

TAGZyme™ Handbook

For
Exoproteolytic cleavage of N-terminal His tags

June 2001



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Contents

Kit Contents	5
Storage Conditions	6
Safety Information	6
Product Use Limitations	7
Product Warranty and Satisfaction Guarantee	7
Technical Assistance	7
Introduction	8
The TAGZyme Principle	9
Proteins with intrinsic DAPase stop points	9
Proteins without intrinsic DAPase stop points	10
Applications for the TAGZyme System	12
TAGZyme pQE Vectors	13
QIAexpress pQE vectors	13
Regulation of expression – pREP4 plasmid	14
<i>E. coli</i> host strains	15
The Cloning Procedure	17
Cleavage Protocols	20
Notes Before Starting	20
His tag design	20
Expression, Ni-NTA purification, and desalting of His-tagged proteins	20
Buffers and enzyme activity	21
DAPase Enzyme	21
Qcyclase Enzyme	21
pGAPase Enzyme	22
Cysteamine activation	22
Stepwise Use of the TAGZyme System	22
Analysis during the TAGZyme procedure	23
Cleavage of N-terminal 6xHis tags using DAPase Enzyme	25
Buffer preparation	25
Desalting	25
■ Protocol 1. DAPase digestion (small-scale pilot experiment) for proteins containing intrinsic DAPase stop points	26

■ Protocol 2. Preparative DAPase digestion for proteins containing intrinsic DAPase stop points	28
■ Protocol 3. Removal of DAPase Enzyme by subtractive IMAC	29
Cleavage of N-terminal His tags using DAPase, Qcyclase, and pGAPase Enzymes	30
Buffer preparation	30
Desalting	30
■ Protocol 4. DAPase – Qcyclase digestion (small-scale pilot experiment)	31
■ Protocol 5. Preparative DAPase – Qcyclase digestion	33
■ Protocol 6. Removal of DAPase and Qcyclase Enzymes by subtractive IMAC	34
■ Protocol 7. pGAPase Digestion	35
■ Protocol 8. Preparative pyroglutamate removal using pGAPase Enzyme	37
■ Protocol 9. Removal of pGAPase Enzyme by subtractive IMAC	38
Troubleshooting Guide	39
Appendix	41
Enzyme specifications	41
Solutions required	44
Use of blunt-end-cutting restriction enzymes to introduce various amino acids at the N-terminus of the mature protein	44
Recommended PCR cloning strategy for use of the vector pQE-TriSystem in combination with TAGZyme cleavage	48
His tags suitable for exoproteolytic cleavage by the TAGZyme system	50
Small-scale subtractive IMAC	51
Recommendations for subtractive IMAC scale-up	51
References	52
Ordering Information	54
QIAGEN Distributors	55

Kit Contents

TAGZyme™ Kit — for processing of approx. 10 mg of tagged protein

Catalog No. 34300

DAPase™ Enzyme (10 U/ml)	0.5 units (50 µl)
Qcyclase™ Enzyme (50 U/ml)	30 units (600 µl)
pGAPase™ Enzyme (25 U/ml)	10 units (400 µl)
Cysteamine-HCl (20 mM)	1000 µl
Ni-NTA Agarose	10 ml
Disposable columns (empty)	20
Handbook	1
Product sheets DAPase Enzyme and Qcyclase/pGAPase Enzymes	each 1

TAGZyme pQE Vector Set

Catalog No. 32932

Vectors TAGZyme pQE-1 and -2	each 25 µg
Handbook	1

TAGZyme DAPase Enzyme (2.5 U) — for processing of approx. 50 mg of tagged protein

Catalog No. 34362

DAPase Enzyme (10 U/ml)	2.5 units (250 µl)
Cysteamine-HCl (20 mM)	1000 µl
Handbook	1
Product sheet DAPase Enzyme	1

TAGZyme Qcyclase/pGAPase Enzymes (150 U/50 U) — for processing of approx. 50 mg of tagged protein

Catalog No. 34342

Qcyclase Enzyme (50 U/ml)	150 units (5 x 600 µl)
pGAPase Enzyme (25 U/ml)	50 units (5 x 400 µl)
Handbook	1
Product sheet Qcyclase/pGAPase Enzymes	1

TAGZyme DAPase Enzyme (50 U)* — for processing of approx. 1 g of tagged protein
Catalog No. Inquire

DAPase Enzyme (10 U/ml)	50 units (5 ml)
Cysteamine-HCl (20 mM)	25 ml
Handbook	1
Product sheet DAPase Enzyme	1

TAGZyme Qcyclase/pGAPase Enzymes (3000 U/1000 U)* — for processing of approx. 1 g of tagged protein
Catalog No. Inquire

Qcyclase Enzyme (50 U/ml)	3000 units (5 x 12.5 ml)
pGAPase Enzyme (25 U/ml)	1000 units (5 x 8 ml)
Handbook	1
Product sheet Qcyclase/pGAPase Enzymes	1

* Bulk enzyme quantities are customized products; delivery may take up to 6 weeks. Enzymes are also available in GMP-grade. Please inquire.

Storage Conditions

DAPase™, Qcyclase™, and pGAPase™ Enzymes, Cysteamine-HCl, and vectors TAGZyme pQE-1 and -2 should be stored at -20°C .

Ni-NTA Agarose should be stored at $2-8^{\circ}\text{C}$. Ni-NTA matrices should not be frozen.

Disposable columns can be stored at room temperature.

Safety Information

When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, please consult the appropriate material safety data sheets (MSDSs). These are available online in convenient and compact PDF format at www.qiagen.com/ts/msds.asp where you can find, view, and print the MSDS for each QIAGEN kit and kit component.

Ni-NTA Agarose

Contains nickel-nitrilotriacetic acid. Harmful, sensitizer, and flammable. Risk and safety phrases*: R10-22-40-42/43. S13-26-36-46.

* R10: Flammable. R22: Harmful if swallowed. R40: Possible risks of irreversible effects. R42/43: May cause sensitization by inhalation and skin contact. S13: Keep away from food, drink, and animal feedingstuffs. S26: In case of contact with eyes, rinse immediately with plenty of water and seek medical advice. S36: Wear suitable protective clothing. S46: If swallowed, seek medical advice immediately and show the container or label.

Product Use Limitations

The TAGZyme™ System is developed, designed, and sold for research purposes only. It is not to be used for human diagnostic or drug purposes or to be administered to humans unless expressly cleared for that purpose by the Food and Drug Administration in the USA or the appropriate regulatory authorities in the country of use. All due care and attention should be exercised in the handling of many of the materials described in this text.

Product Warranty and Satisfaction Guarantee

QIAGEN guarantees the performance of all products in the manner described in our product literature. The purchaser must determine the suitability of the product for its particular use. Should any product fail to perform satisfactorily due to any reason other than misuse, QIAGEN will replace it free of charge or refund the purchase price. We reserve the right to change, alter, or modify any product to enhance its performance and design. If a QIAGEN product does not meet your expectations, simply call your local Technical Service Department or distributor. We will credit your account or exchange the product — as you wish.

A copy of QIAGEN terms and conditions can be obtained on request, and is also provided on the back of our invoices. If you have questions about product specifications or performance, please call QIAGEN Technical Services or your local distributor (see inside front cover).

Technical Assistance

At QIAGEN we pride ourselves on the quality and availability of our technical support. Our Technical Service Departments are staffed by experienced scientists with extensive practical and theoretical expertise in molecular biology and the use of QIAGEN products. If you have any questions or experience any difficulties regarding the TAGZyme System or QIAGEN products in general, please do not hesitate to contact us.

QIAGEN customers are a major source of information regarding advanced or specialized uses of our products. This information is helpful to other scientists as well as to the researchers at QIAGEN. We therefore encourage you to contact us if you have any suggestions about product performance or new applications and techniques.

For technical assistance and more information please call one of the QIAGEN Technical Service Departments or local distributors (see inside front cover).

Introduction

The TAGZyme System is an efficient and specific solution for the complete removal of small N-terminal His tags and other amino acid tags by the use of exopeptidases. The method is based on the use of dipeptidyl aminopeptidase I (DAPase Enzyme) alone or in combination with glutamine cyclotransferase (Qcyclase Enzyme) and pyroglutamyl aminopeptidase (pGAPase Enzyme). These recombinant enzymes contain a C-terminal His tag and can therefore be bound to Ni-NTA matrices. This allows their removal from the reaction solution by Immobilized-Metal Affinity Chromatography (IMAC). This feature has been utilized in the design of a simple process consisting of aminopeptidase cleavage followed by subtractive IMAC. The system can form the backbone of a combined TAGZyme-IMAC strategy for the efficient production of highly purified and homogeneous recombinant proteins (see Figure 1). As the TAGZyme enzymes carry a His tag at their C-terminus, the tag is not digested by the N-terminal exopeptidase DAPase Enzyme.

The use of exopeptidases in the TAGZyme System eliminates the risk of endoproteolytic cleavage within the body of the protein, and the rapid rate of reaction means that sensitive proteins can be processed even at 4°C in a matter of hours.

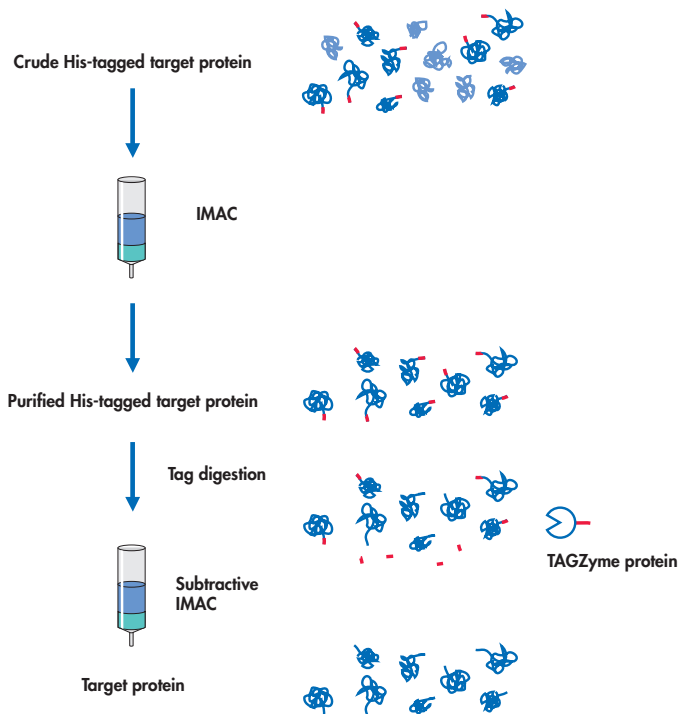


Figure 1. Schematic summary of the TAGZyme procedure.

The TAGZyme Principle

The TAGZyme System makes use of a highly specific and processive exoproteolytic cleavage of N-terminal amino acids for the removal of small affinity tags from proteins (e.g., 6xHis tags). After completion of the digestion, the exoproteolytic enzymes — which carry His tags at the C-terminus — are removed by subtractive IMAC. The efficiency of the total procedure is supplemented by the use of a series of *E. coli* expression vectors, TAGZyme pQE-1 and -2. These expression vectors combine the high-level expression of 6xHis-tagged proteins delivered by the pQE vector series with specially designed His tag-coding and multiple cloning site sequences that allow complete and convenient removal of N-terminal His tags. The two vectors have been optimized for use with the TAGZyme System. Occasionally, problems may be encountered when processing other tags. For an overview of the suitability of other tags for TAGZyme processing, please consult Table 2 (page 17). N-terminal amino acids are cleaved off as dipeptides by dipeptidyl aminopeptidase I (DAPase Enzyme, Figure 2A). After removal of the first N-terminal dipeptide the enzyme progressively cleaves off dipeptides until a stop point is encountered. Stop points are certain amino acids in defined positions within a dipeptide (see Table 1). As the His tags of TAGZyme enzymes appear at the C-terminus they are not subject to digestion.

Table 1. DAPase stop points

Amino acid	DAPase stop point (↓) sequence*
Lysine (Lys, K)	<u>Xaa-Xaa...Xaa-Xaa</u> ↓ Lys-Xaa Xaa-Xaa...
Arginine (Arg, R)	<u>Xaa-Xaa...Xaa-Xaa</u> ↓ Arg-Xaa Xaa-Xaa...
Proline (Pro, P)	<u>Xaa-Xaa...Xaa-Xaa</u> ↓ Xaa-Xaa Pro-Xaa...
Proline (Pro, P)	<u>Xaa-Xaa...Xaa-Xaa</u> ↓ Xaa-Pro Xaa-Xaa...
Glutamine (Gln, Q)	<u>Xaa-Xaa...Xaa-Xaa</u> ↓ Gln [†] -Xaa Xaa-Xaa...

* Natural DAPase stop points (↓) are the following amino acids in the given position within a dipeptide (dipeptides that are cleaved off are underlined).

† In the presence of excess Qcyclase Enzyme.

Proteins with intrinsic DAPase stop points

A range of mature proteins have natural DAPase Enzyme stop points (Table 1) causing the enzyme to release its substrate, i.e., the detagged mature protein, as soon as this amino acid occurs in the N-terminal position. Accordingly, N-terminal His tags containing an even number of amino acid residues can be completely and specifically removed by treatment with DAPase Enzyme alone (Figure 2A). After digestion is complete, the C-terminally His-tagged DAPase Enzyme, residual undigested target protein, and copurified contaminants are removed by subtractive IMAC (Figure 3A). The entire process is typically completed within 45 minutes.

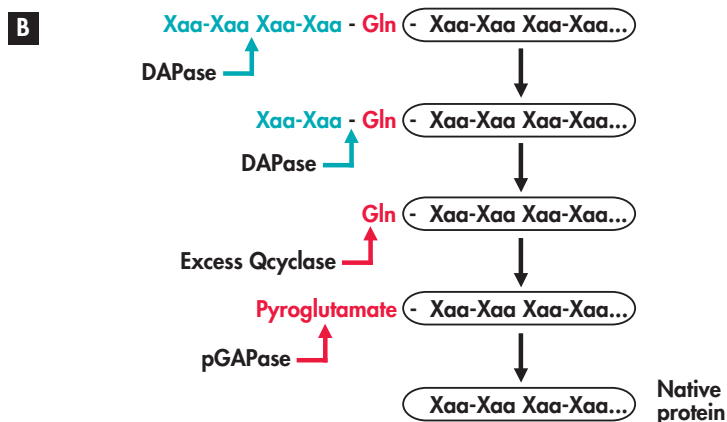
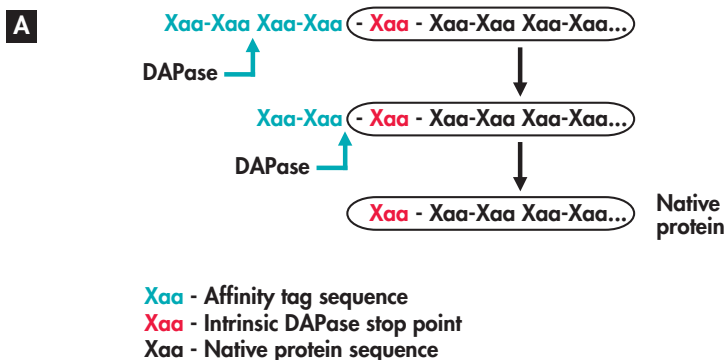


Figure 2. Schematic summary of the overall cleavage strategy. **A** DAPase Enzyme cleavage of a N-terminal His tag from a protein containing a natural stop point to obtain the mature target protein. **B** Cleavage of an N-terminal His tag from a protein making use of a glutamine stop point. Following dipeptide cleavage by DAPase Enzyme, an N-terminal glutamine residue is converted to pyroglutamate that in turn is removed by pGAPase Enzyme action.

Proteins without intrinsic DAPase stop points

cDNA coding for proteins that do not contain a natural stop point can be cloned into a TAGzyme pQE vector in such a way that a glutamine (Gln, Q) residue is introduced into the position between the last cleavable dipeptide and the first authentic amino acid of the target protein. DAPase cleavage is then performed in the presence of a second enzyme, glutamine cyclotransferase (Qcyclase Enzyme), which catalyzes the cyclization of an N-terminal glutamine residue to pyroglutamate (Figure 2B). Presence of excess

Qcyclase Enzyme ensures immediate cyclization of the inserted glutamine residue when the His tag has been digested and the glutamine appears in the N-terminal position. A protein possessing an N-terminal pyroglutamate residue cannot serve as a substrate for DAPase Enzyme and is thus protected against further DAPase digestion. Following the coincubation, both enzymes are removed from the reaction solution by subtractive Ni-NTA IMAC (Figure 3B). The target protein is obtained by cleaving off the N-terminal pyroglutamyl residue through the action of a third enzyme, pyroglutamyl aminopeptidase (pGAPase Enzyme) (Figures 2B and 3B). This process is typically completed within 120 minutes. A glutamine DAPase stop point can be introduced by cloning the protein coding sequence into the expression vector TAGZyme pQE-2. Here, any uneven amino acid position can be chosen for the glutamine residue, and the first amino acid of the target protein must immediately follow. Alternatively, TAGZyme pQE-1 is the vector of choice whenever the sequence of the protein allows cloning into the blunt-ended *PvuII* restriction site, which links the first amino acid of the target protein to the glutamine stop point (Figure 5, page 16).

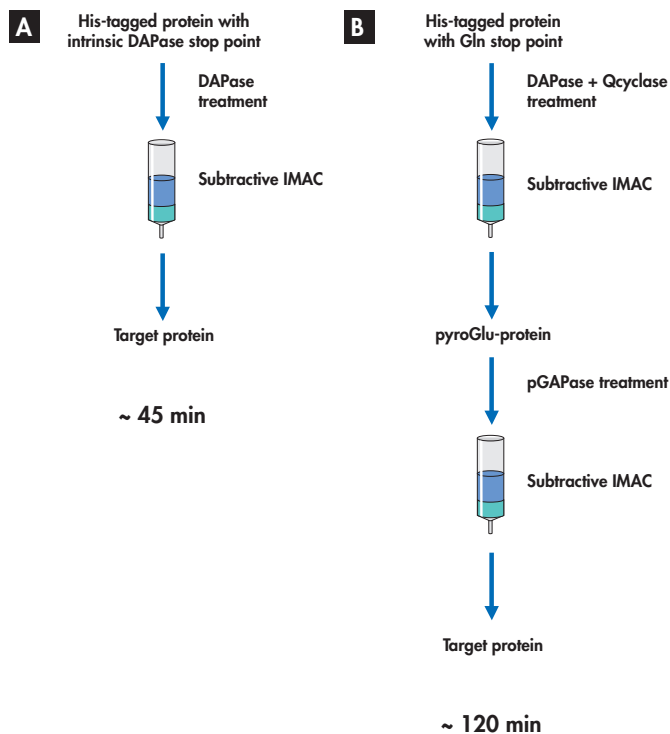


Figure 3. Scheme of the combined cleavage and purification strategy. **A** Procedure for proteins having a natural DAPase stop point. **B** Procedure for proteins with an introduced glutamine DAPase stop point.

Applications for the TAGZyme System

The TAGZyme System is suitable for cleavage of every N-terminal His tag that contains certain sequence characteristics that are described in this handbook.

Therapeutic proteins

In the production of therapeutic proteins for use in humans or animals, it is often desirable to remove any artificial additions such as His tags.

The specificity and the speed of action of the recombinant enzymes in the TAGZyme System make it an ideal tool for production of recombinant proteinaceous therapeutics, where precisely defined cleavage characteristics are required. Due to the independence of this system from sequence-determined cleavage sites, the TAGZyme System provides the highest level of specificity of protein cleavage and target protein integrity. TAGZyme System components are available in various formats including bulk quantities of single enzymes.

Moreover, the TAGZyme System can be combined with Ni-NTA-based IMAC protein purification strategies for which Drug Master Files (Type II) are available for support in regulatory affairs. The subtractive Ni-NTA IMAC processing steps within the TAGZyme procedure can contribute to an increase in the purity of the target protein.

For production where the highest safety standards are required, GMP-quality TAGZyme enzymes are available. Please contact QIAGEN for details (see inside front cover).

Protein crystallography and structure determination

Structure determination of protein crystals has become more and more important in the context of drug screening and rational design of small molecules for protein ligands. In order to elucidate a protein's structure it is often desirable to crystallize the protein in the native state, i. e., without affinity tag additions.

Screening for crystallization conditions is often done in a high-throughput format. QIAGEN offers an automated solution for the production of large amounts of His-tagged protein for this purpose in 96-well format. TAGZyme is an ideal supplementary tool for this automated protein purification. Please contact QIAGEN for further details.

Protein microarrays

Depending on the chemistry of coupling of a purified protein to the surface of a chip and on the chip's intended application, it may be desirable to remove His tags from proteins prior to immobilization.

In combination with an automated solution for the purification of His-tagged proteins in a high-throughput format, TAGZyme is the method of choice to produce a large number of authentic, detagged proteins in a convenient and timesaving procedure.

Please contact QIAGEN for details of available solutions in automated high-throughput protein purification and downstream processing.

Basic research

Because the TAGZyme System is available in a small kit size and protocols are provided for the processing of a large range of proteins, the system is equally suited to His-tag removal from proteins used in small assays in basic research.

TAGZyme pQE Vectors

The vectors TAGZyme pQE-1 and -2 are based on the pQE-30 and pQE-80 vectors for expression of N-terminally 6xHis-tagged proteins in *E. coli*. The His tag has been modified to encode the epitope Met-Lys-His₆ (MKH₆) a short His tag and the N-terminus Met-Lys motif that delivers a high expression level and lowest level of methionine processing in *E. coli* (1). Furthermore, in the rare case of methionine processing in *E. coli* the N-terminal lysine residue would act as a DAPase stop point (see Table 1, page 9) and prevent DAPase from out-of-frame digestion. The presence of this DAPase stop point leaves the protein intact allowing removal of the protein by subtractive IMAC.

QIAexpress pQE vectors

High-level expression of 6xHis-tagged proteins in *E. coli* using the QIAexpress pQE vectors is based on the T5 promoter transcription-translation system. pQE plasmids belong to the pDS family of plasmids (2) and were derived from plasmids pDS56/RBSII and pDS781/RBSII-DHFRS (3). These low-copy plasmids (Figure 4) have the following features:

- Optimized promoter-operator element consisting of phage T5 promoter (recognized by the *E. coli* RNA polymerase) and two *lac* operator sequences which increase *lac* repressor binding and ensure efficient repression of the powerful T5 promoter
- Synthetic ribosomal binding site, RBSII, for high translation rates
- 6xHis-tag coding sequence either 5' or 3' to the cloning region
- Multiple cloning site and translational stop codons in all reading frames for convenient preparation of expression constructs
- Two strong transcriptional terminators: *t*₀ from phage lambda (4), and T1 from the *rrnB* operon of *E. coli*, to prevent read-through transcription and ensure stability of the expression construct
- β -lactamase gene (*bla*) confers resistance to ampicillin (5) at 100 μ g/ml (the chloramphenicol acetyl transferase gene (CAT) present between *t*₀ and T1 is not expressed)
- ColE1 origin of replication (5)

Restriction maps and sequences for the cloning regions of QIAexpress vectors are presented in Figure 5. The entire sequence information is available at www.qiagen.com. A strategy for the use of the pQE-TriSystem vector for protein expression in insect and mammalian cells in combination with the TAGZyme System is outlined in the Appendix, page 48.

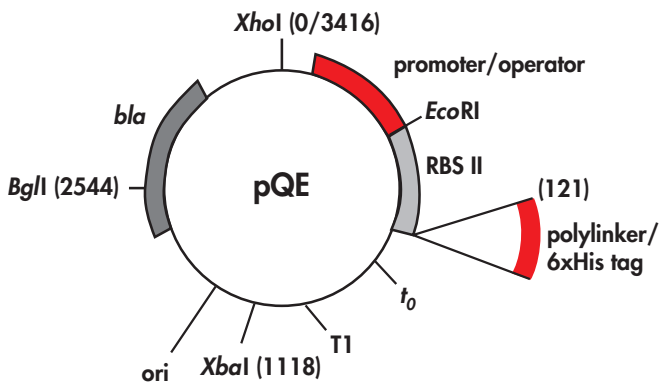


Figure 4. pQE vectors.

Regulation of expression — pREP4 plasmid

The extremely high transcription rate initiated at the T5 promoter can only be efficiently regulated and repressed by the presence of high levels of the *lac* repressor protein. *E. coli* host strains used in the QIAexpress System use a *lac* repressor gene in *trans* or *cis* to the gene to be expressed. In the *trans* system, the host strains contain the low-copy plasmid pREP4 which confers kanamycin resistance and constitutively expresses the *lac* repressor protein encoded by the *lac I* gene (6). The pREP4 plasmid is derived from pACYC and contains the p15A replicon. Multiple copies of pREP4 are present in the host cells that ensure the production of high levels of the *lac* repressor protein that binds to the operator sequences and tightly regulates recombinant protein expression. The pREP4 plasmid is compatible with all plasmids carrying the ColE1 origin of replication, and is maintained in *E. coli* in the presence of kanamycin at a concentration of 25 µg/ml. The *cis*-repressed vectors pQE-80L, -81L, and -82L contain the *lac^q* gene and do not require the presence of pREP4.

Expression of recombinant proteins encoded by pQE vectors is rapidly induced by the addition of isopropyl-β-D-thiogalactoside (IPTG) which binds to the *lac* repressor protein and inactivates it. Once the *lac* repressor is inactivated, the host cell's RNA polymerase can transcribe the sequences downstream from the promoter. The transcripts produced are then translated into the recombinant protein. The special "double operator" system in the pQE expression vectors, in combination with the high levels of the *lac* repressor protein generated by pREP4 or the *lac^q* gene on pQE-80L, pQE-81L, or pQE-82L, ensure tight control at the transcriptional level. The pREP4 plasmid is already present in the QIAexpress *E. coli* strains M15[pREP4] and SG13009[pREP4]. Using pQE-80L, pQE-81L, or pQE-82L with the *cis-lac^q* gene, expression rates are comparable with those obtained using pQE-30, pQE-31, or pQE-32 vectors in combination with pREP4.

***E. coli* host strains**

Any *E. coli* host strain containing both the expression (pQE) and the repressor (pREP4) plasmids can be used for the production of recombinant proteins. The QIAexpress System uses *E. coli* strain M15[pREP4] which permits high-level expression and is easy to handle. Strain SG13009[pREP4] (7) is also supplied and may be useful for the production of proteins that are poorly expressed in M15[pREP4]. Both the M15 and SG13009 strains are derived from *E. coli* K12 and have the phenotype Nal^s , Str^s , Rif^s , Thi^- , Lac^- , Ara^+ , Gal^+ , Mtl^- , F^- , RecA^+ , Uvr^+ , Lon^+ .

E. coli strains that harbor the *lacI^f* mutation, such as XL1 Blue, JM109, and TG1, produce enough *lac* repressor to efficiently block transcription, and are ideal for storing and propagating pQE plasmids. These strains can also be used as expression hosts for expressing nontoxic proteins, but they may be less efficient than the M15[pREP4] strain, and expression is regulated less tightly than in strains harboring the pREP4 plasmid. If the expressed protein is toxic to the cell, "leaky" expression before induction may result in poor culture growth or in the selection of deletion mutants that grow faster than bacteria containing the correct plasmid. Note that *E. coli* strains M15 and SG13009 do not harbor a chromosomal copy of the *lacI^f* mutation, so pREP4 must be maintained by selection for kanamycin resistance. The *cis*-repressed pQE-80L series of vectors can be easily used with any *E. coli* host strain and kanamycin selection is not necessary.

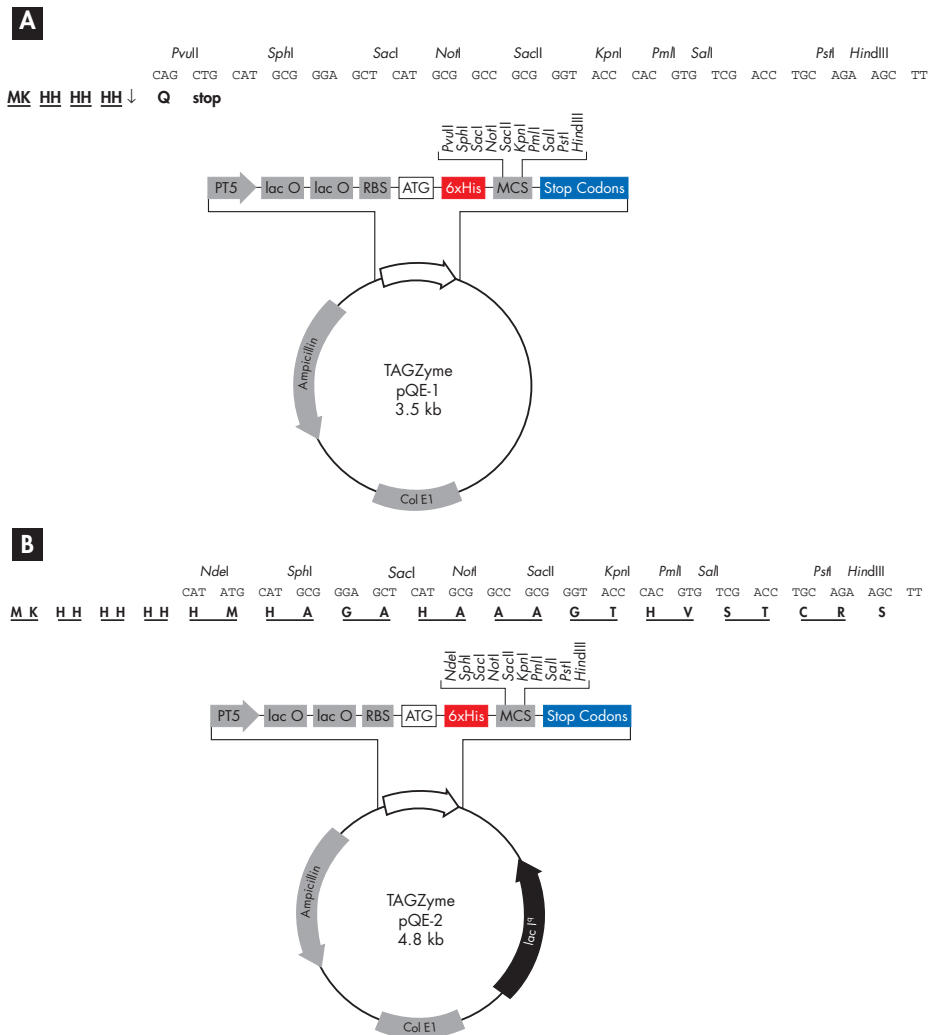


Figure 5. TAGZyme pQE vectors for N-terminal His tag constructs which facilitate exoproteolytic removal of N-terminal residues by TAGZyme enzymes. Restriction sites within the multiple cloning sites, DNA sequences, and the corresponding N-terminal amino acid sequences are shown. **A** DAPase cleaves off the underlined dipeptides and DAPase digestion stops at the glutamine residue (Q) at position “↓” in the presence of excess Qcyclyase. **B** DAPase Enzyme cleaves off the underlined dipeptides until an introduced stop point is reached.

Refer to *The QIAexpressionist* (8) or to www.qiagen.com for further details and sequences of the TAGZyme pQE-1 and -2 vectors.

The Cloning Procedure

The cleavage activity of DAPase Enzyme is dependent upon the amino acid composition of the His tag to be digested, i.e., of the dipeptides to be cleaved. The TAGZyme pQE *E. coli* expression vectors have been specially designed to provide reliable and efficient His tag cleavage.

The TAGZyme pQE-2 tag sequences allow removal of the complete N-terminal tag irrespective of the cloning site of the DNA insert. Vector TAGZyme pQE-1 can be used to insert a glutamine DAPase stop point. See Table 13 in the Appendix for a list of blunt-cutting restriction enzymes that can be used in conjunction with *PvuII* for PCR cloning of expression inserts. After IMAC purification and subsequent treatment with DAPase Enzyme and excess Qcyclase Enzyme, the pyroglutamate residue generated can then be removed by the use of pGAPase Enzyme (see above).

Table 2. Examples of the cleavage rates of various dipeptides by DAPase Enzyme.

Rapid rate of cleavage	Medium rate of cleavage	Slow rate of cleavage	No cleavage = DAPase stop point
Xaa – Arg	Xaa – Asp*	Xaa – Phe [†]	Arg – Xaa
Xaa – Lys	Xaa – Glu*	Gly – Met	Lys – Xaa
His – Ala	Phe – Xaa [†]	Gly – Ser	Xaa – Pro
His – Gln	Ala – Ala	Ser – Met	Xaa – Xbb – Pro
His – Gly	Asp – Asp*, [‡]		Gln – Xaa [§]
His – His	Glu – Glu*, [‡]		
His – Met	Glu – His*		
Ala – His	Gly – Phe [†]		
Gly – His	Ser – Tyr		
Met – His			

* Positively or negatively charged side chains inhibit DAPase Enzyme cleavage, and sequences containing aspartic acid (Asp) or glutamic acid (Glu) can only be digested by DAPase Enzyme at acidic pH while sequences containing histidine (His) residues require a pH above 6.0. Therefore, 6xHis tags containing Glu or Asp can only be digested by DAPase Enzyme at a pH between 6.0 and 6.5.

[†] With a few exceptions, dipeptides containing Phe, Ile, Leu, Tyr, and Trp in either of the two positions of the dipeptide, are subject to slow cleavage.

[‡] Medium to slow cleavage rate.

[§] Gln-Xaa serves as a stop point for DAPase Enzyme only in the presence of Qcyclase Enzyme, which converts the glutamine residue to pyroglutamate (which can be removed by the action of pGAPase Enzyme).

The use of expression vectors other than TAGZyme pQE constructs in conjunction with TAGZyme enzymes is possible. However, since these vectors have not been specifically designed for use with the TAGZyme System, the amino acid sequence to be cleaved off should be carefully analyzed for efficiency of dipeptide cleavage using Table 2. It is also recommended to make use of Table 2 and the guidelines given below whenever a new N-terminal tag is designed for cleavage by DAPase Enzyme or in combination with Qcyclase Enzyme and pGAPase Enzyme. The TAGZyme System is equally suited for use with prokaryotic and eukaryotic expression systems.

In addition to considering the dipeptide composition within the N-terminus to be cleaved, the following guidelines should be followed in order to achieve successful removal of His tags from recombinant proteins using the TAGZyme System.

- The total number of amino acid residues in the tag to be cleaved off should not exceed 30.
- If the target protein contains an intrinsic DAPase stop point (see Table 1) which is to be utilized, the tag must be composed of an even number of residues. If the target protein does not contain a stop point the tag must be C-terminally extended with a glutamine residue (Q) in addition to an even number of residues N-terminal to the glutamine residue.
- Arginine (R) and lysine (K) residues must not be placed in odd-numbered positions of the tag.
- The tag sequence must not contain any proline (P) residues.
- The N-terminal sequence of the tag should be designed to minimize in vivo processing of the N-terminal methionine residue.

Processing of methionine leads to out-of-frame DAPase digestion and results in the accumulation of erroneously processed products. In *E. coli*, the residue adjacent to the initial methionine influences the degree of processing, and a bulky residue should be placed in this position. We recommend lysine (found in TAGZyme pQE-1 and -2 vectors), but arginine, glutamate, or aspartate are also effective as a penultimate residue that reduces methionine processing in *E. coli* (1). Please note that DAPase–Qcyclase Enzyme treatment must be carried out at pH 6.0–6.5 if aspartate or glutamate residues occur in the His-tag sequence to be cleaved (see Table 2 and Table 3).

Table 3. Characteristics of recommended His tag N-termini

N-terminus	Level of methionine processing in <i>E. coli</i>*	Expression level in <i>E. coli</i>†	DAPase Enzyme cleavage rate	Other advantages
Met ¹ Lys ² – His tag	Very low	Very high	Rapid	DAPase Enzyme stop point for out-of-frame digestion‡
Met ¹ Arg ² – His tag	Low	Very high	Rapid	DAPase Enzyme stop point for out-of-frame digestion‡
Met ¹ Glu ² – His tag	Low	High	Medium (only at acidic pH)	
Met ¹ Asp ² – His tag	Low	High	Medium (only at acidic pH)	

* See reference 1 and 11.

† See reference 1.

‡ See also Table 1.

In general, the nucleotide sequence encoding the tag has a strong influence on the expression level and self-complimentary mRNA sequences close to the ATG start codon should be avoided. Furthermore, it has been observed that the amino acids lysine (codon AAA) and arginine (example codon CGT) significantly improve expression if placed next to the start methionine coded by ATG.

The tag sequence should be designed to avoid dipeptides that result in slow DAPase cleavage rates. The rate at which DAPase Enzyme cleaves off different dipeptides from the N-terminus depends on the amino acid residues in the dipeptide. Dipeptides containing an arginine or lysine residue in the c-terminal position are cleaved off very quickly, whereas dipeptides containing a hydrophobic amino acid residue (i.e, Phe, Ile, Leu, Tyr, Trp) are cleaved off relatively slowly. Examples of cleavage rates with respect to dipeptide composition are shown in Table 2, page 17.

Proteins expressed using other pQE vectors that encode N-terminal His tags are poorly processed as they encode the sequence Met-Arg-Gly-Ser. The second dipeptide, Gly-Ser is slowly cleaved by DAPase Enzyme (see Table 2). Furthermore, C-terminal His tags encoded by the pQE vectors pQE-60, -70, -16, and -TriSystem are not removed by the TAGZyme System, as the exoprotease cleaves dipeptides from the N-terminus of proteins.

In some cases, *in vivo* His-tag cleavage can occur, leading to erroneously processed products. Such processing may be observed when arginine residues appear in the middle of His tag sequence or close to the target protein sequence. It is recommended that arginine residues only appear close to the N-terminus of the tag.

In response to out-of-frame digestion resulting from methionine processing or *in vivo* cleavage of the tag, incorporation of DAPase stop points in the tag is recommended (see above).

Erroneously processed products with two or more consecutive histidine residues remaining can be efficiently removed by subtractive Ni-NTA IMAC after DAPase digestion. Lysine, arginine, and alternating glutamine residues (in the presence of Qcyclase Enzyme) are functional stop points. It is recommended to place arginine in the N-terminal sequence of a tag (see above).

Cleavage Protocols

Notes Before Starting

His tag design

Please note that the precise amino acid sequence of a polyhistidine tag and the nucleotide sequence selected to encode it are of great importance for the overall performance of the resulting construct during expression, post-translational processing, purification, and tag removal. For these reasons, we strongly recommend using the pQE-TAGZyme expression vectors that have been optimized for use with the TAGZyme System. If other vectors are used, please follow the guidelines given in this handbook regarding tag design and gene construction strategy.

Expression, Ni-NTA purification, and desalting of His-tagged proteins

For expression and purification of 6xHis-tagged proteins refer to *The QIAexpressionist, a handbook for high-level expression and purification of 6xHis-tagged proteins* (8).

The TAGZyme procedure works well at pH 6.3–7.5 in the absence of imidazole. Because an addition of imidazole or a reduction in pH are usually used for elution of His-tagged proteins from Ni-NTA matrices, the purified target should be desalted before starting the TAGZyme procedure. Desalting can be performed using standard techniques such as gel filtration, ultrafiltration, hollow-fibre modules, or dialysis.

The presence of imidazole leads to a decrease in the cleavage rate, probably due to competitive inhibitory effect on DAPase catalysis. Simple dilution of IMAC elution fractions for direct use in the TAGZyme procedure without prior desalting may be possible but reaction parameters must be optimized in pilot experiments. Imidazole should be diluted to a concentration of 50 mM or lower. The final protein concentration should not be lower than 0.3 mg/ml.

Buffers and enzyme activity

Phosphate buffers are recommended for use with the TAGZyme System due to their low tendency to strip metal ions from IMAC matrices. However, other buffers may be used such as Tris, Bis-Tris, Bis-Tris-Propane, and MES. For further details on the compatibility of reagents with Ni-NTA IMAC matrices and procedures, refer to Table 4 in *The QIAexpressionist* (8) or visit us at www.qiagen.com.

The optimal pH for TAGZyme catalyzed removal of tags, and also for removal of His-tagged contaminants using subtractive IMAC, is 6.7 to 7.5. All the TAGZyme enzymes work well between 4°C and 37°C as outlined in Table 4.

Table 4. Effect of reaction temperature on enzymatic activity

Reaction temperature	Relative activity of TAGZyme enzymes
37°C	100%
Room temperature (20–25°C)	50%
4–6°C	10%

DAPase Enzyme

DAPase Enzyme is inactive in the presence of denaturants (guanidine hydrochloride or urea), even at low concentrations. DAPase Enzyme is 85–100% active in the presence of up to 0.4% CHAPS, Tween® 20, Tween 80, and Triton® X-100 and 60–70% active in the presence of 1% of these detergents.

The enzyme has a broad pH optimum between pH 4 and 8. However, the activity depends on the dipeptides to be cleaved off (see Table 2 and Table 3). The optimal pH of DAPase-catalyzed removal of His tags is pH 6.7 to 7.2. The enzyme's activity is approximately 50% of maximum at pH 6.3 and 7.5 and approximately 10% at pH 5.8 and 8.0. DAPase Enzyme must be activated before use by the reducing agent cysteamine (see protocols).

Qcyclyase Enzyme

Qcyclyase Enzyme has a pH optimum of 8 and shows approximately 60–70% of maximum activity at pH 7 and pH 9.5 and approximately 40% at pH 6.2. Qcyclyase Enzyme is not inactivated by reducing agents such as cysteamine and DTT.

pGAPase Enzyme

pGAPase Enzyme is 100% stable in the presence of 1.6 M guanidine hydrochloride for 140 minutes and shows approximately 85% of maximum activity in the presence of 3.2 M guanidine hydrochloride for 140 minutes. Because pGAPase Enzyme is a cysteine peptidase, urea is not recommended for use with pGAPase Enzyme because the presence of low amounts of the chemical decomposition product cyanate will inactivate the enzyme.

The enzyme is 85–100% active in the presence of up to 0.4% CHAPS, Tween 20, Tween 80, and Triton X-100 and about 60% active in the presence of 1% of these detergents. pGAPase Enzyme is slightly activated by sarkosyl and shows 125% activity in the presence of 1% sarkosyl.

pGAPase Enzyme has a broad pH optimum between pH 6 and 10 with approximately 70% activity at pH 6 and 10. pGAPase Enzyme must be activated before use by the reducing agent cysteamine (see protocols).

TAGZyme Buffer (see below) provides optimal TAGZyme enzyme activity conditions and its use is recommended in TAGZyme procedures.

Cysteamine activation

Cysteamine is used as an activator for DAPase Enzyme and pGAPase Enzyme. It is thought that at a physiological pH, cysteamine, and its oxidized form cystamine, act as a hydrogen donor for the reduction of disulfides in the enzymes.

Stepwise Use of the TAGZyme System

Normally, by following the recommendations below, sufficient cleavage of the target protein will be obtained. However, the actual rate of cleavage of an N-terminal His tag may vary from protein to protein. This can be due to variations in steric accessibility of the tag or due to modifications of amino acid residues. If the optimal cleavage conditions have to be determined for a specific purification process, it is recommended that a pilot DAPase or DAPase–Qcyclase digestion reaction be carried out.

Therefore, the use of the TAGZyme System should include the following steps:

- Pilot digestion to establish optimum enzyme concentrations
- Preparative DAPase or DAPase–Qcyclase digestion
- Subtractive IMAC using Ni-NTA resin
- Digestion with pGAPase Enzyme and second subtractive IMAC (for proteins without intrinsic DAPase stop points)

Analysis during the TAGZyme procedure

We recommend that the efficiency of cleavage reactions is checked by subjecting samples from the different steps of the TAGZyme procedure to SDS-PAGE analysis. The pGAPase Enzyme-catalyzed removal of pyroglutamate cannot be observed directly but may be confirmed by subjecting an aliquot of the fully processed protein to a second round of DAPase treatment and subsequent analysis by SDS-PAGE. The result of efficient pGAPase Enzyme-catalyzed pyroglutamate removal will be quantitative DAPase Enzyme-catalyzed conversion of the deprotected target protein (i.e., without an N-terminal pyroglutamate residue) into truncated forms with increased electrophoretic mobility.

Figure 6, page 24 shows an SDS-PAGE analysis of a TAGZyme-cleaved His-tagged protein. His-tagged human tumor necrosis factor α (hTNF α) expressed in *E. coli* and purified by Ni-NTA IMAC, was subjected successively to DAPase–Qcyclase and pGAPase treatment and the authentic target protein hTNF α was recovered from the reaction solution by subtractive IMAC (lane 5). In addition to the TAGZyme enzymes and residual, unprocessed His-tagged TNF α , minor contaminants were efficiently removed in this step. The completeness of the pGAPase Enzyme-catalyzed removal of the pyroglutamate residue was checked by incubation of an aliquot of the fully processed TNF α with DAPase Enzyme. A quantitative DAPase Enzyme-catalyzed conversion of deprotected TNF α into a truncated form with increased electrophoretic mobility was observed (lane 6) confirming efficient pGAPase Enzyme-catalyzed removal of the pyroglutamate residue.



Figure 6. Removal of the His tag from His-tagged hTNF α using the TAGZyme System.

- 1:** Purified His-tagged hTNF α . (the tag was an alternating tag as described in the Appendix, "His tags suitable for exoproteolytic cleavage by the TAGZyme System").
 - 2:** After incubation for 10 minutes with DAPase and Qcyclase Enzymes at 37°C.
 - 3:** After incubation for 20 minutes with DAPase and Qcyclase Enzymes at 37°C.
 - 4:** After incubation for 30 minutes with DAPase and Qcyclase Enzymes at 37°C.
 - 5:** After completion of the reaction untagged, pyroglutamyl-extended hTNF α was recovered by subtractive IMAC, subjected to pGAPase digestion, and mature hTNF α was recovered in the flow-through fraction of a second round of subtractive IMAC.
 - 6:** An aliquot of the processed protein was incubated with excess DAPase (0.125 U/mg hTNF α) for 2 hours in order to analyze the efficiency of the pGAPase-catalyzed removal of pyroglutamate. The two subunits of His-tagged DAPase Enzyme are visible.
- All samples were subjected to SDS-PAGE and the gel stained by Coomassie® Blue. **M:** markers.

Cleavage of N-terminal 6xHis tags using DAPase Enzyme

The data in Table 5 can be used as a rough guide to the amount of DAPase Enzyme necessary to completely digest the N-terminal tag of a recombinant protein. However, substantial differences in activity may be encountered from protein to protein (see above). Therefore, the figures in Table 5 should be considered as a starting point for the pilot experiments only, and not as a general rule for any protein and reaction scale.

Table 5. Times generally required for DAPase digestion at the given DAPase Enzyme-to-target protein ratio

Amount of target protein	Amount of DAPase Enzyme	Reaction temperature	Required reaction time
1 mg	50 mU	4°C	5 h
50 µg	2.5 mU	20–25°C	60 min
		37°C	30 min

The following section is for DAPase digestion of tagged proteins containing an intrinsic stop point (see above). For the combined DAPase–Qcyclyase and pGAPase digestion (see Protocols 4 and 5).

Buffer preparation

From a 10x stock solution (see Appendix) prepare enough 1x TAGZyme Buffer (20 mM sodium phosphate, pH 7.0; 150 mM NaCl) for desalting and the TAGZyme digestion. Approximately 50 ml 1x TAGZyme Buffer is sufficient for a small-scale experiment.

Note that tags containing glutamate or aspartate residues can only be efficiently cleaved at pH 6.0–6.5. In this case, prepare the TAGZyme Buffer at lower pH (20 mM sodium phosphate, pH 6.0–6.5; 150 mM NaCl).

Desalting

Desalt your His-tagged protein using gel filtration, ultrafiltration dialysis, hollow-fibre filtration, or the method best suited to your needs. It is recommended that proteins are exchanged into 1x TAGZyme Buffer.

Ni-NTA matrices show negligible leaching of nickel ions into the elution buffer (10). However, when using IMAC resins that bind metals more weakly, addition of 5–10 mM EDTA to the eluted protein fraction prior to the desalting procedure is recommended to remove nickel ions from the His tag.

Protocol 1. DAPase digestion (small-scale pilot experiment) for proteins containing intrinsic DAPase stop points

The amount of DAPase Enzyme and the length of incubation time required for complete digestion of the tag depend on the target protein and its concentration. Generally, digestion is complete after treatment for 30 minutes at 37°C with 50 mU DAPase Enzyme per mg protein but the optimal conditions for the processing of a His-tagged protein must be determined in pilot experiments. Table 6 gives guidelines for the conditions required for digestion of 50 µg target protein in TAGZyme buffer. Protein concentration should be at least 0.3 mg/ml. The reaction should take place in a volume of 50 to 300 µl. Larger reaction volumes require longer incubation times due to the dilution of the reactants.

Table 6. Recommendations for DAPase Enzyme digestion pilot experiments

Enzyme/reagent	For processing of 50 µg His-tagged target protein	
	Starting point	Titration range
DAPase Enzyme (1 U/ml)*	2.5 mU (2.5 µl)	0.5–5 mU (0.5–5 µl)
Cysteamine-HCl (2 mM)*	5 µl	1–10 µl

* Dilute an aliquot of the DAPase Enzyme and cysteamine stock solutions according to steps 1 and 2 of protocol 1.

It is recommended that the progress of each digestion be analyzed by SDS-PAGE. Take 5 µl samples from each reaction every 10 minutes, add SDS sample buffer to inactivate the enzyme, and load samples onto an SDS gel including an undigested control. Alternatively, or in addition to varying the enzyme concentration, the incubation temperature can be varied.

Procedure

1. **Prepare a 1/10 dilution of DAPase Enzyme stock solution (10 U/ml) using 1x TAGZyme Buffer.**
2. **Prepare a 1/10 dilution of cysteamine-HCl stock solution (20 mM) using distilled water.**
3. **Mix 1 volume DAPase Enzyme solution (1 U/ml) with 2 volumes cysteamine-HCl (2 mM).**
DAPase Enzyme is activated by cysteamine in this step.
4. **Incubate for 5 min at room temperature. The enzyme mixture must be used within 15 min of preparation.**
During DAPase Enzyme preparation, bring the protein solution to the desired incubation temperature (4–37°C).
5. **Start the digestion by adding the enzyme mix to the temperature-adjusted protein solution.**
6. **Incubate for a length of time that should deliver complete digestion (see Table 5). If desired, take samples during the reaction for SDS-PAGE analysis.**
If removal of DAPase Enzyme is required, please refer to the protocol for small-scale subtractive IMAC in the Appendix, page 51.

Protocol 2. Preparative DAPase digestion for proteins containing intrinsic DAPase stop points

The TAGZyme Kit has been designed to enable processing and purification of at least 10 mg of desalted and IMAC-purified tagged protein. Suitable protein concentrations in digestion reactions are between 0.3 and 5 mg/ml. The amount of DAPase Enzyme (mU) to be used for digestion per mg of desalted protein is established in the pilot DAPase digestion experiment. Table 7 lists the corresponding volumes to be used in a preparative digestion per mg of 6xHis-tagged protein.

Table 7. Recommendations for preparative DAPase digestion

Enzyme/reagent	For processing of 1 mg His-tagged target protein	
	Starting point	Titration range
DAPase Enzyme (10 U/ml)	50 mU (5 μ l)	10–100 mU (1–10 μ l)
Cysteamine-HCl (20 mM)	5 μ l	1–10 μ l

In most cases a linear scaling up of the conditions found to give complete digestion in the pilot experiment will give satisfactory results in a preparative digestion. If desired, a time course can be carried out to verify the optimal digestion conditions determined in the pilot experiments.

- Mix 1 volume DAPase Enzyme solution (10 U/ml) with 1 volume cysteamine-HCl (20 mM).**
DAPase Enzyme is activated by cysteamine in this step.
- Incubate for 5 min at room temperature. The enzyme mixture must be used within 15 min of preparation.**
During DAPase Enzyme preparation, bring the protein solution to the desired incubation temperature (4–37°C).
- Start the digestion by adding the enzyme mix to the temperature-adjusted protein solution.**
- Incubate for a length of time that was found to be sufficient for complete digestion in the pilot experiment. If desired, take samples during the reaction for SDS-PAGE analysis.**

Protocol 3. Removal of DAPase Enzyme by subtractive IMAC

This protocol applies to a cleavage reaction containing 1 mg target protein. Refer to Table 17, page 51 for Ni-NTA IMAC scale up recommendations.

1. **Resuspend the Ni-NTA Agarose suspension by shaking and pipet 1 ml of the 50% suspension (corresponding to 0.5 ml bed volume) into one of the disposable columns provided in the kit.**

Alternatively, pack an LC or FPLC[®] column with 0.5 ml bed volume of Ni-NTA Agarose*.

2. **Equilibrate the column with 5 ml (10 column volumes) 1x TAGZyme Buffer.**

Steps 1 and 2 can be performed during enzyme incubation. When using a chromatography system, do not exceed a flow rate of 0.5 ml/min to ensure quantitative binding of the His-tagged DAPase Enzyme.

3. **Pass the digestion reaction mixture through the column and collect the flow-through fraction.**

Important! The flow-through fraction contains the processed native protein.

4. **Wash the column with 2 ml of 1x TAGZyme Buffer or until the flow-through no longer contains protein. Collect the fraction(s).**

Important! The flow-through fractions contain the processed native protein.

5. **Add the flow-through fraction from step 3 to the protein-containing fractions from step 4. Discard the Ni-NTA resin used in this subtractive step.**

The TAGZyme procedure is finished and the detagged native protein is ready for further applications.

* An HR 5/2 or HR 5/5 FPLC column (Amersham Pharmacia Biotech) is suitable for such a volume of matrix. For processing of larger amounts of protein please refer to the bed-volume size and flow-rate recommendations on page 51. In general, column height should be $\geq 2x$ column diameter.

Cleavage of N-terminal His tags using DAPase, Qcyclase, and pGAPase Enzymes

This section is for the combined DAPase–Qcyclase and pGAPase Enzyme digestion. For the digestion of proteins with a natural stop point using DAPase Enzyme alone see Protocols 1 and 2.

The data in Table 8 can be used as a rough guide to the amounts of DAPase and Qcyclase Enzyme necessary to completely digest the N-terminal tag of a recombinant protein. However, substantial differences in activity may be encountered from protein to protein (see above). Therefore, the figures in Table 8 should be considered as a starting point for the pilot experiments only, and not as a general rule for any protein and reaction scale.

Table 8. Times generally required for DAPase–Qcyclase digestion at the given enzyme-to-target protein ratio

Amount of target protein	Amount of DAPase	Amount of Qcyclase	Reaction temperature	Required reaction time
1 mg	50 mU	3 U	4°C	5 h
50 µg	2.5 mU	150 mU	20–25°C	60 min
			37°C	30 min

Buffer preparation

From a 10x stock solution (see Appendix, page 44) prepare enough 1x TAGZyme Buffer (20 mM sodium phosphate, pH 7.0; 150 mM NaCl) for desalting and the TAGZyme digestion. Approximately 50 ml 1x TAGZyme Buffer is sufficient for a small-scale experiment.

Note: Tags containing glutamate or aspartate residues can only be efficiently cleaved at pH 6.0–6.5. In this case, prepare the TAGZyme Buffer at lower pH (20 mM sodium phosphate, pH 6.0–6.5; 150 mM NaCl). Following cleavage, the pH of the reaction mixture must be increased to between pH 6.7 and 7.5 to enable efficient removal of His-tagged enzymes by IMAC. This can be accomplished by the addition of ~1/100 volume of 1M Tris-Cl.

Desalting

Desalt your His-tagged protein using gel filtration, ultrafiltration dialysis, hollow-fibre filtration, or the method best suited to your needs. It is recommended that proteins are exchanged into 1x TAGZyme Buffer.

Ni-NTA matrices show negligible leaching of nickel ions into the elution buffer (10). However, when using IMAC resins that bind metal ions more weakly, addition of 5–10 mM EDTA to the eluted protein fraction prior to the desalting procedure is recommended to remove nickel ions from the 6xHis tag.

Protocol 4. DAPase–Qcyclase digestion (small-scale pilot experiment)

The amount of DAPase and Qcyclase Enzyme and the length of incubation time required for complete digestion of the His tag depend on the target protein and its concentration. Generally, digestion is complete after treatment for 30 minutes at 37°C with 50 mU DAPase and 3 U Qcyclase Enzyme per mg protein but the optimal conditions for the processing of a tagged protein must be determined in pilot experiments. Table 9 gives guidelines for the conditions required for digestion of 50 µg target protein. Protein concentration should be at least 0.3 mg/ml.

Table 9. Recommendations for pilot DAPase–Qcyclase Enzyme digestion experiments

Enzyme/reagent	For processing of 50 µg His-tagged target protein in 30 minutes	
	Starting point	Titration range
DAPase (1 U/ml)*	2.5 mU (2.5 µl)	0.5–5 mU (0.5–5 µl)
Qcyclase (50 U/ml)	150 mU (3 µl)	30–300 mU (0.6–6 µl)
Cysteamine-HCl (2 mM)*	5 µl	1–10 µl

* Dilute an aliquot of the DAPase Enzyme and cysteamine stock solutions according to steps 1 and 2 of protocol 4.

It is recommended that the progress of each digestion be analyzed by SDS-PAGE. Take 5 µl samples from each reaction every 10 minutes, add SDS sample buffer to inactivate the enzyme, and load samples onto an SDS gel including an undigested control. Alternatively, or in addition to varying the enzyme concentration, the incubation temperature can be varied.

Procedure

1. Prepare a 1/10 dilution of DAPase Enzyme stock solution (10 U/ml) using 1x TAGZyme Buffer.
2. Prepare a 1/10 dilution of cysteamine-HCl stock solution (20 mM) using distilled water.
3. Mix 1 volume DAPase Enzyme solution (1 U/ml) with 2 volumes cysteamine-HCl (2 mM).

DAPase Enzyme is activated by cysteamine in this step.

4. Incubate for 5 min at room temperature. The enzyme mixture must be used within 15 min of preparation.

During DAPase preparation, bring the protein solution to the desired incubation temperature (4–37°C).

5. Add 1.2 volumes of Qcyclase (50 U/ml) to the prepared DAPase.
6. Start the digestion by adding the enzyme mix to the temperature-adjusted protein solution.
7. Incubate for a length of time that should deliver complete digestion (see Table 8, page 30). If desired, take samples during the reaction for SDS-PAGE analysis.

If removal of DAPase and Qcyclase Enzymes is required, please refer to the protocol for small-scale subtractive IMAC in the Appendix, page 51.

Protocol 5. Preparative DAPase–Qcyclase digestion

The TAGZyme Kit has been designed to enable processing and purification of at least 10 mg of desalted and IMAC-purified tagged protein. Suitable protein concentrations in digestion reactions are between 0.3 and 5 mg/ml. The amounts of DAPase and Qcyclase Enzyme to be used for digestion per mg of desalted protein are established in the pilot DAPase–Qcyclase digestion experiment. Table 10 lists the corresponding volumes to be used in a preparative digestion per mg of His-tagged protein.

Table 10. Recommendations for preparative DAPase–Qcyclase digestion

Enzyme/reagent	For processing of 1 mg His-tagged target protein	
	Starting point	Titration range
DAPase (10 U/ml)	50 mU (5 μ l)	10–100 mU (1–10 μ l)
Qcyclase (50 U/ml)	3 U (60 μ l)	0.6–6 U (12–120 μ l)
Cysteamine-HCl (20 mM)	5 μ l	1–10 μ l

In most cases a linear scaling up of the conditions found to give complete digestion in the pilot experiment will give satisfactory results in a preparative digestion. If desired, a time course can be carried out to verify the optimal digestion conditions determined in the pilot experiments.

Procedure

- Mix 1 volume DAPase solution (10 U/ml) with 1 volume cysteamine-HCl (20 mM).**
DAPase is activated by cysteamine in this step.
- Incubate for 5 min at room temperature. The enzyme mixture must be used within 15 min of preparation.**
During DAPase preparation, bring the protein solution and an aliquot of 1x TAGZyme Buffer to the desired incubation temperature (4–37°C).
- Add 12 volumes of Qcyclase (50 U/ml) to the prepared DAPase.**
- Start the digestion by adding the enzyme mix to the temperature-adjusted protein solution.**
- Incubate for a length of time that was found to be sufficient for complete digestion in the pilot experiment. If desired, take samples during the reaction for SDS-PAGE analysis.**

Protocol 6. Removal of DAPase and Qcyclease Enzymes by subtractive IMAC

This protocol applies to a cleavage reaction containing 1 mg target protein. Refer to Table 17, page 51 for Ni-NTA IMAC scale up recommendations.

- 1. Resuspend the Ni-NTA Agarose suspension by shaking and pipet 1 ml of the 50% suspension (corresponding to 0.5 ml bed volume) into one of the disposable columns provided in the kit.**

Alternatively, pack an LC or FPLC column with 0.5 ml bed volume of Ni-NTA Agarose*.

- 2. Equilibrate the column with 5 ml (10 column volumes) 1x TAGZyme Buffer.**

Steps 1 and 2 can be performed during enzyme incubation. When using a chromatography system, do not exceed a flow rate of 0.5 ml/min to ensure quantitative binding of the 6xHis-tagged DAPase and Qcyclease Enzymes.

- 3. Pass the digestion reaction mixture through the column and collect the flow-through fraction.**

Important! The flow-through fractions contain the processed pyroglutamyl-extended protein.

- 4. Wash the column with 2 ml of 1x TAGZyme Buffer or until the flow-through no longer contains protein. Collect the fraction(s).**

Important! The flow-through fractions contain the processed pyroglutamyl-extended protein.

- 5. Add the flow-through fraction from step 3 to the protein-containing fractions from step 4. Discard the Ni-NTA resin used in this subtractive step.**

The DAPase–Qcyclease Enzyme step is finished and the recovered detagged protein is ready for the removal of pyroglutamate by the action of pGAPase Enzyme (see page 35).

* An HR 5/2 or HR 5/5 FPLC column (Amersham Pharmacia Biotech) is suitable for such a volume of matrix. For processing of larger amounts of protein please refer to the bed-volume size and flow-rate recommendations on page 51. In general, column height should be $\geq 2x$ column diameter.

Protocol 7. pGAPase digestion (small-scale pilot experiment)

This step is only necessary for proteins that have been incubated with Qcyclase Enzyme.

Table 11. Times generally required for pGAPase reaction at the given enzyme-to-target protein ratio

Target protein	pGAPase	Reaction temperature	Required reaction time
1 mg	1 U	4–8°C	Overnight (15 h)
50 µg	50 mU	20–25°C	3 h
		37°C	90 min

Generally, digestion with pGAPase Enzyme is complete after treatment for 90 minutes at 37°C with 1.0–1.25 U of pGAPase Enzyme per mg of protein (see Table 11). However, optimal conditions may vary from protein to protein. Therefore, it is recommended that a titration of the enzyme concentration (see Table 12) or a control reaction with DAPase Enzyme (see “Analysis during the TAGZyme Procedure”, page 23) is carried out after completion of the TAGZyme procedure. Alternatively, vary time and/or temperature of incubation. Increase the incubation time when the incubation temperature is decreased.

Table 12. Recommendations for pilot pGAPase pyroglutamate removal experiments

Enzyme/reagent	For processing of 50 µg pyroglutamyl-extended target protein	
	Starting point	Titration range
pGAPase (25 U/ml)	50 mU (2 µl)	10–100 mU (0.4–4 µl)
Cysteamine-HCl (2 mM)*	5 µl	1–10 µl

* Dilute an aliquot of the cysteamine-HCl stock solution according to step 1 of protocol 7.

1. Prepare a 1/10 dilution of cysteamine-HCl stock solution (20 mM) using distilled water.
2. Mix 2 μ l cysteamine-HCl (2 mM) with 2 μ l of pGAPase Enzyme (25 U/ml) per 50 μ g of pyroglutamyl-extended protein.
pGAPase Enzyme is activated by cysteamine in this step.
3. Incubate for 10 min at 37°C. The mixture must be used within 30 min after preparation.
4. Add the activated pGAPase Enzyme to the pyroglutamyl-extended protein contained in the eluate from the first subtractive IMAC.
5. Incubate at the desired temperature. For time-period guidelines refer to Table 11.
If removal of pGAPase Enzyme is required, please refer to the protocol for small-scale subtractive IMAC in the Appendix, page 51.

Protocol 8. Preparative pyroglutamate removal using pGAPase Enzyme

This step is only necessary for proteins that have been incubated with Qcyclase Enzyme.

Generally, digestion with pGAPase Enzyme is complete after treatment for 90 minutes at 37°C with 1.0–1.25 U of pGAPase Enzyme per mg of protein (see Table 11). However, optimal conditions may vary from protein to protein. Therefore, it is recommended that a titration of the enzyme concentration or a control reaction with DAPase Enzyme (see “Analysis during the TAGZyme Procedure”, page 23) is carried out after completion of the TAGZyme procedure. Alternatively, vary time and/or temperature of incubation. Increase the incubation time when the incubation temperature is decreased.

1. **Mix 4 µl cysteamine-HCl (20 mM) with 40 µl of pGAPase Enzyme (25 U/ml) per mg of pyroglutamyl-extended protein.**

pGAPase Enzyme is activated by cysteamine in this step.

2. **Incubate for 10 min at 37°C. The mixture must be used within 30 min after preparation.**
3. **Add the activated pGAPase Enzyme to the pyroglutamyl-extended protein contained in the eluate from the first subtractive IMAC.**
4. **Incubate at the desired temperature. For incubation guidelines refer to Table 11.**

Protocol 9. Removal of pGAPase Enzyme by subtractive IMAC

This protocol applies to a cleavage reaction containing 1 mg target protein. Refer to Table 17, page 51 for Ni-NTA IMAC scale up recommendations.

- 1. Resuspend the Ni-NTA Agarose suspension by shaking and pipet 1 ml of the 50% suspension (corresponding to 0.5 ml bed volume) into one of the disposable columns provided in the kit.**

Alternatively, pack a LC or FPLC column with 0.5 ml bed volume of Ni-NTA Agarose*.

- 2. Equilibrate the column with 5 ml (10 column volumes) 1x TAGZyme buffer.**

Steps 1 and 2 can be performed during enzyme incubation. When using a chromatography system, do not exceed a flow rate of 0.5 ml/min to ensure quantitative binding of the 6xHis-tagged pGAPase Enzyme.

- 3. Pass the digestion reaction mixture through the column and collect the flow-through fraction.**

Important! The flow-through fractions contain the processed native protein.

- 4. Wash the column with 2 ml of 1x TAGZyme buffer or until the flow-through no longer contains protein. Collect the fraction(s).**

Important! The flow-through fractions contain the processed native protein.

- 5. Add the flow-through fraction from step 3 to the protein-containing fractions from step 4. Discard the Ni-NTA resin used in this subtractive step.**

We recommend investigating the efficiency of the pGAPase Enzyme-catalysed removal of pyroglutamate residues by subjecting an aliquot of the fully processed native protein to a post-process DAPase Enzyme treatment and SDS analysis (see Analysis during the TAGZyme procedure, page 23).

The TAGZyme procedure is finished and the detagged native protein is ready for further applications.

* An HR 5/2 or HR 5/5 FPLC column (Amersham Pharmacia Biotech) is suitable for such a volume of matrix. For processing of larger amounts of protein please refer to the bed-volume size and flow-rate recommendations on page 51. In general, column height should be $\geq 2x$ column diameter.

Troubleshooting Guide

Comments and suggestions

End product not sufficiently pure

Poor quality of tagged protein preparation

Refer to *The QIAexpressionist* for guidelines and limitations of Ni-NTA IMAC purification of His-tagged proteins.

Inefficient digestion

When working with proteins purified by IMAC using matrices other than Ni-NTA, metal ions may be leached from the matrix. These metal ions may have an inhibitory effect on digestion. Include EDTA in the desalting procedure prior to digestion.

Check N-terminal amino acid sequence for inefficiently cleaved dipeptides (Table 2, page 17). Check for the presence of DAPase Enzyme stop points in odd-numbered positions in the protein sequence. Check whether pH of the reaction is correct. The pH must be lowered when Glu or Asp residues are in the tag sequence to be cleaved.

Check the pH of the 1x TAGZyme Buffer preparation. pH optimum for the TAGZyme procedure is pH 6.7. to 7.5.

Check for the presence of denaturants. Even low concentrations will inactivate DAPase Enzyme.

Be sure that the length of the tag to be cleaved does not exceed 30 amino acids.

The optimal DAPase Enzyme-to-protein ratio may vary from protein to protein. Determine optimum conditions as described in pilot experiments. In some cases, a certain percentage of the tagged protein is not cleaved, e.g., due to steric hindrance. This residual His-tagged protein will be efficiently removed by subtractive IMAC.

Too many amino acids removed (DAPase digestion continues into the body of the target protein)

DAPase stop point is not present at correct position. Check sequence for correct positioning of stop point (Table 1, page 9).

When making use of glutamine (Q) stop point, be sure to include an excess of Qcyclase Enzyme in the incubation reaction with DAPase Enzyme. Refer to Table 8, page 30 for suitable ratio of DAPase Enzyme to Qcyclase Enzyme.

Comments and suggestions

Continued digestion during pGAPase step	<p>Inefficient first-round subtractive IMAC can lead to DAPase Enzyme being present during pGAPase incubation. Be sure to equilibrate the IMAC column as described in the protocol. Be sure not to exceed the recommended flow rate of 0.5 ml/min. Check pH of column load as binding of DAPase and Qcyclase Enzymes may be inefficient at a pH lower than 7.0.</p> <p>Inefficient subtractive IMAC – refer to <i>The QIAexpressionist</i> for general guidelines for IMAC and its limitations.</p>
Pyroglutamyl-extended protein remains in the final preparation	<p>pGAPase activity was inhibited. Be sure that urea is not present in the pGAPase reaction.</p> <p>Titrate pGAPase concentration to find out optimal concentration for complete digestion. Check for complete digestion by performing a DAPase control reaction as described on page 23.</p>
pGAPase Enzyme present after subtractive IMAC	<p>Subtractive IMAC was inefficient. Refer to <i>The QIAexpressionist</i> for general guidelines for IMAC and its limitations.</p>

Appendix

Enzyme specifications

DAPase Enzyme

Recombinant dipeptidyl peptidase I, polyhistidine-tagged (DPPI/dipeptidyl aminopeptidase I/DAPI/Cathepsin C; EC 3.4.14.1).

Source	Recombinant baculovirus expression vector system expressing the cloned DPPI gene from rat liver
Supplied form	Solution in 3 mM sodium phosphate; 150 mM NaCl; 2 mM cysteamine·HCl; 50% glycerol, pH 6.7–7.0
Purity	>98% (determined by SDS-PAGE)
Concentration	10 units/ml
Storage	–20°C
Stability	9 months at –20°C; 1 week at 2–8°C
Assay conditions	DAPase Enzyme is assayed at 37°C in 20 mM citric acid, 150 mM NaCl, 1 mM EDTA, 5 mM cysteamine, pH 4.5, containing 4 mM Gly-Phe- <i>p</i> -nitroanilide as substrate.
Unit definition	One unit is defined as the amount of enzyme that converts 1 μmol of substrate per minute under the conditions used.
Specific activity	7–11 unit/mg protein (protein determined by Bradford assay using BSA as standard)

Qcyclase Enzyme

Recombinant glutamine cyclotransferase, polyhistidine-tagged (GCT; EC 2.3.2.5)

Source	Recombinant baculovirus expression vector system expressing the cloned glutamine cyclotransferase gene from papaya latex
Supplied form	Solution in 8 mM sodium phosphate; 150 mM NaCl; 50% glycerol, pH 7.0
Purity	>98% (determined by SDS-PAGE)
Concentration	50 units/ml
Storage	-20°C
Stability	1 year at -20°C; 1 week at 2-8°C
Assay conditions	Qcyclase Enzyme (0.5-2 units) is assayed at 37°C in 50 mM Tris-HCl, pH 8.0, containing 2.5 mM Gln-Trp-Glu as substrate. The product (pyroGlu-Trp-Glu) is separated from the substrate by eluting the column with a linear NaCl gradient in 10 mM Tris-HCl, pH 8.0. The portion of Gln-Trp-Glu converted to pyroGlu-Trp-Glu detected at 280 nm is calculated from the respective peak areas.
Unit definition	One unit is defined as the amount of enzyme, which converts 1 μ mol of substrate per minute under the conditions used.
Specific activity	70-110 units/mg protein (protein determined by A_{280})

pGAPase Enzyme

Recombinant pyroglutamyl aminopeptidase, polyhistidine-tagged (PGAP; EC 3.4.19.3)

Source	<i>E. coli</i> expressing the cloned pyroglutamyl aminopeptidase gene from <i>Bacillus amyloliquefaciens</i>
Supplied form	Solution in 6 mM Tris-HCl; 40 mM NaCl; 2 mM EDTA; 2 mM cysteamine-HCl; 50% glycerol, pH 8.0
Purity	>98% (determined by SDS-PAGE)
Concentration	25 units/ml
Storage	-20°C
Stability	1 year at -20°C; 1 week at 2-8°C
Assay conditions	PGAP (0.01-0.025 Units) was assayed at 37°C in 20 mM Tris-HCl, 100 mM NaCl, 5 mM EDTA, 5 mM cysteamine, pH 8.0, containing 2 mM pyroglutamyl- <i>p</i> -nitroanilide as substrate.
Unit definition	One unit is defined as the amount of enzyme, which converts 1 μmol of substrate per minute under the conditions used.
Specific activity	4.5-7 units/mg protein (protein determined by A_{280})

Solutions required

10x TAGZyme Buffer

for 500 ml

200 mM NaH₂PO₄

13.80 g NaH₂PO₄·H₂O (MW 137.99 g/mol)

1.5 M NaCl

43.83 g NaCl (MW 58.44 g/mol)

Adjust to desired pH with NaOH. Filter (0.2 µm) into a sterile storage vessel and store at 2–8°C.

Note: Upon 1:10 dilution pH will shift from 6.3 to 7.0.

Use of blunt-end-cutting restriction enzymes to introduce various amino acids at the N-terminus of the mature protein

Blunt-ended restriction enzyme sites can be introduced at the 5' end of the protein-coding sequence by PCR, and cloned into the TAGZyme pQE-1 vector. Different restriction enzyme sites can be utilized to incorporate specific amino acids at the N-terminus of the mature protein (see Table 13). After expression of the construct, the His tag and glutamine residue are removed using the TAGZyme System.

For example, your (mature) protein of interest starts with the amino acid alanine (Ala). To introduce Ala into amino acid position 10 (immediately following the glutamine residue) in the TAGZyme pQE-1 vector, construct a primer containing the restriction enzyme sequence for *FspI*. A suitable sense PCR primer is shown below. GCA codes for the desired amino acid alanine, and the sequence TGC GCA forms the recognition sequence of *FspI*. *FspI*-restricted PCR products can be blunt-end ligated into *PvuII*-restricted TAGZyme pQE-1 vector, to give a construct encoding for a glutamine residue in an odd-numbered position, followed by the desired N-terminal amino acid, in this case alanine.

PCR sense primer:

N-terminal amino acid sequence: 5' N NNN TGC *FspI* GCA NNN NNN NNN NNN NNN 3'
Ala¹ aa² aa³ aa⁴ aa⁵ aa⁶

Table 13. Restriction enzyme recognition sequences for the incorporation of the indicated amino acid directly after the glutamine residue encoded by the TAGZyme pQE-1 vector*

Amino acid to be introduced	Suitable restriction enzyme	Restriction enzyme recognition sequence
Any	<i>MlyI</i>	GAGTC (N) ₅ ▼ <u>NNN</u>
		CTCAG (N) ₅ ▲ <u>NNN</u> <u>Xaa</u>
Any-Ser	<i>XmnI</i>	GAANN▼ <u>NN^{TTC} N</u>
		CTTNN▲ <u>NNAAG N</u> <u>Xaa-Ser</u>
Any [±] -Cys	<i>MslI</i>	CA Py NN▼ <u>NN Pu TG N</u>
		GT Pu NN▲ <u>NN Py AC</u> <u>Any[±]-Cys</u>
Any [±] -Trp		CA Py NN▼ <u>NN Pu TG N</u>
		GT Pu NN▲ <u>NN Py AC N</u> <u>Any[±]-Trp</u>
Ala	<i>FspI</i>	TGC▼ <u>GCA</u>
		ACG▲ <u>CGT</u> <u>Ala</u>
		<i>SfoI</i>
CCG▲ <u>CGG</u> <u>Ala</u>		
<i>AfeI</i>	AGC▼ <u>GCT</u>	
	TCG▲ <u>CGA</u> <u>Ala</u>	
	Arg	<i>BsrBI</i>
CTC▲ <u>GCC</u> <u>Arg</u>		
<i>NruI</i>		
	AGC▲ <u>GCT</u> <u>Arg</u>	
	Asn	<i>HpaI</i>
CAA▲ <u>TTG</u> <u>Asn</u>		
<i>HincII</i>		
	CA Pu▲ <u>Py TG</u> <u>Asn (AAC)</u>	

Table continued overleaf

Table 13. Continued

Gln-Pro†	<i>MscI</i>	TGG▼ <u>CCA</u> ACC▲GGT
		†Gln-Pro (CCA)
	<i>StuI</i>	AGG▼ <u>CCT</u> TCC▲GGA
		†Gln-Pro (CCT)
Gly	<i>NaeI</i>	GCC▼ <u>GGC</u> CGG▲CCG
		<u>Gly</u>
	<i>SmaI</i>	CCC▼ <u>GGG</u> GGG▲CCC
		<u>Gly</u>
Ile	<i>EcoRV</i>	GAT▼ <u>ATC</u> CTA▲TAG
		<u>Ile</u>
	<i>SspI</i>	AAT▼ <u>ATT</u> TTA▲TAA
		<u>Ile</u>
Leu	<i>PvuII</i>	CAG▼ <u>CIG</u> GTC▲GAC
		<u>Leu</u>
Lys	<i>DraI</i>	TTT▼ <u>AAA</u> AAA▲TTT
		<u>Lys</u>
Lys-Leu, Lys-Pro, Lys-His, Lys-Gln, Lys-Arg	<i>PmeI</i>	GTTT▼ <u>AAAC</u> CAAA▲TTTG
		<u>Lys-Leu/Pro/His/Gln/Arg</u>
Lys-Phe, Lys-Leu, Lys-Ile, Lys-Met, Lys-Val	<i>SwaI</i>	ATTT▼ <u>AAAT</u> TAAA▲TTTA
		<u>Lys-Phe/Leu/Ile/Met/Val</u>
Thr	<i>ScaI</i>	AGT▼ <u>ACT</u> TCA▲TGA
		<u>Thr</u>
Tyr	<i>BstZ17I</i>	GTA▼TAC CAT▲ATG
		<u>Tyr</u>

Table continued overleaf

Table 13. Continued

Val	<i>Bsa</i> I	Py AC▼GT Pu Py TG▲CA Py <u>Val</u>
	<i>Btr</i> I	CAC▼GTC GTG▲CAG <u>Val</u>
	<i>Pml</i> I	CAC▼GTG GTG▲CAC <u>Val</u>
	<i>Sna</i> BI	TAC▼GTA ATG▲CAT <u>Val</u>
Serine in position 2: Ala-Ser, Arg-Ser, Gln-Ser, Glu-Ser, Gly-Ser, Leu-Ser, Lys-Ser, Met-Ser, Pro-Ser, Ser-Ser, Thr-Ser, Trp-Ser, Val-Ser	<i>Psh</i> AI	GACNN▼NNGTC N CTGNN▲NNCAG N <u>Xaa-Ser</u>

* This list may not be complete! Only 5- or 6-nucleotide cutters are listed.

† Use of this restriction site incorporates a proline residue in the position following the glutamine stop. Proline functions as a stop two positions ahead, thus generating a protein with the N-terminal amino acids Gln1-Pro2... Omit Qcyclase Enzyme from the DAPase reaction in this case, as Qcyclase Enzyme will convert the glutamine residue to pyroglutamate.

‡ Any amino acid except Asp, Asn, His, Tyr, Cys, and Phe can be inserted (refer to the notice above† when Pro is incorporated).

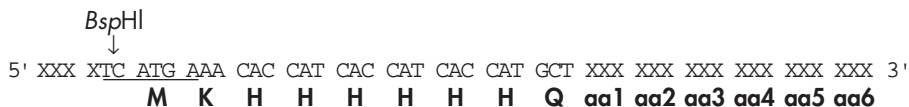
Recommended PCR cloning strategy for use of the vector pQE-TriSystem in combination with TAGZyme cleavage

The pQE-TriSystem vector allows parallel expression of a His-tagged recombinant protein in *E. coli*, baculovirus-infected insect cells, and mammalian cells using a single construct. The vector encodes a C-terminal His tag (which cannot be removed by the TAGZyme System). To make use of this extremely versatile expression vector, an N-terminal His tag must be introduced by PCR. A cloning strategy and primer design recommendations are given below.

- Clone into the most N-terminal restriction site, *Nco*I, to avoid the introduction of slowly cleaved dipeptides (see Table 2, page 17).
- Design a 5' (sense) oligonucleotide primer including the *Nco*I-compatible 5' restriction site *Bsp*HI and including sequences coding for a 6xHis tag (the use of the *Bsp*HI site allows the insertion of a lysine residue as the next amino acid following the start methionine).
- Include a C-terminal stop codon (UAA) after the last amino acid
- Clone into any one of the C-terminal restriction sites (e. g., *Hind*III)

Refer to *The QIAexpressionist* (8) or visit us at www.qiagen.com for more details on the pQE-TriSystem vector.

Design of the 5' (sense) PCR primer with an introduced glutamine stop point*



* If the protein to be expressed contains a natural stop point within the amino acids aa1 – aa3 (see Table 1, page 9) this can be used as a DAPase Enzyme stop point instead of the glutamine residue.

Design of the 3' (antisense) PCR primer including a stop codon (TTA) for cloning into the *Hind*III site

Cloning into restriction sites located 3' of *Nco*I is not recommended, because this will result in the insertion of an alanine residue directly behind the initial methionine. Alanine does not efficiently prevent methionine processing (1) which may result in erroneously processed DAPase Enzyme digestion products. Furthermore, the second N-terminal dipeptide would be Ile-Ser which will be inefficiently cleaved (see Table 2, page 17).

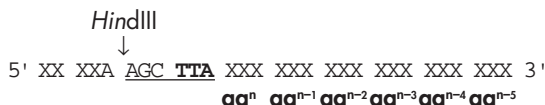


Table 14. The genetic code

First position (5' end)	Second position				Third position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

Table 15. *E. coli* codon usage table. For each codon, frequency of usage (%) and the corresponding amino acid are given

First position	Second position								Third position
	U		C		A		G		
U	2.23	Phe	0.85	Ser	1.62	Tyr	0.52	Cys	U
	1.66	Phe	0.86	Ser	1.22	Tyr	0.65	Cys	
	1.39	Leu	0.72	Ser	0.20	Stop	0.09	Stop	
	1.36	Leu	0.89	Ser	0.02	Stop	1.52	Trp	
C	1.10	Leu	0.70	Pro	1.29	His	2.09	Arg	C
	1.11	Leu	0.55	Pro	0.97	His	2.20	Arg	
	0.39	Leu	0.84	Pro	1.53	Gln	0.36	Arg	
	5.26	Leu	2.32	Pro	2.88	Gln	0.54	Arg	
A	3.03	Ile	0.90	Thr	1.77	Asn	0.88	Ser	A
	2.51	Ile	2.34	Thr	2.17	Asn	1.61	Ser	
	0.44	Ile	0.71	Thr	3.36	Lys	0.21	Arg	
	2.53	Met	1.44	Thr	1.03	Lys	0.12	Arg	
G	1.83	Val	1.53	Ala	3.21	ASp	2.47	Gly	G
	1.53	Val	2.55	Ala	1.91	Asp	2.96	Gly	
	1.09	Val	2.01	Ala	3.94	Glu	0.80	Gly	
	2.59	Val	3.36	Ala	1.78	Glu	1.11	Gly	

His tags suitable for exoproteolytic cleavage by the TAGZyme System

The following His tags have been shown to deliver excellent expression rates in *E. coli* and be well-suited for convenient cleavage using the TAGZyme System. For a more detailed overview, see reference 12.

Table 16. Amino acid and encoding nucleotide sequences for recommended His tags

	1	2	3	4	5	6	7	8	9
Amino acid	M	K	H	H	H	H	H	H	(Q)
Codon	ATG	AAA	CAT	CAC	CAT	CAC	CAT	CAC	(GCT)
Amino acid	M	R	H	H	H	H	H	H	(Q)
Codon	ATG	CGT	CAT	CAC	CAT	CAC	CAT	CAC	(GCT)

Small-scale subtractive IMAC

- Pipet 50 µl Ni-NTA suspension (25 µl settled bed volume) into a microcentrifuge tube and equilibrate by spinning briefly (10 s), removing the supernatant, adding 500 µl TAGZyme buffer, spinning briefly (10 s), and removing the supernatant.
- Add the TAGZyme Enzyme reaction mixture and incubate at 4°C or room temperature for 10 min on a shaker platform or an end-over-end shaker. Ensure that the suspension is mixed well.
- To recover the target protein, spin briefly (10 s), and carefully remove the supernatant. Be sure not to disturb the Ni-NTA matrix, which contains the bound TAGZyme Enzyme.

Recommendations for subtractive IMAC scale-up

The use of a chromatography system with which the flow rate can be precisely controlled is recommended. When processing larger columns the flow rate is a critical factor for the efficient binding of His-tagged proteins to the Ni-NTA matrix. In addition, the use of Ni-NTA Superflow is recommended as it can withstand higher back pressures (up to 10 bar = 1 MPa). Table 17 gives guidelines for flow rates and column dimensions to be used when scaling up subtractive IMAC.

Table 17. Recommended column dimensions and flow rates for Ni-NTA IMAC scale up

Amount of protein to be processed	Ni-NTA bed volume	Column dimensions (internal diameter x length)	Flow rate (ml/min)		Linear flow rate (cm/h)	
			Load	Wash	Load	Wash
Up to 1 mg	0.5 ml	0.5 cm x 2.5 cm	0.5	1.0	150	300
50 mg	10 ml	1.6 cm x 5 cm	5	10	150	300
1 g	200 ml	5 cm x 10.2 cm	50	100	150	300

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Hoffmann-La Roche owns patents and patent applications pertaining to the application of Ni-NTA resin (Patent series: RAN 4100/63: USP 4.877.830, USP 5.047.513, EP 253 303 B1), and to 6xHis-coding vectors and His-labeled proteins (Patent series: USP 5.284.933, USP 5.130.663, EP 282 042 B1). All purification of recombinant proteins by Ni-NTA chromatography for commercial purposes, and the commercial use of proteins so purified, require a license from Hoffmann-La Roche.

TAGZyme technology is licensed under U.S. Patent No. 5,691,169, U.S. Patent No. 5,783,413 and E.U. Patent No. 00759931B1.

Ordering Information

Product	Contents	Cat. No.
TAGZyme Kit	0.5 Units DAPase Enzyme, 30 Units Qcyclase Enzyme, 10 Units pGAPase Enzyme, 20 mM Cysteamine-HCl (1 ml), Ni-NTA Agarose (10 ml), 20 Disposable Columns	34300
TAGZyme pQE Vector Set	TAGZyme pQE-1 and -2 Vector DNA, 25 µg each	32932
TAGZyme DAPase Enzyme (2.5 U)	2.5 Units DAPase Enzyme, 20 mM Cysteamine-HCl (1 ml)	34362
TAGZyme DAPase Enzyme (50 U)*	50 Units DAPase Enzyme, 20 mM Cysteamine-HCl (25 ml)	Inquire
TAGZyme Qcyclase/pGAPase Enzymes (150 U/50 U)	150 Units Qcyclase Enzyme, 50 Units pGAPase Enzyme	34342
TAGZyme Qcyclase/pGAPase Enzymes (3000 U/1000 U)*	3000 Units Qcyclase Enzyme, 1000 Units pGAPase Enzyme	Inquire
Related products		
Ni-NTA Agarose† (25 ml)	25 ml nickel-charged resin (max. pressure: 2.8 psi)	30210
Ni-NTA Superflow† (25 ml)	25 ml nickel-charged resin (max. pressure: 140 psi)	30410
Polypropylene Columns (1 ml)	50/pack, 1 ml capacity	34924

* Bulk enzyme quantities are customized products; delivery may take up to 6 weeks. Enzymes are also available in GMP-grade. Please inquire.

† Available in bulk quantities; please inquire.

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