Supplementary Information

Table ST1. Quantitative comparison of phosphate solubilizing ability to other phosphate-solubilizing bacterial isolates

Name of organism	Comparative study of soluble phosphate concentration*	High range of salinity tolerance	Reference
P5 isolate	10 mg L^{-1} after 5 days or 0.0021 mg. ml^{-1}. day^{-1} with 2.11 mg. ml^{-1}. day^{-1} biomass production	7.5-10 % NaCl	Current study
Pseudomonas sp.	66.2 ± 13.4 mg. L^{-1} after 3 days or 0.022 mg. ml^{-1}. day^{-1}	2.75 % NaCl	Blanco-Vargas *et al.*, 2020; Deshwal and Kumar, 2013
***Serratia* sp.**	89.5 ± 4.7 mg. L^{-1} after 3 days or 0.029 mg. ml^{-1}. day^{-1}	5.8% NaCl	Kulkova *et al.*, 2024; Blanco-Vargas *et al.,* 2020
Bacillus sp.	461.86 mg·L^{-1} after 7-days or 0.066 mg. ml^{-1}. day^{-1}	8% NaCl	Lin *et al.*, 2023; Gul *et al*., 2023
***Micrococcus* sp.**	285.78 µg mL^{-1} after 3 day or 0.095 mg. ml $^{-1}$. day^{-1}	5% NaCl	Joshi *et al.*, 2023; Alvarez-Sastre and Carro, 2022
Streptomyces sp.	320 µg mL^{-1} after 3 day or 0.11 mg. mL^{-1}. day^{-1}	300nM or 17.53% NaCl	Nozari *et al.*, 2021; Joshi *et al.,* 2023
Klebsiella sp.	891.38 ± 18.55 µg mL^{-1} after 3 days or 0.297 mg. ml^{-1}. day^{-1}	6% NaCl	Singh *et al.*, 2015; Joshi *et al.*, 2023

*For quantification used different methods and different media

Table ST2. Correlation among day, biomass concentration, and Orthophosphate concentration of *Bacillus sonorensis* GG2.

Correlation				
***Bacillus sonorensis* GG2**		**Day**	**Biomass Concentration**	**Orthophosphate Concentration**
Day	Pearson Correlation	1	0.931	0.399
	Sig. (2-tailed)		0.003	0.004
Biomass Concentration	Pearson Correlation	0.931	1	0.412
	Sig. (2-tailed)	0.003		0.002
Orthophosphate Concentration	Pearson Correlation	0.399	0.412	1
	Sig. (2-tailed)	0.004	0.002	

Correlation is significant at the 0.05 level (2-tailed). Statistical Analysis by IBM SPSS 26.

Table ST3. Correlation among day, biomass concentration, and Para-nitrophenol concentration of *Bacillus sonorensis* GG2.

Correlation				
***Bacillus sonorensis* GG2**		**Day**	**Biomass Concentration**	**Para-nitrophenol Concentration**
Day	Pearson Correlation	1	1.00	0.888
			0.002	0.001

	Sig. (2-tailed)			
Biomass Concentration	Pearson Correlation	1.00	1	0.889
	Sig. (2-tailed)	0.002		0.001
Para-nitrophenol Concentration	Pearson Correlation	0.888	0.889	1
	Sig. (2-tailed)	0.001	0.001	

Correlation is significant at the 0.05 level (2-tailed). Statistical Analysis by IBM SPSS 26

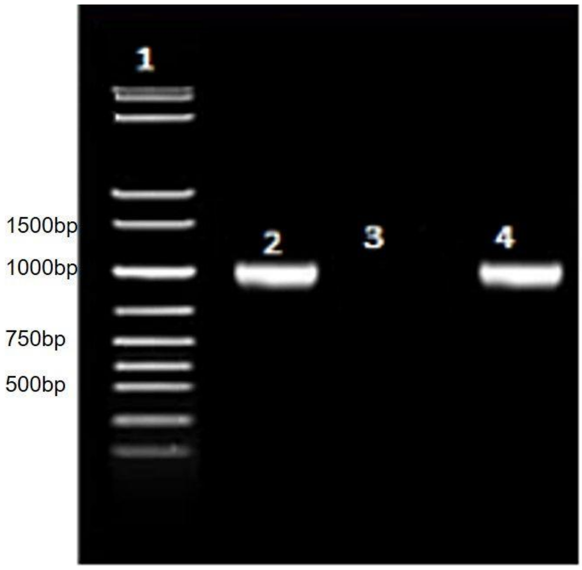


Fig. S1. *Shows a single 1Kb PCR product of 16S rRNA gene on 2% agarose gel (Lane 1: 1KB DNA ladder, Lane 2: 16S amplicon (Positive Control: E. Coli), Lane 3: Negative Control, Lane 4: Sample).*

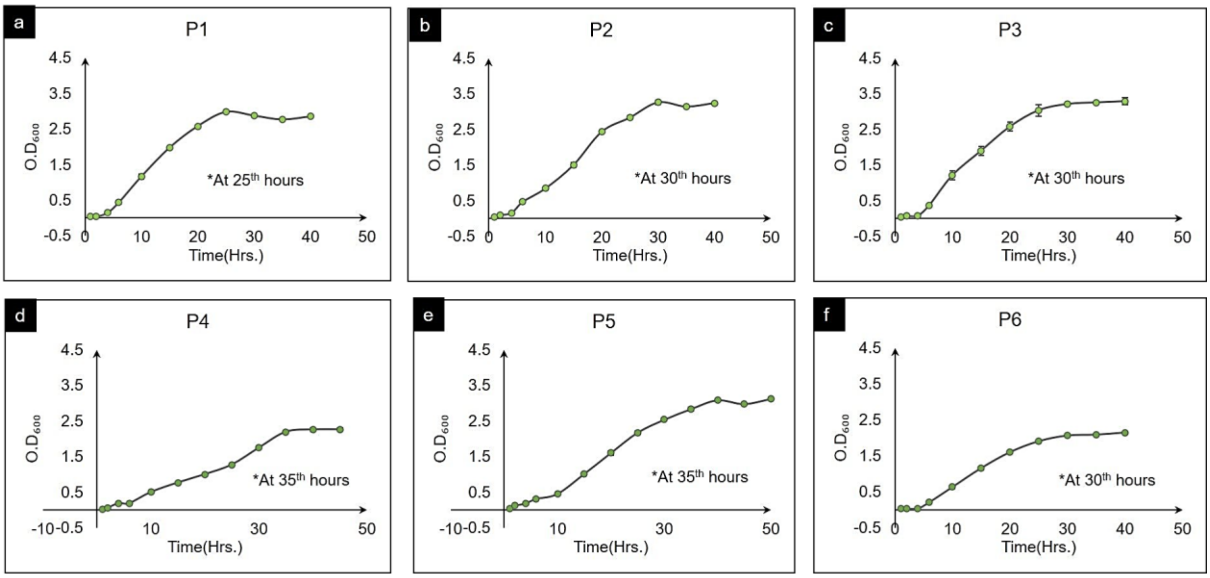


Fig. S2. *Exponential phase study of P-solubilizing bacteria in Pvk medium.*

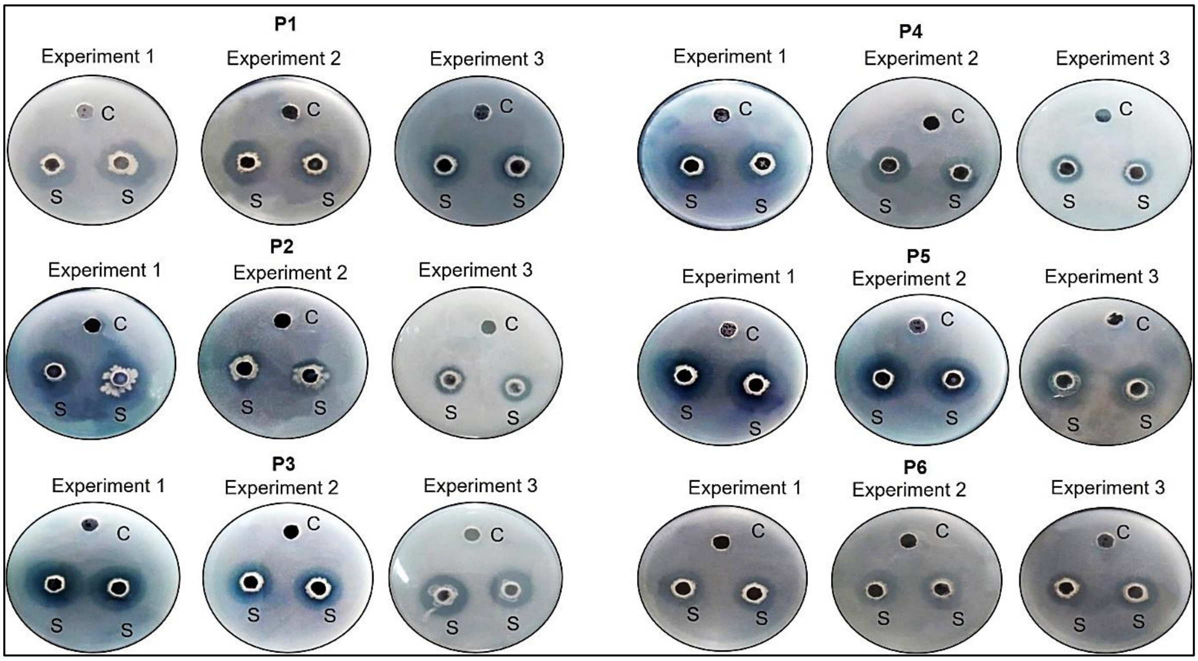


Fig. S3. *Inorganic phosphate solubilization in Pvk medium plate by holo-zone formation (C=control; S= pure culture).*

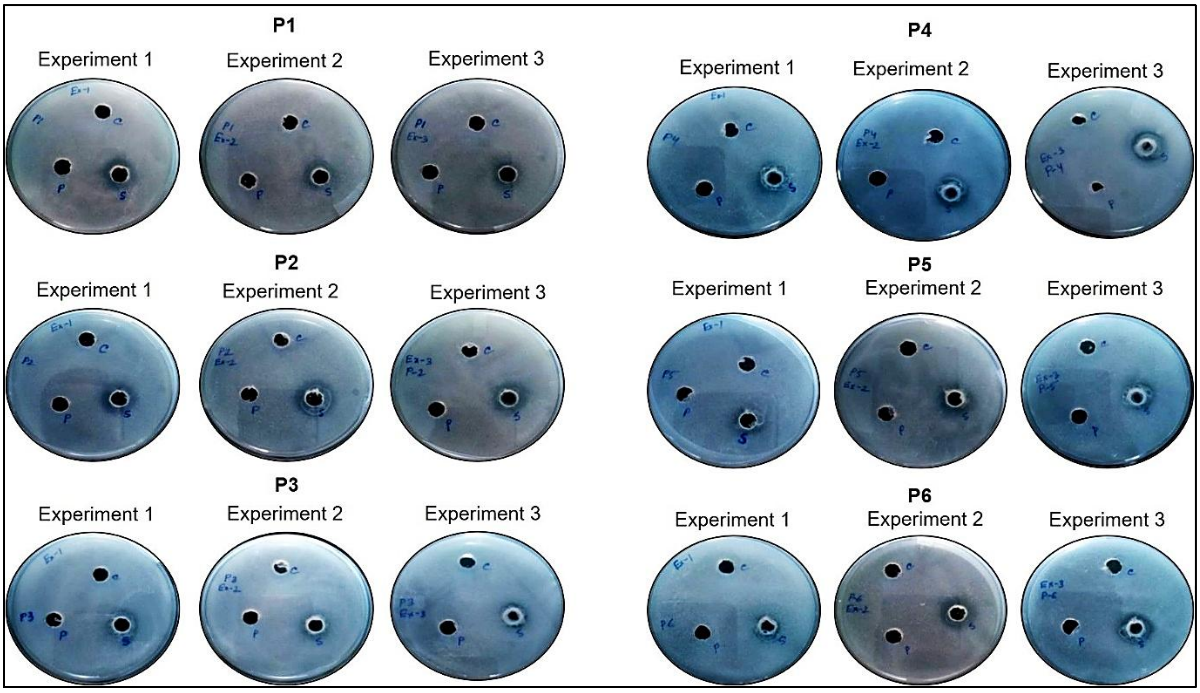
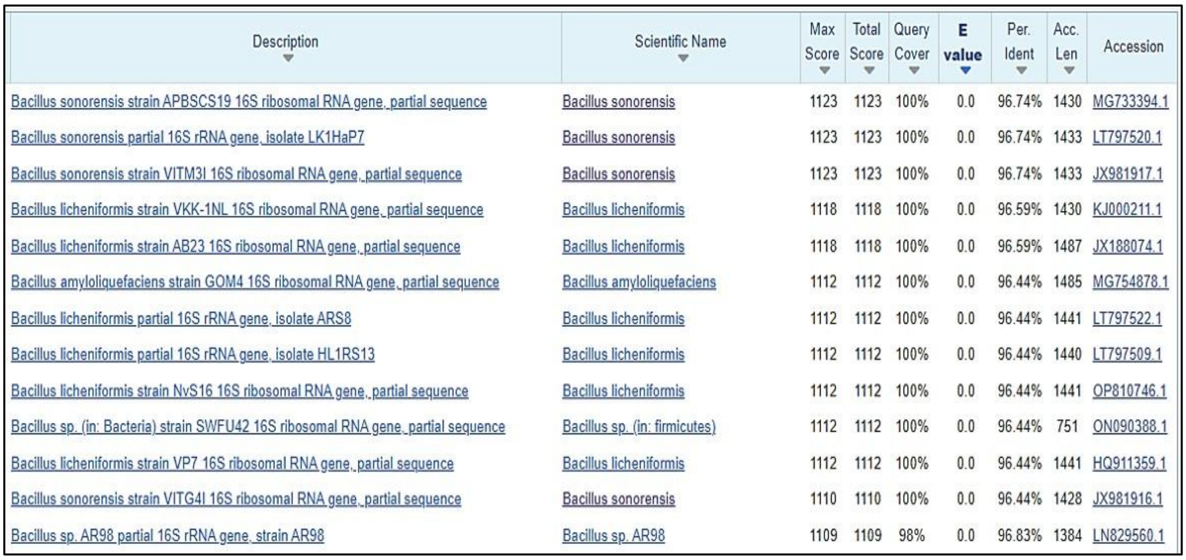


Fig. S4. *Determine the extracellular or intracellular response for P-solubilization in Pvk media, when, C = PBS buffer as a control, P = crude extract of P-solubilizing bacterial isolate (for intracellular response investigation), S = P-solubilizing bacterial alive cell (for extracellular response investigation).*



Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Bacillus sonorensis strain APBSCS19 16S ribosomal RNA gene, partial sequence	Bacillus sonorensis	1123	1123	100%	0.0	96.74%	1430	MG733394.1
Bacillus sonorensis partial 16S rRNA gene, isolate LK1HaP7	Bacillus sonorensis	1123	1123	100%	0.0	96.74%	1433	LT797520.1
Bacillus sonorensis strain VITM3I 16S ribosomal RNA gene, partial sequence	Bacillus sonorensis	1123	1123	100%	0.0	96.74%	1433	JX981917.1
Bacillus licheniformis strain VKK-1NL 16S ribosomal RNA gene, partial sequence	Bacillus licheniformis	1118	1118	100%	0.0	96.59%	1430	KJ000211.1
Bacillus licheniformis strain AB23 16S ribosomal RNA gene, partial sequence	Bacillus licheniformis	1118	1118	100%	0.0	96.59%	1487	JX188074.1
Bacillus amyloliquefaciens strain GOM4 16S ribosomal RNA gene, partial sequence	Bacillus amyloliquefaciens	1112	1112	100%	0.0	96.44%	1485	MG754878.1
Bacillus licheniformis partial 16S rRNA gene, isolate ARS8	Bacillus licheniformis	1112	1112	100%	0.0	96.44%	1441	LT797522.1
Bacillus licheniformis partial 16S rRNA gene, isolate HL1RS13	Bacillus licheniformis	1112	1112	100%	0.0	96.44%	1440	LT797509.1
Bacillus licheniformis strain NvS16 16S ribosomal RNA gene, partial sequence	Bacillus licheniformis	1112	1112	100%	0.0	96.44%	1441	OP810746.1
Bacillus sp. (in: Bacteria) strain SWFU42 16S ribosomal RNA gene, partial sequence	Bacillus sp. (in: firmicutes)	1112	1112	100%	0.0	96.44%	751	ON090388.1
Bacillus licheniformis strain VP7 16S ribosomal RNA gene, partial sequence	Bacillus licheniformis	1112	1112	100%	0.0	96.44%	1441	HQ911359.1
Bacillus sonorensis strain VITG4I 16S ribosomal RNA gene, partial sequence	Bacillus sonorensis	1110	1110	100%	0.0	96.44%	1428	JX981916.1
Bacillus sp. AR98 partial 16S rRNA gene, strain AR98	Bacillus sp. AR98	1109	1109	98%	0.0	96.83%	1384	LN829560.1

Fig. S5. *16S rRNA sequence of P5 bacterial isolates was generated BLAST analysis to compare with the sequences in the NCBI GenBank database. The P5 isolate has been higher similar to Bacillus sonorensis bacterial strain.*

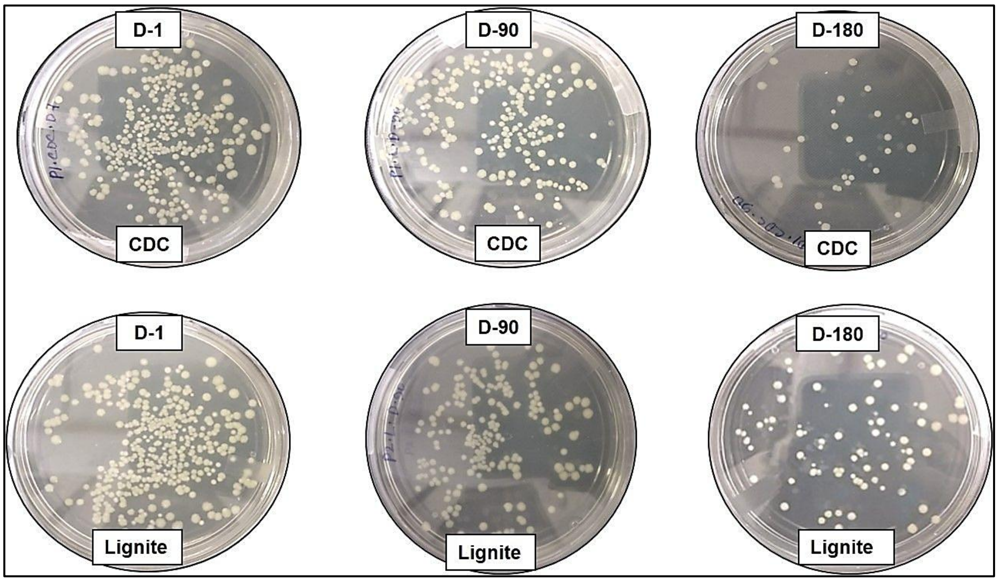


Fig. S6. *Best plate shows of viability study at 0, 90, and 180 days of Bacillus sonorensis GG2 in carriers (CDC and lignite).*

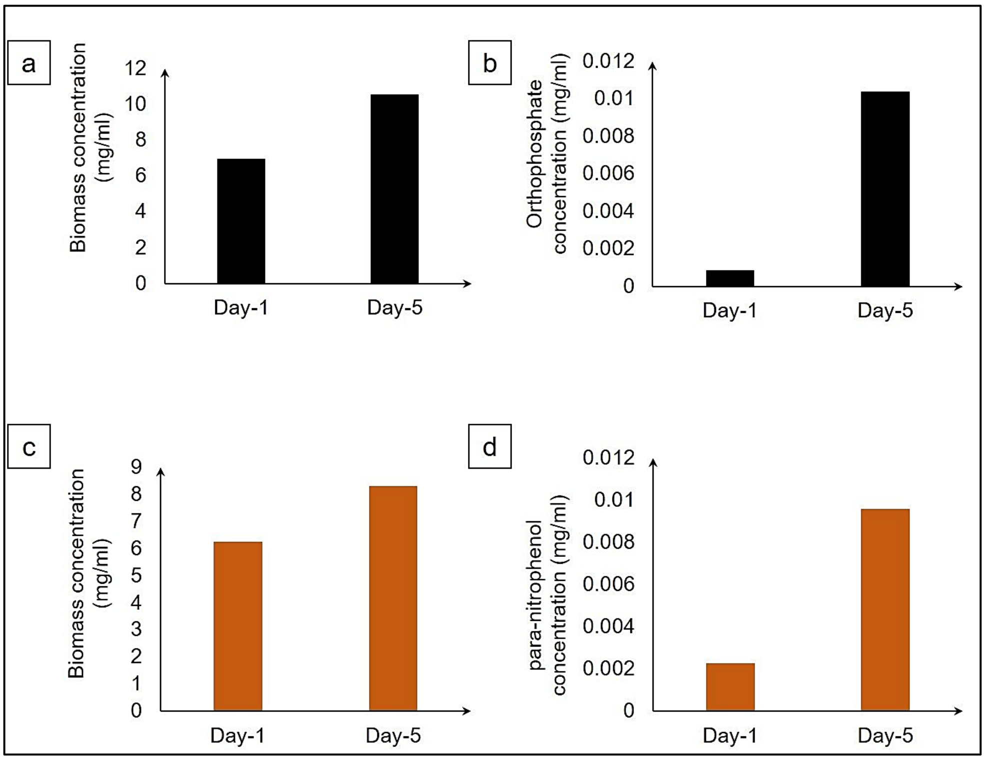


Fig. S7. *Biomass, orthophosphate and para-nitrophenol production profile of Bacillus sonorensis GG2 strain (a) biomass increase profile at study of orthophosphate production, (b) orthophosphate increase profile at 5 days, (c) biomass increase profile at study of para-nitrophenol production (d) para-nitrophenol production at 5 days.*

Supplementary Datafile SD1: Phosphate solubilizing bacterial 16S rRNA sequences in FASTA databases

>*Bacillus sonorensis* GG2 =>*Bacillus sonorensis* GG2_16s rRNA gene
CGGACAGATGGGAGCTTGCTCCCTGATGTCAGCGGCGGACGGGTGAGTAACA
CGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATA
CCGGATGCTTGATTGAACCGCATGGTTCAATTATAAAAGGTGGCTTTTACCTAC
CACTTACAAATGGACCCGCGGCGCATTACCTAGTTGGTGAGGTAACGGCTCAC
CAAGGCAACAATGCGTAGCCAACCTGAAAGGGTGATCGGCCACACTGGAACTG
AAACACGGCCCAAACTCCTACGGGAGGCACCAGTAGGGAATCTTCCCCAAGGG
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AACTCTGTTGTTAGGGAAAAACAAGTACCGTTCAAATAGGGCGGTACCTTGACG
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TCTTAAGTCTAATGTGAAACCCCCCGGCTCAACCGGGAAGGGTCATTGAAAACT
GGGGAACTTGAGTGCAAAAAAGGAAAGGGAAATTCCACGTGTACCGGTGAAAT
GCGTAAAAATGTGAAGGAACACCAGTG GCGAAGGC

>*Priestia megaterium* LsR8 =>*MW423831.1 Priestia megaterium strain NIBSM_LsR8 16S ribosomal RNA gene, partial sequence*
AAGGGGGCGGGGTGCTAATACTGCAAGTCGAGCGAACTGATTAGAAGCTTGCT
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ACTGGGATAACTTCGGGAAACCGAAGCTAATACCGGATAGGATCTTCTCCTTCA
TGGGAGATGATTGAAAGATGGTTTCGGCTATCACTTACAGATGGGCCCGCGGT
GCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCATAGCCGA
CCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTAC
GGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAA
CGCCGCGTGAGTGATGAAGGCTTTCGGGTCG

>*Klebsiella* sp. BRSPKC05 =>*ON038365.1 Klebsiella sp. strain BRSPKC05 16S ribosomal RNA gene, partial sequence*
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>*Enterobacter* sp. LYX-2 =>*OK035565.1 Enterobacter sp. strain LYX-2 16S ribosomal RNA gene, partial sequence*
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>Pseudomonas fluorescens MRPF-2 =>_OP493230.1 Pseudomonas fluorescens strain MRPF-2 16S ribosomal RNA gene, partial sequence_

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>*Rhizobium meliloti* M55241 =>*M55241.1 Rhizobium meliloti 16S ribosomal RNA, partial*

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>*Acinetobacter* sp. PSK.N1 =>*OP741088.1 Acinetobacter sp. strain PSK.N1 16S ribosomal RNA gene, partial sequence*

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>Alcaligenes aquatilis RD03 =>_OP680985.1 Alcaligenes aquatilis strain RD03 16S ribosomal RNA gene, partial sequence_

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>Azospirillum brasilense* AzCast =>*OP882682.1 Azospirillum brasilense strain AzCast 16S ribosomal RNA gene, partial sequence

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>Burkholderia cepacia AF175314 =>_AF175314.1 Burkholderia cepacia 16S ribosomal RNA gene, partial sequence_

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GACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA
GTGGGGAATTTTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTGTGT
GAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAAAGAAAACCTTGGCTC
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CCTGGGAACTGCATTGGTGACTGGCGGGCTAGAGTATGGCAGAGGGGGGTAG
AATTCCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCG
AAGGCAGCCCCCTGGGCCAATACTGACGCTCATGCACGAAAGCGTGGGGAGC
AAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGT
TGGGGATTCATTTCCTTAGTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGG
GAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGC
GGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGA
CATGGTCGGAATCCTGAAGAGATTCGGGAGTGCTCGAAAGAGAACCGGCACAC
AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC
GCAACGAGCGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGA
CTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCC

CTTATGGGTAGGGCTTCACACGTCATACAATGGTCGGAACAGAGGGTTGCCAA
CCCGCGAGGGGGAGCTAATCCCAGAAAACCGATCGTAGTCCGGATTGCACTCT
GCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCG
CGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTG
GGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAGGACGGTCACCACGGTAG
GATTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGG

>Paenibacillus macerans **TLLY7 =>*MT705866.1 Paenibacillus macerans strain TLLY7 16S ribosomal RNA gene, partial sequence***

AGATCGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACCTGATGGAGTGCTT
GCACTCCTGATGGTTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCC
CGTAAGACCGGGATAACTACCGGAAACGGTAGCTAATACCGGATAATCAAGTCT
CTCGCATGGGAGGCTTGGGAAAGGGCGGAGCAATCTGTCACTTACGGATGGG
CCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCGACGATG
CGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCA
GACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGA
CGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGC
CAGGGAAGAACGTCTTCTGGAGTAACTGCCAGGAGAGTGACGGTGCCTGAGAA
GAAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAA
GCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGCTGTTTAAGTCT
GGTGTTTAATCCTGGGGCTCAACTCCGGGTCGCACTGGAAACTGGACGGCTTG
AGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGAT
GTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGACGCTGA
GGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC
GTAAACGATGAGTGCTAGGTGTTAGGGGTTTCGATACCCTTGGTGCCGAAGTA
AACACATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAG
GAATTGACGGGGACCCGCACAAGCAGTGGAGTATGTGGTTTAATTCGAAGCAA
CGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTGTAGAGATATGG
CTTTCCTTCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT
CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGACTTTAGTTGC
CAGCAAGTGAAGTTGGGCACTCTAGAGTGACTGCCGGTGACAAACCGGAGGAA
GGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTA
CTACAATGGCCGGTACAACGGGAAGCGAAGGAGCGATCTGGAGCGAATCCTA

GAAAAGCCGGTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGTCG
GAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCT
TGTACACACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGAG
GTAACCGCAAGGGGCCAGCCGCCGAAGGTGGGGTAGATGATTGGGT

>*Pseudomonas putida* R43 =>*KC990820.1 Pseudomonas putida strain R43 16S ribosomal RNA gene, partial sequence*

CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACG
TTTCGAAAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACC
TTCGGGCCTTGCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGG
TAATGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCA
CACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAAT
ATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGT
CTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAGTAAGCTAATACCTT
GCTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGC
CGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC
GCGTAGGTGGTTCGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAC
TGCATCCAAAACTGGCGAGCTAGAGTACGGTAGAGGGTGGTGGAATTTCCTGT
GTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCA
CCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTA
GATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCCGTTGGAATCCTTG
AGATTTTAGTGGCGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCC
GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCAT
GTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATGCAGAG
AACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCTGACACAGGTGCTGCAT
GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGC
AACCCTTGTCCTTAGTTACCAGCACGTTATGGTGGGCACTCTAAGGAGACTGCC
GGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACG
GCCTGGGCTACACACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGC
GAGGTGGAGCTAATCTCACAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC
TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTG
AATACGTTCCCGGGCCTTGTACACACCGCCCGTCACAACCATGGGTAGTGGGT

>Cytobacillus firmus* NPBR2 *=>MT383634.1 Cytobacillus firmus strain NPBR2 16S ribosomal RNA gene, partial sequence

GAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACGGATGGGAGCT
TGCTCCCAGACCGTCAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTGCC
TGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGATAAYTCTTTYC
CTCACATGAGGRAAAGCTGAAAGATGGCATCTCGCTATCACTTACAGATGGGC
CCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCVACGATGC
GTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAG
ACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGAC
GGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAACTCTGTTGTC
AGGGAAGAACAAGTACCGGAGTAACTGCCGGTACCTTGACGGTACCTGACCAG
AAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGC
GTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGTTCCTTAAGTCTGA
TGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGGAACTTG
AGTGCAGAAGAGAAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGAT
GTGGAGGAACACCAGTGGCGAAGGCGACTCTTTGGTCTGTAACTGACGCTGAG
GCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCG
TAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCAAA
CGCATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGA
ATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACG
CGAAGAACCTTACCAGGTCTTGACATCTCCTGACAACCCTAGAGATAGGGCGTT
CCCCTTCGGGGGACAGGATGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTC
GTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCC
AGCATTCAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGT
GGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTA
CAATGGATGGTACAAAGGGCTGCAAGACCGCGAGGTTAAGCGAATCCCATAAA
ACCATTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATC
GCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTAC
ACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGGGGTAAC
CTTTTGGAGCCAGCCGCCTAAGGTGGGACAGATGATTGG

>Bacillus licheniformis* SQR2 *=>FN650810.1 Bacillus licheniformis partial 16S rRNA gene, strain SQR2

GGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACAC
TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTT
CCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTT
CGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTCGAATAGGGCG
GTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCC
GCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCT
CGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGG
GTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGT
GTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACT
CTCTGGTCTGTA

Supplementary Datafile SD2: Multiple sequence alignment of phosphate solubilizing bacterial based on 16s rRNA gene sequences

Consensus

1. Bacillus sonorensis GG2
2. Priestia megaterium LsR8
3. Klebsiella sp. BRSPKC05
4. Enterobacter sp. LYX-2
5. Pseudomonas fluorescens MRPF-2
6. Rhizobium meliloti M55241
7. Acinetobacter sp. PSK.N1
8. Alcaligenes aquatilis RD03
9. Azospirillum brasilense AzCast
0. Burkholderia cepacia AF175314
1. Paenibacillus macerans TLLY7
2. Pseudomonas putida R43
3. Cytobacillus firmus NPBR2
4. Bacillus licheniformis SQR2

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    GCCCAGACTCCTACGGGAGGCAGCAGT-GGGAAT-TT---CAATGG-CG-AAG-CTGA---AGC-A-GCCGCGTG-GTGA-GAAGG---TTCGG-T-GTAAAGC-CTTT-
             340       350       360       370       380       390       400       410       420       430       440
1   GCCCAAACTCCTACGGGAGGCACCAGTAGGGAATCTTCCCCAAGGGACAAAAGTCTGACGAACCAACCCCCCGTGAGTGATGAAGGTT-TTCGAATCGTAAAACTCTGTT  381
2   GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGCT-TTCGGGTCG------------  401
3   GTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTCGGGTTGTAAAGCACTTTC  346
4   GTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCC-TTCGGGTTGTAAAGTACTTTC  398
5   GTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTC-TTCGGATTGTAAAGCACTTTA  413
6   GCCCAA--------------------------------------------------------------------------------------------------------  260
7   GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCC-TTTTGGTTGTAAAGCACTTTA  399
8   --------------------------------------------------------------------------------------------AGGTCGTAAAGTACTTTT  18
9   GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGCAACCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGCC-TTAGGGTTGTAAAGCTCTTTC  396
10  GCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTGTGTGAAGAAGGCC-TTCGGGTTGTAAAGCACTTTT  398
11  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTT-TTCGGATCGTAAAGCTCTGTT  419
12  GTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTC-TTCGGATTGTAAAGCACTTTA  338
13  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTT-TTCGGATCGTAAAACTCTGTT  418
14  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTT-TTCGGATCGTAAAGCTCTGTT  176

    ----GGGA-GAA------------AA-------------TTGACG-TACC---AGAA-AAGC-CCGGCTAACT-CGTGCCAGCAGCCGCGGTAATACG-AGGG-GCAAGC
             450       460       470       480       490       500       510       520       530       540       550
1   GTTAGGGAAAAACAAGTACCGTTCAAATAGGGCGGTACCTTGACGGTACCTAACCAAAAACCCACGGCTAACTACGTGCCACCACCCGCGGTAATACGTAGGTGGCAAGC  491
2   --------------------------------------------------------------------------------------------------------------  401
3   AGCGGGGAGGAAGGCGGTGAGGTTAATAACCTCACCGA-TTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGC  455
4   AGCGGGGAGGAAGGTGTTGTGGTTAATAACCGCAGCAA-TTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGC  507
5   AGTTGGGAGGAAGGGCAGTAAGTTAATA-CCTTGCTGTTTTGACGTTACCAACAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGC  522
6   --------------------------------------------------------------------------------------------------------------  260
7   AGCGAGGAGGAGGCTTACCTGGTTAATACCCGGGATAAGTGGACGTTACTCGCAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGC  509
8   GGCAGAGAAGAAAAGGTATCCCCTAATA-CGGGATCCTGCTGACGGTATCTGCAGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGC  127
9   GCACGCGACGATGA--------------------------TGACGGTAGCGTGAGAAGAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCGAGC  480
10  GTCCGGAAAGAAAACCTTGGCTCTAATA-CAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGC  507
11  GCCAGGGAAGAACGTCTTCTGGAGTAAC-TGCCAGGAGAGTGACGGTGCCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGC  528
12  AGTTGGGAGGAAGGGCAGTAAGCTAATA-CCTTGCTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGC  447
13  GTCAGGGAAGAACAAGTACCGGAGTAAC-TGCCGGTACCTTGACGGTACCTGACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGC  527
14  GTTAGGGAAGAACAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGC  286

    GTT--TCGGAATTACTGGGCGTAAAGCGCGCG-AGGCGGTT--TTAAGTC-GATGTGAAA-CCCCGGGCTCAACCTGGGAA-TGCATT-GAAACTGG-G-GCT-GAGT--
             560       570       580       590       600       610       620       630       640       650       660
1   GTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGTTTCTTAAGTCTAATGTGAAACCCCCCGGCTCAACCGGGAAGGGTCATTGAAAACTGGGGAACTTGAGTGC  601
2   --------------------------------------------------------------------------------------------------------------  401
3   GTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCT  565
4   GTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCT  617
5   GTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTCAGCAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTACTGAGCTAGAGTAC  632
6   --------------------------------------------------------------------------------------------------------------  260
7   GTTAATCGGATTTACTGGGCGTAAAGCGCGCGTAGGTGGCTAATTAAGTCAAATGTGAAATCCCCGAGCTTAACTTGGGAATTGCATTCGATACTGGTTAGCTAGAGTAT  619
8   GTTAATCTGAATTACTGGGCGTAAAGCGTGTGTTGGCGGTTCGGAAAGAAAGATGTGAAATCCCCGGGCTCAACCTTGGAACTGCATTTTTAACTGCCGAGCTAGAGTAT  237
9   GTTGTTCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGCCCGATCAGTCAGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTTGATACTGTCGGGCTTGAGTTC  590
10  GTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTCGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTGGTGACTGGCGGGCTAGAGTAT  617
11  GTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGCTGTTTAAGTCTGGTGTTTAATCCTGGGGCTCAACTCCGG-GTCGCACTGGAAACTGGACGGCTTGAGTGC  637
12  GTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTCGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCGAGCTAGAGTAC  557
13  GTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGC  637
14  GTTGTCCGGAATTATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGC  396

    -G-AGAGG--GGT-GAATTCCA-GTGTAGCGGTGAAATGCGTAGA-AT-TGGAGGAA-ACC-GTGGCGAAGGCG-CC--CTGG-C--A-ACTGAC-CT-AGG-GCGAAAG
             670       680       690       700       710       720       730       740       750       760       770
1   AAAAAAGGAAAGGGAAATTCCACGTGTACCGGTGAAATGCGTAAAAATGTGAAGGAACACCAGTGGCGAAGGC-------------------------------------  674
2   --------------------------------------------------------------------------------------------------------------  401
3   TGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAG  675
4   TGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAG  727
5   GGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG  742
6   --------------------------------------------------------------------------------------------------------------  260
7   GGGAGAGGATGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCCTAATACTGACACTGAGGTGCGAAAG  729
8   GTCAGAGGGGGGTAGAATTCCACGTGTAGCAGTGAAATGCGTAGATATGTGGAGGAATACCGATGGCGAAGGCAGCCCCCTGGGATAATACTGACGCTCAGACACGAAAG  347
9   CGGAGAGGATGGTGGAATTCCCAGTGTAGAGGTGAAATTCGTAGATATTGGGAAGAACACCGGTGGCGAAGGCGGCCATCTGGACGGACACTGACGCTGAGGCGCGAAAG  700
10  GGCAGAGGGGGGTAGAATTCCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAATACTGACGCTCATGCACGAAAG  727
11  AGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGACGCTGAGGCGCGAAAG  747
12  GGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG  667
13  AGAAGAGAAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTTTGGTCTGTAACTGACGCTGAGGCGCGAAAG  747
14  AGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTA---------------------  485
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     CATG-CCCTTA-G----GGGCTACACACGT-CTACAATGG-----ACA--G-G--GC-A---CGCGAG----AGC--A-C-CA-AAA------TC--AGT-CGGAT-G-A
              1220      1230      1240      1250      1260      1270      1280      1290      1300      1310      1320
1    --------------------------------------------------------------------------------------------------------------  674
2    --------------------------------------------------------------------------------------------------------------  401
3    CATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCATATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAG-TATGTCGTAGTCCGGATTGGA  1217
4    CATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAG-TGCGTCGTAGTCCGGATTGGA  1269
5    CATGGCCCTTACGGCCAGGGCTACACACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCATAAAA-CCGATCGTAGTCCGGATCGCA  1284
6    --------------------------------------------------------------------------------------------------------------  260
7    CATGGCCCTTACGGCCAGGGCTACACACGTGCTACAATGGTCGGTACAAAGGGTTGCTACTGCGCGAGCAGATGCTAATCTCAAAAAG-CCGATCGTAGTCCGGATCGCA  1271
8    --------------------------------------------------------------------------------------------------------------  755
9    CATGGCCCTTATGGGTTGGGCTACACACGTGCTACAATGGCGGTGACAGTGGGATGCGAAGTCGCAAGATGGAGCCAATCCCCAAAAG--CCGTCTCAGTTCGGATTGCA  1242
10   CATGGCCCTTATGGGTAGGGCTTCACACGTCATACAATGGTCGGAACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCCAGAAAA-CCGATCGTAGTCCGGATTGCA  1264
11   CATGCCCCTTATGACCTGGGCTACACACGTACTACAATGGCCGGTACAACGGGAAGCGAAGGAGCGATCTGGAGCGAATCCTAGAAAAGCCGGTCTCAGTTCGGATTGCA  1292
12   CATGGCCCTTACGGCCTGGGCTACACACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCTCACAAAA-CCGATCGTAGTCCGGATCGCA  1210
13   CATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGATGGTACAAAGGGCTGCAAGACCGCGAGGTTAAGCGAATCCCATAAAA-CCATTCTCAGTTCGGATTGCA  1291
14   --------------------------------------------------------------------------------------------------------------  485
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     --CTGCAACTCG--T-C-TGAAG--GGAATCGCTAGTAATCG---ATCAG-ATG---CGG-TGAATACGTTCCCGGG-CTTGTACACACCGCCCGTCAC-ACCA-G-G--
              1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
1    --------------------------------------------------------------------------------------------------------------  674
2    --------------------------------------------------------------------------------------------------------------  401
3    GTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGG-TGAATACGTTCCCGGGC--------------------------------  1294
4    GTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGG-TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAC-ACCATGGGAG  1377
5    GTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGTCACGG-TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAC-ACCATGGGAG  1392
6    --------------------------------------------------------------------------------------------------------------  260
7    GTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGG-TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAC-ACCATGGGAG  1379
8    --------------------------------------------------------------------------------------------------------------  755
9    CTCTGCAACTCGGGTGCATGAAGTTGGAATCGCTAGTAATCGCGGATCAGCACGCCGCGGTTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAC-ACCATGGGAG  1351
10   CTCTGCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGG-TGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCAC-ACCATGGGAG  1372
11   GGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGG-TGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCAC-ACCACGAGAG  1400
12   GTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGG-TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACAACCATGGGTA  1319
13   GGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGG-TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAC-ACCACGAGAG  1399
14   --------------------------------------------------------------------------------------------------------------  485
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     --------------------------------------------------------------------------------------------------------------
              1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540
1    --------------------------------------------------------------------------------------------------------------  674
2    --------------------------------------------------------------------------------------------------------------  401
3    --------------------------------------------------------------------------------------------------------------  1294
4    TGGGTTGCTAAAAGAAGTAGGTAGCTTAACCTTCG--GGAGCGCAGGAACCATAGAGT----------------------------------------------------  1433
5    TGGGTTGC-TCCAGAAGTAGCTAGTCTAACCGCAA--GGGGGACGGTTACCACGGAGTGATTCATGACTGGGGTGAAGTC------------------------------  1469
6    --------------------------------------------------------------------------------------------------------------  260
7    TTTGTTGC-ACCAGAAGTAGGTAGTCTAACCTTAG--GGAGGACGCTTACCACGGTGTGGCCGATGACTGGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCG  1486
8    --------------------------------------------------------------------------------------------------------------  755
9    TTGGCTTT-ACCCGAAGGTGGTGCGCTAACCGGCAACGGAGGCAGCCAACCACGGTCAGGTCAGCGACTGGGGT------------------------------------  1424
10   TGGGTTTT-ACCAGAAGTGGCTAGTCTAACCGCAA--GGAGGACGGTCACCACGGTAGGATTCATGACT-GGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGG----  1474
11   TTTACAAC-ACCCGAAGTCGGTGAGGTAACCGCAA--GGGGCCAGCCGCCGAAGGTGGGGTAGATGATTGGGT-------------------------------------  1470
12   GTGGGT--------------------------------------------------------------------------------------------------------  1325
13   TTTGTAAC-ACCCGAAGTCGGTGGGGTAACCTTTT--GGAGCCAGCCGCCTAAGGTGGGACAGATGATTGG---------------------------------------  1467
14   --------------------------------------------------------------------------------------------------------------  485
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     -------------
              1550
1    -------------  674
2    -------------  401
3    -------------  1294
4    -------------  1433
5    -------------  1469
6    -------------  260
7    GTTGGATCCACCC  1499
8    -------------  755
9    -------------  1424
10   -------------  1474
11   -------------  1470
12   -------------  1325
13   -------------  1467
14   -------------  485
```