

Supplementary file 6. CDSs for biphenyl, benzoate, catechol and protocatechuate degradative pathways found in the metagenome annotation and their genus affiliation based on blastn.

Contig ID	Start	End	Strand	Size (pb)	Relevant closest relative ^a Organism / % identity / % coverage	Genus assignment
Biphenyl to benzoate						
<i>bphA</i> – Biphenyl 2,3-dioxygenase (EC. 1.14.12.18) ^b						
1820	3,271	4,072	+	802 ^c	<i>Rhodococcus</i> sp. HA99 / 99% / 100% ^d	<i>Rhodococcus</i>
3198	1	546	+	546 ^c	<i>Rhodococcus</i> sp. HA99 / 99% / 100% ^d	<i>Rhodococcus</i>
5928	15	1385	+	1,371	<i>Rhodococcus jostii</i> RHA1 / 99% / 100%	<i>Rhodococcus</i>
754	2,959	4,365	+	1407	<i>Rhodococcus opacus</i> B4 / 99% / 100%	<i>Rhodococcus</i>
<i>bphB</i> – Cis 2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC. 1.3.1.56)						
1820	957	2,264	+	1,308	<i>Rhodococcus</i> sp. HA99 / 99% / 100%	<i>Rhodococcus</i>
754	5,179	5,994	+	816	<i>Rhodococcus opacus</i> B4 / 99% / 100%	<i>Rhodococcus</i>
<i>bphC</i> – Biphenyl-2,3-diol 1,2-dioxygenase (EC 1.13.11.59)						
1820	2,294	3,136	+	843	<i>Rhodococcus</i> sp. HA99 / 99% / 100 %	<i>Rhodococcus</i>
754	6,216	7,202	+	987	<i>Rhodococcus opacus</i> B4 / 99% / 100%	<i>Rhodococcus</i>
6144	68	985	+	918	<i>Rhodococcus jostii</i> RHA1 / 100% / 100%	<i>Rhodococcus</i>
<i>bphD</i> – 2,6-dioxo-6-phenylhexa-3-enoate hydrolase (EC. 3.7.1.8)						
11912	491	1103	+	612 ^c	<i>Rhodococcus</i> sp. HA99 / 99% / 100 % ^d	<i>Rhodococcus</i>
3155	1	134	+	134 ^c	<i>Rhodococcus</i> sp. HA99 / 99% / 100 % ^d	<i>Rhodococcus</i>
6144	1108	1879	+	772 ^c	<i>Rhodococcus jostii</i> RHA1 / 99% / 100% ^d	<i>Rhodococcus</i>
4498	50	135	+	86 ^c	<i>Rhodococcus jostii</i> RHA1 / 99% / 100% ^d	<i>Rhodococcus</i>
<i>bphE</i> – 2-hydroxypenta-2,4-dienoate hydratase (EC. 4.2.1.80)						
4498	1,404	2,207	-	804	<i>Rhodococcus jostii</i> RHA1 / 99% / 100%	<i>Rhodococcus</i>
<i>bphF</i> – 4-hydroxy-2-oxovalerate aldolase (EC. 4.1.3.39)						
4498	622	1,392	-	771	<i>Rhodococcus jostii</i> RHA1 / 99% / 99%	<i>Rhodococcus</i>
Benzoate to catechol						
<i>benA</i> – Benzoate 1,2-dioxygenase (EC. 1.14.12.10) ^b						
111	18,548	19,975	+	1,428	<i>Bordetella</i> sp. SCN 67-23 / 98% / 100% ^e	<i>Bordetella</i>
9	422,588	423,931	+	1,344	<i>Bordetella</i> sp. SCN 67-23 / 97% / 99% ^e	<i>Bordetella</i>
6	410,402	411,718	+	1,317	<i>Bordetella</i> sp. SCN 67-23 / 90% / 99% ^e	<i>Bordetella</i>
5	179,942	181,222	-	1,281	<i>Bordetella</i> sp. SCN 67-23 / 98% / 100% ^e	<i>Bordetella</i>
15068	500	820	-	321 ^c	<i>Rhodococcus opacus</i> 1CP / 96% / 93%	<i>Rhodococcus</i>
236	9,268	10,659	-	1,392	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
112	37,082	38,440	+	1,359	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
9887	75	704	+	630 ^c	<i>Pseudomonas</i> sp. DRA535 / 97% / 100%	<i>Pseudomonas</i>
2919	1,784	3,163	+	1,380	<i>Pseudomonas fluorescens</i> FW300-N2E3 / 90% / 100%	<i>Pseudomonas</i>
2676	397	1,785	+	1,389	<i>Pseudomonas umsogensis</i> BS3657 / 91% / 100%	<i>Pseudomonas</i>
<i>benD</i> – 1,6-dihydroxycyclohexa-2,4-diene-1-carboxyate dehydrogenase (EC. 1.3.1.25)						
112	40,122	40,895	+	774	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
12981	491	958	-	468 ^c	<i>Pseudomonas</i> sp. DRA525 / 97% / 99%	<i>Pseudomonas</i>
2301	7	801	+	795	<i>Rhodococcus opacus</i> B4 / 84% / 96%	<i>Rhodococcus</i>
2883	1,760	2,533	-	774	<i>Pseudomonas chlororaphis</i> PCL 1606 / 87% / 199%	<i>Pseudomonas</i>
9	424,440	425,438	+	998	<i>Bordetella</i> sp. SCN 67-23 / 93% / 100% ^e	<i>Bordetella</i>
Catechol ortho-cleavage						
<i>catA</i> – Catechol 1,2-dioxygenase (EC. 1.13.11.1)						
608	4,243	5,178	+	936	<i>Achromobacter</i> sp. MFA1 R4 / 79% / 97%	<i>Achromobacter</i>
17	153,528	154,463	+	936	<i>Bordetella holmesii</i> H903 / 86% / 100%	<i>Bordetella</i>

2	476,792	477,661	-	870	<i>Bordetella</i> sp. SCN 67-23 / 98% / 100% ^e	<i>Bordetella</i>
4	328,457	329,407	-	951	<i>Variovorax</i> sp. YR216 / 78% / 99% ^e	<i>Variovorax</i>
1395	129	977	+	849	<i>Rhodococcus opacus</i> 1CP / 87% / 100%	<i>Rhodococcus</i>
7047	453	1,349	+	897	<i>Rhodococcus jostii</i> RHA1 (pRHL1) / 97% / 100%	<i>Rhodococcus</i>
24924	41	520	+	480 ^c	<i>Rhodococcus opacus</i> 1CP / 95% / 100%	<i>Rhodococcus</i>
10936	190	864	+	675	<i>Rhodococcus opacus</i> 1CP / 94% / 99%	<i>Rhodococcus</i>
61	104,733	105,398	+	666	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
36074	104	349	-	246 ^c	<i>Pseudomonas putida</i> KF715 / 99% / 100%	<i>Pseudomonas</i>
2919	16	615	+	600	<i>Pseudomonas fluorescens</i> FW300-N2E3 / 88% / 100%	<i>Pseudomonas</i>
20	16,531	17,400	+	870	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 100% / 100%	<i>Pseudomonas</i>
1495	1,421	2,350	-	930	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
catB – Muconate cycloisomerase (EC. 5.5.1.1)						
111	2,111	3,181	+	1,071	<i>Cupriavidus taiwanensis</i> LMG19424 / 97% / 100%	<i>Cupriavidus</i>
1495	2,712	3,920	-	1,209	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
14	13,969	15,111	+	1,143	<i>Achromobacter xylosoxidans</i> NH44784-1996 / 86% / 96%	<i>Achromobacter</i>
17	152,301	153,455	+	1,155	<i>Bordetella holmesii</i> H903 / 84% / 97%	<i>Bordetella</i>
18	56,392	57,504	+	1,113	<i>Pseudomonas taeanensis</i> MS-3 / 91% / 100% ^e	<i>Pseudomonas</i>
19746	44	697	-	654 ^c	<i>Rhodococcus opacus</i> 1CP / 88% / 99%	<i>Rhodococcus</i>
21	215,967	217,127	+	1,161	<i>Bordetella</i> sp. SCN 67-23 / 97% / 100% ^e	<i>Bordetella</i>
26	38,750	40,018	+	1,269	<i>Achromobacter ruhlandii</i> SCCH3:ACH 33-1365 / 79% / 86%	<i>Achromobacter</i>
2945	1,180	2,415	+	1,236	<i>Pseudomonas chlororaphis</i> DSM 21509 / 89% / 97%	<i>Pseudomonas</i>
4	156,847	157,971	+	1,125	<i>Achromobacter xylosoxidans</i> NCTC10807 / 82% / 95%	<i>Achromobacter</i>
4	266,785	267,915	-	1,131	<i>Bordetella</i> sp. SCN 67-23 / 96% / 100% ^e	<i>Bordetella</i>
608	3,129	4,190	+	1,062	<i>Bordetella trematum</i> H044680328 / 79% / 98%	<i>Bordetella</i>
6862	1,097	1,615	-	519 ^c	<i>Rhodococcus opacus</i> PD630 / 95% / 99%	<i>Rhodococcus</i>
6	392,792	393,904	-	1,113	<i>Bordetella</i> sp. SCN 67-23 / 96% / 100% ^e	<i>Bordetella</i>
7340	2	790	+	789 ^c	<i>Pseudomonas</i> sp. JY-Q / 96% / 100%	<i>Pseudomonas</i>
82	50,297	51,538	-	1,242	<i>Achromobacter xylosoxidans</i> FDAARGOS / 89% / 90%	<i>Achromobacter</i>
catC – Muconolactone Delta-isomerase (EC. 5.3.3.4)						
1495	2,393	2,683	-	291	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
1	498,412	498,687	-	276	<i>Achromobacter insolitus</i> DSM 23807 / 92% / 100%	<i>Achromobacter</i>
2945	2,426	2,716	+	291	<i>Pseudomonas chlororaphis</i> 189 / 92% / 100%	<i>Pseudomonas</i>
4	157,997	158,275	+	279	<i>Cupriavidus</i> sp. USMAA2-4 / 84% / 75%	<i>Cupriavidus</i>
547	5,965	6,240	-	276	<i>Achromobacter</i> sp. MFA1 R4 / 86% / 99%	<i>Achromobacter</i>
58	86,144	86,419	-	276	<i>Achromobacter denitrificans</i> PR1 / 83% / 99%	<i>Achromobacter</i>
5	390,270	391,439	+	1,179	<i>Cupriavidus basilensis</i> 4G11 / 84% / 99%	<i>Cupriavidus</i>
7340	812	1,102	+	291	<i>Pseudomonas putida</i> KF715 / 100% / 100%	<i>Pseudomonas</i>
catD – 3-oxoadipate enol-lactonase (EC. 3.1.1.24)						
100	19,900	20,745	+	846	<i>Bordetella</i> sp. SCN 67-23 / 93% / 100% ^e	<i>Bordetella</i>
107	1,057	1,866	-	810	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
11202	423	1,106	+	684	-	Unassigned
112	50,528	51,316	+	788	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 100% / 100%	<i>Pseudomonas</i>
117	45,268	46,077	+	810	<i>Variovorax soli</i> NBRC 106424 / 78% / 99% ^e	<i>Variovorax</i>
11	152,279	153,079	+	801	<i>Bordetella</i> sp. SCN 67-23 / 88% / 100% ^e	<i>Bordetella</i>
12	270,910	271,716	-	807	-	Unassigned
18398	312	827	-	516 ^c	<i>Pseudomonas fluorescens</i> Pf29Arp / 90% / 100%	<i>Pseudomonas</i>
1731	330	1,400	+	1,070	<i>Microbacterium chokolatum</i> SIT 101 / 80% / 94%	<i>Microbacterium</i>
18921	26	325	+	300 ^c	<i>Pseudomonas frederiksbergensis</i> ERDD5:01 / 90% / 100%	<i>Pseudomonas</i>
1	497,270	498,049	-	780	<i>Achromobacter xylosoxidans</i> FDAARGOS / 89% / 100%	<i>Achromobacter</i>

1	699,603	700,475	-	873	<i>Achromobacter xylosoxidans</i> A8 / 76% / 81%	<i>Achromobacter</i>
203	25,892	26,659	-	768	<i>Bordetella</i> genomosp. 4 AU14378 / 88% / 100% ^e	<i>Bordetella</i>
20581	328	636	-	309 ^c	<i>Pseudomonas</i> sp. DRA525 / 97% / 100%	<i>Pseudomonas</i>
2165	3,073	3,906	+	834	<i>Pseudomonas</i> sp. GR 6-02 / 93% / 100%	<i>Pseudomonas</i>
21	262,738	263,472	+	735	<i>Bordetella</i> sp. SCN 67-23 / 95% / 98% ^e	<i>Bordetella</i>
2272	2,494	3,294	+	801	-	Unassigned
25865	7	480	+	474 ^c	<i>Pseudomonas putida</i> KF715 / 98% / 100%	<i>Pseudomonas</i>
265	15,499	16,308	-	810	<i>Bordetella</i> genomosp. 4 AU9919 / 94% / 100% ^e	<i>Bordetella</i>
2922	2,160	3,026	+	867	-	Unassigned
2	681,491	682,390	+	900	<i>Bordetella</i> sp. SCN 67-23 / 97% / 100% ^e	<i>Bordetella</i>
315	10,086	10,889	+	804	<i>Microbacterium</i> sp. 69-10 / 88% / 100% ^e	<i>Microbacterium</i>
340	10,454	11,155	+	702	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
397	3,102	4,031	+	930	<i>Pseudomonas lini</i> BS3782 / 79% / 54%	<i>Pseudomonas</i>
4295	1,382	2,164	+	783	<i>Rhodococcus opacus</i> 1CP / 87% / 100%	<i>Rhodococcus</i>
4345	400	1,101	+	702	<i>Stenotrophomonas maltophilia</i> NCTC10257 / 92% / 99%	<i>Stenotrophomonas</i>
4	394,540	395,382	-	843	-	Unassigned
4	473,906	474,721	-	816	<i>Bordetella</i> sp. SCN 67-23 / 96 % 100% ^e	<i>Bordetella</i>
547	4,809	5,588	-	780	<i>Bordetella petrii</i> DSM 12804 / 82% / 99%	<i>Bordetella</i>
58	85,021	85,800	-	780	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
5938	1,430	1,792	+	363 ^c	<i>Cupriavidus metallidurans</i> CH34 / 97% / 100%	<i>Cupriavidus</i>
599	1,455	2,246	-	792	<i>Pseudomonas fluorescens</i> FW300-N2E2 / 83% / 99%	<i>Pseudomonas</i>
5	636,912	637,706	-	795	-	Unassigned
6462	342	1,184	-	843	<i>Cupriavidus nantongensis</i> X1 / 95% / 100%	<i>Cupriavidus</i>
6743	986	1,750	-	765	<i>Pseudomonas brassicacearum</i> DF41 / 89% / 100%	<i>Pseudomonas</i>
6	524,175	524,915	+	741	-	Unassigned
70	89,968	90,801	-	834	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
713	5,786	6,613	+	828	<i>Rhodococcus wratislaviensis</i> IFP 2016 / 98% / 98% ^e	<i>Rhodococcus</i>
7975	1,003	1,506	-	504 ^c	<i>Rhodococcus opacus</i> 1CP / 93% / 100%	<i>Rhodococcus</i>
7	490,999	491,790	+	792	<i>Bordetella</i> sp. SCN 67-23 / 89% / 100% ^e	<i>Bordetella</i>
809	3,085	3,828	+	744	<i>Stenotrophomonas maltophilia</i> ISMMS3 / 98% / 100%	<i>Stenotrophomonas</i>
9	79,595	80,371	+	777	-	Unassigned
9	354,172	354,876	-	705	<i>Bordetella</i> sp. SCN 67-23 / 92% / 99% ^e	<i>Bordetella</i>
9	356,411	357,214	-	804	<i>Bordetella</i> sp. SCN 67-23 / 96% / 100% ^e	<i>Bordetella</i>
9	476,780	477,514	+	735	-	Unassigned
9	499,071	500,237	-	1,167	<i>Bordetella</i> sp. H567 / 71% / 95%	<i>Bordetella</i>
catJ – 3-oxoadipate CoA-transferase (EC. 2.8.3.6)^b						
10	18,572	19,408	+	837	<i>Bordetella petrii</i> DSM 12804 / 99% / 100%	<i>Bordetella</i>
112	46,192	47,040	+	849	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
1218	3,591	4,190	-	600	<i>Bordetella</i> genomosp. 4 AU9919 / 96% / 100% ^e	<i>Bordetella</i>
13	200,003	200,683	+	681	<i>Achromobacter denitrificans</i> PR1 / 87% / 100%	<i>Achromobacter</i>
14	307,980	308,660	+	681	<i>Achromobacter xylosoxidans</i> C54 / 86% / 93%	<i>Achromobacter</i>
15	111,829	112,500	+	672	<i>Cupriavidus</i> sp. USMAA1020 / 76% / 87%	<i>Cupriavidus</i>
181	12,905	13,597	-	693	<i>Bordetella</i> genomosp. 4 AU14378 / 99% / 100% ^e	<i>Bordetella</i>
1	499,344	500,033	-	690	<i>Achromobacter denitrificans</i> PR1 / 95% / 100%	<i>Achromobacter</i>
21008	117	359	+	243 ^c	<i>Cupriavidus taiwanensis</i> STM6070 / 87% / 98% ^e	<i>Cupriavidus</i>
2873	2,331	3,026	-	696	<i>Pseudomonas putida</i> H8234 / 99% / 100%	<i>Pseudomonas</i>
2939	2,324	3,202	-	879	<i>Pseudomonas umsongensis</i> BS3657 / 89% / 100%	<i>Pseudomonas</i>
29	97,821	98,486	+	666	<i>Achromobacter denitrificans</i> PR1 / 89% / 99%	<i>Achromobacter</i>
31	106,759	107,439	-	681	<i>Bordetella</i> genomosp. 4 AU9919 / 99% / 100% ^e	<i>Bordetella</i>

31	167,658	168,491	-	834	<i>Bordetella</i> genomsp. 4 AU9919 / 98% / 100% ^e	<i>Bordetella</i>
33	58,434	59,114	-	681	<i>Achromobacter xylosoxidans</i> FDAARGOS / 88% / 100%	<i>Achromobacter</i>
3	424,890	425,723	-	834	<i>Achromobacter</i> sp. MFA1 R4 / 86% / 100%	<i>Achromobacter</i>
547	6,930	7,601	-	672	<i>Achromobacter insolitus</i> DSM 23807 / 86% / 96%	<i>Achromobacter</i>
58	87,080	87,769	-	690	<i>Achromobacter xylosoxidans</i> FDAARGOS / 81% / 96%	<i>Achromobacter</i>
599	7,166	7,981	-	816	<i>Pseudomonas antarctica</i> PAMC 27494 / 89% / 100%	<i>Pseudomonas</i>
75	70,378	71,259	+	882	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
7	247,488	248,177	+	690	<i>Bordetella</i> genomsp. 13 AU7206 / 82% / 82%	<i>Bordetella</i>
catF – 3-oxoadipyl-CoA thiolase (EC. 2.3.1.174)						
112	47,822	49,027	+	1,206	<i>Pseudomonas</i> sp. A46 / 100% / 100% ^e	<i>Pseudomonas</i>
161	11,915	13,120	+	1,206	<i>Achromobacter denitrificans</i> PR1 / 83% / 100%	<i>Bordetella</i>
185	20,335	21,555	+	1,221	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 100% / 100%	<i>Pseudomonas</i>
1959	1,913	3,124	-	1,212	<i>Pseudomonas fluorescens</i> NCIMB 11764 / 87% / 99%	<i>Pseudomonas</i>
23560	21	569	+	549 ^c	<i>Cupriavidus necator</i> NH9 / 96% / 100%	<i>Cupriavidus</i>
3	62,431	63,636	-	1,206	<i>Achromobacter denitrificans</i> PR1 / 91% / 99%	<i>Achromobacter</i>
48	91,275	92,480	-	1,206	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
599	5,185	6,390	-	1,206	<i>Pseudomonas mediterranea</i> DSM 16733 / 87% / 99%	<i>Pseudomonas</i>
7003	20	343	+	324 ^c	<i>Pseudomonas thivervalensis</i> bs3779 / 96% / 100%	<i>Pseudomonas</i>
7	249,942	251,247	+	1,306	<i>Achromobacter xylosoxidans</i> FDAARGOS / 84% / 99%	<i>Achromobacter</i>
Catechol meta-cleavage						
catE – Catechol 2,3-dioxygenase (EC. 1.13.11.2)						
72	59,515	60,456	+	942	<i>Cupriavidus basilensis</i> 4G11 / 80% / 68%	<i>Cupriavidus</i>
4	313,652	314,605	+	954	<i>Variovorax boronicumulans</i> PHE5-4 / 75% / 95% ^e	<i>Variovorax</i>
11300	64	819	+	756 ^c	-	Unassigned
6	35,272	36,216	+	945	<i>Cupriavidus necator</i> N-1 / 77% / 83%	<i>Cupriavidus</i>
9	84,727	85,671	+	945	<i>Variovorax</i> sp. HW608 / 78% / 86%	<i>Variovorax</i>
HMSH – 2-hydroxy-muconate-6-semialdehyde hydrolase (EC. 3.7.1.9)						
28882	28	351	+	324 ^c	<i>Rhodococcus jostii</i> RHA1 (pRHL2) / 97% / 100%	<i>Rhodococcus</i>
4164	808	1,662	-	855	<i>Stenotrophomonas maltophilia</i> ISMMS3 / 96% / 100%	<i>Stenotrophomonas</i>
4551	649	1,503	-	855	<i>Stenotrophomonas maltophilia</i> ISMMS2 / 99% / 100%	<i>Stenotrophomonas</i>
5	182,597	183,430	-	834	<i>Bordetella</i> sp. SCN 67-23 / 93% / 100% ^e	<i>Bordetella</i>
6	614,076	614,909	+	834	<i>Bordetella</i> sp. SCN 67-23 / 95% / 100% ^e	<i>Bordetella</i>
9	159,463	160,326	-	864	<i>Bordetella</i> sp. SCN 67-23 / 98% / 100% ^e	<i>Bordetella</i>
9	179,065	179,910	+	846	<i>Bordetella</i> sp. SCN 67-23 / 95% / 100% ^e	<i>Bordetella</i>
OEH – 2-oxopent-4-enoate hydratase (EC. 4.2.1.80)						
1040	5,094	5,906	-	813	<i>Pseudomonas</i> sp. TCu-HL1 / 85% / 99%	<i>Pseudomonas</i>
13936	730	957	-	228 ^c	<i>Cupriavidus taiwanensis</i> LMG19424 / 92% / 100%	<i>Cupriavidus</i>
14113	158	376	+	219 ^c	<i>Pseudomonas putida</i> KF715 / 100% / 100%	<i>Pseudomonas</i>
14136	25	810	+	786 ^c	<i>Rhodococcus opacus</i> B4 / 89% / 100%	<i>Rhodococcus</i>
1546	2,468	3,229	-	762	<i>Pseudomonas thivervalensis</i> BS3779 / 93% / 100%	<i>Pseudomonas</i>
15592	66	614	+	549 ^c	<i>Rhodococcus opacus</i> PD630 / 94% / 100%	<i>Rhodococcus</i>
1906	577	1,386	-	810	<i>Pseudomonas veronii</i> R02 / 82% / 97%	<i>Pseudomonas</i>
21574	38	415	+	378 ^c	<i>Pseudomonas putida</i> KF715 / 100% / 100%	<i>Pseudomonas</i>
26	213,432	214,196	-	765	<i>Bordetella</i> genomsp. 4 AU14378 / 95% / 100% ^e	<i>Bordetella</i>
3155	2,410	2,823	-	414 ^c	<i>Rhodococcus</i> sp. HA99 / 100% / 70%	<i>Rhodococcus</i>
3711	1,137	1,856	-	720	<i>Rhodococcus</i> sp. T104 / 99% / 100%	<i>Rhodococcus</i>
3	827,233	828,019	+	787	<i>Achromobacter</i> sp. LC458 / 100% / 100% ^e	<i>Achromobacter</i>
4726	100	342	+	243 ^c	<i>Rhodococcus opacus</i> PD630 / 97% / 100%	<i>Rhodococcus</i>
4978	27	218	+	192 ^c	<i>Rhodococcus</i> sp. HA99 / 100% / 85%	<i>Rhodococcus</i>

7	97,161	97,982	+	822	<i>Herbaspirillum</i> sp. meg3 / 75% / 74%	<i>Herbaspirillum</i>
9987	11	478	+	468 ^c	<i>Rhodococcus opacus</i> B4 / 86% / 100%	<i>Rhodococcus</i>
HOA – 4-hydroxy-2-oxovalerate aldolase (EC. 4.1.3.39)						
1040	3,108	4,136	-	1,029	<i>Pseudomonas</i> sp. TCU-HCL1 / 88% / 100%	<i>Pseudomonas</i>
113	10,502	11,515	-	1,014	<i>Pseudomonas putida</i> PC2 / 83% / 98%	<i>Pseudomonas</i>
18447	569	709	-	141 ^c	<i>Rhodococcus opacus</i> M213 / 91% / 100% ^e	<i>Rhodococcus</i>
24567	84	572	-	489 ^c	<i>Rhodococcus opacus</i> PD630 / 91% / 96%	<i>Rhodococcus</i>
28962	187	510	-	324 ^c	<i>Cupriavidus taiwanensis</i> LMG19424 / 94% / 100%	<i>Cupriavidus</i>
75	90,408	91,442	+	1,035	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
900	5,999	6,793	-	795	<i>Pseudomonas veronii</i> 1YdBTEX2 / 90% / 99%	<i>Pseudomonas</i>
9020	249	1,277	+	1,029	<i>Pseudomonas</i> sp. A3(2016) / 91% / 100%	<i>Pseudomonas</i>
9	25,590	26,597	-	1,008	<i>Ralstonia eutropha</i> H16 / 86% / 98 %	<i>Ralstonia</i>
Benzoate to protocatechuate						
<i>pobA</i> – 4-hydroxybenzoate 3-monooxygenase (EC. 1.14.13.2)						
3	787,153	788,382	-	1230	<i>Achromobacter</i> sp. LC458 / 99% / 100% ^e	<i>Achromobacter</i>
3586	2,454	2,813	-	360 ^c	<i>Ralstonia eutropha</i> jnP134 / 81% / 96%	<i>Ralstonia</i>
4	551,587	552,774	+	1188	-	Unassigned
5	374,041	375,210	-	1170	<i>Bordetella</i> sp. SCN 67-23 / 97% / 100% ^e	<i>Bordetella</i>
7	626,017	627,192	-	1176	<i>Bordetella</i> sp. SCN 68-11 / 98% / 100% ^e	<i>Bordetella</i>
9393	116	1,297	-	1182	<i>Rhodococcus opacus</i> R7 / 89% / 98%	<i>Rhodococcus</i>
921	5,196	6,389	+	1194	<i>Pseudomonas chlororaphis</i> 189 / 82% / 100%	<i>Pseudomonas</i>
41	133,618	134,805	-	1188	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 00% / 100%	<i>Pseudomonas</i>
1127	23	391	+	369 ^c	<i>Pseudomonas thivervalensis</i> BS3779 / 95% 100%	<i>Pseudomonas</i>
21084	25	387	+	363 ^c	<i>Pseudomonas putida</i> KF715 / 100% / 100%	<i>Pseudomonas</i>
Protocatechuate ortho-cleavage						
<i>pcaG</i> – Protocatechuate 3,4-dioxygenase (EC. 1.13.11.3)^b						
3	783,331	783,919	-	609	<i>Achromobacter</i> sp. LC458 / 99% / 100% ^e	<i>Achromobacter</i>
3	627,864	628,439	+	576	<i>Achromobacter</i> sp. LC458 / 98% / 100% ^e	<i>Achromobacter</i>
13	56,633	57,223	-	591	<i>Bordetella petrii</i> DSM 12804 / 97% / 100%	<i>Bordetella</i>
27628	19	459	+	441 ^c	<i>Cupriavidus nantongensis</i> X1 / 93% / 100%	<i>Cupriavidus</i>
32	194,965	195,624	-	660	<i>Ralstonia solanacearum</i> CFBP2957 / 79% / 93%	<i>Ralstonia</i>
112	30,341	30,946	+	606	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
4247	1,815	2,420	+	606	<i>Pseudomonas</i> sp. DRA525 / 98% / 100%	<i>Pseudomonas</i>
7003	1,088	1,654	+	567	<i>Pseudomonas fluorescens</i> F113 / 93% / 100%	<i>Pseudomonas</i>
13344	24	575	+	552	<i>Pseudomonas resinovorans</i> NBRC 106553 / 83% / 99%	<i>Pseudomonas</i>
<i>pcaB</i> – 3-carboxy-cis,cis-muconate cycloisomerase (EC. 5.5.1.2)						
112	49,157	50,518	+	1,362	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
11647	475	1,113	-	639 ^c	<i>Pseudomonas putida</i> H8234 / 99% / 100%	<i>Pseudomonas</i>
127	24,939	26,294	+	1,356	<i>Achromobacter</i> sp. MFA1 R4 / 83% / 98%	<i>Achromobacter</i>
13	59,484	60,896	-	1,413	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
14	181,983	183,329	-	1,347	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
25258	31	381	+	351 ^c	<i>Ralstonia pickettii</i> DTP0602 / 81% / 83%	<i>Ralstonia</i>
25969	332	529	-	198 ^c	<i>Agrobacterium tumefaciens</i> Ah5 / 100% / 100%	<i>Agrobacterium</i>
3806	1,072	2,436	+	1,365	<i>Pseudomonas thivervalensis</i> BS3779 / 92% / 100%	<i>Pseudomonas</i>
3	628,462	629,844	+	1,383	<i>Cupriavidus necator</i> NH9 / 75% / 69%	<i>Cupriavidus</i>
599	2,259	3,620	-	1,362	<i>Pseudomonas fluorescens</i> FW300-N2E3 / 82% / 100%	<i>Pseudomonas</i>
59	6,409	7,773	+	1,365	<i>Bordetella</i> genomosp. 4 AU14378/ 91% / 100% ^e	<i>Bordetella</i>
7	633,205	634,506	-	1,302	<i>Bordetella</i> sp. SCN 68-11 / 90% / 99% ^e	<i>Bordetella</i>
9	500,241	501,602	-	1,362	<i>Bordetella</i> sp. SCN 67-23 / 97% / 100% ^e	<i>Bordetella</i>

<i>pcaC</i> – 4-carboxymuconolactone decarboxylase (EC. 4.1.1.44)						
112	51,393	51,788	+	396	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 100% / 100%	<i>Pseudomonas</i>
119	27,082	27,573	+	492	<i>Bordetella</i> genomosp. 13 AU7206 / 79% / 100% ^e	<i>Bordetella</i>
11	270,047	270,466	+	420	<i>Delftia acidovorans</i> ANG1 / 82% / 77%	<i>Delftia</i>
1246	4,333	4,715	-	383	<i>Pseudomonas thivervalensis</i> BS3779	<i>Pseudomonas</i>
12	145,225	145,623	+	399	<i>Delftia tsuruhatensis</i> CM13 / 84% / 97%	<i>Delftia</i>
13145	229	444	-	216 ^c	<i>Pseudomonas putida</i> NBRC 14164 / 95% / 100%	<i>Pseudomonas</i>
13595	104	493	-	390 ^c	<i>Pseudomonas</i> sp. FGI182 / 99% / 100%	<i>Pseudomonas</i>
13	59,036	59,491	-	456	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
14207	102	335	+	234 ^c	<i>Pseudomonas lini</i> BS3782 / 87% / 94	<i>Pseudomonas</i>
15	89,181	90,483	-	1,303	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
16868	85	324	+	240 ^c	<i>Cupriavidus nantongensis</i> X1 / 87% / 91%	<i>Cupriavidus</i>
16	202,370	202,720	-	351	<i>Achromobacter</i> sp. LC458 / 97% / 100% ^e	<i>Achromobacter</i>
1833	2,365	3,018	+	654	<i>Pseudomonas fluorescens</i> FW300-N2C3 / 86% / 99%	<i>Pseudomonas</i>
2034	3,231	3,661	-	431	<i>Pseudomonas brassicacearum</i> BS3663 / 94% / 100%	<i>Pseudomonas</i>
20	228,919	229,290	+	372	<i>Pseudomonas putida</i> W619 / 95% / 100%	<i>Pseudomonas</i>
215	7,947	9,140	+	1,194	<i>Burkholderia</i> sp. CCGE1002 / 92% / 98%	<i>Burkholderia</i>
22323	197	589	-	393 ^c	<i>Pseudomonas putida</i> KF715 / 97% / 98%	<i>Pseudomonas</i>
22	38,149	38,559	-	411	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
22	199,358	199,735	+	378	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
24	82,371	82,736	+	366	<i>Achromobacter</i> sp. LC458 / 100% / 100% ^e	<i>Achromobacter</i>
2591	1,384	1,779	-	396	<i>Pseudomonas fluorescens</i> FW300-N2E3 / 89% / 91%	<i>Pseudomonas</i>
30268	67	471	+	405 ^c	<i>Pseudomonas granadensis</i> LMG 27940 / 94% / 99%	<i>Pseudomonas</i>
388	2,639	3,049	-	411	<i>Bordetella</i> genomosp. 4 AU14378 / 99% / 99% ^e	<i>Bordetella</i>
403	5,304	5,723	+	420	<i>Mycobacterium</i> sp. PH-06/ 86% / 90%	<i>Mycobacterium</i>
403	8,326	8,658	+	333	<i>Microbacterium</i> sp. Leaf159 / 89% / 91% ^e	<i>Microbacterium</i>
4268	2,094	2,486	-	393	<i>Rhodococcus jostii</i> RHA1 / 92% / 98%	<i>Rhodococcus</i>
599	1,052	1,444	-	393	<i>Pseudomonas chlororaphis</i> DSM 21509 / 90% / 98%	<i>Pseudomonas</i>
5	279,378	279,764	-	387	-	Unassigned
67	100,860	101,261	+	402	<i>Bordetella</i> genomosp. 4 AU14378 / 100% / 100% ^e	<i>Bordetella</i>
7068	877	1311	-	435	<i>Rhodococcus</i> sp. SC4 / 93% / 95% ^e	<i>Rhodococcus</i>
709	4,449	4,838	-	390	<i>Pseudomonas</i> sp. GR 6-02 / 94% / 100%	<i>Pseudomonas</i>
70	87,514	87,903	-	390	<i>Pseudomonas pseudoalcaligenes</i> KF707 / 99% / 100%	<i>Pseudomonas</i>
8962	311	811	-	501	<i>Bordetella</i> genomosp. 13 AU7206 / 81% / 79%	<i>Bordetella</i>
Protocatechuate meta-cleavage						
<i>ligA</i> – Protocatechuate 4,5-dioxygenase (EC. 1.13.11.8) ^b						
7	628,030	628,392	-	363	<i>Bordetella</i> sp. SCN 68-11 / 97% / 100% ^e	<i>Bordetella</i>
4	552,801	553,166	+	366	-	Unassigned
36342	5	388	-	384	<i>Pseudomonas putida</i> H8234 / 99% / 100%	<i>Pseudomonas</i>
21	257,598	257,957	+	360	-	Unassigned
<i>ligC</i> – 2-hydroxy-4-carboxymuconate semialdehyde hemiacetal dehydrogenase (EC. 1.1.1.312)						
11	21,264	22,241	+	978	<i>Bordetella</i> sp. SCN 67-23 / 97% / 97% ^e	<i>Bordetella</i>
<i>ligI</i> – 2-pyrone-4,6-dicarboxylate lactonase (EC. 3.1.1.57)						
119	7,921	8,634	+	714	<i>Bordetella</i> genomosp. 4 AU14378 / 96% / 100% ^e	<i>Bordetella</i>
14	108,326	109,186	-	861	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
14	210,070	210,759	+	690	-	Unassigned
14	210,922	211,764	+	843	-	Unassigned
150	38,888	39,757	+	870	<i>Bordetella</i> genomosp. 4 AU9919 / 85% / 97% ^e	<i>Bordetella</i>

15	114,273	115,118	+	846	<i>Bordetella petrii</i> DSM 12804 / 95% / 100%	<i>Bordetella</i>
1	431,616	432,515	+	900	<i>Bordetella hinzii</i> H568 / 80% / 93%	<i>Bordetella</i>
232	20,516	20,974	+	459	-	Unassigned
2697	2,059	2,865	-	807	-	Unassigned
26	140,818	141,606	+	789	<i>Achromobacter piechaudii</i> ATCC 43553 / 75% / 97% ^e	<i>Achromobacter</i>
26	217,119	217,988	+	870	<i>Bordetella</i> genomosp. 4 AU14378 / 90% / 100% ^e	<i>Bordetella</i>
28	83,031	83,924	+	894	<i>Bordetella petrii</i> DSM 12804 / 97% / 100%	<i>Bordetella</i>
2	12,960	13,772	-	813	<i>Bordetella</i> sp. SCN 67-23 / 87% / 100% ^e	<i>Bordetella</i>
2	110,475	111,356	-	882	<i>Bordetella</i> sp. SCN 67-23 / 96% / 100% ^e	<i>Bordetella</i>
31	46,133	46,924	-	792	<i>Bordetella</i> genomosp. 4 AU9919 / 89% / 100% ^e	<i>Bordetella</i>
343	6,231	6,803	-	573	<i>Bordetella petrii</i> DSM 12804 / 80% / 89%	<i>Bordetella</i>
3	201,832	202,779	+	948	<i>Achromobacter xylosoxidans</i> FDAARGOS_147 / 80% / 63%	<i>Achromobacter</i>
463	4,151	5,011	-	861	<i>Bordetella</i> genomosp. 4 AU9919 / 89% / 100% ^e	<i>Bordetella</i>
47	65,020	65,835	-	816	<i>Achromobacter denitrificans</i> PR1 / 83% / 99%	<i>Achromobacter</i>
52	102,803	103,684	-	882	<i>Bordetella petrii</i> DSM 12804 / 98% / 100%	<i>Bordetella</i>
67	43,900	44,733	+	834	<i>Bordetella</i> genomosp. 11 AU8856 / 76% / 99% ^e	<i>Bordetella</i>
6	173,530	174,378	-	849	<i>Variovorax paradoxus</i> B4 / 75% / 80%	<i>Variovorax</i>
6	252,644	253,456	-	813	<i>Bordetella</i> genomosp. 8 AU19157 / 78% / 81%	<i>Bordetella</i>
6	256,622	257,512	+	891	<i>Bordetella</i> sp. SCN 67-23 / 96% / 93% ^e	<i>Bordetella</i>
6	385,117	385,986	-	870	<i>Bordetella petrii</i> DSM 12804 / 80% / 96%	<i>Bordetella</i>
71	36,020	36,895	+	876	<i>Burkholderia gladioli</i> BSR3 / 81% / 96%	<i>Burkholderia</i>
742	6,958	7,857	+	900	<i>Bordetella petrii</i> DSM 12804 / 76% / 93%	<i>Bordetella</i>
7	632,330	633,208	-	879	<i>Bordetella</i> sp. SCN 68-11 / 94% / 98% ^e	<i>Bordetella</i>
83	63,919	64,620	-	702	<i>Advenella kashmirensis</i> WT001 / 76% / 63%	<i>Advenella</i>
86	71,625	72,320	-	696	<i>Bordetella</i> genomosp. 4 AU14378 / 89% / 100% ^e	<i>Bordetella</i>
8	467,326	468,303	+	978	<i>Achromobacter</i> sp. MFA1 R4 / 85% / 88%	<i>Achromobacter</i>
9	18,452	19,252	+	801	<i>Bordetella</i> sp. SCN 67-23 / 81% / 100%	<i>Bordetella</i>
ligJ – 4-oxalmesaconate hydratase (EC. 4.2.1.83)						
111	33,440	34,447	+	1,008	<i>Rhodococcus</i> sp. DK17 / 82% / 100% ^e	<i>Rhodococcus</i>
14	319,940	320,659	-	720	<i>Achromobacter</i> sp. MFA1 R4 / 83% / 98%	<i>Achromobacter</i>
160	14,292	15,011	+	720	<i>Bordetella petrii</i> DSM 12804 / 81% / 100%	<i>Bordetella</i>
32089 ^d	258	443	-	186 ^c	<i>Burkholderia</i> sp. NRF60-BP8 / 89% / 98%	<i>Burkholderia</i>
5	537,561	538,568	-	1,008	<i>Afipia</i> sp. GAS231 / 78% / 79%	<i>Afipia</i>
72	57,398	58,420	+	1,023	<i>Xanthomonas campestris</i> ICMP 21080 / 80% / 99%	<i>Xanthomonas</i>
762	2,813	3,814	+	1,002	<i>Microbacterium azadirachtae</i> ARN176 / 92% / 100% ^e	<i>Microbacterium</i>
ligK – 4-hydroxy-4-methyl-2-oxoglutarate aldolase (EC. 4.1.3.17)						
14	319,221	319,943	-	723	<i>Bordetella petrii</i> DSM 12804 / 99% / 100%	<i>Bordetella</i>
5	541,762	542,469	+	708	<i>Bordetella</i> sp. SCN 67-23 / 97% / 100% ^e	<i>Bordetella</i>
71	35,237	35,938	+	702	<i>Pseudomonas citronellolis</i> P3B5 / 76% / 90%	<i>Pseudomonas</i>
Benzoate degradation via benzoyl--CoA formation						
bclA – Benzoate--CoA ligase (EC. 6.2.1.25)						
14	289,927	291,486	+	1,560	<i>Achromobacter xylosoxidans</i> FDAARGOS / 86% / 99%	<i>Achromobacter</i>
245	7,166	8,740	+	1,575	<i>Achromobacter ruhlandii</i> SCCH3:ACH 33-1365 / 79% / 98%	<i>Achromobacter</i>
33	68,141	69,685	-	1,545	<i>Achromobacter xylosoxidans</i> A8 / 87% / 100%	<i>Achromobacter</i>
7	464,984	466,573	-	1,590	<i>Variovorax denitrificans</i> PR1 / 79% / 96%	<i>Bordetella</i>
boxA – Benzoyl-CoA 2,3-epoxidase (EC. 1.14.13.208)^b						
14	282,185	283,435	-	1251	<i>Achromobacter xylosoxidans</i> FDAARGOS / 84% / 99%	<i>Achromobacter</i>
245	744	2,015	-	1272	<i>Achromobacter ruhlandii</i> SCCH3:ACH 33-1365 / 79% / 98%	<i>Achromobacter</i>
33	74,745	76,019	+	1275	<i>Achromobacter xylosoxidans</i> FDAARGO / 84% / 99%	<i>Achromobacter</i>

7	473,260	474,534	+	1275	<i>Variovorax paradoxus</i> S110 / 80% / 97%	<i>Variovorax</i>
<i>boxC</i> – 2,3-epoxybenzoyl-CoA dihydrolase (EC. 4.1.2.44)						
14	284,919	286,574	-	1,656	<i>Achromobacter ruhlandii</i> SCCH3:ACH 33-1365 / 85% / 98%	<i>Achromobacter</i>
245	3,581	5,239	-	1,659	<i>Achromobacter ruhlandii</i> SCCH3:ACH 33-1365 / 80% / 98%	<i>Achromobacter</i>
33	71,460	73,148	+	1,689	<i>Achromobacter xylosoxidans</i> DFAARGOS_147 / 87% / 95%	<i>Achromobacter</i>
7	470,145	471,785	+	1,641	<i>Variovorax paradoxus</i> S110 / 80% / 99%	<i>Bordetella</i>
<i>boxD</i> – 3,4-dehydroadipyl-CoA semialdehyde dehydrogenase (NADP(+)) (EC. 1.2.1.77)						
7	466,653	468,233	-	1,581	<i>Variovorax</i> sp. HW608 / 77% / 93%	<i>Variovorax</i>
14	288,300	289,883	+	1,584	<i>Bordetella petrii</i> DSM 12804 / 98% 100%	<i>Bordetella</i>

^a Based on blastn against the nt NCBI database on April, 2017. Cutoff with a minimum of 75% identity and 50% cover.

^b Only alpha subunits of multimeric enzymes are considered.

^c Partial sequence.

^d Complete CDS could be reconstructed from two segments assigned to the same species.

^e Blastp against nr NCBI database was used instead (April, 2017, cutoff with a minimum of 75% identity and 50% cover.) due to lack of significant results using blastn against nt NCBI database.