

**Synthesis of silver nanoparticles and their role against a  
thiazolekinase enzyme from *Plasmodium falciparum***

A thesis submitted in fulfilment of the requirements for the degree of  
**Master of Science**

**Department of Biochemistry, Microbiology and Biotechnology**

**Faculty of Science**

**Rhodes University**

By

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## Abstract

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Malaria, a mosquito-borne infectious disease, caused by the protozoan *Plasmodium* genus, is the greatest health challenges worldwide. The plasmodial vitamin B<sub>1</sub> biosynthetic enzyme *PfThzK* diverges significantly, both structurally and functionally from its counterpart in higher eukaryotes, thereby making it particularly attractive as a biomedical target. In the present study, *PfThzK* was recombinantly produced as 6×His fusion protein in *E. coli* BL21, purified using nickel affinity chromatography and size exclusion chromatography resulting in 1.03% yield and specific activity 0.28 U/mg. The enzyme was found to be a monomer with a molecular mass of 34 kDa. Characterization of the *PfThzK* showed an optimum temperature and pH of 37 °C and 7.5 respectively, and it is relatively stable ( $t_{1/2}$ =2.66 h). Ag nanoparticles were synthesized by NaBH<sub>4</sub>/tannic acid, and characterized by UV-vis spectroscopy and transmission electron microscopy. The morphologies of these Ag nanoparticles (in terms of size) synthesized by tannic acid appeared to be more controlled with the size of 7.06±2.41 nm, compared with those synthesized by NaBH<sub>4</sub>, with the sized of 12.9±4.21 nm. The purified *PfThzK* was challenged with Ag NPs synthesized by tannic acid, and the results suggested that they competitively inhibited *PfThzK* (89 %) at low concentrations (5-10 μM) with a  $K_i$  = 6.45 μM.

**Keywords: Ag nanoparticles, synthesis, methylhydroxyethylthiazolekinase (*PfThzK*)**

# Declaration

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I, Jia Yao, hereby declare that this thesis is my own, unaided work. It is being submitted for the degree of Master of Science at Rhodes University. It has not been submitted before for any other degree or examination in any other university.

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Author's Signature

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Date

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## List of Abbreviations

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$\mu\text{g}$	Microgram
$\mu\text{M}$	Micromolar ( $\mu\text{moles/litre}$ )
$\mu\text{L}$	Microlitre
$\mu\text{mol}$	Micromole
6 $\times$ His-tag	Hexahistidine purification tag
A	Absorbance
Ag	Silver
BCA	Bicinchoninic acid
bp	Base pair
CAM	Chloramphenicol
Da	Dalton
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
<i>E. coli</i>	<i>Escherichia coli</i>
EDTA	Ethylenediaminetetraacetic acid
FPLC	Fast protein liquid chromatography
HIV	Human immunodeficiency virus
$k_{cat}$	Enzyme turn-over number
kDa	Kilodalton
$K_i$	Inhibitor constant
$K_m$	Michaelis-Menten constant

NPs	Nanoparticles
PCR	Polymerase chain reaction
PEG	Polyethylene glycol
SEM	Scanning electron microscopy
SDS	Sodium dodecyl sulphate
SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
TEM	Transmission electron microscopy
UV-vis	Ultraviolet-visible

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## List of outputs

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# Chapter 1

## Literature review

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### 1.1. Malaria

Malaria, a mosquito-borne infectious disease, caused by the protozoan *Plasmodium* genus, especially by four species, *P. falciparum*, *P. vivax*, *P. malariae* and *P. ovale*, is the greatest health challenges worldwide. Malaria is becoming the most prevalent parasitic disease in the world. In 2006, there were an estimated 247 million malaria episodes causing over 1.25 million deaths, of which 86% were in Africa (Gardella *et al.*, 2008). Around 80% of malaria cases in Africa were in 13 countries in 2006, and approximately 109 countries were endemic for malaria in 2008, 45 of which were in Africa. There were an estimated 216 million malaria episodes worldwide in 2010, and 81% of those cases occurred in Africa, followed by South East Asia with 13%, and Eastern Mediterranean regions with 5%. There were an estimated 655 thousand malaria deaths in the world in 2010, and 91% of those were in Africa region, followed by South East Asia with 6% and Eastern Mediterranean with 3%; about 86% of these cases were children under 5 years old (WHO<sup>1</sup>, 2012). The reason for such high morbidity and death rate in Africa is because 91% of these cases were due to *P. falciparum*, the most prevalent of the four malarial parasites. As shown in Figure 1.1, Africa, South-East Asia, Eastern Mediterranean and South America regions were the most affected areas in the world by 2011. As people migrated, there was an increase of globalization in business and commerce, and also an increase in travel with more and more people from malaria-free

countries being exposed to the disease. It is reported that every year about 25 thousand travelers return with malaria after visiting endemic countries, and 0.4% of these die from the infection (Gyang, 2009).

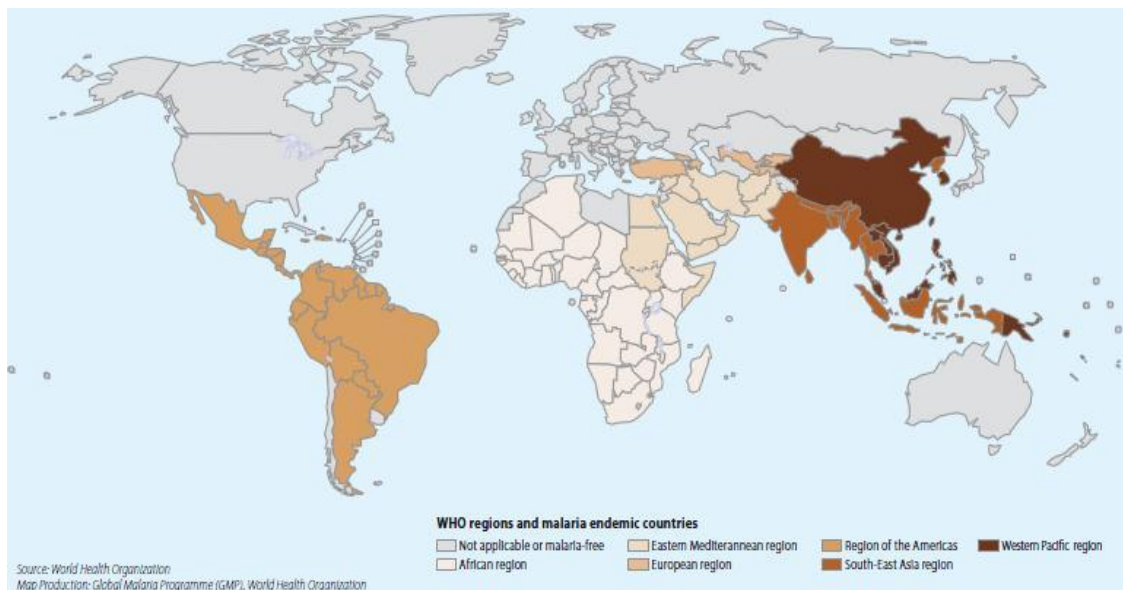
The number of global malaria episodes has risen from 223 million in 2000 to 237 million cases in 2005, and the estimation of the world population that is at risk with malaria has recently been challenged using a combination of data (Table 1.1). It was indicated that there were more than 500 million episodes of clinical malaria, from *P. falciparum* in 2002, which was considerably higher than the 400 million cases reported by the World Health Organization (WHO<sup>1</sup>, 2012).

**Table 1.1.** Estimates of malaria cases and deaths by WHO Region, 2011.  
Source: World Health Organization 2012.

Region	Estimated cases ('000s)			% <i>P. falciparum</i>	Confirmed cases reported	Reported/estimated
	Estimate	Lower	Upper			
Africa	174 000	113 000	239 000	98%	20 000	11%
Americas	1 000	1 000	1 000	34%	1 000	59%
Eastern Mediterranean	10 000	8 000	14 000	82%	1 000	10%
Europe	0.2	0.2	0.2	0%	0.2	87%
South-East Asia	28 000	23 000	35 000	54%	2 000	9%
Western Pacific	2 000	2 000	2 000	77%	257	13%
World	216 000	149 000	274 000	91%	24 000	11%

Region	Estimated deaths			% <5
	Estimate	Lower	Upper	
Africa	596 000	468 000	837 000	91%
Americas	1 000	1 000	2 000	29%
Eastern Mediterranean	15 000	1 000	38 000	60%
Europe	0	0	0	4%
South-East Asia	38 000	28 000	50 000	31%
Western Pacific	5 000	3 000	6 000	41%
World	655 000	537 000	907 000	86%

There are several reasons that contribute to the increasing malarial burden. First, it is the drug resistance. In Africa and part of Southeast Asia, *P. falciparum* is resistant to almost all the antimalarial drugs and *P. vivax* is almost chloroquine resistant. Second, it is insecticide resistance. Third, it is climatic changes. Global warming may contribute to the spread of the malaria vector into some non-endemic countries. Fourth, it is travel. Travel from malaria-free countries to malarial endemic countries is an increasingly important cause of malaria. As every year, in Europe, approximately 7 thousand imported malarial cases have been reported (Behrens *et al.*, 2008).



**Figure 1.1.** Malaria affected countries, prevention of reintroduction countries and malaria-free countries at the end of 2011.  
Source: World Health Organization 2012.

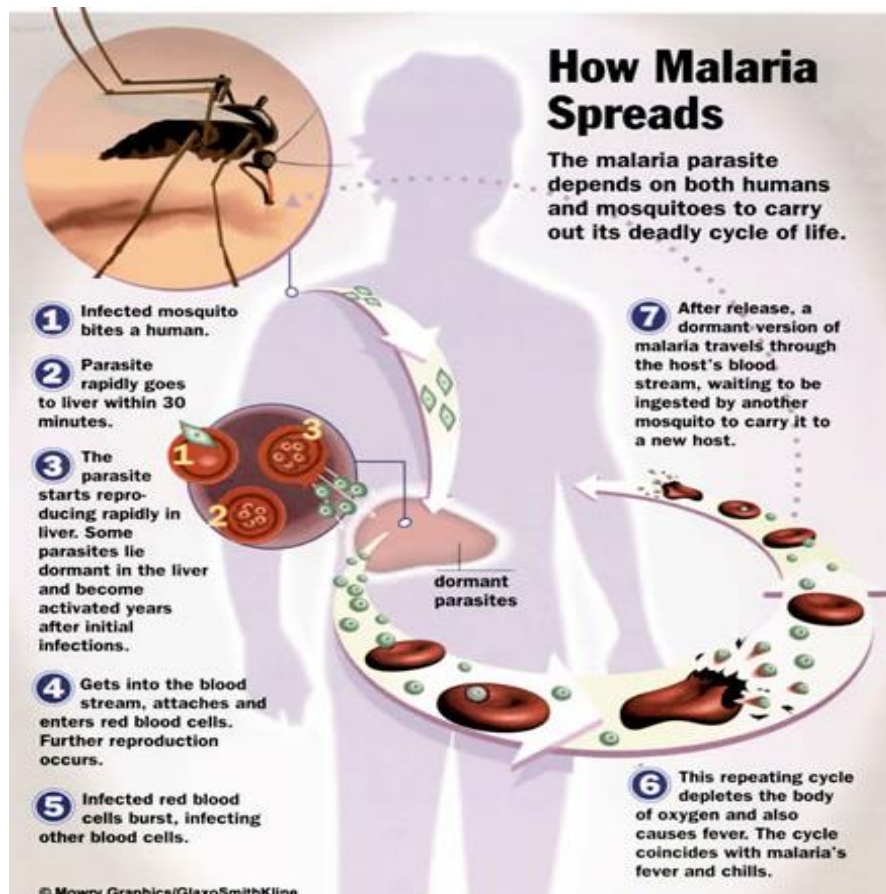
### 1.1.1. Life-cycle of malaria

Malaria is transmitted to humans by the bite of the female *Anopheles* mosquito vector. The female *Anopheles* mosquito injects approximately 15-20 sporozoites each time which

then migrate to the liver within a few minutes and invade the hepatocytes by an unknown mechanism, to form hepatic schizonts (Lindner *et al.*, 2012).

A sporozoite of *P. falciparum* generates about 30,000 new parasites, which develop slowly in liver cells into hypnozoites, which remain for months in the tissue. These hypnozoites could induce new relapses of the disease up to two years after the initial infection. Meanwhile, the asexual blood stages (late trophozoites and schizonts) of the parasite are the main etiological agents in malaria, causing the symptoms of the disease to appear about two weeks after the mosquito-vectored sporozoite injection (WHO<sup>2</sup>, 2006). These asexual stages are the main target of the antimalarial drugs (Wells *et al.*, 2009). The schizonts rupture to form merozoites, which are released into the bloodstream where they enter the red blood cells, and remain relatively inactive metabolically for about 10–15 hours. The parasite then undergoes a rapid growth phase over the next 25 hours, constituting the trophozoite stage, digesting the majority of the hemoglobin and growing to fill more than 50% of the volume of the host cells. It takes 1-2 weeks for hepatic schizonts to rupture, and the young trophozoites to consume the hemoglobin in the red cells and to develop into schizonts and eventually to rupture, and release more merozoites to invade more blood cells, and cause fever symptoms. At the end of the trophozoite stage, the parasite divides several times (the schizont stage) before the host cell lyses to release the newly formed merozoites that continue the cycle (See Figure 1.2). This concerted cell lysis results in the classical malaria symptoms, which are mainly headache, periodically recurrent high fever (every 48–72 hours), myalgia, anemia, hepatitis and splenomegaly (Santos-Magalhaes *et al.*, 2010). Moreover, neurological symptoms may occur resulting in death in the case of severe *P. falciparum* infection.

After several asexual life-cycles, certain parasites develop into sexual forms. In *P. falciparum* malaria, it takes approximately 10 days to produce gametocytes. A female *Anopheles* mosquito fuses the male and female gametocytes in their midgut to form a zygote, and the zygote eventually develops new sporozoites to complete the whole life-cycle. In *P. vivax* and *P. ovale* malarias a few of the sporozoites in the liver remain as dormant hypnozoites that may cause a relapse of malaria after several years. In contrast, the *P. malariae* malarias do not have the hypnozoite stages but may remain in the blood for several years.



**Figure 1.2.** Life-cycle of malaria.

Source: [http://www.travelhealth.co.uk/diseases/malaria\\_lifecycle.htm](http://www.travelhealth.co.uk/diseases/malaria_lifecycle.htm)

### 1.1.2. Strategies for malaria control

Strategy for the control of malaria is to reduce the malaria disease burden to a level, which is no longer a problem to public health. These include vector control with residual insecticide spraying, larva control and personal protection, such as insecticide treated bednets and insect repellent spray (Rozendaal, 1997). Studies on the development of an effective malaria vaccine and a transgenic mosquito which cannot transmit malaria are ongoing but neither is likely to be available soon.

The antimalarial drugs commonly used are classified as 5 compounds: quinolines and aryaminoalcohols, the antifols, the artemisinin derivatives, the hydroxynaphtha-quinones and antibacterial agents.

Quinolines and aryaminoalcohols include amodiaquine, chloroquine, quinine and mefloquine. Quinine is an ancient drug and is used for the treatment of severe malaria especially that from *P. falciparum*. Side-effects, however, are quite common, including hearing impairment (van Huyssteen, 2010), dizziness and vertigo (Croft *et al.*, 2001). Quinine may cause hypoglycaemia and renal failure (Trampuz *et al.*, 2003). Chloroquine is especially used against the mature trophozoite stage, but extensive resistant has recently been reported (Olliaro, 2001). Side-effects include headache, hair loss, convulsions (Deen *et al.*, 2008), and it is also known to stimulate psoriasis in some cases (Ferreira, 2010), it is considerably toxic in an overdose and can induce severe cardiac arrhythmias.

Antifols are folate biosynthesis inhibitors, and include pyrimethamine, proguanil, chloroproguanil and trimethoprim. Pyrimethamine and proguanil act as prodrugs to

inhibit plasmodial dihydrofolate reductase (DHFR). Pyrimethamine and proguanil should be used in combination with sulpha drugs because resistance can be developed quickly if it is issued alone (Gregson and Plowe, 2005). Pyrimethamine and proguanil induce abdominal pain, vomiting and diarrhoea (Hatz, 2001).

Artemisinin derivatives include artemisinin, dihydroartemisinin and artesunate. These drugs were originally derived from *Artemisia annua*, and were used in traditional Chinese medicine for fever a thousand years ago. These drugs act fast, and are the most commonly used for the treatment of malaria, nowadays. Side-effects such as mild gastrointestinal disturbances (Sevene *et al.*, 2010), dizziness and tinnitus (Ehrhardt and Meyer, 2009), have been reported, but in general these drugs are extremely tolerated. The only weakness of these drugs is that they are only suitable to treat uncomplicated malaria because of the short half-life (Ndiaye *et al.*, 2011).

Antibacterial drugs are those with antimalarial activity, such as clindamycin and tetracyclines. These drugs are weak antimalarials that act slowly, and could only be used in combination with other drugs (Nosten *et al.*, 2006). They commonly induce gastrointestinal effects, such as vomiting and diarrhoea (van Boxtel, 2001). Rashes and drug fever have been also been reported, along with haemolytic anaemia.

### **1.1.3. Genomic field for malaria investigation**

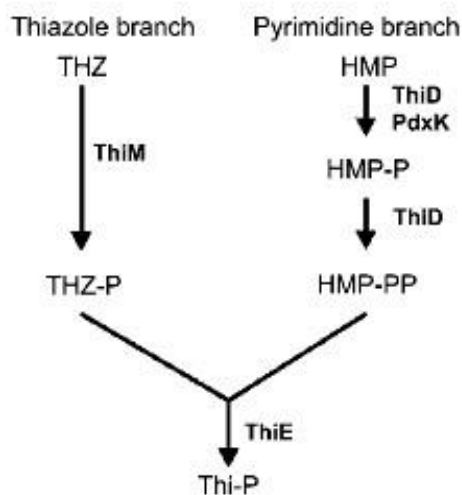
Due to the complexity of the parasites life cycle and the development of drug resistance (WHO<sup>2</sup>, 2008), it is really essential to work out novel drug targets and develop new chemotherapeutics. The publication of the *P. falciparum* genome sequence in 2002 (Gardner *et al.*, 2002), and that of *P. vivax* in 2008 (Dharia *et al.*, 2010) opened a new

door with the genomic knowledge to understand the malaria pathogens and also provide new tools to develop malaria therapy. These genome sequences can be investigated to describe biological pathways and also hypothesize possible functions for malaria genes. The database research allow people to identify novel biological pathways present in the parasite and so far give people an idea about interesting targets for subsequent research. The isoprenoids biosynthesis pathway in the parasite was identified by the genomic sequence information (Ralph *et al.*, 2004), and subsequently, the *Pfdxr* gene was identified as a target of fosmidomycin resistance (Zhang *et al.*, 2011).

According to the predominantly intracellular life cycle of *P. falciparum*, interfering with the salvage system for cofactors and metabolites could be a possible target (Huthmacher *et al.*, 2006; Muller *et al.*, 2010) with the life cycle of mosquito being disrupted, and the malarial parasite being controlled. One possible target is the thiamine metabolizing enzyme responsible for the synthesis of B group vitamins such as vitamin B<sub>1</sub>, B<sub>6</sub> and B<sub>9</sub>. Humans cannot synthesize the vitamin and require it as an additive form within their diet. Bacteria, fungi, plants and the malarial parasite, on the other hand, possess a biosynthetic pathway for the vitamin incorporating the thiamine metabolizing enzymes (Muller *et al.*, 2009).

Vitamin B<sub>1</sub> exists ubiquitously in all organisms as a cofactor for carbohydrate metabolism (Muller and Kappes, 2007; Knockel, 2008). The biosynthetic pathway of vitamin B<sub>1</sub> in *Escherichia coli* and *Saccharomyces cerevisiae* is fully understood (Sprenger *et al.*, 1997; Himmeldirk *et al.*, 1998; Settembre *et al.*, 2003; Nosaka, 2006). The plasmodial pathway identified three vitamin B<sub>1</sub> biosynthetic enzymes: a) 5-(2-hydroxy-ethyl)-4-methylthiazole (THZ) kinase (ThiM or *PfThzK*); b) 4-amino-5-hydroxymethyl-2-

methylpyrimidine (HMP) HMP-P kinase (ThiD) and c) thiaminephosphate synthase (ThiE) (Figure 1.3).



**Figure 1.3.** Reaction scheme of the enzymes involved in thiamine phosphate biosynthesis.

(Wrenger, 2006)

Two independent synthesis branches are combined in the biosynthesis of thiamine. The biosynthesis of thiamine phosphate is divided into two branches, the thiazole branch and the pyrimidine branch. In *E. coli*, the precursor of pyrimidine branch is 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP), which has to be phosphorylated in two steps to 4-amino-2-methyl-5-hydroxymethyl pyrimidine diphosphate (HMP-PP) by HMP/HMP-P kinase (ThiD). The first phosphorylation, however, can also be effected by pyridoxine kinase (PdxK), which is involved in the activation of vitamin B<sub>6</sub>, as demonstrated for the parasites *Trypanosoma brucei* and *P. falciparum* (Yang *et al.*, 1998; Besteiro *et al.*, 2002; Cassera *et al.*, 2004; Bozdech and Ginsburg, 2005; Rapala-Kozik *et al.*, 2007; Knockel *et al.*, 2008; Muller *et al.*, 2010). HMP itself is synthesized in bacteria

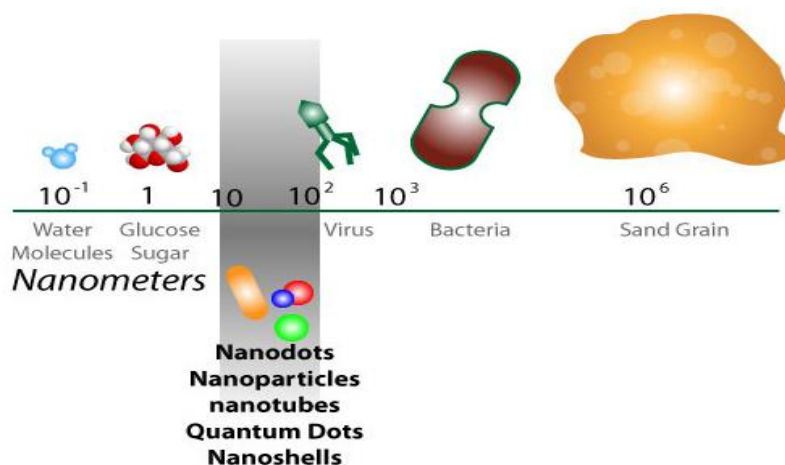
by the HMP biosynthesis enzyme, whereas it has been suggested that in eukaryotes pyridoxine and histidine are possibly bonded to HMP (Webb *et al.*, 2007; Jurgenson *et al.*, 2009). The thiamine biosynthesis branch starts with 5-(2-hydroxyethyl)-4-methylthiazole (THZ), which is converted by THZ kinase (ThiM) to 4-methyl-5-(2-phosphoethyl)-thiazole (THZ-P). Finally, the thiazole and pyrimidine moieties, HMP-PP and THZ-P, are merged to form thiamine phosphate (Thi-P) by thiamine phosphate synthase (ThiE) (Wrenger *et al.*, 2006; Jurgenson *et al.*, 2009).

To develop new antimalarial drugs, several rules must be considered. These novel drugs should only target the parasite, with no or harmless effects on the human host. An example of this would be the enzymes involved in vitamin biosynthesis pathways which are absent in the host. One promising target is the thiamine metabolizing enzyme methylhydroxyethylthiazolekinase from *P. falciparum* (*PfThzK*), which diverges significantly, both structurally and functionally from its counterpart in higher eukaryotes, thereby making it particularly attractive as a biomedical target (Wrenger *et al.*, 2006).

## 1.2. Nanotechnology

The term ‘nano’ is adapted from the Greek word meaning ‘dwarf’, when used as a prefix, it implies  $10^{-9}$ . A nanometer (nm) is one billionth of a meter, or roughly the length of three atoms side by side. The research of nanotechnology often centres around three primary studies and applied science: nano-materials, nano-instrumentation and nano-medicine. Nanotechnology refers to the study of particles that can be classified as a certain number below sizes of 100 nm, often on a molecular or atomic scale. A DNA molecule is 2.5 nm wide, a protein approximately 50 nm, and a flu virus about 100 nm, a

human hair is approximately 10,000 nm thick. By comparing the scale and size of known objects one is able to grasp the concept of nanotechnological research (Figure 1.4) (Keiper, 2003; Du Mont, 2008; Toumey, 2010). Nanotechnology involves the design, synthesis, and characterization of materials and devices that have a functional organization in at least one dimension on the nanometer scale ranging from a few nm up to 100 nm (Chen and Li, 2007; Tasker *et al.*, 2007; Varadan *et al.*, 2008; Thakkar *et al.*, 2010; Shrestha, 2012).



**Figure 1.4.** Nanoscale and examples of objects of different sizes.  
(<http://angiebiotech.com/nanotechnology-nanoparticle-fight-infection/>)

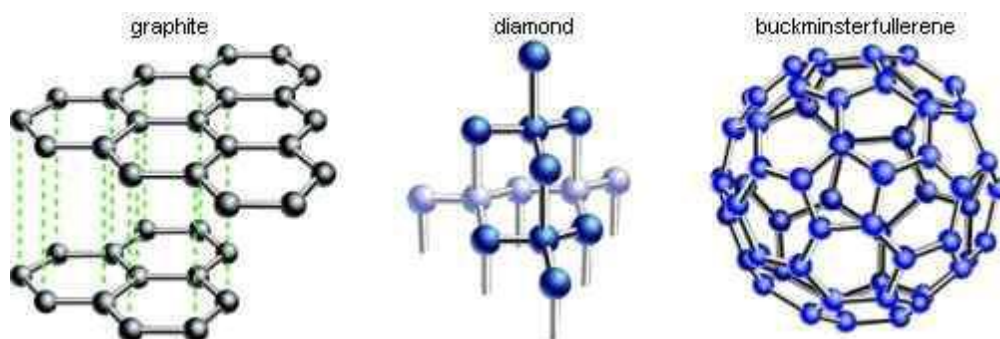
### 1.2.1. Nanomaterials and nanoparticles

Nanomaterials are those materials with unique physical properties derived from the inherent nanoscale dimensions, and leading to large surface to volume ratio (Barth *et al.*, 2005). The term nanoparticle is often mentioned interchangeably with nanomaterial but typically defines the individual molecules that make up the nanomaterial in bulk. Nanoparticles are really of scientific interest because they connect bulk materials and atomic or molecular structures (Martin *et al.*, 2006). There are many reasons for this, one

being the fact that nanoparticles possess a very high surface-to-volume aspect ratio. In the case of silver nanoparticles (AgNPs), this allows them to easily interact with other particles and to increase their antibacterial efficiency (Ju-Nam and Lead, 2008; Zhang *et al.*, 2008; Veerapandian and Yun, 2011; Wu *et al.*, 2011; Wiarachai *et al.*, 2012). This effect is extremely robust, and as little as 1 g of AgNPs is known to impart antibacterial properties on hundreds of square meters of substrate material. Recently the most investigated nanomaterials include carbon nanomaterials such as fullerenes, nanotubes and buckyballs; quantum dots (QDs); metal nanoparticles such as gold and silver nanoparticles (Burgess, 2012).

#### 1.2.1.1. Fullerenes

Fullerenes are those hollow-cage molecules composed entirely of carbon atoms, in a form of a sphere, an ellipsoid or a tube. They were discovered as a third form of carbon-based molecules besides diamond and graphite as shown in Figure 1.5 (Smalley and Yakobson, 1998). Due to the unique physical and chemical properties of these forms of carbon molecules, a great deal of research on fullerenes technological applications has been carried out, especially on material science and electronics (Sato *et al.*, 1995; Hodak and Girifalco, 2001; Bosi *et al.*, 2003; Hayashi *et al.*, 2004), even on medical therapeutics such as tumour diagnostics recently (Bakry *et al.*, 2007; Takagi *et al.*, 2008; Lee *et al.*, 2009; Sharma *et al.*, 2011; Chen *et al.*, 2012). According to the structural variations, fullerenes can be separated into different types, such as buckyballs, nanotubes, megatubes, polymers, and fullerene rings (Ray, 2012).



**Figure 1.5.** The structures of those three different forms of carbon-based molecules: Graphite; Diamond and Fullerene.  
(<http://www.designanduniverse.com/articles/diamond.php>)

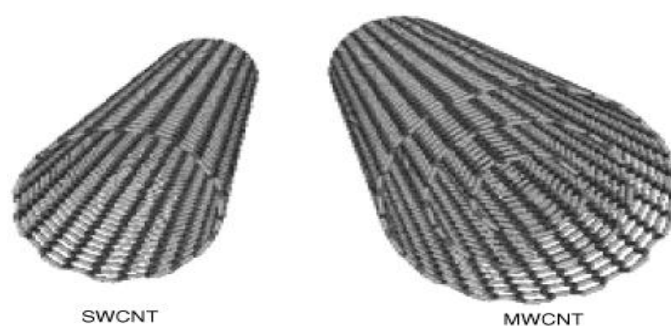
The most studied fullerene is  $C_{60}$ , also referred to as buckminsterfullerene, which was named after Richard Buckminster Fuller, is the most stable fullerene and also the most abundant in nature (Yadav and Kumar, 2008). The  $C_{60}$  fullerene molecule consists of 60 carbon atoms, with a total of 12 pentagons and 20 hexagons, resembles a soccer ball, and all the rings are fused and all double bonds are conjugated. There are 120 symmetrical operations, like the rotations around the axis and reflections in a plane, which makes the  $C_{60}$  molecule with the largest symmetrical operations, the most symmetric molecule (Parag and Ashish, 2005).  $C_{60}$  fullerene and their derivatives have potential antiviral activity, which has strong implications on the treatment of acquired immunodeficiency syndrome (AIDS), which based on those biological properties including their unique molecular architecture and antioxidant activity (Judd *et al.*, 2001; Du Toit *et al.*, 2010; Kar and Knecht, 2012). It has been shown that the amino acid derivatives of fullerene  $C_{60}$  are potentially to inhibit human immunodeficiency virus (HIV) and human

cytomegalovirus replication (Yu *et al.*, 2002; Hegde *et al.*, 2006; Bakry *et al.*, 2007; Hu *et al.*, 2010).

It was reported that fullerenes have potential biological antioxidant property, which is based on the fact that fullerenes possess a great deal of conjugated double bonds and low lying unoccupied molecular orbitals, and easily take up an electron (Mateo-Alonso *et al.*, 2006; Witte, 2008; Yeung *et al.*, 2011). It was shown that some polar group-derivatized fullerene, such as polyhydroxylated fullerenes and C<sub>60</sub> tris-acid are able to generate a large amount of oxygen free radicals (Lai *et al.*, 2000; Isakovic *et al.*, 2006; Markovic and Trajkovic, 2008;), which are necessary to protect cell growth from induced apoptotic injuries (Chen *et al.*, 2004; Hu *et al.*, 2007; Partha and Conyers, 2009; Rebecca *et al.*, 2009; Badireddy *et al.*, 2012). Fullerenes have also been investigated for skin cells on cytoprotective action against ultraviolet A radiation recently (Xiao *et al.*, 2006; Xiao *et al.*, 2010; Saitoh *et al.*, 2011).

Carbon nanotubes (CNTs) are carbon sheets rolled up into a nanoscale-tube, including single-wall carbon nanotubes (SWCNTs) and those with additional graphene tubes around the core of an SWCNT named multi-wall CNTs (MWCNTs) shown as Figure 1.6. Three methods were employed to synthesize CNTs so far, including arc-discharge (Hutchison *et al.*, 2001; Sugai *et al.*, 2003; Keidar *et al.*, 2008), laser ablation (Kokal *et al.*, 2000; Scott *et al.*, 2001) and chemical vapor deposition (Chhowalla *et al.*, 2001; Hofmann *et al.*, 2003; Reina *et al.*, 2008; Kumar and Ando, 2010). For the first two methods, solid-state carbon precursors are used to synthesize nanotube structure, however, producing an excess of by-products. The chemical vapor deposition (CVD) methods employ hydrocarbon gases as carbon atoms sources to nucleate the growth of CNTs with

organized patterns of nanotube structure on surface, comprising both SWCNTs and MWCNTs (Terrones, 2004). The CNTs have been utilized in the construction of various detection devices, such as gas sensors (Li *et al.*, 2003; Zhang *et al.*, 2006; Du *et al.*, 2007), electrochemical detectors (Wang and Musameh, 2003; Cui *et al.*, 2007; Meng *et al.*, 2009) and biosensors with immobilized biomolecules (Wohlstadter *et al.*, 2003; Tripathi *et al.*, 2006; Maehashi *et al.*, 2007; Sanchez *et al.*, 2008).

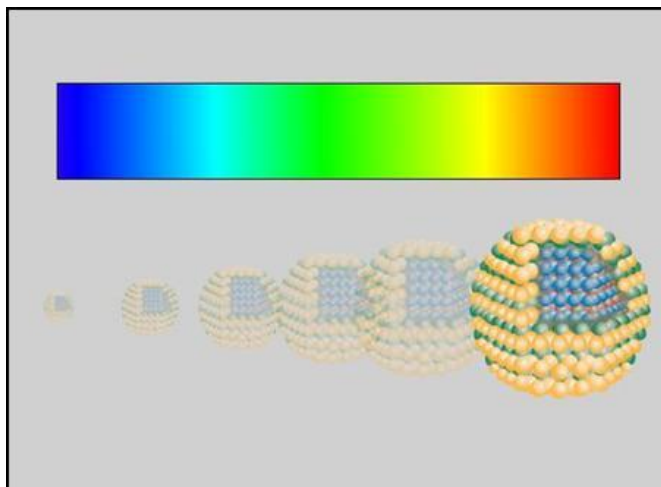


**Figure 1.6.** The structures of single-wall carbon nanotube (SWCNT) and multi-wall carbon nanotube (MWCNT). (Scarselli *et al.*, 2012)

#### 1.2.1.2. Quantum dots

Quantum dots (QDs) are semiconductor nanocrystals with unique size-dependent optical properties (Hoshino *et al.*, 2004), that can emit light in all colours of the spectrum depending on their size (Figure 1.7). Fluorescent QDs are able to be conjugated with bioactive antibodies (Goldman *et al.*, 2002; Hoshino *et al.*, 2005) or ligands (Gao *et al.*, 2004; Sperling *et al.*, 2008), to target specific cellular structures, such as peroxisomes (Fu *et al.*, 2006), DNA (Fu *et al.*, 2004; Raymond *et al.*, 2005; Kim *et al.*, 2007) and cell membrane receptors (Bannai *et al.*, 2007; Smith *et al.*, 2008; Yum *et al.*, 2009). Bioconjugated QDs are employed as tools for site-specific gene and drug delivery (Suri *et al.*, 2007; Mishra *et al.*, 2010; Parveen *et al.*, 2012) and also explored for the creation

of flat-panel light-emitting diode (LED) displays (Tan *et al.*, 2007; Rizzo *et al.*, 2007; Jang *et al.*, 2010).

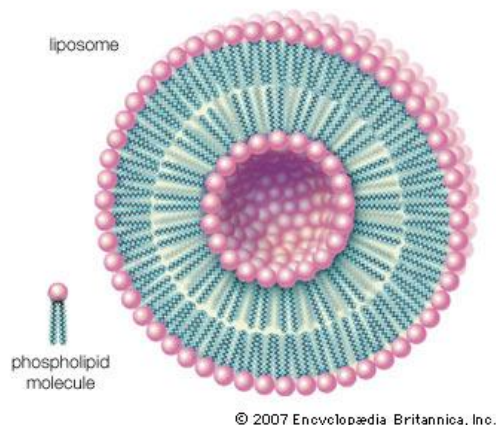


**Figure 1.7.** The size-dependent spectrum property of Quantum dots. Aerospace Concepts consultant. (<http://www.concepts.aero/system/files/quantum-dots.jpg>)

### 1.2.1.3. Liposome

A liposome is an artificial spherical vesicle with a membrane composed of phospholipids bilayer (Figure 1.8). Liposomes are designed to deliver drug or genetic material into a cell (Shaheen *et al.*, 2006; Wasankar *et al.*, 2012), and are composed of naturally-derived phospholipids with mixed lipid chain (Kolusheva *et al.*, 2000; Goldenbogen *et al.*, 2011), or of pure components (Fox *et al.*, 2011; Ranjan, 2012). Liposomes are commonly classified into multilamellar vesicles (MLV), large unilamellar vesicles (LUV), and small unilamellar vesicles (SUV), according to their lamellarity and size (Mujoriya *et al.*, 2011; Tejera-Garcia *et al.*, 2011; Akbarzadeh *et al.*, 2013). It has been shown that liposomes can be utilized for plenty of therapeutic areas, such as drug/ protein delivery (Tan *et al.*, 2010; Al-Jamal and Kostarelos, 2011; Vivero-Escoto, 2013); antimicrobial, antifungal

and antiviral therapy (Nakonechny *et al.*, 2010; Malmsten, 2011; Xu and Burgess, 2012); tumour therapy (Zhang *et al.*, 2010; Kueffer *et al.*, 2013); gene delivery (Candiani *et al.*, 2010; He *et al.*, 2010) and immunology (Alving, 2006; Henriksen-Lacey *et al.*, 2010; Altin, 2012).



**Figure 1.8.** The structure of liposome. Encyclopædia Britannica. (<http://www.britannica.com/EBchecked/media/92244/Phospholipids-can-be-used-to-form-artificial-structures-called-liposomes>)

### 1.2.2. Metal nanoparticles

It has shown that the properties of metallic nanoparticles differ substantially from their constituent atoms or bulk counterparts, including electronic, physical, and also chemical properties (Rivera-Gil *et al.*, 2010; Sau *et al.*, 2010; Rivera-Gil *et al.*, 2012). Because of their small size, metal nanoparticles have a very large surface area-to-volume ratio, which affects their individual as well as interaction properties (Mahmoudi *et al.*, 2011). They also perform a high fraction of edge- and corner-like curved regions, which have more coordinatively unsaturated atoms than the flat surface, leading to higher surface energy and its affections of surface bonding properties and chemical reactivity (Pozun *et al.*,

2011; Zasada *et al.*, 2011; Pacchioni and Freund, 2012). Furthermore, one of the motivations of the studies of metallic nanoparticles is their unique optical properties, especially from copper, gold and silver. Metallic nanoparticles can strongly couple with incident light through excitation of their surface plasmon resonances, leading to collective oscillations of the free conduction electrons near the interface between the metal nanoparticle and ambient (Banerjee *et al.*, 2010; Paudel and Leuenberger, 2012; Losurdo *et al.*, 2013). This coupling leads to unique optical properties, named as localized surface plasmon resonance (LSPR), particularly in gold and silver (Ringe *et al.*, 2010; Larginho and Baptista, 2012).

#### 1.2.2.1. Application of metallic nanoparticles

The optical properties of metal nanoparticles and their arrays have been exploited for a great deal of applications such as controlling the growth of nanoparticles by enhancing optical forces (Messina *et al.*, 2011; Ni *et al.*, 2012); improving efficiency of photovoltaic devices by increasing light absorption (Atwater and Polman, 2010; Han and Chen, 2010); photothermal destruction of cancer cells (Huang and El-Sayed, 2010; Fan *et al.*, 2012) and pathogenic bacteria (Alkilany *et al.*, 2012; Rosenberg and Petrie, 2012); enhancement in the sensitivity of sensors and spectroscopies (Margueritat *et al.*, 2011; Pryce *et al.*, 2011); energy transport and storage (Liu and Lee, 2010; Ferrier *et al.*, 2012; Solis-Jr *et al.*, 2012).

Metal nanoparticles have possible and potential applications in various areas. For example, nanoparticles can be induced to merge into a solid at relatively low temperatures, often without melting, leading to improved and easy-to-create coatings for electronic applications, which are the basic property for capacitors (Thakkar *et al.*, 2010;

Sengar and Mehta, 2012). Furthermore, nanoparticles possess a wavelength below the critical light wavelength, that makes them more transparent and useful for applications in cosmetics (Julia and Li, 2011; Chen *et al.*, 2012), coatings (Yu *et al.*, 2010; Stojanovic *et al.*, 2012), and packaging (Jeong *et al.*, 2010). Metal nanoparticles can be attached, nondestructively, to single strands of DNA thus opening up avenues for medical diagnostic applications (Poon *et al.*, 2010; Busson *et al.*, Rosarin and Mirunalini, 2011). Nanoparticles can pass through the vasculature, the blood brain barrier and localize any target organ (Na *et al.*, 2011; Krol *et al.*, 2012; Wang *et al.*, 2012) which can, potentially, lead to novel therapeutic, imaging and biomedical applications.

**Table 1.2.** Examples of metal nanoparticles potential applications.

Nanoparticles	Applications	References
Copper Metal NPs	Biosensor; drug delivery; Alzheimer's therapeutics	Bracey <i>et al.</i> , 2009; Liu <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2013
Gold Metal NPs	Biomarker; biosensors; colouration; drug delivery system; tumour therapeutics	Hong <i>et al.</i> , 2010; Nash <i>et al.</i> , 2010; Alhasan <i>et al.</i> , 2012; Lee <i>et al.</i> , 2012
Palladium Metal NPs	Biosensor; drug delivery system;	Lu <i>et al.</i> , 2011; Das <i>et al.</i> , 2013
Platinum Metal NPs	Biosensor; drug delivery system	Su <i>et al.</i> , 2010; Mclamore <i>et al.</i> , 2011
Ruthenium Metal NPs	Drug delivery	Kenezevic <i>et al.</i> , 2012; Wang <i>et al.</i> , 2012
Silver Metal NPs	Antibacterial and antifungal agent; biosensor; coating	Marambio-Jones and Hoek, 2010; Arnaout and Gunsch, 2012; Singh <i>et al.</i> , 2012;

### 1.2.2.2. Synthesis of metallic nanoparticles

There are two alternative approaches for the synthesis of metal nanoparticles: the ‘bottom-up’ approach and the ‘top-down’ approach. The former means self assembly, or the construction of a structure atom-by-atom, molecule-by-molecule, or cluster-by-cluster (Strackarn *et al.*, 2012). In this approach, initially the nanostructured building blocks are formed and, subsequently, assembled into the final material using chemical or biological procedures (Thakkar *et al.*, 2010; Orbach *et al.*, 2012). A typical advantage of the bottom-up approach is the enhanced possibility of obtaining metal nanoparticles with considerably less defects and more homogeneous chemical composition (Sau and Rogach, 2010). In the top-down approach, a suitable starting material is reduced in size using physical, mechanical or chemical methods (Singh *et al.*, 2010; Ambrosi *et al.*, 2012; Yadav *et al.*, 2012). A major drawback of the top-down approach is the imperfection of the surface structure which could impact on physical properties and also surface chemistry due to the high aspect ratio (Shahbazi *et al.*, 2012; Suresh, 2012; von Freymann *et al.*, 2013).

Several methods and recipes for the preparation of metal nanoparticles have been reported so far, and only those that are common and well established will be mentioned.

#### 1.2.2.2.1. Chemical reduction method

The traditional and most widely used method for synthesis of metal nanoparticles is using wet-chemical procedures. A typical procedure involves growing nanoparticles in a liquid medium containing various reactants, in particular reducing agents such as sodium borohydride or potassium bitartrate or methoxypolyethylene glycol (Polte *et al.*, 2010; van Heusden *et al.*, 2010; Abeylath and Amiji, 2011; Singh *et al.*, 2011). To prevent the

aggregation of metal nanoparticles, a stabilizing agent such as sodium dodecyl/benzyl sulfate or polyvinyl pyrrolidone is also necessary in the reaction mixture (Badawy *et al.*, 2010; Goldshleger *et al.*, 2012). It was reported that ion exchange resins have been used to produce nickel nanoparticles varying in size 3-5 nm (Railsback *et al.*, 2010). Generally, the chemical methods are low-cost and rapid for high volume (Rangappa *et al.*, 2010; Lu *et al.*, 2011; Kim *et al.*, 2012); however, their drawbacks include contamination from chemicals, toxic solvents and the generation of hazardous by-products, and furthermore there is limited control on the shape and size of the nanoparticle (Malekzadeh and Halali, 2011; Virkutyte and Varma, 2011). Interestingly, several developed chemical approaches for controlled-size and shape nanoparticles have been reported recently. For example, stable Pt/Ru nanoparticles with 2.1-2.8 nm in diameter were synthesized by ethanol (Liu *et al.*, 2011; Wang *et al.*, 2011). Tannic acid was used as both reducing and stabilizing agent to synthesize spherical gold (Aromal and Philip, 2012), nickel (Dutta and Dolui, 2011) and silver nanoparticles (Yi *et al.*, 2011). Green, effective chemical routes for the synthesis of nanoparticles are getting more and more attractive.

#### 1.2.2.2.2. Biological synthesis

Biosynthetic methods employ the resources available in nature to prepare metal nanoparticles (Han *et al.*, 2012). It was reported that a number of biological materials have been involved in biosynthetic pathways, including algae, bacteria, fungi, plant and yeast (Table 1.3). There are quite a few reports of algae being used as a biomaterial for the synthesis of metal nanoparticles. *Sargassum wightii* was the first marine algae reported to be used to synthesize stable extracellular gold particles under relatively simple conditions (Singaravelu *et al.*, 2007). Prokaryotic bacteria are the most common

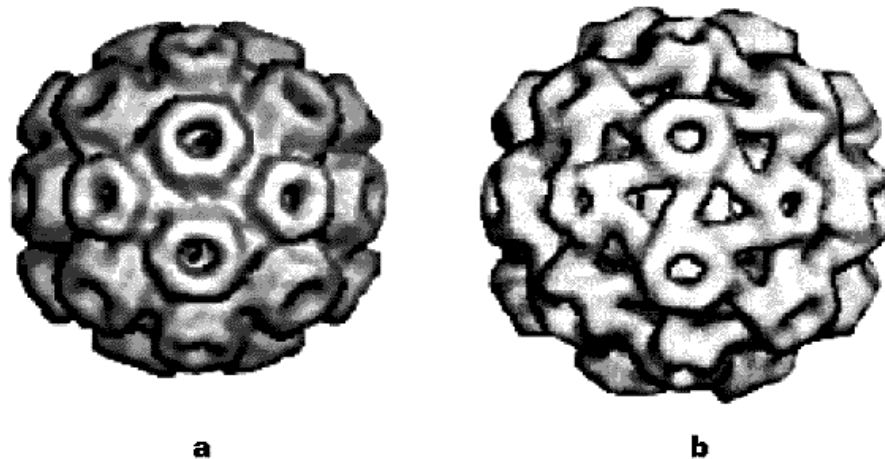
biological resources employed in metal nanoparticle synthesis because of their relative ease of manipulation (Mondal *et al.*, 2011). It was reported that the crystalline Ag nanoparticles could be extracellularly produced when silver-resistant *Morganella sp.* RP-43 was exposed to silver nitrate (AgNO<sub>3</sub>), and it was the first report that elucidates the molecular evidence of silver resistance in bacteria (Parik *et al.*, 2008). The first intracellularly synthesized nanoparticles was cadmium sulfide (CdS), by incubating *E. coli* with cadmium chloride (CdCl<sub>2</sub>) and sodium sulfide (Na<sub>2</sub>S), and it showed that the formation of nanoparticles was markedly affected by physiologic parameters (Sweeney *et al.*, 2004). Fungi have been reported as a kind of ideal biomaterial to synthesize metal nanoparticles. One of the distinct advantages is that fungi showed the ease in their scale-up, just using thin solid substrate fermentation for the synthesis of metal nanoparticles (Ahmad *et al.*, 2002; Ahmad *et al.*, 2005). Plant leaf extract has been exploited to synthesize gold, silver and platinum nanoparticles with different size depending on the pH (Sharma *et al.*, 2007; Kumar and Yadav, 2009; Mubarak-Ali *et al.*, 2011; Vinod *et al.*, 2011).

**Table 1.3.** Some examples of microorganisms involving in metal nanoparticles synthesis.

Microorganism	Type of nanoparticles	References
<b>Algae</b>		
<i>Sargassum wightii</i>	Au	Oza <i>et al.</i> , 2012
<b>Bacteria</b>		
<i>Clodtridium thermoaceticum</i>	CdS	Thakkar <i>et al.</i> , 2010
<i>Escherichia coli</i>	Ag, Au	Aubin-Tam and Hamad-Schifferli, 2005; Shahverdi <i>et al.</i> , 2007
<i>Klebsiella pneumoniae</i>	Ag, CdS	Krumov <i>et al.</i> , 2009; Mokhtari <i>et al.</i> , 2009
<i>Lactobacillus strains</i>	Ag, Au	Nair and Pradeep, 2002; Vaidyanathan <i>et al.</i> , 2009

<b>Fungi</b>		
<i>Trichoderma asperellum</i>	Ag, Au	Mukherjee <i>et al.</i> , 2008; Mukherjee <i>et al.</i> , 2012
<i>Verticillium</i>	Ag, Au	Sharma <i>et al.</i> , 2007
<b>Plant</b>		
<i>Azadirachta indica</i>	Ag, Au	Leela and Willner, 2004; Rajasekharreddy <i>et al.</i> , 2010
<i>Diopyros kaki</i>	Pt	Song <i>et al.</i> , 2010
<i>Eucalyptus hybrida</i>	Ag	Dubey <i>et al.</i> , 2009
<i>Magnolia kobus</i>	Au	Song <i>et al.</i> , 2009
<i>Terminalia catappa</i>	Au	Ankamwar, 2010
<b>Yeast</b>		
MKY3	Ag	Katz and Wilner, 2004

It was reported that viruses have been investigated as a biomaterial to synthesize gold and silver nanoparticles (Kramer *et al.*, 2004; Loo *et al.*, 2006; Niikura *et al.*, 2009). The viral capsids act as molecular containers for the encapsulation of genomic nucleic acid, and they can also be used as constrained reaction vessels for packaging and entrapment of synthetic nanoparticles (Liepoold *et al.*, 2005). One of the distinct advantages is that a virus can provide an ideal protein cage structure. An excellent example is icosahedral cowpea chlorotic mottle virus (CCMV) (Figure 1.9). The CCMV capsids undergoes a pH and metal-ion dependent swelling, which results in a reversible structural transition of the capsid (open or closed), releasing the interior of the protein cage to the medium (Renggli *et al.*, 2011). The virus also presents a confined environment and unique protein surface topology, including polarity, residue charge and surface relief (Slocik *et al.*, 2005). The metal nanoparticles synthesized in the virus protein cage are tiny enough to cross cell membranes and make them potential for medical applications. Generally, the biological methods are environmentally friendly, but high-cost and slow for high-volume due to the complicated preparation procedure and specific temperature and pH conditions.



**Figure 1.9.** Cryo-electron microscopy and image reconstruction of the cowpea chlorotic mottle virus. a), in an unswollen condition induced by low pH; b), in a swollen condition induced by high pH.  
(Douglas and Young, 1998)

### 1.2.3. Safety of nanotechnology

Nanotechnology is an emerging science, and the novel and unique properties of nanoparticles may pose a health risk to humans and the environment. It is estimated that the average person consumes 1012 submicron-sized particles per day, from the food additives consisting primarily of titanium dioxide ( $\text{TiO}_2$ ) and aluminosilicates (Stem and McNeil, 2008). Correspondingly, the study of the hazardous effects of these particles, particulate toxicology, has been underway for many decades. Therefore due to the potential nanomaterial risks, there has been a dramatic increased concern to safety research. Potential routes of nanoparticle exposure include inhalation, dermal, oral and in the case of biomedical applications, the toxicity resulting from nanoparticle exposure could occur via the lungs and skin (Papp *et al.*, 2008).

The toxicology of nanoparticles should involve the study of the interactions of those ultrafine particles with biological systems and the environment, and also the investigation of their potential risk at a molecular level (Lai and Sayre, 2009; Yildirimer *et al.*, 2011; Yah *et al.*, 2012). A number of studies on the effects of nanoparticles on biological cells, tissues, animals and environment system have been carried out (Braydich-Stolle *et al.*, 2010; Shvedova *et al.*, 2010; Celardo *et al.*, 2011). For example, the metallic nanoshells, as a drug delivery agent have been extensively studied for the controlled release in chemotherapy (Rosler *et al.*, 2001; Xu *et al.*, 2006; Gu *et al.*, 2007; Haidar, 2010; Huschka *et al.*, 2012). They are generally composed of inert metals such as gold or titanium, and each of these platforms is inert and biocompatible. It was reported that a significant fraction of the particles is retained in the body after administration, and this can lead to toxicity (Wang and Thanou, 2010; Werner *et al.*, 2012). Therefore, most of the work on metal nanoparticle drug delivery has been in the preclinical stage.

### **1.3. Present research**

#### **1.3.1. Hypothesis**

Silver nanoparticles of controlled size and shape can significantly interfere with the activity of methylhydroxyethylthiazolekinase enzyme from *Plasmodium falciparum* thereby introducing a new, promising and potential approach to control malaria.

#### **1.3.2. Objectives**

- Chemical synthesis of silver nanoparticles by reducing a silver salt with NaBH<sub>4</sub> or tannic acid.

- Cloning, expression, purification and characterization of the biomedical target: methylhydroxyethylthiazolekinase from *Plasmodium falciparum* (PfThzK).
- *In vitro* evaluation of these silver nanoparticles against methylhydroxyethylthiazolekinase from *Plasmodium falciparum* (PfThzK).

## Chapter 2

# Isolation of the genes encoding methylhydroxyethylthiazolekinase from *Plasmodium falciparum* (PfThzK)

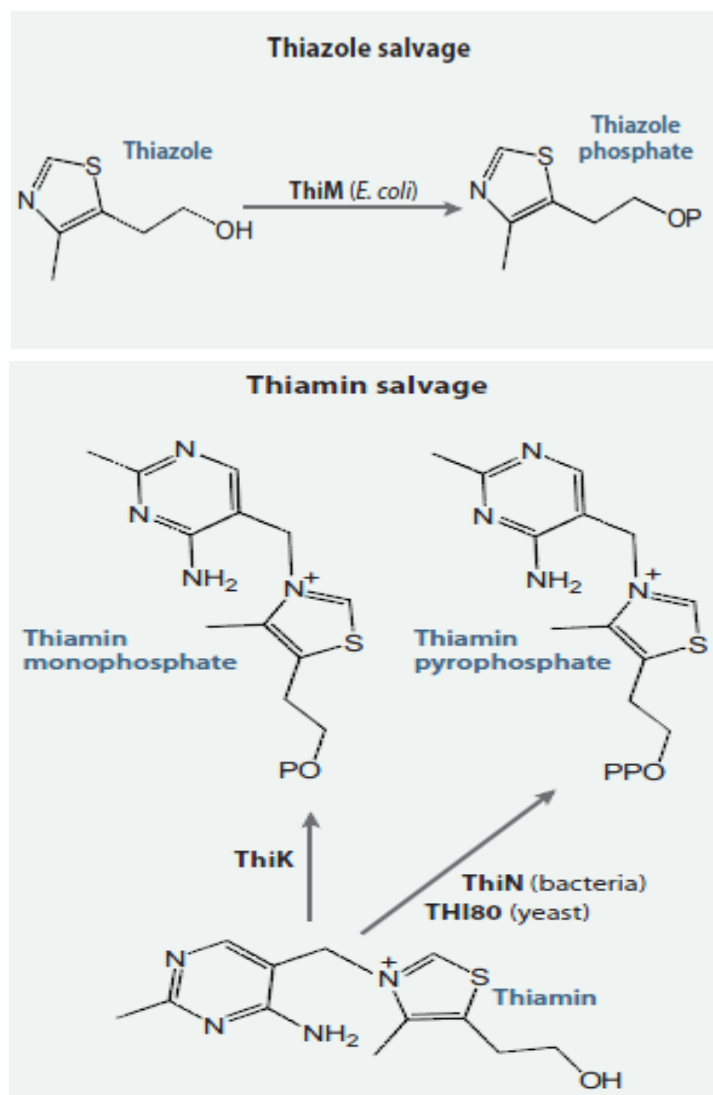
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### 2.1. Introduction

Vitamin B<sub>1</sub> (thiamine) is an essential cofactor for several key enzymes of carbohydrate metabolism, and it occurs ubiquitously in all organisms. Humans obtain it from their diet, and in the case of bacteria, fungi, plants and malaria parasite, it is synthesized *de novo*. And then thiamine has to be salvaged by thiamine pyrophosphokinase to be active cofactor thiamine pyrophosphate (Thi-PP) (Begley *et al.*, 1999; Wightman and Meacock, 2003).

#### 2.1.1. Biosynthesis of thiamine phosphate in *P. falciparum*

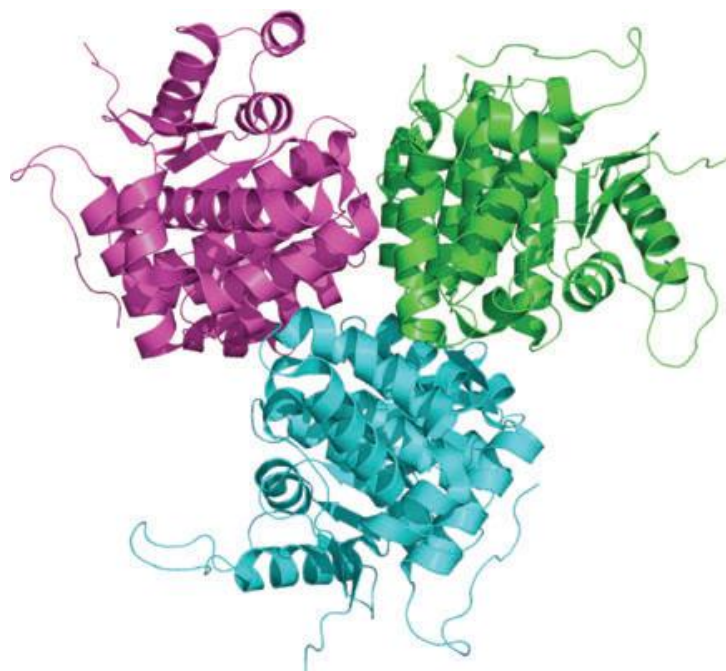
The biosynthetic pathway of vitamin B<sub>1</sub> in *Escherichia coli* and *Saccharomyces cerevisiae* is well understood (Scott and Phillips, 1997; Taylor *et al.*, 1998; Begley *et al.*, 1999; Mizote *et al.*, 1999; Wightman and Meacock, 2003). In bacteria the thiazole can be converted to thiazole-phosphate (THZ-P) by ThiM (thiazole kinase of bacteria); thiamine or components of thiamine, can be salvaged (Figure 2.1). In bacteria, thiamine can be converted to thiamine-phosphate by thiamine kinase (ThiK), or be converted to thiamine-diphosphate by thiamine pyrophosphokinase (ThiN), the corresponding enzyme in higher organism such as yeast for example, is THI80 (Jurgenson *et al.*, 2009).



**Figure 2.1.** Salvage pathways for thiazole and thiamine in *E. coli*.

ThiM from *Bacillus subtilis* and *Salmonella typhimurium* have been biochemically characterized (Zhang *et al.*, 1997; Petersen and Downs, 1997), and the structure of the *B. subtilis* ThiM was determined (Campobasso *et al.*, 2000). ThiM from *B. subtilis* is a trimer, and each protomer contains 9  $\beta$ -strands and 12  $\alpha$ -helices (Figure 2.2). The corresponding enzyme in *P. falciparum*, PfThzK, hasn't been structurally characterized

by X-ray, but it was evaluated to be a monomer, with a molecular mass of 34 kDa (Wrenger, 2006).

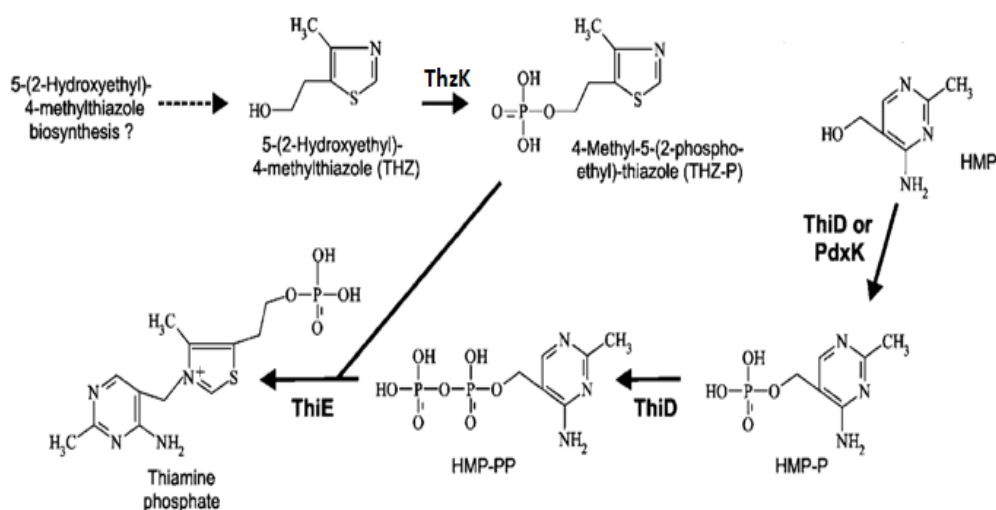


**Figure 2.2.** X-ray structure of thiazolekinase from *B. subtilis* (Jurgenson *et al.*, 2009).

The plasmodial pathway identified three vitamin B<sub>1</sub> biosynthetic enzymes: a) 5-(2-hydroxy-ethyl)-4-methylthiazole (THZ) kinase (ThzK), b) 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP) HMP-P kinase (ThiD) and c) thiamine phosphate synthase (ThiE). The biosynthesis of thiamine phosphate is divided into two branches: the thiazole branch and the pyrimidine branch. The thiamine biosynthesis branch starts with 5-(2-hydroxyethyl)-4-methylthiazole (THZ), which is activated and converted by THZ kinase (ThzK) to 4-methyl-5-(2-phosphoethyl)-thiazole (THZ-P). The precursor of the pyrimidine branch is 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP), which has

to be phosphorylated in two steps to 4-amino-2-methyl-5-hydroxymethyl pyrimidine diphosphate (HMP-PP) by HMP/HMP-P kinase (ThiD). The first phosphorylation, however, can also be effected by pyridoxine kinase (PdxK), which is involved in the activation of vitamin B<sub>6</sub>, as demonstrated for the parasites *Trypanosoma brucei* and *P. falciparum* (Morett *et al.*, 2003; Wrenger *et al.*, 2005). HMP itself is synthesized in bacteria by the HMP biosynthesis enzyme, whereas it has been suggested that in eukaryotes pyridoxine and histidine are possibly bound to HMP (Wrenger *et al.*, 2006). Finally, the thiazole and pyrimidine moieties, HMP-PP and THZ-P, are merged to form thiamine phosphate (Thi-P) by thiamine phosphate synthase (ThiE) (Figure 2.3).

Arbitrary use of malarial chemotherapeutic agents increased drug resistance and a loss in efficiency. Therefore, new antimalarial drugs and novel drug targets are urgently required. These drugs should be developed to target only parasites and not be harmful to the human host. The three enzymes involved in the parasitic metabolic thiamine synthetic pathway, ThiD, ThiE and ThzK are absent in the human host, especially, ThzK which is structurally and functionally different from the corresponding enzymes in bacteria and yeasts; this makes ThzK ideal as a potential drug target.



**Figure 2.3.** Thiamine phosphate biosynthesis in *P. falciparum* (Wrenger *et al.*, 2006).

The 5-(2-hydroxyethyl)-4-methylthiazole (THZ) synthesized *de novo* will be phosphorylated to THZ-P by THZ-kinase (ThzK). In the pyrimidine branch, 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP) is phosphorylated to HMP-P by either the pyridoxinekinase (PdxK) or the HMP-(P)-kinase (ThiD). Subsequently, HMP-P is phosphorylated to HMP-PP by HMP-(P)-kinase. THZ-P and HMP-PP are merged to thiamine phosphate in a reaction catalysed by thiamine synthase (ThiE).

### 2.1.2. Gene sequence encoding *PfThzK* used in this study

Polymerase chain reaction (PCR) amplification of the genomic DNA using primers based on published sequence data is commonly used to isolate the gene encoding specific proteins of interest. However, the entire *P. falciparum* genome sequence was only published in 2002, and it is the most A-T rich genome sequenced to date. Very few studies on cloning of ThzK gene from *P. falciparum* were published so far (Gerdner *et al.*, 2002; Wrenger *et al.*, 2006).

The opening reading frame (ORF) encoding for the methylhydroxyethylthiazolekinase comprises 909 base pairs (bp), the sequence data (NCBI Reference Sequence: AY166865) is shown in Appendix 1.

## 2.2. Materials and methods

### 2.2.1. Chemicals and reagents

All the chemicals and reagents utilized to prepare strain cultures and amplify *PfThzK* gene are described in Appendix 2 (Media and Buffers).

### 2.2.2. Genomic DNA, bacterial strains, plasmids and culture

#### conditions

*P. falciparum* 3D7 genomic DNA (MRA-120G, MR4) was used as a template to amplify *PfThzK* gene sequence, which was purchased from American Type Culture Collection (ATCC). Oligonucleotides and restriction enzymes, *NdeI* and *EcoRI*, which were used for the design of primers and double digestion, were obtained from IDT® (South Africa). Recombinant plasmids were expressed in *E. coli* strains JM109 or *E. coli* BL21 (DE3) containing pRARE (Invitrogen), those strains were grown at 37 °C at 160 rpm under aeration in LB media or on LA plates (Appendix 2) supplemented with antibiotics to which the plasmids conferred resistance (30 µg/ml kanamycin or/and 34 µg/ml chloramphenicol).

The plasmids used in this chapter are pSmart and pET28b(+), where 30 µg/ml kanamycin was used as antibiotic marker. Plasmid pSmart was used as a cloning vector and pET28b(+) was used to generate target proteins fused with a N-terminal His-tag, and therefore these target proteins could be subsequently purified by Ni-affinity chromatography.

### 2.2.3. PCR amplification

The ORFs encoding for *PfThzK* were amplified by polymerase chain reaction from *P. falciparum* 3D7 genomic DNA (MRA-120G, MR4) using oligonucleotides: *PfThzK-NdeI*: 5'-CATATGAGAAAATATAATTTTTTTTACAAAAAGTCGC-3'; *PfThzK-EcoRI*: 5'-GAATTCTTATGCTACTTTGTAAATATCTACGATTTGG-3' (Table 2.1). PCR of the plasmidial constructs was performed in a total reaction volume of 50 µl using Phusion®

Hot Start II polymerase (Finzymes, Thermo Scientific, Finland) by Thermal Cycler (MJ Mini™, Bio-RAD) and using the following thermal cycling program: initial denaturation for 2 min at 98 °C, followed by 35 cycles of 20 sec at 95 °C, 10 sec at 64 °C, 10 sec at 59 °C, 1 min at 60 °C, and 8 min at 60 °C (Table 2.2).

**Table 2.1** Oligonucleotide primers used for PCR amplification.

Primer	Sequence	Temperature
<i>PfThzK-NdeI</i>	5'-CATATGAGAAAATATAATTTTTTTACAAAAAGTCGC-3'	54.0 °C
<i>PfThzK-EcoRI</i>	5'-GAATTCTTATGCTACTTTGTAAATATCTACGATTTGG-3'	56.4 °C

The PCR amplification and DNA products were analyzed by electrophoresis (90V; 60 min) on 0.8% agarose gel in TAE buffer (0.04 M Tris-HCl, 1 mM EDTA pH 8.0, 0.021 mM glacial acetic acid) containing 0.6 µg/ml ethidium bromide. The products were visualized using Uviprochemi gel imaging system (UVitec) or VIBER LOURMAT (ECX-1.5L) with low radiation UV source, and the DNA products were then isolated from the gel using Biospin Gel Extraction Kit (BioFlux, Bioer Technology Co., Ltd) based on the manufacturer's instructions (Appendix 3). The nucleic acid concentrations were determined with a Nanodrop 2000 spectrophotometer (Thermo Scientific).

**Table 2.2a.** PCR reaction components.

Component	50 $\mu$ l reaction	Final concentration
H <sub>2</sub> O	16.5	
5xPhusion® HF Buffer	10	1x
dNTPs	1	0.8 mM
Forward primer ( <i>PfThzK-NdeI</i> )	10	0.5 $\mu$ M
Reverse primer ( <i>PfThzK-EcoRI</i> )	10	0.5 $\mu$ M
Template DNA	2	25 ng/ $\mu$ l
Phusion® Hot Start II DNA polymerase	0.5	0.02 U/ $\mu$ l

**Table 2.2b.** PCR thermal cycling program.

Cycle step	Temperature	Time	Cycles
Initial denaturation	98 °C	2 min	1
Denaturation	98 °C	20 sec	
Annealing	64 °C	10 sec	
Annealing	59 °C	10 sec	35
Extension	60 °C	1 min	
Final extension	60 °C	8 min	1
Cooling	4 °C	$\infty$	1

#### 2.2.4. Ligation

The cleaned DNA products (approximately 900 bp) isolated from the gel were ligated into pSmart Vector system (Lucigen). Each ligation was carried out as per manufacturer's instructions, with a total volume of 10  $\mu$ l, containing PEG4000 (1  $\mu$ l), 10 $\times$ ligation buffer,

T4 DNA ligase, pSmart vector and DNA product with 1:1 molar ratio of vector: insert DNA (see Table 2.3). Each ligation was performed at 4 °C overnight.

**Table 2.3.** Ligation components

Component	10 µl reaction	Final concentration
H <sub>2</sub> O	0	
Insert DNA	6	4.2 ng/µl
PEG4000 (50%)	1	5%
10xLigation buffer	1	1x
T4 DNA ligase	1	0.3 U/µl
pSmart vector	1	25 ng/µl

### 2.2.5. Transformation and cloning

Competent *E. coli* strains JM109 and *E. coli* BL21 (DE3) cells (Invitrogen) were prepared according to the modified methods described before (Hanahan, 1983; Chung *et al.*, 1989), with the procedure as follows :

- A single colony of *E. coli* cells was inoculated into 5 ml LB medium, and incubated overnight at 37 °C with aeration.
- The overnight culture (1.0 ml) was inoculated into SOB media (20 g/L tryptone, 5 g/L yeast extract, 0.584 g/L NaCl, 0.186 g/L KCl, 2.034 g/L MgCl<sub>2</sub>, 2.464 g/L MgSO<sub>4</sub>), and grown at 37 °C with aeration at 160 rpm until OD<sub>600</sub> reached 0.6.
- The culture was cooled (ice-water bath; 10 min), and centrifuged (3,000 × g; 10 min; 4 °C).
- The pellets were resuspended in 80 ml pre-cooled TB buffer (2.6 g/L HEPES, 2.203 g/L CaCl<sub>2</sub>, 18.638 g/L KCl, 10.886 g/L MnCl<sub>2</sub>, pH 6.7) followed by a second centrifugation (3,000 × g; 10 min; 4 °C) and resuspended in 20 ml pre-cooled TB buffer (Appendix 2).

- DMSO was added to the suspension to a final concentration of 7% (1.4 ml DMSO/20ml suspension), and the mixture was cooled (ice; 10 min), then divided into aliquots (100 µl) and stored at -80 °C until required.

Competent *E. coli* JM109 cells (100 µl aliquot) were thawed on ice and ligated product *PfThzK*-pSmart (10 µl) was added. The mixture was placed on ice (30 min), followed by heating (42 °C; 40 sec), cooling (ice-water bath; 2 min) and then treated with 250 µl pre-warmed SOC media (20 g/L tryptone, 5 g/L yeast extract, 0.584 g/L NaCl, 0.186 g/L KCl, 2.034 g/L MgCl<sub>2</sub>, 2.464 g/L MgSO<sub>4</sub>), and then incubated (37 °C, 60 min).

The *PfThzK*-pSmart-JM109 culture was plated onto LA plates (Appendix 2) containing 30 µg/ml of kanamycin, and incubated at 37 °C overnight. Single transformation colonies were selected and inoculated into a LB culture (5 ml; containing 30 µg/ml of kanamycin) and incubated (37 °C; 16 h). The DNA of the gene with interest was isolated by BioSpin Plasmid Extraction Kit (BioFlux, Bioer Technology Co., Ltd) according to the manufacturer's instructions (Appendix 4).

### 2.2.6. Sequencing

Restriction fragment length polymorphism was used as a screening method in double digestion using *EcoRI* and *NdeI* restriction enzymes. The double digestion was performed (10 µl; 37 °C; 12 h), the digested products sequenced (Inqaba Biotechnical Industries, Pty, Ltd; South Africa) and aligned with the reference sequence from NCBI database.

The pSmart plasmids containing the desired insert were double digested by *EcoRI* and *NdeI* and then ligated to pET28b(+) using the same method (Section 2.2.4). The pET28b(+) plasmid containing the desired insert were cleaned from the agarose gel by

BioSpin Gel Extraction Kit (BioFlux, Bioer Technology Co., Ltd) according to the same protocol describe before (Section 2.2.5). The cleaned *PfThzK*-pET28b(+) were ligated and the products transformed into competent *E. coli* BL21 [DE3 (with pRARE)] cells then inoculated onto LA plates containing 30 µg/ml kanamycin and 34 µg/ml chloramphenicol. Positive transformants selected (Section 2.2.5) were then ready for expression.

**Table 2.4.** Double digestion components.

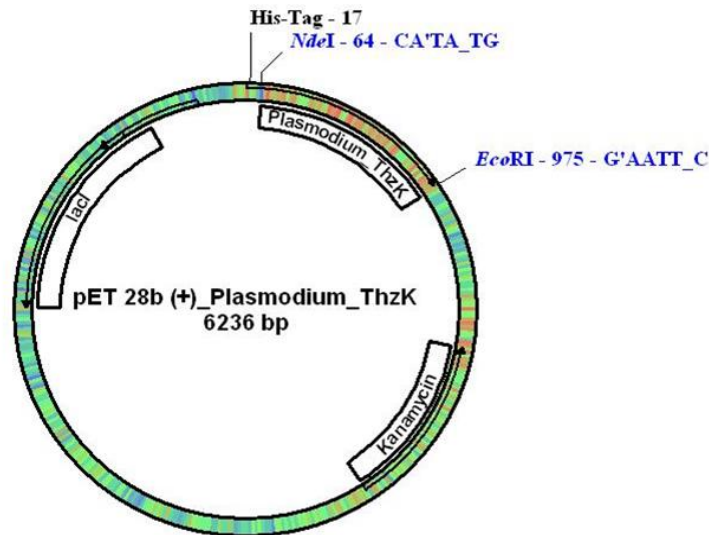
Component	10 µl reaction
H <sub>2</sub> O	6 µl
Isolated plasmid	2 µl
Buffer O	1 µl
<i>NdeI</i>	0.5 µl
<i>EcoRI</i>	0.5 µl

## 2.3. Results and discussion

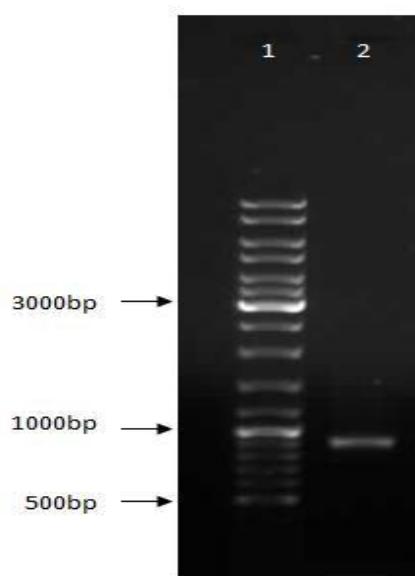
### 2.3.1. PCR amplification

Two primers *PfThzK-NdeI* and *PfThzK-EcoRI* were designed to amplify and express the *PfThzK* gene as described in Section 2.2.3. Vector pET28b(+) were utilized for fusion proteins and hexa-Histidine tags (Figure 2.4).

The *PfThzK* gene was successfully amplified by PCR (Section 2.2.3), after agarose electrophoresis it contained a band of approximately 900 bp (Figure 2.5), which agrees with NCBI database (909 bp), and it was also confirmed by Bozdech (2005) and Wrenger (2006).



**Figure 2.4.** Vector map of pET28b(+) containing His-tag binding site, *NdeI* and *EcoRI* cloning sites, and the kanamycin resistance gene.

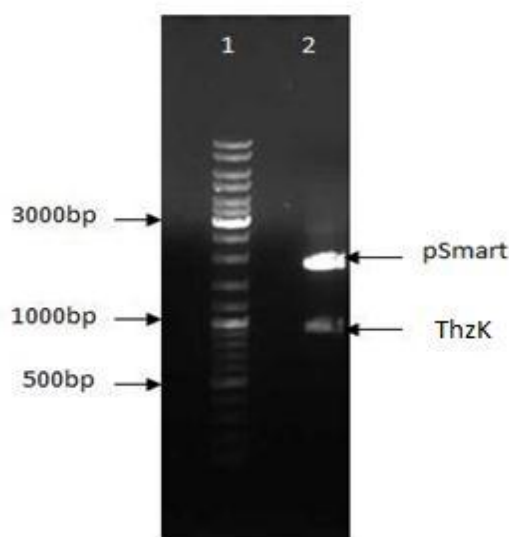


**Figure 2.5.** Agarose gel electrophoresis of the PCR amplified *PfThzK* gene. Lane 1 represents the DNA marker; lane 2 represents the amplified *PfThzK* gene (approximate 900 bp).

### 2.3.2. Transforming and cloning

The amplified *PfThzK* gene was cleaned by Biospin Gel Extraction Kit (Section 2.2.3), the concentration of isolated genomic DNA was 138.4 ng/ $\mu$ l, and it was pure of good quality ( $A_{260}/A_{280} = 1.9$ ), which could be used for subsequent experiments.

Double digestion with *EcoRI* and *NdeI* restriction enzymes was performed (Section 2.2.6) and the agarose electrophoretogram contained 2 bands: one of approximately 900 bp and another around 1.8 kb, which confirmed that the insert was the gene of interest (Figure 2.6).



**Figure 2.6.** Agarose gel electrophoresis of the double digestion with *NdeI* and *EcoRI* restriction enzymes. Lane 1 represents the DNA marker; lane 2 represents the double digested products: *PfThzK* (909 bp), pSmart (1.8 kb).

The double digested products were sent to Inqaba Biotech Industries (South Africa) for sequencing (Section 2.2.6), and alignment of the insert showed 99.9% identity (908/909) to the reference gene (Figure 2.7). The ORF encoding for *PfThzK* was identified on

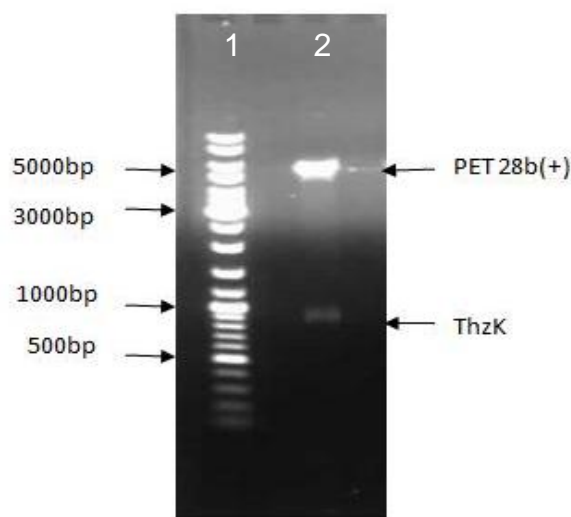
chromosome12 by BLAST analysis (<http://blast.ncbi.nlm.nih.gov>). The ORF comprises 909 bp and does not contain any introns. The *PfThzK* gene sequence shows moderate sequence identities of 99% and 99% to *P. falciparum* 3D7 chromosome12 (AE014188.3) and *P. falciparum* ThzK mRNA (AY166865.1) respectively.

Pf_ThzK_NCBI	1	ATGAGAAAATATAAATTTTTFACAAAAAGTCGGCTFATTCTCTACCTTAACCAAATAAAT	60
Pf_ThzK	1	ATGAGAAAATATAAATTTTTFACAAAAAGTCGGCTFATTCTCTACCTTAACCAAATAAAT	60
Pf_ThzK_NCBI	61	AGCGTTAAGGAATATCATGATGATATAATAAAGTGCATTGAGAAAAGTTCGGGTATATAAT	120
Pf_ThzK	61	AGCGTTAAGGAATATCATGATGATATAATAAAGTGCATTGAGAAAAGTTCGGGTATATAAT	120
Pf_ThzK_NCBI	121	CCTCTGTTCATTGTATACTAATAGAGTAACCCTGAAAAGGTGGCAAACAGTTTATTCG	180
Pf_ThzK	121	CCTCTGTTCATTGTATACTAATAGAGTAACCCTGAAAAGGTGGCAAACAGTTTATTCG	180
Pf_ThzK_NCBI	181	GCCTTTGGCTCTTCTCCGGCTATGATTGATAATCCTAAGGAAGTTGAAGAATTGGCTAAA	240
Pf_ThzK	181	GCCTTTGGCTCTTCTCCGGCTATGATTGATAATCCTAAGGAAGTTGAAGAATTGGCTAAA	240
Pf_ThzK_NCBI	241	ATAGCTTCATGTACTTATTTCAACTTAGGGTTACATACGACCGCAGGTAGAAAATATAAT	300
Pf_ThzK	241	ATAGCTTCATGTACTTATTTCAACTTAGGGTTACATACGACCGCAGGTAGAAAATATAAT	300
Pf_ThzK_NCBI	301	TTATTAGAAAAGTTAAGAAAAGAATGTATGAAAGATAAATTTATGTTAATTATAGATCCA	360
Pf_ThzK	301	TTATTAGAAAAGTTAAGAAAAGAATGTATGAAAGATAAATTTATGTTAATTATAGATCCA	360
Pf_ThzK_NCBI	361	ATAGCTGTTGGAGCAACAACCTATAGAACTAATGTTATTAAGATATAAATTTAAAATGC	420
Pf_ThzK	361	ATAGCTGTTGGAGCAACAACCTATAGAACTAATGTTATTAAGATATAAATTTAAAATGC	420
Pf_ThzK_NCBI	421	CAACCTAATGTAATAAAAAGTAAATATGCTGAAATTTATFATTTAGATAAAGGAGAATTT	480
Pf_ThzK	421	CAACCTAATGTAATAAAAAGTAAATATGCTGAAATTTATFATTTAGATAAAGGAGAATTT	480
Pf_ThzK_NCBI	481	TTGGGGAAGGGGTGTAGATAGTAATAATAACAATACTCATAATGAAACAGATGTAATTAAT	540
Pf_ThzK	481	TTGGGGAAGGGGTGTAGATAGTAATAATAACAATACTCATAATGAAACAGATGTAATTAAT	540
Pf_ThzK_NCBI	541	ACTGCCAGAAATGTTGCATTAATAATAAATTGTGCTGTAGTAGTTACATCAAAAACAGAT	600
Pf_ThzK	541	ACTGCCAGAAATGTTGCATTAATAATAAATTGTGCTGTAGTAGTTACATCAAAAACAGAT	600
Pf_ThzK_NCBI	601	TATAATGTTAGTCCATGTTCTCATTATGTAGCCAAAATTAATTGTGATTTAAAATTCGT	660
Pf_ThzK	601	TATAATGTTAGTCCATGTTCTCATTATGTAGCCAAAATTAATTGTGATTTAAAATTCGT	660
Pf_ThzK_NCBI	661	ACAAAAATTAACGGGTCAAGGTTGTTCTGTTGGTGGCCCTTGTGCAGCAGCTACTTCAGTA	720
Pf_ThzK	661	ACAAAAATTAACGGGTCAAGGTTGTTCTGTTGGTGGCCCTTGTGCAGCAGCTACTTCAGTA	720
Pf_ThzK_NCBI	721	TATCCTCAAAAACCCATTCATAGCATGTATATCTGCTACTCTTATATATAAATGGCAGCA	780
Pf_ThzK	721	TATCCTCAAAAACCCATTCATAGCATGTATATCTGCTACTCTTATATATAAATGGCAGCA	780
Pf_ThzK_NCBI	781	TTCAAAGCATATCAAAAAGAAAAGTATCCAGGTTCCCTAAGTCATAAATTATGATGAT	840
Pf_ThzK	781	TTCAAAGCATATCAAAAAGAAAAGTATCCAGGTTCCCTAAGTCATAAATTATGATGAT	840
Pf_ThzK_NCBI	841	ATTTAATTAATTCACATAATCCTCAATTTCTCAATTTCCAATTCGTAGATATTTACAAA	900
Pf_ThzK	841	ATTTAATTAATTCACATAATCCTCAATTTCTCAATTTCCAATTCGTAGATATTTACAAA	900
Pf_ThzK_NCBI	901	GCAGCATAA	909
Pf_ThzK	901	GTAGCATAA	909

**Figure 2.7.** Sequence alignments of the reference ThzK from *P. falciparum* database and the cloned gene from *P. falciparum*. The cloned *PfThzK* gene showed 99.9% identity to the reference gene, mismatch: 1 bp.

The desired insert was separated from pSmart plasmid after double digestion with *EcoRI* and *NdeI*, and it was cleaned from the gel and ligated into pET28b(+) in *E. coli* BL21 cells (Section 2.2.6). These cells were inoculated onto LA plates (containing 30 µg/ml kanamycin and 34 µg/ml chloramphenicol) and incubated at 37 °C overnight.

Seven colonies were grown and selected for plasmid extraction (Section 2.2.5), agarose gel electrophoresis contained 2 bands (Figure 2.8), one of approximate 900 bp represented *PfThzK* (909 bp) and another of about 5 kb, represented pET28b(+) vector (5,368 bp), and the insert with correct size was selected after double digestion which was used for expression experiments.



**Figure 2.8.** Agarose gel electrophoresis of the double digestion with *NdeI* and *EcoRI* restriction enzymes. Lane 1 represents the DNA marker; lane 2 represents the double digested products: *PfThzK* (909 bp), pET28b(+) (5,368 bp).

The *PfThzK* gene was amplified and identified in the present study through cloning of its genomic DNA by PCR with Phusion® Hot Start II polymerase. This was the second approach to amplify *ThzK* gene from *P. falciparum* by PCR method. In the present study, *NdeI* and *EcoRI* restriction enzymes were utilized to design shorter primers compared to previous studies (Wrenger, 2006). The Phusion polymerase employed in this study offered accurate and progressive performance. The PCR program was modified and different from the one commonly used: Higher denature temperature. This is because the

Phusion® Hot Start II polymerase combines the DNA polymerase and is reversibly bound, which inhibits the 3'-5' exonuclease activity of the polymerase, preventing degradation of the primers and DNA polymerase. Due to the high thermostability of Phusion polymerase, a temperature of 98 °C or even higher can be used. A longer extension process was employed in this study because of the complexity of *PfThzK* gene.

In conclusion, methylhydroxyethylthiazolekinase gene was successfully amplified and pure *PfThzK* gDNA was transformed into pET28(+) vectors, which were ready for protein expression. The deduced protein sequence of ORF encoding for the *P. falciparum* methylhydroxyethylthiazolekinase consists of 302 amino acids and has a molecular mass of 34 kDa. The amino acid sequence shows moderate sequence identities 39%, 35% and 33% to *Clostridium sporogenes* (accession no. ZP 02994013.1), *Spirosoma linguale* (accession no. YP003388301.1) and *Arthrobacter arilaitensis* (accession no. YP003915272.1), respectively. The *PfThzK* protein shows homology to the C-terminus and is only approximately half of the size of its fungal counterparts, whereas its bacterial homologues are of the same size (Wrenger, 2006).

## Chapter3

# Expression, purification and characterization of methylhydroxyethylthiazolekinase (*PfThzK*)

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### 3.1. Introduction

High concentration of pure protein is necessary for laboratorial analysis *in vitro*, however, the ‘traditional’ or ‘conventional’ purification methods, which extract protein from its source, can’t meet these requirements, because the products are potentially pathogenic and the yields are really low, making it more expensive.

The Gram-negative bacteria *E. coli* is the most frequently used prokaryotic expression system available and it has evolved as a standard organism for the production of enzymes for analytical and diagnostic use. The gene encoding the target protein is introduced to the cell as part of an expression vector (Neidhardt *et al.*, 1996; Hottenrott *et al.*, 1997; Banyex, 1999).

Promoters are DNA sequences which direct RNA polymerase binding and transcription initiation. *E. coli* has seven different types of promoter, and some are commonly used, such as *lac*, *T7* and *trp* (Oehler *et al.*, 1994; Hasan and Szybalski, 1995).

#### 3.1.1. *T7* RNA polymerase heterologous expression system

The *T7* polymerase system is highly processive and recognizes conserved sequences covering a region between -17 and +6 bp relative to the mRNA starting site (Ramos *et al.*,

2004). It is the strongest promoter described for microorganisms so far and it is quite efficient, leading to an accumulation of the desired protein of about 40-50% of total cell protein (Dubendorff and Studier, 1991; Savalia *et al.*, 2010). One of the most useful systems for expression of recombinant proteins in *E. coli* is the pET vector series, which is based on the *T7* phage RNA polymerase promoter (Ramos *et al.*, 2004). The expression of the recombinant protein using these plasmids is tightly regulated and, when induced, produces high levels of transcripts and recombinant proteins (Oliveria *et al.*, 2001).

However, it has several drawbacks. One problem of using the *T7* expression system may result in plasmid or expression instability due to the leaky expression (Sagawa *et al.*, 1996). If the desired recombinant protein is toxic to host cells, this leads to low or negligible expression (Miroux and Walker, 1996).

### **3.1.2. The Histidine-tags to improve heterologous expression**

A DNA sequence containing six histidine residues is frequently used in vectors for production of recombinant proteins, leading to the expression of a recombinant protein with 6xHis-tag fused to its N- or C-terminus. Several pET vectors have a 6xHis-tag which permits the purification of recombinant protein on metal charged columns (Crowe *et al.*, 1994). Expressed His-tag recombinant proteins can be purified and detected easily because the histidine residues bind to several types of immobilized metal ions, such as nickel, cobalt and copper (Hoffman and Roeder, 1991; Franken *et al.*, 2000). Nickel is the most frequently used metal ion for purification of His-tagged proteins, because nickel provides good binding efficiency. The problem of using nickel affinity chromatography,

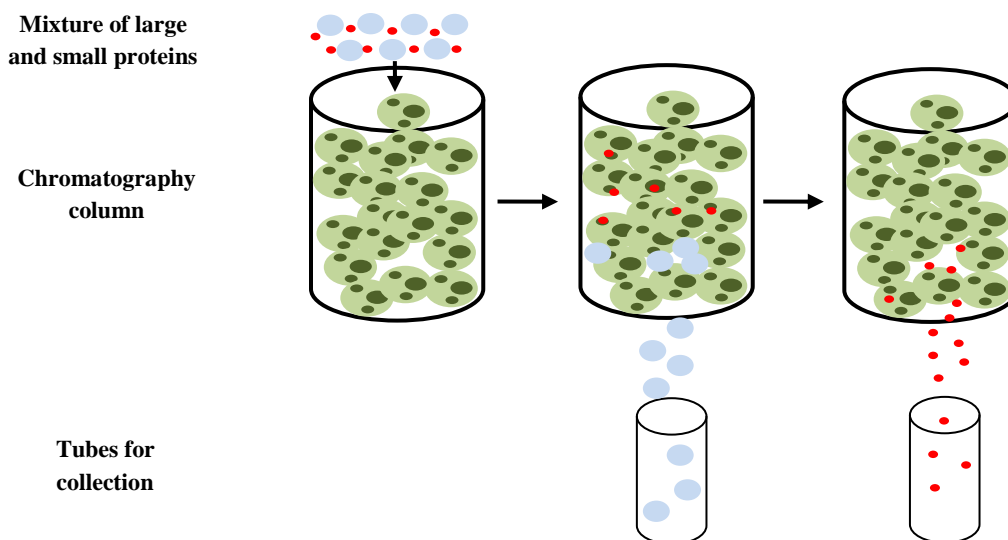
however, is that nickel also tends to bind unspecific proteins that contain any histidine clusters (Muller *et al.*, 1998).

For nickel affinity chromatography, His-tags are likely to bind to resins in near-neutral buffer conditions. Moreover, in a typical binding buffer, low-concentration imidazole helps wash out any unspecific proteins that contain histidine clusters. Elution of His-tagged protein from the resin is then carried out with a subsequent elution using a high concentration of imidazole (Schmitt *et al.*, 1993; Arnau *et al.*, 2006; Ganesana *et al.*, 2011).

### **3.1.3. Size exclusion chromatography**

Size exclusion chromatography (SEC) is a chromatographic procedure in which particles are separated based on their size. It is commonly used for separating large molecules or macromolecular complexes such as proteins and industrial polymers. Separation is achieved by the different exclusion from the pores of the packing material. The principle feature of SEC is its gentle non-adsorptive interaction with the sample, enabling high retention of biomolecular activity (Wen *et al.*, 1996; De Nobili and Chen, 1999; Al-Bokari *et al.*, 2002). A protein mixture is poured into a column, which contains a suspension of tiny beads with different-sized macroscopic pores (Figure 3.1). As the proteins pass through the column, the larger proteins can only fit into fewer pores and thus have a more direct and faster path through the beads. In contrast, the smaller proteins can fit through more pores and take a meandering and longer path as they get caught in various holes and thus, take a longer time to flow through the column. As time passes, the eluates containing the larger proteins pass through quickly, while smaller proteins will

elute later. For the separation of biomolecules in aqueous or aqueous/organic mobile phases, SEC is referred to as gel filtration chromatography. The main application of gel filtration chromatography is the fractionation of proteins and other water-soluble polymers (Kieft, 1991; Bollag, 1995).



**Figure 3.1** Size exclusion chromatography columns contain beads with various pores. The larger proteins, which fit in fewer pores, take a more direct path through the column and elute first. The smaller proteins are slower to elute as they meander in and out of pores.

## 3.2. Materials and methods

### 3.2.1. Reagents and chemicals

All reagents used in purification and characterization of the *PfThzK* in this chapter are detailed in Appendix 2.

### 3.2.2. Plasmids and culture conditions

The *PfThzK*-pET28(+) constructs from the previous study (Section 2.3.2) were stored at -20 °C. LA plates and LB media (Appendix 2) with two antibiotics were used for colony selection (30 µg/ml kanamycin and 34 µg/ml chloramphenicol in ethanol). Auto-induction media (Table 3.1) were used to over-express *PfThzK* proteins.

**Table 3.1.** Auto-induction components.

Auto-induction media	Component	Final concentration	Sterilization
20×NPS	0.5 M (NH <sub>4</sub> ) <sub>2</sub> SO <sub>4</sub> 1 M KH <sub>2</sub> PO <sub>4</sub> 1 M Na <sub>2</sub> HPO <sub>4</sub>	50 ml/ L	Filter sterilize
50×5052	250 g/L Glycerol 25 g/L Glucose 100 g/L α-Lactose	20 ml/L	Filter sterilize
MgSO <sub>4</sub>	1M MgSO <sub>4</sub>	2 ml/L	Filter sterilize
ZY	10 g/L Tryptone 5 g/L yeast extract	928 ml	Autoclave
Antibiotics	30 µg/ml kanamycin 34 µg/ml chloramphenicol	1 ml/L	

### 3.2.3. Expression of *PfThzK* protein

The *PfThzK*-pET28(+) constructs were transformed into *E. coli* BL21 competent cells and plated out on LA with 30 µg/ml kanamycin and 34 µg/ml chloramphenicol. Positive colonies were selected and inoculated to LB broth with the same antibiotic pressure, and incubated in a rotary shaker (160 rpm; 37 °C; 14 h). The culture was inoculated into the auto-induction media (10 ml culture/1 L auto-induction media) and dispensed into ten 500 ml sterile flasks (100 ml per flask), incubated in a rotary shaker (160 rpm; 20 °C; 36 h). One flask was randomly chosen and used for induction study: 1 ml of culture from this flask was taken every 2 hours for 36 h, washed with Tris-HCl buffer (50 mM; pH

7.0), pelleted by centrifugation ( $1,500 \times g$ ; 5 min), frozen ( $-80\text{ }^{\circ}\text{C}$ ) and retained as “Induction sample1-18 (IS1-IS18)”.

The cultures in other flasks were centrifuged ( $5,000 \times g$ ; 20 min;  $4\text{ }^{\circ}\text{C}$ ) in an Avanti® J-E centrifuge and a JA-14 rotor (Beckman Coulter) after 36 h incubation period. The cell pellet was resuspended in Tris-HCl buffer (50 ml; 50 mM; pH 7.0), centrifuged at  $5,000 \times g$ ; 20 min;  $4\text{ }^{\circ}\text{C}$ ), and the cell pellet weighed, then resuspended in the same buffer (20 ml buffer/1 g cells). The cells suspensions were lysed using lysozyme (1 mg lysozyme/1 ml suspension), incubated in a rotary shaker (160 rpm;  $37\text{ }^{\circ}\text{C}$ ; 1 h), and finally stored at  $-80\text{ }^{\circ}\text{C}$ .

#### **3.2.4. Purification of *PfThzK* protein**

The frozen cell lysate was thawed at  $4\text{ }^{\circ}\text{C}$  overnight, the unbroken cells and debris were removed by centrifugation ( $2,700 \times g$ ; 30 min;  $4\text{ }^{\circ}\text{C}$ ), an aliquot of supernatant (1.0 ml) was retained for “total protein (T)”, and the remaining supernatant clarified by ultra-centrifugation ( $28,000 \times g$ ,  $4^{\circ}\text{C}$ , 90 min) with an Optima™ L-90K centrifuge (Beckman Coulter). An aliquot of this supernatant (1.0 ml) was saved as “clarified protein (C)”.

The recombinant protein *PfThzK* was then purified by nickel affinity and size exclusion chromatography. The “clarified protein” (150 ml) mixed with 50 ml binding buffer (50 mM NaCl, 50 mM Tris-HCl, pH 7.5) was loaded onto a His-trap FF column (5 ml, Amersham Biosciences) at 5 ml/min, which was pre-washed by binding buffer, and the bound protein eluted with elution buffer (0.5 M NaCl, 0.5 M imidazole, 20 mM Tris-HCl, pH 7.5) in a linear 0-0.5 M imidazole gradient. An aliquot of the active fractions (1.0 ml) was retained for “His-trap fractions (H)”, and the remaining active fractions pooled and

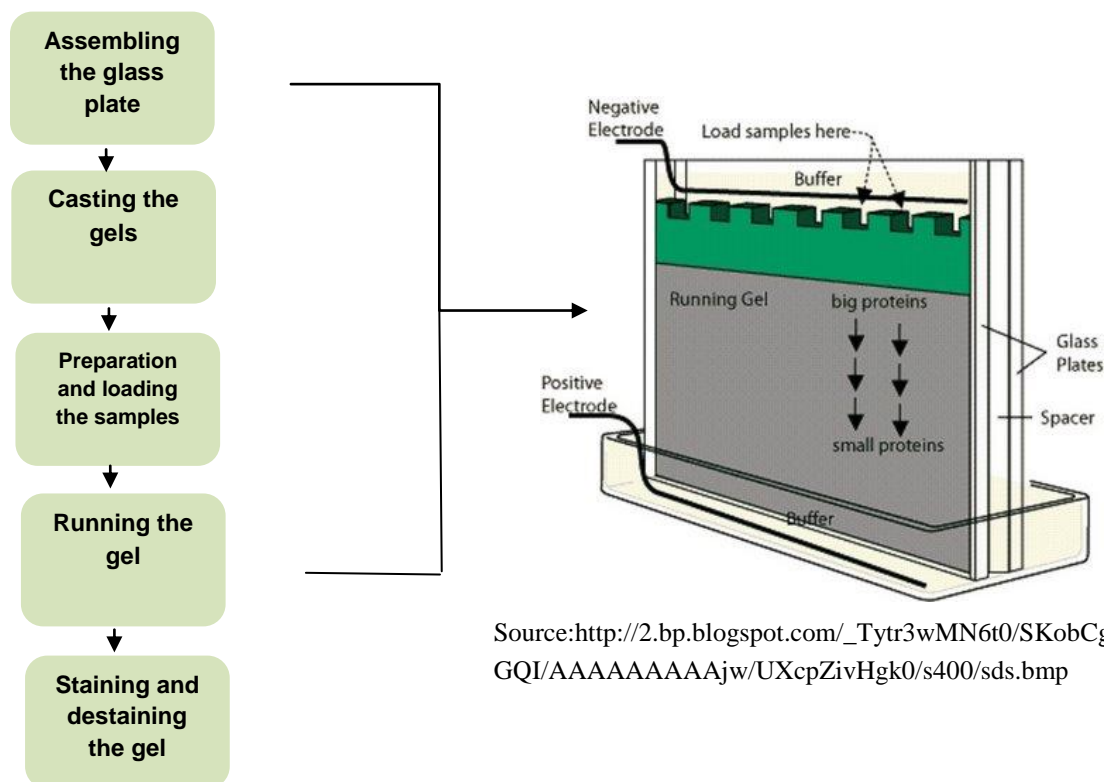
concentrated to 2 ml by Vivaspin2 centrifugal concentrators MWCO 10,000 (Sartorius Stedim Biotech, Germany). The concentrated sample was loaded onto Sephacryl S100HR gel filtration column, equilibrated and eluted using gel filtration buffer (50 mM NaCl, 50 mM Tris-HCl, pH 7.5) at 1 ml/min. An aliquot of the active fractions (1.0 ml) was retained for “gel filtration fractions (G)”, and the remainder pooled and dialyzed (50 mM Tris-HCl, pH 7.0, 16 h, 4 °C). The dialyzed protein (D) was then ready for subsequent analysis.

### **3.2.5. Characterization of recombinant *Pf*ThzK protein**

#### **3.2.5.1. SDS-PAGE analysis**

Sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) is the most widely used method for analyzing protein mixtures qualitatively and also for evaluation of purity of protein during protein purification steps. The protein sample is boiled in loading buffer containing  $\beta$ -mercaptoethanol, which disrupts the secondary, tertiary and quaternary structure of the protein by destroying the disulphide bridges. This leads to the opening up of the protein into a linear rod-shaped structure coating with a series of negatively charged SDS molecules of constant charge density per unit mass, thus facilitating electrophoretic mobility (Wilson and Walker, 1994).

Polyacrylamide gels were prepared by the free radical polymerization of acrylamide and the cross linking agent tetramethylethylenediamine (TEMED) bisacrylamide (Figure 3.2), the procedure is detailed in Appendix 5.



**Figure 3.2.** The flow chat of SDS-PAGE and the setting of electrophoresis gel.

The proteins present in each fraction from the previous step were determined by SDS-PAGE electrophoresis using 10% resolving gel and 4% stacking gel (Laemmli, 1970). PageRuler™ Prestained Protein Ladder (Fermentas) was used as molecular weight markers and an estimation of the molecular weights of protein bands visualized on the gels. Electrophoresis was carried out using the Mini-PROTEAN3 Electrophoresis System (Bio-Rad) with SDS running buffer (Appendix 2) at 100 V until the desired separation had been achieved. Bands of protein were visualized on the SDS-PAGE gels by staining with Coomassie Blue (Fairbanks *et al.*, 1971). Three staining solutions, each containing 10% acetic acid and progressively lower concentrations of Coomassie Brilliant Blue R-

250 were used, and the staining and destaining protocol is shown in Appendix 6. All solutions used for SDS-PAGE analysis of proteins are listed in Appendix 2.

### 3.2.5.2. Protein concentration

Protein concentrations were evaluated using the Pierce® BCA Protein Assay Kit (Thermo SCIENTIFIC), which is based on bicinchoninic acid (BCA) for the colorimetric detection and quantification of total protein. This method is highly sensitive to the colorimetric detection of the cuprous cation. The purple-coloured reaction product of the assay is water-soluble and exhibits a strong absorbance at 562 nm that is linear with an increased protein concentration over a broad working range (20-2,000 µg/ml). Protein concentrations in this study were determined with reference to standards of bovine serum albumin (Appendix 7). A series of dilutions of known concentration was prepared, and 50 µl of each sample was added to 1 ml of the working reagent, vortexed, and then incubated (60 °C; 30 min). The absorbance was read at 562 nm with a Spectroquant® Pharo300 spectrophotometer (Merck Pty Ltd).

### 3.2.5.3. *Pf*ThzK activity determination

Purified *Pf*ThzK activities were determined by an improved molybdate method, which is based on the colorimetric determination of inorganic phosphate (Fiske and Subbarow, 1925). In the enzyme assay reaction, *Pf*ThzK converts 5-(2-hydroxyethyl)-4-methylthiazole to 4-methyl-5-(2-phosphoethyl)-thiazole (THZ-P) and inorganic phosphate “Pi”, which reacts with ammonium molybdate to produce a coloured complex (Chifflet *et al.*, 1988). This activity assay should be carried out in an acidic solution containing excess ascorbic acid to prevent the complex from slowly oxidizing. The “Pi”

concentrations in the samples were determined by extrapolation from the inorganic phosphate standard curve, which was prepared by serial dilutions of a standard phosphate solution. The enzyme assay was in a standard condition with a total volume of 97  $\mu$ l consisting of Tris-HCl buffer (29 mM, pH 7.5),  $MgSO_4$  (6 mM), ATP (3 mM) and THZ (3 mM). The reaction mixture was incubated at a certain temperature for 10 min and stopped by heating (100  $^{\circ}C$ , 2 min).

Sample (80  $\mu$ l) was placed in a 96-well microtitre plate, followed by 160  $\mu$ l of Reagent C [0.65%  $(NH_4)_2MoO_4$ ; 9% Ascorbic acid]. The mixture was allowed to stand (10 min; room temperature) for colour development, and the absorbance of each solution read at 700 nm by microtitre plate reader (Biotek Epoch). All the reagents used and the standard curve are shown in Appendix 8.

#### 3.2.5.4. The temperature profile of *PfThzK*

The optimum temperature for the purified *PfThzK* was determined under the same enzyme assay conditions (Section 3.2.5.3). The purified *PfThzK* was incubated at varying temperatures ranging from 10-80  $^{\circ}C$ , and then 6  $\mu$ l of each sample was added to enzyme assay reactions.

#### 3.2.5.5. The pH profile of *PfThzK*

The optimum pH condition for purified *PfThzK* was determined under the same enzyme assay conditions (Section 3.2.5.3). The purified *PfThzK* was incubated with a 0.1 M buffer cocktail (0.1 M sodium acetate pH 3.5-5, MES pH 5.5-6.5 and Tris-HCl pH 7-9), and then 6  $\mu$ l of each sample was added to enzyme assay reactions.

### 3.2.5.6. The thermal stability of purified *PfThzK*

The optimal temperature and pH were used to determine the thermal stability of purified *PfThzK*. Pre-activated *PfThzK* activity at time zero was considered to be 100% relative activity, and the activity was measured at 30 min interval for 5 h. A half-life ( $t_{1/2}$ ), which is the time required for the enzyme to lose 50% of its initial activity, was also measured.

### 3.2.5.7. Kinetic study

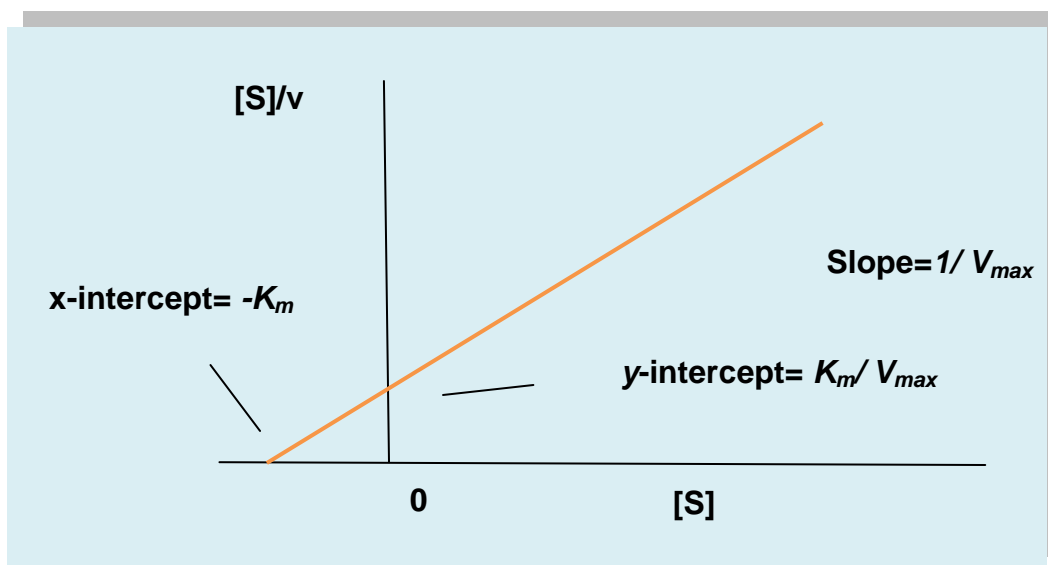
For analysis of the substrate THZ specificity of *PfThzK*, the standard assay was executed with varying concentrations of THZ between 0 and 0.3 mM. The reaction products were treated as per the standard and measurement was carried out at 700 nm (Appendix 7) as described in section 3.2.5.3.

Enzyme-catalyzed reactions are characterized by the formation of a complex between the enzyme and its substrate (the ES complex). The Michaelis-Menten equation is the rate equation for a one-substrate enzyme catalyzed reaction. It quantitatively relates the initial rate, the maximum rate, and the initial substrate concentration to the Michaelis constant  $K_m$ .

$$v_0 = \frac{V_{\max}[S]}{K_m + [S]}$$

Hanes-Woolf Plot is one of the linear plots of the Michaelis-Menten Equation:

$$\frac{[S]}{v} = \frac{1}{V_{\max}}[S] + \frac{K_m}{V_{\max}}$$



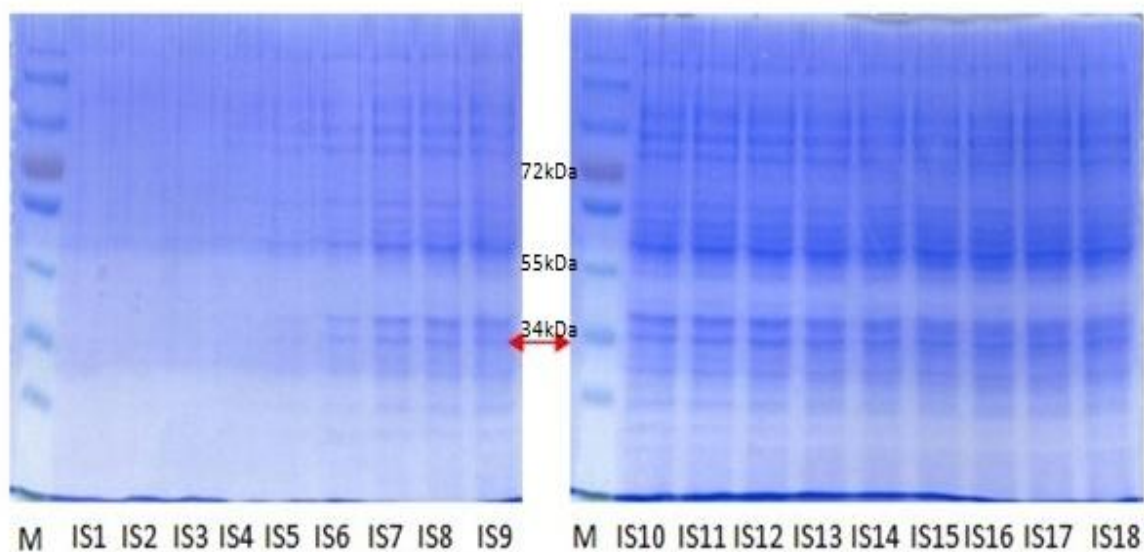
**Figure 3.3.** Hanes-Woolf Plot.

Where  $V_{max}$  is the activity of the enzyme approached at saturating concentrations of substrate,  $K_m$  is the concentration of substrate required to produce a velocity that 50% of  $V_{max}$  (Gilbert, 2000).

### 3.3. Results and discussions

#### 3.3.1. Expression of recombinant *PfThzK*

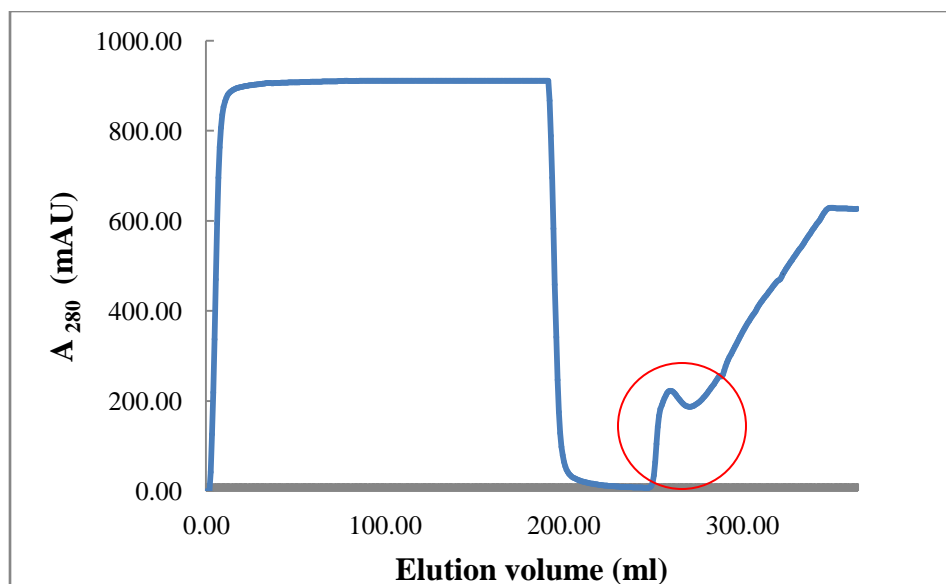
SDS-PAGE was carried out with each sample (Figure 3.4). The bands represent *PfThzK* (around 34 kDa) were visible from sample IS5-IS18, indicating that after 10-hour induction period, certain amount of proteins was expressed by the cells. Low concentration of protein was noticed after 10-hour induction (IS5) while the most protein was expressed after 32 h induction (IS16).



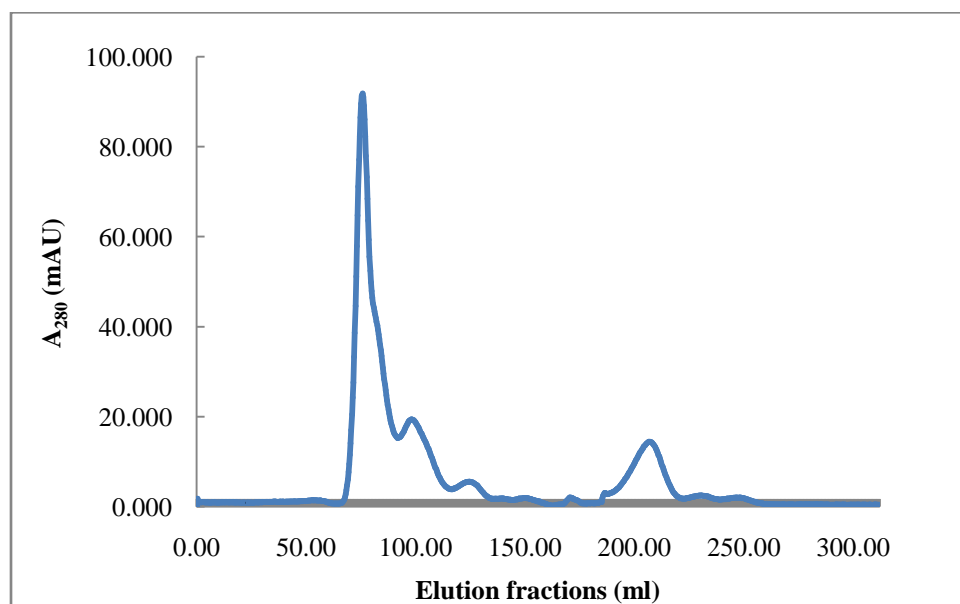
**Figure 3.4.** SDS-PAGE analysis of the auto-induction study. (M): marker, (IS1-IS18): samples of auto-induction culture from time 2 h to time 36 h with 2 h intervals.

### 3.3.2. Purification of recombinant *PfThzK*

The expressed protein was applied to a Ni-affinity column and all of the collected fractions (Figure 3.5) were analyzed by SDS-PAGE electrophoresis to detect which fractions contained *PfThzK*. The fractions of interest were then concentrated and loaded onto a gel filtration column, and eluted by 50 mM Tris-HCl with 50 mM NaCl, the elution profile is shown in Figure 3.6. One main protein peak was observed between elution volumes 60-100 ml, indicating that *PfThzK* was monomer.



**Figure 3.5.** Elution profile obtained from nickel affinity resin. Flow rate: 5 ml/min, elution fraction size: 5ml. The bound proteins shown in red were the fractions collected.

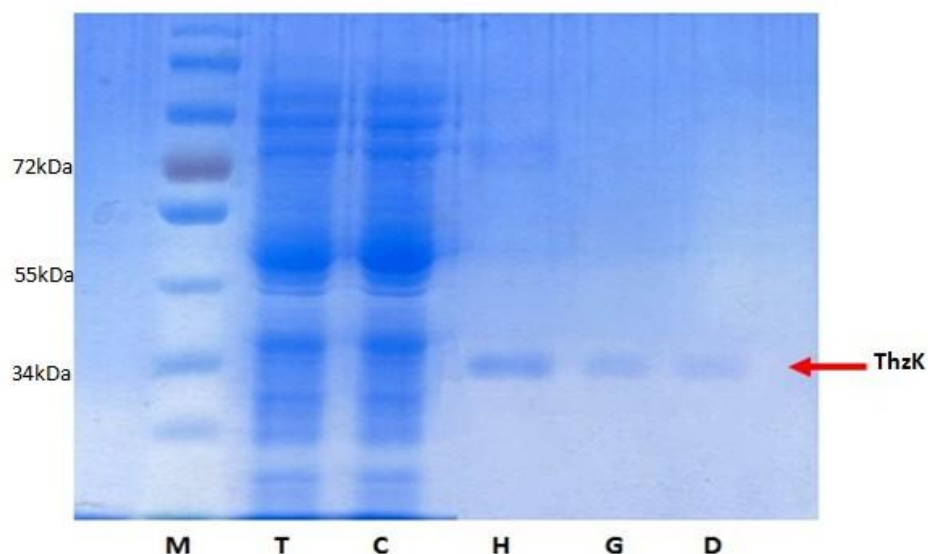


**Figure 3.6.** Protein elution profile obtained from size exclusion chromatography (Sephacryl S100HR gel filtration column).

After each purification step, SDS-PAGE was employed to determine the molecular weight of the protein(s) as shown in Figure 3.7. Several bands were observed from the first two samples, reflecting various soluble proteins in the “Total protein” sample. After nickel-affinity chromatography, from the third band, only a few intensive bands were observed, indicating that the majority of those soluble proteins were unbound proteins, and had been washed out through His-trap column. After size exclusion chromatography, only one intensive band of 34 kDa was observed, corresponding to *PfThzK*. Dialysis, as the final purification step, removed some of the contaminating bands and also the salts from gel filtration buffer. Samples from each purification step were collected:

- The supernatant of post-centrifuged frozen cell lysate (Total protein “T”)
- The supernatant of post-ultracentrifugation (Clarified protein “C”)
- His-trap nickel affinity chromatography (“H”)
- Gel filtration chromatography (“G”)
- Dialysis (“D”)

A summary of the purification procedure after centrifugation, ultracentrifugation, His-trap nickel affinity chromatography, gel filtration chromatography and dialysis is shown in Table 3.2. After His-trap Ni-affinity, the amount of total protein decreased from 166.44 mg to 4.89 mg, indicating that most of the expressed proteins were unbound, and washed out, which can be also observed from SDS-PAGE analysis (Figure 3.7). It also resulted in the loss of total activity from 21.30  $\mu\text{mol}/\text{min}/\text{ml}$  of the starting material to 0.22  $\mu\text{mol}/\text{min}/\text{ml}$  after final dialysis. The specific activity, however, increased accordingly at every step.



**Figure 3.7.** 10% SDS-PAGE analysis of each purification step. (M): marker, (T), (C), (H), (G) and (D) indicates each step during purification. Total protein “T”: The supernatant of post-centrifuged frozen cell lysate; Clarified protein “C”: The supernatant of post-ultracentrifugation; “H”: His-trap nickel affinity chromatography; “G”: Gel filtration chromatography; “D”: Dialysis.

**Table 3.2.** Purification table of *PfThzK*. The enzyme activity was calculated in U, which means the amount of the enzyme catalyzing the conversion of 1  $\mu\text{mol}$  of substrate per minute ( $\text{U} = \mu\text{mol}/\text{min}/\text{ml}$ ).

Purification step	Volume (ml)	Total protein (mg)	Total activity (U)	Specific activity (U/mg)	Purification fold	Yield (%)
Post centrifuge	170	174.62	21.30	0.12	1	100
Post ultracentrifuge	167	166.44	19.46	0.11	0.92	91.4
His-trap	25	4.89	0.62	0.13	1.04	2.9
Gel filtration	25	0.95	0.26	0.27	2.26	1.23
Dialysis	24.8	0.80	0.22	0.28	2.33	1.03

### 3.3.3. Characterization of recombinant *PfThzK*

#### 3.3.3.1. SDS-PAGE analysis and protein concentration

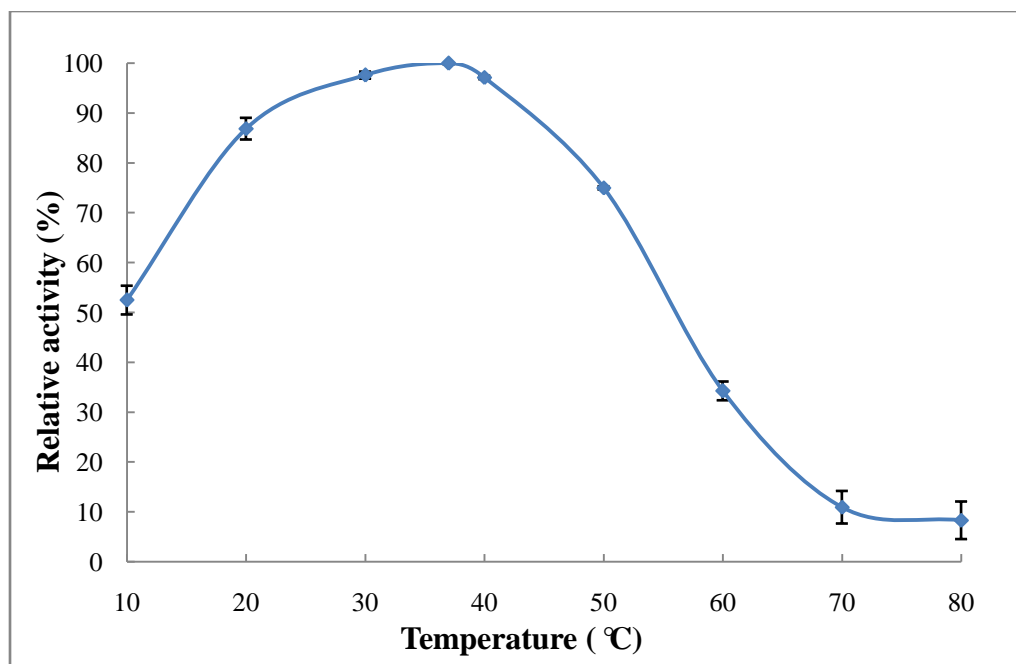
SDS-PAGE analysis and protein concentration determination were carried out after each purification step and after dialysis, only one single band of 34 kDa was observed (Figure 3.7).

The final concentration of purified *PfThzK* was 32.26 µg/ml. It was also noticed that after dialysis, protein concentration was quite low for characterization, thus pure *PfThzK* was concentrated by Vivaspin2 centrifugal concentrators MWCO 10,000 (Sartorius Stedim Biotech, Germany) for subsequent analysis.

#### 3.3.3.2. Temperature optimum profile

The activities were determined over a range of temperatures, from 10 °C to 80 °C, and the temperature curve follows a typical bell shape (Figure 3.8). The rate of enzymatic reaction increases as the temperature increases from 10 °C to 30 °C with a maximum *PfThzK* activity seen at 37 °C.

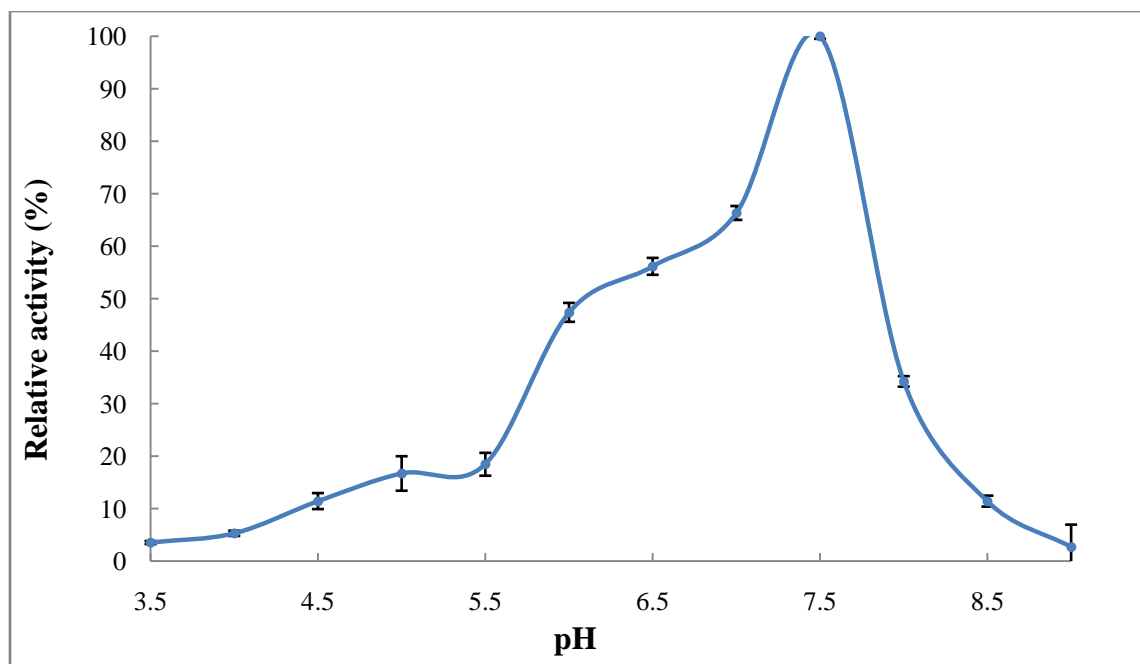
Previous studies on ThzK characterized from *Bacillus subtilis* and *E. coli* had also found an optimal temperature of 35-37 °C range (Zhang *et al.*, 1997; Begley *et al.*, 1999). The downside to this reaction, was noted at 50 °C and higher temperatures, because protein structures could be disrupted, leading to inactivation and denaturation (Hohmann and Meacock, 1998). At 60 °C and higher temperatures, the bigger error bars represent the larger variability of data, and also reflect that *PfThzK* were denatured at those temperatures and the measurements were not really accurate according to the low activities.



**Figure 3.8.** Temperature profile of purified *PfThzK* enzyme. Hundred percent activity (0.027 U/ml) was observed at 37 °C.

### 3.3.3.3. pH optimum profile

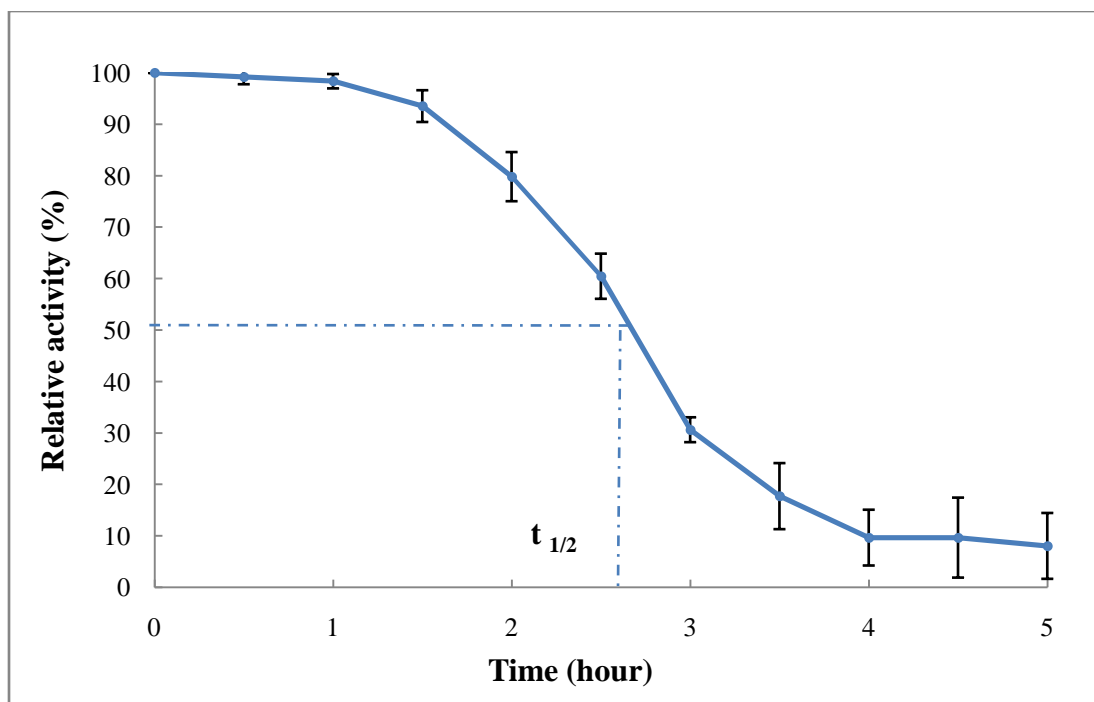
The rate of enzyme activity is commonly influenced by the structure of enzyme. The change in pH results in breaking of the ionic bonds which hold the tertiary structure of the enzyme together and the enzyme loses its functional shape, particularly the shape of the active site. Most enzymes normally present a strong dependence of activity on the pH conditions, so it is important to optimize the pH of purified *PfThzK* (Dixon, 1952; Wikinson, 1960; Dyson and Noltmann, 1967). The purified *PfThzK* in this study had an optimal pH at 7.5 (Figure 3.9). Previous studies on ThzK from *B. subtilis* had an optimal pH to be pH 7-7.5 (Zhang *et al.*, 1997).



**Figure 3.9.** pH profile of the purified *PfThzK* enzyme. Hundred percent activity (0.028 U/ml) was observed at pH 7.5.

#### 3.3.3.4. Thermal stability of purified *PfThzK*

The purified *PfThzK* was incubated with thiazole at the optimum conditions (37 °C; pH 7.5) and the enzyme activities were determined at 30 min intervals for 5 hours. The slight activity loss was observed during the first 1 hour, and then enzyme activity decreased rapidly with the increased incubation time (Figure 3.10). The evident activity loss from 0.027 U/ml to 0.0051 U/ml during 1.5 h-3.5 h incubation periods, and after 3.5 hour incubation, 80% of the activity had been lost, thereafter slight decrease was observed. The purified *PfThzK* in this study had a half life of 2.66 hours ( $t_{1/2}=2.66$ ).



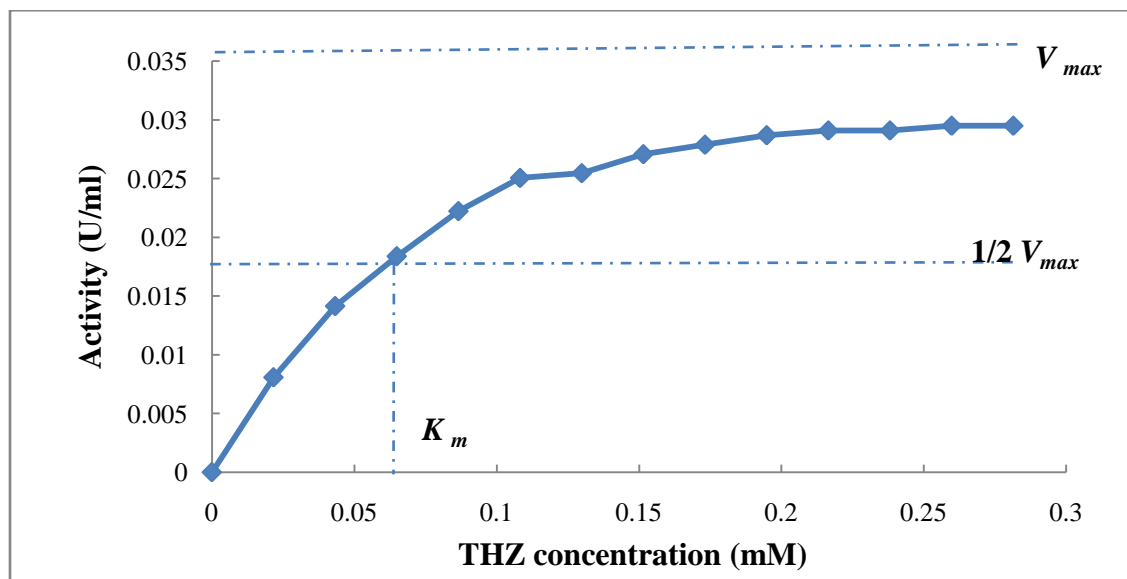
**Figure 3.10.** Thermal stability of purified *PfThzK*. The 100% activity was 0.029 U/ml, the initial enzyme activity at time zero.

### 3.3.3.5. Kinetic study

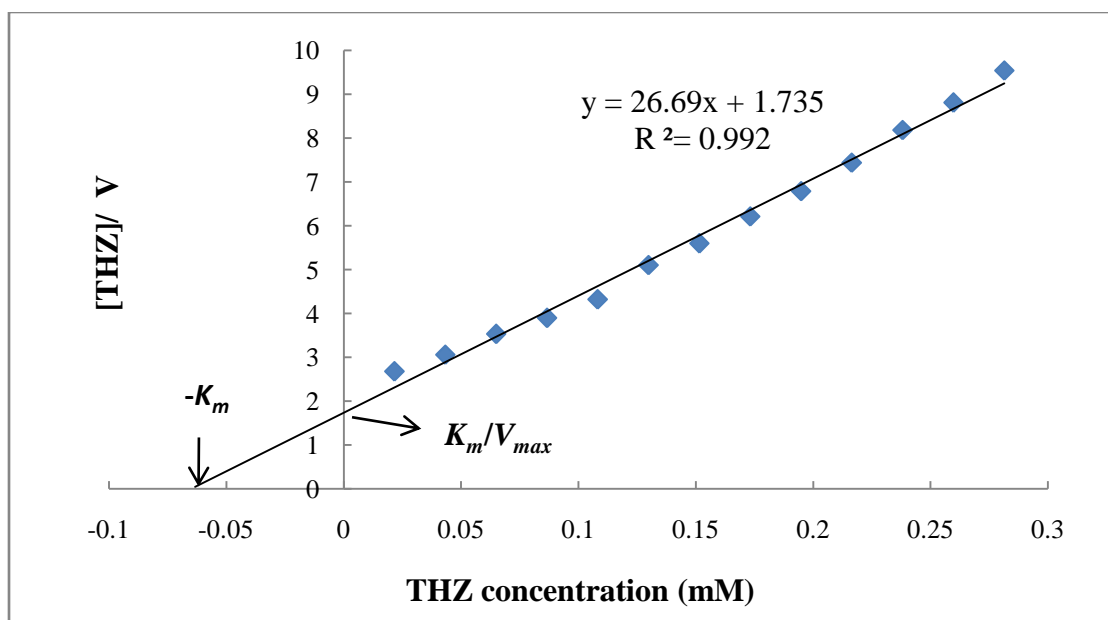
The effect of substrate concentration on the purified *PfThzK* was evaluated by measuring the *PfThzK* activity with a range of THZ concentration of (0-0.3 mM). The activities curve followed Michaelis-Menten, the *PfThzK* activity increased hyperbolically with the increased THZ concentration from 0-0.06 mM, and the activity remained relatively constant according to the substrate saturation (Figure 3.11).

The initial velocity of the reaction at different substrate concentrations was measured, and kinetic parameters  $K_m$  and  $V_{max}$  values were calculated by using Hanes–Woof ( $[S]/v$ - $[S]$  plot) analysis (Figure 3.12). The Michaelis constant ( $K_m$ ) value of *PfThzK* was found to be 0.065 mM while the specific activity was 295.04 nmol/mg which is a little higher

than previous study of  $249 \pm 14$  nmol/mg (Wrenger *et al.*, 2006).  $V_{max}$  calculated from the inverse of the slope (Figure 3.12) is  $0.037 \mu\text{mol}/\text{min}/\text{ml}$ .



**Figure 3.11.** Michaelis-Menten plot of purified *PfThzK* enzyme activity versus THZ concentration.



**Figure 3.12.** Hanes-Woolf plot of purified *PfThzK* enzyme activity versus THZ concentration.

### 3.4 Conclusions

To summarize, the ORF encoding methylhydroxyethylthiazolekinase from *P. falciparum* (*PfThzK*) was cloned into the expression vector pET28b(+) and recombinantly expressed in *E. coli* BL21 (DE3) in auto-induction medium with a yield of 0.8 mg/L of bacteria culture. The expressed protein was purified by nickel affinity chromatography and the purity of the recombinant enzyme was assessed by SDS-PAGE analysis. *PfThzK* eluted as a single peak corresponding to a molecular mass of 34 kDa, suggesting a monomeric structure. The optimal temperature and pH were 37 °C and 7.5 respectively, and the specific activity was found to be 295.04 nmol/mg, with a  $k_{cat}$  value of 0.149 s<sup>-1</sup>. The kinetic parameters of the *PfThzK* were also analyzed with a  $V_{max}$  value of 0.037 μmol/min/ml and  $K_m$  value of 0.065 mM, which was 2-fold higher than the counterpart from *B. subtilis* (Zhang *et al.*, 1997). Furthermore, the specific activity of *PfThzK* is a little higher than that in previous study (Wrenger, 2006), but 10-fold higher comparing to *B. subtilis* value (Campobasso *et al.*, 2000). In addition, the catalytic efficiency was calculated to be  $2.3 \times 10^3 \text{ M}^{-1}\text{s}^{-1}$ , which is slightly higher than that from a previous study of  $2 \times 10^3 \text{ M}^{-1}\text{s}^{-1}$  (Wrenger, 2006).

## Chapter 4

# Synthesis of Ag Nanoparticles and Interaction with methylhydroxyethylthiazolekinase

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### 4.1. Introduction

Nanotechnology and nanoparticles have been increasingly recognized for their potential applications in aerospace engineering, nano-electronics, environmental remediation, medical healthcare and consumer products in the past decade (Gerber and Lang, 2006; Sing *et al.*, 2009). It is estimated that of all the metal nanoparticles in consumer products, silver nanoparticles (Ag NPs) have the highest degree of applications of commercialization (Maynard and Michelson, 2007). Various Ag NPs applications have been reported recently, ranging from disinfection medical devices and home appliances to water treatment (Vigneshwaran *et al.*, 2007; Tolaymat *et al.*, 2010). Moreover, the unique plasmon–resonance optical scattering properties of Ag NPs allow them to be used in bio-sensing and imaging applications (Dubas and Pimpan, 2008; Schrand *et al.*, 2008). Furthermore, Ag NPs have also shown the important potential applications in the treatment of disease (Moghimi *et al.*, 2001; Panyam and Labhasetwar, 2003), for example, Ag NPs have been shown to interact with the HIV-1 virus and inhibit the virus to bind host cells *in vitro* (Elechiguerra *et al.*, 2005).

The metallic nanoparticles have shown significant mechanical, electronic, magnetic, optical and catalytic properties, which are highly influenced by their size, shape and

composition (Buzea *et al.*, 2007; Das and Marsili, 2011; Burda *et al.*, 2005). Therefore, the specific synthetic route should be improved upon according to the properties of metal nanoparticles (Perez-Juste *et al.*, 2005; Cuenya, 2010; Chen and Liu, 2011). Numerous approaches to synthesize Ag NPs have been published recently, such as microwave treatment (Salkar *et al.*, 1999); phase transfer processes (Li *et al.*, 2002); laser ablation (Dolgaev *et al.*, 2002); photochemical synthesis (Mallick *et al.*, 2004); micro-emulsion (Husel *et al.*, 2004) and  $\gamma$ -irradiation (Shin *et al.*, 2004). Chemical synthetic routes (Kheybari *et al.*, 2010; Sadeghi *et al.*, 2010; Prabhu *et al.*, 2010; Khan *et al.*, 2011; Hussain *et al.*, 2011; Dawyet *et al.*, 2012) and biological routes (Shahverdi *et al.*, 2007; Masurkar *et al.*, 2011; Chaudhari *et al.*, 2012; Chan and Mashitah, 2012) for Ag NPs have been extensively used to improve the methods with the latter having been designed to be more environmental and eco-friendly. The chemical reduction methods, however, involve the synthesis of Ag NPs with well-controlled size in which silver ions are reduced by reductants and stabilizer or protective agents to prevent these NPs from aggregation (van Dong *et al.*, 2012).

#### **4.1.1. Characterization of nanoparticles**

Nanoparticles must be characterized to understand their unique properties, such as size, shape, surface charge, and adsorption, in terms of application of these nanoparticles (Rivera-Gil *et al.*, 2012). A number of methods are currently used to characterize nanoparticles, and the most commonly used are introduced as followed.

#### 4.1.1.1. Ultraviolet-visible spectroscopy

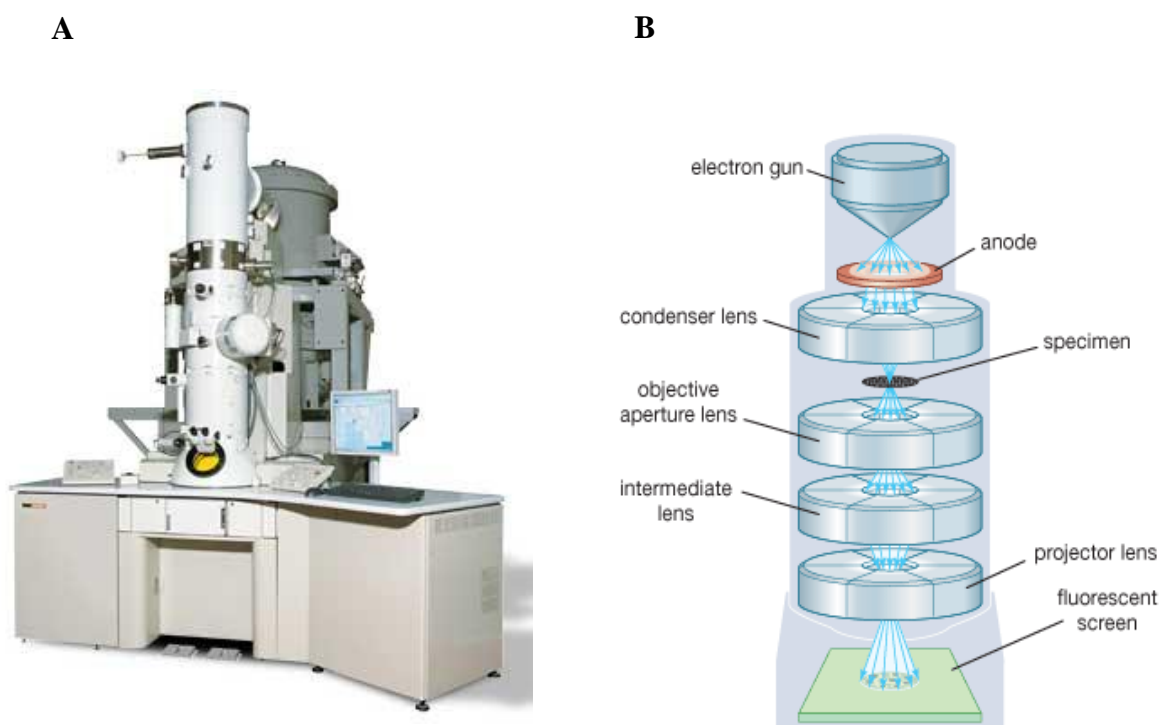
Ultraviolet and visible spectrometers (Uv-vis spectrometers) have been generally employed in the laboratory for many years and have become the most important analytical instrument in the modern day research (Milone, 2012). For a liquid sample, a standard spectroscopy measures direct transmittance as a percentage, which represents the percentage of the incident beam of light transmitted by the sample. The value is then used to calculate absorbance, which is widely used to measure concentration in liquid solutions (Smith, 2011; Tripathi *et al.*, 2012). Gold and silver nanoparticles have been extensively characterized by this technique due to their unique plasmon nature and optical properties, such as concentration and aggregation state (Chandra *et al.*, 2010; Cheng *et al.*, 2011; Prathna *et al.*, 2011; Lombardi *et al.*, 2012).

#### 4.1.1.2. Transmission electron microscopy

Nanoparticles always present different shapes and sizes, which can be usually detected by transmission electron microscopy (TEM) (Figure 4.1). TEM is a microscopy technique, which transmit a beam of electrons through an ultra-thin specimen, and interact with the specimen (Kruse, 2009; Gahlaut, 2012). The denser parts of specimen absorb more electrons, and make them look darker on the resulting image (Briggman and Bock, 2012; Staniewicz *et al.*, 2012). The remarkable advantage of TEM is that they give images with high resolutions. The drawback, however, is that they can be used only on thin specimens, artefacts such as folds, bubbles, can be found on the image (Findlay *et al.*, 2009; Ong *et al.*, 2011; Akhtar, 2012; Fultz and Howe, 2012). Furthermore, the slicing and staining process is complex and expensive (Dudkiewicz *et al.*, 2011).

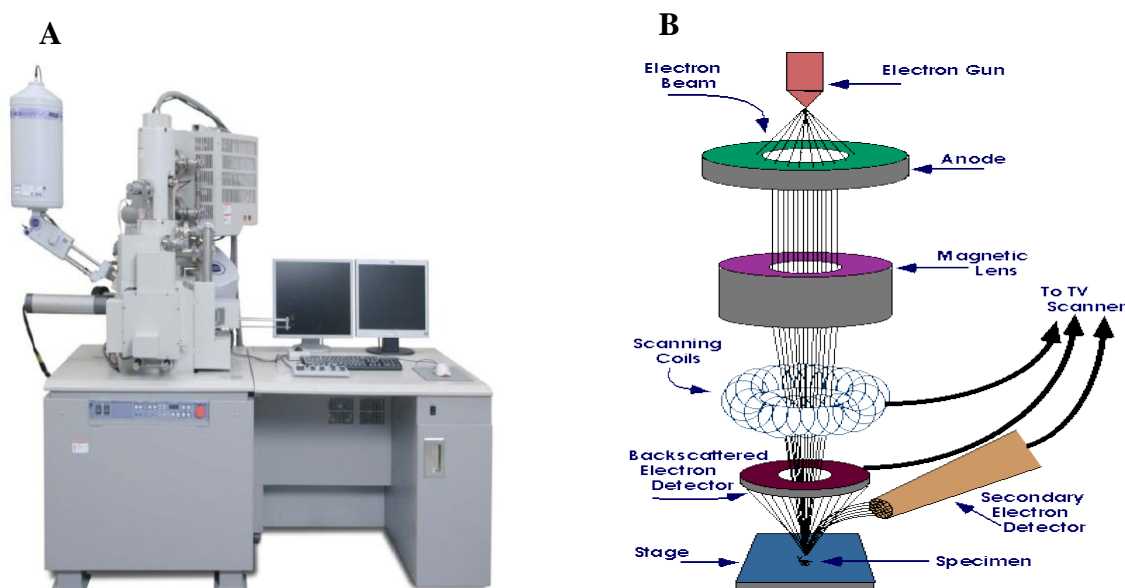
### 4.1.1.3. Scanning electron microscopy

The scanning electron microscopy (SEM) is an electron microscope (Figure 4.2) which produces an image of a sample by scanning it with a focused beam of electrons, and the electrons interact with sample electrons, producing various signals which can be detected as the information of the sample surface topography and composition (Ayache *et al.*, 2010; Vermeij *et al.*, 2012; Maco *et al.*, 2013). The specimens can be observed in high vacuum, low vacuum and the environmental SEM specimens can be observed in wet conditions (Gandolfi *et al.*, 2010).



**Figure 4.1.** Transmission electron microscope (TEM). A) A conventional TEM instrument (JEM-2100F, JEOL); B) Schematic representation of the TEM. (JEOL global solutions provider for advanced technology; A pocket merlin, 2008).

For a standard SEM, an electron is thermionically emitted from an electron gun which is fitted with a tungsten or lathan hexaboride cathode filament. The tungsten filament is the most commonly used because of its higher melting temperature (Li *et al.*, 2012). The electron beam generally has an energy ranging from 0.2 keV to 50 keV, which is much lower than TEM with voltage of 300 keV. It is focused by two condenser lenses to a spot about 0.4 nm to 5 nm in diameter (Guan, 2010; Dellby, 2012; Zhou, 2013). The  $1^\circ$  electrons lose energy by repeated random scattering and absorption within the specimen, which extend from less than 0.1-5  $\mu\text{m}$  into the surface. The energy exchange between the electron beam and the sample leads to the reflection of high-energy electrons by elastic scattering, emission of  $2^\circ$  electrons can be picked up by specialized detectors depending on the type of different instrumentations. SEM is a valuable tool to determine the purity of nanoparticles, and also quite important to determine the level of dispersion and uniformity of metal nanoparticles.



**Figure 4.2.** Scanning electron microscope (SEM). A) A conventional SEM instrument (Hitachi SU6600, Direct Industry); B) Schematic representation of the SEM. (Direct Industry-The Virtual Industrial Exhibition; Schweitzer, Radiological and Environmental Management, 2013).

### 4.1.2. The objectives of this chapter

The objectives of this chapter are:

- i. Synthesis of Ag NPs by both sodium borohydride and tannic acid.
- ii. Characterization of Ag NPs by UV-vis spectrophotometer and transmission electron microscopy (TEM).
- iii. Evaluate the effect of Ag NPs on the methylhydroxyethylthiazolekinase activity *ex P. falciparum*.

## 4.2. Materials and methods

### 4.2.1. Materials

Silver nitrate ( $\text{AgNO}_3$ ) and sodium borohydride ( $\text{NaBH}_4$ ) were obtained from Merck (South Africa). Tannic acid ( $\text{C}_{76}\text{H}_{52}\text{O}_{46}$ ) was purchased from Sigma-Aldrich (South Africa). All the reagents and buffers were prepared using deionized water obtained from Milli-Q system.

### 4.2.2. Methods

#### 4.2.2.1. Nanoparticles synthesis

##### 4.2.2.1.1. Synthesis of Ag nanoparticles with $\text{NaBH}_4$

Ag nanoparticles were synthesized in the presence of ice-cold  $\text{NaBH}_4$  as described by Solomon (2007) with some modifications.  $\text{AgNO}_3$  (1.0 mM) was added dropwise (about 1 drop per second) to ice-cold  $\text{NaBH}_4$  (2.0 mM) in an ice-bath. The reaction mixture was

stirred vigorously on a magnetic stir plate until full reaction was achieved as determined by visual change in colour.

#### 4.2.2.1.2. Synthesis of Ag nanoparticles with tannic acid

Ag nanoparticles were synthesized in the presence of tannic acid as described by Sivaraman (2009) with some modifications.  $\text{AgNO}_3$  (2.95 mM) was added as one portion to tannic acid solution (0.15 mM), while stirring at room temperature. The stirring was continued till there was no further change in colour.

#### 4.2.2.2. Characterization

##### 4.2.2.2.1. UV-visible spectroscopy

Samples were 10-fold diluted with deionized water and a spectral scan between 250-900 nm was carried out using a UV-visible spectrophotometer (Spectroquant Pharo 300, Merck) to evaluate plasmon resonance associated with the synthesized Ag nanoparticles.

##### 4.2.2.2.2. Transmission electron microscopy (TEM)

Samples were 10-fold diluted with deionized water, and one drop of sample was applied on a carbon-coated copper grid, excess sample was removed using blotting paper after one minute, the grid was air-dried at room temperature. The electron photographs of nanoparticles were taken by JEOL JEM-1210 TEM operating at 80 keV. The Ag nanoparticle sizes were determined by analysis of 200 particles from 5-10 photographs of each sample using 'Scandium' computer software.

### 4.2.2.3. Effect of Ag nanoparticles on *PfThzK* activity

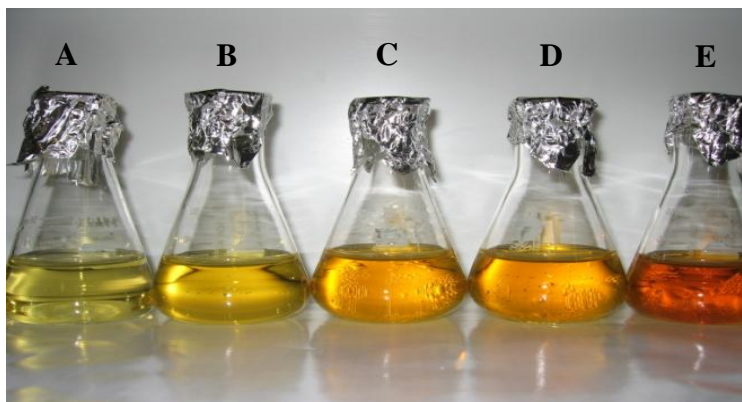
Constant concentrations of Ag nanoparticles (5, 10, 15, 20, 25, 30  $\mu\text{M}$ ) were prepared by diluting the synthesized sample with deionized water. Ag nanoparticles were incubated with purified *PfThzK* under standard condition (29 mM Tris-HCl, pH 7.5; 6 mM  $\text{MgSO}_4$ , 3 mM ATP, 3 mM THZ) for up to 5 hours, varying periods of incubation at intervals of 10, 20, 30, 60, 90, 120, 150, 180, 300 minutes were applied. The thiazolekinase activity was determined colorimetrically at 700 nm as described in Chapter 3 (3.2.5.3). To determine the inhibitor constant value  $K_i$ , purified *PfThzK* was treated with Ag NPs (5, 10, 15, 20, 25, 30  $\mu\text{M}$ ) in the presence of varying amounts of the substrate THZ (0.05-0.3 mM), the inhibition was monitored by determining the kinetic properties of the enzyme by Hanes-Woolf plot.  $K_i$  was calculated using equation:  $K_i = \frac{[NPs] \cdot V_{max}^*}{V_{max} - V_{max}^*}$ . Where [NPs] = concentration of Ag nanoparticles;  $V_{max}$  and  $V_{max}^*$  = maximum enzyme catalyzed reaction in absence and presence of nanoparticles respectively.

## 4.3. Results and discussion

### 4.3.1. Synthesis of Ag nanoparticles.

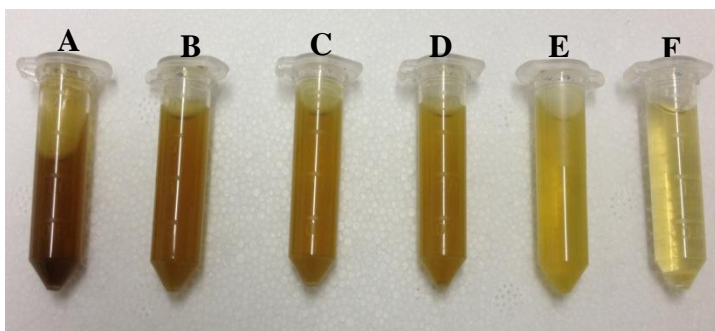
A fixed concentration of  $\text{AgNO}_3$  was added dropwise to chilled  $\text{NaBH}_4$  solution in an ice-bath with stirring, the concentration of Ag salt to  $\text{NaBH}_4$  ratios of 1:6-1:30. A rapid colour change was observed from colourless to yellow and brownish with increased colour intensity depending on the amount of Ag metal present in the solution (Figure 4.3). The change of colour was the first indication of nanoparticles formation. Aggregation and precipitation was noticed from the molar ratio of  $\text{AgNO}_3$  to  $\text{NaBH}_4$  less than 1: 7.5

[sample (D) and (E)]. A large excess of  $\text{NaBH}_4$  was needed both to reduce the ionic silver and to stabilize the silver nanoparticles that form, which was also reported in literature (Khan and Talib, 2010; Eising *et al.*, 2011).



**Figure 4.3.** The Ag nanoparticles synthesized with  $\text{NaBH}_4$  at different molar ratios of metal salt to  $\text{NaBH}_4$ : A) 1:30; B) 1:15; C) 1:10; D) 1:7.5; E) 1:6.

Tannic acid as a reducing agent and stabilizer was also employed to synthesize Ag nanoparticles. When  $\text{AgNO}_3$  (2.95 mM) was added to tannic acid solution with stirring, a rapid colour change was observed from yellow to brown (Figure 4.4). Furthermore, no aggregation was noticed even after several months (Sivaraman *et al.*, 2009). Tannic acid has been studied for its anti oxidant properties, and also as a chelating agent for several inorganic cations (Gonzalez *et al.*, 2010; Yi *et al.*, 2011).



**Figure 4.4.** The Ag nanoparticles synthesized with different concentrations of tannic acid: A) 60  $\mu\text{M}$ ; B) 50  $\mu\text{M}$ ; C) 40 M; D) 30  $\mu\text{M}$ ; E) 20  $\mu\text{M}$ ; F) 10  $\mu\text{M}$ .

### 4.3.2. Characterization of Ag nanoparticles

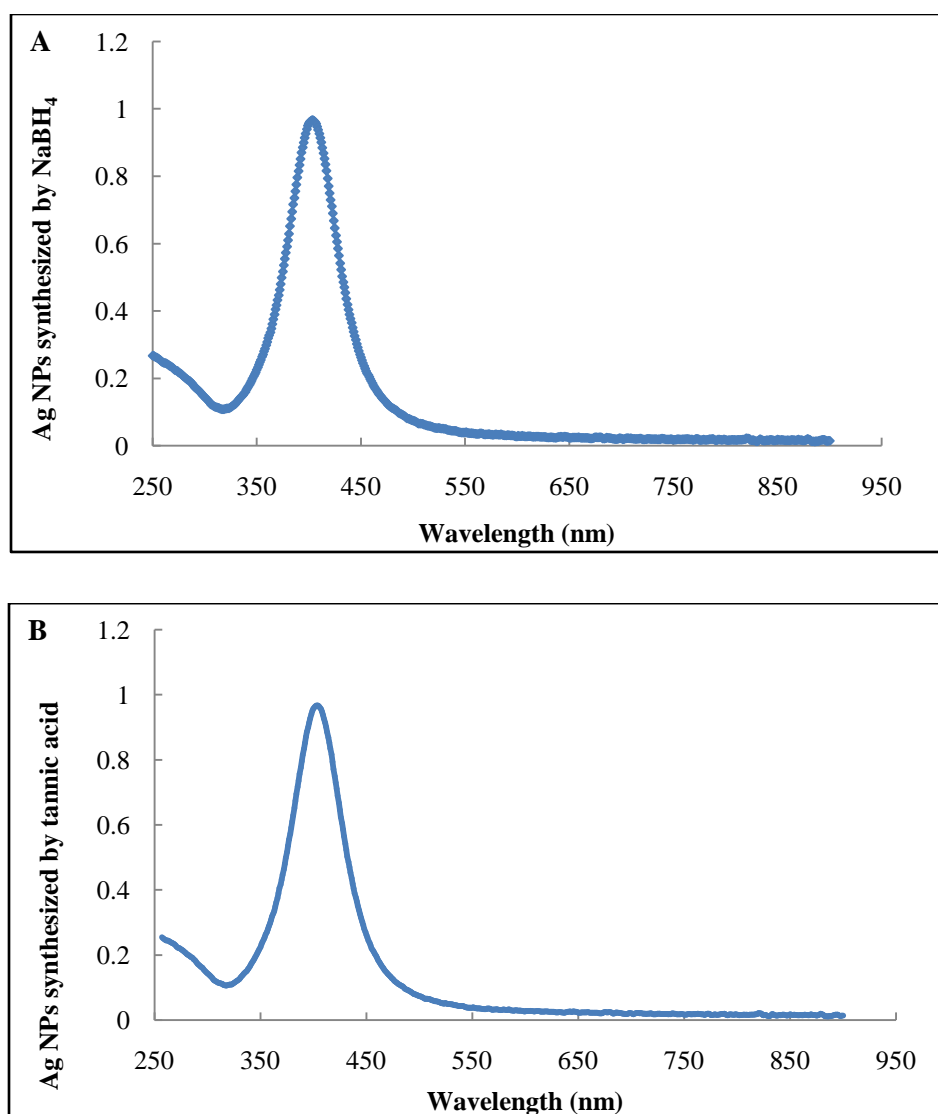
#### 4.3.2.1. UV-visible spectroscopy

Synthesized Ag nanoparticles were characterized by UV-visible spectroscopy and the absorption maximum was analyzed by a spectral scan between 200-900 nm. The UV-vis absorption spectrum of silver nanoparticles synthesized using  $\text{NaBH}_4$  and tannic acid as reducing agent are shown in Figure 4.5. The UV-vis absorption spectrum reveals the formation of silver nanoparticles by showing surface plasmon absorption maxima at 403 nm and 410 nm respectively. The position and shape of the plasmon absorption depends on the particles size, shape and the dielectric constant of the surrounding medium (Amendola *et al.*, 2010; Khan *et al.*, 2012; Mahmoud *et al.*, 2012). It was also reported that the increased particles size or particle aggregation may lead to the shift of SPR maximum shift (Jain and El-Sayed, 2010; Ringe *et al.*, 2010).

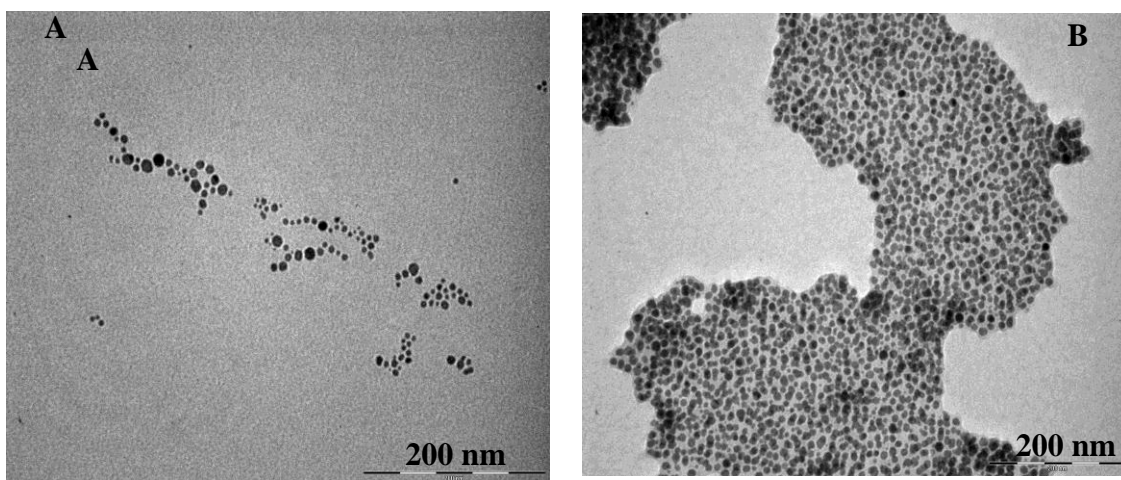
#### 4.3.2.2. Transmission electron microscopy analysis

Nanoparticles samples were characterized by TEM in order to confirm the synthesis of Ag and also to determine the shape and size of Ag nanoparticles (Figure 4.6). In general, the silver particles are spherical. Analysis of 200 particles in each set of experimental sample, the average size of Ag nanoparticles synthesized with  $\text{NaBH}_4$  is  $12.9 \pm 4.21$  nm, which was in good agreement to that reported in literature (Dong *et al.*, 2010; Yu *et al.*, 2011). For those Ag nanoparticles synthesized with tannic acid, the mean size is  $7.06 \pm 2.41$  nm, which was also mentioned before (Sivaraman *et al.*, 2009). It was reported that the size of synthesized Ag nanoparticles depends on the initial molar ratio (MR) of tannic acid to  $\text{AgNO}_3$ , and the smaller size could be achieved when  $\text{MR}=0.05$ . It was also

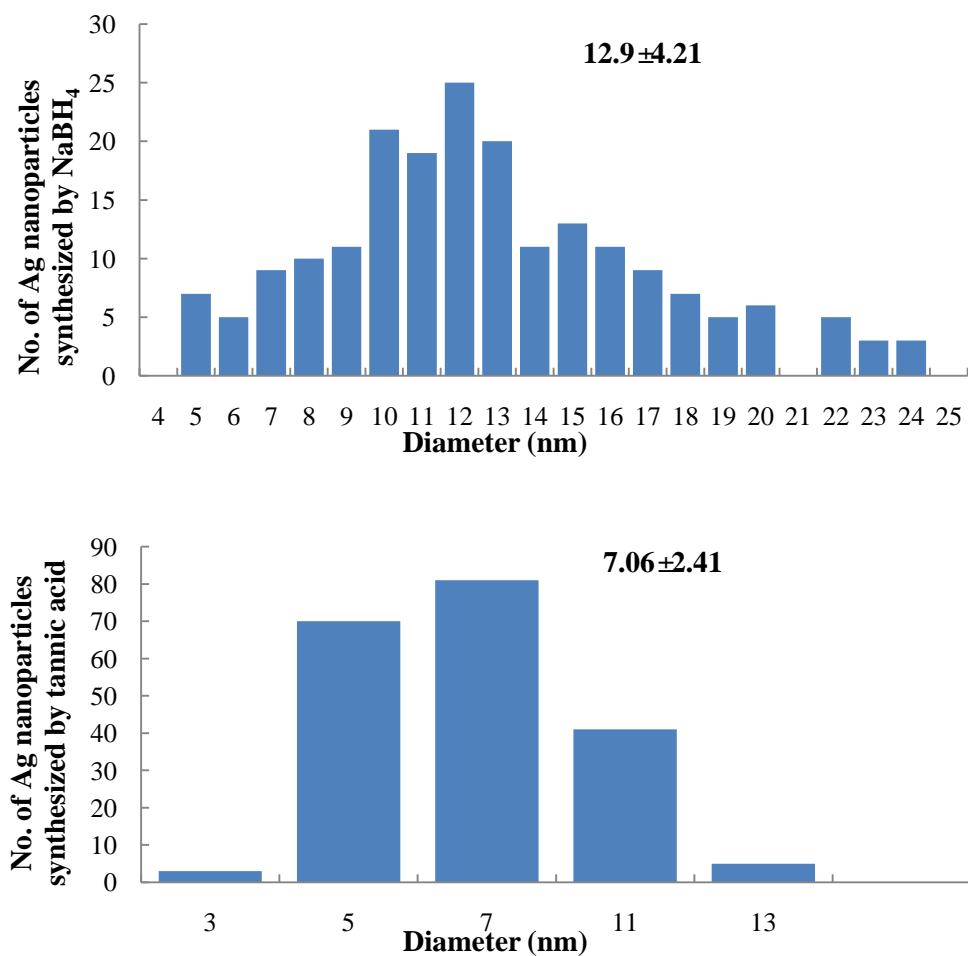
reported that the small Ag nanoparticles with more surface area and more active site were potential for higher antimicrobial activity and inhibitory effects (Jin *et al.*, 2010; Kin *et al.*, 2010; Das *et al.*, 2012). Considering the size and stability of Ag nanoparticles synthesized by these two methods, the nanoparticles synthesized by tannic acid were used for subsequent experiment.



**Figure 4.5.** UV-visible absorbance spectra of Ag nanoparticles showing the typical surface plasmon resonance. A) Ag nanoparticles synthesized by NaBH<sub>4</sub>; B) Ag nanoparticles synthesized by tannic acid.



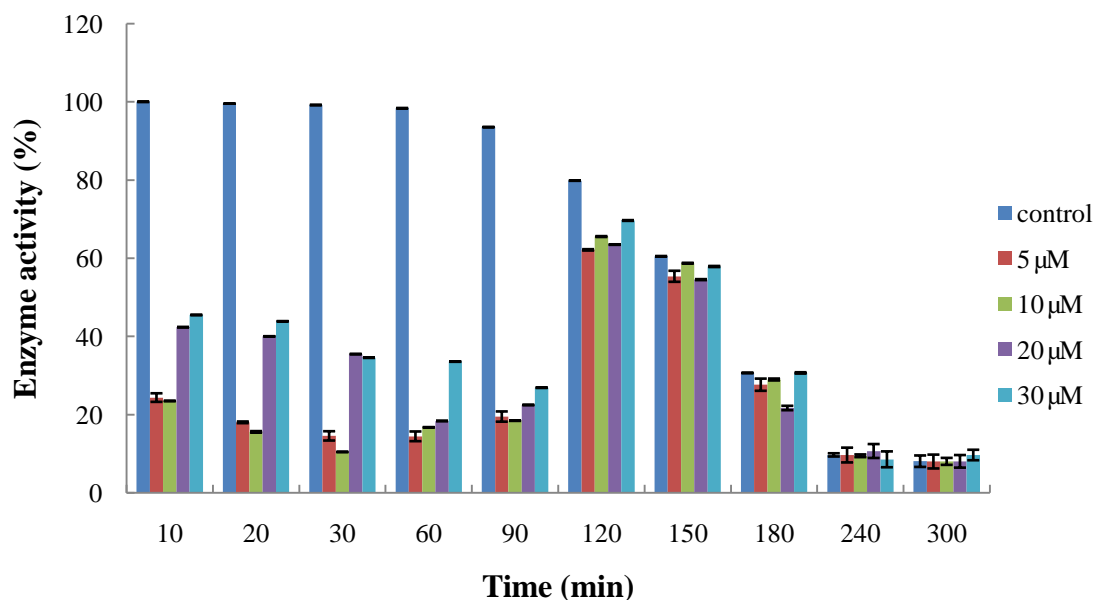
**Figure 4.6.** TEM images of Ag nanoparticles synthesized by A)  $\text{NaBH}_4$ ; B) tannic acid.



**Figure 4.7.** Size distribution of Ag nanoparticles synthesized by  $\text{NaBH}_4$ :  $12.9 \pm 4.21$  nm; tannic acid:  $7.06 \pm 2.41$  nm.

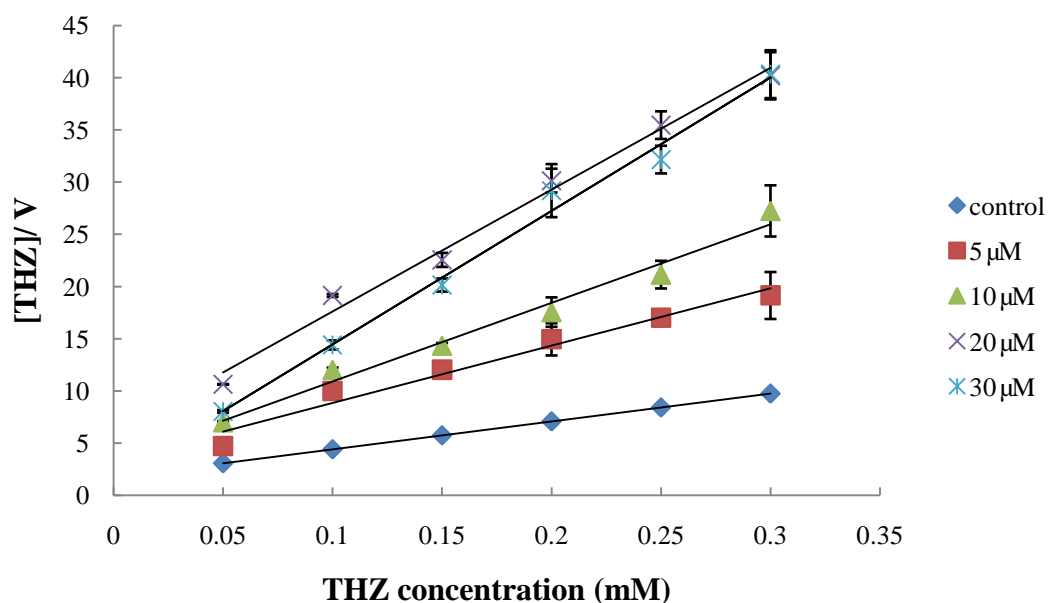
### 4.3.3. Effect of Ag nanoparticles on *PfThzK* activity

The effect of Ag nanoparticles on methylhydroxyethylthiazolekinase was investigated by the method described in 4.2.2.3 with thiazole as substrate. The activity of control (*PfThzK* without Ag nanoparticles) was assayed together at the same experimental conditions. For time dependence it was noticed that there was an increase inhibition during the first 60 min, the strongest inhibition (89% inhibition) was obtained when *PfThzK* was incubated with 10  $\mu\text{M}$  Ag NPs for 30 min. Furthermore, higher inhibition was observed with lower concentration of Ag NPs (10-20  $\mu\text{M}$ ). Interestingly, enzyme activity was restored to the value of control after *PfThzK* was incubated with Ag NPs for longer than 2 hours. It is probably because with the time, the nanoparticles aggregated and dissociated from *PfThzK* and restored its activity.



**Figure 4.8.** The *PfThzK* inhibitory effects of AgNPs

For substrate dependence (Figure 4.9), *PfThzK* was competitively inhibited at all the concentrations of Ag NPs (5-30  $\mu\text{M}$ ). The  $V_{max}$  decreased in the presence of Ag NPs (see Table 4.1), with the inhibitory constant value  $K_i$  of 6.54  $\mu\text{M}$ .



**Figure 4.9.** Hanes-Woolf plot showing influence of Ag NPs on purified *PfThzK*.

**Table 4.1.** Kinetic parameters determined from the interaction of Ag NPs on *PfThzK* using different substrate concentrations.

Ag NPs concentration	0 (control)	5 $\mu\text{M}$	10 $\mu\text{M}$	20 $\mu\text{M}$	30 $\mu\text{M}$
$K_m$ (mM)	0.065	0.064	0.05	0.0507	0.013
$V_{max}$ ( $\mu\text{mol}\cdot\text{min}^{-1}\cdot\text{ml}^{-1}$ )	0.037	0.0203	0.0139	0.00858	0.0078
$k_{cat}$ ( $\text{s}^{-1}$ )	0.15	0.082	0.056	0.034	0.032

Ag Nanoparticles were successfully synthesized by NaBH<sub>4</sub> and tannic acid, and the comparison of these two chemical processes concluded that the tannic acid route was milder and more eco-friendly. Relatively uniform sized and shaped Ag nanoparticles synthesized by tannic acid were utilized to determine the influences of Ag NPs on *PfThzK*, and it was shown that *PfThzK* was competitively inhibited with the inhibitory constant value  $K_i$  of 6.54  $\mu\text{M}$ , 89% inhibition was observed when *PfThzK* was incubated with 10  $\mu\text{M}$  Ag NPs for 30 min. The present work is the first study that evaluated the effects of Ag nanoparticles on the activities of methylhydroxyethylthiazolekinase from *Plasmodium falciparum*, and the inhibition effects of Ag nanoparticles on *PfThzK* could be utilized to disrupt the metabolism of vitamin B<sub>1</sub> in the parasite, which could be potential used to control malaria disease.

## Chapter 5

### Conclusions

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#### 5.1. General conclusions

##### 5.1.1. Isolation, expression, purification and characterization of

###### *PfThzK*

*PfThzK* is a very important enzyme in plasmodial vitamin B<sub>1</sub> biosynthesis and was recombinantly produced as 6×His fusion protein in *E. coli* BL21, with a yield of 0.8 mg per litre of bacteria culture. The enzyme was then successfully over-produced and purified by Ni-affinity chromatography and size exclusion chromatography. Purified *PfThzK* activity was analyzed by an improved molybdate method, and the optimal conditions determined as 37 °C, pH 7.5, and the specific activity was found to be 295.04 nmol/mg, with  $V_{max}$  value of 0.037 μmol/min/ml and  $K_m$  value of 65 μM. ThzK enzyme activity in *B. subtilis* had been found, and the apparent  $K_m$  value for thiazole was reported to be 34 μM (Campobasso *et al.*, 2000), which is comparable to the plasmodial counterpart in this study.

##### 5.1.2. Synthesis of Ag nanoparticles

Metallic nanoparticles are becoming more attractive in various fields of science because of their high surface energy and high surface-to-volume properties (Chaudhari *et al.*, 2012). Ag nanoparticles are the most applicable of all the metal nanoparticles in

consumer products (Maynard and Michelson, 2007); and Ag nanoparticles have been one of the most interesting metallic nanoparticles in research due to their exceptional properties (Perez-Juste *et al.*, 2005). The metallic nanoparticles have shown significant mechanical, electronic, magnetic, optical and catalytic properties, which are highly influenced by their size, shape and composition (Buzea *et al.*, 2007; Das and Marsili, 2011; Burda *et al.*, 2005). Therefore, the specific synthesized route should be selected according to the properties of metal nanoparticles (Perez-Juste *et al.*, 2005; Cuenya, 2010; Chen and Liu, 2011). Recently biological synthetic routes have been designed to be environmentally friendly, however, the improved chemical synthetic pathways for silver nanoparticles have been shown to be more versatile, and more environmentally friendly (Khan *et al.*, 2011; Dawy *et al.*, 2012). In the present study, Ag nanoparticles were synthesized by two chemical methods, the Ag ions were reduced by NaBH<sub>4</sub> and tannic acid and possessed optical properties similar to those reported in the literature. Moreover, the tannic acid synthetic method is more ideal, as the conditions of synthesis were generally mild and simple. The morphologies of these Ag nanoparticles (in terms of size) appeared to be more controlled with the size of 7.06±2.41 nm, compared with those synthesized by NaBH<sub>4</sub>, with the size of 12.9±4.21 nm. Furthermore, no extra stabilizer was needed for this method since tannic acid acted as a reducing agent and stabilizer thereby preventing aggregation and precipitation of the Ag nanoparticles.

### **5.1.3. Interaction of Ag nanoparticles with *PfThzK***

The potential neurotoxicity of Ag nanoparticles was determined by an *in vitro* study of their effects on the enzymatic activity of *PfThzK*, a very important enzyme in plasmodial vitamin B<sub>1</sub> biosynthesis pathway. It was noticed that the enzymatic activity was inhibited

with the inhibitory constant value  $K_i$  of 6.54  $\mu\text{M}$ . Heavy metals, especially Ag nanoparticles have been reported to be toxic as they bind to functional groups of proteins leading to protein deactivation and denaturation (Valodkar *et al.*, 2011; Elzoghby *et al.*, 2012).

The inhibition of Ag nanoparticles on *PfThzK* produces a new potential approach to control malaria disease. Conversely, the present study also demonstrated that *PfThzK* may still be novel biomedical targets in the combat against malaria. As introduced in Chapter 1, *PfThzK* are only found in *Plasmodium* parasite and not in humans, because they are responsible for the metabolism of vitamin B<sub>1</sub>. The inhibition effects of Ag nanoparticles on methylhydroxyethylthiazolekinase have possible clinical applications in the treatment of malaria disease.

## 5.2. Future work

The present work is the first study that evaluated the effects of Ag nanoparticles on the activities of *PfThzK*, and it can be considered as the beginning of future work relevant to vitamin B<sub>1</sub> biosynthetic enzymes. The results of this research also cause other research questions, which may increase the knowledge and understanding of the therapy of malaria disease. From this study, it would be more interesting to carry out many relevant researches as following:

As introduced in Chapter 1, there are three key enzymes involved in plasmodial vitamin B<sub>1</sub> biosynthetic pathways: 1) 5-(2-hydroxy-ethyl)-4-methylthiazole (THZ) kinase (*PfThzK*); 2) 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP) HMP-P kinase (*PfThiD*) and 3) thiamine phosphate synthase (*PfThiE*). In the present study, only

*PfThzK* was purified and evaluated, and it would be of interest to see the effect of Ag nanoparticles on the other two enzymes.

It is reported that it is possible to synthesize Ag nanoparticles by biological methods, such as cowpea chlorotic mosaic virus (CCMV). The virus cage is small enough to enter the blood brain barrier which must be important and specific for cerebral malaria. It is important to evaluate the activation/inhibition of the NPs synthesized by virus protein on *PfThzK* and other plasmodial vitamin B<sub>1</sub> biosynthetic enzymes.

Recently, various nanoparticles have been studied at laboratory level, such as copper, gold, platinum and silver. From the present study, it's becoming more interesting to determine the activation/inhibition of different nanoparticles on *PfThzK*, and contribute more knowledge and understanding to nanotechnology and malaria therapy.

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## Appendices

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### Appendix 1: *PfThzK* sequence

```
1 atgagaaaatataatTTTTTTTACAAAAAGTCGCTTATTCTCTACCTTAACCAAAAATAAAT
61 agcgTTAAGGAATATCATGATGATATAATAAAGTGCATTGAGAAAGTTCGGGTATTAAAT
121 cctcttgTTCATTGTATAACTAATAGAGTAACCACTGAAAAGGTGGCAAACAGTTTATTG
181 gcctttggctcttctccggctatgattgataatcctaaggaagttgaagaatttgctaaa
241 atagcttcatgtacttatttcaacttagggttacatacgacgcaggtagaaaatattaat
301 ttattagaaaagTTAAGAAAAGAATGTATGAAAGATAAATTTATGTTAATTATAGATCCA
361 atagctgTTGGAGCAACAACCTATAGAACTAATGTTATTAAGATATAATTTTAAAATGC
421 caacctaatgtaataaaaaggtaatatTgctgaaatttattatttagataaaggagaattt
481 ttgggggaagggTGTAGATAGTAATAATAACAATACTCATAATGAAACAGATGTAATTAAT
541 agtgccagaaatgTTGCATTAAAATATAATTGTGCTGTAGTAGTTACATCAAAAACAGAT
601 tatattgTTAGTCCATGTTCTCATTATGTAGCCAAAATTAATTGTGATTTAAAAATCTG
661 acaaaaattactgggTcaggttgTtctgTtggtgccctttgtgcagcagctacttcagta
721 tatcctcaaaacccattcatagcatgtatatctgctactcttatataaaattggcagca
781 ttcaaagcatatcaaaaagaaaagtatccaggttcctaagtcataaaattattgatgat
841 atttattactattcacataatcctcattttctcaatttccaaatcgtagatatttacaaa
901 gcagcataa
```

## Appendix 2: Media and Buffers

*Table A1.* Media and Buffers

<b>Luria Broth (LB)</b>	10 g/L tryptone 5 g/L yeast extract 10 g/L NaCl	Autoclave
<b>Luria Agar (LA)</b>	10 g/L tryptone 5 g/L yeast extract 10 g/L NaCl 15 g/L agar	Autoclave
<b>TAE</b>	0.04 M Tris-HCl 1 mM EDTA pH 8.0 0.021 mM glacial acetic acid	
<b>SOB</b>	20 g/L tryptone 5 g/L yeast extract 0.584 g/L NaCl 0.186 g/L KCl 2.034 g/L MgCl <sub>2</sub> 2.464 g/L MgSO <sub>4</sub>	Autoclave
<b>SOC</b>	20 g/L tryptone 5 g/L yeast extract 0.584 g/L NaCl 0.186 g/L KCl 2.034 g/L MgCl <sub>2</sub> 2.464 g/L MgSO <sub>4</sub>	Add 20 ml/L of sterile glucose after autoclave
<b>TB buffer</b>	2.6 g/L HEPES pH6.7 2.203 g/L CaCl <sub>2</sub> 18.638 g/L KCl 10.886 g/L MnCl <sub>2</sub>	Mix all the components except MnCl <sub>2</sub> , adjust pH to 6.7 with KOH/HCL, then add MnCl <sub>2</sub> , and filter sterilize (0.22 μm)
<b>Tris-HCl</b>	121.14 g/mol Tris Powder Hydrochloric acid	Adjust with HCl to desired pH value Dilute with dH <sub>2</sub> O to desired concentration
<b>Binding buffer</b>	0.5 M NaCl 20 mM imidazole 20 mM Tris-HCl	Adjust pH to 7.5, degas and filter
<b>Elution buffer</b>	0.5 M NaCl 0.5 M imidazole 20 mM Tris-HCl	Adjust pH to 7.5, degas and filter
<b>Gel filtration buffer</b>	50 mM NaCl 50 mM Tris-HCl	Adjust pH to 7.5, degas and filter
<b>10% Resolving gel</b>	0.972 ml 30% Acrylamide 485 μl 3M Tris, pH8.8 2.188 ml dH <sub>2</sub> O 91 μl 10% SDS 12.5 μl 10% APS 2.5 μl TEMED	TEMED should be added last.
<b>4% Stacking gel</b>	0.2 ml 30% Acrylamide 105 μl 0.5M Tris, pH6.8 1.185 ml dH <sub>2</sub> O 15 μl 10% SDS 15 μl 10% APS 1.5 μl TEMED	TEMED should be added last.

<b>SDS-PAGE loading buffer</b>	1.6 ml dH <sub>2</sub> O 0.5 ml 0.5 M Tris, pH6.8 0.8 ml 50% glycerol 0.8 ml 10% SDS 0.2 ml 2- βmercaptoethanolbromophenol blue 0.1 ml acetic acid	2-βmercaptoethanolbromophenol blue should be added just before use.
<b>SDS-PAGE running buffer</b>	25 mMTris powder 192 mM glycine 0.1% SDS	
<b>Fairbanks A</b>	0.05% Coomassie Blue 25% isopropanol 10% acetic acid	
<b>Fairbanks B</b>	0.005% Coomassie Blue 10% isopropanol 10% acetic acid	
<b>Fairbanks C</b>	0.002% Coomassie Blue 10% acetic acid	
<b>Fairbanks D</b>	10% acetic acid	

## Appendix 3: Biospin Gel Extraction Kit Protocol

(BioFlux, Bioer Technology Co., Ltd)

**1. Excise the DNA fragment from the agarose gel with a clean scalpel.**

Minimize the size of the gel slice by removing extra agarose.

**2. Weigh the gel slice and add 3 volume of Extraction Buffer to 1 volume of gel slice (100 mg=100 µl).**

Add 300 µl Extraction Buffer to each 100 mg gel, and the gel slice should not be more than 400 mg per test.

**3. Incubate at 50 °C until the gel melts in a heating block and vortex the tube every 2 minutes during the incubation.**

Usually, it takes 10 min. If the colour of the mixture is purple then add 10 µl of 3 M sodium acetate (pH5.0), and mix. The colour will return to yellow.

**4. Optional: Add 1 volume of isopropanol to 1 volume of gel and mix.**

No need to add isopropanol in the case the fragments > 500 bp and < 4 kb.

**5. Apply the sample to Spin column, centrifuge for 1 min at 6,000 × g. Discard the flow-through.**

If the sample volume is more than 750 µl, simply load and spin again.

**6. Add 500 µl Extraction Buffer to Spin column, centrifuge for 30-60 s at 12,000 × g. Discard the flow-through.**

**7. Add 750 µl Wash buffer to Spin column, centrifuge for 30-60s at 12,000 × g. Discard the flow-through.**

If the DNA will be used for salt sensitive applications, let the spin column stand for 2-5min after addition of Wash Buffer, before centrifugation.

**8. Centrifuge for an additional 1min at 12,000 × g and transfer the Spin column to a sterile 1.5 ml microcentrifuge tube.**

Recommend to centrifuge according to this step; otherwise, there will be residual liquid in the column.

**9. Add 30-100 µl Elution Buffer, H<sub>2</sub>O or TE Buffer to the Spin column and let it stand for 1 min at room temperature.**

The volume of Elution Buffer could be adjusted according to needs, but no less than 20  $\mu$ l.

**10. Centrifuge for 1min at 12,000  $\times$  g. The buffer in the microcentrifuge tube contains the DNA.**

The extracted DNA can be used directly for downstream molecular biological experiment. Store at -20  $^{\circ}$ C.

## Appendix 4: Biospin Plasmid DNA Extraction Kit Protocol

(BioFlux, Bioer Technology Co., Ltd)

- 1. Add 2 ml cultured bacteria to 2 ml microcentrifuge tube.**
- 2. Centrifuge at 10,000 × g for 30 s, and discard the supernatant.**

Step 1 and 2 could be repeated for more than once to collect enough cells.
- 3. Resuspend pelleted bacteria cells in 250 µl Resuspension Buffer and No cell clumps should be visible after resuspension of the pellets.**
- 4. Add 250 µl Lysis Buffer and gently invert the tube 4-6 times to mix.**

Do not vortex, as this will result in shearing of genomic DNA. Do not allow this step for more than 5 min.
- 5. Add 350 µl Neutralization Buffer and gently invert the tube 4-6 times to mix.**

The solution should become cloudy and no local precipitate should be visible.
- 6. Centrifuge for 10 min at 13,000 × g until a compact white pellet form.**
- 7. Apply the supernatant to the Spin column and centrifuge for 1 min at 6000 × g. Discard the flow-through.**
- 8. Add 650 µl Wash Buffer to the Spin column and centrifuge for 1 min at 12,000 × g. Discard the flow-through.**
- 9. Repeat step 8.**
- 10. Centrifuge for an additional 1 min at 12,000 × g and transfer the Spin column to a sterile 1.5 ml microcentrifuge tube.**

Recommend to centrifuge according to this step; otherwise, there will be residual liquid in the column.
- 11. Add 50 µl Elution Buffer to the Spin column and let it stand for 15 min at 37 °C.**

The volume of Elution Buffer could be adjusted according to needs.
- 12. Centrifuge for 1 min at 12,000 × g. The buffer in microcentrifuge tube contains the plasmid DNA.**
- 13. The purified plasmid DNA can be used directly for kinds of downstream molecular biological experiments. Store at -20 °C.**

## **Appendix 5: Fairbanks Coomassie Blue Protein Staining and Destaining Protocol**

(Fairbanks *et al.*, 1971)

- 1. After electrophoresis, the gels are placed in a microwavable container, and approximately 100 ml of Fairbanks A staining solution was added.**
- 2. The gel in the solution is then heated in a conventional microwave oven on full power until the solution reaches boiling point (about 2 min).**
- 3. Cool the gel and solution to room temperature for approximately 5 min with gentle shaking.**
- 4. The Fairbanks A solution is then discarded and the gel rinsed in distilled water at room temperature for a few seconds.**

After this step, protein bands containing 100 ng or more are easily observed.

- 5. Add approximately 100 ml of Fairbanks B solution and proceed as in steps 2-4.**

After this step, protein bands containing 50 ng or more are easily observed.

- 6. Add approximately 100 ml of Fairbanks C solution and proceed as in steps 2-4.**

After this step, protein bands containing 25 ng or more are easily observed.

- 7. Add approximately 100 ml of Fairbanks D solution (destaining solution) and repeat steps 2-4.**

After this step, protein bands containing 5 ng or more are easily observed.

A water- clear background can be achieved by repeating step 7 two or three times, or if the gel is left shaking in the destaining solution for 15 or more minutes.

Also, the procedure can be stopped at any of the steps once the desired results are achieved, followed by destaining as in step 7.

All solutions used here are shown in Appendix 2.

## Appendix 6: BCA protein Assay and standard

### A. Preparation of diluted BSA Standard, and 1 ml of 2.0 mg/ml albumin was used as stock.

Use Table A2 as a guide to prepare a set of protein standards.

**Table A2.** Preparation of diluted albumin standards.

Vial	Volume of Diluent (µl)	Volume and source of BSA (µl)	Final BSA concentration (µg/ml)
A	0	300 of stock	2,000
B	125	375 of stock	1,500
C	325	325 of stock	1,000
D	175	175 of vial B	750
E	325	325 of vial C	500
F	325	325 of vial E	250
G	325	325 of vial F	125
H	400	100 of vial G	25
I	400	0	0=Blank

### B. Preparation of BCA working reagent (WR)

1. Use the following formula to determine the total volume of WR required:

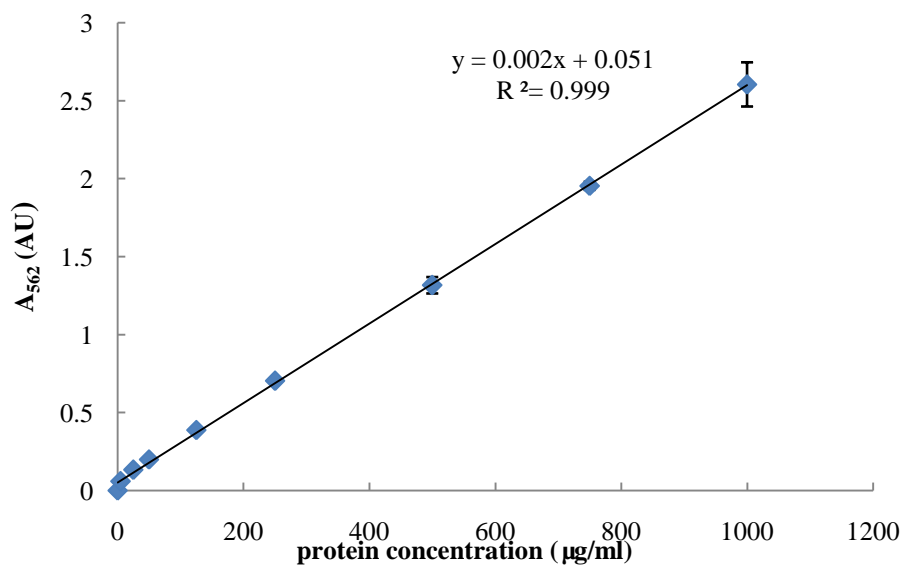
$$(\text{standards} + \text{samples}) \times (3 \text{ replicates}) \times (\text{volume of WR per sample}) = \text{WR required}$$

2. Prepare WR by mixing 50 parts of BCA reagent A with 1 part of BCA reagent B (50:1).

### C. 2 ml Eppendorf-tube procedure (sample to WR ratio = 1:20)

1. Pipette 50 µl of each standard and unknown sample replicate into 2 ml-eppendorf tube.
2. Add 1ml of the WR to each tube, and mix well.
3. Incubate at 60 °C for 30 min, and cool down to room temperature.
4. Read absorbance at 562 nm.

### D. BCA standard curve



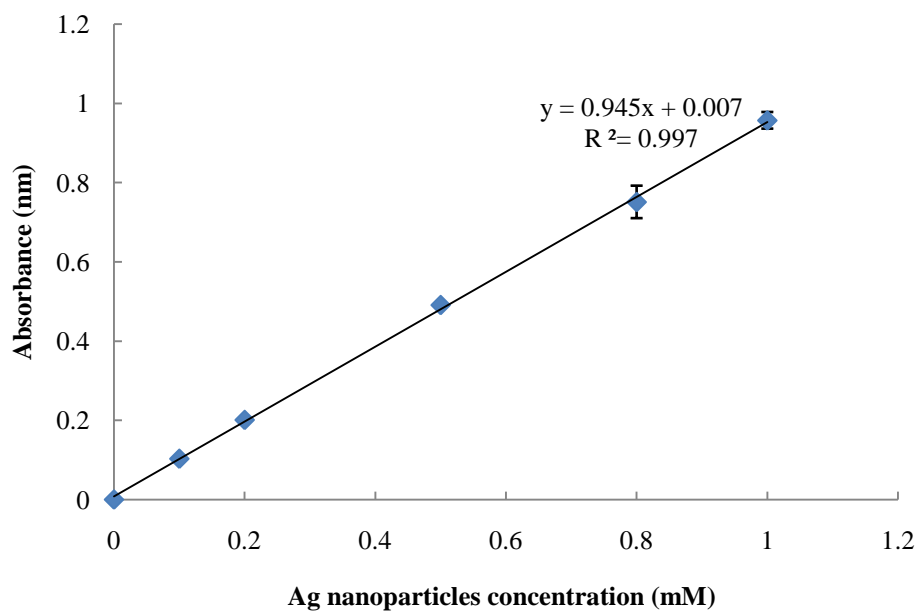
*Figure A1.* BCA standard curve.

## Appendix 7: Ag nanoparticles standard

Preparation of diluted Ag nanoparticles standard as Table A3, and 1 ml of 1 mM Ag NPs was used as stock. The samples were read at 400 nm.

*Table A3.* Preparation of Ag nanoparticles standard.

	1	2	3	4	5	6
1mM stock ( $\mu\text{l}$ )	0	10	20	50	80	100
dH <sub>2</sub> O ( $\mu\text{l}$ )	1000	990	980	950	920	900
Final concentration (mM)	0	0.1	0.2	0.5	0.8	1.0



*Figure A2.* The Ag nanoparticles standard.

## Appendix 8: Molybdate assay and phosphate standard

**A. Preparation of diluted Na<sub>2</sub>HPO<sub>4</sub> Standard as Table A4, and 1 ml of 1 mM Na<sub>2</sub>HPO<sub>4</sub> was used as stock.**

*Table A4.* Preparation of diluted Na<sub>2</sub>HPO<sub>4</sub>.

	1	2	3	4	5	6	7	8	9	10
<b>1mM stock (μl)</b>	0	10	20	30	40	50	80	90	100	120
<b>dH<sub>2</sub>O (μl)</b>	100 0	990	980	970	960	950	920	910	900	880
<b>Final concentration (μM)</b>	0	10	20	30	40	50	80	90	100	120

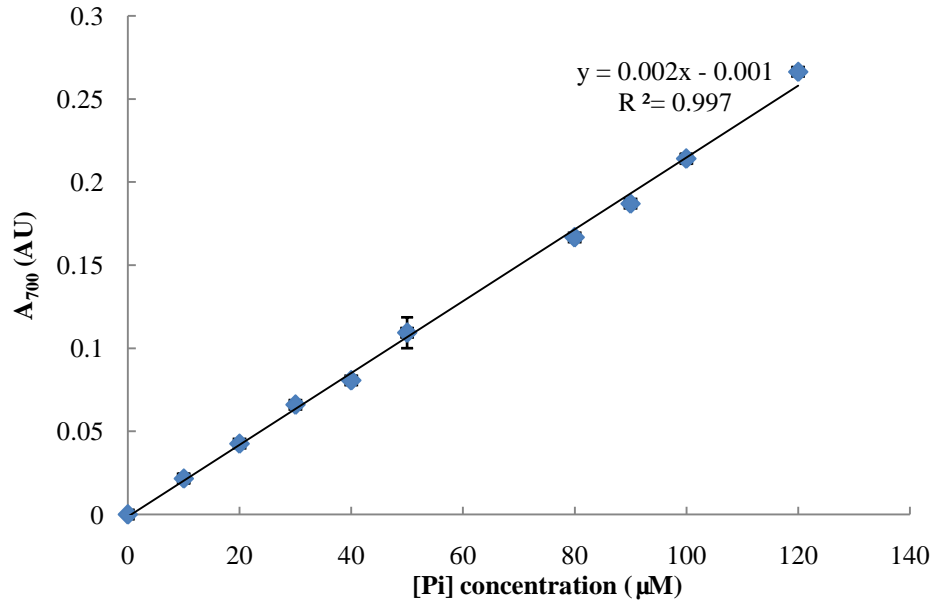
**B. Preparation of Molybdate assay reagents.**

- Reagent A: 2 g of ammonium molybdate is dissolved in 9 ml of concentrated H<sub>2</sub>SO<sub>4</sub>. This is diluted with 200 ml of dH<sub>2</sub>O and make up to 310 ml.
- Reagent B: 9% Ascorbic solution is prepare by dissolving 18 g of L-ascorbic acid in a little quantity of dH<sub>2</sub>O, and then fill up to 200 ml.
- Reagent C: prepare just before use by mixing A and B in 4:1 ratio.

**C. Protocol of Molybdate assay**

- 80 μl of each sample is placed in microtite plate.
- 160 μl of reagent C is added to each sample and allow to stand for 10 min at room temperature for colour development.
- Read absorbance at 700 nm

**D. Phosphate standard curve:**



**Figure A3.** Phosphate standard curve