

Table S1. Putative taxonomic affiliation of [FeFe]-hydrogenase sequences obtained from Prony metagenome P27.

OTU	MG-RAST ID	Taxonomy (Phylum ; Class ; Order)	Highly similar sequence retrieved from Genbank		
			% similarity	(Genbank accession number)	Species - clone
P27_hydA14	D4ZHLFP1:60:D2HDNACXX:3:2107:8059:82633:ACACGA	Firmicutes; Clostridia; Clostridiales	75.5	(YP_008699055)	hydrogenase, Fe-only [Clostridium autoethanogenum DSM 10061]
P27_hydA114	D4ZHLFP1:60:D2HDNACXX:3:1109:13172:94760:ACACGA	Firmicutes; Clostridia; Clostridiales	68.2	(WP_023062885)	hydrogenase, Fe-only [Clostridium thermocellum]
P27_hydA1	D4ZHLFP1:60:D2HDNACXX:3:1311:20647:55845:ACACGA	Firmicutes; Clostridia; Clostridiales	48.1	(WP_023062885)	hydrogenase, Fe-only [Clostridium thermocellum]
P27_hydA7	D4ZHLFP1:60:D2HDNACXX:3:2315:12483:17223:ACACGA	Firmicutes; Clostridia; Clostridiales	77.4	(WP_023062885)	hydrogenase, Fe-only [Clostridium thermocellum]
P27_hydA136	D4ZHLFP1:60:D2HDNACXX:3:2306:7045:37162:ACACGA	Firmicutes; Clostridia; Clostridiales	49.7	(GAE89903)	hydrogenase [Clostridium straminisolvens JCM 21531]
P27_hydA45	D4ZHLFP1:60:D2HDNACXX:3:2308:14654:24288:ACACGA	Firmicutes; Clostridia; Clostridiales	65.9	(GAE89903)	hydrogenase [Clostridium straminisolvens JCM 21531]
P27_hydA129	D4ZHLFP1:60:D2HDNACXX:3:2306:11382:44214:ACACGA	Firmicutes; Clostridia; Clostridiales	72.4	(YP_005047780)	hydrogenase, Fe-only [Clostridium clariflavum DSM 19732]
P27_hydA13	D4ZHLFP1:60:D2HDNACXX:3:2102:8481:71964:ACACGA	Firmicutes; Clostridia; Clostridiales	75.1	(YP_008699055)	hydrogenase, Fe-only [Clostridium autoethanogenum DSM 10061]
P27_hydA84	D4ZHLFP1:60:D2HDNACXX:3:1106:2370:35020:ACACGA	Firmicutes; Clostridia; Clostridiales	76.3	(WP_0221116126)	hydrogenase Fe-only [Clostridium sp. CAG:169]
P27_hydA85	D4ZHLFP1:60:D2HDNACXX:3:2305:8704:48944:ACACGA	Firmicutes; Clostridia; Clostridiales	85.1	(YP_001036861)	hydrogenase, Fe-only [Clostridium thermocellum ATCC 27405]
P27_hydA48	D4ZHLFP1:60:D2HDNACXX:3:1108:1705:91727:ACACGA	Firmicutes; Clostridia; Clostridiales	78.6	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA5	D4ZHLFP1:60:D2HDNACXX:3:1314:8272:100789:ACACGA	Firmicutes; Clostridia; Clostridiales	80.9	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA106	D4ZHLFP1:60:D2HDNACXX:3:2306:18633:67353:ACACGA	Firmicutes; Clostridia; Clostridiales	71.6	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA101	D4ZHLFP1:60:D2HDNACXX:3:2314:5473:6798:ACACGA	Firmicutes; Clostridia; Clostridiales	48.5	(YP_001113004)	hydrogenase [Desulfotomaculum reducens MI-1]
P27_hydA24	D4ZHLFP1:60:D2HDNACXX:3:2314:9285:21359:ACACGA	Firmicutes; Clostridia; Clostridiales	90.0	(YP_004545921)	hydrogenase Fe-only [Desulfotomaculum ruminis DSM 2154]
P27_hydA27	D4ZHLFP1:60:D2HDNACXX:3:1305:16629:82167:ACACGA	Firmicutes; Clostridia; Clostridiales	77.8	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA107	D4ZHLFP1:60:D2HDNACXX:3:1114:19745:58907:ACACGA	Firmicutes; Clostridia; Clostridiales	77.4	(YP_001113007)	hydrogenase [Desulfotomaculum reducens MI-1]
P27_hydA11	D4ZHLFP1:60:D2HDNACXX:3:2116:12176:59324:ACACGA	Firmicutes; Clostridia; Clostridiales	77.8	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA111	D4ZHLFP1:60:D2HDNACXX:3:2106:3631:63778:ACACGA	Firmicutes; Clostridia; Clostridiales	79.0	(WP_008410064)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P27_hydA134	D4ZHLFP1:60:D2HDNACXX:3:1303:11680:47793:ACACGA	Firmicutes; Clostridia; Clostridiales	97.1	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA135	D4ZHLFP1:60:D2HDNACXX:3:2316:14697:15311:ACACGA	Firmicutes; Clostridia; Clostridiales	94.0	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA123	D4ZHLFP1:60:D2HDNACXX:3:2302:3021:14439:ACACGA	Firmicutes; Clostridia; Clostridiales	81.6	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA19	D4ZHLFP1:60:D2HDNACXX:3:1309:20698:19893:ACACGA	Firmicutes; Clostridia; Clostridiales	91.0	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA51	D4ZHLFP1:60:D2HDNACXX:3:2110:4908:93477:ACACGA	Firmicutes; Clostridia; Clostridiales	95.0	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 7711]
P27_hydA90	D4ZHLFP1:60:D2HDNACXX:3:2308:4104:27466:ACACGA	Firmicutes; Clostridia; Clostridiales	90.5	(YP_001113004)	hydrogenase [Desulfotomaculum reducens MI-1]
P27_hydA91	D4ZHLFP1:60:D2HDNACXX:3:2301:6794:9875:ACACGA	Firmicutes; Clostridia; Clostridiales	95.0	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 7711]
P27_hydA92	D4ZHLFP1:60:D2HDNACXX:3:2312:14796:69310:ACACGA	Firmicutes; Clostridia; Clostridiales	95.9	(YP_004545921)	hydrogenase Fe-only [Desulfotomaculum ruminis DSM 2154]
P27_hydA68	D4ZHLFP1:60:D2HDNACXX:3:1115:15760:55593:ACACGA	Firmicutes; Clostridia; Clostridiales	66.6	(YP_004969732)	hydrogenase, Fe-only [Desulfosporosinus orientis DSM 765]
P27_hydA93	D4ZHLFP1:60:D2HDNACXX:3:2316:7439:59410:ACACGA	Firmicutes; Clostridia; Clostridiales	84.3	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA96	D4ZHLFP1:60:D2HDNACXX:3:2302:9663:61279:ACACGA	Firmicutes; Clostridia; Clostridiales	68.2	(WP_008410064)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P27_hydA59	D4ZHLFP1:60:D2HDNACXX:3:1307:7139:36512:ACACGA	Firmicutes; Clostridia; Clostridiales	90.5	(YP_007946226)	hydrogenase, Fe-only [Desulfotomaculum gibsoniae DSM 7213]
P27_hydA37	D4ZHLFP1:60:D2HDNACXX:3:1311:12003:89454:ACACGA	Firmicutes; Clostridia; Clostridiales	90.9	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 7711]
P27_hydA38	D4ZHLFP1:60:D2HDNACXX:3:2313:17826:33583:ACACGA	Firmicutes; Clostridia; Clostridiales	90.9	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA128	D4ZHLFP1:60:D2HDNACXX:3:1303:17006:29935:ACACGA	Firmicutes; Clostridia; Clostridiales	93.0	(WP_008410059)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P27_hydA130	D4ZHLFP1:60:D2HDNACXX:3:2115:12121:70737:ACACGA	Firmicutes; Clostridia; Clostridiales	84.0	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA131	D4ZHLFP1:60:D2HDNACXX:3:2110:11779:25039:ACACGA	Firmicutes; Clostridia; Clostridiales	90.9	(WP_008410059)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P27_hydA79	D4ZHLFP1:60:D2HDNACXX:3:1315:7322:7202:ACACGA	Firmicutes; Clostridia; Clostridiales	63.2	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA8	D4ZHLFP1:60:D2HDNACXX:3:2109:10707:54209:ACACGA	Firmicutes; Clostridia; Clostridiales	93.6	(YP_004518238)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA97	D4ZHLFP1:60:D2HDNACXX:3:1309:12380:17569:ACACGA	Firmicutes; Clostridia; Clostridiales	72.0	(YP_004496996)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P27_hydA61	D4ZHLFP1:60:D2HDNACXX:3:2304:9197:41505:ACACGA	Firmicutes; Clostridia; Clostridiales	85.9	(YP_004497002)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P27_hydA63	D4ZHLFP1:60:D2HDNACXX:3:1106:12199:34111:ACACGA	Firmicutes; Clostridia; Clostridiales	91.0	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 7711]
P27_hydA64	D4ZHLFP1:60:D2HDNACXX:3:2303:2598:25384:ACACGA	Firmicutes; Clostridia; Clostridiales	92.0	(YP_004545921)	hydrogenase Fe-only [Desulfotomaculum ruminis DSM 2154]
P27_hydA72	D4ZHLFP1:60:D2HDNACXX:3:1302:19141:50190:ACACGA	Firmicutes; Clostridia; Clostridiales	65.1	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P27_hydA43	D4ZHLFP1:60:D2HDNACXX:3:2314:1930:100125:ACACGA	Firmicutes; Clostridia; Clostridiales	73.6	(WP_022271995)	hydrogenase Fe-only [Eubacterium siraeum CAG:80]
P27_hydA125	D4ZHLFP1:60:D2HDNACXX:3:2314:16699:37745:ACACGA	Firmicutes; Clostridia; Clostridiales	79.3	(YP_077035)	Fe hydrogenase [Symbiobacterium thermophilum IAM 14863]
P27_hydA126	D4ZHLFP1:60:D2HDNACXX:3:2310:17631:29511:ACACGA	Firmicutes; Clostridia; Clostridiales	49.7	(YP_003640841)	hydrogenase, Fe-only [Thermincola potens JR]
P27_hydA47	D4ZHLFP1:60:D2HDNACXX:3:1313:3186:85130:ACACGA	Firmicutes; Clostridia; Clostridiales	71.2	(YP_003640841)	hydrogenase, Fe-only [Thermincola potens JR]
P27_hydA75	D4ZHLFP1:60:D2HDNACXX:3:2314:7403:99385:ACACGA	Firmicutes; Clostridia; Clostridiales	67.0	(WP_021908252)	hydrogenase Fe-only [Eubacterium sp. CAG:146]
P27_hydA53	D4ZHLFP1:60:D2HDNACXX:3:2304:9596:32957:ACACGA	Firmicutes; Clostridia; Clostridiales	98.0	(YP_006910651)	[Fe] hydrogenase, large subunit HymC [Dehalobacter sp. DCA]
P27_hydA56	D4ZHLFP1:60:D2HDNACXX:3:2307:5017:82140:ACACGA	Firmicutes; Clostridia; Clostridiales	75.1	(YP_003640841)	hydrogenase, Fe-only [Thermincola potens JR]
P27_hydA78	D4ZHLFP1:60:D2HDNACXX:3:2308:19195:51114:ACACGA	Firmicutes; Clostridia; Halanaerobiales	59.3	(YP_003826883)	NAD(P)-dependent iron-only hydrogenase iron-iron [Acetohalobium arabaticum DSM 5501]
P27_hydA52	D4ZHLFP1:60:D2HDNACXX:3:1313:15591:68584:ACACGA	Firmicutes; Clostridia; Thermoanaerobacterales	76.6	(YP_003239720)	hydrogenase, Fe-only [Ammonifex degensii KC4]
P27_hydA31	D4ZHLFP1:60:D2HDNACXX:3:1101:20130:2900:ACACGA	Firmicutes; Clostridia; Thermoanaerobacterales	78.6	(ACA51661)	HydA [Thermoanaerobacterium saccharolyticum JW/SL-YS485]
P27_hydA117	D4ZHLFP1:60:D2HDNACXX:3:2316:6701:34903:ACACGA	Firmicutes; Clostridia; Thermoanaerobacterales	98.6	(YP_007298421)	hydrogenase, Fe-only [Thermoanaerobacterium thermosaccharolyticum M0795]
P27_hydA121	D4ZHLFP1:60:D2HDNACXX:3:2315:6287:77241:ACACGA	Firmicutes; Clostridia; Thermoanaerobacterales	97.8	(YP_007298421)	hydrogenase, Fe-only [Thermoanaerobacterium thermosaccharolyticum M0795]
P27_hydA4	D4ZHLFP1:60:D2HDNACXX:3:2315:14097:33168:ACACGA	Firmicutes; Clostridia; Thermoanaerobacterales	87.0	(GAF24846)	iron only hydrogenase large subunit, C-terminal [Moorella thermoacetica Y72]
P27_hydA35	D4ZHLFP1:60:D2HDNACXX:3:2308:15765:97985:ACACGA	Thermotogae; Thermotogae; Thermotogales	96.3	(YP_005096723)	hydrogenase, Fe-only [Marinitoga piezophila KA3]

P27_hydA18	D4ZHLFP1:60:D2HDNACXX:3:2313:17713:85556:ACACGA	<i>Thermotogae; Thermotogae; Thermotogales</i>	83.2	(YP_005470551)	hydrogenase, Fe-only [<i>Ferrihydrobacterium pennivorans</i> DSM 9078]
P27_hydA23	D4ZHLFP1:60:D2HDNACXX:3:1114:2287:87019:ACACGA	<i>Thermotogae; Thermotogae; Thermotogales</i>	82.8	(YP_004659299)	hydrogenase large subunit domain-containing protein [<i>Thermotoga thermarum</i> DSM 5069]
P27_hydA26	D4ZHLFP1:60:D2HDNACXX:3:1107:12202:54331:ACACGA	<i>Thermotogae; Thermotogae; Thermotogales</i>	54.3	(YP_002534027)	NADP-reducing hydrogenase, subunit D [<i>Thermotoga neapolitana</i> DSM 4359]
P27_hydA133	D4ZHLFP1:60:D2HDNACXX:3:1311:8497:2283:ACACGA	<i>Thermotogae; Thermotogae; Thermotogales</i>	89.0	(YP_005096723)	hydrogenase, Fe-only [<i>Marinitoga piezophila</i> KA3]
P27_hydA108	D4ZHLFP1:60:D2HDNACXX:3:2311:19981:34912:ACACGA	<i>Deltaproteobacteria; Syntrophobacterales</i>	90.1	(YP_844976)	hydrogenase, Fe-only [<i>Syntrophobacter fumaroxidans</i> MPOB]
P27_hydA70	D4ZHLFP1:60:D2HDNACXX:3:2312:3330:10832:ACACGA	<i>Deltaproteobacteria; Syntrophobacterales</i>	97.1	(YP_844976)	hydrogenase, Fe-only [<i>Syntrophobacter fumaroxidans</i> MPOB]
P27_hydA103	D4ZHLFP1:60:D2HDNACXX:3:2309:13748:77439:ACACGA	<i>Deltaproteobacteria; Desulfuovibrionales</i>	90.1	(YP_002952160)	Fe hydrogenase [<i>Desulfuovibrio magneticus</i> RS-1]
P27_hydA15	D4ZHLFP1:60:D2HDNACXX:3:2312:18659:40581:ACACGA	<i>Deltaproteobacteria; Desulfuovibrionales</i>	84.3	(WP_006921111)	hydrogenase, Fe-only, partial [<i>Desulfuovibrio magneticus</i>]
P27_hydA118	D4ZHLFP1:60:D2HDNACXX:3:2101:19990:24288:ACACGA	<i>Deltaproteobacteria; Desulfuromonadales</i>	82.0	(YP_004198598)	hydrogenase, Fe-only [<i>Geobacter</i> sp. M18]
P27_hydA16	D4ZHLFP1:60:D2HDNACXX:3:2305:7417:37924:ACACGA	<i>Deltaproteobacteria; Desulfobacterales</i>	87.8	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus</i> DSM 2032]
P27_hydA21	D4ZHLFP1:60:D2HDNACXX:3:2315:11400:82351:ACACGA	<i>Deltaproteobacteria; Desulfobacterales</i>	77.8	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus</i> DSM 2032]
P27_hydA74	D4ZHLFP1:60:D2HDNACXX:3:1310:5971:76924:ACACGA	<i>Deltaproteobacteria; Desulfobacterales</i>	71.2	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus</i> DSM 2032]
P27_hydA119	D4ZHLFP1:60:D2HDNACXX:3:2116:8151:3767:ACACGA	<i>Synergistetes; Synergistia; Synergistales</i>	81.3	(YP_003316672)	hydrogenase [<i>Thermanaerovibrio acidaminovorans</i> DSM 6589]
P27_hydA104	D4ZHLFP1:60:D2HDNACXX:3:2301:7976:40736:ACACGA	<i>Synergistetes; Synergistia; Synergistales</i>	78.6	(YP_003316672)	hydrogenase [<i>Thermanaerovibrio acidaminovorans</i> DSM 6589]
P27_hydA110	D4ZHLFP1:60:D2HDNACXX:3:1313:7546:14195:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	95.0	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana</i> DSM 8902]
P27_hydA124	D4ZHLFP1:60:D2HDNACXX:3:2304:6980:81620:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	77.8	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana</i> DSM 8902]
P27_hydA3	D4ZHLFP1:60:D2HDNACXX:3:2311:2271:81749:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	87.4	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA32	D4ZHLFP1:60:D2HDNACXX:3:2313:10656:87661:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	96.0	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA25	D4ZHLFP1:60:D2HDNACXX:3:2314:19579:3636:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	90.5	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA49	D4ZHLFP1:60:D2HDNACXX:3:2116:7098:31541:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	71.6	(WP_018525843)	hydrogenase Fe-only [<i>Spirochaeta alkalica</i>]
P27_hydA46	D4ZHLFP1:60:D2HDNACXX:3:2305:18503:27092:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	75.1	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana</i> DSM 8902]
P27_hydA54	D4ZHLFP1:60:D2HDNACXX:3:2306:9291:27493:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	75.1	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana</i> DSM 8902]
P27_hydA55	D4ZHLFP1:60:D2HDNACXX:3:2308:18720:99679:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	90.9	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA71	D4ZHLFP1:60:D2HDNACXX:3:2308:7319:15774:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	85.9	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA73	D4ZHLFP1:60:D2HDNACXX:3:1107:7828:16538:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	95.9	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA86	D4ZHLFP1:60:D2HDNACXX:3:1312:2867:61608:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	70.1	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA87	D4ZHLFP1:60:D2HDNACXX:3:2308:16490:49170:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	78.2	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA88	D4ZHLFP1:60:D2HDNACXX:3:1116:7681:64020:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	88.6	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA89	D4ZHLFP1:60:D2HDNACXX:3:2312:19934:93270:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	87.4	(YP_005061073)	hydrogenase, Fe-only [<i>Sphaerochaeta pleomorpha</i> str. Grapes]
P27_hydA9	D4ZHLFP1:60:D2HDNACXX:3:2113:4052:37186:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	82.0	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA94	D4ZHLFP1:60:D2HDNACXX:3:1313:19524:59750:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	88.6	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae</i> DSM 11293]
P27_hydA95	D4ZHLFP1:60:D2HDNACXX:3:2315:16166:74536:ACACGA	<i>Spirochaetes; Spirochaetia; Spirochaetales</i>	81.3	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana</i> DSM 8902]
P27_hydA12	D4ZHLFP1:60:D2HDNACXX:3:2306:15468:39944:ACACGA	<i>Bacteroidetes; Bacteroidia; Bacteroidales</i>	81.3	(AGY54346)	Iron hydrogenase 1 [<i>Bacteroidales</i> bacterium CF]
P27_hydA57	D4ZHLFP1:60:D2HDNACXX:3:1307:6493:50547:ACACGA	<i>Bacteroidetes; Bacteroidia; Bacteroidales</i>	72.4	(WP_010803103)	[FeFe] hydrogenase, group A [<i>Parabacteroides</i>]
P27_hydA120	D4ZHLFP1:60:D2HDNACXX:3:2312:6660:84593:ACACGA	Paddy field soil, Japan	79.0	(BAM65990)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA10	D4ZHLFP1:60:D2HDNACXX:3:1306:1891:68256:ACACGA	Paddy field soil, Japan	99.4	(BAM66117)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA100	D4ZHLFP1:60:D2HDNACXX:3:1313:6957:74344:ACACGA	Paddy field soil, Japan	94.7	(BAM65873)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA102	D4ZHLFP1:60:D2HDNACXX:3:2308:10616:100738:ACACGA	Paddy field soil, Japan	77.4	(BAM65979)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA82	D4ZHLFP1:60:D2HDNACXX:3:2309:13108:22639:ACACGA	Paddy field soil, Japan	82.8	(BAM65975)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA83	D4ZHLFP1:60:D2HDNACXX:3:1113:15517:30091:ACACGA	Paddy field soil, Japan	82.8	(BAM66175)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA80	D4ZHLFP1:60:D2HDNACXX:3:2115:2278:49486:ACACGA	Paddy field soil, Japan	79.0	(BAM66042)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA76	D4ZHLFP1:60:D2HDNACXX:3:2309:7462:55567:ACACGA	Paddy field soil, Japan	94.0	(BAM66088)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA58	D4ZHLFP1:60:D2HDNACXX:3:2302:12090:96382:ACACGA	Paddy field soil, Japan	82.4	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA62	D4ZHLFP1:60:D2HDNACXX:3:2313:1840:13283:ACACGA	Paddy field soil, Japan	90.1	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA40	D4ZHLFP1:60:D2HDNACXX:3:2305:19590:12472:ACACGA	Paddy field soil, Japan	82.0	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA41	D4ZHLFP1:60:D2HDNACXX:3:2311:18282:13431:ACACGA	Paddy field soil, Japan	80.1	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA29	D4ZHLFP1:60:D2HDNACXX:3:2108:7635:75958:ACACGA	Paddy field soil, Japan	99.4	(BAM66039)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA22	D4ZHLFP1:60:D2HDNACXX:3:1116:13594:62969:ACACGA	Paddy field soil, Japan	81.3	(BAM66042)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA20	D4ZHLFP1:60:D2HDNACXX:3:2316:13431:6449:ACACGA	Paddy field soil, Japan	70.9	(BAM65871)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA127	D4ZHLFP1:60:D2HDNACXX:3:1111:13539:41334:ACACGA	Paddy field soil, Japan	62.0	(BAM66154)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P27_hydA81	D4ZHLFP1:60:D2HDNACXX:3:2314:16120:39436:ACACGA	Saline microbial mat community, Mexico	98.2	(ACM67558)	iron-dependent hydrogenase [uncultured organism] clone="hydA_2
P27_hydA81	D4ZHLFP1:60:D2HDNACXX:3:2314:16120:39436:ACACGA	Yellowstone Geothermal Ecosystem, USA	96.3	(ADC53604)	[FeFe]-hydrogenase, [uncultured bacterium] clone E4_24
P27_hydA116	D4ZHLFP1:60:D2HDNACXX:3:2304:16632:31364:ACACGA	Oil fields subDjected to CO ₂ and water-flooding	77.4	(AGU38562)	[FeFe]-hydrogenase, partial [uncultured prokaryote] clone="FeFe-Hyd_W4-27
P27_hydA65	D4ZHLFP1:60:D2HDNACXX:3:2113:3477:30709:ACACGA	Saline microbial mat community, Mexico	97.1	(ACM67583)	iron-dependent hydrogenase [uncultured organism] clone="hydA_60
P27_hydA17	D4ZHLFP1:60:D2HDNACXX:3:2302:13048:20570:ACACGA	Water of high temperature petroleum reservoir	85.5	(AGU38562)	[FeFe]-hydrogenase, production water of high temperature petroleum reservoir
P27_hydA33	D4ZHLFP1:60:D2HDNACXX:3:1114:20033:69531:ACACGA	Yellowstone Geothermal Ecosystem, USA	93.2	(ADC53598)	[FeFe]-hydrogenase, [uncultured bacterium]