Within the global livestock production trade, *Fasciola hepatica* remains a parasite of significant detriment in terms of economics, veterinary impact and food safety. The emergence of drug resistance within multiple distinct *F. hepatica* populations has led to the urgent search for alternative chemotherapies as a means of control. Of the drug discovery strategies available to parasitologists, drug repositioning reduces pre-clinical development time by taking advantage of existing research. Among *F. hepatica* candidates to enter such an approach are the histone modifying enzymes (HMEs). HMEs are a diverse class of proteins involved in catalysing (writers), reversing (erasers) and recognising (readers) post-translational modifications on proteins (including histones). Considering the significant developmental changes that occur during the *F. hepatica* life cycle, in addition to promising HME inhibition studies in the related blood fluke, *Schistosoma mansoni*, HMEs represent highly attractive targets for further study. Here, we present the first complete bioinformatic characterisation of the histone acetylation machinery (histone acetyl transferases – HATs (writers); histone deacetylases – HDACs (erasers) and bromodomain containing proteins – BCPs (readers)) in *F. hepatica*. Briefly, BLAST searches were performed against available *F. hepatica* genomic and transcriptomic datasets using known HAT, HDAC and BCP protein sequences with an *E*-value cut-off of $1e^{-10}$. BioMart searches were also performed against a *F. hepatica* genome in WormBase ParaSite using InterPro accessions for each domain to ensure retrieval of novel sequences which may be missed by homology-based methods. Matched sequences were subsequently annotated using InterPro domain scans and were manually checked in alignments against their reference sequences to confirm the presence of key functional residues according to existing literature and UniProt records. Of the proteins putatively identified, 9 were HAT orthologues, 13 were HDAC orthologues and 40 were BCP orthologues. Among the putatively identified BCP proteins, the simultaneous presence of multiple functional domains was observed, including 5 sequences which contained both HAT and BCP domains. Domain architecture annotation indicates the conservation of key functional motifs and residues present in the human and *S. mansoni* orthologues, some of which have been confirmed by RT-PCR and sequencing. Mining of existing RNA-Seq data revealed the differential expression of these HATs, HDACs and BCPs during aspects of *F. hepatica* development. The results of these and future functional genomics/whole organism compound screening investigations will provide evidence for the importance of HMEs in *F. hepatica* lifecycle transitions and highlight repositioned compounds suitable for further development as next-generation flukicides.