

**Figure S1: Pipeline for modeling GST-like interactions in MSCs.** Global approach used to identify GST-like folds in AIMP and aaRSs and to model their association into MSCs with ColabFold. The occurrence of canonical interfaces 1, 1' and 2 in the resulting models suggest a positive interaction between GST-like domains.

Table S1. (A) Annotation of GST-like containing protein genes in EupathDB. (B) Additional domains identified in *Apicomplexa* aaRSs (except GST-like domains)

A

	AIMPs and AARSs					Translation factors			
	AIMP	ERS	MRS	QRS	YRS	EF1-β	EF1-γ	EF1-α	EF1-δ
<i>P. berghei</i>	PBANKA_1306200	PBANKA_1362000	PBANKA_0518700	PBANKA_1346600	PBANKA_1222800	PBANKA_0814200	PBANKA_1352000	PBANKA_1133300	PBANKA_1218900
<i>P. chabaudi</i>	PCHAS_1309400	PCHAS_1366600	PCHAS_0518800	PCHAS_1351200	PCHAS_1223400	PCHAS_0814500	PCHAS_1356600	PCHAS_1133800	PCHAS_1219600
<i>P. falciparum</i>	PF3D7_1442300	PF3D7_1349200	PF3D7_1034900	PF3D7_1331700	PF3D7_0807900	PF3D7_0913200	PF3D7_1338300	PF3D7_1357100	PF3D7_0319600
<i>P. knowlesi</i>	PKNH_1240000	PKNH_1251700	PKNH_0620100	PKNH_1268800	PKNH_0110800	PKNH_0711100	PKNH_1263000	PKNH_1114500	PKNH_0821600
<i>P. vivax</i>	PVP01_1264700	PVP01_1205600	PVP01_0620000	PVP01_1222900	PVP01_0112500	PVP01_0711600	PVP01_1216400	PVP01_1114900	PVP01_0820600
<i>P. yoelii</i>	PY17X_1310000	PY17X_1367700	PY17X_0519800	PY17X_1351500	PY17X_1226000	PY17X_0817500	PY17X_1357200	PY17X_1134900	PY17X_1222100
<i>B. bigemina</i>	BBBOND_0102100	BBBOND_0404120	BBBOND_0207070	BBBOND_0307760	BBBOND_0202210	BBBOND_0110635	BBBOND_0200780	BBBOND_0108320	
<i>B. bovis</i>	BBOV_III010240	BBOV_III011840	BBOV_I001970	BBOV_II006400	BBOV_II002250	BBOV_IV003370	BBOV_II000890	BBOV_IV010620	
<i>B. microti</i>	BMR1_01G02705	BmR1_04g04960	BMR1_02g02000	BMR1_03g03040	BMR1_01G00295	BMR1_03g01425	BMR1_02g03070	BMR1_03g03725	
<i>T. annulata</i>	TA11475	TA17035	TA05325	TA12530	TA08075	TA16305	TA08705	TA06720	
<i>T. orientalis</i>	TOT_020000112	TOT_010001344	TOT_030000712	TOT_020000303	TOT_040000556	TOT_010001036	TOT_040000424	TOT_010000685	
<i>T. parva</i>	TpMuguga_02g00124	TpMuguga_01g01053	TpMuguga_03g00137	TpMuguga_02g00322 TpMuguga_02g02375	TpMuguga_04g00367	TpMuguga_01g01096	TpMuguga_04g00492	TpMuguga_01g00726	
<i>C. hominis</i>	Chro.40444	Chro.80098	Chro.80398	Chro.10244	Chro.60344	Chro.20423	Chro.70492	Chro.60459	
<i>C. muris</i>	CMU_018940	CMU_024700	CMU_006170	CMU_028890	CMU_031000	CMU_003010	CMU_014590	?	
<i>C. parvum</i>	cgd4_3880	cgd8_790	cgd8_3460	cgd1_2130	cgd6_2970	cgd2_3950	cgd7_4450	cgd6_3990	
<i>T. gondii</i>	TGME49_223140	TGME49_263870	TGME49_289300	TGME49_217460-126	TGME49_251880	TGME49_226410	TGME49_300140	TGME49_294800	TGME49_219140
<i>N. caninum</i>	NCLIV_006150	NCLIV_024090	NCLIV_041650	NCLIV_062220	NCLIV_066920	NCLIV_046550	NCLIV_064580	NCLIV_014180	NCLIV_061340

B

	ARS	CRS	DRS	FRS-α	FRS-β	GRS	HRS	IRS	KRS	LRS	NRS	PRS	RRS	SRS	TRS	VRS	YRS	WRS
Nter	<i>Plasmodium</i>	ASP	ASP	K-rich helix	DNA-binding		ASP	?	K-rich helix	K-rich helix		K-rich helix	Ybak			ASP		Ala-X
	<i>Toxoplasma</i>		?	K-rich helix	DNA-binding		ASP	?	-	K-rich helix		K-rich helix	Ybak			ASP		Ala-X
	<i>Neospora</i>		?	K-rich helix	DNA-binding		ASP	?	-	K-rich helix		K-rich helix	Ybak					Ala-X
	<i>Babesia</i>			K-rich helix	DNA-binding		ASP	?	-	K-rich helix		K-rich helix	Ybak					Ala-X
	<i>Theileria</i>	ASP		K-rich helix	DNA-binding		ASP	?	-	K-rich helix		K-rich helix	Ybak			ASP		Ala-X
	<i>Cryptosporidium</i>			K-rich helix	DNA-binding			?	-	K-rich helix		K-rich helix	Ybak					
Cter	<i>Plasmodium</i>								Zn binding		tRNA binding		Zn binding					
	<i>Toxoplasma</i>								Zn binding		tRNA binding		Zn binding					
	<i>Neospora</i>								Zn binding		tRNA binding		Zn binding					
	<i>Babesia</i>								Zn binding		tRNA binding		Zn binding					
	<i>Theileria</i>								Zn binding		tRNA binding		Zn binding					
	<i>Cryptosporidium</i>								Zn binding		tRNA binding		Zn binding					

ASP: Apicoplast Signal Peptide  
?: Peptide with no functional prediction  
Apicomplex-specific domain  
Eukaryote-specific domain

**A**

***PLASMODIUM***

*P. vivax*  
*P. yoelii*  
***P. berghei***  
*P. knowlesi*  
*P. falciparum*  
*P. chabaudi*

[illegible]

## ***THEILERIA***

*T.annulata*  
*T.orientalis*  
***T.parva***

[illegible]

## ***BABESIA***

*B. microti*  
*B. bigemina*  
***B. bovis***

[illegible]

*B. microti*  
*B. bigemina*  
***B. bovis***

**$\alpha 7$**

YNHIDALVKK  
FRHVSTWAQN  
YKHVSTWVQN  
.:\*.:.:.

## CRYPTOSPORIDIUM

*C. hominis*  
***C. parvum***  
*C. muris*

**RIDIU**

MDK---FGDISTAGRKKLNDYLSTRSYMNGVSPTQDDV EALYMIKAGG-FCDFQHI **CRYV**SHIQS  
MDK---FGDISTAGRKKLNDYLSTRSYMNGVSPQDDV EALYMIMKAGG-FCDFQHI **CRYV**SHIQS  
MLKIKGFGLDSTLEGKKKLDFLSNRTYFNGVNPQNDC NLVSELLAGTKYCSFPHI **CRYLEH**MRH  
\* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \*

## ***TOXOPLASMA/NEOSPORA***

*T. gondii*  
*N. caninum*


  
 MVVPDFGNLKS DIGVKLNEYLASRSFITGYS**ATQDDAI**IFSKLLGAPNATK FVDAS**RWY**RHVS HFSVPVQKAAM
   
 MVVPDFGNLKS DIGVKLNEYLASRSFITGY**ATQDDAI**IFSKLLGAPNATK FVDAS**RWY**RHVS HFSVPVQKAAM
   
 \*\*\*\*\*

# B

# PLASMODIUM

*P. vivax*  
*P. yoelii*  
***P. berghei***  
*P. knowlesi*  
*P. falciparum*  
*P. chabaudi*

*P. vivax*  
*P. yoelii*  
***P. berghei***  
*P. knowlesi*  
*P. falciparum*  
*P. chabaudi*

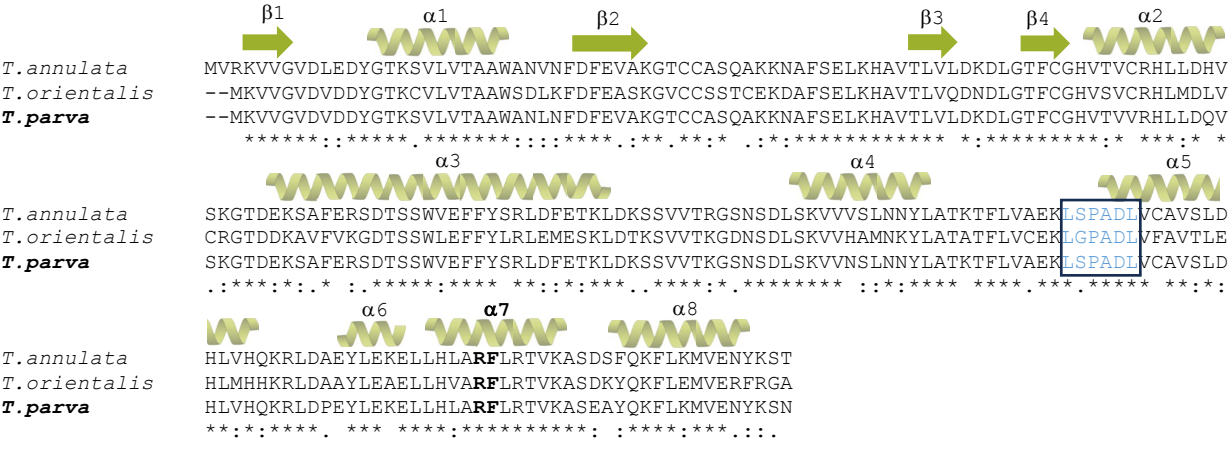
[illegible]

*P. vivax*  
*P. yoelii*  
***P. berghei***  
*P. knowlesi*  
*P. falciparum*  
*P. chabaudi*

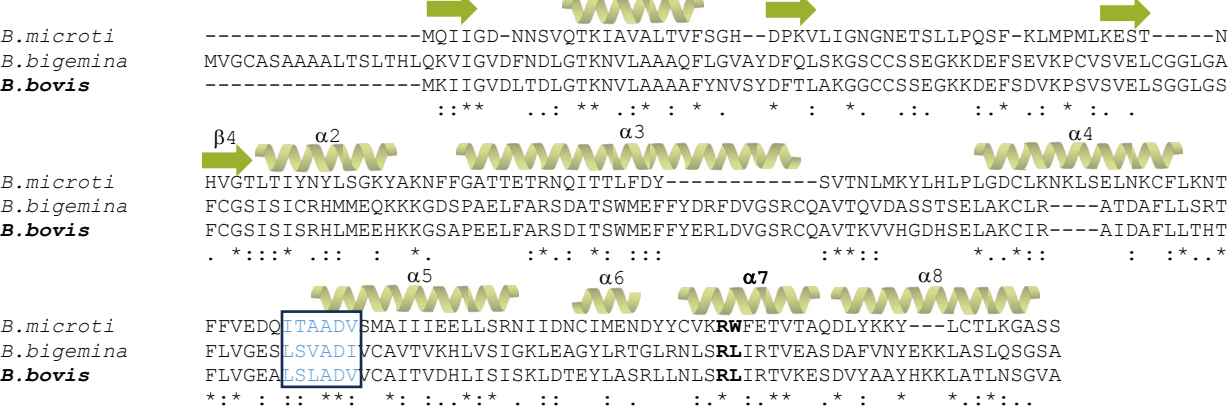
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Figure S2

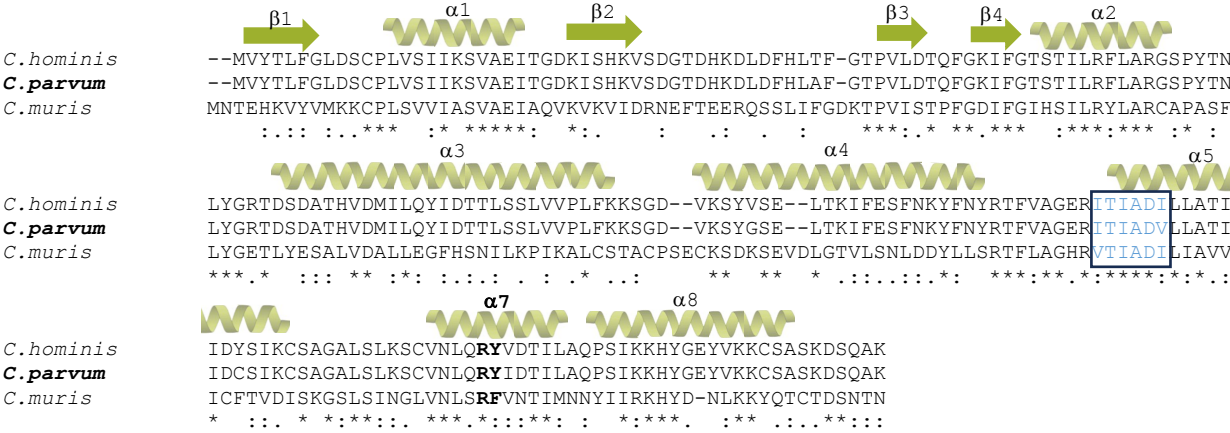
# THEILERIA



# BABESIA



# CRYPTOSPORIDIUM



# TOXOPLASMA/NEOSPOA

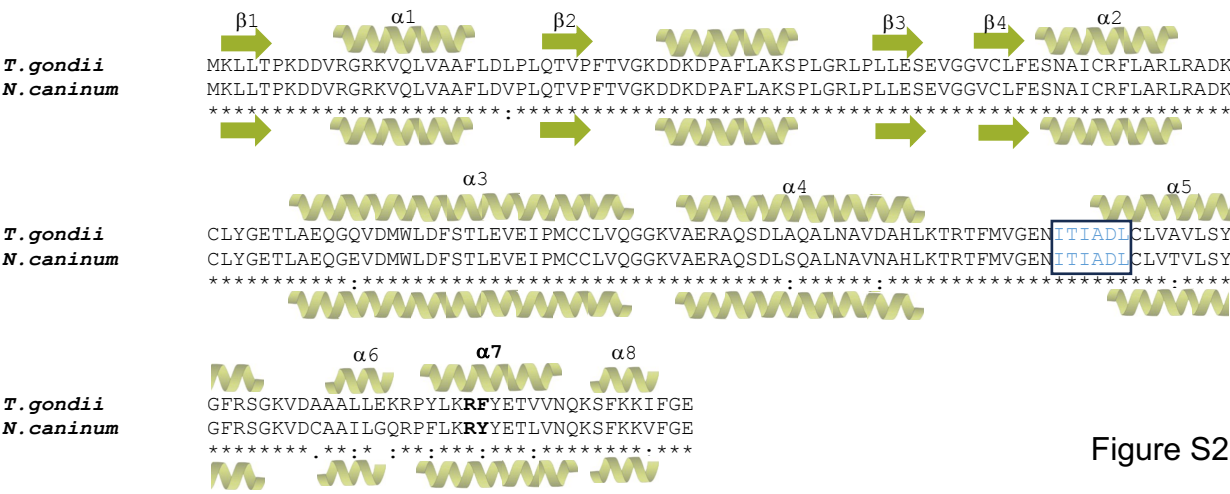


Figure S2

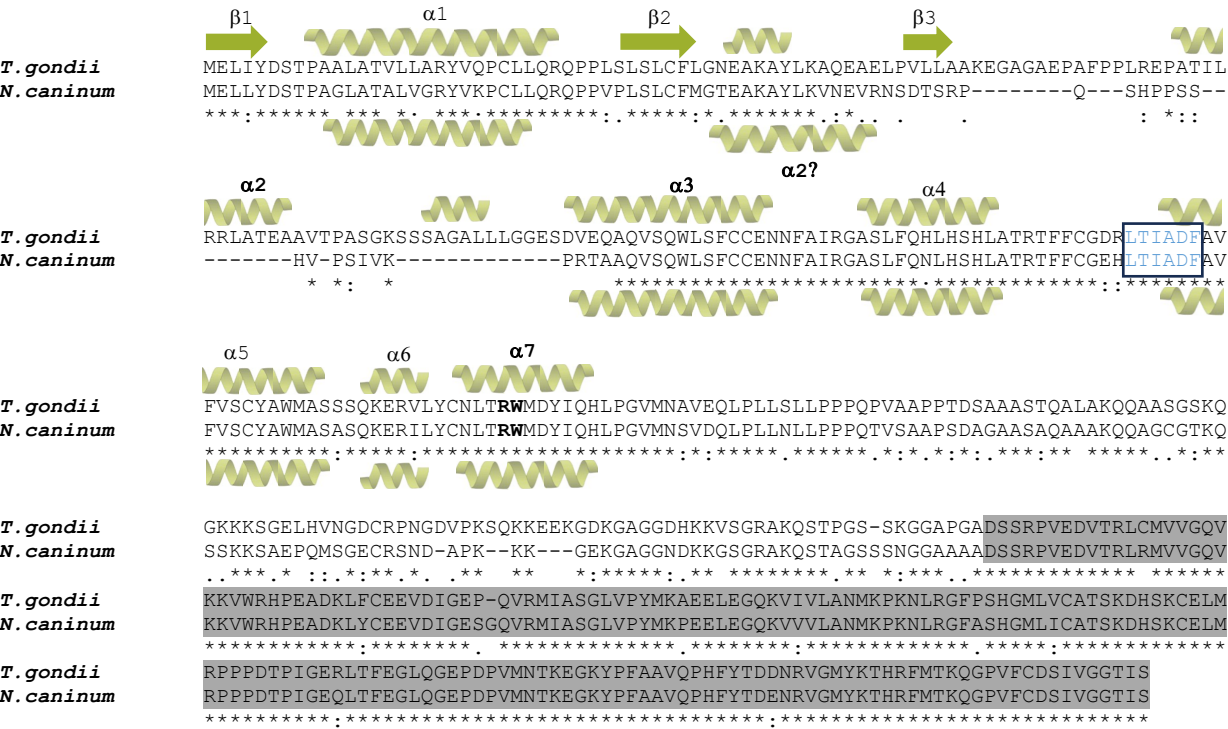
***PLASMODIUM*** (tRip)



[illegible][illegible]

Figure S2

**TOXOPLASMA (Tg-p43) / NEOSPORA (Nc-p47)**



**Phylogenetic tree based on full sequence alignments of Apicomplexa AIMP**

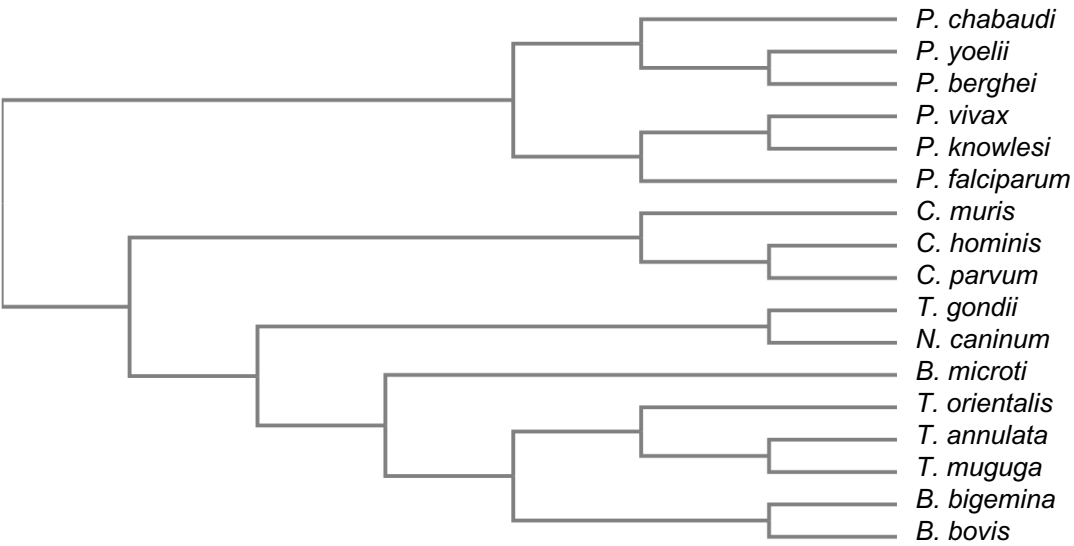
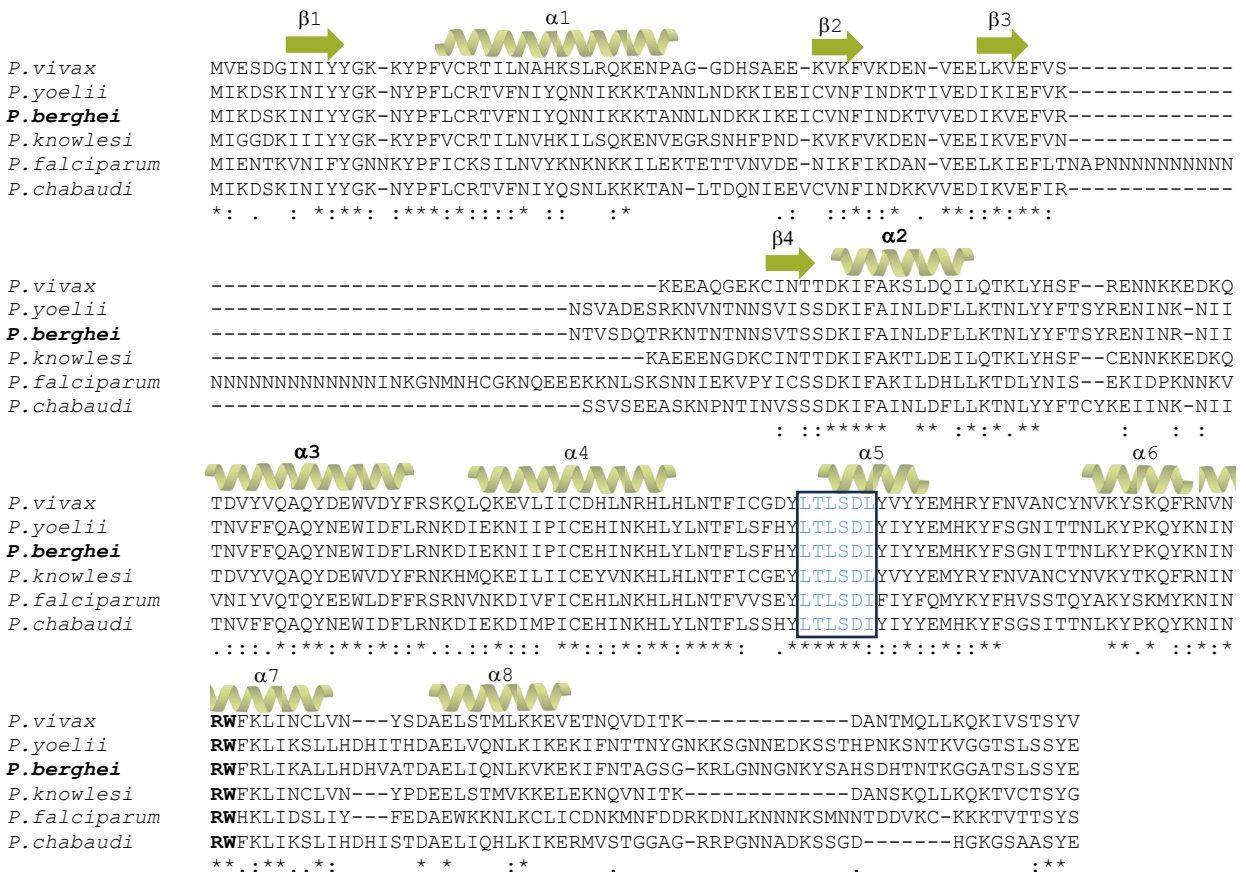


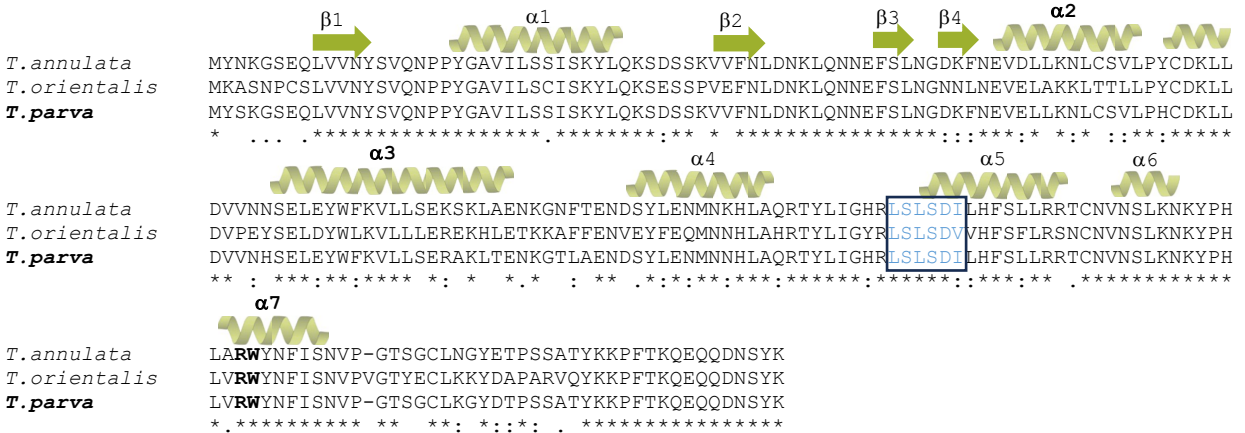
Figure S2

## D GST-like ERSs

# PLASMODIUM



## ***THEILERIA***



## **BABESIA**

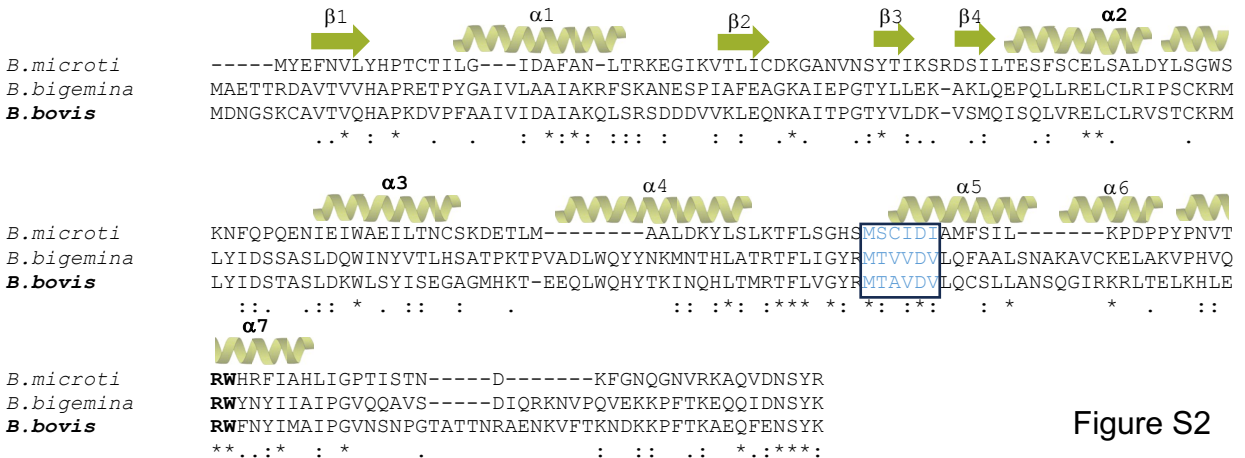


Figure S2

TOXOPLASMA / NEOSPORA

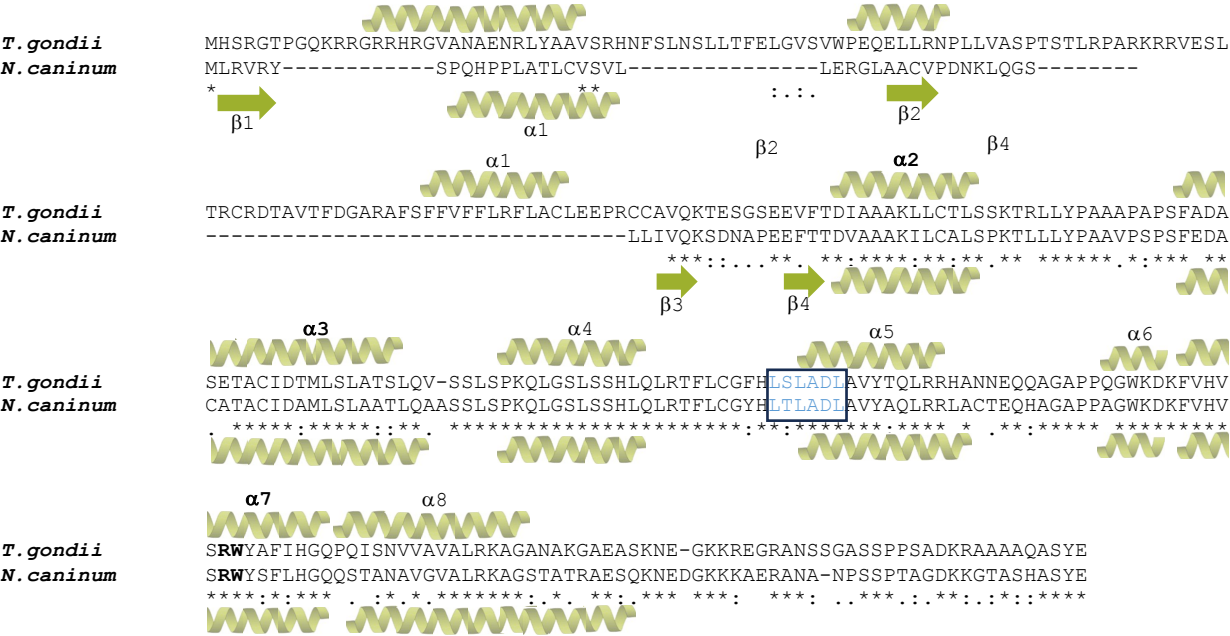
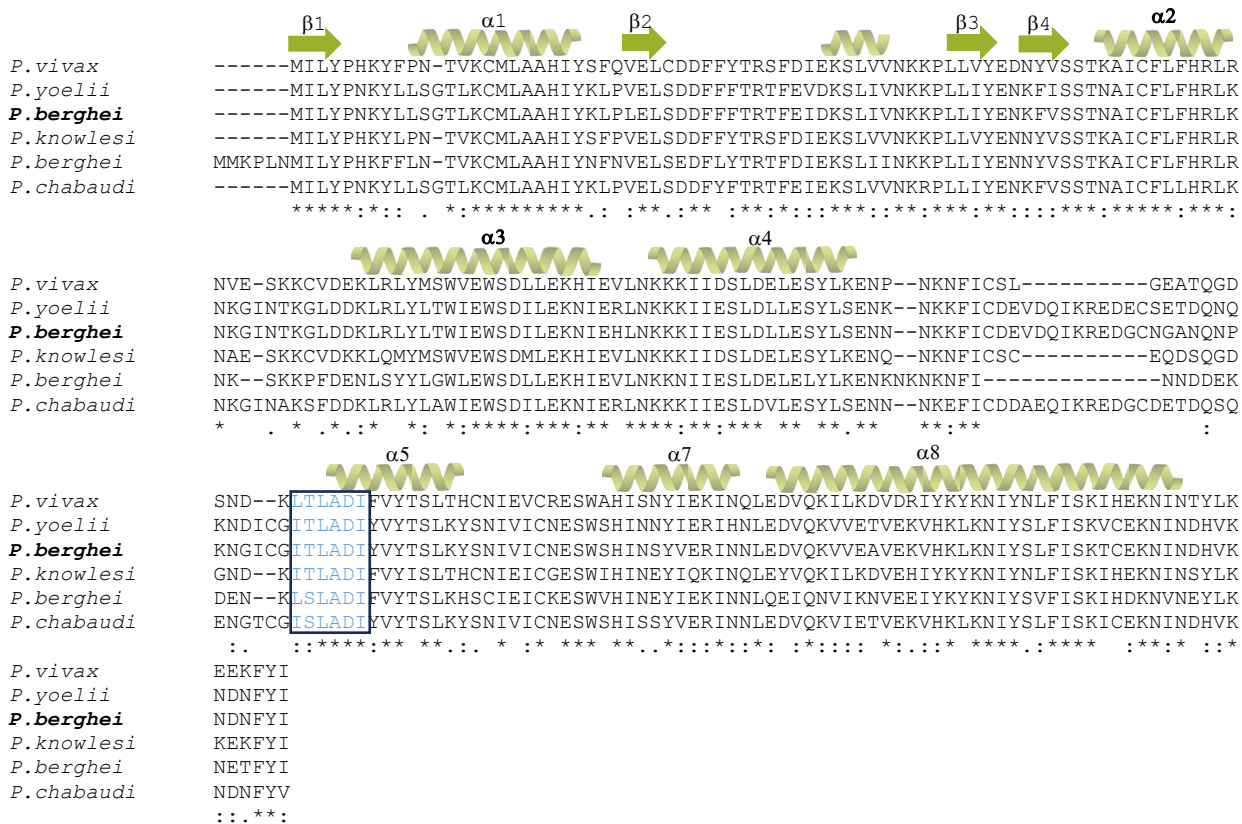


Figure S2

# E

## PLASMODIUM



## THEILERIA

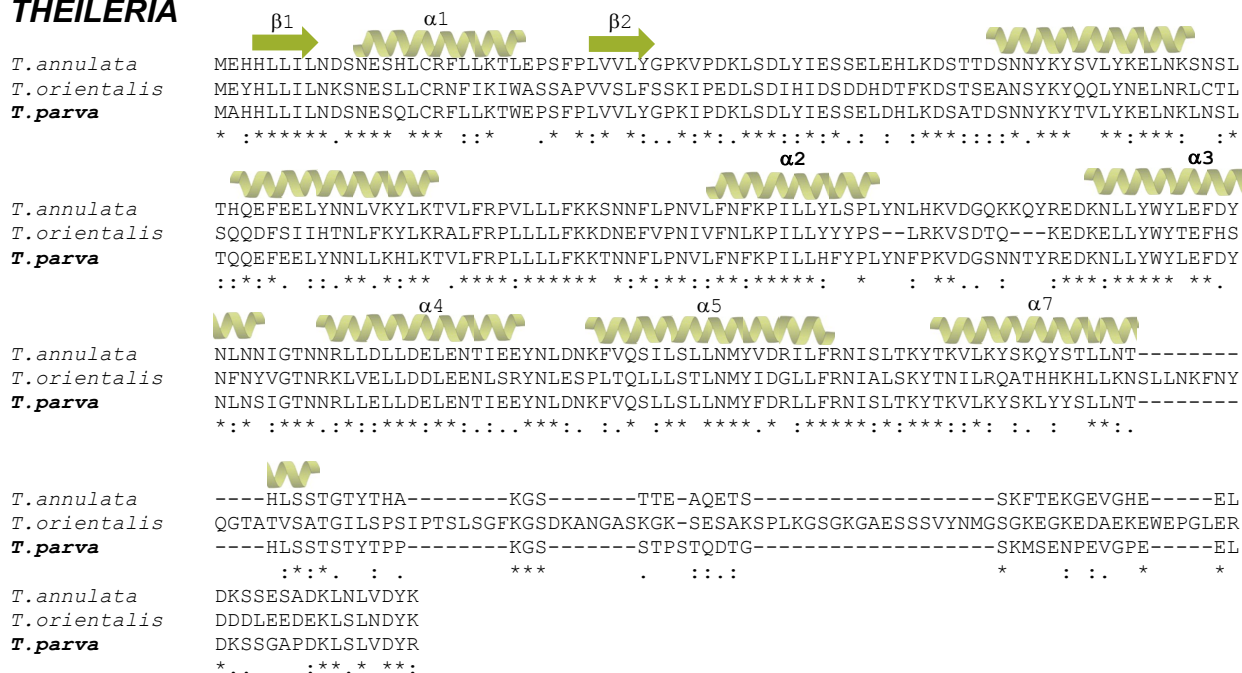


Figure S2

*B. bigemina*  
***B. bovis***  
*B. microti*



**F**

# PLASMODIUM

Species	Sequence
*P. vivax*	MEHVEKIYIRNKAEKSDNFFYFYFNWVKLNFTCLIISENSSSLRSSVLELLNGKKVLVSEINVCEALFRLACGGI----
*P. yoelii*	MEHIEKIYIKNKSDLGNEFFYFYFNWVKEKFNISLIVISENSSLRHNIVLELSDGNNLSLNELNSCAIFHLIISNDK----
*P. berghei*	MEHVEKIYIKNTSDLGNEFFYFYFNWIKKFNISLIINESNSLRHNIVLELSEGNISLNELNSCVIFHIIIRNSH----
*P. knowlesi*	MENVEKIYIRNKADLSDNFFYFYFNWVKLNFTCLIISENSSSLRSSILLELLNGKKVLVSEINACEALFRLTCGGV----
*P. falciparum*	---MEKIYSKNKLDYLSIIFNFYSWYKRHFKGTLLINENSNIKNTTLELLNGKKLLNEINACEAILKLNHHEHYDSS
*P. chabaudi*	MEPIEKIYIKNKSDLGNEFFYFYFNWIKKFNISLIISESSSLRHNIVLELPEGYKLPVLELNSCVIFRIICNGY----

:\*\*\* :\* : . : \* \* \* \* \* : : \* \* \* \* \* : : : \* \* . : : \* \* \* \* \* : : :

P. vivax -----SGE-----SSGGVSG-----EISDVSCHH  
 P. yoelii -----NSKNS-----KN-N-----QNNKHIWNNEFE-----SEQDVEENP  
 P. berghei -----NKK-----DNWGNFE-----NEQDVEENP  
 P. knowlesi -----SNAV-----GTVS-----CTVNCLSNGPVSG-----AQRDDFANR  
 P. falciparum SGTCNVNNINQPNNNNNNNKENINDNNNNNNKENINDNNNNNNKINNPCSTNSFNISFSTNNYNNFNNPCCSFSCNIYDY  
 P. chabaudi -----NKN-----NIWGNFE-----NEKDKEENP

P. vivax RIDALYAEELKFFLKGRLASDKPVDQFLERVEAEMALQ--KGFCCKER--LSFLEDFLFSIFKKAKVDQVEG--NKYPH  
 P. yoelii -FRISQIEELKNFLKNILLQKKKLENNFYERIEKEMMNKNNNIFSKDK--LRYIDFLFLFCILKKNKIEKIN--NKYEH  
 P. berghei -FKIVQIEELKQFLKNILLQKKKLENDFFEKIEENEMIKNNNIFAKDK--LRYVDFLLFCILKKNKIEKIN--PKYEN  
 P. knowlesi CRDTRLGEEELKFYLKEKLASEKPVDEQFLQRVEAEMALQ--KVFCCKDK--LSFLEDFLFSIFKKGKVEKLKDPGRYPH  
 P. falciparum -YDILKIEELKDFLKDFILRNKKINKEFFDTIEEDMTMWWKIFFFGQKKRTPEFLDFLLFYILKKENIHFFEE-ETRYIN  
 P. chabaudi -FKIVQIEELKHFLKDTLLQKKKLLDNDFFEKIEENEMICKN-TIFSKDK--LKYTDFLLFYILKQNKIEKIN--PKYEN

\*\*\* \*\* : . \* : : \* : : \* : \* : : : \* \* \* \* \* : : : : : \* : :

P. vivax LGAWLSKNN---FP--IKEEDMNSFAS  
 P. yoelii LNNWYLQNN---IS--VKEESMNSFTN  
 P. berghei LNNWFLKNN---IS--IKEESMSSFTN  
 P. knowlesi LSAWFSKNN---FT--IKEEDMNSFAS  
 P. falciparum LHNWFLKNKIYDISNDKKEDNTPSACN  
 P. chabaudi LNNWFLKNN---IS--IKEESMNSFTN

\* \* \* : : \* \* \* \* \* \*

## ***TOXOPLASMA / NEOSPORA***

***T. gondii***  
***N. caninum***

β1 α1 β2 β3

MALSPGAVLRLITRLASLPPLSTVTDVVLAYIEQNLKSAGDFTFSVQPDTSSTPAAPFRIAIVETKKKEQPSPIAAGEALSD  
MALSPGAVIRVTRLSSLPPLSTVTDVVLSYLEQHLKSAGGFTFSVPDTS SSPATPFRIAIVETKKGEAPRPIAGGEALSD  
\*\*\*\*\*:\*.\*\*\*:\*\*\*\*\*:\*.\*\*:\*

α2 α3 α4

YAAARCIARLAASTGDPFASLLKASGAPGGVEAAVDVCEQWAAFYGVSGKAPEASDNPGLSACIDFFARRFSTSSSFLFG  
YAAARCVARLAASTGGVFACLLNENGATESADGAVDACEQWAAFCGVPGKTP EAAEHPLGTACIEFFTRRFSTSSAFLCN  
\*\*\*\*\*:\*\*\*\*\*. \*\*.\*\*: \*\*. . .: \*\*.\*\*\*\*\* \*\*.\*:\*\*\*::\*:\*:\*:\*:\*:\*:\*:\*:\*:\*:\*\* .

α5 α7

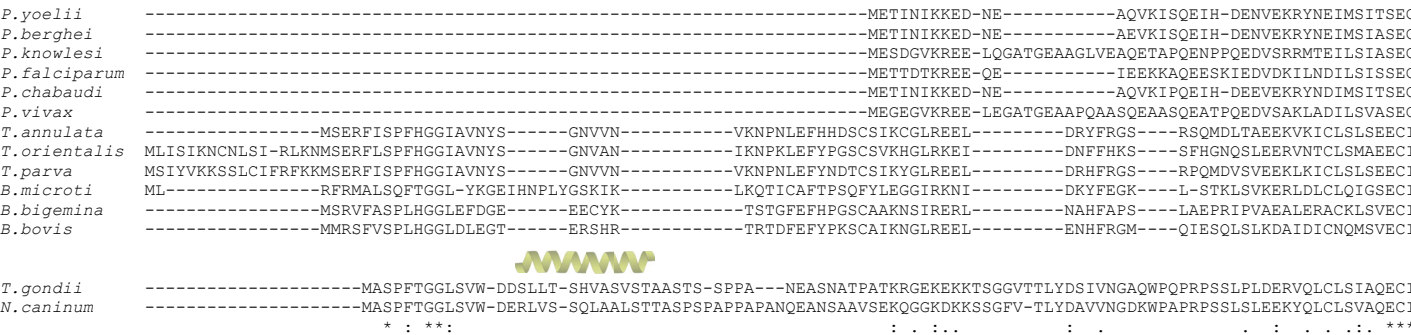
TPQPSLADMTL FALLKAHPAAQTALSSALRTSETAAKHFFSSWSACVAKAIPGAGALSGAGAKGTDRAKKGSGEMVG-QGA  
TPNPSLADMTL FALKLTQPAHTALLSALRTSGEAAKHFSAWSSSI AKALPGATTLSGAGVFPD-GSAQGNRGEISGATGA  
\*\*:\*

***T. gondii***  
***N. caninum***

GVASEAVDGPDATTS  
GASPESTDGPDATAS  
\*.\*:\*.\*.\*.\*.\*.\*.\*.\*.\*.\*

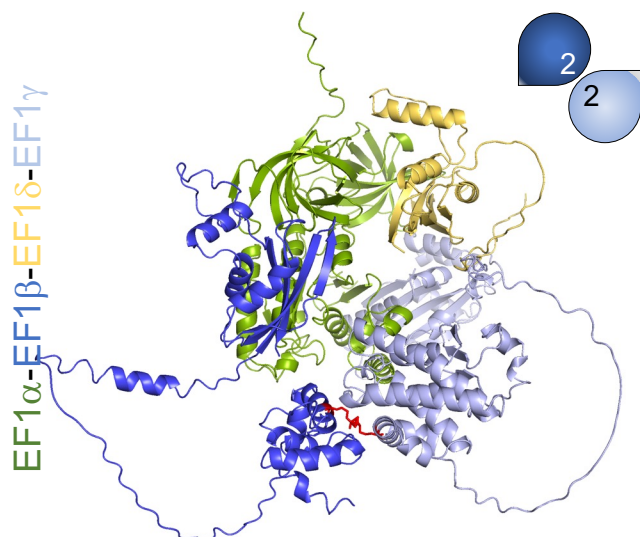
Figure S2

G N-terminal extensions of YRSs

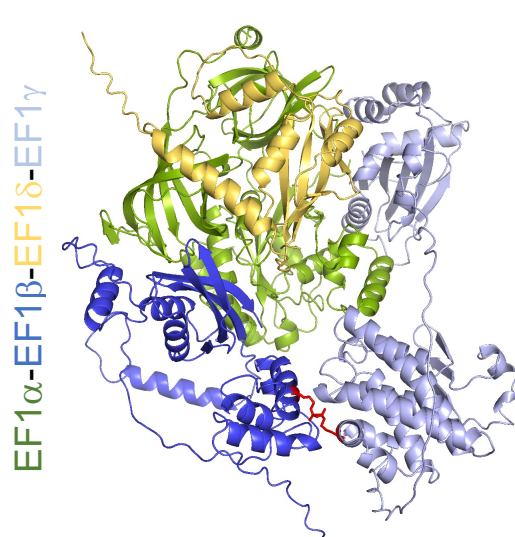


**Figure S2. Sequence alignment of GST-like domains present in *Apicomplexa* EF1 and multi-synthetase complexes.** Protein alignments were performed with M-Coffee [22]. The corresponding EupathDB annotations are given in Table S1. The complete sequences of AIMP<sub>s</sub> are shown with their EMAPII-like domain highlighted in grey. For EF1 subunits and aaRS<sub>s</sub>, alignments were performed on the full-length protein sequences, but only the GST-like domains involved in protein-protein interactions are shown. The RW motif in helix  $\alpha$ 7 and involved in interface 2 is highlighted in bold. The N-capping box ( $\phi$ -S/T-X-X-D- $\phi$ ) is shown in blue in the central helix  $\alpha$ 5, when present in the sequence. The GST-like domain of EF1 $\beta$  is reduced to only 3  $\alpha$ -helices including  $\alpha$ 5 and  $\alpha$ 7 which are sufficient to form an interface 2 with EF1 $\gamma$ . The strains used to run ColabFold modeling are indicated in bold and the corresponding secondary structures are displayed above the sequences or below for *N. caninum* proteins.

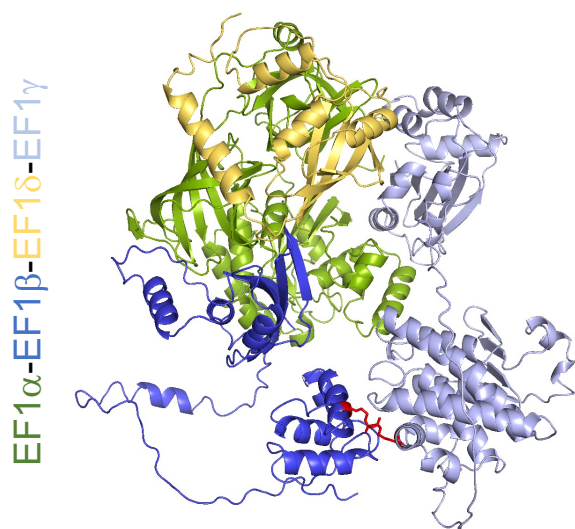
*P. berghei*



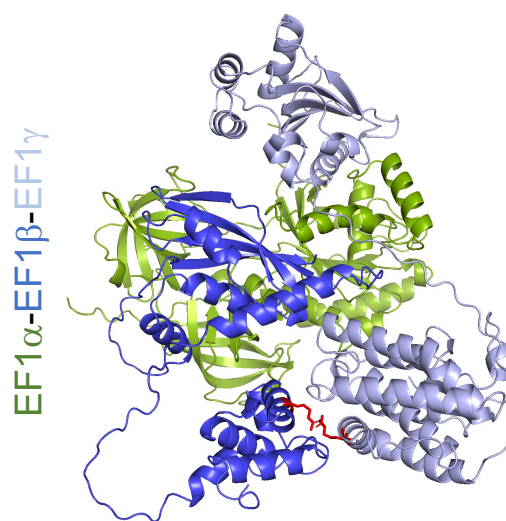
*T. gondii*



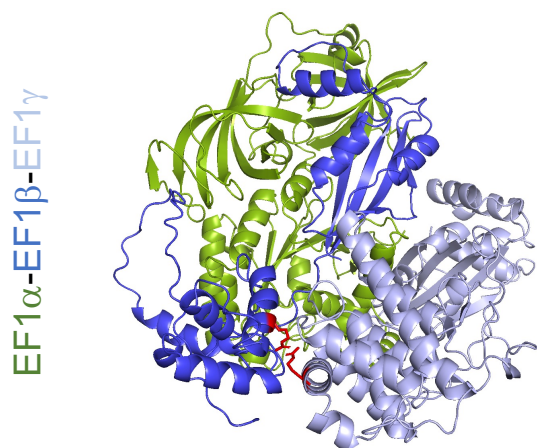
*N. caninum*



*C. parvum*



*T. parva*



*B. bovis*

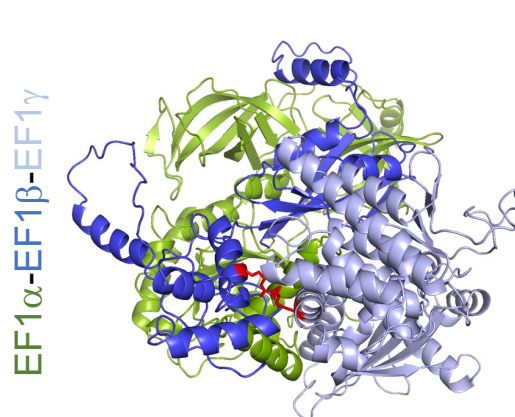


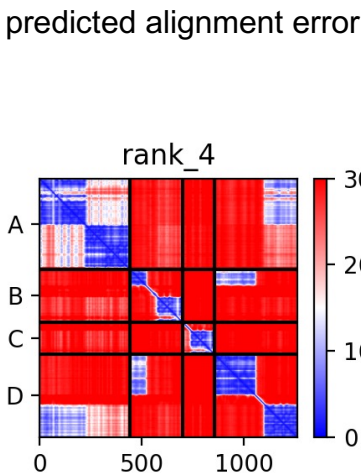
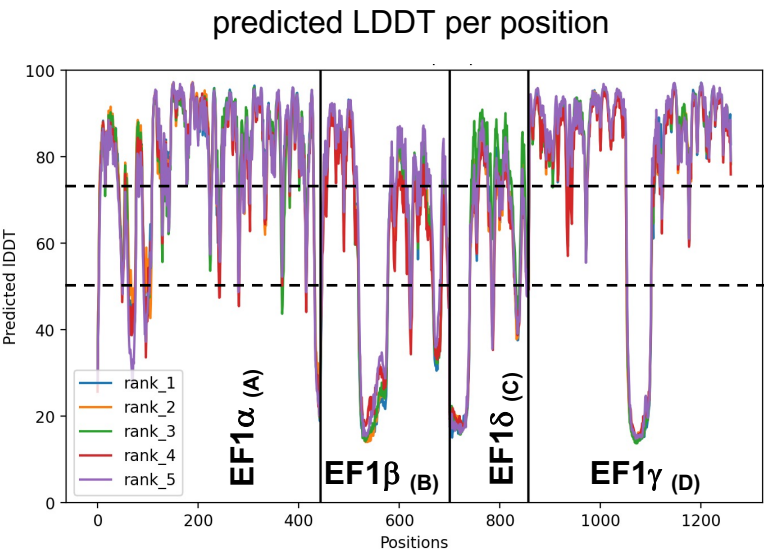
Figure S3

**Figure S3. Similarities between EF1 complexes in the *Apicomplexa* phylum.** Molecules are colored in blue for EF1 $\beta$ , light blue for EF1 $\gamma$ , green for EF1 $\alpha$ , and yellow for EF1 $\delta$ . All models are shown in "cartoon". GST-like domains are schematized with drop shapes, with the same color code. *Plasmodia*, *Toxoplasma* and *Neospora* complexes are tetramers while EF1 is a trimer (EF1 $\beta$ , EF1 $\gamma$ , and EF1 $\alpha$ ) in *Babesia*, *Theileria* and *Cryptosporidium*, due to the impossibility to identify subunit EF1 $\delta$  in the corresponding genomes. All EF1 $\beta$ -EF1 $\gamma$  heterodimers involve interface 2 shown in red; the parameters for each AlphaFold model are shown in Figure S4.

EF1

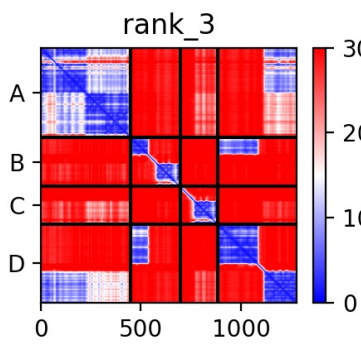
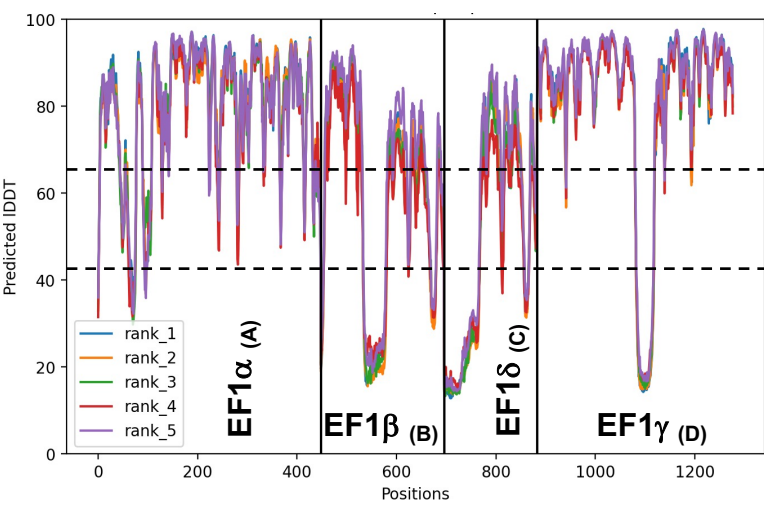
*Plasmodium*

**pTM**  
Rank\_1: 0.44  
Rank\_2: 0.43  
Rank\_3: 0.44  
Rank\_4: 0.48  
Rank\_5: 0.48



*Toxoplasma*

**pTM**  
Rank\_1: 0.45  
Rank\_2: 0.41  
Rank\_3: 0.5  
Rank\_4: 0.47  
Rank\_5: 0.48



*Neospora*

**pTM**  
Rank\_1: 0.45  
Rank\_2: 0.42  
Rank\_3: 0.50  
Rank\_4: 0.45  
Rank\_5: 0.49

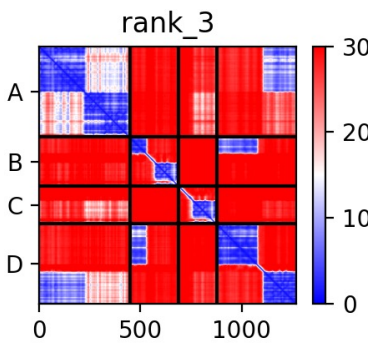
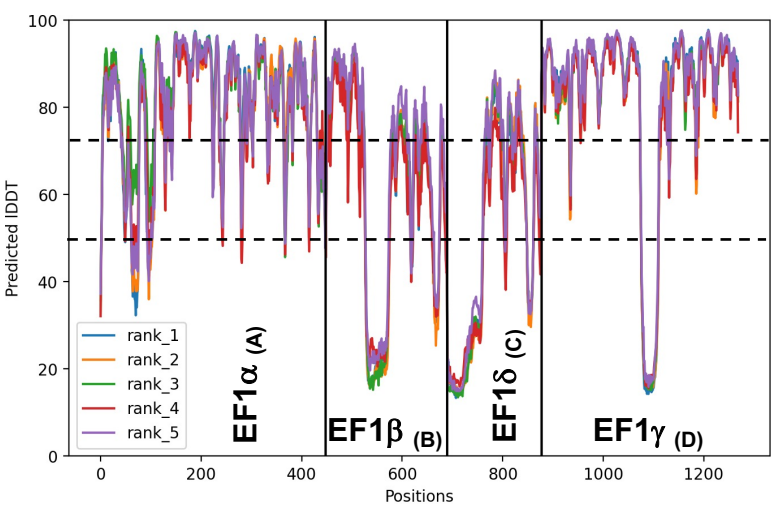


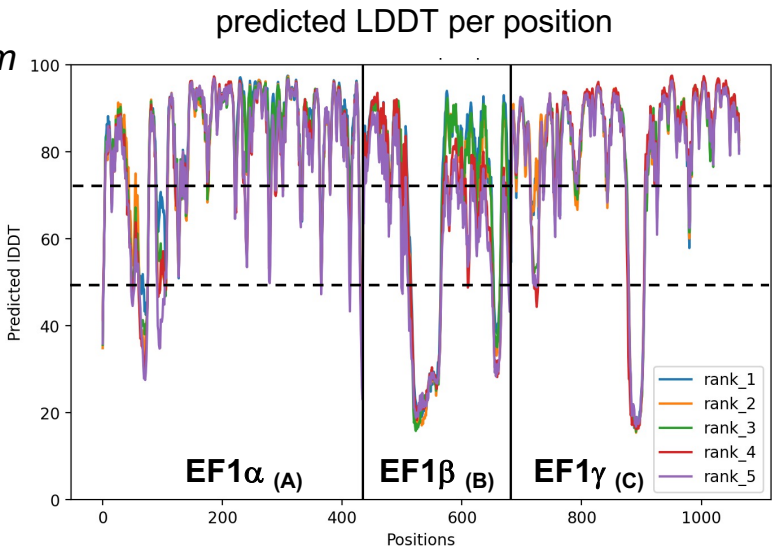
Figure S4

EF1

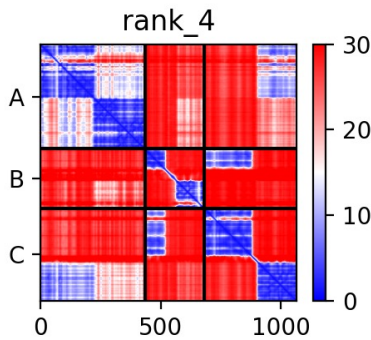
*Cryptosporidium*

pTM

Rank\_1: 0.48  
Rank\_2: 0.49  
Rank\_3: 0.56  
Rank\_4: 0.58  
Rank\_5: 0.57



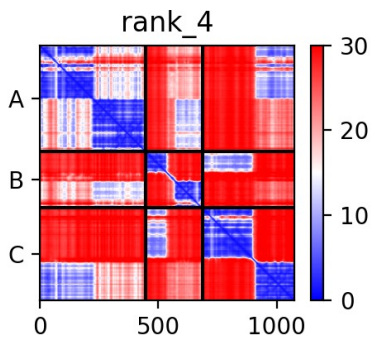
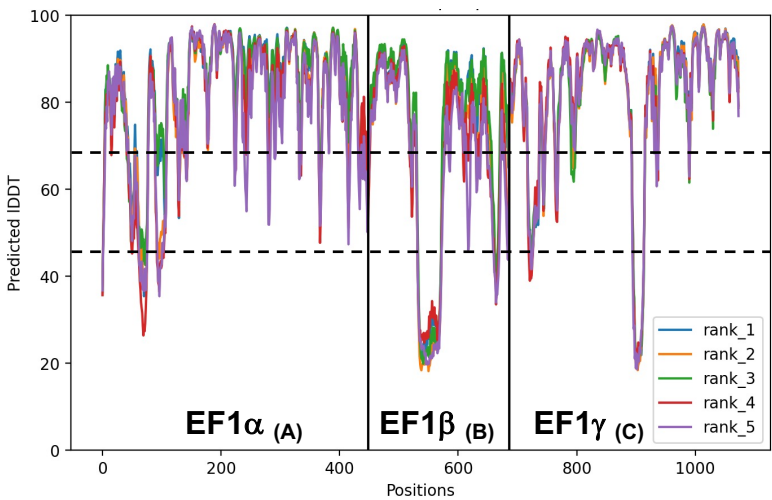
predicted alignment error



*Theileria*

pTM

Rank\_1: 0.51  
Rank\_2: 0.47  
Rank\_3: 0.59  
Rank\_4: 0.59  
Rank\_5: 0.57



*Babesia*

pTM

Rank\_1: 0.51  
Rank\_2: 0.52  
Rank\_3: 0.63  
Rank\_4: 0.74  
Rank\_5: 0.6

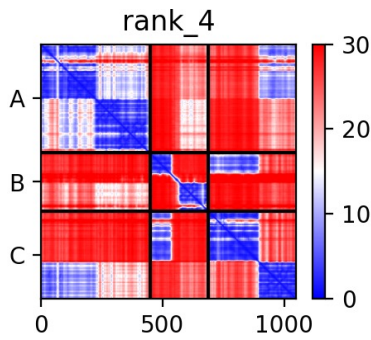
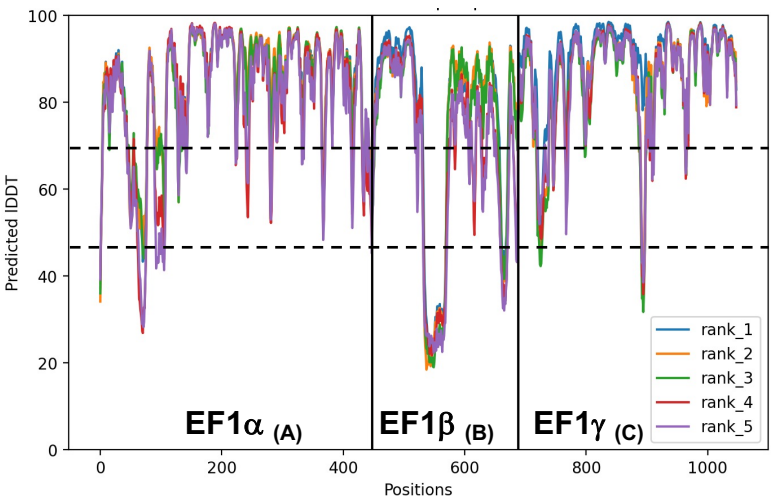


Figure S4

**Figure S4. Confidence metrics of the ColabFold predictions for EF1 GST-like backbones.**

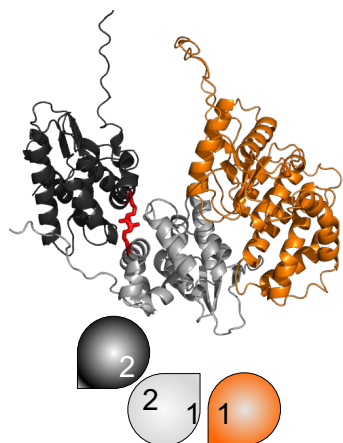
Models were ranked by pTM (predicted Template Modeling) scores, which measures the overall topological accuracy of the predictions. Predictions with pTM scores higher than 0.5 and showing the known GST-like interfaces 1, 1' and 2 were considered relevant and are highlighted in bold. The central plots show the pLDDT (predicted Local Distance Difference Test) scores per position. Regions predicted with high confidence are identified by pLDDT > 70, while disordered regions are identified by pLDDT < 50 and are presented as long filaments (not shown in graphical representations). The PAE (predicted aligned error) plot on the left indicates that the relative positions of domains are well predicted (blue).

ERS-AIMP-MRS

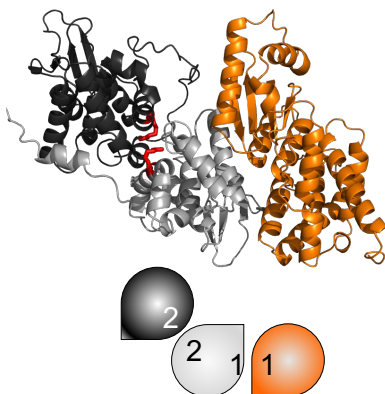
QRS-ERS-AIMP-AIMP-ERS-QRS

MRS-tRip-ERS-ERS-tRip-MRS

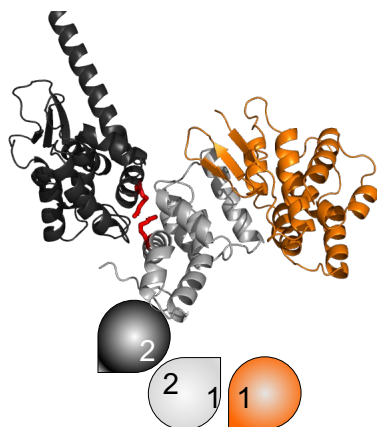
**A** *Theileria parva*



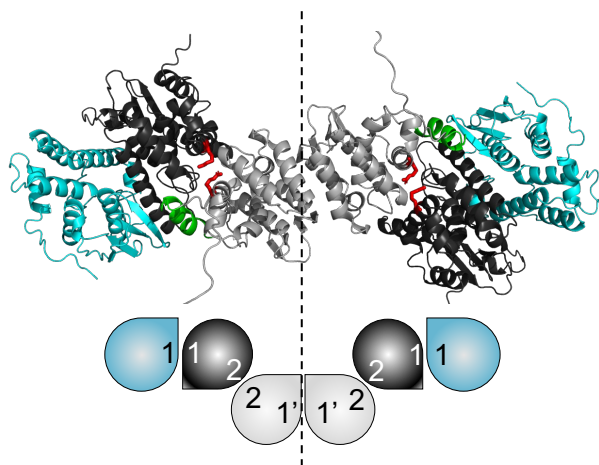
**B** *Babesia bovis*



**C** *Saccharomyces cerevisiae*



**D** *Plasmodium berghei*



**E** *Toxoplasma gondii*

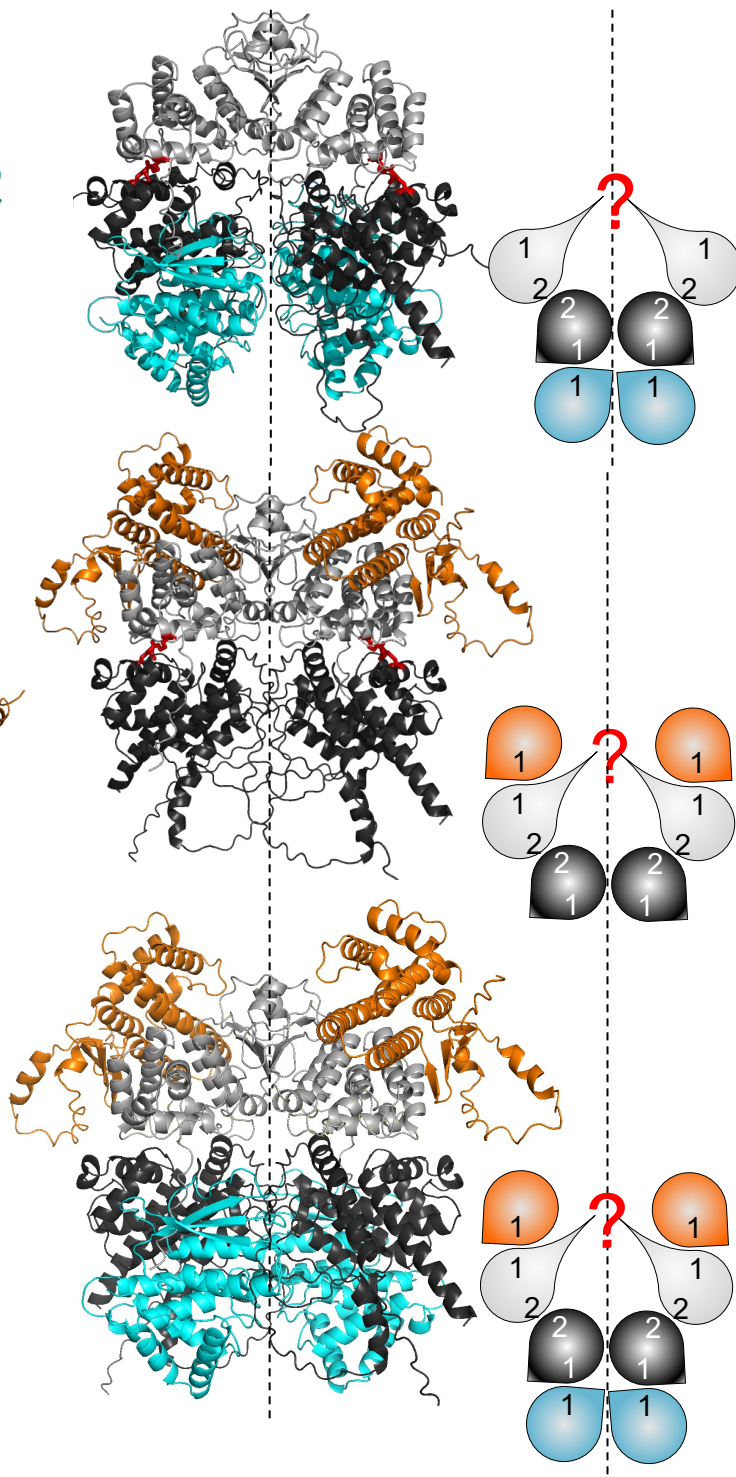


Figure S5

**Figure S5. Diversity of multi-synthetase complexes in the *Apicomplexa* phylum.** All complexes are shown in "cartoon" with the same color codes and schematized below with drop shapes colored grey for AIMP, black for ERS, blue for QRS, and orange for MRS, all displaying interfaces 1/1' and 2. In *Theileria* (**A**) and *Babesia* (**B**), MSCs are organized into AIMP-ERS-MRS trimers similar to the Arc1p-ERS-MRS trimer determined for *S. cerevisiae* MSC (**C**) [28,49]. (**D**) The M- and Q- complexes of *Plasmodium* were determined experimentally [17,18]. They both involve equivalent GST-like domains but organize differently. In the Q-complex, symmetry is imposed by the tRip homodimer (interface 1',[13]) that binds ERS via interface 2, which in turn binds QRS (interface 1). Alternatively, the M-complex is organized around the ERS homodimer. Accordingly, the tRip transmembrane helices  $\alpha 8$  (green) are equidistant and similarly oriented. (**E**) Two *Toxoplasma* MSCs have been modeled to mimic *Plasmodium* Q- and M-complexes. Both models show homodimerization of *Tg*-p43 through an unknown interface (?). This homomeric interaction, if biologically relevant, would allow the formation of a unique MSC (dimer of tetramers, Figure 4C). Moreover, the transmembrane helix  $\alpha 8$  is not predicted for *Tg*-p43.

# MSC

*S. cerevisiae*

predicted LDDT per position

predicted alignment error

pTM

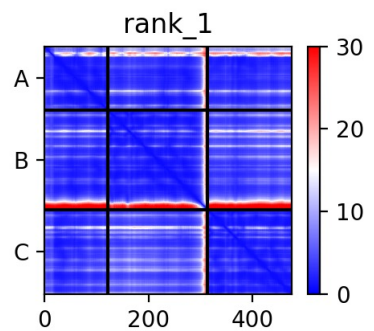
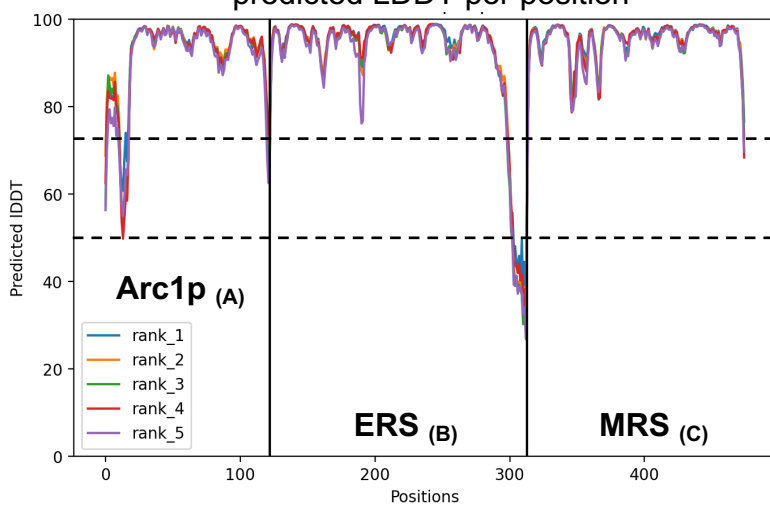
Rank\_1: 0.91

Rank\_2: 0.91

Rank\_3: 0.90

Rank\_4: 0.91

Rank\_5: 0.90



*Theileria*

pTM

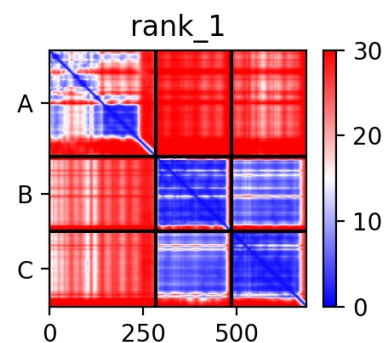
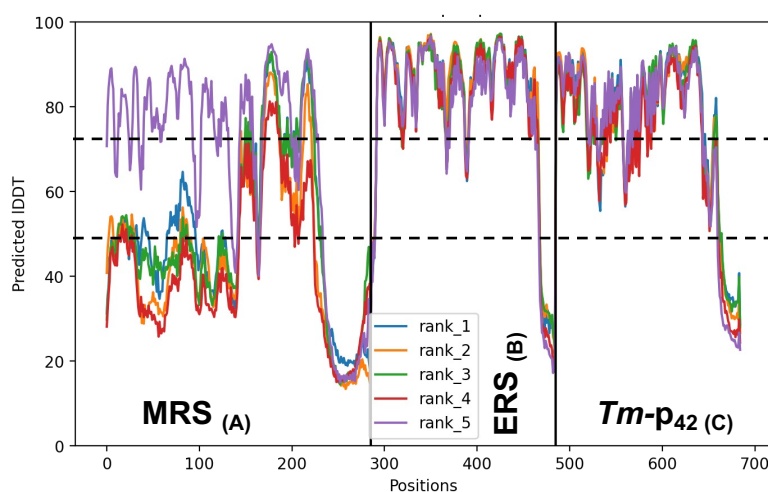
Rank\_1: 0.58

Rank\_2: 0.57

Rank\_3: 0.56

Rank\_4: 0.57

Rank\_5: 0.57



*Babesia*  
(custom templates)

pTM

Rank\_1: 0.90

Rank\_2: 0.89

Rank\_3: 0.89

Rank\_4: 0.89

Rank\_5: 0.88

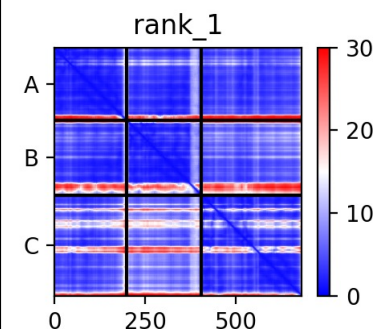
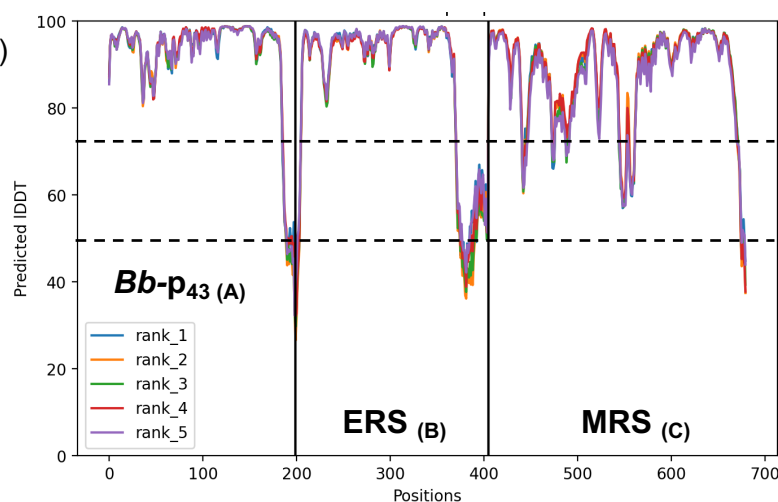
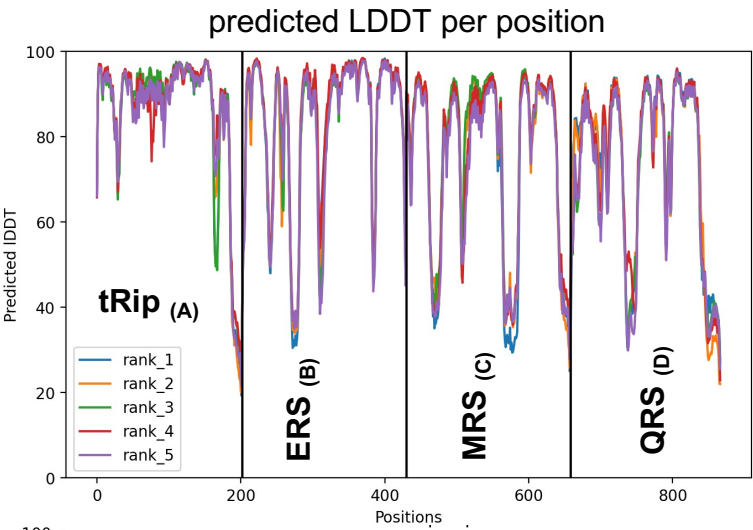


Figure S6

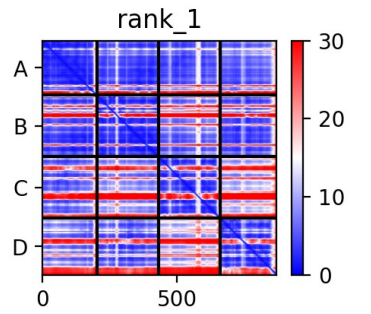
# MSC

## *Plasmodium*

**pTM**  
Rank\_1: 0.85  
Rank\_2: 0.84  
Rank\_3: 0.83  
Rank\_4: 0.83  
Rank\_5: 0.83

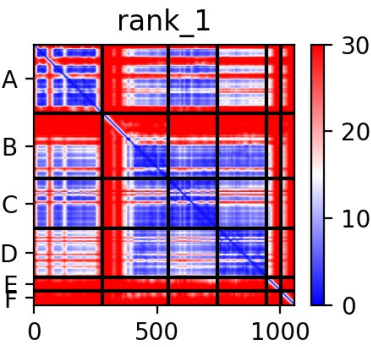
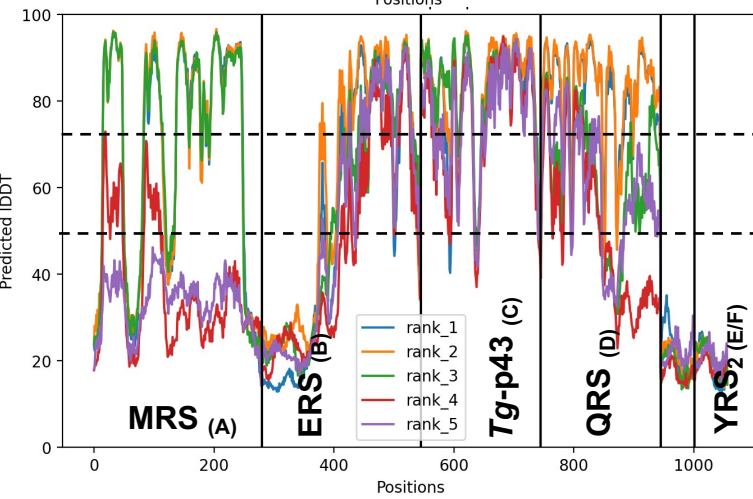


predicted alignment error



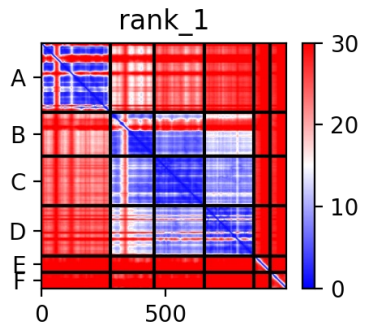
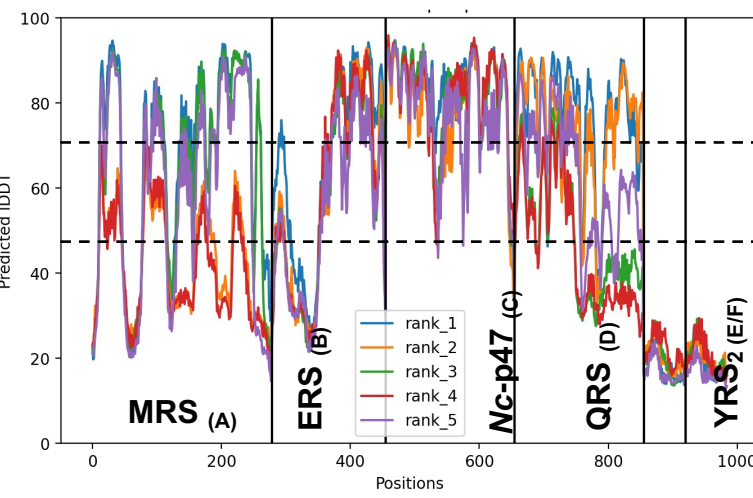
## *Toxoplasma*

**pTM**  
Rank\_1: 0.69  
Rank\_2: 0.39  
Rank\_3: 0.69  
Rank\_4: 0.61  
Rank\_5: 0.41



## *Neospora*

**pTM**  
Rank\_1: 0.49  
Rank\_2: 0.39  
Rank\_3: 0.58  
Rank\_4: 0.38  
Rank\_5: 0.32

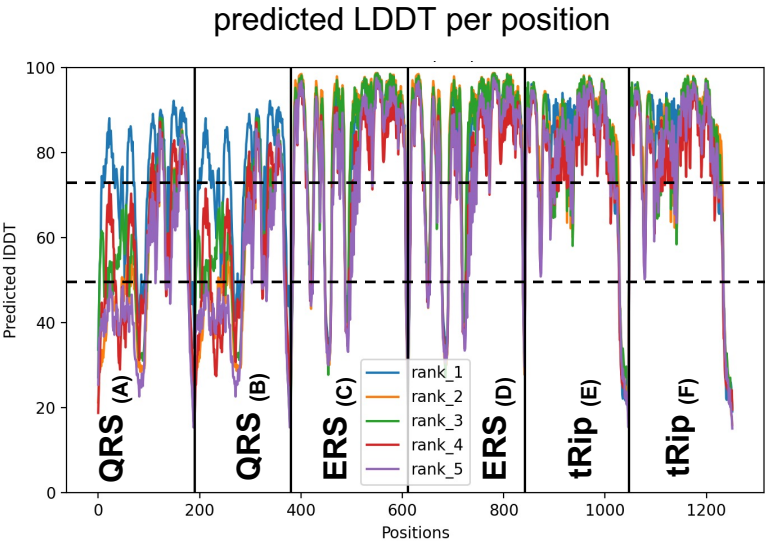


**Figure S6. Confidence metrics of the ColabFold predictions for GST-like interaction network of *S. cerevisiae* and *Apicomplexa* parasites. See legend Figure S5**

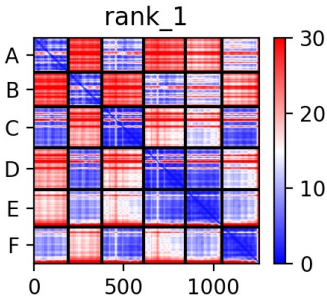
MSC

*Plasmodium*  
Q-complex

**pTM**  
**Rank\_1: 0.70**  
Rank\_2: 0.66  
Rank\_3: 0.66  
Rank\_4: 0.45  
Rank\_5: 0.43



predicted alignment error



*Plasmodium*  
M-complex

**pTM**  
**Rank\_1: 0.74**  
**Rank\_2: 0.72**  
Rank\_3: 0.45  
Rank\_4: 0.36  
Rank\_5: 0.36

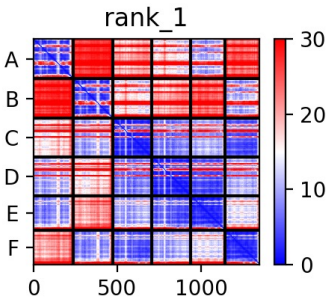
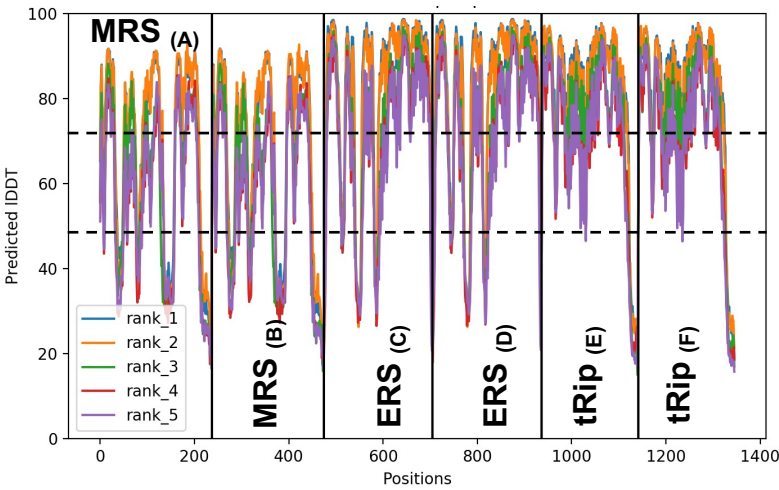
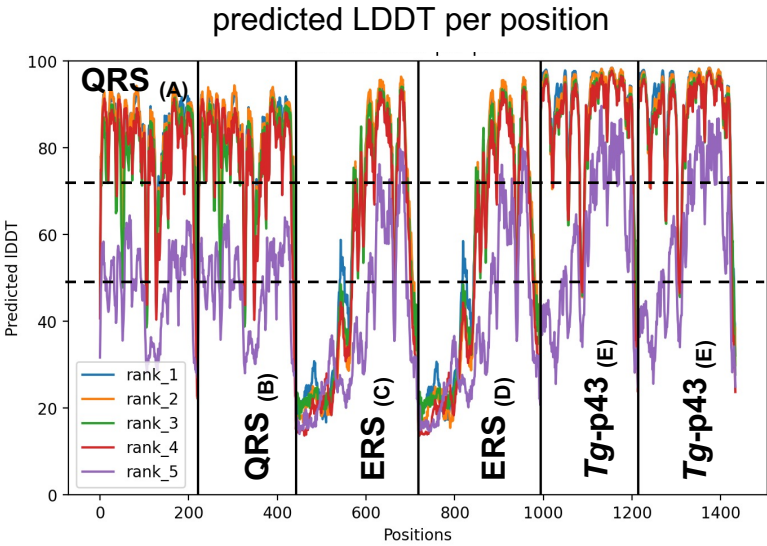


Figure S7

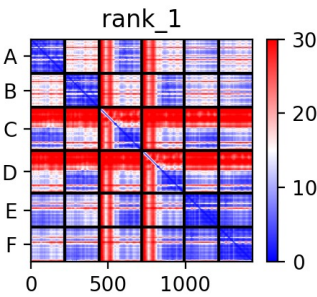
MSC

*Toxoplasma*  
Q-complex

**pTM**  
Rank\_1: 0.73  
Rank\_2: 0.72  
Rank\_3: 0.66  
Rank\_4: 0.65  
Rank\_5: 0.32



predicted alignment error



*Toxoplasma*  
M-complex

**pTM**  
Rank\_1: 0.73  
Rank\_2: 0.69  
Rank\_3: 0.69  
Rank\_4: 0.56  
Rank\_5: 0.49

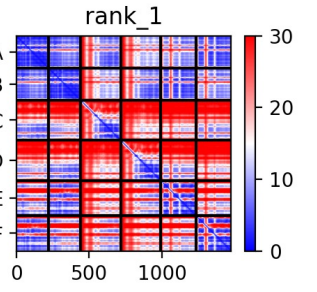
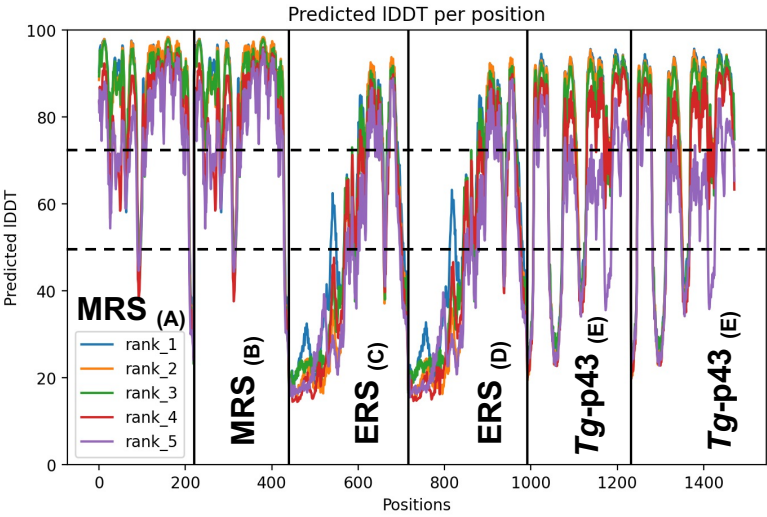


Figure S7. Confidence metrics of the ColabFold predictions for M- and Q-MSC GST-like backbones in *Plasmodium*, *Toxoplasma* and *Neosporidium*. See legend Figure S5