

# Supplementary Materials: Distribution in Different Organisms of Amino Acid Oxidases with FAD or a Quinone As Cofactor and Their Role as Antimicrobial Proteins in Marine Bacteria

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**Table S1.** Amino acid oxidases (AAOs) from microbial sources. Marine microorganisms are shown in bold. \* cofactor and/or activity attributed for high similarity with LodA. ND, not determined. NA, not accessible. LAAOs, L-amino acid oxidases. DAAOs, D-amino acid oxidases. LASPOs, L-aspartate oxidases. CTQ, cysteine tryptophilquinone.

Microorganism (Enzyme Name)	Activity (Main Substrate)	Cofactor	Oligomeric Structure/Mass Molecular	Various	Accession Number	Reference
<b>AAOs with Quinone Cofactor (LodA-Like Proteins)</b>						
<b><i>Marinomonas mediterranea</i> MMB-1 (LodA)</b>	L-Lysine $\epsilon$ -oxidase (L-Lys)	CTQ	Homotetramer (80.9 $\times$ 4 kDa). Crystal structure solved, PDB ID: 2YMW	Antimicrobial. Biofilms dispersion. Extracellular	AA Y33849	[1,2]
<b><i>Marinomonas mediterranea</i> MMB-1 (GoxA)</b>	Glycine oxidase (Gly)	CTQ	76.2 kDa	Other substrates: Gly ethyl ester	ADZ90918	[3,4]
<b><i>Pseudoalteromonas tunicata</i> D2 (AlpP)</b>	L-Lysine $\epsilon$ -oxidase (L-Lys)	* CTQ	110 kDa	Antimicrobial. Biofilms dispersion	Q7X018	[5,6]
<i>Chromobacterium violaceum</i>	ND	ND	ND	Antimicrobial. Biofilms dispersion	AAQ60932	[6]
<i>Caulobacter crescentus</i>	ND	ND	ND	Antimicrobial. Biofilms dispersion	NP_419374	[6]
<b><i>Pseudoalteromonas flavipulchra</i> JG1 (PfaP)</b>	* L-Lysine $\epsilon$ -oxidase (* L-Lys)	* CTQ	77 kDa	Antimicrobial. pI = 4.6	AFB71049	[7]
<b><i>Pseudoalteromonas flavipulchra</i> C2</b>	Broad spectrum oxidase (L-Lys > L-Met > L-Glu > L-Leu > L-Gln > L-Tyr > L-Phe)	ND	60 kDa	Antimicrobial. pI = 9.4. It contains a 9-residues peptide similar to AlpP	NA	[8]

**Table S1. Cont.**

<i>Pseudoalteromonas luteoviolacea</i>	Broad spectrum oxidase (L-Met > L-Gln > L-Leu > L-Phe > L-Glu > L-Trp)	ND	Oligomer (110 kDa)	Antimicrobial	NA	[9]
<i>Rheinheimera aquatica</i> GR5	* L-Lysine $\epsilon$ -oxidase (L-Lys)	* CTQ	Monomer (71 kDa)	Antimicrobial. pI = 3.6. It contains a 19-residue peptide similar to AlpP and LodA	NA	[10]
<b>DAAOs</b>						
<i>Rubrobacter xylanophilus</i> (RxDAO)	D-Amino acid oxidase (neutral and basic D-aa)	FAD	Monomer (24,1 kDa)	Thermostable. pH opt = 7.5–10. T <sup>a</sup> opt = 65 °C	BAP18969	[11]
<i>Arthrobacter protophormiae</i> (ApDAO)	D-Amino acid oxidase (neutral and hydrophobic D-aa)	FAD	Homodimer (34.6 × 2 kDa)	pI = 4.2. pH opt = 6.5–8.5	AAP70489	[12]
<i>Rhodospiridium toruloides</i> (RgDAO)	D-Amino acid oxidase	FAD	Homodimer (40 × 2 kDa). Crystal structure solved, PDB ID: 1C0L		P80324	[13]
<i>Fusarium solani</i>	D-Amino acid oxidase	FAD	40 kDa	Oxidizes Cephalosporin C	P24552	[14]
<b>LASPOs</b>						
<i>Bacillus subtilis</i> 168	L-Aspartate oxidase (L-Asp)	FAD	Monomer-Dimer equilibrium (55–110 kDa)	NAD <sup>+</sup> biosynthesis. Inhibited by iminoaspartate, succinate, fumarate, oxalacetate and D-Asp	NP_390665	[15]
<i>Escherichia coli</i> K12	L-Aspartate oxidase (L-Asp)	FAD	Monomer-Dimer equilibrium (60.3–120 kDa). Crystal structure solved, PDB ID: 1KNP	NAD <sup>+</sup> biosynthesis. Inhibited by iminoaspartate, succinate and fumarate. pI = 5.6	P10902	[16,17]
<i>Pyrococcus horikoshii</i> OT-3	L-Aspartate oxidase (L-Asp)	FAD	Homotrimer (51,925 × 3 kDa)	Thermostable. pH opt = 8.6. T <sup>a</sup> opt = 90 °C	O57765	[18]
<i>Sulfolobus tokodaii</i>	L-Aspartate oxidase (L-Asp)	FAD	Monomer (53.6 kDa). Crystal structure solved, PDB ID 2E5V)	Other substrates: L-Asn. T <sup>a</sup> opt = 79–87,5 °C	WP_0109792 15	[19,20]

**Table S1. Cont.**

<i>Pseudoalteromonas</i> <b>sp. B3</b>	Broad spectrum oxidase (L-Leu > L-Lys > L-Tys > L-Asn > L-Gln > L-Met > L-cystine > L-Arg > L-Trp > L-Glu)	FAD	60 kDa	Homology with LASPOs	AJZ73816	[21]
<b>Fungal AAOs</b>						
<i>Neurospora crassa</i>	Broad spectrum oxidase (L-His > aminobutyric > L-canavanine > L-Tyr > D, L-Ornithine > D, L-Phe > L-Leu)	FAD	ND	L-aa catabolism	CAD21325	[22,23]
<i>Aspergillus nidulans</i>	Broad spectrum oxidase (L-His > aminobutyric > L-canavanine > L-Tyr > D, L-ornithine > D, L-Phe > L-Leu)	FAD	ND	L-aa catabolism	AAT84085	[24]
<i>Laccaria bicolor</i> S238N	Broad spectrum oxidase (L-Phe, L-His, L-Met, L-Leu, and L-Lys)	FAD	ND	L-aa catabolism. Nitrogen mineralization. pI = 6.2	DAA34975	[25,26]
<i>Hebeloma cylindrosporum</i>	Broad spectrum oxidase (L-Glu > L-Gln > L-Ornithine > L-Asn > L-Leu > L-His > L-Phe)	FAD	70 and 140 kDa	L-aa catabolism. Nitrogen mineralization. pI = 6.2. pH opt = 7–8	ADM80414	[25,26]
<i>Aspergillus fumigatus</i> P13	Broad spectrum oxidase (L-Tyr > L-Phe > L-Pro > L-Ser > L-Leu/L-Ala > L-Asp)	ND	ND	Non active on D-aa	ND	[27]
<i>Trichoderma viride</i> (LysOX)	L-Lysine $\alpha$ -oxidase (L-Lys)	FAD	Homodimer (55 $\times$ 2 kDa). Crystal structure solved, PDB ID: 3X0V	Antitumoral. Other substrates: L-Ornithine > L-Arg > L-Phe. pI = 4.2. pH opt = 4.5-10. T <sup>a</sup> opt = 50 °C	BAR88116	[28,29]
<i>Trichoderma harzianum</i> ETS 323	Broad spectrum oxidase (L-Phe > L-Lys > L-Glu > L-Ala)	FAD	Monomer-Dimer equilibrium (63.5 kDa)	Biocontrol agent. Extracellular. pH opt = 7	ADD91592	[30,31]

**Table S1. Cont.**

<i>Saccharomyces cerevisiae</i>	L-Lysine oxidase (L-Lys)	ND	ND	L-Lys biosensor. Other substrates: L-Arg, L-Asn. pH opt = 7,5. T <sup>a</sup> opt = 30 °C	NA	[32]
<i>Coprinus</i> sp. SF-1 (Tod)	L-Tryptophan oxidase (L-Trp and derivatives)	FAD	68 kDa	Other substrates: L -Phe and L-Tyr. T <sup>a</sup> opt = 35–43 °C. pH opt = 7	NA	[33]
<b>Other enzymes with AAO activity</b>						
<i>Bacillus subtilis</i> 168 (GoxB)	Glycine oxidase (Gly)	FAD	Homotetramer (42 × 4 kDa). Crystal structure solved, PDB ID: 1NG4	Other substrates: Sarcosine, N-ethyl-Gly, D-Pro, D-Ala	O31616	[34,35]
<i>Geobacillus kaustophilus</i> HTA426 (GoxK)	Glycine oxidase (Gly)	FAD	Homotetramer (42 × 4 kDa)	Other substrates: Sarcosine, N-ethyl-Gly, D-Pro, D-Ala. Thermostable	BAD74908	[36]
<i>Bacillus</i> sp. B-0618 (MSox)	Sarcosine oxidase (sarcosine)	FAD	Monomer (43.8 kDa). Crystal structure solved, PDB ID: 2A89	Other substrates: L-Pro, N-ethyl-Gly, N-methyl- D L-Ala, N-methyl-D L-Val, N-methyl-L-Leu	BAA03967	[37,38]
<i>Streptococcus oligofermentans</i> (SoAAO)	Aminoacetone oxidase (aminoacteone)	FAD	43 kDa. Crystal structure solved, PDB ID: 4CNK	Antioxidant and microbial competition. Other substrates: L-Asp > L-Trp > L-Lys > L-Ile > L-Arg > L-Apn > L-Gln	ACA52024	[39–41]
<i>Rhodococcus opacus</i> DSM 43250	Broad spectrum oxidase (all the proteinogenic aa except Gly, L-Thr and L-Pro)	FAD	Homodimer (53 × 2 kDa). Crystal structure solved, PDB ID: 2JB2	pI = 4,8. pH opt = 8–9. T <sup>a</sup> opt = 30 °C	AAL14831	[42,43]
<i>Rhodococcus</i> sp. AIU Z-35-1	Broad spectrum oxidase (L-Ala > Nα-Z-L-Lys > L-His > L-Tyr > L-ornithine > L-Gln)	FAD	Homodimer (51 × 2 kDa)	pI = 4.8. pH opt = 8–8,5. N-terminal homology with <i>Rhodococcus opacus</i> DSM 43250 LAO.	NA	[44,45]
<i>Rhodococcus</i> sp. AIU LAB-3	Broad spectrum oxidase (L-Ala > L-Gln > Nα-Z-L-Lys> L-m > L-Arg > L-Phe > L-Met > L-Lys)	FAD	Homodimer (52,5×2 kDa)	pH opt = 6–8.5. T <sup>a</sup> opt = 45 °C. N-terminal homology with <i>Rhodococcus opacus</i> DSM 43250 LAO.	NA	[45]

**Table S1. Cont.**

<i>Bacillus carotarum</i> 2Pfa	Broad spectrum oxidase (L-Leu > L-Lys > L-Arg > L-Met > L-Asn)	FAD	Homodimer (54×2 kDa)	Other substrates: D-isomers. pI = 4.8. pH opt = 8–8.5	NA	[46]
<i>Cellulomonas cellulans</i> AM8	Broad spectrum oxidase (all the proteinogenic aa except Gly, L-Pro and L-Thr)	FAD	55 kDa	Extracellular. pH opt=6,5-7,5	NA	[47]
<i>Corynebacterium</i> sp. A20	Broad spectrum oxidase (all the proteinogenic aa except L-Asp, L-Thr, L-Pro and Gly)	ND	130-140 kDa	L-aa catabolism	NA	[48]
<i>Morganella morgani</i>	Broad spectrum oxidase (L-Leu > L-Phe > L-Trp > L-Met > L-Tyr)	FAD	ND	T <sup>a</sup> opt = 35–43 °C	NA	[49]
<i>Streptomyces</i> sp. X-119-6	L-Glutamate oxidase (L-Glu)	FAD	Hexamer $\alpha_2\beta_2\gamma_2$ [(42 + 17 + 10) × 2 kDa]. Crystal structure solved, PDB ID: 2E1M	L-Glu biosensor. Extracellular. pH opt = 7. T <sup>a</sup> opt = 58 °C	BAB93449	[50–52]
<i>Streptomyces endus</i>	L-Glutamate oxidase (L-Glu)	FAD	Dimer (45 × 2 KDa)	pI = 6.2. pH opt = 6.5–8. T <sup>a</sup> opt = 30–45 °C	NA	[53]
<i>Streptomyces platensis</i> NTU3304	L-Glutamate oxidase (L-Glu)	FAD	Heterotrimer of 78 kDa (39, 19 and 16 kDa)	L-Glu biosensor	AAK15071	[54]
<i>Streptomyces violascens</i>	L-Glutamate oxidase (L-Glu)	FAD	Monomer (60 kDa)	Other substrates: L-Gln	NA	[55]
<i>Streptomyces</i> sp. Z-11-6	L-Glutamate oxidase (L-Glu)	FAD	Tetramer $\alpha_2\beta_2$ [(25 + 22.5) × 2 kDa]	Extracellular	NA	[56]
<i>Pseudomonas</i> sp. AIU 813	L-Lysine $\alpha$ -oxidase/monooxygenase (L-Lys)	FAD	Homodimer (54.5 × 2 kDa). Crystal structure solved, PDB ID: 3WE0	Other substrates: L-Ornithine > L-Arg. Induced by L-Lys. pI = 4.6. pH opt = 7	BAO51829	[57,58]
<i>Pseudomonas</i> sp. P-501 (PAO)	L-Phenylalanine oxidase (deaminating and decarboxylating) (L-Phe)	FAD	Heterodimer $\alpha_2\beta_2$ [(10 + 60) × 2 kDa]. Crystal structure solved, PDB ID: 3AYJ	Other substrates: L-Tyr > L-Met > L-NorLeu > L-Trp. L-Phe is mainly oxygenated and L-Met is mainly oxidized	BAD66877	[59–61]
<i>Pseudomonas savastanoi</i> (TMO)	Tryptophan 2-monooxygenase (L-Trp)	FAD	62 kDa	Biosynthesis of indoleacetic acid	EFW87519	[62]

**Table S1. Cont.**

<i>Ralstonia solanacearum</i> (PTMO)	L-Tryptophan monooxygenase (L-Trp)	FAD	Heterodimer $\alpha_2\beta_2$ [(9.2 + 64.5) × 2 kDa].	Other substrates: L-Tyr, L-Trp, L-Met and L-Phe. L-Phe and L-Tyr are mainly oxygenated. L-Met is mainly oxidized. L-Trp is both oxygenated and oxidized. Homology with PAO	NA	[63]
<i>Chromobacterium violaceum</i> (VioA)	L-Tryptophan oxidase (L-Trp and derivatives)	FAD	48 kDa	Violacein biosynthesis. pH opt = 9,25	Q9S3V1	[64]
<i>Lechevalieria aerocolonigenes</i> ATCC 39243 (RebO)	L-Tryptophan oxidase (L-Trp and derivatives)	FAD	Homodimer (54 × 2 kDa)	Rebeccamycin biosynthesis	BAC15750	[65]
<i>Streptomyces</i> sp. TP-A0274 (StaO)	L-Tryptophan oxidase (L-Trp and derivatives)	FAD	Homodimer (57x2 kDa)	Staurosporine biosynthesis. L-Trp biosensor. No activity on other L-aa. pH opt = 7–8	BAC55210	[66]
<i>Aquimarina</i> sp. <b>antisso-27</b>	Broad spectrum oxidase (L-Leu > L-Ile > L-Met > L-Val)	ND	190 kDa	Algicide and antimicrobial. pI = 9,4	NA	[67]
<i>Synechococcus elongatus</i> PCC 6301 and PCC 7942	Basic L-aa oxidase (L-Arg > L-Lys > L-ornithine > L-His)	FAD	50 kDa	Catabolism of Arg. Periplasmic. pI= 8,5	CAA88452	[68,69]
<i>Synechococcus cedrorum</i> PCC 6908	Basic L-aa oxidase (L-Arg > L-Lys > L-ornithine > L-His)	FAD	Homodimer (49 × 2 kDa)	pI = 8.5	NA	[69]
<i>Chlamydomonas reinhardtii</i>	Broad spectrum oxidase (all the proteinogenic aa except L-Cys)	FAD	Oligomer $\alpha_x\beta_x$ [(66 + 135) × X kDa].	L-aa catabolism. Periplasmic	EDP07010	[70]

**Table S2.** Representative amino acid oxidases (AAOs) from animals. Marine organisms are shown in bold. ND, not determined.

<b>Organism (Enzyme Name)</b>	<b>Activity (Main Substrate)</b>	<b>Cofactor</b>	<b>Oligomeric Structure /Mass Molecular</b>	<b>Various</b>	<b>Accession Number</b>	<b>Reference</b>
Gastropods						
<i><b>Aplysia californica</b></i> (Escapin)	L-Lysine and L-arginine oxidase (L-Lys, L-Arg)	FAD	Monomer (60 kDa)	Antimicrobial. Defence against predators	Q6IWZ0	[71]
<i><b>Aplysia kurodai</b></i> (Aplysianin A)	L-Lysine and L-arginine oxidase (L-Lys, L-Arg)	FAD	Homotetramer (85 × 4 kDa)	Antimicrobial	BAA11867	[72,73]
<i><b>Aplysia californica</b></i> (Aplysianin A)	L-Lysine and L-arginine oxidase (L-Lys, L-Arg)	FAD	Homotetramer (85 × 4 kDa)	Antimicrobial. It shares 85% amino acid sequence identity with Aplysianin A from <i>A. kurodai</i>	NP_001191524	[74]
<i><b>Achatina fulica</b></i> (Achacin)	Broad spectrum oxidase (L-Met > L-Leu > L-Trp > L-Lys > L-Arg > L-Phe > L-Cys > L-Asn)	FAD	56 kDa	Antimicrobial	CAA45871	[75,76]
Vertebrates						
<i><b>Sebastes schlegelii</b></i> (SSAP)	L-Lysine oxidase (L-Lys)	FAD	Homodimer (53 × 2 kDa)	Antimicrobial. Innate immunity of fish skin	BAF43314	[77]
<i>Danio rerio</i> (Isoform X1)	ND	FAD	ND	Predicted LAAO	XP_009289996	NCBI
<i><b>Bothrops jararacussu</b></i> (BjsuLAAO)	Aromatic and hydrophobic amino acids oxidase (L-Met > L-Leu > L-Phe > L-Ile > L-Trp > L-Tyr)	FAD	Homodimer (56 × 2 kDa). Crystal structure solved, PDB ID: 4e0v	Antimicrobial. Present in the snake venom	AAR31182	[78]

**Table S2. Cont.**

<i>Crotalus durissus cumanensis</i> (CdcLAAO)	Aromatic and hydrophobic amino acids oxidase	FAD	Monomer (55 kDa)	Antimicrobial. Present in the snake venom	K9N7B7	[79]
<i>Homo sapiens</i> (IL4I1)	Aromatic amino acid oxidase (L-Phe > L-Trp > L-Tyr)	FAD	~70 kDa	Regulator of immune system	Q96RQ9	[80,81]
<i>Homo sapiens</i> (hDAAO)	D-Amino acid oxidase (D-Ala, D-Ser, D-Pro, Gly)	FAD	Homodimer (39.4 × 2 kDa)	Involved in D-Ser catabolism	NP_001908	[82]
<i>Homo sapiens</i> (DDO)	D-Aspartate oxidase (D-Asp, N-methyl-D-aspartate, D-Glu)	FAD	37 kDa	Involved in D-Asp catabolism	BAI44653	[83,84]



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