Supplementary

Sequence Fig A for EC 2.5.1.49

97.64% sequence similarity

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Upper line: pae49 (Genome data base), from 28 to 403
Lower line: pae49 (1st BASE), from 6 to 382

pae49 (Genome data base): pae49 (1st BASE) identity= 97.64 %( 372/381)
gap=5.69 %( 23/404)

1   CGTGTTCTGCGAAACCATCGGCAACCCGGCGGGCAACATCATCGACCTGCAGGCACTGGC
                               |||   || ||||||||||||||||||||||||
1   ......................CGGNNGGCCNNCATCATCATCGACCTGCAGGCACTGGC

61  CGACGCCGCTCACCGCCACGGCGTGCCACTGATCGTCGACAACACGGTAGCCACCCCGGT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
39  CGACGCCGCTCACCGCCACGGCGTGCCACTGATCGTCGACAACACGGTAGCCACCCCGGT

121 GCTCTGCCGGCCGTTCGAGCACGGCGCCGACATCGTCGTGCACTCGCTGACCAAGTACAT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
99  GCTCTGCCGGCCGTTCGAGCACGGCGCCGACATCGTCGTGCACTCGCTGACCAAGTACAT

181 GGGCGGCCACGGCACCAGCATCGGCGGGATCGTGGTCGACTCCGGCAAATTCGACTGGGC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
159 GGGCGGCCACGGCACCAGCATCGGCGGGATCGTGGTCGACTCCGGCAAATTCGACTGGGC

241 GGCGAACAAGTCGCGCTTCCCGCTGCTGAACACGCCCGATCCGTCCTACCACGGCGTCAC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
219 GGCGAACAAGTCGCGCTTCCCGCTGCTGAACACGCCCGATCCGTCCTACCACGGCGTCAC

301 CTACACCGAGGCCTTCGGACCCGCCGCCTTCATCGGCCGCTGCCGGGTGGTACCGCTGCG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
279 CTACACCGAGGCCTTCGGACCCGCCGCCTTCATCGGCCGCTGCCGGGTGGTACCGCTGCG

361 CAACATGGGCGCGGCGCTCTCGCCGTTCAACG.CCTTCCTCATC
    |||||||||||||||||||||||||||||||| |||||||||||
339 CAACATGGGCGCGGCGCTCTCGCCGTTCAACGCCCTTCCTCATCA
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95.01 % sequence similarity

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Upper line:  pae49 (Genome database), from 41 to 403
Lower line:  pst49 (1st BASE), from 19 to 382

pae49 (Genome database); pst49 (1st BASE) identity= 95.01 %(362/381)
gap=5.69%(23/404)

1   CGTGTTCTGCGAAACCATCGGCAACCCGGCGGGCAACATCATCGACCTGCAGGCACTGGC
                                             |||||||||||||||||||
1   ......................CNNNNNCGCCNNNNNNNNNTCGACCTGCAGGCACTGGC

61  CGACGCCGCTCACCGCCACGGCGTGCCACTGATCGTCGACAACACGGTAGCCACCCCGGT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
39  CGACGCCGCTCACCGCCACGGCGTGCCACTGATCGTCGACAACACGGTAGCCACCCCGGT

121 GCTCTGCCGGCCGTTCGAGCACGGCGCCGACATCGTCGTGCACTCGCTGACCAAGTACAT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
99  GCTCTGCCGGCCGTTCGAGCACGGCGCCGACATCGTCGTGCACTCGCTGACCAAGTACAT

181 GGGCGGCCACGGCACCAGCATCGGCGGGATCGTGGTCGACTCCGGCAAATTCGACTGGGC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
159 GGGCGGCCACGGCACCAGCATCGGCGGGATCGTGGTCGACTCCGGCAAATTCGACTGGGC

241 GGCGAACAAGTCGCGCTTCCCGCTGCTGAACACGCCCGATCCGTCCTACCACGGCGTCAC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
219 GGCGAACAAGTCGCGCTTCCCGCTGCTGAACACGCCCGATCCGTCCTACCACGGCGTCAC

301 CTACACCGAGGCCTTCGGACCCGCCGCCTTCATCGGCCGCTGCCGGGTGGTACCGCTGCG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
279 CTACACCGAGGCCTTCGGACCCGCCGCCTTCATCGGCCGCTGCCGGGTGGTACCGCTGCG

361 CAACATGGGCGCGGCGCTCTCGCCGTTCAACG.CCTTCCTCATC
    |||||||||||||||||||||||||||||||| |||||||||||
339 CAACATGGGCGCGGCGCTCTCGCCGTTCAACGCCCTTCCTCATCA
```

96.34 % sequence similarity

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Upper line: pae49 (1st BASE), from 19 to 382
Lower line: pst49 (1st BASE), from 19 to 382

pae49 (1st BASE): pst49 (1st BASE) identity= 96.34 %( 369/383) gap=0.00
%( 0/383)

1   CGGNNGGCCNNCATCATCATCGACCTGCAGGCACTGGCCGACGCCGCTCACCGCCACGGC
    |  ||   | |         ||||||||||||||||||||||||||||||||||||||||
1   CNNNNNCGCCNNNNNNNNNNTCGACCTGCAGGCACTGGCCGACGCCGCTCACCGCCACGGC

61  GTGCCACTGATCGTCGACAACACGGTAGCCACCCCGGTGCTCTGCCGGCCGTTCGAGCAC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61  GTGCCACTGATCGTCGACAACACGGTAGCCACCCCGGTGCTCTGCCGGCCGTTCGAGCAC

121 GGCGCCGACATCGTCGTGCACTCGCTGACCAAGTACATGGGCGGCCACGGCACCAGCATC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GGCGCCGACATCGTCGTGCACTCGCTGACCAAGTACATGGGCGGCCACGGCACCAGCATC

181 GGCGGGATCGTGGTCGACTCCGGCAAATTCGACTGGGCGGCGAACAAGTCGCGCTTCCCG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GGCGGGATCGTGGTCGACTCCGGCAAATTCGACTGGGCGGCGAACAAGTCGCGCTTCCCG

241 CTGCTGAACACGCCCGATCCGTCCTACCACGGCGTCACCTACACCGAGGCCTTCGGACCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGCTGAACACGCCCGATCCGTCCTACCACGGCGTCACCTACACCGAGGCCTTCGGACCC

301 GCCGCCTTCATCGGCCGCTGCCGGGTGGTACCGCTGCGCAACATGGGCGCGGCGCTCTCG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 GCCGCCTTCATCGGCCGCTGCCGGGTGGTACCGCTGCGCAACATGGGCGCGGCGCTCTCG

361 CCGTTCAACGCCCTTCCTCATCA
    |||||||||||||||||||||||
361 CCGTTCAACGCCCTTCCTCATCA
```