

The biosynthetic pathway of 2-azahypoxanthine in fairy-ring forming fungus

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Supplementary table 1

Main features of sequence data.

	FLX+	GAllx
Number of raw reads	915,457	137,529,366
Length of reads (bp)	376,450,318	13,890,465,966
Av. of length of reads (bp)	411	101
Number of high-quality reads		
Number of reads	915,457	79,179,992
Length of reads (bp)	376,450,318	7,514,231,108
Av. of length of reads (bp)	411	94.9

Supplementary table 2

Assembly summary.

Number of scaffolds	812
N50 (bp)	178878
Total size of scaffolds (bp)	36644714
Maximum scaffold length (bp)	899431
Minimum scaffold length (bp)	1999
Average scaffold length (bp)	45129

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 aactggtagattctaaacttatcccaatgtcagGGCATCGTCTTTCTTGACATATTCCTCTTCTCCGTGA
G I V F L D I F P L L R D

 TCCTATCACTTTTGAAACACTCATCAGCATTTTGTCCACCATGTAAACATCATATACTATCACCAAGTCAC
P I T F E T L I T H F V H H V T S Y T I T K S P

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T R K I D V I V G L D A R G F L L G P I I A L

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R L G A A F V P V R K Q G K L P G P C V G A S Y

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E K E Y G V

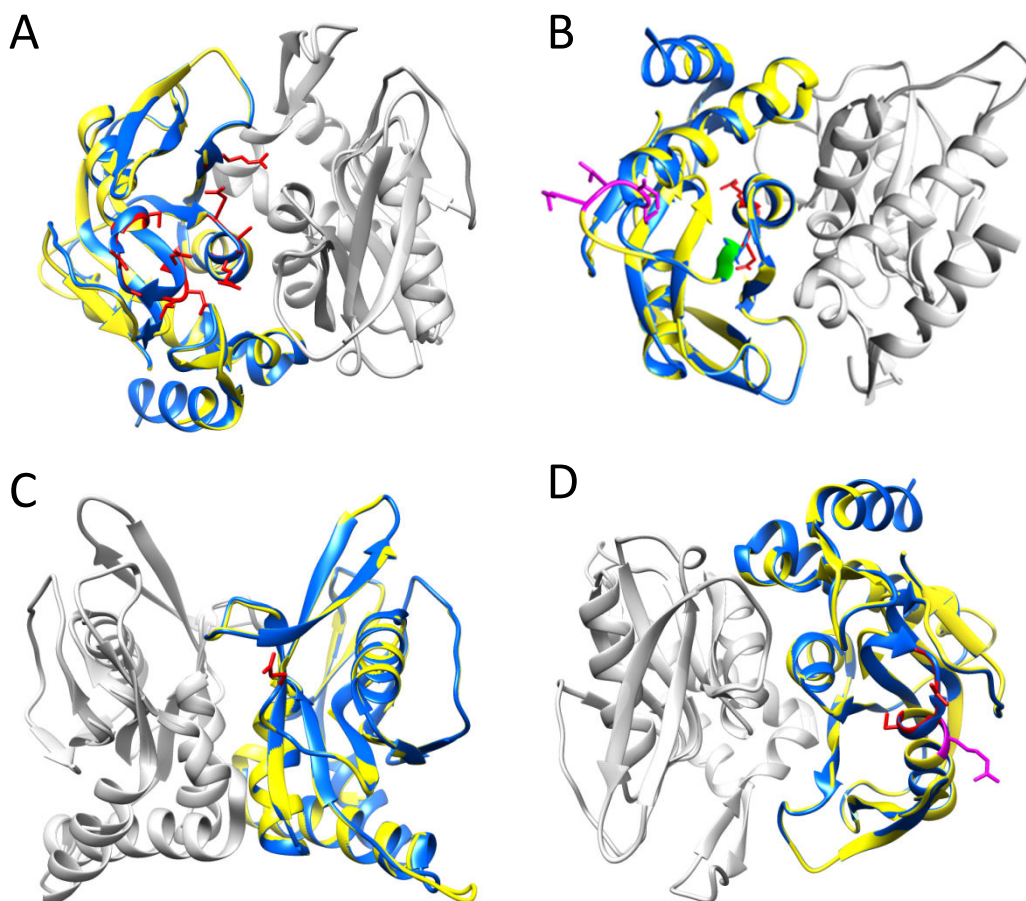
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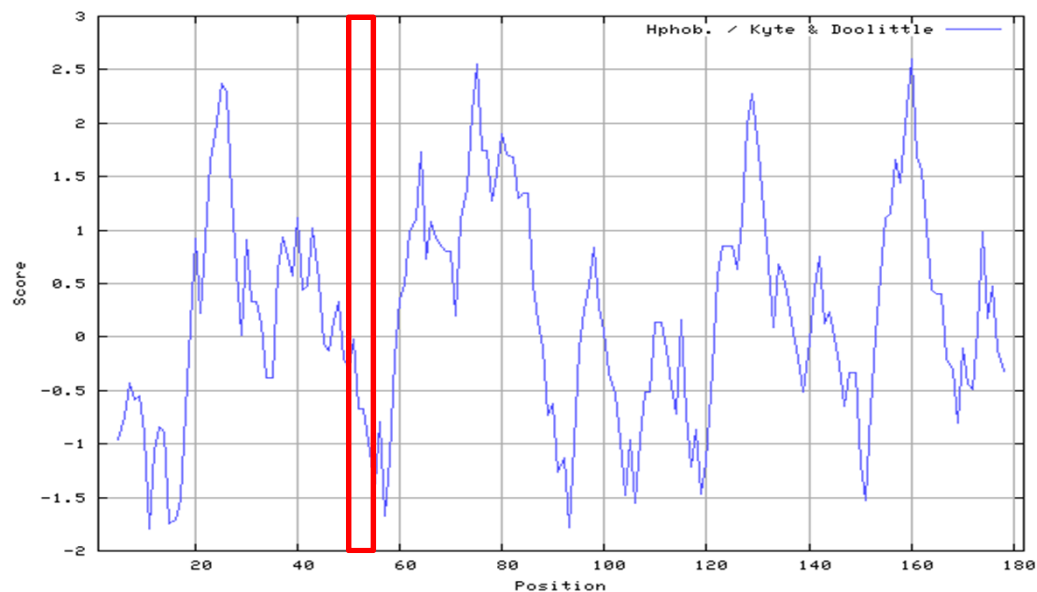
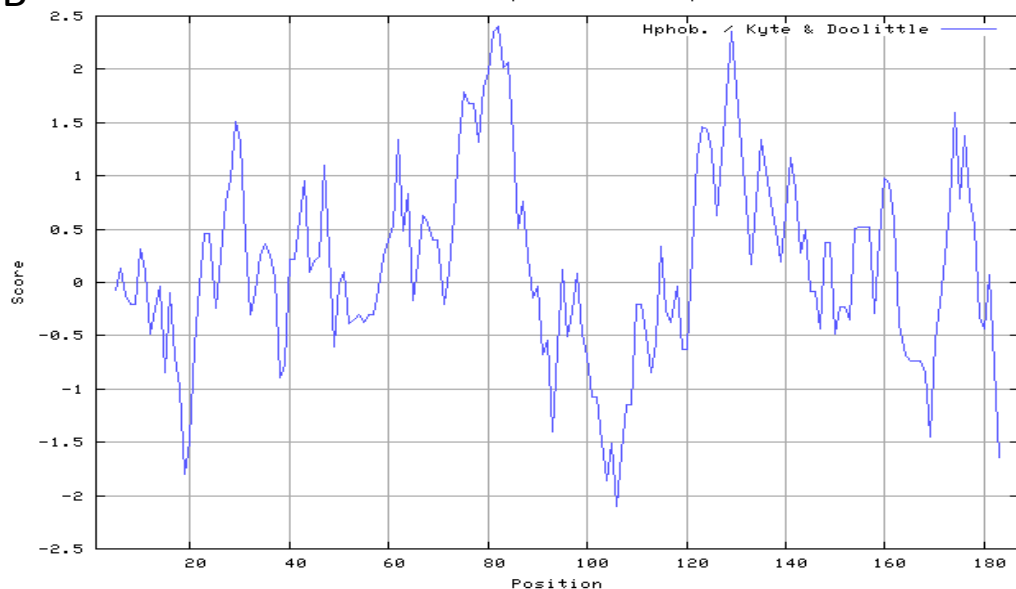
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A A G E L V A K Q G G K T L E Y L F I I E L M F

 TCTTCAGGGCTGGAACCAAGTTGGATGCTCCGGCATACTCGATCGTTCAATCGGATGATTGA
F R A G T K L D A P A Y S I V Q S D D *

Supplementary Figure 2. The genomic DNA and the deduced amino acid sequence of *L. sordida* *APRT* gene. Upper case ; exon sequences, lower case ; intron sequences ; bold upper case ; predicted amino acid sequence. Note that the underlines of the introns display GT-AG consensus for splicing sites.



Supplementary Figure 3. Structures of APRTs in *L. sordida* and *S. cerevisiae*. Three-dimensional structural modeling was carried out on SwissModel server with the *S. cerevisiae* (Protein data bank code, 1G2Q) as the template. Ribbon diagram shows the overlap of the *S. cerevisiae* APRT monomer (blue) and *L. sordida* APRT monomer (yellow). (A) Putative phosphoribosyl pyrophosphate (PRPP)-binding motifs and 5'-phosphate contact region of *L. sordida*. The conserved amino acid residues related in the PRPP and 5'-phosphate binding are shown in red. (B) The missing region in *L. sordida* APRT. A missing region (51-Thr-Ile-Thr-Lys-54), citrate contact region (67-Asp-Ala-Arg-69) and alpha-helix (62-Val-Ile-Val-Gly-Leu-66) near 5' citrate contact region are shown in magenta, red and green, respectively. (C) Glu-116 positioned on the dimer surface. Glu-116 conserved between *L. sordida* and *P. involutes* is shown in red. (D) Arg-139 is component of a-helix near 5' phosphate binding motif. Arg-139 and 5' phosphate binding motif (133-Ala-Thr-Gly-Gly-Ser-137) are shown in magenta and red, respectively.

A**B**

Supplementary Figure 4. Hydropathy Plot for *L. sordida* APRT(A) and *S. cerevisiae* APRT (B) (Protein data bank code, 1G2Q). Hydropathy plot was created using the ProtScale tool (<http://web.expasy.org/protscale/>). The missing region in *L. sordida* APRT is boxed in red.