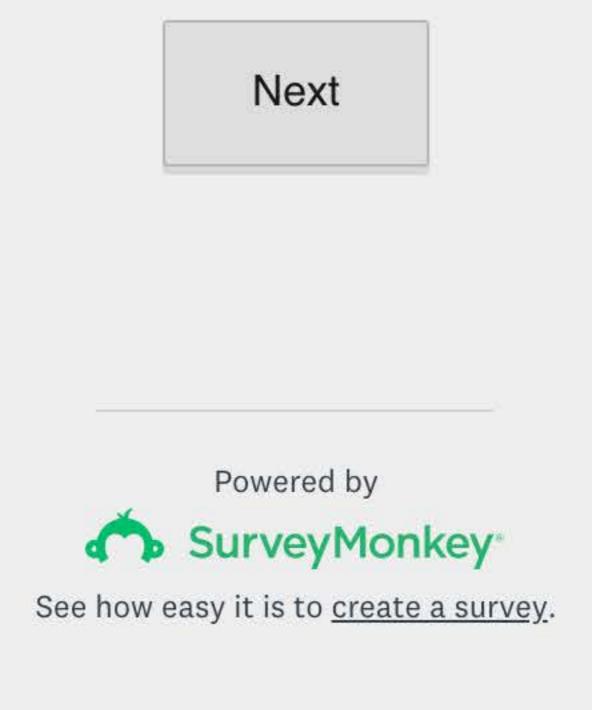
IPG Survey

We want to improve NCBI's products and services. We would like to learn more about how this site helps you with your work, and what we can do better. Please click "next" below to get started.

OMB Control Number: 0925-0648

Expiration Date: 05/31/2021

Public reporting burden for this collection of information is estimated to average 4 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a current valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to NIH Project Clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-0648). Do not return the completed form to this address.



Privacy & Cookie Policy

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

Bioinformatics professional	
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 F	Protein Groups (IPG)?
Daily	
Weekly	
Monthly	
Yearly	
This is my first visit	
Triio io iriy iirot viole	
I. Do you want to know the source of the protei	n names in an IPG?
Yes	
) No	
5. What was your primary motivation for visiting	g IPG today?
Determine the taxonomic distribution for a set of iden	tical proteins
Find an exemplar sequence for a set of identical prot	reins (e.g. "best" accession)
Find all sequence records representing a set of ident	
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 a	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)	
S Did vou find what vou were looking for?	
6. Did you find what you were looking for?	
Yes	
) No	
the IPG web page ?	ing IPG today, how easy was it to find what you were looking for on
Very easy	
Easy	
Neither easy nor difficult	
Difficult	
Very difficult	
8. Considering your <i>primary</i> motivation for visit	ing IPG today, how easy was it to download/retrieve the data you
	이 가게 되는 이번 가장 이번 지원 이번 가게 되었다. 그는 이번 이 경우를 가장 이 전에 가장 이 없는 것이 되었다면 하는데 되었다.
were looking for? Very easy	
were looking for? Very easy Easy	
were looking for? Very easy Easy Neither easy nor difficult	
were looking for? Very easy Easy Neither easy nor difficult Difficult	
were looking for? Very easy Easy Neither easy nor difficult	
were looking for? Very easy Easy Neither easy nor difficult Difficult	
 Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 	
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your <i>primary</i> motivation for visit	ting IPG today, will you also use the NCBI Protein database to
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your <i>primary</i> motivation for visit accomplish some part or all of this task?	ing IPG today, will you also use the NCBI Protein database to
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your <i>primary</i> motivation for visit accomplish some part or all of this task? Yes	ting IPG today, will you also use the NCBI Protein database to
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your <i>primary</i> motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient	ting IPG today, will you also use the NCBI Protein database to
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your <i>primary</i> motivation for visit accomplish some part or all of this task? Yes	ting IPG today, will you also use the NCBI Protein database to
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein	
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein	ing IPG today, will you also use the NCBI Protein database to n with data from IPG? Please check all that apply.
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein	n with data from IPG? Please check all that apply.
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your <i>primary</i> motivation for visit 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	n with data from IPG? Please check all that apply. Tor other sequence similarity search tool)
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAST	n with data from IPG? Please check all that apply. Tor other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.)
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAST) Perform a multiple alignment to other proteins (e.g. u	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) s protein has been identified
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAST) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) s protein has been identified
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) s protein has been identified
Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) s protein has been identified
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) s protein has been identified
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify)	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch)
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify)	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) s protein has been identified
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify)	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch)
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify)	In with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect	n with data from IPG? Please check all that apply. Tor other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. possible taxonomic mis-classifications (i.e. possible taxonomic mis-classifications) Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. customs)	In with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms?
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Cenerate a taxonomic tree of organisms in which this evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p. Other (please specify) 11. In addition to the website, do you retrieve day Yes, using other computational approaches (e.g. cus No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used.	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Cenerate a taxonomic tree of organisms in which this evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p. Other (please specify) 11. In addition to the website, do you retrieve day Yes, using other computational approaches (e.g. cus No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used.	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Mich of the following tasks do you perform Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) th the data you are seeking today at NCBI, including other NCBI and
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Cearch for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) th the data you are seeking today at NCBI, including other NCBI and
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website 12. Please outline the workflow that you use without-NCBI resources used.	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Search for related proteins or IPGs (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using other computational approaches (e.g. cus No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the service of the process of the	In with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) sprotein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be? the IPG pages to a friend or colleague?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this is evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p.) Other (please specify) 11. In addition to the website, do you retrieve day Yes, using other computational approaches (e.g. cus) No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the likely is it that you would recommend to Not at all likely	In with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and bout the IPG pages, what would it be? The IPG pages to a friend or colleague? Extremely likely
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this is evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p.) Other (please specify) 11. In addition to the website, do you retrieve day Yes, using other computational approaches (e.g. cus) No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the likely is it that you would recommend to Not at all likely	In with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) sprotein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and put the IPG pages, what would it be? the IPG pages to a friend or colleague?
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus) No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the second of the second o	In with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein/has been identified arta from IPG using any of the following mechanisms? ata from IPG using any of the following mechanisms? ath the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be? the IPG pages to a friend or colleague? Extremely likely
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this is evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p.) Other (please specify) 11. In addition to the website, do you retrieve day Yes, using other computational approaches (e.g. cus) No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the likely is it that you would recommend to Not at all likely	In with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) protein has been identified ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and bout the IPG pages, what would it be? The IPG pages to a friend or colleague? Extremely likely
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus) No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the surface of the process of the process used that all likely is it that you would recommend to the surface of the process used that all likely	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) sprotein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? Ath the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be? Extremely likely 1 5 6 7 8 9 10
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Cenerate a taxonomic tree of organisms in which this accomplish some part or all of the proteins (e.g. using BLAS) Perform a multiple alignment to other proteins (e.g. using BLAS) Considering your primary motivation for visit accomplish some part or all of this task? Yes No, IPG is sufficient I'm not familiar with NCBI Protein Generate a taxonomic tree of organisms in which this is a taxonomic tree of organisms in which this is a taxonomic mis-classifications (i.e. p. Other (please specify) Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the workflow that you use with non-NCBI resources used.	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) sprotein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? Ath the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be? Extremely likely 1 5 6 7 8 9 10
Were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus) No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the surface of the process of the process used that all likely is it that you would recommend to the surface of the process used that all likely	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) sprotein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? Ath the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be? Extremely likely 1 5 6 7 8 9 10
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS') Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve day Yes, using other computational approaches (e.g. cus) No, I only use the website 12. Please outline the workflow that you use with non-NCBI resources used. 13. If there was one thing you could change about the subject of the process of the	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) sprotein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? stom scripts) the the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be? Extremely likely 1 5 6 7 8 9 10
were looking for? Very easy Easy Neither easy nor difficult Difficult Very difficult Not Applicable 9. Considering your primary motivation for visit 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 Search for related proteins or IPGs (e.g. using BLAS' Perform a multiple alignment to other proteins (e.g. u Generate a taxonomic tree of organisms in which this Evaluate the gene neighborhood in one or more taxa Look for possible taxonomic mis-classifications (i.e. p Other (please specify) 11. In addition to the website, do you retrieve do Yes, using the E-Utilities / EDirect Yes, using other computational approaches (e.g. cus No, I only use the website 12. Please outline the workflow that you use withon-NCBI resources used. 13. If there was one thing you could change about all likely 14. How likely is it that you would recommend to the standard of the stand	n with data from IPG? Please check all that apply. For other sequence similarity search tool) sing COBALT, MAFFT, muscle, kalign, etc.) sprotein has been identified protein/taxonomic mismatch) ata from IPG using any of the following mechanisms? Ath the data you are seeking today at NCBI, including other NCBI and but the IPG pages, what would it be? Extremely likely 1 5 6 7 8 9 10

See how easy it is to <u>create a survey</u>.

IPG Survey, Contact Us

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.

