

Supplemental Table 2: Genome Properties of *Hyphomonas neptunium* ATCC 15444<sup>T</sup>

<u>property</u>	<u>state</u>	<u>value</u>	<u>assigned by</u>	<u>prediction</u>	<u>experiment</u>	<u>curator comment</u>
2-aminoethylphosphate degradation	none found	0	RULES	1		
4-hydroxyphenylacetate degradation	not supported	0.1	RULES	1		
5-aminolevulinate biosynthesis	YES		RULES	1		
5-aminolevulinate biosynthesis (glutamate pathway)	NO		RULES	1		
5-aminolevulinate biosynthesis from succinyl-CoA and glycine	YES	1	RULES	1		
6S RNA (eubacterial RNA polymerase regulator)	uncurated	0	RULES	1		
acetyl-CoA -- acetate interconversion via acetyl phosphate	none found	0	RULES	1		
acetyl-CoA biosynthesis from acetate, direct	YES	1	RULES	1		
acetyl-CoA carboxylase complex	YES	0.75	HYBRID	1		
addAB pathway	some evidence	0.5	RULES	1		
addiction module, hig class	YES	1	RULES	1		
addiction module, ParE class	none found	0	RULES	1		
addiction module,	none found	0	RULES	1		

RelE-RelB class			S			
addiction modules	YES	1	RULE S	1		
aerobic respiration	some evidence		RULE S	1		
arginine biosynthesis from ornithine, carbamoyl-p and aspartate	YES	1	RULE S	1		
arginine catabolism to glutamate via arginine succinyltransferase (AST)	some evidence	0.6	RULE S	1		
arsenical resistance system	YES	1	RULE S	1		
arsenite oxidase	none found	0	RULE S	1		
aspartate semialdehyde biosynthesis from aspartate	YES	1	RULE S	1		
attenuation system: tryptophanase	none found	0	RULE S	1		
bacterial cell division septum system	some evidence	0.6	RULE S	1		
bacteriochlorophyll biosynthesis from chlorophyllide a	none found	0	RULE S	1		
beta-ketoadipate degradation to succinyl-CoA and acetyl-CoA	some evidence	0.67	RULE S	1		
biofilm participation	YES		haft			TIGR paper
biotin biosynthesis	YES	0.75	HYBRI D	1		
cell shape	ROD		cpark	0	1	From Bergey's

						Manual. Cells are oval to rod in shape
chaperone system: DnaK-DnaJ-GrpE	YES	1	RULE S	1		
chaperone system: GroEL/GroES	YES	1	RULE S	1		
chaperone system: thermosome/prefoldin	none found	0	RULE S	1		
chlorophyll biosynthesis from chlorophyllide a	none found	0	RULE S	1		
chlorophyllide a biosynthesis from protoporphyrin IX	none found	0	RULE S	1		
chorismate biosynthesis via shikimate	YES	1	HYBRID	1		
circadian clock system KaiABC	none found	0	RULE S	1		
class I (aerobic) ribonucleotide reductase	YES	1	RULE S	1		
class II (B12-dependent) ribonucleotide reductase	YES	1	RULE S	1		
class III (anaerobic) ribonucleotide reductase	none found	0	RULE S	1		
clpXP degradation machine	YES	1	RULE S	1		
cobalamin-utilizing enzymes	YES	4	RULE S	1		
cobalt import system (ABC transporter: 3.A.1.18.1)	none found	0	RULE S	1		

cobalt import system (adapted nickel transporters)	none found	0	RULE S	1		
cobalt import system (CbtAB - proposed)	none found	0	RULE S	1		
cobalt import system (CbtC - proposed)	none found	0	RULE S	1		
cobalt import systems	NO	0	RULE S	1		
cobyrrinic acid diamide biosynthesis, aerobic pathway	not supported	0.08	RULE S	1		
cobyrrinic acid diamide biosynthesis, anaerobic pathway	not supported	0.09	RULE S	1		
coenzyme A biosynthesis from pantothenate	YES	1	RULE S	1		
Coenzyme B12 biosynthesis - overview	some evidence		RULE S	1		
Coenzyme B12 biosynthesis from cob(II)yrinate diamide	YES	1	RULE S	1		
coenzyme PQQ biosynthesis	none found	0	RULE S	1		
competence-related genes	none found	0	RULE S	1		
count of DNA molecules	QUANTITATIVE	1	RULE S			
count of predicted proteins	QUANTITATIVE	3521	RULE S			
count of TRAP transporter clusters	QUANTITATIVE	1	RULE S	1	0	

count of tRNAs	QUANTITATIVE	43	RULE S			
CRISPR RAMP module	none found	0	RULE S	1		
CRISPR region	NO	0	haft	1		by repfind and HMMs
CRISPR system, Aperi subtype (Archaea specific)	none found	0	RULE S	1		
CRISPR system, Dpsyc subtype	none found	0	RULE S	1		
CRISPR system, Dvulg subtype	none found	0	RULE S	1		
CRISPR system, Ecoli subtype	none found	0	RULE S	1		
CRISPR system, Hmari subtype	none found	0	RULE S	1		
CRISPR system, Mtube subtype (RAMP-like)	none found	0	RULE S	1		
CRISPR system, Nmeni subtype	none found	0	RULE S	1		
CRISPR system, Tneap subtype	none found	0	RULE S	1		
CRISPR system, Ypest subtype	none found	0	RULE S	1		
cyanophycin-like storage polymers	none found	0	RULE S	1		
cysteine biosynthesis from serine	YES	1	RULE S	1		
cysteine biosynthesis, tRNA-dependent	NO	0	RULE S	1		
cytochrome (quinone) oxidase, aa3 type, QoxABCD	none found	0	RULE S	1		
cytochrome	YES	1	RULE S	1		

(quinone) oxidase, bd type			S			
cytochrome (quinone) oxidase, bo type	not supported	0.2	RULE S	1		
cytochrome c based oxygen reduction and quinone re-oxidation	YES		RULE S	1		
cytochrome c oxidase, cbb3-type	YES	1	RULE S	1		
cytochrome c oxidase, mitochondrial, caa3-type	some evidence	0.75	RULE S	1		
cytochrome c oxidases	YES		RULE S	1		
cytochrome c reductase	YES	1	RULE S	1		
D-xylose utilization (conversion to D-xylulose-5-phosphate)	none found	0	RULE S	1		
degradation of tyrosine via homogentisate	some evidence	0.75	RULE S	1		
dissimilatory sulfate reduction	none found	0	RULE S	1		
DNA dinucleotide thermophily metric RR+YY-RY-YR	QUANTITATIVE	-0.008	RULE S			
DNA GC content	QUANTITATIVE	61.93	RULE S			
DNA polymerase III, bacterial	some evidence	0.75	RULE S	1		
DNA size (megabases)	QUANTITATIVE	3.705	RULE S			
dTDP-L-rhamnose	YES	1	RULE	1		

biosynthesis from glucose-1-phosphate			S			
ectoine biosynthesis	YES	1	RULE S	1		
electron transfer (transport) chain	some evidence		RULE S	1		
endospore formation minimal gene set	none found	0	RULE S	1		
Entner-Doudoroff pathway	some evidence	0.5	RULE S	1		
ethanolamine catabolism to acetaldehyde	none found	0	RULE S	1		
ethanolamine degradation organelle	none found	0	RULE S	1		
F and P-type conjugation systems (type IV secretion), common components	some evidence	0.22	RULE S	1		
F-type conjugation system	not supported		RULE S	1		
F-type conjugation system (type IV secretion) specific components	none found	0	RULE S	1		
F1/F0 ATPase	YES	1	selengt	1		
flagella	YES		haft	1	1	PMID:10758848
flagella, bacterial type	some evidence	0.48	HYBRID	1		
formaldehyde detoxification, glutathione-dependent	YES	1	RULE S	1		

fucose catabolism	none found	0	RULE S	1		
functional gene clustering - property level	QUANTITATIVE	48	RULE S			
GABA utilization	some evidence	0.33	RULE S	1		
galactose-6-phosphate degradation via tagatose-6-phosphate	none found	0	RULE S	1		
gas vesicle	none found	0	RULE S	1		
GatABC aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase complex	YES	1	RULE S	1		
glucosylglycerol biosynthesis	none found	0	RULE S	1		
glutathione biosynthesis	YES	1	RULE S	1		
glycine betaine biosynthesis from choline	some evidence	0.5	HYBRID	1		
glycine cleavage system	YES	1	RULE S	1		
glycogen system	none found	0	RULE S	1		
glyoxylate shunt	YES	1	selengt	1		
histidine biosynthesis from ribose-5-phosphate	YES	1	RULE S	1		
histidine degradation to glutamate	YES	1	RULE S	1		
HMM hit percentage	SUFFICIENT	71	RULE S			

Hybrid NRPS-PKS natural product biosynthesis genes	NO	0	RULE S	1		
inteins	none found	0	RULE S	1		
intrinsic pathogen of animals	NO		haft			PMID:10758848
intrinsic pathogen of humans	NO		haft			PMID:10758848 marine
IPP biosynthesis	YES		RULE S	1		
IPP biosynthesis via deoxyxylulose	YES	0.8	HYBRID	1		
IPP biosynthesis via mevalonate	NO		RULE S	1		
iron-sulfur cluster assembly iscSUA-hscBA-fdx system	none found	0	RULE S	1		
iron-sulfur cluster assembly SUF system	some evidence	0.75	RULE S	1		
iron-sulfur cluster assembly systems	some evidence		RULE S	1		
isoleucine biosynthesis from threonine and pyruvate	YES	1	RULE S	1		
KDO(2)-lipid A (Re LPS) biosynthesis and delivery	some evidence	0.89	RULE S	1		
Leloir pathway (galactose/glucose interconversion)	some evidence	0.25	RULE S	1		
leucine biosynthesis from pyruvate and acetyl-CoA	YES	1	RULE S	1		
lipoprotein localization system	none found	0	RULE S	1		

lolABCDE						
lipoprotein system lgt/lsp/lnt	YES	1	RULE S	1		
LPS inner core biosynthesis, ketodeoxyoctonate and heptose type	some evidence	0.2	RULE S	1		
LPXTG/sortase system	none found	0	RULE S	1		
lysine biosynthesis	YES		RULE S	1		
lysine biosynthesis from aspartate semialdehyde, acylated pathway	YES	1	RULE S	1		
lysine biosynthesis via alpha-aminoadipate (AAA pathway)	not supported	0.25	RULE S	1		
mannosylglycerate biosynthesis	none found	0	RULE S	1		
menaquinone biosynthesis	none found	0	RULE S	1		
mesophile	YES		haft			
methanogenesis	NO		selengut	1	0	
methionine biosynthesis from homoserine	some evidence	0.75	RULE S	1		
minCDE system	none found	0	RULE S	1		
mismatch repair	YES	1	RULE S	1		
molybdate ABC transporter	none found	0	RULE S	1		
molybdopterin biosynthesis	some evidence	0.6	RULE S	1		
mreBCD system	some evidence	0.33	RULE S	1		

Na <sup>+</sup> -translocating NADH-quinone reductase	none found	0	RULE S	1		
NAD(P) biosynthesis from L-aspartate and DHAP	YES	0.75	selengt	1		
NADH dehydrogenase I	YES	1	selengt	1		
NADH dehydrogenase, Sno(Mnh)ABCDE FG)	YES	1	RULE S	1		
nickel import ABC transporter	none found	0	RULE S	1		
nickel-dependent hydrogenase	none found	0	RULE S	1		
nitrogen fixation	none found	0	RULE S	1		
nonhomologous end-joining, bacterial type	none found	0	RULE S	1		
nucleoside catabolism	none found	0	RULE S	1		
nucleotide excision repair	YES	1	RULE S	1		
ornithine biosynthesis from glutamate, acetylated branch	YES	1	RULE S	1		
outer membrane	YES		haft			
oxygen reduction and quinone re-oxidation	YES		RULE S	1		
oxygen requirement	aerobic		haft		1	PMID:10758848
pantothenate biosynthesis from aspartate and 2-oxoisovalerate	some evidence	0.75	RULE S	1		

pentose phosphate cycle	some evidence	0.89	RULE S	1		
PEP-CTERM	none found	0	RULE S	1		
peptidoglycan(mur ein) biosynthesis	YES	1	RULE S	1		
Percent A (Ala)	QUANTITATIVE	12.737	RULE S			
Percent C (Cys)	QUANTITATIVE	0.831	RULE S			
Percent D (Asp)	QUANTITATIVE	5.714	RULE S			
Percent E (Glu)	QUANTITATIVE	6.194	RULE S			
Percent F (Phe)	QUANTITATIVE	3.759	RULE S			
Percent G (Gly)	QUANTITATIVE	8.745	RULE S			
Percent H (His)	QUANTITATIVE	1.836	RULE S			
Percent I (Ile)	QUANTITATIVE	5.192	RULE S			
Percent K (Lys)	QUANTITATIVE	3.397	RULE S			
Percent L (Leu)	QUANTITATIVE	9.796	RULE S			
Percent M (Met)	QUANTITATIVE	2.569	RULE S			
Percent N (Asn)	QUANTITATIVE	2.612	RULE S			
Percent P (Pro)	QUANTITATIVE	5.343	RULE S			
Percent Q (Gln)	QUANTITATIVE	3.06	RULE S			
Percent R (Arg)	QUANTITATIVE	6.675	RULE S			
Percent S (Ser)	QUANTITATIVE	5.587	RULE S			

Percent T (Thr)	QUANTITATIVE	5.382	RULES			
Percent V (Val)	QUANTITATIVE	6.862	RULES			
Percent W (Trp)	QUANTITATIVE	1.378	RULES			
Percent Y (Tyr)	QUANTITATIVE	2.32	RULES			
periplasmic nitrate reductase	none found	0	RULES	1		
phage: major features	some evidence	1	RULES	1		
phenylacetic acid catabolism	none found	0	RULES	1		
phenylalanine biosynthesis from chorismate	YES	1	RULES	1		
phosphate ABC transporter (pstSCAB-phoU)	some evidence	0.75	RULES	1		
phosphonates ABC transport	some evidence	0.67	RULES	1		
phosphonates C-P lyase system	none found	0	RULES	1		
photosynthesis	NO		haft			
polyhydroxyalkanoic acids	YES	1	HYBRID	1		
polyketide biosynthesis, type I	YES	1	RULES	1		
Potassium-transporting ATPase KdpFABC	none found	0	RULES	1		
prokaryotic N-terminal cleavage/methylation, type IV pilin-like	some evidence	6	RULES	1		

proline biosynthesis from glutamate	YES	1	RULE S	1		
propionyl-CoA catabolism via methylcitric acid	none found	0	RULE S	1		
protein average length	QUANTITATIVE	316	RULE S			
protein-coding palindromic elements	none found	0	RULE S	1		
protocatechuate degradation to beta-ketoadipate	none found	0	RULE S	1		
protoheme from protoporphyrin IX	YES	1	RULE S	1		
protoporphyrin IX biosynthesis from uroporphyrinogen III	some evidence	0.67	RULE S	1		
PTS transport system	some evidence	0.6	RULE S	1		
purine (inosine-5'-phosphate) biosynthesis from ribose-5-phosphate	YES	1	RULE S	1		
pyrimidine (uridine-5'-phosphate) de novo biosynthesis	YES	1	RULE S	1		
pyrrolysine	NO	0	haft	1	0	
pyruvate fermentation to acetoin	none found	0	RULE S	1		
recBCD pathway	none found	0	RULE S	1		
recFOR recombination pathway	YES	1	RULE S	1		
reduction of	YES	1	RULE	1		

oxidized methionine			S			
release factor 2 programmed frameshift	YES	1	haft	1		
resistance to mercury	some evidence	0.33	HYBRID	1		
Resistance to Reactive Oxygen Species (ROS)	YES	4	RULE S	1		
restriction enzyme system, type I	YES	1	RULE S	1		
Rhamnose catabolism	none found	0	RULE S	1		
riboflavin, FAD and FMN from GTP and ribulose-5-P	YES	1	RULE S	1		
ribonucleotide reduction	YES		RULE S	1		
ribosome, bacterial, large subunit	YES	0.97	HYBRID	1		
ribosome, bacterial, small subunit	YES	1	RULE S	1		
RNA polymerase, bacterial	YES	1	RULE S	1		
Rnf-type electron transport complex	none found	0	RULE S	1		
ruvABC Holliday junction complex	YES	0.67	HYBRID	1		
Sec system preprotein translocase	YES	1	RULE S	1		
selenocysteine	YES	1	HYBRID	1		
sequenced plasmids	NO	0	RULE S			
signal recognition system, bacterial	some evidence	0.75	RULE S	1		

single complex oxygen reduction and quinone re-oxidation	YES		RULE S	1		
siroheme biosynthesis from uroporphyrinogen-III	YES	1	RULE S	1		
SMC-ScpA-ScpB complex	YES	1	RULE S	1		
SOS response	YES	1	RULE S	1		
species	Hyphomonas neptunium		Taxon_lo			
spermidine biosynthesis from arginine (via agmatine)	none found	0	RULE S	1		
sporadically distributed four-gene operon	none found	0	RULE S	1		
spore formation	NO		haft			
sulfate reduction to sulfide, assimilatory	not supported	0.5	RULE S	1		
sulfate/thiosulfate ABC transporter	none found	0	RULE S	1		
sulfite reductase complex, Salmonella/Clostridium type	none found	0	RULE S	1		
superoxide dismutase, nickel-type	none found	0	RULE S	1		
Tat (Sec-independent) protein export	YES	1	RULE S	1		
TaxID	EXACT	228405	Taxon_lo			
TCA cycle	YES	1	HYBRI	1		

			D			
temperature environment	mesophilic		haft			
tetrahydrofolate biosynthesis from GTP and PABA	YES	1	RULE S	1		
tetrahydromethanopterin S-methyltransferase complex	none found	0	RULE S	1		
thiamine/TPP ABC transporter ThiBPQ	none found	0	RULE S	1		
thiamine: hydroxyethylthiazole from 1-deoxy-D-xylulose-5-phosphate, cysteine, either Tyr or Gly	some evidence	0.5	RULE S	1		
thiamine: hydroxymethylpyrimidine pyrophosphate from aminoimidazole ribotide	YES	1	RULE S	1		
thiamine: TPP from HMP-PP and HET-P	YES	1	RULE S	1		
thiotemplate type non-ribosomal peptide biosynthesis	PARTIAL	1	RULE S	1		
threonine biosynthesis from aspartate semialdehyde	YES	1	RULE S	1		
Ti-type conjugation system	none found	0	RULE S	1		
tmRNA trans-	YES	1	RULE	1		

translation system			S			
Tol-Pal system	some evidence	0.4	RULE S	1		
TonB-dependent transport	none found	0	RULE S	1		
transcription termination - antitermination Nus factors	YES	1	selengt	1		
Transcription-Coupled Nucleotide Excision Repair	YES	1	RULE S	1		
TRAP-T (tripartite ATP-independent periplasmic transporters) family transporters	YES	1	RULE S	1		
trehalose biosynthesis, OtsAB pathway	YES	1	HYBRID	1		
trehalose biosynthesis, TreYZ pathway	none found	0	RULE S	1		
trehalose utilization	none found	0	RULE S	1		
tRNA aminoacylation	YES	0	RULE S	1		
tRNA-Asn direct aminoacylation	none found	0	RULE S	1		
tRNA-Gln direct aminoacylation	none found	0	RULE S	1		
tryptophan biosynthesis from ribose-5-phosphate	YES	1	RULE S	1		
type I secretion	not supported	0.25	RULE S	1		
type II secretion	some evidence	0.89	RULE S	1		

type III secretion	NO		haft	1		
tyrosine biosynthesis from chorismate	YES	1	RULE S	1		
ubiquinone biosynthesis from chorismate, aerobic	some evidence	0.83	RULE S	1		
uncharacterized gene pair TIGR02612/TIGR02613	none found	0	RULE S	1		
uncharacterized gene pair TIGR02683/TIGR02684	none found	0	RULE S	1		
uncharacterized gene pair TIGR02687/TIGR02688	none found	0	RULE S	1		
urea carboxylase/allophanate hydrolase pathway	none found	0	RULE S	1		
urease	none found	0	RULE S	1		
uroporphyrinogen III biosynthesis from 5-aminolevulinate	YES	1	RULE S	1		
V-type ATPase	none found	0	RULE S	1		
valine biosynthesis from pyruvate	YES	1	RULE S	1		