

Supplementary Table S3: Comparison of the genome properties of *P. glucodililyticus* DD6b with all completely sequenced type strains belonging to genus *Pedobacter*, as on 05-th of December 2014.

Genome Name	<i>P. agri</i> PB92	<i>P. borealis</i> DSM 19626	<i>P. glucosidilyticus</i> DD6b	<i>P. glucosidilyticus</i> DSM 23534	<i>P. heparinus</i> HIM 762-3, DSM 2366	<i>P. oryzae</i> DSM 19973
GenBank Project ID	PRJNA84275	PRJNA236461	PRJNA246159	PRJNA188803	PRJNA27949	PRJNA185613
IMG Genome ID	2548876984	2585427687	2590828803	2523533576	644736398	2523231054
GenBank Accession	AJLG000000000	J AUG000000000	JMTN000000000	AULF000000000	CP001681	AUHA000000000
Genome Size	5141552	5544917	3872381	4021020	5167383	3445768
Gene Count	5188	5008	3352	3524	4339	3122
Coding Base Count %	87.71	85.13	90.65	90.54	93.36	90.92
GC	.38	.38	.35	.34	.42	.38
COG Count	2182	2391	1910	1913	2320	1784
COG %	42.06	47.74	56.98	54.28	53.47	57.14
KEGG Count	788	866	823	812	879	760
KEGG %	15.19	17.29	24.55	23.04	20.26	24.34
KOG Count	639	717	641	636	760	633
KOG %	12.32	14.32	19.02	18.05	17.52	20.28
Pfam Count	3559	3549	2646	2749	3458	2435
Pfam %	68.6	70.87	78.94	78.01	79.7	77.99
TIGRfam Count	1091	1119	1005	1025	1156	917
TIGRfam %	34.36	22.34	29.98	29.09	26.64	29.37
Signal Peptide Count	658	729	482	448	691	371
Transmembrane Count	1108	1105	749	767	1051	774
w/ Func Pred %	65.11	66.79	77.86	52.07	66.26	75.3
Scaffold Count	379	216	93	62	1	10
rRNA Count	3	3	3	7	7	6
tRNA Count	49	51	38	41	45	37
CRISPR Count	0	0	1(46)	1(4)	0	0