GUIDE TO AROMATIC AMINO-ACID BIOSYNTHESIS ACRONYMS

Functional Reaction[a]	Acronyms for Analog or Sub-homolog Types [b]	Query Tags (*gi* number)	Organisms
2-Keto-3-deoxy-D-*arabino*-heptulosonate 7-phosphate (DAHP) synthase	$AroA_{I\alpha}$ $AroA_{I\beta}$ $AroA_{II}$ *$AroA_{II}$	21646940 4980844 81555637 410486	*Chlorobium tepidum* (Ctep) *Thermotoga maritima* (Tmar) *Helicobacter pylori* (Hpyl) *Lycopersicon esculentum* (Lesc)
2-Keto-3-deoxy-D-*manno*-octulosonate 8-phosphate (KDOP) synthase [c]	KdsA	67466688	*Escherichia coli* (Ecol)
2-Amino-3,7-dideoxy-D-threo-hept-6-ulosonate (ADTH) synthase	AroA'	1591105	*Methanococcus jannaschii* (Mjan)
Dehydroquinate synthase I	AroB *AroB	5822049 18425036	*Emericella nidulans* (Enid) *Arabidopsis thaliana* (Atha)
Dehydroquinate synthase II	AroB'	1591882	*Methanococcus jannaschii* (Mjan)
Dehydroquinase[d]	$AroC_I$ *$AroC_I$• $AroC_{II}$	17433709 15230703 61219243	*Salmonella typhimurium* (Styp) *Arabidopsis thaliana* (Atha) *Mycobacterium tuberculosis* (Mtub)
Shikimate dehydrogenase[d]	AroD •AroD	16131162 15230703	*Escherichia coli* (Ecol) *Arabidopsis thaliana* (Atha)
Shikimate kinase	$AroE_I$ *$AroE_I$ $AroE_{II}$	114199 30692396 14194467	*Erwinia chrysanthemi* (Echr) *Arabidopsis thaliana* (Atha) *Methanococcus jannaschii* (Mjan)
Enolpyruvylshikimate-3-phosphate (EPSP) synthase	AroF *AroF	2506201 15225450	*Escherichia coli* (Ecol) *Arabidopsis thaliana* (Atha)
Chorismate synthase	AroG *AroG	114183 18402389	*Escherichia coli* (Ecol) *Arabidopsis thaliana* (Atha)

Anthranilate synthase (α subunit) ¥ PABA synthase (α subunit) ¥	TrpAa *TrpAa PabAa *PabAa•	14973317 18410376 16129766 30684045	*Streptococcus pneumoniae* (Spne) *Arabidopsis thaliana* (Atha) *Escherichia coli* (Ecol) *Arabidopsis thaliana* (Atha)
Anthranilate synthase (β subunit) ¥ PABA[e] synthase (β subunit) ¥ **PABA synthase** // Anthranilate synthase (β subunit)¥	TrpAb *TrpAb PabAb •PabAb **PabAb** // TrpAb	14973316 21594026 16131239 30684045 129521	*Streptococcus pneumoniae* (Spne) *Arabidopsis thaliana* (Atha) *Escherichia coli* (Ecol) *Arabidopsis thaliana* (Atha) *Bacillus subtilis* (Bsub)
PABA synthase (γ subunit); 4-Amino-4-deoxy-chorismate lyase	PabAc *PabAc	1787338 22327924	*Escherichia coli* (Ecol) *Arabidopsis thaliana* (Atha)
Anthranilate Phosphoribosyl-transferase	TrpB *TrpB	14973315 15238711	*Streptococcus pneumoniae* (Spne) *Arabidopsis thaliana* (Atha)
Phosphoribosyl-anthranilate isomerase **PR-5-amino-1-PR-4-imidazole carboxamide** // PR-anthranilate isomerase[e]	$TrpC_I$ *$TrpC_I$ **HisD** // $TrpC_{II}$	14973313 30680348 45593458	*Streptococcus pneumoniae* (Spne) *Arabidopsis thaliana* (Atha) Mycobacterium tuberculosis (Mtub)
Indoleglycerol-phosphate synthase	TrpD *TrpD	14973314 15238914	*Streptococcus pneumoniae* (Spne) *Arabidopsis thaliana* (Atha)
Tryptophan synthase (α subunit)	$TrpEa_\alpha$ *$TrpEa_\alpha$ $TrpEa_\beta$	25291883 18410104 004320	*Streptococcus pneumoniae* (Spne) *Arabidopsis thaliana* (Atha) *Sulfolobus sulfataricus* (Ssul)
Tryptophan synthase (β subunit)	$TrpEb_\alpha$ *$TrpEb_\alpha$ $TrpEb_\beta$	25291905 15239755 1004319	*Streptococcus pneumoniae* (Spne) *Arabidopsis thaliana* (Atha) *Sulfolobus sulfataricus* (Ssul)
Chorismate mutase	$AroH_I$ *$AroH_I$ $AroH_{II}$	2495875 14794421 24212657	*Methanococcus jannaschii* (Mjan) *Pseudomonas aeruginosa* (Paer) *Bacillus subtilis* (Bsub)

	$AroH_{III}$ *$AroH_{III}$	6325317 18406100	*Saccharomyces cereviseae* (Scer) *Arabidopsis thaliana* (Atha)
Arogenate dehydrogenase¥	$TyrA_a$ *$TyrA_a$	62389124 15218283	*Corynebacterium glutamicus* (Cglu) *Arabidopsis thaliana* (Atha)
Prephenate dehydrogenase¥	$TyrA_p$•ACT	143815	*Bacillus subtilis* (Bsub)
Cyclohexadienyl dehydrogenase¥	$TyrA_c$	56551316	*Zymomonas mobilis* (Zmob)
Prephenate dehydratase ¥	$PheA_{Ip}$•ACT	130048	*Bacillus subtilis* (Bsub)
Arogenate dehydratase¥	$PheA_{Ia}$•ACT *$PheA_{Ia}$•ACT	58000965 79317657	*Gluconobacter oxydans* (Goxy) *Arabidopsis thaliana* (Atha)
Cyclohexadienyl dehydratase	*$PheA_{IIc}$	2997758	*Pseudomonas aeruginosa* (Paer)
Aromatic aminotransferase	$AroJ_{I\alpha}$	85676806	*Escherichia coli* (Ecol)
	$AroJ_{I\beta}$ *$AroJ_{I\beta}$	1574093 14794424	*Haemophilus influenzae* (Hinf) *Pseudomonas aeruginosa* (Paer)
	$AroJ_{I\gamma}$	6318592	*Lactococcus lactis* (Llac)

aEnzymes in a box that are marked with the symbol ¥ following the name currently cannot be distinguished from one another with great confidence using the query-tag sequences given.

bSpacing within a box indicates distinctly separated analog or sub-homolog groupings, with the exception of what is covered in footnote**a**. Asterisk superscripts indicate signal peptides in prokaryotes, whereas green asterisk superscripts indicate transit peptides in higher plants.

cUse this query to assure that a putative $AroA_{I\beta}$ sequence is not in fact a KdsA sequence.

dThe convention of a bullet indicates the fusion of the two indicated domains in *$AroC_I$•AroD proteins of higher plants.

eAbbreviations: PABA, 4-aminobenzoate; PR, phosphoribosyl.