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1. Which professional category best describes you? Please select only one.

- Bioinformatics professional
 Life Science Researcher
 Educator
 Student
 Healthcare professional
 Technician
 Librarian / Information Specialist
 Computer Scientist / Software Developer
 Other (please specify)

2. Please pick one category that best describes your organization.

- College or University
 Research Institute
 Commercial / Industry
 Government
 Non-profit Organization
 Hospital/health care organization
 Other (please specify)

3. How frequently do you use NCBI's Identical Protein Groups (IPG)?

- Daily
 Weekly
 Monthly
 Yearly
 This is my first visit

4. Do you want to know the source of the protein names in an IPG?

- Yes
 No

5. What was your primary motivation for visiting IPG today?

- Determine the taxonomic distribution for a set of identical proteins
 Find an exemplar sequence for a set of identical proteins (e.g. "best" accession)
 Find all sequence records representing a set of identical proteins
 Find the corresponding nucleotide coordinates for a protein's coding sequence (CDS) in one or more organisms
 Identify genome assemblies on which this protein is annotated
 Find the best name for a protein
 Look at a graphical display of a protein sequence
 Find relevant literature
 View a protein in its genomic context(s)
 Evaluate the domain structure of a protein
 Other (please specify)

6. Did you find what you were looking for?

- Yes
 No

7. Considering your *primary* motivation for visiting IPG today, how easy was it to find what you were looking for on the IPG web page ?

- Very easy
 Easy
 Neither easy nor difficult
 Difficult
 Very difficult

8. Considering your *primary* motivation for visiting IPG today, how easy was it to download/retrieve the data you were looking for?

- Very easy
 Easy
 Neither easy nor difficult
 Difficult
 Very difficult
 Not Applicable

9. Considering your *primary* motivation for visiting IPG today, will you also use the NCBI Protein database to accomplish some part or all of this task?

- Yes
 No, IPG is sufficient
 I'm not familiar with NCBI Protein

10. Which of the following tasks do you perform with data from IPG? Please check all that apply.

- Search for related proteins or IPGs (e.g. using BLAST or other sequence similarity search tool)
 Perform a multiple alignment to other proteins (e.g. using COBALT, MAFFT, muscle, kalign, etc.)
 Generate a taxonomic tree of organisms in which this protein has been identified
 Evaluate the gene neighborhood in one or more taxa
 Look for possible taxonomic mis-classifications (i.e. protein/taxonomic mismatch)
 Other (please specify)

11. In addition to the website, do you retrieve data from IPG using any of the following mechanisms?

- Yes, using the E-Utilities / EDirect
 Yes, using other computational approaches (e.g. custom scripts)
 No, I only use the website

12. Please outline the workflow that you use with the data you are seeking today at NCBI, including other NCBI and non-NCBI resources used.

13. If there was one thing you could change about the IPG pages, what would it be?

14. How likely is it that you would recommend the IPG pages to a friend or colleague?

Not at all likely

Extremely likely

0	1	2	3	4	5	6	7	8	9	10
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We welcome your input! Please contact us at suggest@ncbi.nlm.nih.gov if you would like to provide additional feedback about the IPG resource.

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