BIOINFORMATION

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Supplementary material:

Table 1: List of the apicoplast associated drug targets of *Toxoplasma gondii ME49* having pathogen specific unique biochemical pathways

Sl. No	Drug Target Name	Predicted Function
1	Mov34/MPN/PAD-1 domain	It acts as a regulatory submit of 26 proteasome
2	Thioredoxin reductase	It reduces thioredoxin using NADPH
3	Succinyl Co-A ligase	It is a ADP-forming beta subunit
4	RNA binding	It is involved in Post-transcriptional events
5	Long chain fatty acid CoA ligase	It catalyses bio-activation of fatty acids
6	Heat shock protein 90((Putative)	It has molecular Chaperon activity
7	60S Ribosomal protein L23(Putative)	It is involved in Binding activity
8	Hypothetical protein TGME49_112400	No definite function could be identified
9	Signal Recognition particle 54 kda	The protein is involved in rRNA modification guide activity
10	L-isoaspartate O-methyl transferase	This protein recognises & catalyses the repair of damaged DNA
11	Pyruvate Kinase	It is involved in Glycolysis
12	Succinate- semi aldehyde dehydrogenase	It catalyses metabolic reactions of fatty acids
13	DNA polymerase delta catalytic subunit	It is involved in DNA replication and repair
14	Actin -like family protein ARP4a	It has ATPase activity
15	Ras family domain	It acts as potential tumour suppressor
16	5-aminolevulinic acid synthase	It possess pyridoxal phosphate binding
17	Ankyrin repeat	It has a mediatory role in protein-protein interactions
18	Kelch motif domain	It is involved in cell fusion mechanism

Table 2: Fold based modeling of selected proteins using fold –recognition based computational tool Phyre2 (Protein Homology/analogY Recognition Engine V 2.0). Selected template, Coverage, residues aligned fold descriptor, and super family for each protein are given

Protein	SCOP Code/protein PDBID	Coverage (%)	Residues aligned	Fold/PDB descriptor	Super family	Family
Long chain fatty acid CoA ligase	d1pg4a_	95 %	Residues 23-739	Acetyl-CoA synthetase-like	Acetyl CoA synthetase	Acetyl-CoA synthetase
Succinate-semi aldehyde dehydrogenase	c3ed6B_	97%	Residues 14-565	Betaine aldehyde dehydrogenase	Oxidoreductase	Oxidoreductase