

# QconCAT inquiry form



Dear valued customer,  
thank you very much for your request.

To receive an appropriate quotation, please answer the following questions to the best of your knowledge and return the order inquiry form to PolyQuant via E-mail (info@polyquant.com) or fax (+49-9405-96999-28). Any information you provide will be treated with the highest confidentiality independent of a CDA<sup>3</sup>. If you have any questions, please do not hesitate to contact us.

For internal use:	<b>Name</b>	<input type="text"/>
	<b>Position</b>	<input type="text"/>
	<b>Company/Institute</b>	<input type="text"/>
	<b>Street Address</b>	<input type="text"/>
	<b>Zip Code</b>	<input type="text"/>
	<b>City</b>	<input type="text"/>
	<b>Country</b>	<input type="text"/>
	<b>Telephone/Fax</b>	<input type="text"/>
	<b>E-mail</b>	<input type="text"/>
	<b>VAT-ID</b>	<input type="text"/>

## 1) General information:

**Name of QconCAT:**

(your preferred name for the construct)

**Source (organism/matrix):**

(e.g. bacteria, yeast, cultured cells,  
mouse/kidney, human/plasma, plant/leaves etc)

**Number of proteins to quantify:**

**Total number of peptides for quantification:**

**MS-data for peptides available<sup>1</sup>:**  Yes  No <sup>1</sup>(the peptides have been detected previously e.g. by the customer)

**Peptide selection by:**  Customer  PolyQuant  Customer/PolyQuant

MTA<sup>2</sup> necessary  Yes  No

<sup>2</sup>Material transfer agreement

CDA<sup>3</sup> necessary:  Yes  No

<sup>3</sup>Confidentiality disclosure agreement

The QconCAT(s) will be used for:  Exploratory/Discovery Analysis  
 High-throughput analysis

## 2) Gene construct information

Gene construct exists:  Yes  No

Select yes if gene construct exists and continue with 3)  
Select no if gene construct(s) should be designed by PolyQuant

Protein Optimization:  Yes  No

Select yes if PolyQuant shall shuffle peptides to optimize the properties of the QconCAT  
Select no if the order of the peptides needs to remain as provided by the customer

## 3) Expression specific information

Labeling option:  unlabeled  13C Arg/Lys  13C, 15N Arg/Lys  15N

other (please specify):

Purity:  crude extract

IMAC purified (6 M GdnHCl)

IMAC purified (8 M Urea)

IMAC purified, dialysed

requires additional buffer screen to identify suitable storage buffer

## 4) Other services

I would like to receive peptide libraries and iRT values for my QconCAT (Skyline file)

Short gradient (free of charge)

Long gradient (extra fee)

PolyQuant performs absolute protein quantification of the target proteins (full service project)

Discovery proteomics to identify peptides suitable for quantification by PolyQuant

Development of protein extraction protocol by PolyQuant

Comment: