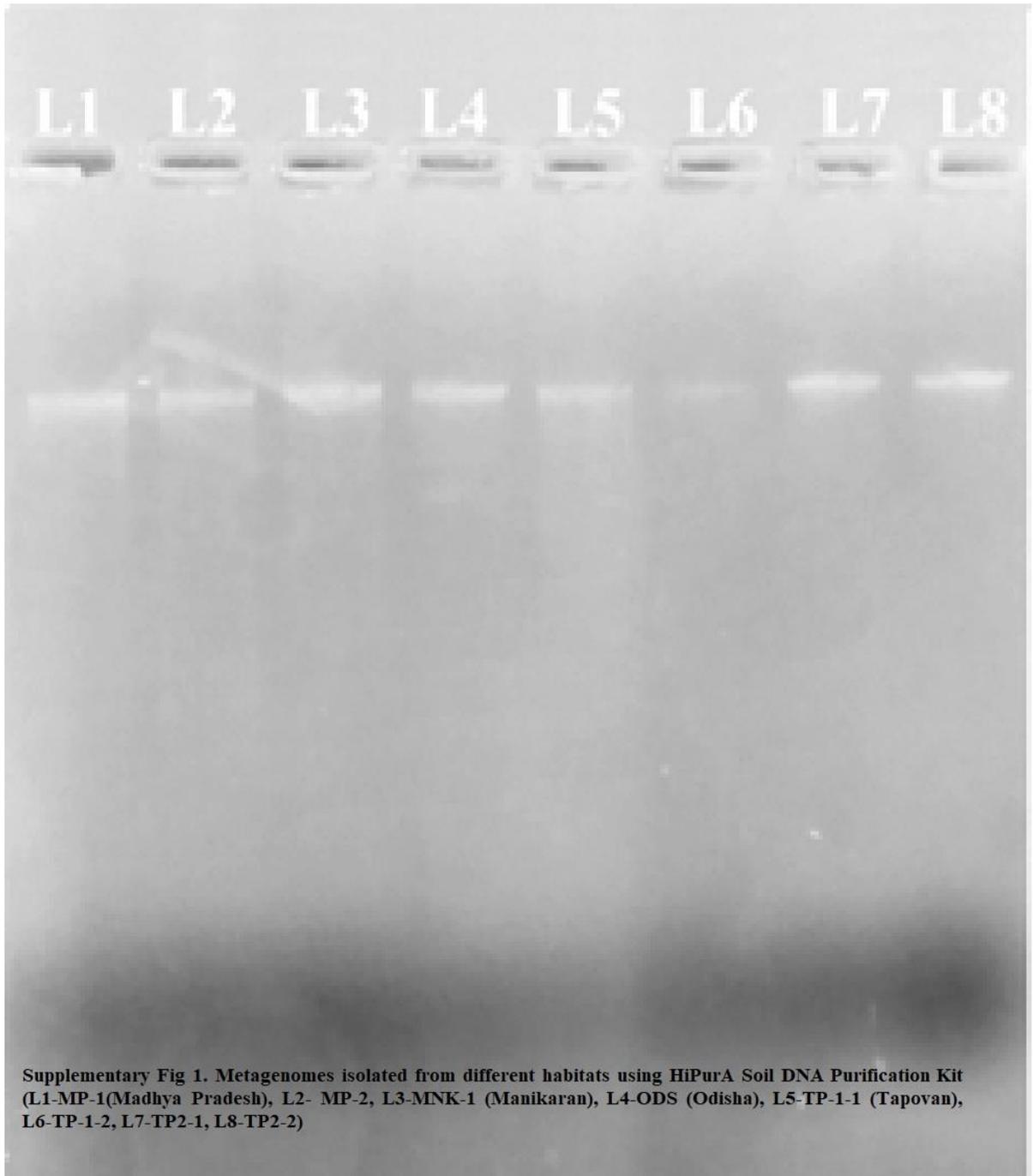


## Supplementary Information



>Forward ODS\_Amylase 9

```
AGGGGACAGTCCTCTAGTTTCTAGTTCAGTCGCCCTGTCAAGCC AAGGATCGACCAACGGGGACTGAATCTGCCGTTTCAGA
TTTAACCGCGGTTCAATGGGTTCCGAATGTCGGGTTGTTCTCACGGCTCTGCCGGGGAAAAATTTTGTGCCCTTGATTC
GCCGCTTTAAAGAACGAGCCAAATAGAAGGGAATGGGCCTTCCCTGTCTCCCGAGAAATGTCATGGTGGGGAGGT
AATCAACGGAGAGATCCGCACCCATAATGTTTTCCTCGCTTTTAAAGA TCAAATCAATTTTGTGTTTCAAGGCAGGAAAT
TCGGGGTGGGAGTCTCCCTTCCACCCGGACGTAATCCCGAAAAAAAACATGAGGACCCTCCAGATTACCTGTGAG
AATAAAAAACGGAAAGCAACGGTTTAAACAAAAATTTGGACAAAATCCACTCAAAACGAATTTGCCCTCTTGTGTTGG
GGGGCCAGGGGGTTATCGAACCAAAAGGGTAAATCCAACATGTTTCAAATGGGGAAGCCTTTGTGTA AAAACGAAACA
CCACTGGTTGAAACAAATTTTCCCTCAATATCAATAAACCCCGCCCTCCCTCTGTGTTCCTCATGGCCAAACGAGT
GTGTGACATGTAGTAGATAGAAATTTCCCCCAACGATCAACACACCACCATGAAAATGGAATATTAATAATTTTG
ATGTATTTGTTCCTCCACCAATCAGTCTTTTATTGAATGACAGCGGTGCAAAAGATCCAACTCTCCCTAGGCAC
CAAAATTAATAATACCAGACCAGTGAAGCTCGCGGCTGACATCCAGTATATAATGACTTTTATCTTACGGAGCTA
TGTGGTTATCCACTTACATGGTAAGCGCAAGTGTAGTCTCTATACATCCCAATCGACACAGATCTGACCCCTGGCCT
CAGTATATCCATGTCAG
```

>Reverse ODS\_Amylase 9

```
NNNNNNNNNATGCTGACGCTGTTATTTGCGCTCATCTTCTGTGCTGCTCATTTCTGTCAGCAGCGGGGCAAAATC
TTAATGGGACGGTGTATGTCAGTATTTTGAATGGTACATGCCCAATGACGGCCAACATTTGGAAGCGCTTGCAAAAACG
ACTCGGCATATTTGGCTGAACACGGTATATACGTCCGCTTGGATTTCCCGCCGATATAAGGGAACGAGCCAAAGCGG
ATGTGGGCTACGGTGTCTTACGACCTTTATGATTTAGGGGAGTTTCATCAAAAAGGGACGGTTCGGACAAAGTACG
GCACAAAAGGAGAGCTGCAATCTGCGATCAAAAGTCTTCAATCCCGGACATTAACGTTTACGGGGAATGTTGTCAT
TCAACCACAAAAGGCGGGCTGATGCGACCGAAGATGTAACCGCGGTGAAAGTGTATCCCGCTGACCGCAACCGCG
TAATTTACAGGAGAACACCGAATAAAGCCATGGACACATTTTCTATTTTCCGGGGCGCGGAGCACATACAGCGATTT
TAAATGGCATTTGGTACCATTGTGACGGAACCGATTTGGACGAGTCCGAAAGCTGAACCGCATCTATAAGTTTCAA
GGAAAAGCTTTGGGATTTGGAAAGTTTCCAATGAAAACGGCAACTATGATTAATTTGATGTATGCCGACATCGATTAT
GACCATCTGATGTCAGCAGCAAAATTAAGAGATGGGGCACTTGGTATGCCAAATGAACATGCAATTTGACGTTTTC
CGTCTGTATGCTGTCAAAACACATTAATTTTCTTTTGTCCGGGATTTGGTTAATCAATGTCAGGGAAAAACGGGGA
AGGAAATGTTTACGGTAGCTGAATATTTGGCAGAAATGACATGGGGCGCGTGGAAAACATTTTGAACAAAACAAAT
TTAATCATTTACAGTGTGTGACGTGCCCTTCAATATCAGTTCATGCTGCAATCGACACAGGGAGGGCGCTATGATAT
GAGGAAATGTCTGAACAGTACGGTCGTTTCAAGCATCCGTTGAAAGCGGTTACATTTGTCGATAAACCATGATACA
CAGCCGGGGCAATCGCTGTAGTCTGACGTCTCAAACATGGTTTAAAGCCGCTTGCTTACGCTTATTTCAACAAGGG
AATCTGGAACCCCTCAGGTTTCTCCGGGAATGTACGGGACGAAAGGAAATCCANCCCGAAATTTCTGCTTGA
AACCAAAATGAAACCGATTTTAAANCGAAAAACCTTTGGTTCCGGGCCACCTNATTTTFTNNCCCCATTANNNTTC
CCGTGGGA AAAGGAAGAAAACCTNNTTTC AAANNCGNNTTGNCGCTTTNNAAAA NAGACCCCGGGGGAAAAA
AAAATTTTNGCCGAAAACCCGAAAGGAGAAAATTTTCAAANN TTGGGACGGNNINNNATATAAAAAGGGGGT
ANATCTANNNGCCGGCTNNTTNTTTTTAAAAGAAAAAAAANAAGAATTTANNNNNNTTTTNTTTTTT
```

**Supplementary Fig 2. The nucleotide sequence of cloned amylase gene fragment amplified from e-DNA of Atri geothermal Spring of Odisha**



**Supplementary Fig 3. Homology modelling of the translated gene sequence coding protein showing similarity with alpha amylase using Phyre 2 program**

**a**

XXXLLTLLFALIFLLPHSAAAAANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEHGITAVWI  
 PPAYKGT SQADVGYGAYDLYDLGEFHQKGTVRTKYGTGKELQSAIKSLHSRDIINVYGDVVINH K  
 GGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDES R K  
 LNRIYKFGKAWDWEVSNENGN DYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAV K  
 HIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHVSFVDPVPLHYQFHAAS T Q  
 GGGYDMRKL LNSTVVSKHPLKAVTFVDNHDTQPGQSLESTVQTWFKPLAYAFIL TRESGNPQV F  
 SGNCTGRKETPXRNSCLET KIEPILXRKNLWFRPTXFFXPLXFPVVGKGRKXFXKXLLXKXDP  
 GGGKNFXPKNPEKEKFSXXGTXXX-XGGX SXXPAXXFLKEKXRI XXXFFF F

**b** amylase A, partial [*Bacillus licheniformis*]

Sequence ID: [AMJ27400.1](#) Length: 469 Number of Matches: 1

Range 1: 1 to 398 [GenPept](#) [Graphics](#) [Next Match](#) [Previous](#)

| Score          | Expect | Method   | Identities   | Positives    | Gaps      | Frame |
|----------------|--------|--|--------------|--------------|-----------|-------|
| 780 bits(2015) | 0.0    | Compositional matrix adjust.                                   | 377/398(95%) | 384/398(96%) | 1/398(0%) | +3    |
| Query 48       |        | PHSAAAAANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEHGITAVWIPPAYKGT SQAD |              |              | 227       |       |
| Sbjct 1        |        | PHSAAAAANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEHGITAVWIPPAYKGT SQAD |              |              | 60        |       |
| Query 228      |        | VGYGAYDLYDLGEFHQKGTVRTKYGTGKELQSAIKSLHSRDIINVYGDVVINH KGGADATE |              |              | 407       |       |
| Sbjct 61       |        | VGYGAYDLYDLGEFHQKGTVRTKYGTGKELQSAIKSLHSRDIINVYGDVVINH KGGADATE |              |              | 120       |       |
| Query 408      |        | DVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDES RKLNR  |              |              | 587       |       |
| Sbjct 121      |        | DVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDES RKLNR  |              |              | 180       |       |
| Query 588      |        | IYKFQKAWDWEVSNENGN DYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAV    |              |              | 767       |       |
| Sbjct 181      |        | IYKFQKAWDWEVSNENGN DYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAV    |              |              | 240       |       |
| Query 768      |        | KHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHVSFVDPVPLHYQFH |              |              | 947       |       |
| Sbjct 241      |        | KHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHVSFVDPVPLHYQFH |              |              | 300       |       |
| Query 948      |        | AASTQGGGYDMRKL LNSTVVSKHPLKAVTFVDNHDTQPGQSLESTVQTWFKPLAYAFIL T |              |              | 1127      |       |
| Sbjct 301      |        | AASTQGGGYDMRKL LNSTVVSKHPLKAVTFVDNHDTQPGQSLESTVQTWFKPLAYAFIL T |              |              | 360       |       |
| Query 1128     |        | RESGNPQVFSGNCTG-RKETPXRNSCLET KIEPILXRK                        | 1238         |              |           |       |
| Sbjct 361      |        | R+SG P VFSG+ G ++ +P L+ KIEPIL +                               | 398          |              |           |       |

**Supplementary Fig 4 a.** Longest ORF in the sequence of the cloned gene present in T vector. **b.** Sequence of the cloned gene analysed using BLASTx tool using translated nucleotide sequence as query and searching protein database.

```

Query 371  GGTCAACAACCAAAAGGCGCGCTGATGCGACCGAAGATGTAACCGCGTTGAAGTCGA 430
Sbjct 570  GGTCAACAACCAAAAGGCGCGCTGATGCGACCGAAGATGTAACCGCGTTGAAGTCGA 629
Query 431  TCCCCGTGACCCGAACCGCGTAATTTCAAGGAGAACACCGAATTAAGCCTGGACACATTT 490
Sbjct 630  TCCCCGTGACCCGAACCGCGTAATTTCAAGGAGAACACCGAATTAAGCCTGGACACATTT 689
Query 491  TCATTTTCCGGGGCGCGGAGCACATACAGCGATTTAAATGGCATTGGTACCATTTTGA 550
Sbjct 690  TCATTTTCCGGGGCGCGGAGCACATACAGCGATTTAAATGGCATTGGTACCATTTTGA 749
Query 551  CCGAACCGATTGGGACGAGTCCCGAAAGCTGAACCGCATCTATAAGTTTCAAGGAAAAGGC 610
Sbjct 750  CCGAACCGATTGGGACGAGTCCCGAAAGCTGAACCGCATCTATAAGTTTCAAGGAAAAGGC 809
Query 611  TTGGGATTGGGAAGTTTCCAATGAAAACGGCAACTATGATTATTTGATGTATGCCGACAT 670
Sbjct 810  TTGGGATTGGGAAGTTTCCAATGAAAACGGCAACTATGATTATTTGATGTATGCCGACAT 869
Query 671  CGATTATGACCATCCTGATGTCGACGACAGAAATTAAGAGATGGGGCACTTGGTATGCCAA 730
Sbjct 870  CGATTATGACCATCCTGATGTCGACGACAGAAATTAAGAGATGGGGCACTTGGTATGCCAA 929
Query 731  TGAAC TGCAATTGGACGGTTCCCGTCTTGATGCTGTCAAACACATTAATTTTCTTTTTT 790
Sbjct 930  TGAAC TGCAATTGGACGGTTCCCGTCTTGATGCTGTCAAACACATTAATTTTCTTTTTT 989
Query 791  GCGGGATTGGGTTAATCATGTGAGGAAAAAACGGGGAAGGAAATGTTTACGGTAGCTGA 850
Sbjct 990  GCGGGATTGGGTTAATCATGTGAGGAAAAAACGGGGAAGGAAATGTTTACGGTAGCTGA 1049
Query 851  ATATTGGCAGAATGACTTGGGCGCGCTGAAAACTATTTGAACAAAACAAATTTAATCA 910
Sbjct 1050  ATATTGGCAGAATGACTTGGGCGCGCTGAAAACTATTTGAACAAAACAAATTTAATCA 1109
Query 911  TTCAGTGTGTTGACGTGCCGCTTCAATATCAGTTCATGCTGATCGACACAGGGAGGCGG 970
Sbjct 1110  TTCAGTGTGTTGACGTGCCGCTTCAATATCAGTTCATGCTGATCGACACAGGGAGGCGG 1169

Query 971  CTATGATATGAGGAAATTGCTGAACAGTACGGTCGTTTCCAAGCATCCGTTGAAAGCGGT 1030
Sbjct 1170  CTATGATATGAGGAAATTGCTGAACAGTACGGTCGTTTCCAAGCATCCGTTGAAAGCGGT 1229
Query 1031  TACATTTGTCGATAACCATGATACACAGCCGGGGCAATCGCTTGAGTCGACTGTCCAAAC 1090
Sbjct 1230  TACATTTGTCGATAACCATGATACACAGCCGGGGCAATCGCTTGAGTCGACTGTCCAAAC 1289
Query 1091  ATGGTTTAAGCCGCTTGCTTACGCTTTTATTCTCACAGGGAATCTGSAACCCCTCAGGT 1150
Sbjct 1290  ATGGTTTAAGCCGCTTGCTTACGCTTTTATTCTCACAGGGAATCTGSAACCCCTCAGGT 1349
Query 1151  TTTCTCCGGGAAT-TGTACGGGACGAAAGGAAACT-CCANCCGAAATTCCTGCCTTGAA 1208
Sbjct 1350  TTTCTACGGGATATGTACGGGACGAAAGGAGACTCCACGCGGAAATTCCTGCCTTGAA 1409

Query 1209  AC-CAAAATTGAACCGATTTTAAAN-CGAAAAAC 1241
Sbjct 1410  ACACAAAATTGAACCGATCTTAAAAGCGAGAAAAAC 1444

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**Supplementary fig 5. BLAST n search exhibiting nucleotide similarity of query sequence with amylase gene of *Bacillus licheniformis* 548.**