Function
Histone demethylase that demethylates 'Lys-4' of histone H3, a specific tag for epigenetic transcriptional activation, thereby acting as a corepressor. Required for de novo DNA methylation of a subset of imprinted genes during oogenesis. Acts by oxidizing the substrate by FAD to generate the corresponding imine that is subsequently hydrolyzed. Demethylates both mono- and di-methylated 'Lys-4' of histone H3. Has no effect on tri-methylated 'Lys-4', mono-, di- or tri-methylated 'Lys-9', mono-, di- or tri-methylated 'Lys-27', mono-, di- or tri-methylated 'Lys-36' of histone H3, or on mono-, di- or tri-methylated 'Lys-20' of histone H4.

Sequence similarities
Belongs to the flavin monoamine oxidase family. Contains 1 CW-type zinc finger. Contains 1 SWIRM domain.

Domain
The SWIRM domain may act as an anchor site for a histone tail.

Cellular localization
Nucleus.

Form
There are 3 isoforms produced by alternative splicing.

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