxygenase	<i>C. necator</i> H16	88	100	Q0K7X7 (294)
		<i>kynU2</i>	RMET_RS26570 (409) KynU2	Kynureninase	<i>P. fluorescens</i>	53	100	P83788 (416)
	2-aminobenzoate	<i>abmG</i>	RMET_RS11035 (553) AbmG	2-aminobenzoate-CoA ligase	<i>A. evansii</i> KB740	58	99	Q93FC0 (542)