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*Immune responses directed at egg proteins during experimental infection with the liver fluke *Fasciola hepatica**

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Moxon et al - supplementary data

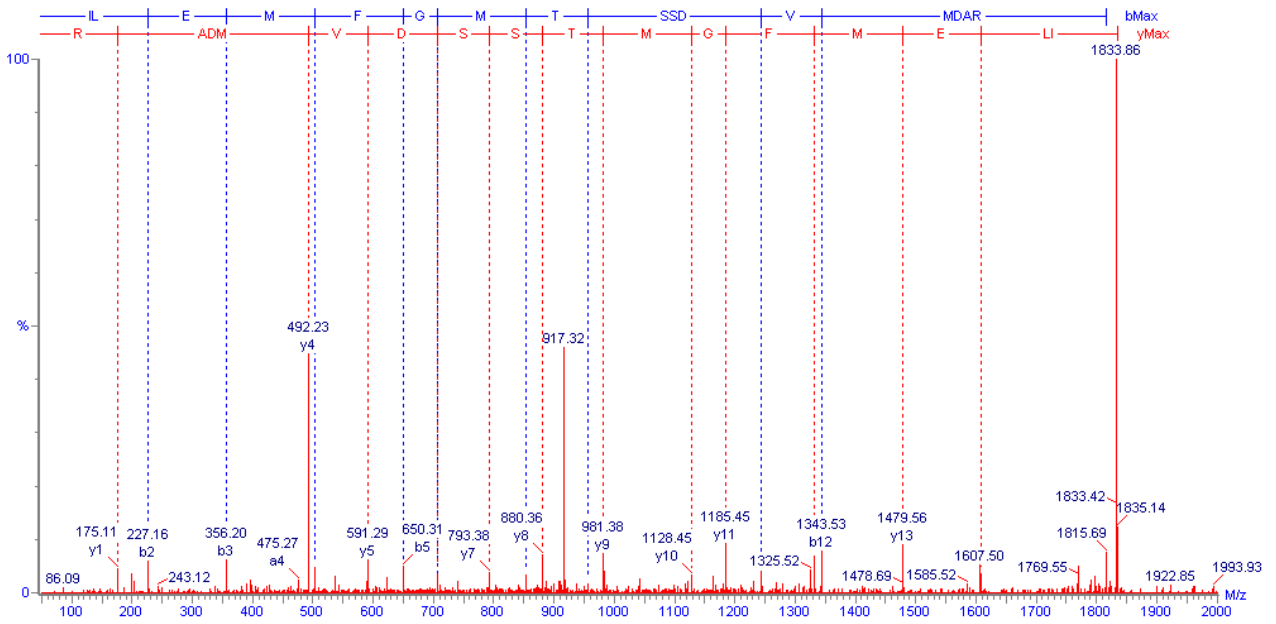


Figure S1. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 917.8, with a 2+ charge taken from a protein band with an apparent molecular weight of 61.6 kDa. Interpretation of the b and y ion series revealed the peptide sequence ILEFFGMTSSDVM DAR, matching a peptide from a protein disulphide isomerase expressed by *Fasciola hepatica*

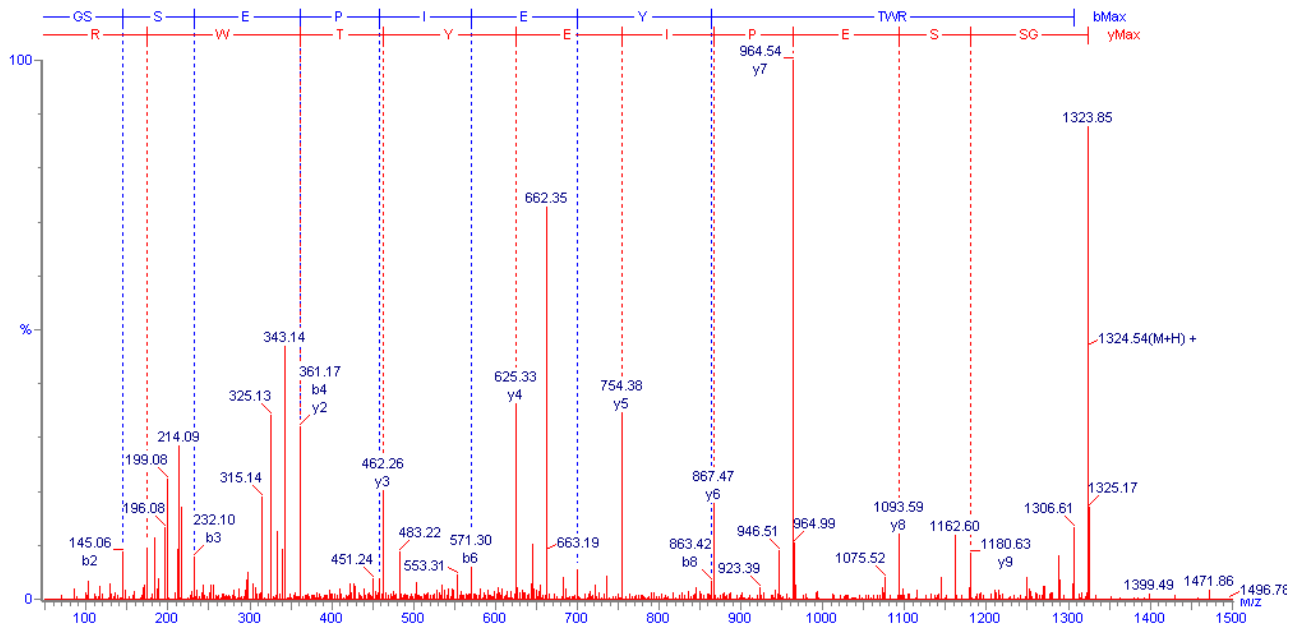


Figure S2. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 634.3, with a 2+ charge taken from a protein band with an apparent molecular weight of 61.6 kDa. Interpretation of the b and y ion series revealed the peptide sequence GSSEPIETWR, matching a peptide from a protein disulphide isomerase expressed by *Fasciola hepatica*

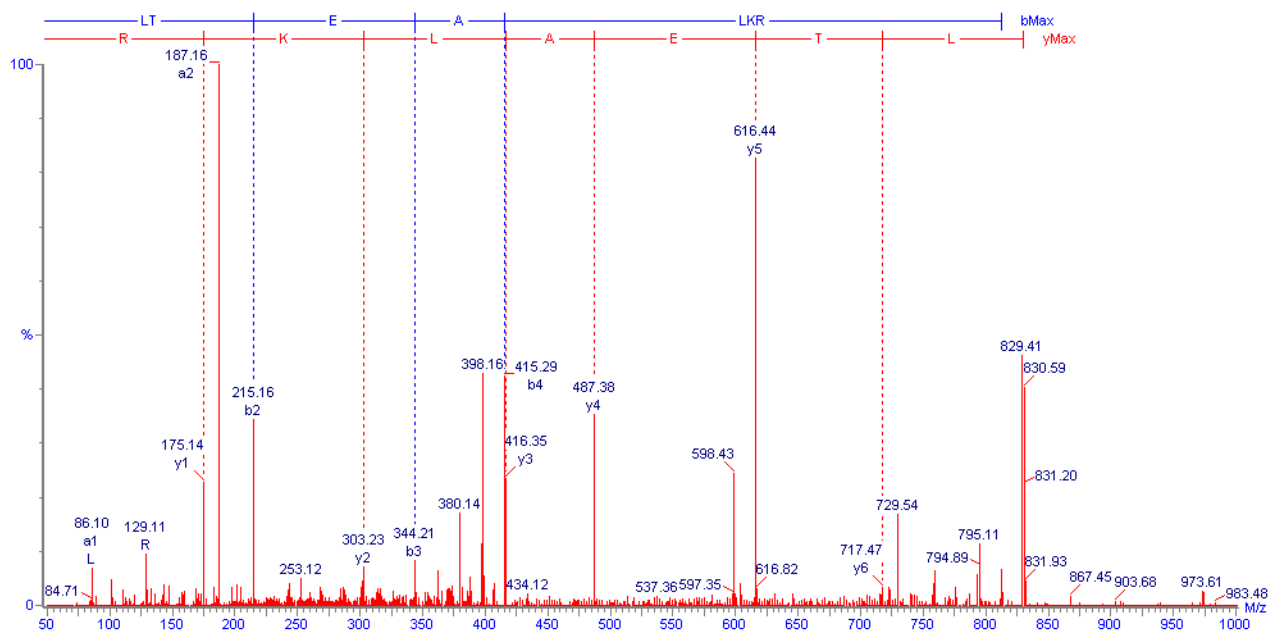


Figure S3. MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 415.7 with a 2+ charge taken from a protein band with apparent molecular mass of 61.6 kDa. Interpretation of the b and y ion series revealed the peptide sequence LEALKR. Underlined text denotes deviation from expected protein cleavage specificity. A mass error of 0.02 Da was observed. BLAST analysis against an in-house translated database of *F. hepatica* transcript revealed near-exact matches to clones showing significant homology to a SJCHGC08954 protein expressed by *Schistosoma japonicum* (GenBank accession number AAW27684, BLAST score $1e-11$).

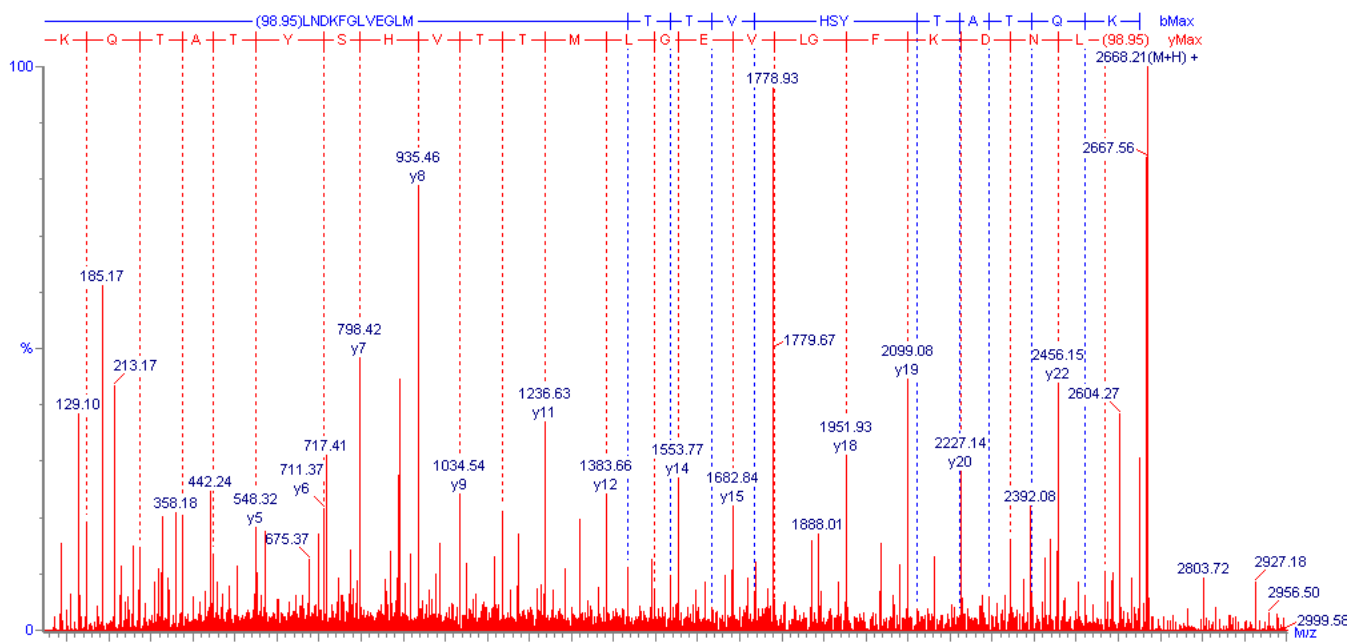


Figure S4. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 890.3, with a 3+ charge taken from a protein band with an apparent molecular weight of 44 kDa. Interpretation of the b and y ion series revealed the peptide sequence INDKFGIVEGLM-TTVHSYATQK, matching a peptide from a glyceraldehyde phosphate dehydrogenase expressed by *Fasciola hepatica*. Note, leucine and isoleucine residues of identical mass were exchanged to improve sequence homology.

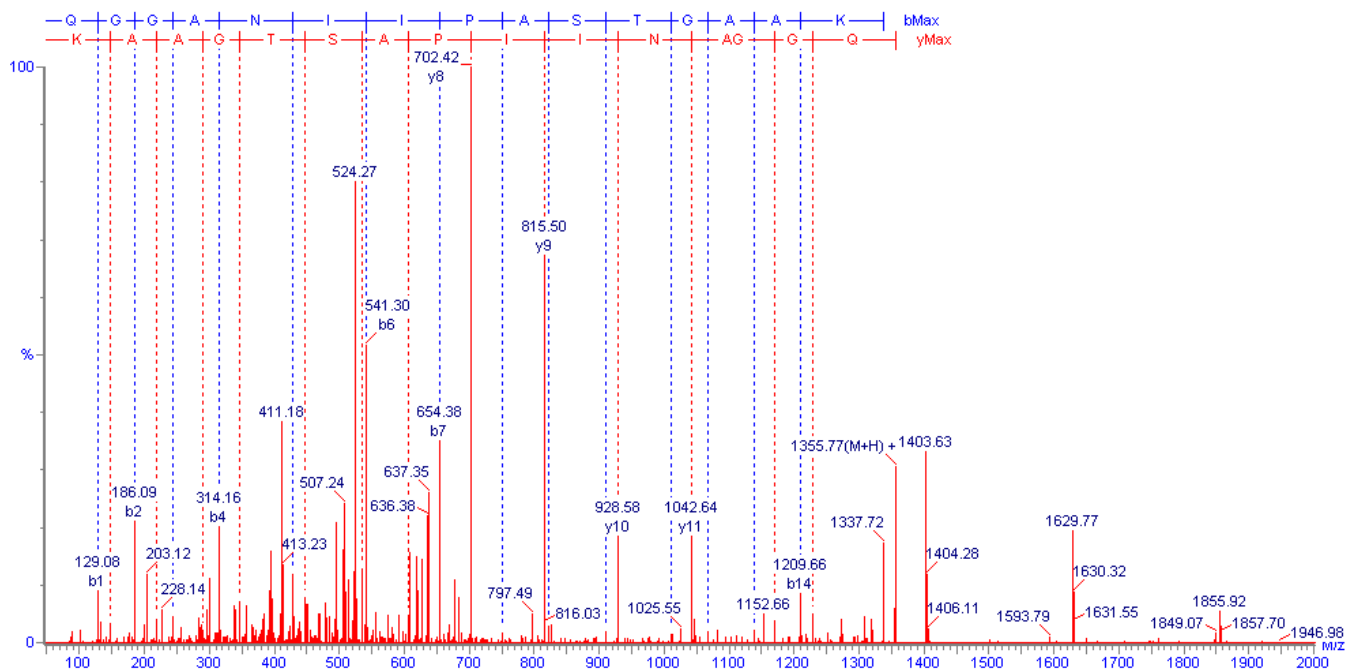


Figure S5. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 678.4, with a 2+ charge taken from a protein band with an apparent molecular weight of 44 kDa. Interpretation of the b and y ion series revealed the peptide sequence QGQNIIPASTGAAK, matching a peptide from a glyceraldehyde phosphate dehydrogenase expressed by *Fasciola hepatica*. Note, leucine and isoleucine residues of identical mass were exchanged to improve sequence homology.

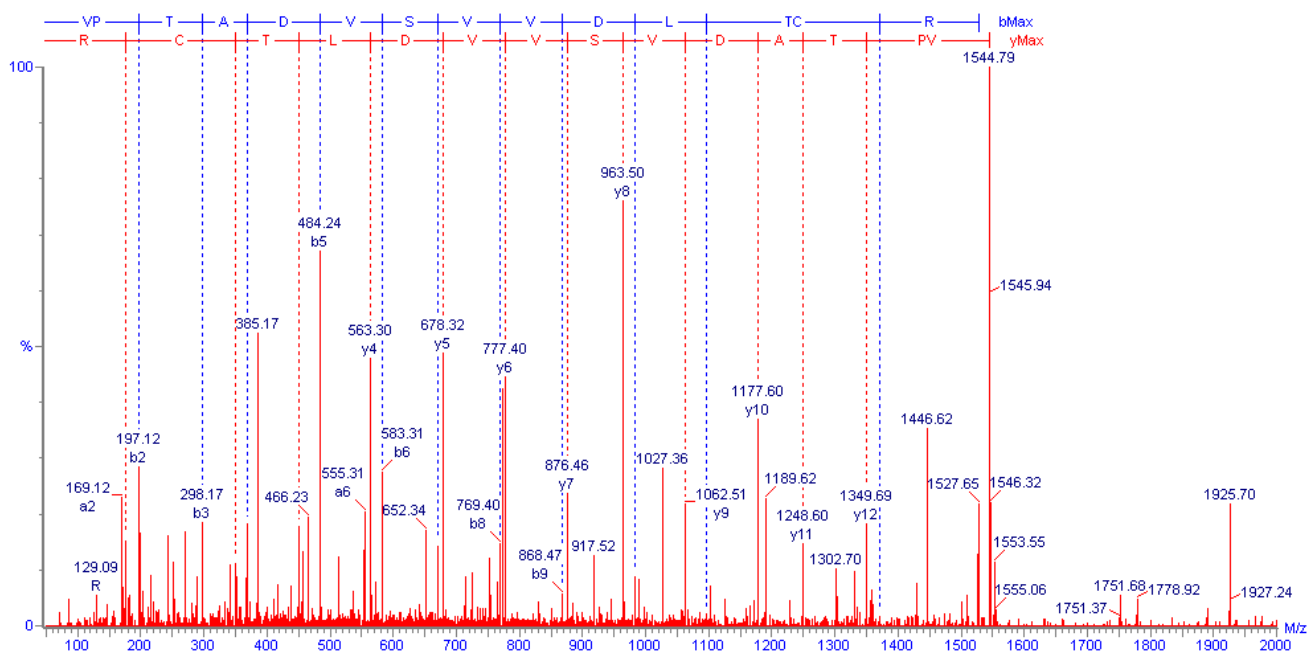


Figure S6. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 773.4, with a 2+ charge taken from a protein band with an apparent molecular weight of 44 kDa. Interpretation of the b and y ion series revealed the peptide sequence VPTADSVVDLTCR, matching a peptide from a glyceraldehyde phosphate dehydrogenase expressed by *Petromyzon marinus*.

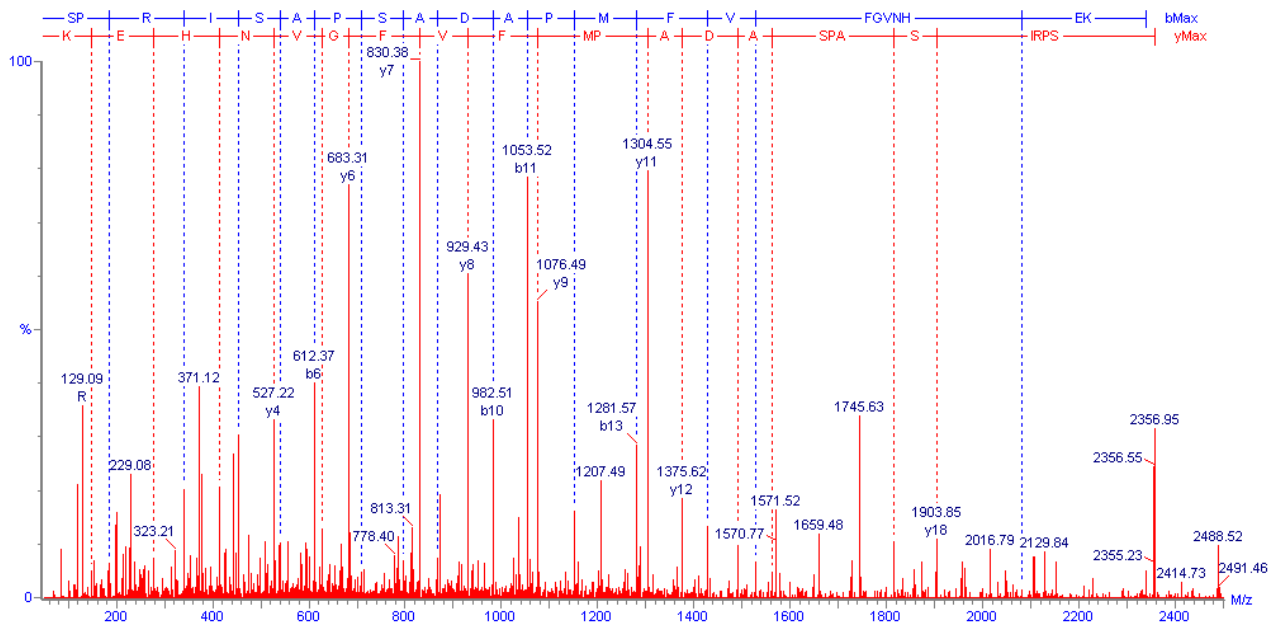


Figure S7. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 786.4, with a 3+ charge taken from a protein band with an apparent molecular weight of 44 kDa. Interpretation of the b and y ion series revealed the peptide sequence SPRISAPSADAPMFVFGVNH EK, matching a peptide from a glyceraldehyde phosphate dehydrogenase expressed by *Petromyzon marinus*.

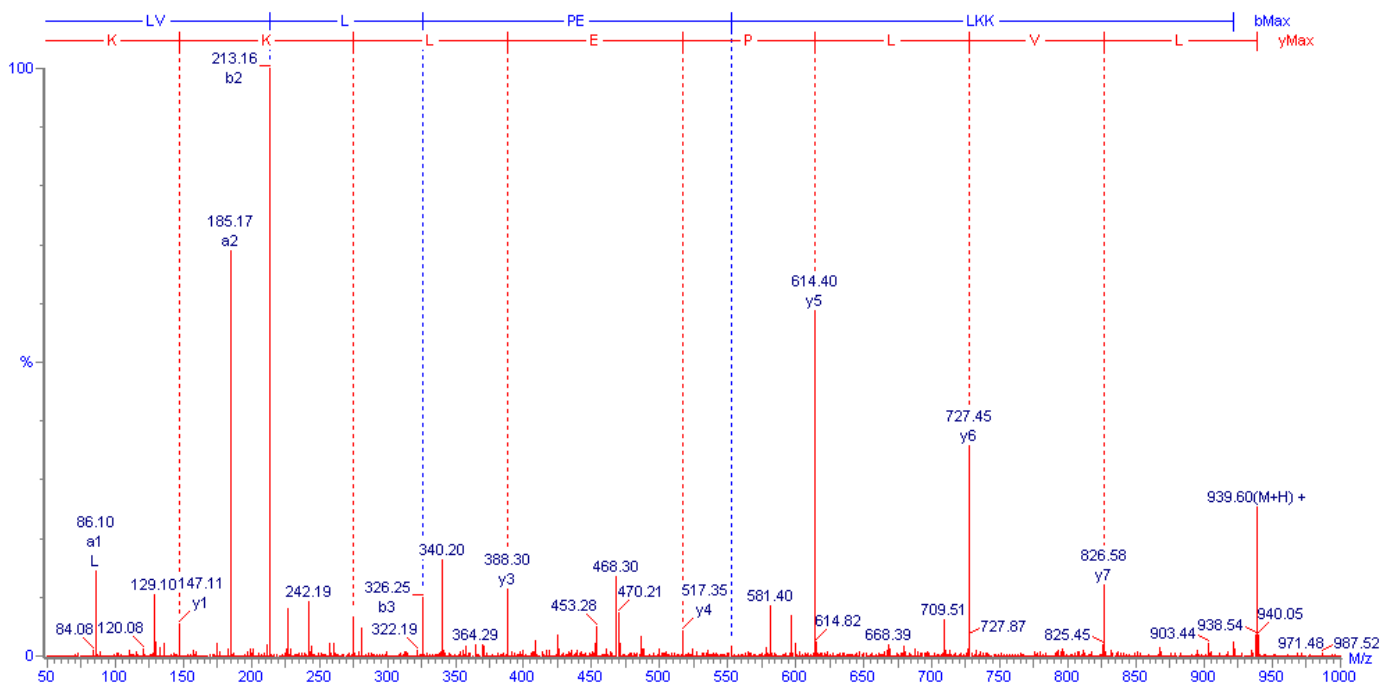


Figure S8. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 470.3, with a 2+ charge taken from a protein band with an apparent molecular weight of 44 kDa. Interpretation of the b and y ion series revealed the peptide sequence LVK L L PE P L LKK V L, matching a peptide from a mitochondrial malate dehydrogenase expressed by *Clonorchis sinensis*.

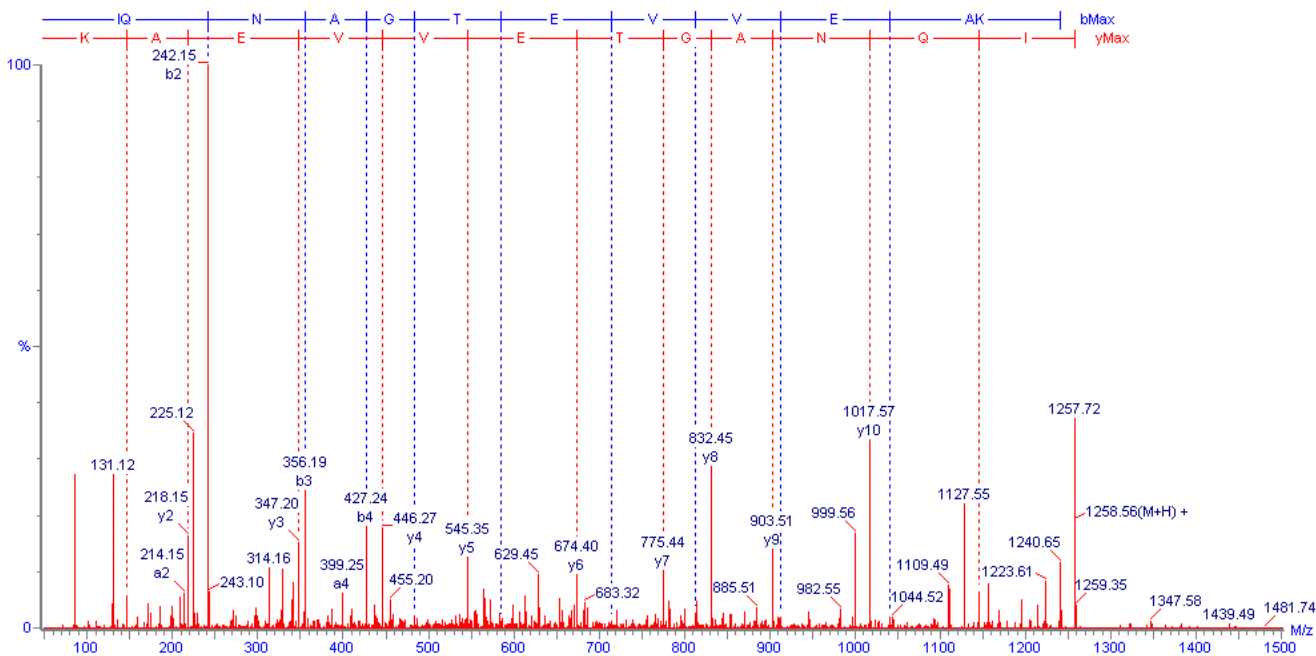


Figure S9. Representative MS/MS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 629.8, with a 2+ charge taken from a protein band with an apparent molecular weight of 44 kDa. Interpretation of the b and y ion series revealed the peptide sequence IQNAGTEVVEAK, matching a peptide from a mitochondrial malate dehydrogenase expressed by *Clonorchis sinensis*.

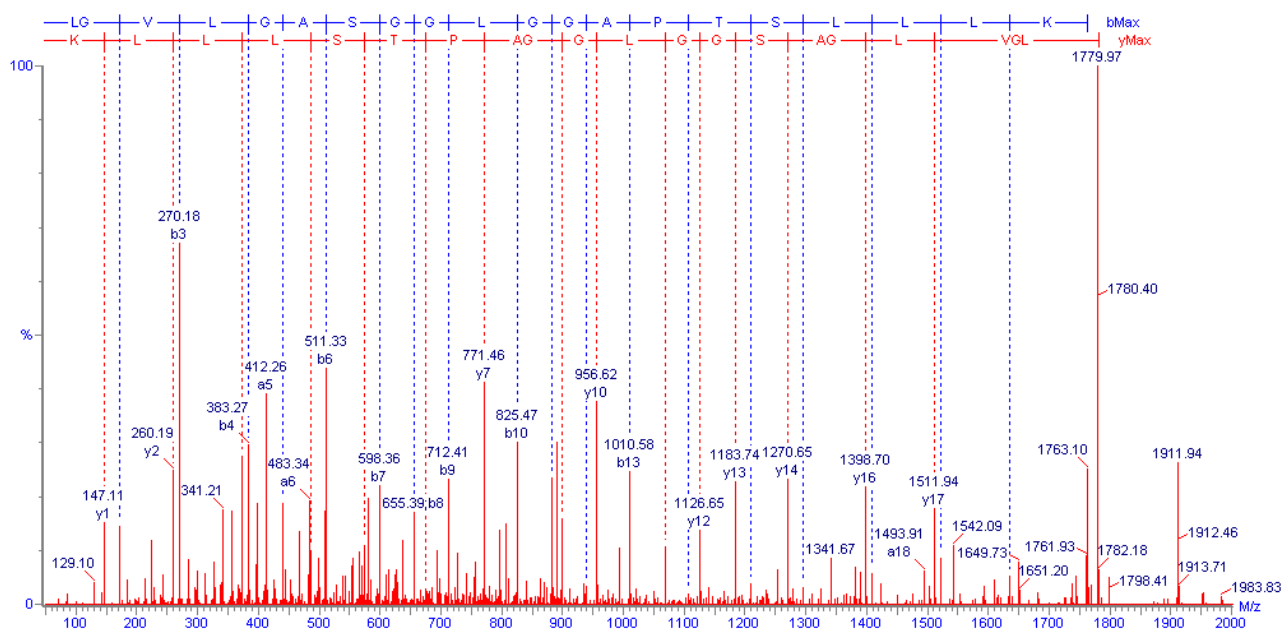


Figure S10. MS/MS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 891 with a 2+ charge taken from a protein band with apparent molecular mass of 44 kDa. Interpretation of the b and y ion series revealed the peptide sequence LGVLGASGGIGGAPTSLLLK. No deviation from expected protein cleavage specificity was noted. A mass error of 0.02 Da was observed. BLAST analysis against an in-house translated database of *F. hepatica* transcript revealed significant matches to a SJCHGC01653 protein expressed by *Schistosoma japonicum* (GenBank accession number AAW25914).

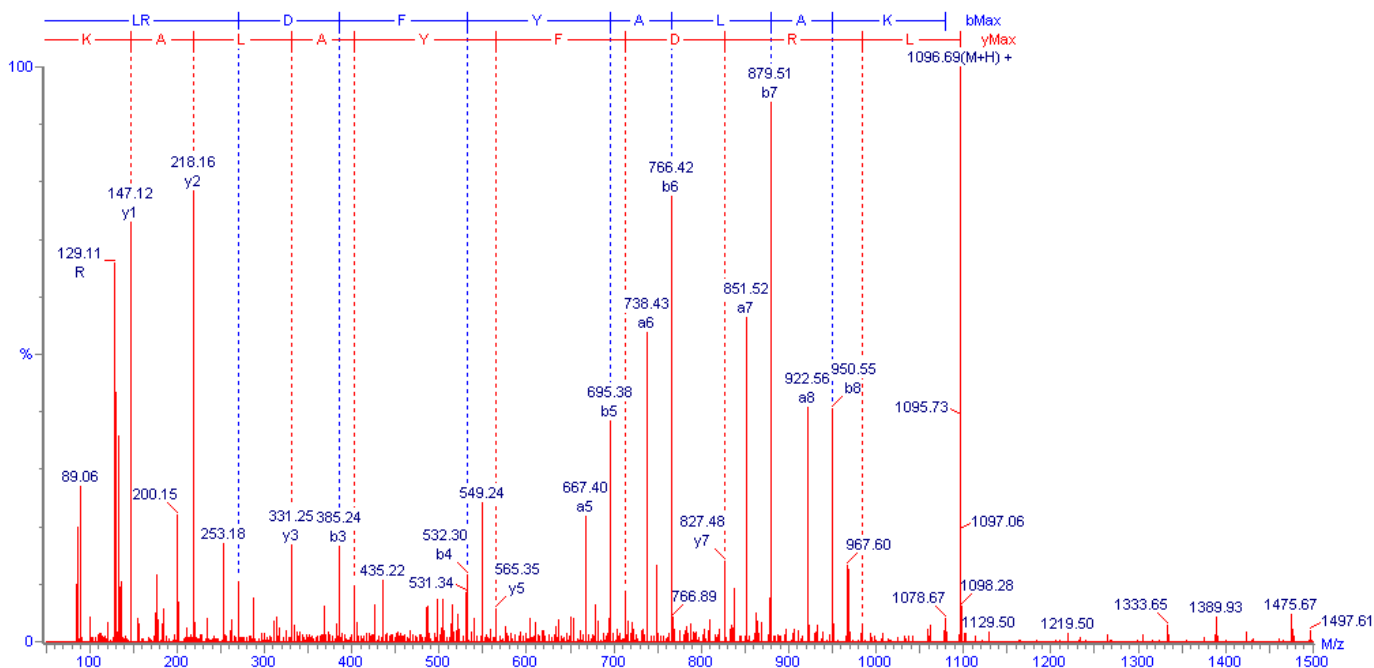


Figure S11. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 548.8, with a 2+ charge taken from a protein band with an apparent molecular weight of 31.9 kDa. Interpretation of the b and y ion series revealed the peptide sequence LRDFYALAK, matching a peptide from a yolk ferritin expressed by *Paragonimus westermani*.

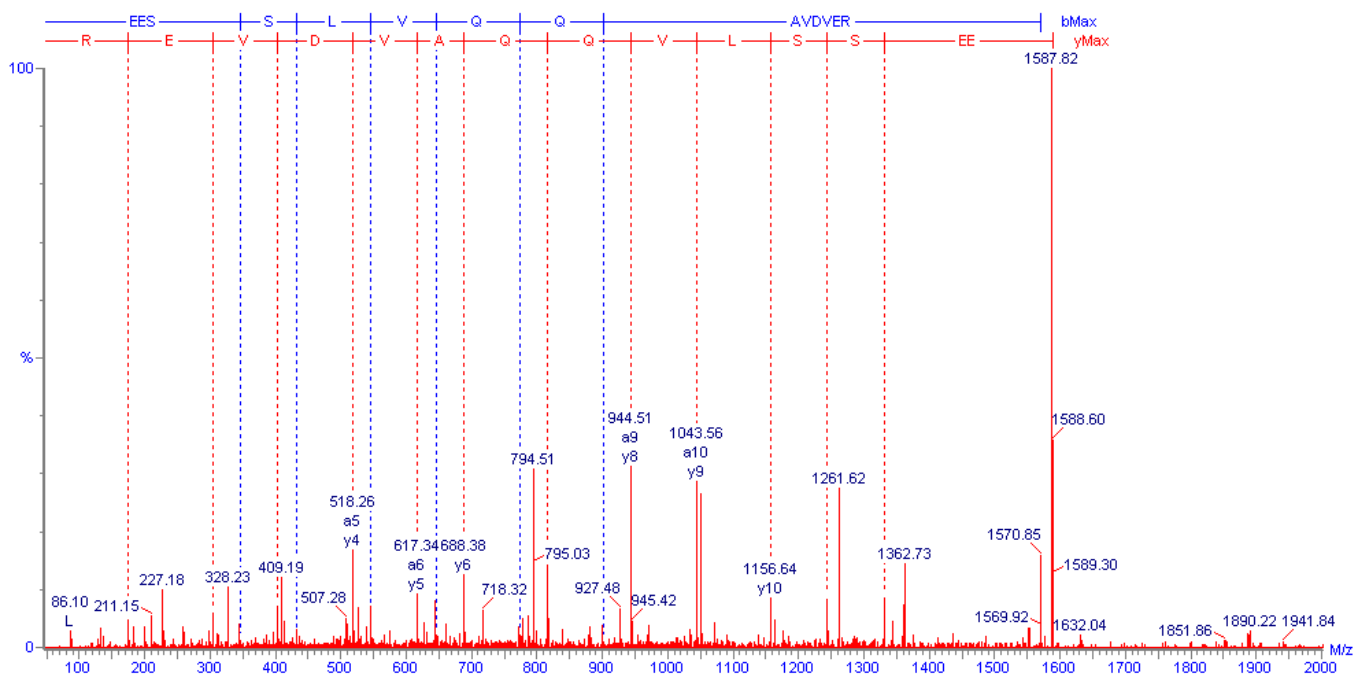


Figure S12. Representative MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 794.9, with a 2+ charge taken from a protein band with an apparent molecular weight of 31.9 kDa. Interpretation of the b and y ion series revealed the peptide sequence EESLVQQAQVLDVLR, matching a peptide from a yolk ferritin expressed by *Paragonimus westermani*.

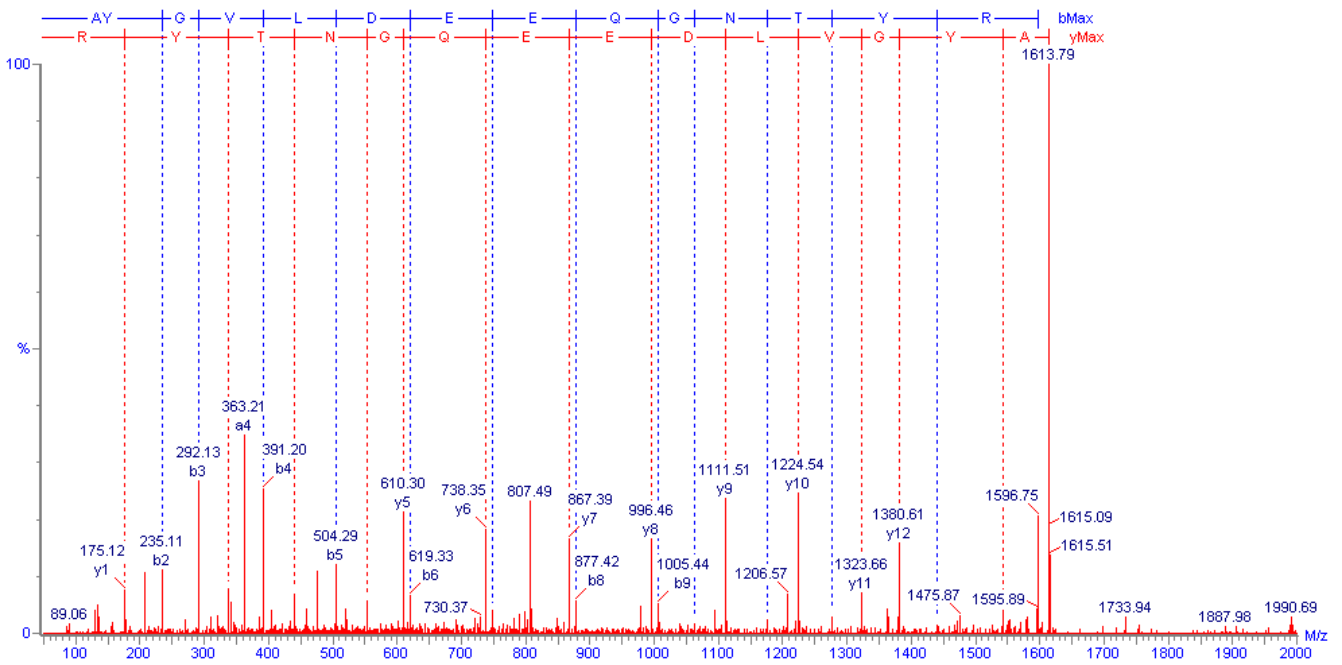


Figure S13. MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 807.9 with a 2+ charge taken from a protein band with apparent molecular mass of 31.9 kDa. Interpretation of the b and y ion series revealed the peptide sequence AYGVLDEEQGNTYR. No deviation from expected protein cleavage specificity was noted. A mass error of 0.02 Da was observed. BLAST analysis against an in-house translated database of *F. hepatica* transcript revealed significant matches to EST clones (7e-4) encoding a thioredoxin peroxidase expressed by *Fasciola hepatica* (GenBank accession number ABY85785, 8e-113).

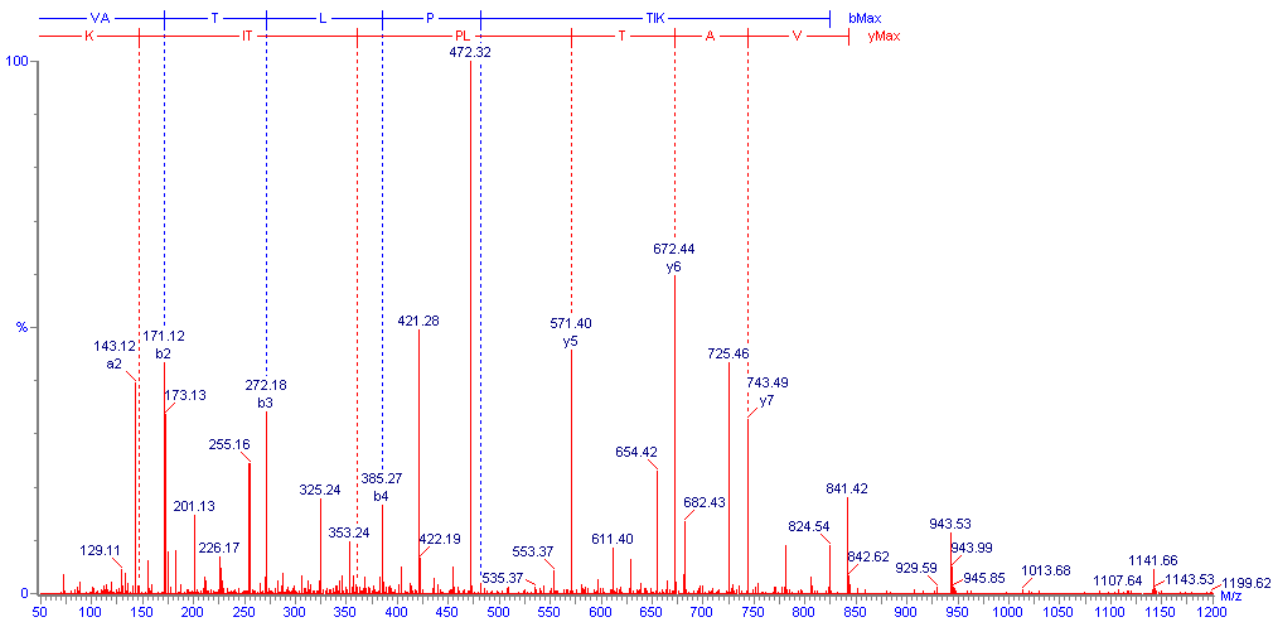


Figure S14. MSMS sequence analysis using peptide sequencer (MassLynx v. 5.0, Micromass, UK) of a precursor ion m/z 421.7 with a 2+ charge taken from a protein band with apparent molecular mass of 31.9 kDa. Interpretation of the b and y ion series revealed the peptide sequence VATLPTIK. No deviation from expected protein cleavage specificity was noted. A mass error of 0.02 Da was observed. BLAST analysis against an in-house translated database of *F. hepatica* transcript revealed near-identical matches to EST clones encoding a phosphoglycerate kinase expressed by *Fasciola hepatica* (GenBank accession number AAZ17561, 7e-100).