



Supporting Information

for

Identification of the new prenyltransferase Ubi-297 from marine bacteria and elucidation of its substrate specificity

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Beilstein J. Org. Chem. **2022**, 18, 722–731. doi:10.3762/bjoc.18.72

Sequence analysis and copies of MS/MS and NMR spectra

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Table S1: List of all Ptases used in all-against-all pairwise sequence similarity network and phylogenetic tree

Nr	Accession/ ID*	Gene Product
1	1122191.4.peg.195	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter antarcticus</i> DSM 21422
2	1121859.3.peg.1165	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Echinicola pacifica</i> DSM 19836
3	1121859.3.peg.1481	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Echinicola pacifica</i> DSM 19836
4	1121859.3.peg.361	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Echinicola pacifica</i> DSM 19836
5	1122191.4.peg.1189	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter antarcticus</i> DSM 21422
6	1122191.4.peg.2126	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter antarcticus</i> DSM 21422
7	1122191.4.peg.3274	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter antarcticus</i> DSM 21422
8	1137271.3.peg.647	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Saccharomonospora</i> sp. CNQ490
9	1137271.3.peg.2500	Aromatic prenyltransferase 1, UbiA family [<i>Saccharomonospora</i> sp. CNQ490
10	1197874.4.peg.1286	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter thermophilus</i> strain HT7-2
11	1197874.4.peg.2089	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter thermophilus</i> strain HT7-2
12	1197874.4.peg.222	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter thermophilus</i> strain HT7-2
13	1197874.4.peg.3133	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter thermophilus</i> strain HT7-2
14	1137271.3.peg.2913	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Saccharomonospora</i> sp. CNQ490
15	1206753.3.peg.805	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter spongiicola</i> strain DSM 25233
16	1206753.3.peg.2854	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter spongiicola</i> strain DSM 25233
17	1206753.3.peg.1779	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter spongiicola</i> strain DSM 25233
18	1206753.3.peg.3728	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter spongiicola</i> strain DSM 25233
19	1206816.3.peg.1205	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter vacoletii</i> strain DSM 25230
20	1206816.3.peg.161	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter vacoletii</i> strain DSM 25230
21	1206816.3.peg.1605	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter vacoletii</i> strain DSM 25230
22	1236486.3.peg.383	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Flavobacterium aquaticum</i> strain CGMCC 1.12398
23	1236486.3.peg.1831	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Flavobacterium aquaticum</i> strain CGMCC 1.12398
24	1236486.3.peg.771	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Flavobacterium aquaticum</i> strain CGMCC 1.12398
25	1236486.3.peg.2092	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Flavobacterium aquaticum</i> strain CGMCC 1.12398
26	1236486.7.peg.991	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Flavobacterium aquaticum</i> strain 1Y8A
27	1236486.7.peg.355	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Flavobacterium aquaticum</i> strain 1Y8A
28	1236486.7.peg.1767	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Flavobacterium aquaticum</i> strain 1Y8A
29	1236486.7.peg.2298	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Flavobacterium aquaticum</i> strain 1Y8A
30	1392498.4.peg.1577	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter forsetii</i> DSM 18668
31	1392498.4.peg.2850	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter forsetii</i> DSM 18668
32	1392498.4.peg.3593	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter forsetii</i> DSM 18668
33	1392498.4.peg.742	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter forsetii</i> DSM 18668
34	143224.4.peg.2004	Aromatic prenyltransferase 1, UbiA family [<i>Zobellia uliginosa</i> strain MAR_2009_138
35	143224.4.peg.1185	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Zobellia uliginosa</i> strain MAR_2009_138
36	143224.4.peg.2755	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Zobellia uliginosa</i> strain MAR_2009_138
37	143224.4.peg.3880	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Zobellia uliginosa</i> strain MAR_2009_138

38	143224.8.peg.3999	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Zobellia uliginosa</i> strain DSM 2061
39	143224.8.peg.3051	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Zobellia uliginosa</i> strain DSM 2061
40	143224.8.peg.265	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Zobellia uliginosa</i> strain DSM 2061
41	143224.8.peg.1269	Aromatic prenyltransferase 1, UbiA family [<i>Zobellia uliginosa</i> strain DSM 2061
42	1608400.3.peg.849	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Algibacter amylolyticus</i> strain RU-4-M-4
43	1608400.3.peg.587	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Algibacter amylolyticus</i> strain RU-4-M-4
44	1608400.3.peg.2023	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Algibacter amylolyticus</i> strain RU-4-M-4
45	1608400.3.peg.3167	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Algibacter amylolyticus</i> strain RU-4-M-4
46	1608400.5.peg.850	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Algibacter amylolyticus</i> strain DSM 29199
47	1608400.5.peg.589	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Algibacter amylolyticus</i> strain DSM 29199
48	1608400.5.peg.1276	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Algibacter amylolyticus</i> strain DSM 29199
49	1608400.5.peg.1668	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Algibacter amylolyticus</i> strain DSM 29199
50	1658664.4.peg.1849	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter flavus</i> strain C3 strain KCTC 42508
51	1658664.4.peg.3317	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter flavus</i> strain C3 strain KCTC 42508
52	1658664.4.peg.617	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter flavus</i> strain C3 strain KCTC 42508
53	1658664.4.peg.2331	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter flavus</i> strain C3 strain KCTC 42508
54	1775173.3.peg.1572	hypothetical protein [<i>Polaribacter pacificus</i> strain CGMCC 1.15763
55	1775173.3.peg.1367	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Polaribacter pacificus</i> strain CGMCC 1.15763
56	1775173.3.peg.988	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Polaribacter pacificus</i> strain CGMCC 1.15763
57	1775173.3.peg.1950	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Polaribacter pacificus</i> strain CGMCC 1.15763
58	228956.4.peg.716	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter sedimenticola</i> strain DSM 19840
59	228956.4.peg.1171	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter sedimenticola</i> strain DSM 19840
60	228956.4.peg.2235	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter sedimenticola</i> strain DSM 19840
61	228956.4.peg.2939	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter sedimenticola</i> strain DSM 19840
62	228957.5.peg.2049	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter orientalis</i> strain DSM 16471
63	228957.5.peg.2580	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter orientalis</i> strain DSM 16471
64	228957.5.peg.651	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter orientalis</i> strain DSM 16471
65	228957.5.peg.246	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter orientalis</i> strain DSM 16471
66	228958.3.peg.335	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter aquivivus</i> strain DSM 16478
67	228958.3.peg.1364	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter aquivivus</i> strain DSM 16478
68	228958.3.peg.3570	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter aquivivus</i> strain DSM 16478
69	228958.3.peg.2310	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter aquivivus</i> strain DSM 16478
70	228959.3.peg.1400	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter ulvicola</i> strain DSM 15366
71	228959.3.peg.271	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter ulvicola</i> strain DSM 15366
72	228959.3.peg.2970	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter ulvicola</i> strain DSM 15366
73	228959.3.peg.2320	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter ulvicola</i> strain DSM 15366
74	2489054.3.peg.102	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Arenibacter</i> sp. GUO666
75	2489054.3.peg.1062	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Arenibacter</i> sp. GUO666
76	2489054.3.peg.2793	Aromatic prenyltransferase 1, UbiA family [<i>Arenibacter</i> sp. GUO666
77	2489054.3.peg.3362	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Arenibacter</i> sp. GUO666

78	252356.13.peg.1335	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter</i> MS6
79	252356.13.peg.2206	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter</i> MS6
80	252356.13.peg.297	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter</i> MS6
81	313603.6.peg.1920	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter</i> sp. HTCC2170
82	252356.13.peg.3531	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter</i> MS6
83	313603.6.peg.2860	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter</i> sp. HTCC2170
84	313603.6.peg.867	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter</i> sp. HTCC2170
85	320912.15.peg.1774	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter dokdonensis</i> strain MAR_2009_71
86	320912.15.peg.60	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter dokdonensis</i> strain MAR_2009_71
87	320912.15.peg.2606	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter dokdonensis</i> strain MAR_2009_71
88	320912.15.peg.709	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter dokdonensis</i> strain MAR_2009_71
89	388413.5.peg.816	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Algoriphagus</i> sp. PR1
90	388413.5.peg.2653	Aromatic prenyltransferase 1, UbiA family [<i>Algoriphagus</i> sp. PR1
91	388413.5.peg.2670	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Algoriphagus</i> sp. PR1
92	388413.5.peg.2771	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Algoriphagus</i> sp. PR1
93	429344.6.peg.730	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter polysiphoniae</i> strain DSM 23514
94	429344.6.peg.2764	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter polysiphoniae</i> strain DSM 23514
95	429344.6.peg.3072	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter polysiphoniae</i> strain DSM 23514
96	440514.5.peg.3165	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter stanieri</i> strain DSM 19891
97	440514.5.peg.2094	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter stanieri</i> strain DSM 19891
98	440514.5.peg.245	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter stanieri</i> strain DSM 19891
99	440514.5.peg.427	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter stanieri</i> strain DSM 19891
100	471857.5.peg.1109	Aromatic prenyltransferase 1, UbiA family [<i>Saccharomonospora viridis</i> DSM 43017
101	471857.5.peg.1596	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Saccharomonospora viridis</i> DSM 43017
102	561365.3.peg.1410	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Maribacter arcticus</i> strain DSM 23546
103	471857.5.peg.302	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Saccharomonospora viridis</i> DSM 43017
104	561365.3.peg.1994	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Maribacter arcticus</i> strain DSM 23546
105	561365.3.peg.1178	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Maribacter arcticus</i> strain DSM 23546
106	561365.3.peg.2786	Aromatic prenyltransferase 1, UbiA family [<i>Maribacter arcticus</i> strain DSM 23546
107	63186.21.peg.2087	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Zobellia galactanivorans</i> strain OII3
108	63186.21.peg.896	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Zobellia galactanivorans</i> strain OII3
109	63186.21.peg.2425	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Zobellia galactanivorans</i> strain OII3
110	63186.21.peg.4811	Aromatic prenyltransferase 1, UbiA family [<i>Zobellia galactanivorans</i> strain OII3
111	63186.3.peg.1224	Similar to (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase [<i>Zobellia galactanivorans</i> strain Dsij
112	63186.3.peg.2343	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB [<i>Zobellia galactanivorans</i> strain Dsij
113	63186.3.peg.489	Aromatic prenyltransferase 1, UbiA family [<i>Zobellia galactanivorans</i> strain Dsij
114	63186.3.peg.3937	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) [<i>Zobellia galactanivorans</i> strain Dsij
115	B1KKU2	UBIA_SHEWM 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella woodyi</i> (strain ATCC 51908 / MS32) OX=392500 GN=ubiA PE=3 SV=1
116	B0TRE7	UBIA_SHEHH 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella halifaxensis</i> (strain HAW-EB4) OX=458817 GN=ubiA PE=3 SV=1
117	Q66FH0	UBIA_YERPS 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953) OX=273123 GN=ubiA PE=3 SV=1

118	B2SXA0	UBIA_PARPJ 4-hydroxybenzoate octaprenyltransferase OS= <i>Paraburkholderia phytofirmans</i> (strain DSM 17436 / LMG 22146 / PsJN) OX=398527 GN=ubiA PE=3 SV=1
119	Q1C0T8	UBIA_YERPA 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pestis</i> bv. Antiqua (strain Antiqua) OX=360102 GN=ubiA PE=3 SV=1
120	Q9PH76	UBIA_XYLFA 4-hydroxybenzoate octaprenyltransferase OS= <i>Xylella fastidiosa</i> (strain 9a5c) OX=160492 GN=ubiA PE=3 SV=2
121	C3K4C4	UBIA_PSEFS 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas fluorescens</i> (strain SBW25) OX=216595 GN=ubiA PE=3 SV=1
122	Q7MZB6	UBIA_PHOLL 4-hydroxybenzoate octaprenyltransferase OS= <i>Photobacterium laumondii</i> subsp. <i>laumondii</i> (strain DSM 15139 / CIP 105565 / TT01) OX=243265 GN=ubiA PE=3 SV=1
123	B2SF41	UBIA_FRATM 4-hydroxybenzoate octaprenyltransferase OS= <i>Francisella tularensis</i> subsp. <i>mediasiatica</i> (strain FSC147) OX=441952 GN=ubiA PE=3 SV=1
124	A6TGU9	UBIA_KLEP7 4-hydroxybenzoate octaprenyltransferase OS= <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> (strain ATCC 700721 / MGH 78578) OX=272620 GN=ubiA PE=3 SV=1
125	A1RFH5	UBIA_SHESW 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella</i> sp. (strain W3-18-1) OX=351745 GN=ubiA PE=3 SV=1
126	Q57GZ3	UBIA_SALCH 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella choleraesuis</i> (strain SC-B67) OX=321314 GN=ubiA PE=3 SV=1
127	B4TDL7	UBIA_SALHS 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella heidelberg</i> (strain SL476) OX=454169 GN=ubiA PE=3 SV=1
128	Q87F82	UBIA_XYLFT 4-hydroxybenzoate octaprenyltransferase OS= <i>Xylella fastidiosa</i> (strain Temecula1 / ATCC 700964) OX=183190 GN=ubiA PE=3 SV=1
129	A7MPP0	UBIA_CROS8 4-hydroxybenzoate octaprenyltransferase OS= <i>Cronobacter sakazakii</i> (strain ATCC BAA-894) OX=290339 GN=ubiA PE=3 SV=1
130	Q3K4G3	UBIA_PSEPF 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas fluorescens</i> (strain Pf0-1) OX=205922 GN=ubiA PE=3 SV=1
131	A4W5F3	UBIA_ENT38 4-hydroxybenzoate octaprenyltransferase OS= <i>Enterobacter</i> sp. (strain 638) OX=399742 GN=ubiA PE=3 SV=1
132	Q5F9S8	UBIA_NEIG1 4-hydroxybenzoate octaprenyltransferase OS= <i>Neisseria gonorrhoeae</i> (strain ATCC 700825 / FA 1090) OX=242231 GN=ubiA PE=3 SV=1
133	A9N9X0	UBIA_COXBR 4-hydroxybenzoate octaprenyltransferase OS= <i>Coxiella burnetii</i> (strain RSA 331 / Henzerling II) OX=360115 GN=ubiA PE=3 SV=1
134	Q02E04	UBIA_PSEAB 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas aeruginosa</i> (strain UCBPP-PA14) OX=208963 GN=ubiA PE=3 SV=1
135	A4VGN3	UBIA_PSEU5 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas stutzeri</i> (strain A1501) OX=379731 GN=ubiA PE=3 SV=1
136	B2K1U4	UBIA_YERPB 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pseudotuberculosis</i> serotype IB (strain PB1/+) OX=502801 GN=ubiA PE=3 SV=1
137	A4YAV1	UBIA_SHEPC 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella putrefaciens</i> (strain CN-32 / ATCC BAA-453) OX=319224 GN=ubiA PE=3 SV=1
138	Q1BYZ6	UBIA_BURCA 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia cenocepacia</i> (strain AU 1054) OX=331271 GN=ubiA PE=3 SV=1
139	A8GKB7	UBIA_SERP5 4-hydroxybenzoate octaprenyltransferase OS= <i>Serratia proteamaculans</i> (strain 568) OX=399741 GN=ubiA PE=3 SV=2
140	Q5ZVL0	UBIA_LEGPH 4-hydroxybenzoate octaprenyltransferase OS= <i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 / ATCC 33152 / DSM 7513) OX=272624 GN=ubiA PE=3 SV=1
141	B7UPK1	UBIA_ECO27 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O127:H6 (strain E2348/69 / EPEC) OX=574521 GN=ubiA PE=3 SV=1
142	Q49A47	UBIA_BLOPB 4-hydroxybenzoate octaprenyltransferase OS= <i>Blochmannia pennsylvanicus</i> (strain BPEN) OX=291272 GN=ubiA PE=3 SV=1
143	C3LPT6	UBIA_VIBCM 4-hydroxybenzoate octaprenyltransferase OS= <i>Vibrio cholerae</i> serotype O1 (strain M66-2) OX=579112 GN=ubiA PE=3 SV=1
144	B5FQQ8	UBIA_SALDC 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella dublin</i> (strain CT_02021853) OX=439851 GN=ubiA PE=3 SV=1
145	Q6LVS3	UBIA_PHOPR 4-hydroxybenzoate octaprenyltransferase OS= <i>Photobacterium profundum</i> (strain SS9) OX=298386 GN=ubiA PE=3 SV=1
146	Q1R3P6	UBIA_ECOUT 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain UTI89 / UPEC) OX=364106 GN=ubiA PE=3 SV=1
147	A8FQF8	UBIA_SHESH 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella sediminis</i> (strain HAW-EB3) OX=425104 GN=ubiA PE=3 SV=1
148	Q3BYM7	UBIA_XANC5 4-hydroxybenzoate octaprenyltransferase OS= <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10) OX=316273 GN=ubiA PE=3 SV=1
149	Q39JF0	UBIA_BURL3 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia lata</i> (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383) OX=482957 GN=ubiA PE=3 SV=1
150	Q4K3L9	UBIA_PSEF5 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5) OX=220664 GN=ubiA PE=3 SV=1
151	B1JVZ5	UBIA_BURCC 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia cenocepacia</i> (strain MC0-3) OX=406425 GN=ubiA PE=3 SV=1
152	P57970	UBIA_PASMU 4-hydroxybenzoate octaprenyltransferase OS= <i>Pasteurella multocida</i> (strain Pm70) OX=272843 GN=ubiA PE=3 SV=1
153	Q0A5V9	UBIA_ALKEH 4-hydroxybenzoate octaprenyltransferase OS= <i>Alkalilimnicola ehrlichii</i> (strain ATCC BAA-1101 / DSM 17681 / MLHE-1) OX=187272 GN=ubiA PE=3 SV=1
154	A1AIL7	UBIA_ECOK1 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O1:K1 / APEC OX=405955 GN=ubiA PE=3 SV=1
155	Q62H69	UBIA_BURMA 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia mallei</i> (strain ATCC 23344) OX=243160 GN=ubiA PE=3 SV=2
156	B6J612	UBIA_COXB1 4-hydroxybenzoate octaprenyltransferase OS= <i>Coxiella burnetii</i> (strain CbuK_Q154) OX=434924 GN=ubiA PE=3 SV=1
157	B1J454	UBIA_PSEPW 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas putida</i> (strain W619) OX=390235 GN=ubiA PE=3 SV=1

158	Q3JBS8	UBIA_NITOC 4-hydroxybenzoate octaprenyltransferase OS= <i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 / C-107) OX=323261 GN=ubiA PE=3 SV=1
159	Q12S01	UBIA_SHEDO 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella denitrificans</i> (strain OS217 / ATCC BAA-1090 / DSM 15013) OX=318161 GN=ubiA PE=3 SV=2
160	Q7VQU0	UBIA_BLOFL 4-hydroxybenzoate octaprenyltransferase OS= <i>Blochmannia floridanus</i> OX=203907 GN=ubiA PE=3 SV=1
161	B5BJV7	UBIA_SALPK 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella paratyphi</i> A (strain AKU_12601) OX=554290 GN=ubiA PE=3 SV=1
162	A5F4H4	UBIA_VIBC3 4-hydroxybenzoate octaprenyltransferase OS= <i>Vibrio cholerae</i> serotype O1 (strain ATCC 39541 / Classical Ogawa 395 / O395) OX=345073 GN=ubiA PE=3 SV=1
163	A9QYL1	UBIA_YERPG 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pestis</i> bv. Antiqua (strain Angola) OX=349746 GN=ubiA PE=3 SV=1
164	A7FN99	UBIA_YERP3 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pseudotuberculosis</i> serotype O:1b (strain IP 31758) OX=349747 GN=ubiA PE=3 SV=1
165	Q0BI45	UBIA_BURCM 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia ambifaria</i> (strain ATCC BAA-244 / AMMD) OX=339670 GN=ubiA PE=3 SV=1
166	A6WT76	UBIA_SHEB8 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella baltica</i> (strain OS185) OX=402882 GN=ubiA PE=3 SV=1
167	A3QIF2	UBIA_SHELP 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella loihica</i> (strain ATCC BAA-1088 / PV-4) OX=323850 GN=ubiA PE=3 SV=1
168	Q1CE95	UBIA_YERPN 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pestis</i> bv. Antiqua (strain Nepal516) OX=377628 GN=ubiA PE=3 SV=1
169	Q8EJJ5	UBIA_SHEON 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella oneidensis</i> (strain MR-1) OX=211586 GN=ubiA PE=3 SV=1
170	A5IBS2	UBIA_LEGPC 4-hydroxybenzoate octaprenyltransferase OS= <i>Legionella pneumophila</i> (strain Corby) OX=400673 GN=ubiA PE=3 SV=1
171	A7ZUR2	UBIA_ECO24 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O139:H28 (strain E24377A / ETEC) OX=331111 GN=ubiA PE=3 SV=1
172	Q1I2R3	UBIA_PSEE4 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas entomophila</i> (strain L48) OX=384676 GN=ubiA PE=3 SV=1
173	P0AGK1	UBIA_ECOLI 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain K12) OX=83333 GN=ubiA PE=1 SV=1
174	A8AN88	UBIA_CITK8 4-hydroxybenzoate octaprenyltransferase OS= <i>Citrobacter koseri</i> (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) OX=290338 GN=ubiA PE=3 SV=1
175	B0RMR4	UBIA_XANCB 4-hydroxybenzoate octaprenyltransferase OS= <i>Xanthomonas campestris</i> pv. campestris (strain B100) OX=509169 GN=ubiA PE=3 SV=1
176	B6I5Q5	UBIA_ECOSE 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain SE11) OX=409438 GN=ubiA PE=3 SV=1
177	A1KSZ7	UBIA_NEIMF 4-hydroxybenzoate octaprenyltransferase OS= <i>Neisseria meningitidis</i> serogroup C / serotype 2a (strain ATCC 700532 / DSM 15464 / FAM18) OX=272831 GN=ubiA PE=3 SV=1
178	A1U6P5	UBIA_MARHV 4-hydroxybenzoate octaprenyltransferase OS= <i>Marinobacter hydrocarbonoclasticus</i> (strain ATCC 700491 / DSM 11845 / VT8) OX=351348 GN=ubiA PE=3 SV=1
179	B1IUL2	UBIA_ECOLC 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain ATCC 8739 / DSM 1576 / Crooks) OX=481805 GN=ubiA PE=3 SV=1
180	Q8XGZ7	UBIA_SALTI 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella typhi</i> OX=90370 GN=ubiA PE=3 SV=1
181	Q6D9I8	UBIA_PECAS 4-hydroxybenzoate octaprenyltransferase OS= <i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672) OX=218491 GN=ubiA PE=3 SV=1
182	Q1LJ64	UBIA_CUPMC 4-hydroxybenzoate octaprenyltransferase OS= <i>Cupriavidus metallidurans</i> (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) OX=266264 GN=ubiA PE=3 SV=1
183	A4Y0P0	UBIA_PSEMY 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas mendocina</i> (strain ymp) OX=399739 GN=ubiA PE=3 SV=1
184	A1WVM9	UBIA_HALHL 4-hydroxybenzoate octaprenyltransferase OS= <i>Halorhodospira halophila</i> (strain DSM 244 / SL1) OX=349124 GN=ubiA PE=3 SV=2
185	Q9HTK0	UBIA_PSEAE 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=ubiA PE=3 SV=1
186	Q4FR08	UBIA_PSYA2 4-hydroxybenzoate octaprenyltransferase OS= <i>Psychrobacter arcticus</i> (strain DSM 17307 / VKM B-2377 / 273-4) OX=259536 GN=ubiA PE=3 SV=1
187	B0BPA2	UBIA_ACTPJ 4-hydroxybenzoate octaprenyltransferase OS= <i>Actinobacillus pleuropneumoniae</i> serotype 3 (strain JL03) OX=434271 GN=ubiA PE=3 SV=1
188	B2I675	UBIA_XYLF2 4-hydroxybenzoate octaprenyltransferase OS= <i>Xylella fastidiosa</i> (strain M23) OX=405441 GN=ubiA PE=3 SV=1
189	B5QZ59	UBIA_SALEP 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella enteritidis</i> PT4 (strain P125109) OX=550537 GN=ubiA PE=3 SV=1
190	B5F1Q3	UBIA_SALA4 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella agona</i> (strain SL483) OX=454166 GN=ubiA PE=3 SV=1
191	Q5PL17	UBIA_SALPA 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella paratyphi</i> A (strain ATCC 9150 / SARB42) OX=295319 GN=ubiA PE=3 SV=1
192	A1T087	UBIA_PSYIN 4-hydroxybenzoate octaprenyltransferase OS= <i>Psychromonas ingrahamii</i> (strain 37) OX=357804 GN=ubiA PE=3 SV=1
193	A6W3L5	UBIA_MARMS 4-hydroxybenzoate octaprenyltransferase OS= <i>Marinomonas</i> sp. (strain MWYL1) OX=400668 GN=ubiA PE=3 SV=1
194	B7V5P9	UBIA_PSEA8 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas aeruginosa</i> (strain LESB58) OX=557722 GN=ubiA PE=3 SV=1
195	B2SS70	UBIA_XANOP 4-hydroxybenzoate octaprenyltransferase OS= <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain PXO99A) OX=360094 GN=ubiA PE=3 SV=1
196	Q0HQR8	UBIA_SHESR 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella</i> sp. (strain MR-7) OX=60481 GN=ubiA PE=3 SV=1
197	Q83F93	UBIA_COXBU 4-hydroxybenzoate octaprenyltransferase OS= <i>Coxiella burnetii</i> (strain RSA 493 / Nine Mile phase I) OX=227377 GN=ubiA PE=3 SV=1

198	A4IYU3	UBIA_FRATW 4-hydroxybenzoate octaprenyltransferase OS= <i>Francisella tularensis</i> subsp. <i>tularensis</i> (strain WY96-3418) OX=418136 GN=ubiA PE=3 SV=1
199	Q5WWR8	UBIA_LEGPL 4-hydroxybenzoate octaprenyltransferase OS= <i>Legionella pneumophila</i> (strain Lens) OX=297245 GN=ubiA PE=3 SV=1
200	Q5QUP3	UBIA_IDILO 4-hydroxybenzoate octaprenyltransferase OS= <i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR) OX=283942 GN=ubiA PE=3 SV=1
201	Q5H5R3	UBIA_XANOR 4-hydroxybenzoate octaprenyltransferase OS= <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain KACC10331 / KXO85) OX=291331 GN=ubiA PE=3 SV=1
202	A7NA50	UBIA_FRATF 4-hydroxybenzoate octaprenyltransferase OS= <i>Francisella tularensis</i> subsp. <i>holarctica</i> (strain FTNF002-00 / FTA) OX=458234 GN=ubiA PE=3 SV=1
203	C5B704	UBIA_EDWI9 4-hydroxybenzoate octaprenyltransferase OS= <i>Edwardsiella ictaluri</i> (strain 93-146) OX=634503 GN=ubiA PE=3 SV=1
204	A6VEG6	UBIA_PSE7 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas aeruginosa</i> (strain PA7) OX=381754 GN=ubiA PE=3 SV=1
205	O52366	UBIA_PROST 4-hydroxybenzoate octaprenyltransferase OS= <i>Providencia stuartii</i> OX=588 GN=ubiA PE=3 SV=1
206	Q7MQ87	UBIA_VIBVY 4-hydroxybenzoate octaprenyltransferase OS= <i>Vibrio vulnificus</i> (strain YJ016) OX=196600 GN=ubiA PE=3 SV=1
207	C1DK47	UBIA_AZOVD 4-hydroxybenzoate octaprenyltransferase OS= <i>Azotobacter vinelandii</i> (strain DJ / ATCC BAA-1303) OX=322710 GN=ubiA PE=3 SV=1
208	Q3YUU4	UBIA_SHISS 4-hydroxybenzoate octaprenyltransferase OS= <i>Shigella sonnei</i> (strain Ss046) OX=300269 GN=ubiA PE=3 SV=1
209	Q8PQD5	UBIA_XANAC 4-hydroxybenzoate octaprenyltransferase OS= <i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306) OX=190486 GN=ubiA PE=3 SV=1
210	B1XC39	UBIA_ECODH 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain K12 / DH10B) OX=316385 GN=ubiA PE=3 SV=1
211	Q1GXB3	UBIA_METFK 4-hydroxybenzoate octaprenyltransferase OS= <i>Methylobacillus flagellatus</i> (strain KT / ATCC 51484 / DSM 6875) OX=265072 GN=ubiA PE=3 SV=1
212	Q31DM4	UBIA_HYDCU 4-hydroxybenzoate octaprenyltransferase OS= <i>Hydrogenovibrio crunogenus</i> (strain XCL-2) OX=317025 GN=ubiA PE=3 SV=1
213	A8GZR0	UBIA_SHEPA 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella pealeana</i> (strain ATCC 700345 / ANG-SQ1) OX=398579 GN=ubiA PE=3 SV=1
214	Q7CPB4	UBIA_SALTY 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella typhimurium</i> (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ubiA PE=1 SV=1
215	B6ENU2	UBIA_ALISL 4-hydroxybenzoate octaprenyltransferase OS= <i>Aliivibrio salmonicida</i> (strain LFI1238) OX=316275 GN=ubiA PE=3 SV=1
216	B1LPK5	UBIA_ECOSM 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain SMS-3-5 / SECEC) OX=439855 GN=ubiA PE=3 SV=1
217	A3CZR1	UBIA_SHEB5 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella baltica</i> (strain OS155 / ATCC BAA-1091) OX=325240 GN=ubiA PE=3 SV=1
218	B1JNE6	UBIA_YERPY 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pseudotuberculosis</i> serotype O:3 (strain YPIII) OX=502800 GN=ubiA PE=3 SV=1
219	Q0SXQ7	UBIA_SHIF8 4-hydroxybenzoate octaprenyltransferase OS= <i>Shigella flexneri</i> serotype 5b (strain 8401) OX=373384 GN=ubiA PE=3 SV=1
220	B7VMA0	UBIA_VIBA3 4-hydroxybenzoate octaprenyltransferase OS= <i>Vibrio atlanticus</i> (strain LGP32) OX=575788 GN=ubiA PE=3 SV=1
221	Q1QSG2	UBIA_CHRSD 4-hydroxybenzoate octaprenyltransferase OS= <i>Chromohalobacter salexigens</i> (strain ATCC BAA-138 / DSM 3043 / CIP 106854 / NCIMB 13768 / 1H11) OX=290398 GN=ubiA PE=3 SV=1
222	Q87U39	UBIA_PSESM 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000) OX=223283 GN=ubiA PE=3 SV=1
223	A5WB34	UBIA_PSEP1 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas putida</i> (strain ATCC 700007 / DSM 6899 / BCRC 17059 / F1) OX=351746 GN=ubiA PE=3 SV=1
224	Q15ZT9	UBIA_PSEA6 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudoalteromonas atlantica</i> (strain T6c / ATCC BAA-1087) OX=342610 GN=ubiA PE=3 SV=2
225	A9MH90	UBIA_SALAR 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella arizonae</i> (strain ATCC BAA-731 / CDC346-86 / RSK2980) OX=41514 GN=ubiA PE=3 SV=1
226	Q48AL9	UBIA_COLP3 4-hydroxybenzoate octaprenyltransferase OS= <i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681) OX=167879 GN=ubiA PE=3 SV=1
227	A9M390	UBIA_NEIM0 4-hydroxybenzoate octaprenyltransferase OS= <i>Neisseria meningitidis</i> serogroup C (strain 053442) OX=374833 GN=ubiA PE=3 SV=1
228	Q9JV93	UBIA_NEIMA 4-hydroxybenzoate octaprenyltransferase OS= <i>Neisseria meningitidis</i> serogroup A / serotype 4A (strain DSM 15465 / Z2491) OX=122587 GN=ubiA PE=3 SV=1
229	A0KEP9	UBIA_AERHH 4-hydroxybenzoate octaprenyltransferase OS= <i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240) OX=380703 GN=ubiA PE=3 SV=1
230	Q5NGI4	UBIA_FRATT 4-hydroxybenzoate octaprenyltransferase OS= <i>Francisella tularensis</i> subsp. <i>tularensis</i> (strain SCHU S4 / Schu 4) OX=177416 GN=ubiA PE=3 SV=1
231	Q7CKP5	UBIA_YERPE 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pestis</i> OX=632 GN=ubiA PE=3 SV=1
232	C0Q4D9	UBIA_SALPC 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella paratyphi</i> C (strain RKS4594) OX=476213 GN=ubiA PE=3 SV=1
233	B7MJ30	UBIA_ECO45 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O45:K1 (strain S88 / ExPEC) OX=585035 GN=ubiA PE=3 SV=1
234	Q3JNX1	UBIA_BURP1 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia pseudomallei</i> (strain 1710b) OX=320372 GN=ubiA PE=3 SV=2
235	Q7VL38	UBIA_HAEDU 4-hydroxybenzoate octaprenyltransferase OS= <i>Haemophilus ducreyi</i> (strain 35000HP / ATCC 700724) OX=233412 GN=ubiA PE=3 SV=1
236	B7NS04	UBIA_ECO71 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O7:K1 (strain IAI39 / ExPEC) OX=585057 GN=ubiA PE=3 SV=1
237	Q8DD49	UBIA_VIBVU 4-hydroxybenzoate octaprenyltransferase OS= <i>Vibrio vulnificus</i> (strain CMCP6) OX=216895 GN=ubiA PE=3 SV=1

238	Q2NR07	UBIA_SODGM 4-hydroxybenzoate octaprenyltransferase OS= <i>Sodalis glossinidius</i> (strain morsitans) OX=343509 GN=ubiA PE=3 SV=1
239	B7M7V3	UBIA_ECO8A 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O8 (strain IAI1) OX=585034 GN=ubiA PE=3 SV=1
240	A0Q4X3	UBIA_FRATN 4-hydroxybenzoate octaprenyltransferase OS= <i>Francisella tularensis</i> subsp. novicida (strain U112) OX=401614 GN=ubiA PE=3 SV=1
241	Q12GA4	UBIA_POLSJ 4-hydroxybenzoate octaprenyltransferase OS= <i>Polaromonas</i> sp. (strain JS666 / ATCC BAA-500) OX=296591 GN=ubiA PE=3 SV=1
242	Q21DY7	UBIA_SACD2 4-hydroxybenzoate octaprenyltransferase OS= <i>Saccharophagus degradans</i> (strain 2-40 / ATCC 43961 / DSM 17024) OX=203122 GN=ubiA PE=3 SV=1
243	Q83IP7	UBIA_SHIFL 4-hydroxybenzoate octaprenyltransferase OS= <i>Shigella flexneri</i> OX=623 GN=ubiA PE=3 SV=1
244	Q9KVP7	UBIA_VIBCH 4-hydroxybenzoate octaprenyltransferase OS= <i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=ubiA PE=3 SV=1
245	A4JBP9	UBIA_BURVG 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia vietnamiensis</i> (strain G4 / LMG 22486) OX=269482 GN=ubiA PE=3 SV=1
246	Q5X5D5	UBIA_LEGPA 4-hydroxybenzoate octaprenyltransferase OS= <i>Legionella pneumophila</i> (strain Paris) OX=297246 GN=ubiA PE=3 SV=1
247	B7LAY8	UBIA_ECO55 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain 55989 / EAEC) OX=585055 GN=ubiA PE=3 SV=1
248	Q2SNV5	UBIA_HAHCH 4-hydroxybenzoate octaprenyltransferase OS= <i>Hahella chejuensis</i> (strain KCTC 2396) OX=349521 GN=ubiA PE=3 SV=1
249	B0KQB7	UBIA_PSEPG 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas putida</i> (strain GB-1) OX=76869 GN=ubiA PE=3 SV=1
250	B3H1F9	UBIA_ACTP7 4-hydroxybenzoate octaprenyltransferase OS= <i>Actinobacillus pleuropneumoniae</i> serotype 7 (strain AP76) OX=537457 GN=ubiA PE=3 SV=1
251	B1YTH7	UBIA_BURA4 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia ambifaria</i> (strain MC40-6) OX=398577 GN=ubiA PE=3 SV=1
252	A4TRU8	UBIA_YERPP 4-hydroxybenzoate octaprenyltransferase OS= <i>Yersinia pestis</i> (strain Pestoides F) OX=386656 GN=ubiA PE=3 SV=1
253	Q0TA22	UBIA_ECOL5 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O6:K15:H31 (strain 536 / UPEC) OX=362663 GN=ubiA PE=3 SV=1
254	A9N1L3	UBIA_SALPB 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella paratyphi</i> B (strain ATCC BAA-1250 / SPB7) OX=1016998 GN=ubiA PE=3 SV=1
255	A9AGE2	UBIA_BURM1 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia multivorans</i> (strain ATCC 17616 / 249) OX=395019 GN=ubiA PE=3 SV=1
256	Q4UZN6	UBIA_XANC8 4-hydroxybenzoate octaprenyltransferase OS= <i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain 8004) OX=314565 GN=ubiA PE=3 SV=1
257	Q14HY6	UBIA_FRAT1 4-hydroxybenzoate octaprenyltransferase OS= <i>Francisella tularensis</i> subsp. <i>tularensis</i> (strain FSC 198) OX=393115 GN=ubiA PE=3 SV=1
258	Q145H3	UBIA_PARXL 4-hydroxybenzoate octaprenyltransferase OS= <i>Paraburkholderia xenovorans</i> (strain LB400) OX=266265 GN=ubiA PE=3 SV=1
259	A1TJR2	UBIA_ACIAAC 4-hydroxybenzoate octaprenyltransferase OS= <i>Acidovorax citrulli</i> (strain AAC00-1) OX=397945 GN=ubiA PE=3 SV=1
260	B4TQQ2	UBIA_SALSV 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella schwarzengrund</i> (strain CVM19633) OX=439843 GN=ubiA PE=3 SV=1
261	B0U042	UBIA_FRAP2 4-hydroxybenzoate octaprenyltransferase OS= <i>Francisella philomiragia</i> subsp. <i>philomiragia</i> (strain ATCC 25017 / FSC 153 / O#319-036) OX=484022 GN=ubiA PE=3 SV=1
262	A1WKC0	UBIA_VEREI 4-hydroxybenzoate octaprenyltransferase OS= <i>Verminephrobacter eiseniae</i> (strain EF01-2) OX=391735 GN=ubiA PE=3 SV=1
263	A7N0X0	UBIA_VIBCB 4-hydroxybenzoate octaprenyltransferase OS= <i>Vibrio campbellii</i> (strain ATCC BAA-1116 / BB120) OX=338187 GN=ubiA PE=3 SV=1
264	B5R7T3	UBIA_SALG2 4-hydroxybenzoate octaprenyltransferase OS= <i>Salmonella gallinarum</i> (strain 287/91 / NCTC 13346) OX=550538 GN=ubiA PE=3 SV=1
265	Q46XG9	UBIA_CUPPJ 4-hydroxybenzoate octaprenyltransferase OS= <i>Cupriavidus pinatubonensis</i> (strain JMP 134 / LMG 1197) OX=264198 GN=ubiA PE=3 SV=1
266	Q8PDE8	UBIA_XANCP 4-hydroxybenzoate octaprenyltransferase OS= <i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25) OX=190485 GN=ubiA PE=3 SV=1
267	Q1Q996	UBIA_PSYCK 4-hydroxybenzoate octaprenyltransferase OS= <i>Psychrobacter cryohalolentis</i> (strain ATCC BAA-1226 / DSM 17306 / VKM B-2378 / K5) OX=335284 GN=ubiA PE=3 SV=1
268	B9MBT5	UBIA_ACJET 4-hydroxybenzoate octaprenyltransferase OS= <i>Acidovorax ebreus</i> (strain TPSY) OX=535289 GN=ubiA PE=3 SV=1
269	A1W307	UBIA_ACISJ 4-hydroxybenzoate octaprenyltransferase OS= <i>Acidovorax</i> sp. (strain JS42) OX=232721 GN=ubiA PE=3 SV=1
270	A3N0I2	UBIA_ACTP2 4-hydroxybenzoate octaprenyltransferase OS= <i>Actinobacillus pleuropneumoniae</i> serotype 5b (strain L20) OX=416269 GN=ubiA PE=3 SV=1
271	C4L7X6	UBIA_TOLAT 4-hydroxybenzoate octaprenyltransferase OS= <i>Tolomonas auensis</i> (strain DSM 9187 / TA4) OX=595494 GN=ubiA PE=3 SV=1
272	B8E613	UBIA_SHEB2 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella baltica</i> (strain OS223) OX=407976 GN=ubiA PE=3 SV=1
273	Q9K083	UBIA_NEIMB 4-hydroxybenzoate octaprenyltransferase OS= <i>Neisseria meningitidis</i> serogroup B (strain MC58) OX=122586 GN=ubiA PE=3 SV=1
274	B2TX76	UBIA_SHIB3 4-hydroxybenzoate octaprenyltransferase OS= <i>Shigella boydii</i> serotype 18 (strain CDC 3083-94 / BS512) OX=344609 GN=ubiA PE=3 SV=1
275	A9L4Q8	UBIA_SHEB9 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella baltica</i> (strain OS195) OX=399599 GN=ubiA PE=3 SV=1
276	A4G1Y9	UBIA_HERAR 4-hydroxybenzoate octaprenyltransferase OS= <i>Hermiimonas arsenicoxydans</i> OX=204773 GN=ubiA PE=3 SV=1
277	B1XRV6	UBIA_POLNS 4-hydroxybenzoate octaprenyltransferase OS= <i>Polynucleobacter necessarius</i> subsp. <i>necessarius</i> (strain STIR1) OX=452638 GN=ubiA PE=3 SV=1

278	A9KGW7	UBIA_COXBN 4-hydroxybenzoate octaprenyltransferase OS=Coxiella burnetii (strain Dugway 5J108-111) OX=434922 GN=ubiA PE=3 SV=1
279	Q0VTA7	UBIA_ALCBS 4-hydroxybenzoate octaprenyltransferase OS=Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2) OX=393595 GN=ubiA PE=3 SV=1
280	A1S2M4	UBIA_SHEAM 4-hydroxybenzoate octaprenyltransferase OS=Shewanella amazonensis (strain ATCC BAA-1098 / SB2B) OX=326297 GN=ubiA PE=3 SV=1
281	A2SMA7	UBIA_METPP 4-hydroxybenzoate octaprenyltransferase OS=Methylibium petroleiphilum (strain ATCC BAA-1232 / LMG 22953 / PM1) OX=420662 GN=ubiA PE=3 SV=1
282	Q21S73	UBIA_RHOFT 4-hydroxybenzoate octaprenyltransferase OS=Rhodoferrax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) OX=338969 GN=ubiA PE=3 SV=1
283	Q2Y5S3	UBIA_NITMU 4-hydroxybenzoate octaprenyltransferase OS=Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) OX=323848 GN=ubiA PE=3 SV=1
284	Q4ZLB4	UBIA_PSEU2 4-hydroxybenzoate octaprenyltransferase OS=Pseudomonas syringae pv. syringae (strain B728a) OX=205918 GN=ubiA PE=3 SV=1
285	Q327U7	UBIA_SHIDS 4-hydroxybenzoate octaprenyltransferase OS=Shigella dysenteriae serotype 1 (strain Sd197) OX=300267 GN=ubiA PE=3 SV=1
286	B0U2A2	UBIA_XYLFM 4-hydroxybenzoate octaprenyltransferase OS=Xylella fastidiosa (strain M12) OX=405440 GN=ubiA PE=3 SV=1
287	Q5E207	UBIA_ALIF1 4-hydroxybenzoate octaprenyltransferase OS=Aliivibrio fischeri (strain ATCC 700601 / ES114) OX=312309 GN=ubiA PE=3 SV=1
288	Q87KM9	UBIA_VIBPA 4-hydroxybenzoate octaprenyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) OX=223926 GN=ubiA PE=3 SV=1
289	P0AGK2	UBIA_ECOL6 4-hydroxybenzoate octaprenyltransferase OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) OX=199310 GN=ubiA PE=3 SV=1
290	B4RK00	UBIA_NEIG2 4-hydroxybenzoate octaprenyltransferase OS=Neisseria gonorrhoeae (strain NCCP11945) OX=521006 GN=ubiA PE=3 SV=1
291	Q6F9N8	UBIA_ACIAD 4-hydroxybenzoate octaprenyltransferase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=ubiA PE=3 SV=2
292	Q31TU8	UBIA_SHIBS 4-hydroxybenzoate octaprenyltransferase OS=Shigella boydii serotype 4 (strain Sb227) OX=300268 GN=ubiA PE=3 SV=1
293	A0KSE2	UBIA_SHESA 4-hydroxybenzoate octaprenyltransferase OS=Shewanella sp. (strain ANA-3) OX=94122 GN=ubiA PE=3 SV=1
294	C6DKC9	UBIA_PECCP 4-hydroxybenzoate octaprenyltransferase OS=Pectobacterium carotovorum subsp. carotovorum (strain PC1) OX=561230 GN=ubiA PE=3 SV=1
295	Q0I0W3	UBIA_HAES1 4-hydroxybenzoate octaprenyltransferase OS=Haemophilus somnus (strain 129Pt) OX=205914 GN=ubiA PE=3 SV=1
296	Q5P5M0	UBIA_AROAE 4-hydroxybenzoate octaprenyltransferase OS=Aromatoleum aromaticum (strain EbN1) OX=76114 GN=ubiA PE=3 SV=2
297	A4STB5	UBIA_AERS4 4-hydroxybenzoate octaprenyltransferase OS=Aeromonas salmonicida (strain A449) OX=382245 GN=ubiA PE=3 SV=2
298	Q0BNI0	UBIA_FRATO 4-hydroxybenzoate octaprenyltransferase OS=Francisella tularensis subsp. holarctica (strain OSU18) OX=393011 GN=ubiA PE=3 SV=1
299	A5CXV6	UBIA_VESOH 4-hydroxybenzoate octaprenyltransferase OS=Vesicomyosocius okutanii subsp. Calyptogena okutanii (strain HA) OX=412965 GN=ubiA PE=3 SV=2
300	P0AGK3	UBIA_ECO57 4-hydroxybenzoate octaprenyltransferase OS=Escherichia coli O157:H7 OX=83334 GN=ubiA PE=3 SV=1
301	A0K4Q5	UBIA_BURCH 4-hydroxybenzoate octaprenyltransferase OS=Burkholderia cenocepacia (strain HI2424) OX=331272 GN=ubiA PE=3 SV=1
302	Q63R13	UBIA_BURPS 4-hydroxybenzoate octaprenyltransferase OS=Burkholderia pseudomallei (strain K96243) OX=272560 GN=ubiA PE=3 SV=2
303	B4T1S9	UBIA_SALNS 4-hydroxybenzoate octaprenyltransferase OS=Salmonella newport (strain SL254) OX=423368 GN=ubiA PE=3 SV=1
304	B0UUY3	UBIA_HISS2 4-hydroxybenzoate octaprenyltransferase OS=Histophilus somni (strain 2336) OX=228400 GN=ubiA PE=3 SV=1
305	Q2A564	UBIA_FRATH 4-hydroxybenzoate octaprenyltransferase OS=Francisella tularensis subsp. holarctica (strain LVS) OX=376619 GN=ubiA PE=3 SV=1
306	Q0AGZ9	UBIA_NITEC 4-hydroxybenzoate octaprenyltransferase OS=Nitrosomonas eutropha (strain DSM 101675 / C91 / Nm57) OX=335283 GN=ubiA PE=3 SV=1
307	Q608Z9	UBIA_METCA 4-hydroxybenzoate octaprenyltransferase OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) OX=243233 GN=ubiA PE=3 SV=1
308	A1JRU3	UBIA_YERE8 4-hydroxybenzoate octaprenyltransferase OS=Yersinia enterocolitica serotype O:8 / biotype 1B (strain NCTC 13174 / 8081) OX=393305 GN=ubiA PE=3 SV=1
309	B7LL12	UBIA_ESCF3 4-hydroxybenzoate octaprenyltransferase OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) OX=585054 GN=ubiA PE=3 SV=1
310	A1VJ21	UBIA_POLNA 4-hydroxybenzoate octaprenyltransferase OS=Polaromonas naphthalenivorans (strain CJ2) OX=365044 GN=ubiA PE=3 SV=1
311	Q2P8F5	UBIA_XANOM 4-hydroxybenzoate octaprenyltransferase OS=Xanthomonas oryzae pv. oryzae (strain MAFF 311018) OX=342109 GN=ubiA PE=3 SV=1
312	Q07XN2	UBIA_SHEFN 4-hydroxybenzoate octaprenyltransferase OS=Shewanella frigidimarina (strain NCIMB 400) OX=318167 GN=ubiA PE=3 SV=1
313	Q3SLJ4	UBIA_THIDA 4-hydroxybenzoate octaprenyltransferase OS=Thiobacillus denitrificans (strain ATCC 25259) OX=292415 GN=ubiA PE=3 SV=1
314	B7MRH2	UBIA_ECO81 4-hydroxybenzoate octaprenyltransferase OS=Escherichia coli O81 (strain ED1a) OX=585397 GN=ubiA PE=3 SV=1
315	A6SUU0	UBIA_JANMA 4-hydroxybenzoate octaprenyltransferase OS=Janthinobacterium sp. (strain Marseille) OX=375286 GN=ubiA PE=3 SV=1
316	Q0HN13	UBIA_SHESM 4-hydroxybenzoate octaprenyltransferase OS=Shewanella sp. (strain MR-4) OX=60480 GN=ubiA PE=3 SV=1
317	A3MPC2	UBIA_BURM7 4-hydroxybenzoate octaprenyltransferase OS=Burkholderia mallei (strain NCTC 10247) OX=320389 GN=ubiA PE=3 SV=1

318	Q0K739	UBIA_CUPNH 4-hydroxybenzoate octaprenyltransferase OS= <i>Cupriavidus necator</i> (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) OX=381666 GN=ubiA PE=3 SV=2
319	B6J375	UBIA_COXB2 4-hydroxybenzoate octaprenyltransferase OS= <i>Coxiella burnetii</i> (strain CbuG_Q212) OX=434923 GN=ubiA PE=3 SV=1
320	A1K2P1	UBIA_AZOSB 4-hydroxybenzoate octaprenyltransferase OS= <i>Azoarcus</i> sp. (strain BH72) OX=418699 GN=ubiA PE=3 SV=1
321	B5FCB4	UBIA_ALIFM 4-hydroxybenzoate octaprenyltransferase OS= <i>Aliivibrio fischeri</i> (strain MJ11) OX=388396 GN=ubiA PE=3 SV=1
322	A3NZ16	UBIA_BURP0 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia pseudomallei</i> (strain 1106a) OX=357348 GN=ubiA PE=3 SV=1
323	B7NFY4	UBIA_ECOLU 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O17:K52:H18 (strain UMN026 / ExPEC) OX=585056 GN=ubiA PE=3 SV=1
324	Q8XVY9	UBIA_RALSO 4-hydroxybenzoate octaprenyltransferase OS= <i>Ralstonia solanacearum</i> (strain GMI1000) OX=267608 GN=ubiA PE=3 SV=1
325	Q88C65	UBIA_PSEPK 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) OX=160488 GN=ubiA PE=3 SV=1
326	B5Z181	UBIA_ECO5E 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O157:H7 (strain EC4115 / EHEC) OX=444450 GN=ubiA PE=3 SV=1
327	B2JGG3	UBIA_PARP8 4-hydroxybenzoate octaprenyltransferase OS= <i>Paraburkholderia phymatum</i> (strain DSM 17167 / CIP 108236 / LMG 21445 / STM815) OX=391038 GN=ubiA PE=3 SV=1
328	A3NDA6	UBIA_BURP6 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia pseudomallei</i> (strain 668) OX=320373 GN=ubiA PE=3 SV=1
329	Q48BQ5	UBIA_PSE14 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudomonas savastanoi</i> pv. phaseolicola (strain 1448A / Race 6) OX=264730 GN=ubiA PE=3 SV=1
330	A4SZT5	UBIA_POLAQ 4-hydroxybenzoate octaprenyltransferase OS= <i>Polynucleobacter asymbioticus</i> (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1) OX=312153 GN=ubiA PE=3 SV=1
331	B8CTT5	UBIA_SHEPW 4-hydroxybenzoate octaprenyltransferase OS= <i>Shewanella piezotolerans</i> (strain WP3 / JCM 13877) OX=225849 GN=ubiA PE=3 SV=1
332	Q2SZ16	UBIA_BURTA 4-hydroxybenzoate octaprenyltransferase OS= <i>Burkholderia thailandensis</i> (strain ATCC 700388 / DSM 13276 / CIP 106301 / E264) OX=271848 GN=ubiA PE=3 SV=2
333	Q3IHW5	UBIA_PSET1 4-hydroxybenzoate octaprenyltransferase OS= <i>Pseudoalteromonas translucida</i> (strain TAC 125) OX=326442 GN=ubiA PE=3 SV=1
334	C5A133	UBIA_ECOBW 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain K12 / MC4100 / BW2952) OX=595496 GN=ubiA PE=3 SV=1
335	B5XXZ2	UBIA_KLEP3 4-hydroxybenzoate octaprenyltransferase OS= <i>Klebsiella pneumoniae</i> (strain 342) OX=507522 GN=ubiA PE=3 SV=1
336	Q82TP2	UBIA_NITEU 4-hydroxybenzoate octaprenyltransferase OS= <i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) OX=228410 GN=ubiA PE=3 SV=2
337	A8A7E0	UBIA_ECOHS 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> O9:H4 (strain HS) OX=331112 GN=ubiA PE=3 SV=1
338	Q47J11	UBIA_DECAR 4-hydroxybenzoate octaprenyltransferase OS= <i>Dechloromonas aromatica</i> (strain RCB) OX=159087 GN=ubiA PE=3 SV=1
339	A8F1B6	COXX_RICM5 Protoheme IX farnesyltransferase OS= <i>Rickettsia massiliae</i> (strain Mtu5) OX=416276 GN=ctaB PE=3 SV=2
340	A6U6U6	COXX_SINMW Protoheme IX farnesyltransferase OS= <i>Sinorhizobium medicae</i> (strain WSM419) OX=366394 GN=ctaB PE=3 SV=1
341	Q2IPE5	COXX_ANADE Protoheme IX farnesyltransferase OS= <i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C) OX=290397 GN=ctaB PE=3 SV=2
342	Q1BTD0	COXX_BURCA Protoheme IX farnesyltransferase OS= <i>Burkholderia cenocepacia</i> (strain AU 1054) OX=331271 GN=ctaB PE=3 SV=1
343	Q6G4C6	COXX_BARHE Protoheme IX farnesyltransferase OS= <i>Bartonella henselae</i> (strain ATCC 49882 / DSM 28221 / Houston 1) OX=283166 GN=ctaB PE=3 SV=1
344	Q325H3	CYOE_SHIBS Protoheme IX farnesyltransferase OS= <i>Shigella boydii</i> serotype 4 (strain Sb227) OX=300268 GN=cyoE PE=3 SV=1
345	A5CXZ0	CYOE_VESOH Protoheme IX farnesyltransferase OS= <i>Vesicomyxosocius okutanii</i> subsp. <i>Calyptogena okutanii</i> (strain HA) OX=412965 GN=cyoE PE=3 SV=1
346	Q3K773	CYOE2_PSEPF Protoheme IX farnesyltransferase 2 OS= <i>Pseudomonas fluorescens</i> (strain Pf0-1) OX=205922 GN=cyoE2 PE=3 SV=1
347	P0AEA5	CYOE_ECOLI Protoheme IX farnesyltransferase OS= <i>Escherichia coli</i> (strain K12) OX=83333 GN=cyoE PE=1 SV=1
348	Q12IC7	CYOE_SHEDO Protoheme IX farnesyltransferase OS= <i>Shewanella denitrificans</i> (strain OS217 / ATCC BAA-1090 / DSM 15013) OX=318161 GN=cyoE PE=3 SV=1
349	B1JDU9	CYOE2_PSEPW Protoheme IX farnesyltransferase 2 OS= <i>Pseudomonas putida</i> (strain W619) OX=390235 GN=cyoE2 PE=3 SV=1
350	A7FLD4	CYOE_YERP3 Protoheme IX farnesyltransferase OS= <i>Yersinia pseudotuberculosis</i> serotype O:1b (strain IP 31758) OX=349747 GN=cyoE PE=3 SV=1
351	Q87IH5	CYOE2_VIBPA Protoheme IX farnesyltransferase 2 OS= <i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633) OX=223926 GN=cyoE2 PE=3 SV=1
352	Q3J6R6	CYOE_NITOC Protoheme IX farnesyltransferase OS= <i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 / C-107) OX=323261 GN=cyoE PE=3 SV=1
353	P44739	MENA_HAEIN 1,4-dihydroxy-2-naphthoate octaprenyltransferase OS= <i>Haemophilus influenzae</i> (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=menA PE=3 SV=1
354	P32166	MENA_ECOLI 1,4-dihydroxy-2-naphthoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain K12) OX=83333 GN=menA PE=1 SV=1
355	Q1H1S8	COXX_METFK Protoheme IX farnesyltransferase OS= <i>Methylobacillus flagellatus</i> (strain KT / ATCC 51484 / DSM 6875) OX=265072 GN=ctaB PE=3 SV=1
356	Q2IR91	COXX_RHOP2 Protoheme IX farnesyltransferase OS= <i>Rhodopseudomonas palustris</i> (strain HaA2) OX=316058 GN=ctaB PE=3 SV=1
357	Q3SLW5	COXX_THIDA Protoheme IX farnesyltransferase OS= <i>Thiobacillus denitrificans</i> (strain ATCC 25259) OX=292415 GN=ctaB PE=3 SV=1

358	P9WIP2	MENA_MYCTO 1,4-dihydroxy-2-naphthoate octaprenyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain CDC 1551 / Oshkosh) OX=83331 GN=menA PE=3 SV=1
359	P9WIP3	MENA_MYCTU 1,4-dihydroxy-2-naphthoate octaprenyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain ATCC 25618 / H37Rv) OX=83332 GN=menA PE=1 SV=1
360	Q7U021	COXX_MYCBO Protoheme IX farnesyltransferase OS= <i>Mycobacterium bovis</i> (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=ctaB PE=3 SV=1
361	Q1B9B1	COXX_MYCSS Protoheme IX farnesyltransferase OS= <i>Mycobacterium</i> sp. (strain MCS) OX=164756 GN=ctaB PE=3 SV=2
362	Q83NK0	COXX_TROW8 Protoheme IX farnesyltransferase OS= <i>Tropheryma whipplei</i> (strain TW08/27) OX=218496 GN=ctaB PE=3 SV=1
363	P65651	MENA_MYCBO 1,4-dihydroxy-2-naphthoate octaprenyltransferase OS= <i>Mycobacterium bovis</i> (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=menA PE=3 SV=1
364	O07134	MENA_MYCLE 1,4-dihydroxy-2-naphthoate octaprenyltransferase OS= <i>Mycobacterium leprae</i> (strain TN) OX=272631 GN=menA PE=3 SV=1
365	A3PZB2	COXX_MYCSJ Protoheme IX farnesyltransferase OS= <i>Mycobacterium</i> sp. (strain JLS) OX=164757 GN=ctaB PE=3 SV=1
366	Q4JVK2	COXX_CORJK Protoheme IX farnesyltransferase OS= <i>Corynebacterium jeikeium</i> (strain K411) OX=306537 GN=ctaB PE=3 SV=1
367	A1UFQ0	COXX_MYCSK Protoheme IX farnesyltransferase OS= <i>Mycobacterium</i> sp. (strain KMS) OX=189918 GN=ctaB PE=3 SV=2
368	A5CRS6	COXX_CLAM3 Protoheme IX farnesyltransferase OS= <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> (strain NCPPB 382) OX=443906 GN=ctaB PE=3 SV=1
369	A4FBP2	COXX2_SACEN Protoheme IX farnesyltransferase 2 OS= <i>Saccharopolyspora erythraea</i> (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338) OX=405948 GN=ctaB2 PE=3 SV=1
370	B8H7N5	COXX_PSECP Protoheme IX farnesyltransferase OS= <i>Pseudarthrobacter chlorophenolicus</i> (strain ATCC 700700 / DSM 12829 / CIP 107037 / JCM 12360 / KCTC 9906 / NCIMB 13794 / A6) OX=452863 GN=ctaB PE=3 SV=1
371	A1KIP0	COXX_MYCBP Protoheme IX farnesyltransferase OS= <i>Mycobacterium bovis</i> (strain BCG / Pasteur 1173P2) OX=410289 GN=ctaB PE=3 SV=1
372	A1SJR1	COXX_NOC SJ Protoheme IX farnesyltransferase OS= <i>Nocardioide</i> sp. (strain ATCC BAA-499 / JS614) OX=196162 GN=ctaB PE=3 SV=1
373	A1R6I0	COXX_PAEAT Protoheme IX farnesyltransferase OS= <i>Paenarthrobacter aurescens</i> (strain TC1) OX=290340 GN=ctaB PE=3 SV=1
374	A0QHX0	COXX_MYCA1 Protoheme IX farnesyltransferase OS= <i>Mycobacterium avium</i> (strain 104) OX=243243 GN=ctaB PE=3 SV=2
375	Q0S0I5	COXX_RHOJR Protoheme IX farnesyltransferase OS= <i>Rhodococcus jostii</i> (strain RHA1) OX=101510 GN=ctaB PE=3 SV=2
376	Q5YTS1	COXX_NOCFA Protoheme IX farnesyltransferase OS= <i>Nocardia farcinica</i> (strain IFM 10152) OX=247156 GN=ctaB PE=3 SV=1
377	Q6AF34	COXX_LEIXX Protoheme IX farnesyltransferase OS= <i>Leifsonia xyli</i> subsp. <i>xyli</i> (strain CTCB07) OX=281090 GN=ctaB PE=3 SV=1
378	Q6A7G0	COXX_CUTAK Protoheme IX farnesyltransferase OS= <i>Cutibacterium acnes</i> (strain DSM 16379 / KPA171202) OX=267747 GN=ctaB PE=3 SV=2
379	A4QEE9	COXX_CORGB Protoheme IX farnesyltransferase OS= <i>Corynebacterium glutamicum</i> (strain R) OX=340322 GN=ctaB PE=3 SV=1
380	A9WT38	COXX_RENSM Protoheme IX farnesyltransferase OS= <i>Renibacterium salmoninarum</i> (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235) OX=288705 GN=ctaB PE=3 SV=1
381	C1AN96	COXX_MYCBT Protoheme IX farnesyltransferase OS= <i>Mycobacterium bovis</i> (strain BCG / Tokyo 172 / ATCC 35737 / TMC 1019) OX=561275 GN=ctaB PE=3 SV=1
382	A0PPP7	COXX_MYCUA Protoheme IX farnesyltransferase OS= <i>Mycobacterium ulcerans</i> (strain Agy99) OX=362242 GN=ctaB PE=3 SV=1
383	A0QWY2	COXX_MYCS2 Protoheme IX farnesyltransferase OS= <i>Mycolicibacterium smegmatis</i> (strain ATCC 700084 / mc(2)155) OX=246196 GN=ctaB PE=3 SV=1
384	A1T8M8	COXX_MYCVP Protoheme IX farnesyltransferase OS= <i>Mycolicibacterium vanbaalenii</i> (strain DSM 7251 / JCM 13017 / NRRL B-24157 / PYR-1) OX=350058 GN=ctaB PE=3 SV=1
385	A1QRH1	COXX_MYCTF Protoheme IX farnesyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain F11) OX=336982 GN=ctaB1 PE=3 SV=1
386	A5U2F4	COXX_MYCTA Protoheme IX farnesyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain ATCC 25177 / H37Ra) OX=419947 GN=ctaB PE=3 SV=1
387	Q47ND5	COXX_THEFY Protoheme IX farnesyltransferase OS= <i>Thermobifida fusca</i> (strain YX) OX=269800 GN=ctaB PE=3 SV=1
388	A0JWQ8	COXX_ARTS2 Protoheme IX farnesyltransferase OS= <i>Arthrobacter</i> sp. (strain FB24) OX=290399 GN=ctaB PE=3 SV=1
389	B1MC66	COXX_MYCA9 Protoheme IX farnesyltransferase OS= <i>Mycobacteroides abscessus</i> (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543) OX=561007 GN=ctaB PE=3 SV=1
390	A4F9B0	COXX1_SACEN Protoheme IX farnesyltransferase 1 OS= <i>Saccharopolyspora erythraea</i> (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338) OX=405948 GN=ctaB1 PE=3 SV=2
391	A4X9F8	COXX_SALTO Protoheme IX farnesyltransferase OS= <i>Salinispora tropica</i> (strain ATCC BAA-916 / DSM 44818 / CNB-440) OX=369723 GN=ctaB PE=3 SV=2
392	Q83GF8	COXX_TROWT Protoheme IX farnesyltransferase OS= <i>Tropheryma whipplei</i> (strain Twist) OX=203267 GN=ctaB PE=3 SV=1
393	A8KYS6	COXX_FRASN Protoheme IX farnesyltransferase OS= <i>Frankia</i> sp. (strain EAN1pec) OX=298653 GN=ctaB PE=3 SV=1
394	P9WFR7	COXX_MYCTU Protoheme IX farnesyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain ATCC 25618 / H37Rv) OX=83332 GN=ctaB PE=3 SV=1
395	P9WFR6	COXX_MYCTO Protoheme IX farnesyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain CDC 1551 / Oshkosh) OX=83331 GN=ctaB PE=3 SV=1
396	Q829U3	COXX_STRAW Protoheme IX farnesyltransferase OS= <i>Streptomyces avermitilis</i> (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680) OX=227882 GN=ctaB

		PE=3 SV=2
397	A8LW09	COXX_SALAI Protoheme IX farnesyltransferase OS= <i>Salinispora arenicola</i> (strain CNS-205) OX=391037 GN=ctaB PE=3 SV=1
398	Q9XAC2	COXX_STRCO Protoheme IX farnesyltransferase OS= <i>Streptomyces coelicolor</i> (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ctaB PE=3 SV=2
399	A4TC38	COXX_MYCGI Protoheme IX farnesyltransferase OS= <i>Mycolicibacterium gilvum</i> (strain PYR-GCK) OX=350054 GN=ctaB PE=3 SV=1
400	B0REI2	COXX_CLAMS Protoheme IX farnesyltransferase OS= <i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i> (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) OX=31964 GN=ctaB PE=3 SV=1
401	Q8FT77	COXX_COREF Protoheme IX farnesyltransferase OS= <i>Corynebacterium efficiens</i> (strain DSM 44549 / YS-314 / AJ 12310 / JCM 11189 / NBRC 100395) OX=196164 GN=ctaB PE=3 SV=2
402	B1W108	COXX_STRGG Protoheme IX farnesyltransferase OS= <i>Streptomyces griseus</i> subsp. <i>griseus</i> (strain JCM 4626 / NBRC 13350) OX=455632 GN=ctaB PE=3 SV=2
403	Q6NH44	COXX_CORDI Protoheme IX farnesyltransferase OS= <i>Corynebacterium diphtheriae</i> (strain ATCC 700971 / NCTC 13129 / Biotype gravis) OX=257309 GN=ctaB PE=3 SV=2
404	A0LTZ0	COXX_ACIC1 Protoheme IX farnesyltransferase OS= <i>Acidothermus cellulolyticus</i> (strain ATCC 43068 / 11B) OX=351607 GN=ctaB PE=3 SV=1
405	A6WC46	COXX_KINRD Protoheme IX farnesyltransferase OS= <i>Kineococcus radiotolerans</i> (strain ATCC BAA-149 / DSM 14245 / SRS30216) OX=266940 GN=ctaB PE=3 SV=1
406	Q8NQ66	COXX_CORGL Protoheme IX farnesyltransferase OS= <i>Corynebacterium glutamicum</i> (strain ATCC 13032 / DSM 20300 / BCRC 11384 / JCM 1318 / LMG 3730 / NCIMB 10025) OX=196627 GN=ctaB PE=3 SV=1
407	Q9CCN4	COXX_MYCLE Protoheme IX farnesyltransferase OS= <i>Mycobacterium leprae</i> (strain TN) OX=272631 GN=ctaB PE=3 SV=2
408	Q741B3	COXX_MYCPA Protoheme IX farnesyltransferase OS= <i>Mycolicibacterium paratuberculosis</i> (strain ATCC BAA-968 / K-10) OX=262316 GN=ctaB PE=3 SV=1
409	Q0RH20	COXX_FRAAA Protoheme IX farnesyltransferase OS= <i>Frankia alni</i> (strain ACN14a) OX=326424 GN=ctaB PE=3 SV=2
410	Q2JCG7	COXX_FRACC Protoheme IX farnesyltransferase OS= <i>Frankia casuarinae</i> (strain DSM 45818 / CECT 9043 / Ccl3) OX=106370 GN=ctaB PE=3 SV=1
411	Q9Y5Z9	UBIA1_HUMAN UbiA prenyltransferase domain-containing protein 1 OS= <i>Homo sapiens</i> OX=9606 GN=UBIAD1 PE=1 SV=1
412	Q96H96	COQ2_HUMAN 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Homo sapiens</i> OX=9606 GN=COQ2 PE=1 SV=1
413	E7FB98	UBIA1_DANRE UbiA prenyltransferase domain-containing protein 1 OS= <i>Danio rerio</i> OX=7955 GN=ubiad1 PE=1 SV=1
414	P0AGK1	UBIA_ECOLI 4-hydroxybenzoate octaprenyltransferase OS= <i>Escherichia coli</i> (strain K12) OX=83333 GN=ubiA PE=1 SV=1
415	Q96H96	COQ2_HUMAN 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Homo sapiens</i> OX=9606 GN=COQ2 PE=1 SV=1
416	P32378	COQ2_YEAST 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) OX=559292 GN=COQ2 PE=1 SV=1
417	Q9VHS7	COQ2_DROME 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Drosophila melanogaster</i> OX=7227 GN=Coq2 PE=2 SV=1
418	Q93YP7	COQ2_ARATH 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PPT1 PE=2 SV=1
419	Q10252	COQ2_SCHPO 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843) OX=284812 GN=ppt1 PE=1 SV=2
420	Q298G6	COQ2_DROPS 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Drosophila pseudoobscura pseudoobscura</i> OX=46245 GN=Coq2 PE=3 SV=1
421	Q54U71	COQ2_DICDI 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Dictyostelium discoideum</i> OX=44689 GN=coq2 PE=3 SV=1
422	Q66JT7	COQ2_MOUSE 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Mus musculus</i> OX=10090 GN=Coq2 PE=2 SV=2
423	Q8I7J4	COQ2_CAEL 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Caenorhabditis elegans</i> OX=6239 GN=coq-2 PE=3 SV=2
424	Q16QL3	COQ2_AEDAE 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Aedes aegypti</i> OX=7159 GN=coq2 PE=3 SV=1
425	Q499N4	COQ2_RAT 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Rattus norvegicus</i> OX=10116 GN=Coq2 PE=2 SV=1
426	Q2KIQ4	COQ2_BOVIN 4-hydroxybenzoate polyprenyltransferase, mitochondrial OS= <i>Bos taurus</i> OX=9913 GN=COQ2 PE=2 SV=1
427	A1JHN0	HSTC_CHLRE Homogentisate solanesyltransferase, chloroplastic OS= <i>Chlamydomonas reinhardtii</i> OX=3055 GN=HST PE=1 SV=1
428	Q8VWJ1	HPT1_ARATH Homogentisate phytyltransferase 1, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=HPT1 PE=1 SV=1
429	Q1ACB3	HSTC_ARATH Homogentisate solanesyltransferase, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=HST PE=1 SV=1
430	A0A077K8G3	CGT1A_CITLI Coumarin 8-geranyltransferase 1, chloroplastic OS= <i>Citrus limon</i> OX=2708 GN=CIPT1 PE=1 SV=1
431	Q7XB14	HGGT_HORVU Homogentisate geranylgeranyltransferase OS= <i>Hordeum vulgare</i> OX=4513 GN=HGGT PE=1 SV=1
432	P73726	HGGT_SYNY3 Homogentisate phytyltransferase OS= <i>Synechocystis</i> sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=slr1736 PE=1 SV=1
433	A0A077K9K6	CGT1B_CITLI Coumarin 8-geranyltransferase 1b, chloroplastic OS= <i>Citrus limon</i> OX=2708 GN=CI-PT1b PE=1 SV=1
434	Q0DAK7	HGGT_ORYSJ Homogentisate geranylgeranyltransferase, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=HGGT PE=2 SV=2
435	B7FA90	HPT1_ORYSJ Probable homogentisate phytyltransferase 1, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=HPT1 PE=2 SV=1

436	Q0D576	HPT2_ORYSJ Probable homogentisate phytyltransferase 2, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=HPT2 PE=3 SV=2
437	Q7XB13	HGGT_WHEAT Homogentisate geranylgeranyltransferase OS= <i>Triticum aestivum</i> OX=4565 GN=HGGT PE=2 SV=1
438	P9WFR5	DPPRS_MYCTU Decaprenyl-phosphate phosphoribosyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv3806c PE=1 SV=1
439	P9WFR4	DPPRS_MYCTO Decaprenyl-phosphate phosphoribosyltransferase OS= <i>Mycobacterium tuberculosis</i> (strain CDC 1551 / Oshkosh) OX=83331 GN=MT3913 PE=3 SV=1
440	A0R626	DPPRS_MYCS2 Decaprenyl-phosphate phosphoribosyltransferase OS= <i>Mycobacterium smegmatis</i> (strain ATCC 700084 / mc(2)155) OX=246196 GN=MSMEG_6401 PE=3 SV=1
441	Q8NLQ9	DPPRS_CORGL Decaprenyl-phosphate phosphoribosyltransferase OS= <i>Corynebacterium glutamicum</i> (strain ATCC 13032 / DSM 20300 / BCRC 11384 / JCM 1318 / LMG 3730 / NCIMB 10025) OX=196627 GN=cg3189 PE=3 SV=1
442	Q5W6H5	CHLG_ORYSJ Chlorophyll synthase, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CHLG PE=2 SV=1
443	Q9M3W5	CHLG_AVESA Chlorophyll synthase, chloroplastic OS= <i>Avena sativa</i> OX=4498 GN=CHLG PE=1 SV=1
444	Q38833	CHLG_ARATH Chlorophyll synthase, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CHLG PE=2 SV=1
445	A4F5C0	A4F5C0_STIAU Prenyltransferase OS= <i>Stigmatella aurantiaca</i> OX=41 GN=auaA PE=4 SV=1

* Accession numbers/ IDs are taken from PATRIC database (1-114) and UniProt database (115-445).

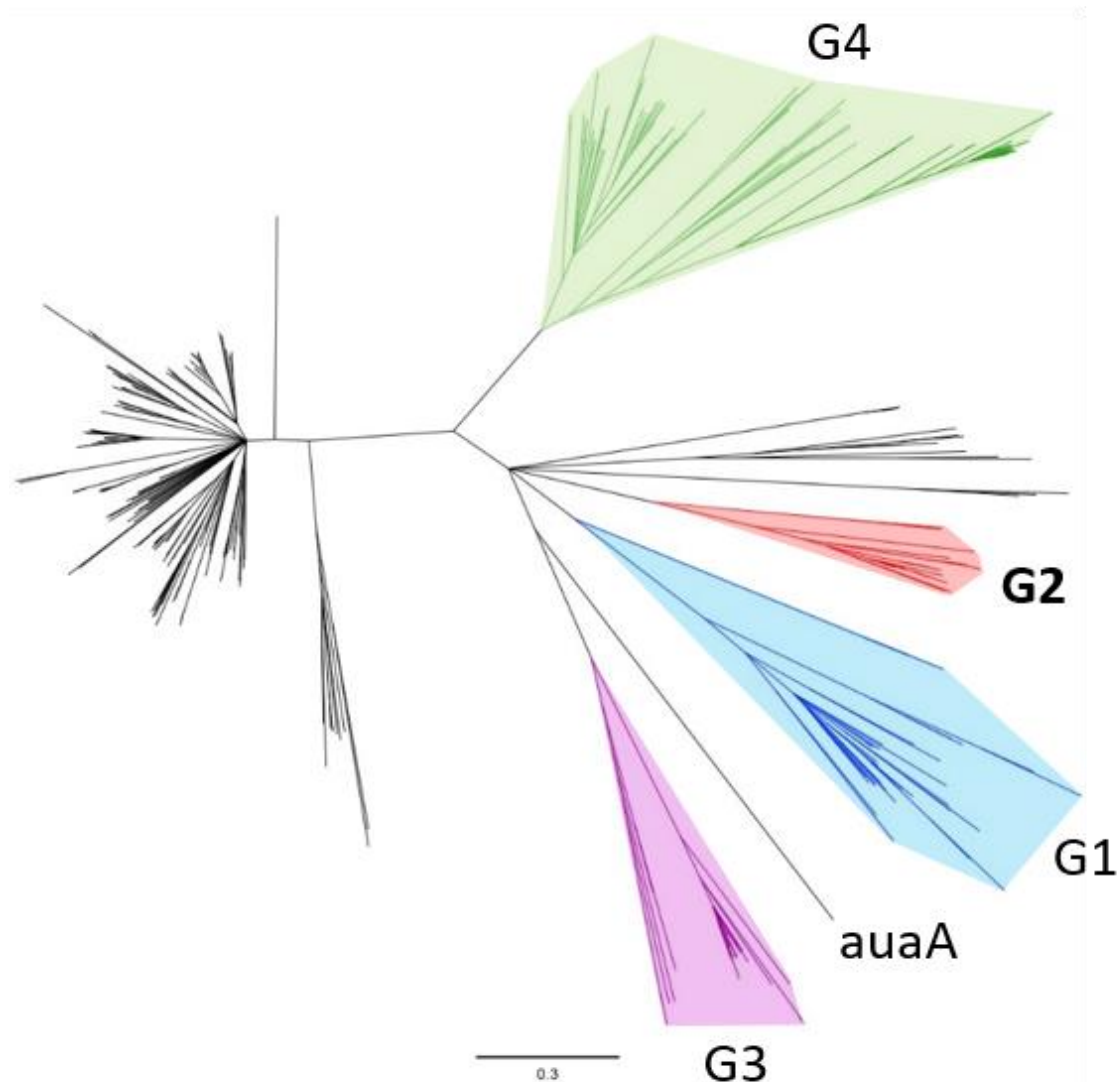


Figure S1: Phylogenetic tree of Ptases from marine Flavobacteria, *Sacharomonospora* and Uniprot database. G1: 1,4-dihydroxy-2-naphthoate polyprenyltransferase (blue), G2: UbiA-like PTases (red), G3: (S)-2,3-di-O-geranylgeranylglyceryl phosphate synthase (purple), G4: Protoheme IX farnesyltransferase (green). Phylogenetic tree was constructed using clustal omega multiple alignment and neighbor-joining method. 500 replicates were used for bootstrap resampling method.

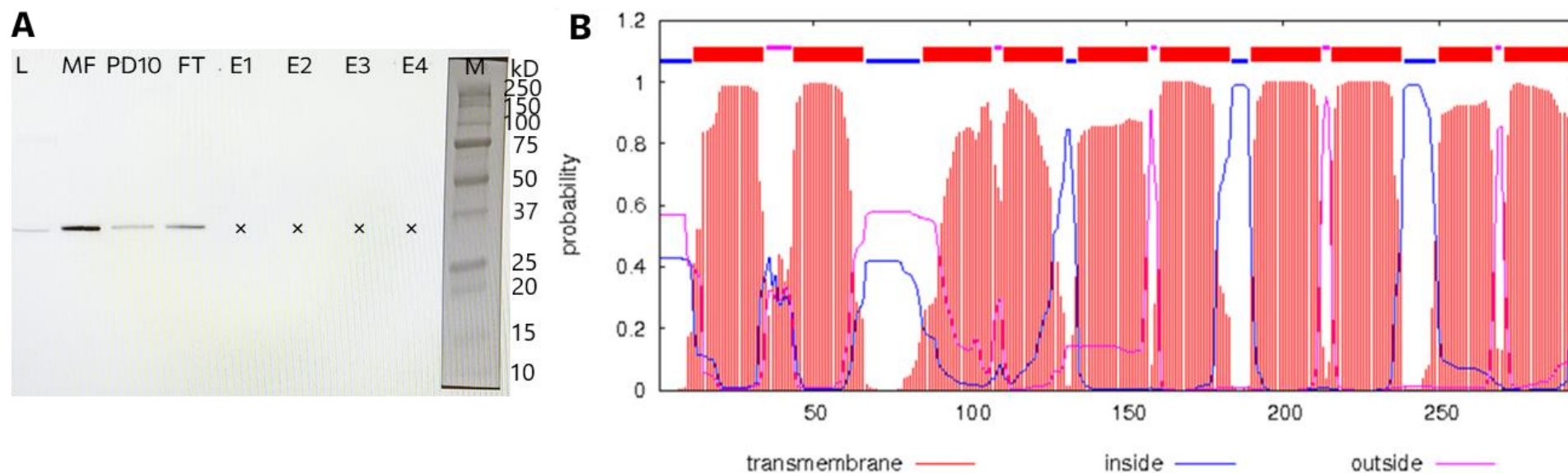


Figure S2: A) Heterologous expression of G2 UbiA-297 of *Maribacter* sp. MS6 in *E. coli*. Lanes from left to right: Crude lysate (L), membrane fraction (MF), PD10 column flow through (PD10), NiNTA flow through (FT), NiNTA elution1- 100 mM imidazole (E1), NiNTA elution 2-150 mM imidazole (E2), NiNTA elution3- 200 mM imidazole (E3), NiNTA elution4- 300 mM imidazole (E4), Biorad all blue protein marker (M) and size indication of marker in kD. B) TMHMM posterior probabilities for G2 UbiA-297 of *Maribacter* sp. MS6.

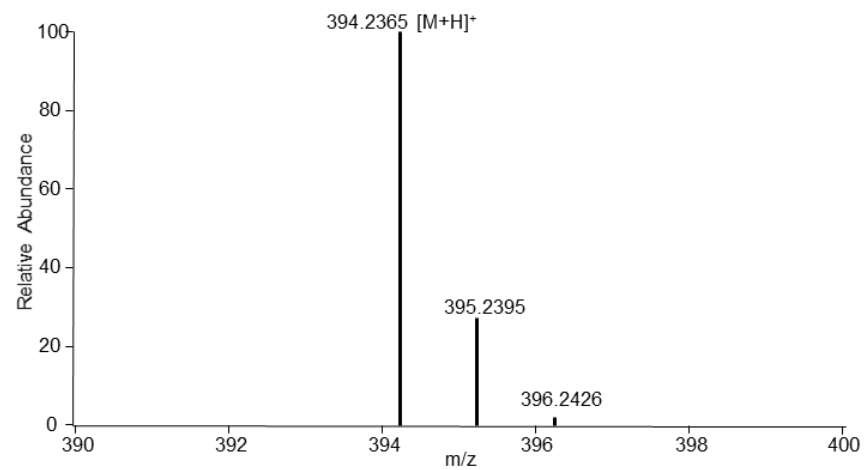
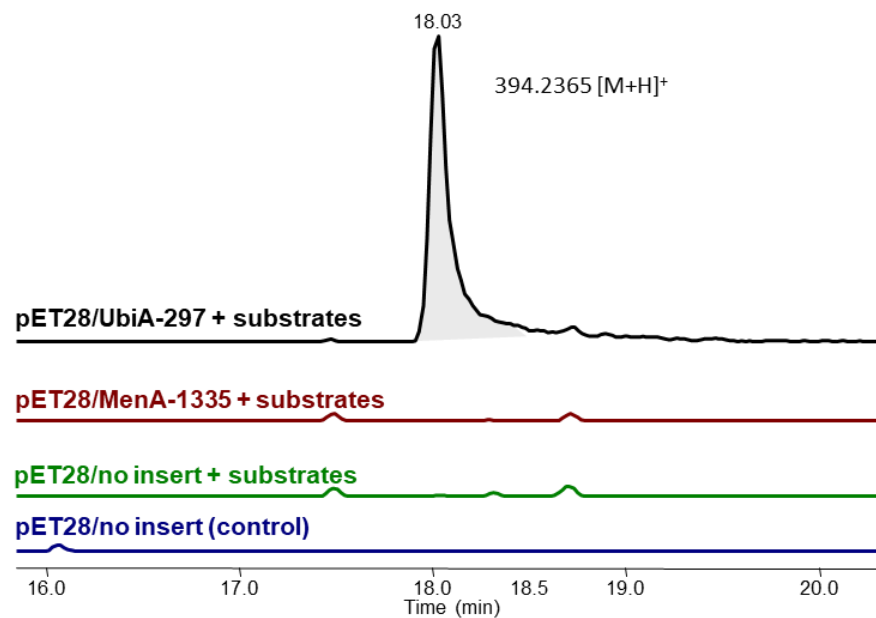


Figure S3: Extracted ion chromatogram (EIC for m/z 378.2428) for the in vivo assay extracts of UbiA-297 using 8-HQA and FPP as substrates and HRMS of product peak at RT 18.03 min.

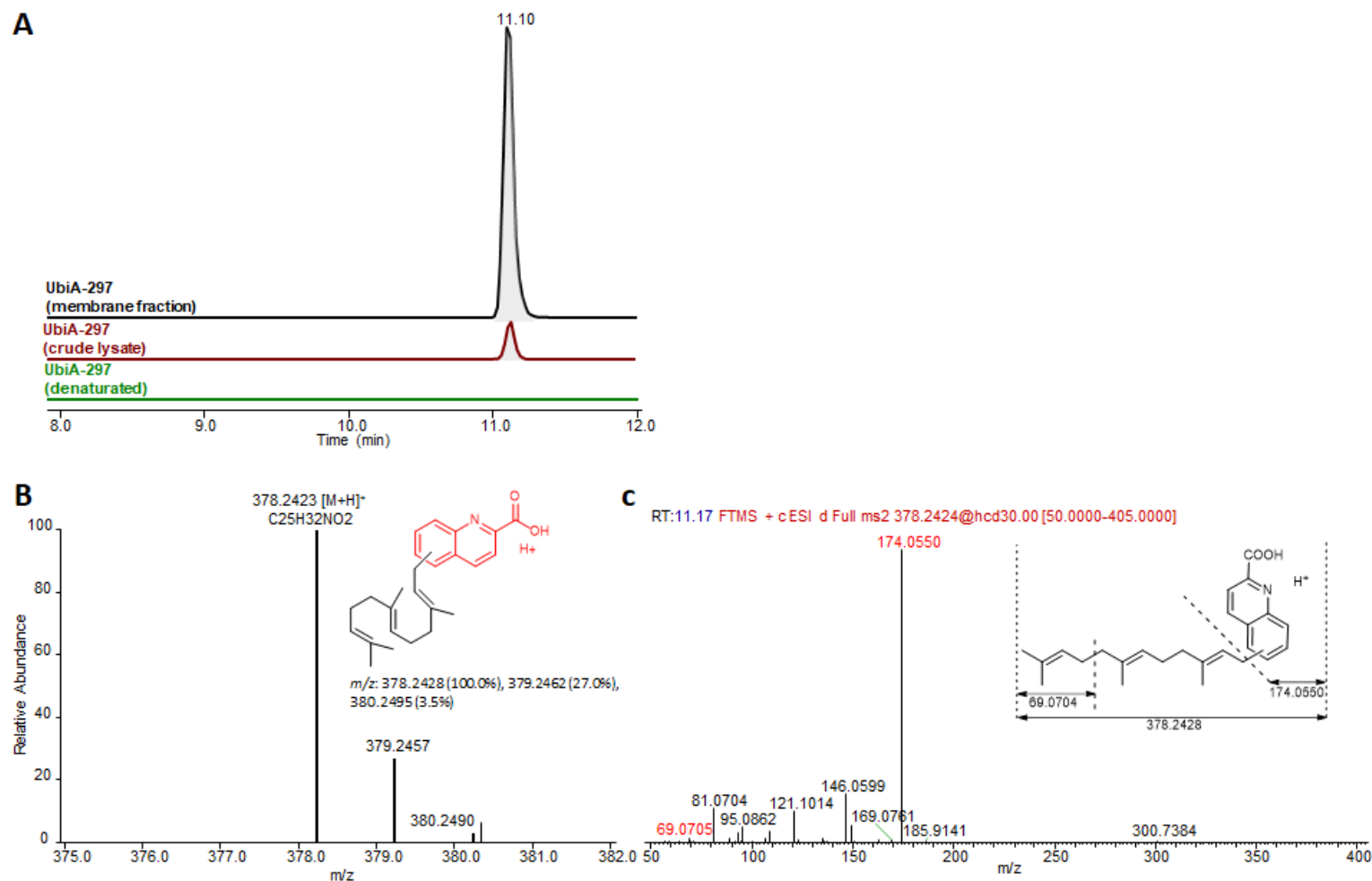


Figure S4: HRMS/MS analysis of the *in vitro* assays using quinaldic acid and FPP as substrates (short gradient, 15 min run). A) Extracted ion chromatogram (EIC for m/z 378.2428) for the assay extracts of UbiA-297 membrane fraction, crude protein lysate, and denaturated membrane fraction. Fixed ion intensity scale (1.05×10^7) was applied to all chromatograms; B) MS-spectrum of the peak at 11.10 min from the membrane fraction assay of UbiA-297; C) MS/MS fragmentation of prenylated product at m/z 378.2424. (Putative fragmentation pattern of farnesylated quinaldic acid is depicted).

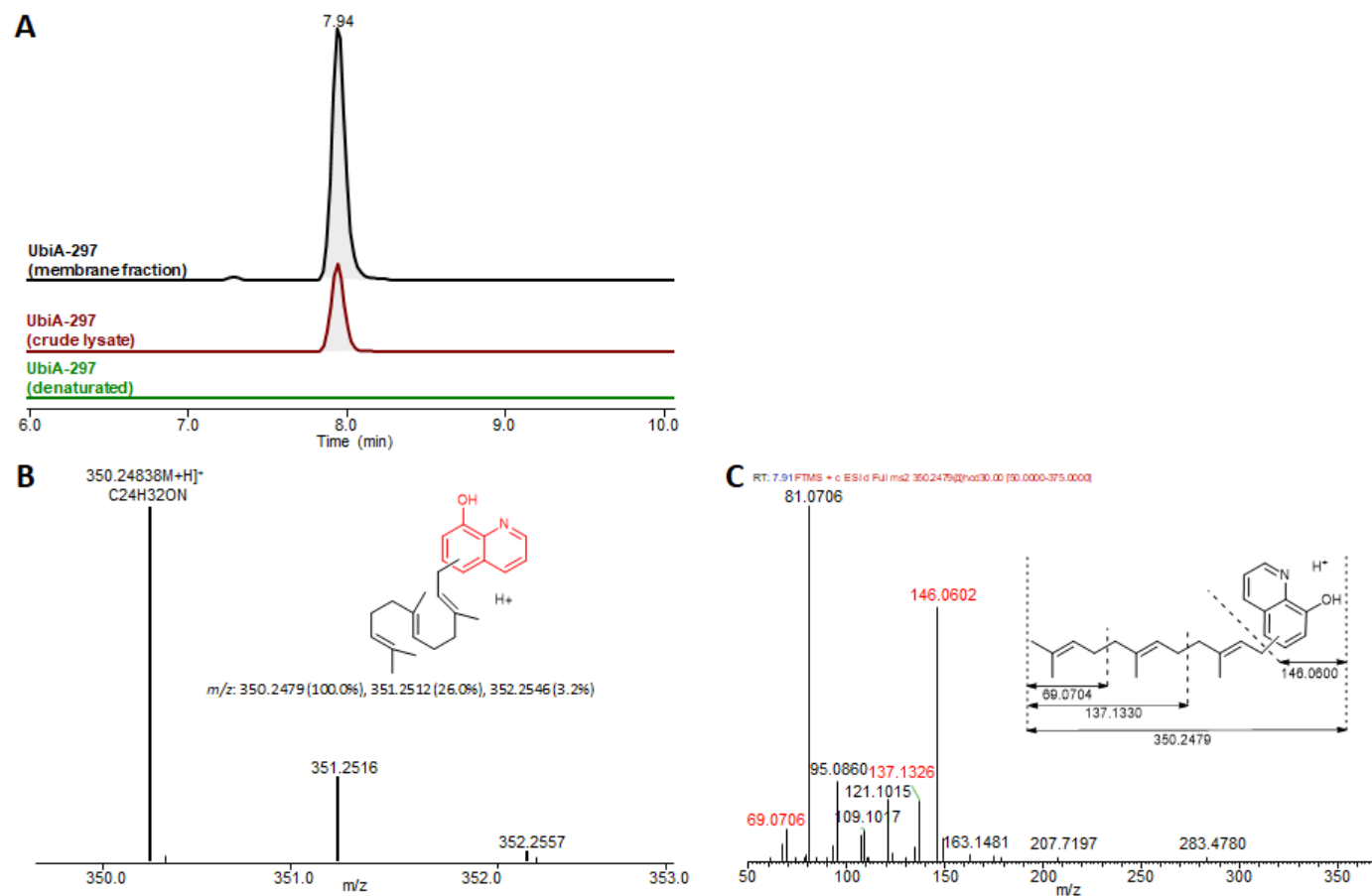


Figure S5: HRMS/MS analysis of the *in vitro* assays using 8-hydroxyquinoline and FPP as substrates (short gradient, 15 min run). A) Extracted ion chromatogram (EIC for *m/z* 350.2479) for the assay extracts of UbiA-297 membrane fraction, crude protein lysate, and denaturated membrane fraction. Fixed ion intensity scale (2.82E6) was applied to all chromatograms; B) MS-spectrum of the peak at 11.10 min from the membrane fraction assay of UbiA-297; C) MS/MS fragmentation of prenylated product at *m/z* 350.2479. (Putative fragmentation pattern of farnesylated 8-hydroxyquinoline is depicted).

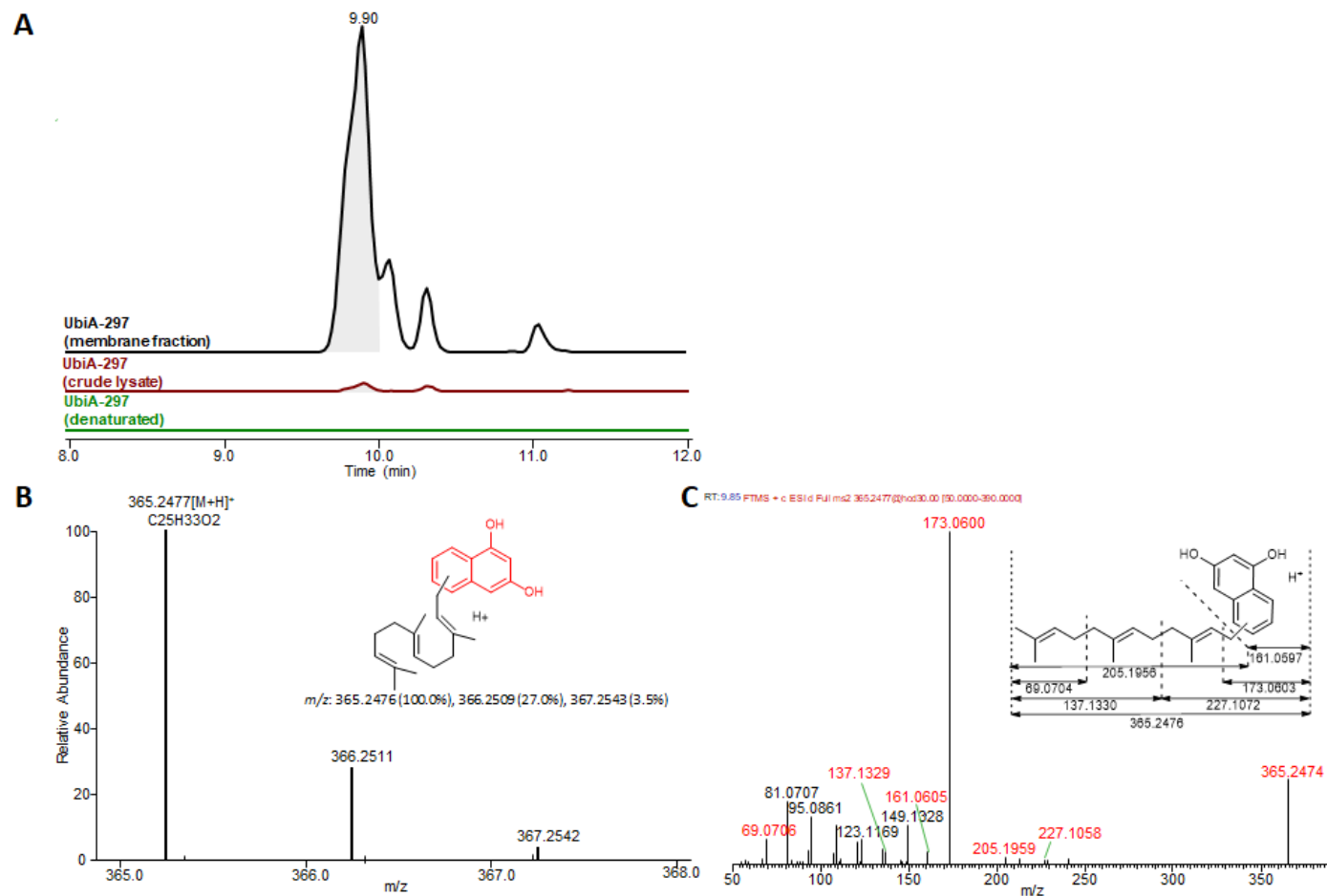


Figure S6: HRMS/MS analysis of the in vitro assays using 1,3-dihydroxynaphtalene and FPP as substrates (short gradient, 15 min run). A) Extracted ion chromatogram (EIC for m/z 365.2476) for the assay extracts of UbiA-297 membrane fraction, crude protein lysate, and denaturated membrane fraction. Fixed ion intensity scale (2.05×10^6) was applied to all chromatograms; B) MS-spectrum of the peak at 11.10 min from the membrane fraction assay of UbiA-297; C) MS/MS fragmentation of prenylated product at m/z 365.2474. (Putative fragmentation pattern of farnesylated 1,3-dihydroxynaphtalene is depicted).

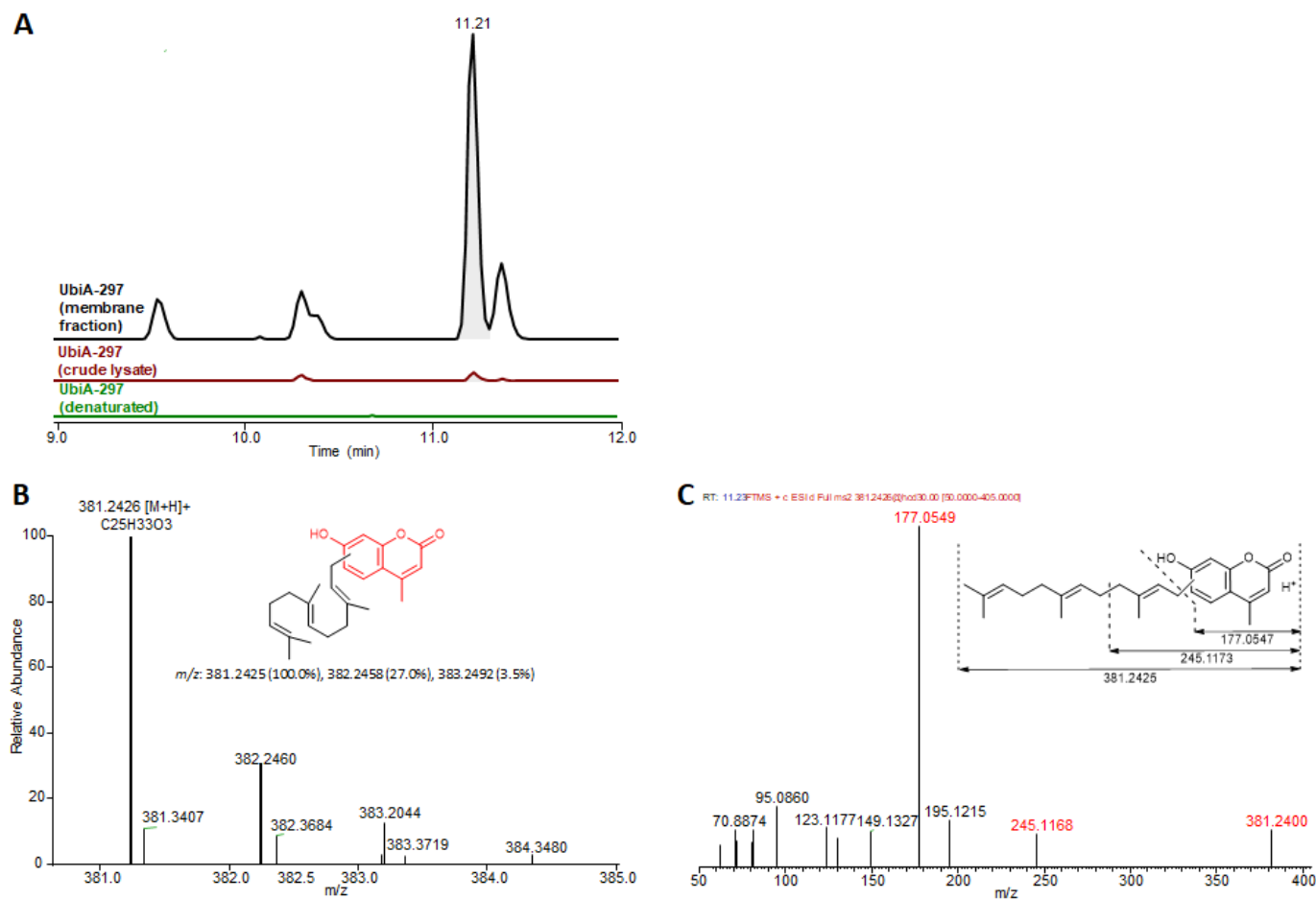


Figure S7: HRMS/MS analysis of the *in vitro* assays using 4-methylumbelliferone and FPP as substrates (short gradient, 15 min run). A) Extracted ion chromatogram (EIC for m/z 381.2425) for the assay extracts of UbiA-297 membrane fraction, crude protein lysate, and denaturated membrane fraction. Fixed ion intensity scale ($7.45E5$) was applied to all chromatograms; B) MS-spectrum of the peak at 11.10 min from the membrane fraction assay of UbiA-297; C) MS/MS fragmentation of prenylated product at m/z 381.2425. (Putative fragmentation pattern of farnesylated 4-methylumbelliferone is depicted).

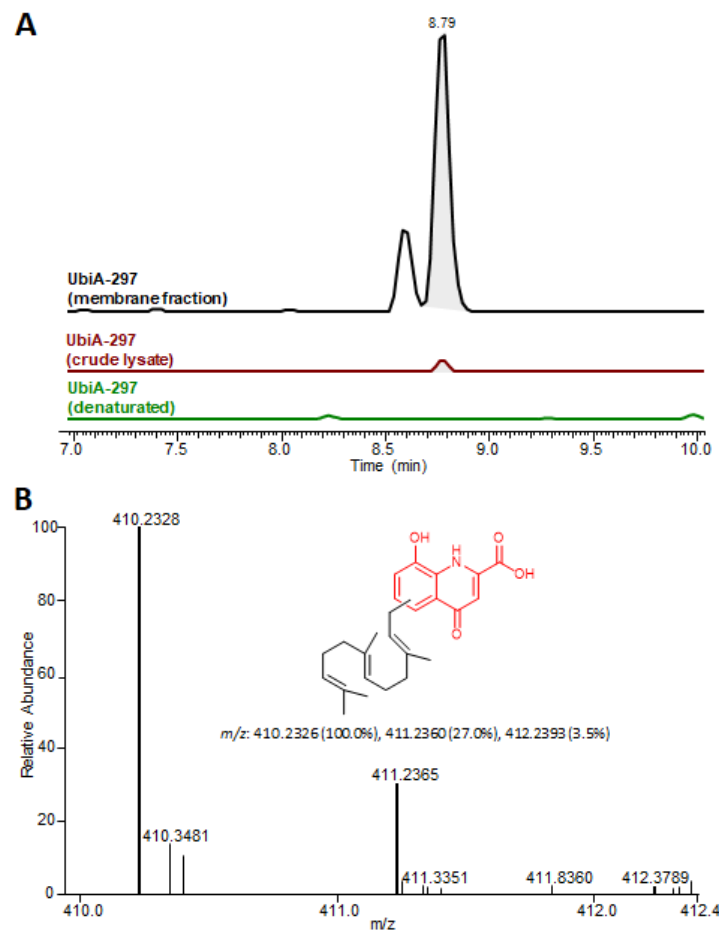


Figure S8: HRMS/MS analysis of the *in vitro* assays using xanthurenic acid and FPP as substrates (short gradient, 15 min run). A) Extracted ion chromatogram (EIC for m/z 410.2326) for the assay extracts of UbiA-297 membrane fraction, crude protein lysate, and denaturated membrane fraction. Fixed ion intensity scale ($3.14E5$) was applied to all chromatograms; B) MS-spectrum of the peak at 11.10 min from the membrane fraction assay of UbiA-297.

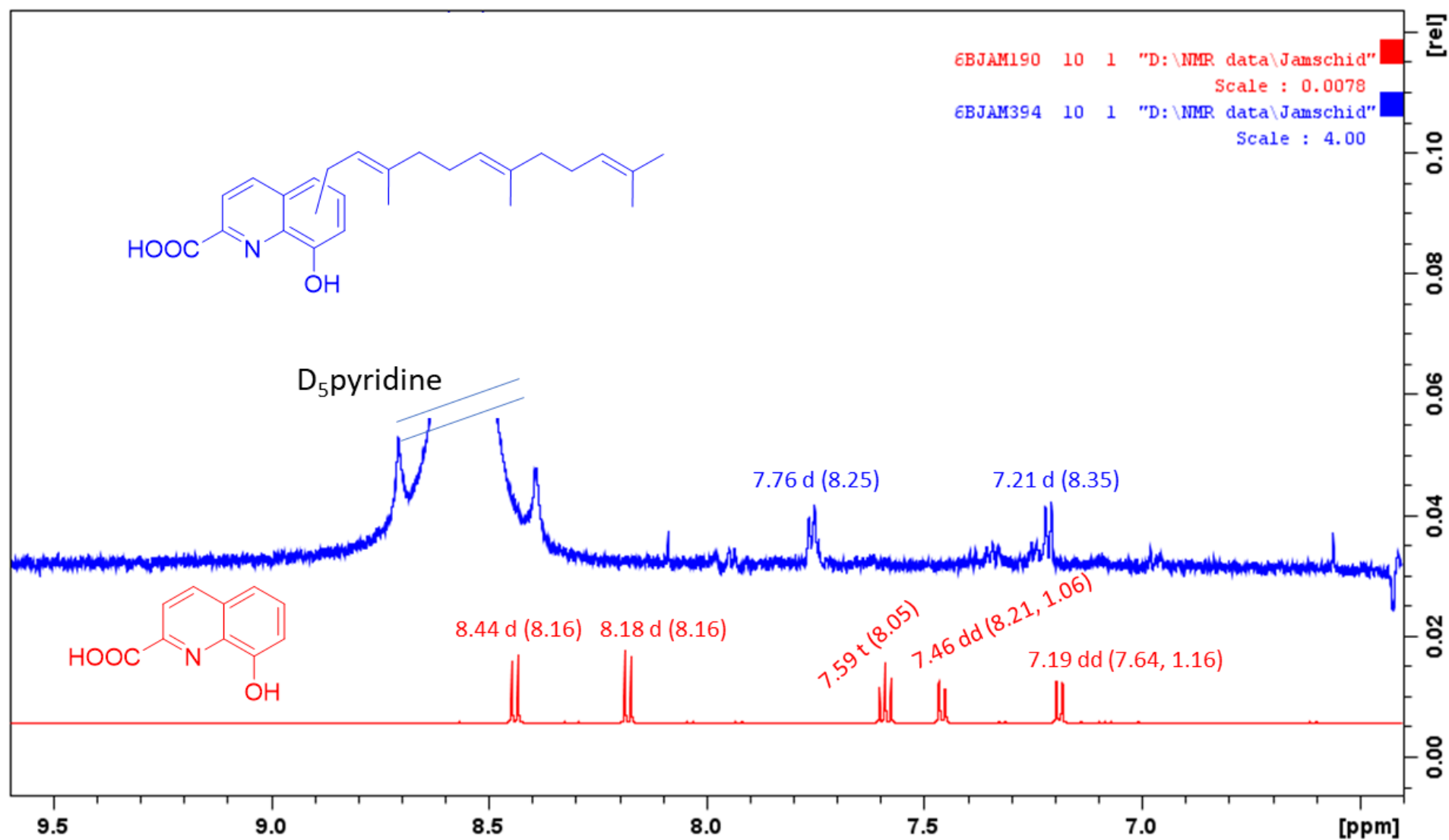


Figure S9: Overlaid ^1H NMR spectra of A) isolated product with m/z 394.2376 (blue), and B) starting material 8-HQA (red), 600 MHz (d_5 -pyridine).