

## Line-By-Line Instructions for Filling in a Target Request Record

Below are the fields contained in the "Target Request" record, example answers, and any answer directives. Fields marked with \* on this sheet are required; when filling in the form you can determine whether all required fields have been filled by choosing Target Request > Verify Request". When the request is submitted there will be automatic notification if required fields have not been filled. Filling in the fields that are not required is desirable and may speed the process of review as well as increase the chance of acceptance of your target.

### GENERAL REQUEST INFORMATION

\*Recipient Lab: CESG [Choose from pull-down menu]  
\*Request Title [YOUR CHOICE]  
Request Status [changeable by author only by submitting form]  
Email Notification [refers to record author]

### PRINCIPLE INVESTIGATOR

\*Name  
\*Email  
Email notification  
\*Phone  
\*Address

### ALTERNATE CONTACT INFORMATION

Name  
Email  
Email Notification  
Phone  
Address

### TARGET DESCRIPTION

\*Main ID [An identifier from a major database]  
\*Secondary ID [YOUR CHOICE]  
\*Unigene ID [NCBI Identifier]  
ORF Type [Choose from pull-down menu]  
Source Organism E. coli [If available on the pull-down menu, choose organism name from the list. If the organism name is not available in the pull-down, fill in the Genus/Species/ and (optional) strain fields]  
Source DB Name NCBI [Database source of Protein Main ID]  
Source DB Version [Version number of Database Source]  
Source DB Date [Date that information was taken from Database.]  
\*ORF Nucleotide Sequence [MUST EXACTLY MATCH TARGET PROTEIN TO BE EXPRESSED. After entering DNA sequence, press "=" button or any other white cell to calculate parameters corresponding to the protein to be made]  
Sig peptide length [Fill in only if known to be present and give your best guess of length]  
Trans membrane [Check the box if your answer is "Yes." If not sure, do not check the box]  
Predicted Function [If known or predicted, describe in 100 characters or less]  
\*Abstract [Describe your interest in the structure of the protein in 4000 characters or less]  
Competition for Structure [Is anyone else known to be working on the structure? If "Yes," give details in 100 characters or less]  
Submitted material [Select from the pull-down menu, noting the guidelines in panel below. If choosing "Other," fill in the "Details" field. If your sample does not meet these criteria, we encourage you to contact us directly to further discuss the situation]

**Line-By-Line Instructions for Filling in a Target Request Record (page 2)**

If you choose "cDNA" as Submitted Material, these additional fields will appear:

**cDNA source** Mammalian Gene Collection (MGC)

**Cloning Plasmid** pENTR

**Cloning Plasmid Construct** pENTR-GAF3

**Expression Plasmid** pET15b

**Expression Plasmid Construct** pET15b-GAF3

**Plasmid Antibiotic Marker** ampicillin

**cDNA Amount** 2 ug

**cDNA volume** 10 ul

**cDNA Concentration** 0.2 ug/ul

If you choose "Protein" as Submitted Material, these additional fields will appear:

**Form** [\[Choose from pulldown menu\]](#)

**Expression system scientific name** E. coli

**Expression system strain** BL21

**Expression system vector type** plasmid

**Expression system plasmid name** pET15b

**Manipulated source details** [\[Any other expression information that might be useful\]](#)

**Component List** [as many as applicable; Additional lines may be added by pressing "+" button to right](#)

**Protein concentration** [Choose unit, enter concentration](#)

**Solvent** H2O

**Buffer** 5 mM Bis Tris

**Added Salt** 50 mM NaCl

**Reductant** 5 mM DTT

**Lock Solvent** (NMR samples only): 5% D2O

**Internal Reference Compound** [\(NMR samples only\): 0.3 mM DSS](#)

**Labeling** [Choose Semet, 15N, 15N and 13C, or None, and set % incorporation \(usually 100%\)](#)

**pH** [\[Set type and enter pH value\]](#)

**Ionic strength** 7.0 mM

**Sample Volume (µL)** 300

**Publication** [\[Enter any reference information that might be useful, by cut-and-paste.\]](#)

**Images** [\[Attach any images that might be useful by pressing "+", and then browsing for the file, and selecting it. \(.jpg, .png, and .gif files are supported\)\]](#)

**File** [\[Attach any files that might be useful by pressing "+", and then browsing for the file, and selecting it. \(Text, Word, Excel, CSV, Sequence, PDF, and Powerpoint files are supported\).\]](#)