

**Xuqian Tan**  
**A13642946**  
**xut006@ucsd.edu**

### Questions:

[Q1] Tell me the name of a protein you are interested in. Include the species and the accession number. This can be a human protein or a protein from any other species as long as its function is known.

If you do not have a favorite protein, select human RBP4 or KIF11. Do not use beta globin as this is in the worked example report that I provide you with online.

Name: Cellular tumor antigen p53 isoform b

Accession: NP\_001119586

Species: Homo Sapiens

[Q2] Perform a BLAST search against a DNA database, such as a database consisting of genomic DNA or ESTs. The BLAST server can be at NCBI or elsewhere. Include details of the BLAST method used, database searched and any limits applied (e.g. Organism).

Method: TBLASTN (2.7.1) search against nematode ESTs

Database: Expressed Sequence Tags (est)

Organism: Zebra Fish (taxid:7955)

The screenshot shows the NCBI BLAST search interface. At the top, there are tabs for 'blastn', 'blastp', 'blastx', 'tblastn', and 'tblastx'. The 'tblastn' tab is selected. Below the tabs, there is a header 'TBLASTN search translated nucleotide databases using a protein query. more...'. On the right, there are links for 'Reset page' and 'Bookmark'.

The main form is divided into several sections:

- Enter Query Sequence:** A text box contains 'NP\_001119586'. There is a 'Clear' button and a 'Query subrange' section with 'From' and 'To' input fields.
- Or, upload file:** A 'Choose File' button and a 'No file chosen' message.
- Job Title:** A text box contains 'NP\_001119586:cellular tumor antigen p53 isoform...'. Below it is a prompt 'Enter a descriptive title for your BLAST search'.
- Align two or more sequences:** A checkbox that is currently unchecked.
- Choose Search Set:** A section with several options:
  - Database:** A dropdown menu showing 'Expressed sequence tags (est)'.
  - Organism:** A text box contains 'zebra fish (taxid:7955)'. There is an 'exclude' checkbox and a '+' button. Below it is a prompt 'Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown'.
  - Exclude:** A section with two checkboxes: 'Models (XM/XP)' and 'Uncultured/environmental sample sequences'.
  - Limit to:** A checkbox for 'Sequences from type material'.
  - Entrez Query:** A text box for 'Enter an Entrez query to limit search'.
- BLAST:** A blue button.
- Search database:** A text box containing 'Expressed sequence tags (est) using Tblastn (search translated nucleotide databases using a protein query)'. There is a checkbox for 'Show results in a new window'.
- Algorithm parameters:** A link at the bottom left.
- Note:** A yellow box at the bottom right stating 'Parameter values that differ from the default are highlighted in yellow and marked with a sign'.

Chosen match: Accession CK142355, a 785 base pair clone from Danio rerio. See below for alignment details.



[Download](#) [GenBank](#) [Graphics](#)

AGENCOURT\_16822121 NIH\_ZGC\_10 Danio rerio cDNA clone IMAGE:7048922 5', mRNA sequence

Sequence ID: [CK142355.1](#) Length: 785 Number of Matches: 1

Range 1: 23 to 640 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
292 bits(747)	5e-101	Compositional matrix adjust.	139/206(67%)	158/206(76%)	0/206(0%)	+2
Query 92	PLSSSVPSQKTYQGSYGFRLLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTP				151	
	P +S+VP Y G++GFRL F SGTAKSVTCTYSP LNK+ CQLAKTCPVQ+ VD P					
Sbjct 23	PTTSTVPETSDYPGAHGFRLLRFPQSGTAKSVTCTYSPDLNKLKQLAKTCPVQMVDVAP				202	
Query 152	PPGTRVRAMAIYKQSQHMTVEVRRCPHHERCSDSDGLAPPQHILIRVEGNLRVEYLDDRNT				211	
	P G+ VRA AIYK+S+H+ EVVRRCPHHER D D LAP HLIRVEGN R Y +D T					
Sbjct 203	PQGSVVRATAIYKKSEHVAEVVRRCPHHERTPDGDNLAPAGHLIRVEGNQRANYREDNIT				382	
Query 212	FRHSVVVPYEPPEVGSDCCTTIHNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFE				271	
	RHSV VPYE P++G++ TT+ NYMCNSSCMGGMNRRPILTIITLE G LLGR SFE					
Sbjct 383	LRHSVFVPYEAPQLGAEWTTVLLNYMCNSSCMGGMNRRPILTIITLETXEGQLLGRRSFE				562	
Query 272	VRVCACPGRRDRRTEENLRKKGEPHH		297			
	VRVCACPGRDR+T E+ +K P H					
Sbjct 563	VRVCACPGRDRKTXGEHFQKT*RPKH		640			

#### Alignment details:

AGENCOURT\_16822121 NIH\_ZGC\_10 Danio rerio cDNA clone IMAGE:7048922 5', mRNA sequence

Sequence ID: [CK142355.1](#) Length: 785 Number of Matches: 1

Related Information

[UniGene](#)-clustered expressed sequence tags

Range 1: 23 to 640 [GenBank](#) [Graphics](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
292 bits(747)	5e-101	Compositional matrix adjust.	139/206(67%)	158/206(76%)	0/206(0%).	+2
Query 92	PLSSSVPSQKTYQGSYGFRLLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTP				151	
	P +S+VP Y G++GFRL F SGTAKSVTCTYSP LNK+ CQLAKTCPVQ+ VD P					
Sbjct 23	PTTSTVPETSDYPGAHGFRLLRFPQSGTAKSVTCTYSPDLNKLKQLAKTCPVQMVDVAP				202	
Query 152	PPGTRVRAMAIYKQSQHMTVEVRRCPHHERCSDSDGLAPPQHILIRVEGNLRVEYLDDRNT				211	
	P G+ VRA AIYK+S+H+ EVVRRCPHHER D D LAP HLIRVEGN R Y +D T					
Sbjct 203	PQGSVVRATAIYKKSEHVAEVVRRCPHHERTPDGDNLAPAGHLIRVEGNQRANYREDNIT				382	
Query 212	FRHSVVVPYEPPEVGSDCCTTIHNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFE				271	
	RHSV VPYE P++G++ TT+ NYMCNSSCMGGMNRRPILTIITLE G LLGR SFE					
Sbjct 383	LRHSVFVPYEAPQLGAEWTTVLLNYMCNSSCMGGMNRRPILTIITLETXEGQLLGRRSFE				562	
Query 272	VRVCACPGRRDRRTEENLRKKGEPHH		297			
	VRVCACPGRDR+T E+ +K P H					
Sbjct 563	VRVCACPGRDRKTXGEHFQKT*RPKH		640			

[Q3] Gather information about this “novel” protein. At a minimum, show me the protein sequence of the “novel” protein as displayed in your BLAST results from [Q2] as FASTA format (you can copy and paste the aligned sequence subject lines from your BLAST result page if necessary) or translate your novel DNA sequence using a tool called EMBOSS Transeq at the EBI. Don’t forget to translate all six reading frames; the ORF (open reading frame) is likely to be the longest sequence without a stop codon. It may not start with a methionine if you don’t have the complete coding region. Make sure the sequence you provide includes a header/subject line and is in traditional FASTA format.

Chosen sequence:

>A. Danio rerio protein (sequence taken from BLAST result)

```
PTTSTVPETSDYPGAHGFRRLRFPQSGTAKSVTCTYSPDLNKLCCQLAKTCPVQMVDVAPPQGSVVRATAIYKKSEHVAEVRRCF
HHERTPDGDNLAPAGHLIRVEGNQRANYREDNITLRHSVFVPYEAPQLGAEWTTVLLNYMCNSSCMGGMNRRPILTIITLETXEGQ
LLGRRSFEVRVCACPRDRKTXGEHFQKT*RPKH
```

Name: Danio rerio cDNA clone

Species: Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

[Q4] Prove that this gene, and its corresponding protein, are novel. For the purposes of this project, “novel” is defined as follows. Take the protein sequence (your answer to [Q3]), and use it as a query in a blastp search of the nr database at NCBI.

Details:

A BLASTP search against NR database (see setup in first screen-shot below) yielded a top hit result is to a protein from Danio rerio.

The screenshot shows the NCBI BLAST search interface. At the top, there's a navigation bar with "BLAST" and "blast suite" links, and a header with "Home", "Recent Results", "Saved Strategies", and "Help". Below this is the "Standard Protein BLAST" section. The main area is divided into several sections: "Enter Query Sequence" where the protein sequence is pasted, "Or, upload file" with a file selection button, "Job Title" with a text input, and "Align two or more sequences" with a checkbox. The "Choose Search Set" section includes "Database" (Non-redundant protein sequences (nr)), "Organism" (with a text input and an "exclude" checkbox), "Exclude" (with checkboxes for "Models (XM/XP)", "Non-redundant RefSeq proteins (WP)", and "Uncultured/environmental sample sequences"), and "Entrez Query" (with a text input and a "Create custom database" link). The "Program Selection" section shows the "Algorithm" dropdown set to "blastp (protein-protein BLAST)". At the bottom, there's a "BLAST" button and a checkbox for "Show results in a new window".

See additional screen shots below for top hits and selected alignment details:

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	<a href="#">cellular tumor antigen p53 isoform 1 [Danio rerio]</a>	407	407	97%	6e-141	95.50%	<a href="#">NP_001258749.1</a>
<input type="checkbox"/>	<a href="#">tumor suppressor p53 [Danio rerio]</a>	407	407	97%	7e-141	95.50%	<a href="#">AAO85406.1</a>
<input type="checkbox"/>	<a href="#">cellular tumor antigen p53 isoform X1 [Danio rerio]</a>	407	407	97%	9e-141	95.50%	<a href="#">XP_005165158.1</a>
<input type="checkbox"/>	<a href="#">cellular tumor antigen p53 isoform 2 [Danio rerio]</a>	407	407	97%	9e-141	95.50%	<a href="#">XP_571402.1</a>
<input type="checkbox"/>	<a href="#">cellular tumor antigen p53 isoform 3 [Danio rerio]</a>	406	406	97%	9e-141	95.50%	<a href="#">NP_001315516.1</a>
<input type="checkbox"/>	<a href="#">Tumor protein p53 [Danio rerio]</a>	407	407	97%	1e-140	95.50%	<a href="#">AAH95597.1</a>
<input type="checkbox"/>	<a href="#">p53beta isoform [Danio rerio]</a>	402	402	97%	5e-140	95.50%	<a href="#">AJD19814.1</a>
<input type="checkbox"/>	<a href="#">PREDICTED: cellular tumor antigen p53-like isoform X2 [Sinocyclocheilus rhinocerosus]</a>	365	365	97%	1e-124	85.50%	<a href="#">XP_016391431.1</a>
<input type="checkbox"/>	<a href="#">PREDICTED: cellular tumor antigen p53-like isoform X1 [Sinocyclocheilus rhinocerosus]</a>	365	365	97%	1e-124	85.50%	<a href="#">XP_016391429.1</a>

Download
GenPept
Graphics

Next
Previous
Descriptions

cellular tumor antigen p53 isoform 1 [Danio rerio]

Sequence ID: [NP\\_001258749.1](#)
Length: 374
Number of Matches: 1

Range 1: 61 to 260

GenPept
Graphics

Next Match

Previous Match

Score	Expect	Method	Identities	Positives	Gaps
407 bits(1046)	6e-141	Compositional matrix adjust.	191/200(96%)	193/200(96%)	0/200(0%)
Query 1	PTTSTVPETSDYPGAGHGRFLRFPQSGTAKSVCTCTSPDLNKLKQLAKTCPQVMVVDVAP				60
Sbjct 61	P TSTVPETSDYPG HGRFLRFPQSGTAKSVCTCTSPDLNKL CQLAKTCPQVMVVDVAP				120
Query 61	PQGSVVRATAIYKSEHVAEVVRRCPHHERTPDGNLAPAGHLIRVEGNQRANYREDNIT				120
Sbjct 121	PQGSVVRATAIYKSEHVAEVVRRCPHHERTPDGNLAPAGHLIRVEGNQRANYREDNIT				180
Query 121	LRHSVFVPYEPOLGAETWTLINYMNSSCMGGMNRRPILTTITLETXEQQLGRRSFE				180
Sbjct 181	LRHSVFVPYEPOLGAETWTLINYMNSSCMGGMNRRPILTTITLET EGQLLGRRSFE				240
Query 181	VRVCACPGDRDKTXGEHFK 200				
Sbjct 241	VRVCACPGDRDKT +F+K 260				

Related Information

[Gene](#) - associated gene details

[New! Genome Data Viewer](#) - aligned genomic context

Download
GenPept
Graphics

Next
Previous
Descriptions

tumor suppressor p53 [Danio rerio]

Sequence ID: [AAO85406.1](#)
Length: 369
Number of Matches: 1

Range 1: 60 to 259

GenPept
Graphics

Next Match

Previous Match

Score	Expect	Method	Identities	Positives	Gaps
407 bits(1045)	7e-141	Compositional matrix adjust.	191/200(96%)	193/200(96%)	0/200(0%)
Query 1	PTTSTVPETSDYPGAGHGRFLRFPQSGTAKSVCTCTSPDLNKLKQLAKTCPQVMVVDVAP				60
Sbjct 60	P TSTVPETSDYPG HGRFLRFPQSGTAKSVCTCTSPDLNKL CQLAKTCPQVMVVDVAP				119
Query 61	PQGSVVRATAIYKSEHVAEVVRRCPHHERTPDGNLAPAGHLIRVEGNQRANYREDNIT				120
Sbjct 120	PQGSVVRATAIYKSEHVAEVVRRCPHHERTPDGNLAPAGHLIRVEGNQRANYREDNIT				179
Query 121	LRHSVFVPYEPOLGAETWTLINYMNSSCMGGMNRRPILTTITLETXEQQLGRRSFE				180
Sbjct 180	LRHSVFVPYEPOLGAETWTLINYMNSSCMGGMNRRPILTTITLET EGQLLGRRSFE				239
Query 181	VRVCACPGDRDKTXGEHFK 200				
Sbjct 240	VRVCACPGDRDKT +F+K 259				

Related Information

[Gene](#) - associated gene details

**[Q5]** Generate a multiple sequence alignment with your novel protein, your original query protein, and a group of other members of this family from different species. A typical number of proteins to use in a multiple sequence alignment for this assignment purpose is a minimum of 5 and a maximum of 20 - although the exact number is up to you. Include the multiple sequence alignment in your report. Use Courier font with a size appropriate to fit page width.

Side-note: Indicate your sequence in the alignment by choosing an appropriate name for each sequence in the input unaligned sequence file (i.e. edit the sequence file so that the species, or short common, names (rather than accession numbers) display in the output alignment and in the subsequent answers below). The goal in this step is to create an interesting an alignment for building a phylogenetic tree that illustrates species divergence.

Re-labeled sequences for alignment:

```
>Human_p53 gi|9606|ref|NP_001119586.1| cellular tumor antigen p53 isoform b  
[Homo sapiens]
```

PLSSSVPSQKTYQGSYGFRGLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPQGTRVRAMAIYKQSQH  
MTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLLDRNTFRHSVVVPYEPPEVGSDCCTTIHYNMCMNSSCMGG  
MNRRLPILTIITLEDSSGNLLGRNSFEVRVCACPGDRDRTEENLRKKGEPHH

>Danio\_rerio\_protein (sequence taken from BLAST result)  
PTTSTVPETSDYPGAHGFRLRFPQSGTAKSVTCTYSPDLNKLKLCQLAKTCPVQMVVDVAPPQGSVVRATAIYKKSEH  
VAEVVRRCPHHERTPDGDNLAPAGHLIRVEGNQRANYREDNITLRHSVFPYEPQLGAEWTTVLLNYMCMNSSCMGG  
MNRRLPILTIITLETXEGQLLGRRSFEVRVCACPGDRDKTXGEHFQKT\*RPKH

>Ray-finned\_fish gi|307959|ref|XP\_016391431.1| PREDICTED: cellular tumor  
antigen p53-like isoform X2 [Sinocyclocheilus rhinocerosus]  
PPTASVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSADLNKLFCQLAKTCPVQMVVDVAPPQGSVIRATAIYKKSEH  
VAEVVRRCPHHERTPDGDALAPPAHLIRMEGNSRAVYREDDITYRHSVVVPYEPQLGAEWTTVLYNFMCMNSSCMGG  
MNRRLPILTIITLETHEGQLLGRRSFEVRVCACPGDRDKTEESNFRK

>Golden-line\_barbel gi|1608454|ref|XP\_016321636.1| PREDICTED: cellular tumor  
antigen p53-like isoform X2 [Sinocyclocheilus anshuiensis]  
PPTASVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSADLNKLFCQLAKTCPVQMVVDVAPPQGSVIRATAIYKKSEH  
VAEVVRRCPHHERTPDGDALAPPAHLIRMEGNSRAVYREDDITYRHSVVVPYEPQLGAEWTTVLYNFMCMNSSCMGG  
MNRRLPILTIITLETHEGQLLGRRSFEVRVCACPGDRDKTEESNFRK

>Grass\_carp gi|7959|. |ANP93608.1| tumor antigen p53 [Ctenopharyngodon idella]  
PPTSTVPIATDYPGEHGFKLQFPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDVAPPQGSVLRATAIYKKSEH  
VAEVVRRCPHHERTPDTDGLAPAAHLIRVEGNLRATYKEDDVTSRHSVVVPYEPQLGAGFTTVLYNYMCMNSSCMGG  
MNRRLPILTIITLETQDGQMLGRRSFEVRVCACPGDRDKTEESNFRK

>Gold\_fish gi|7957|ref|XP\_026112491.1| cellular tumor antigen p53-like  
isoform X2 [Carassius auratus]  
PPTASVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMLVDVAPPQGSVIRATAIYKKSEH  
VAEVVRRCPHHERTPDGDVLAPPAHLIRVEGNLAVYREDDITHRHSVAVPYEPQLGAEWTTVLYNFMCMNSSCMGG  
MNRRLPILTIITLETHEGQLLGRRSFEVRVCACPGDRDKTEESNFGK

>Common\_carp gi|7962|ref|XP\_018953153.1| PREDICTED: cellular tumor antigen  
p53-like isoform X2 [Cyprinus carpio]  
PPTSSVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMLVDVAPPQGSVIRATAIYKKSEH  
VADVRRCPHHERTLDDGDLAPPAHLIRVEGNRAVYREDDMTYRHSVVVPYEPQLGAEWTTVLYNFMCMNSSCMGG  
MNRRLPILTIITLETHDQQLLGRRSFEVRVCACPGDRDKTEESNFRK

#### Alignment:

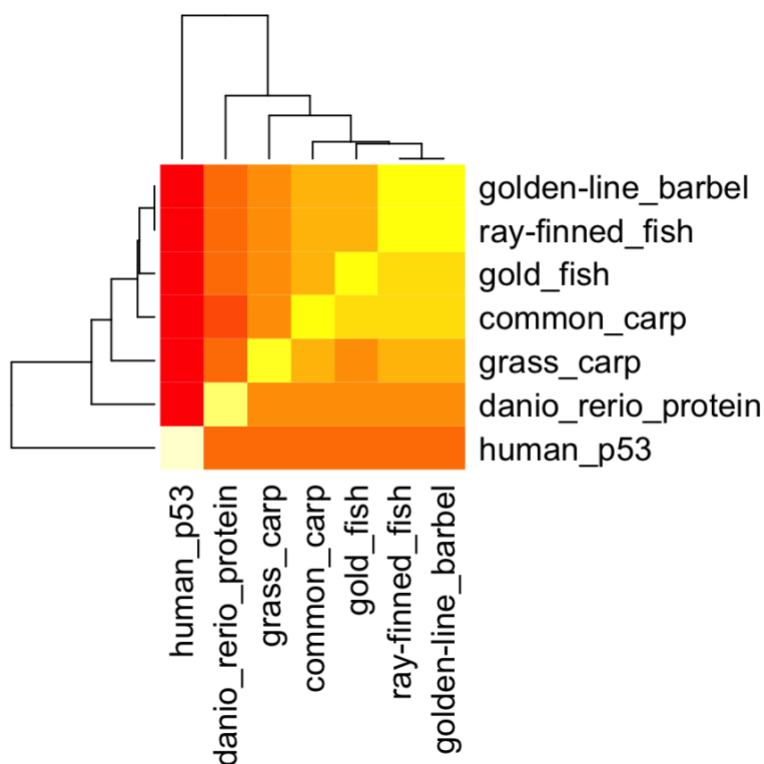
Obtained using MUSCLE (version 3.8) at EBI:

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

Human_p53	PLSSSVPSQKTYQGSYGFRGLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTP
Danio_rerio_protein	PTTSTVPETSDYPGAHGFRLRFPQSGTAKSVTCTYSPDLNKLKLCQLAKTCPVQMVVDVAP
Grass_carp	PPTSTVPIATDYPGEHGFKLQFPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDVAP
Common_carp	PPTSSVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMLVDVAP
Gold_fish	PPTASVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMLVDVAP
Ray-finned_fish	PPTASVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSADLNKLFCQLAKTCPVQMVVDVAP
Golden-line_barbel	PPTASVPVATDYPGEHGFKLGFPQSGTAKSVTCTYSADLNKLFCQLAKTCPVQMVVDVAP
	* :::** . * * :*. * * :*****. ***.:*****: ** :*
Human_p53	PPGTRVRAMAIYKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLLDRNT
Danio_rerio_protein	PQGSVVRATAIYKKSEHVAEVVRRCPHHERTPDGDNLAPAGHLIRVEGNQRANYREDNIT
Grass_carp	PQGSVLRATAIYKKSEHVAEVVRRCPHHERTPDTDGLAPAAHLIRVEGNLRATYKEDDVIT
Common_carp	PQGSVIRATAIYKKSEHVADVRRCPHHERTLDDGDLAPPAHLIRVEGNSRAVYREDDMT
Gold_fish	PQGSVIRATAIYKKSEHVAEVVRRCPHHERTPDGDVLAPPAHLIRVEGNSLAVYREDDIT
Ray-finned_fish	PQGSVIRATAIYKKSEHVAEVVRRCPHHERTPDGDALAPPAHLIRMEGNSRAVYREDDIT



sequence identity matrix (again using a function within the Bio3D package). Then generate a heatmap plot and add to your report. Do make sure your labels are visible and not cut at the figure margins.



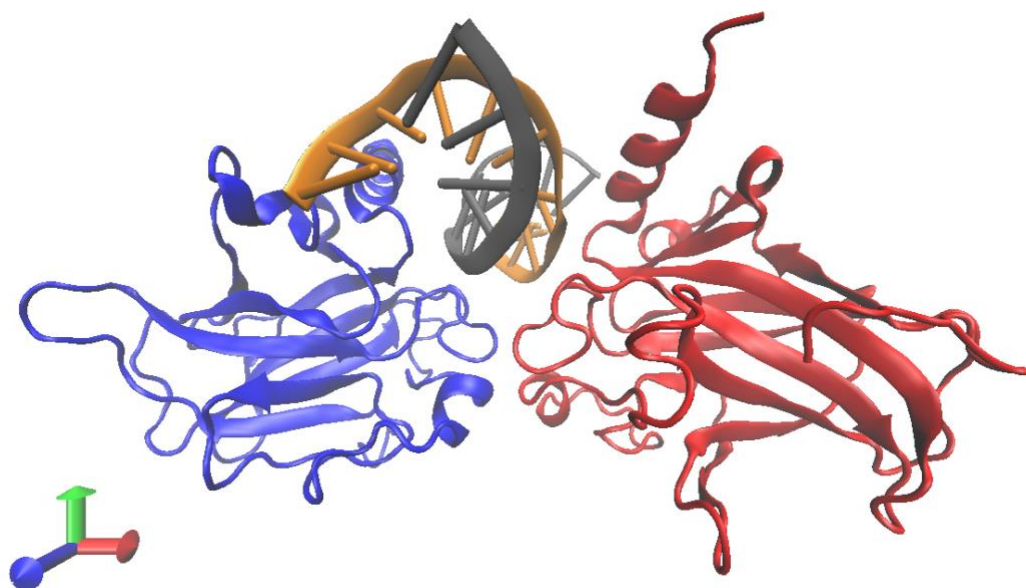
**[Q8]** Using R/Bio3D (or an online blast server if you prefer), search the main protein structure database for the most similar atomic resolution structures to your aligned sequences. List the top 3 unique hits (i.e. not hits representing different chains from the same structure) along with their Evalue and sequence identity to your query. Please also add annotation details of these structures. For example include the annotation terms PDB identifier (structureId), Method used to solve the structure (experimentalTechnique), resolution (resolution), and source organism (source).

ID	Technique	Resolution	Source	Evalue	Identity
3EXJ	X-RAY DIFFRACTION	2.0	Mus musculus	8.99e-89	74.603
1GZH	X-RAY DIFFRACTION	2.6	Homo sapiens	9.26e-88	71.574
3LX5	X-RAY DIFFRACTION	1.9	Streptococcus thermophilus	5.50e+00	29.577



[Q9] Generate a molecular figure of one of your identified PDB structures using VMD. You can optionally highlight conserved residues that are likely to be functional. Please use a white or transparent background for your figure (i.e. not the default black). Based on sequence similarity. How likely is this structure to be similar to your “novel” protein?

It would be likely to have similar structure to my “novel protein” since protein have over 70% sequence similarity.



[Q10] Perform a “Target” search of ChEMBL ( <https://www.ebi.ac.uk/chembl/> ) with your novel sequence. Are there any Target Associated Assays and ligand efficiency data reported that may be useful starting points for exploring potential inhibition of your novel protein?

CHEMBL details 9 Binding Assay (CHEMBL3883306) and 0 Functional Assays; No ligand efficiency data.

<https://www.ebi.ac.uk/chembl/target/inspect/CHEMBL3883306>

ChEMBL Assay ID	Assay Source	Assay Type	Assay Organism	Description	Activity Count	Reference	
<a href="#">CHEMBL3223544</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human SJSA-1 cells expressing amplified MDM2 and wild-type p53 assessed as induction of p21 protein expression at 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223540</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human A2780 CP70 cells expressing p53 mutant gene assessed as induction of MDM2 protein expression at 0.2 to 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223543</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human A2780 cells expressing wild-type p53 assessed as induction of MDM2 protein expression at 0.2 to 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223542</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human A2780 cells expressing wild-type p53 assessed as induction of p53 protein expression at 0.2 to 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223538</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human A2780 CP70 cells expressing p53 mutant gene assessed as induction of p21 protein expression at 0.2 to 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223546</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human SJSA-1 cells expressing amplified MDM2 and wild-type p53 assessed as induction of MDM2 protein expression at 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223541</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human A2780 cells expressing wild-type p53 assessed as induction of p21 protein expression at 0.2 to 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223545</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human SJSA-1 cells expressing amplified MDM2 and wild-type p53 assessed as induction of p53 protein expression at 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓
<a href="#">CHEMBL3223539</a>	Scientific Literature	B	Homo sapiens	Inhibition of MDM2/MDMX-p53 interaction in human A2780 CP70 cells expressing p53 mutant gene assessed as induction of p53 protein expression at 0.2 to 5 uM after 4 hrs by western blot analysis	3	<a href="#">MedChemComm. (2013) 4:9:1297</a>	✓

Showing 1 to 9 of 9 entries

[https://www.ebi.ac.uk/chembl/assay/results/1/chembl\\_id/asc/tab/keyword](https://www.ebi.ac.uk/chembl/assay/results/1/chembl_id/asc/tab/keyword)