

## Find-a-Gene Project

[Q1]

**Protein name:** Tumor protein p53**Species:** *Homo sapiens***Accession number:** NP\_000537.3**Function known:** Encodes tumor suppressor protein; regulates expression of target genes by inducing apoptosis, DNA repair, or changes in metabolism

[Q2]

**BLAST method:** TBLASTN**Database searched:** Expressed sequence tags (est)**Limits applied:** Fishes (taxid: 7898)

Translated BLAST: tblastn

TBLASTN search translated nucleotide databases using a protein query: [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

NP\_000537.3

Clear Query subrange

From To

Or, upload file

Choose File No file chosen

Job Title

NP\_000537:cellular tumor antigen p53 isoform...

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database

Expressed sequence tags (est)

Organism

fishes (taxid:7898)

☐ exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

☐ Limit to

Sequences from type material

Entrez Query

Enter an Entrez query to limit search

[YouTube](#) [Create custom database](#)

**BLAST**

Search database est using Tblastn (search translated nucleotide databases using a protein query)

☐ Show results in a new window

[Algorithm parameters](#)

Note: Parameter values that differ from the default are highlighted in yellow and marked with a sign

## Search output list:

**Information** Your search is limited to records that include: fishes (taxid:7898)

Job Title NP\_000537:cellular tumor antigen p53 isoform...

RID [DDZXAW9Z01R](#) Search expires on 06-04 09:40 am [Download All](#)

Program TBLASTN [Citation](#)

Database est [See details](#)

Query ID NP\_000537.3

Description cellular tumor antigen p53 isoform a [Homo sapiens]

Molecule type amino acid

Query Length 393

Other reports [?](#)

**Filter Results**

Organism only top 20 will appear ☐ exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity E value Query Coverage

to to to

**Filter** **Reset**

**Descriptions** Graphic Summary Alignments Taxonomy

**Sequences producing significant alignments** Download Manage Columns Show 100

☒ select all 100 sequences selected [GenBank](#) [Graphics](#)

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<a href="#">ypa1-26-C02 Yellow perch ovarian library 1 Perca flavescens cDNA, mRNA sequence</a>	281	281	68%	2e-91	52.90%	<a href="#">GO654865.1</a>
<a href="#">EST_omor_rpc_4939 omorgc mixed tissue Osmerus mordax cDNA Osmerus mordax cDNA clone omor_rpc_505_235_rev 5' mRNA sequen</a>	238	238	67%	3e-74	49.62%	<a href="#">EL540986.1</a>
<a href="#">JGI_CAA5844.rev CAAX Pimephales promelas testis 7-8 month adults, males and females pooled (L) Pimephales promelas cDNA clone C</a>	293	293	64%	5e-96	57.68%	<a href="#">DT317081.1</a>
<a href="#">CLJ392-K04.y1d-s SHGC-CLJ2 Gasterosteus aculeatus cDNA clone CLJ392-K04 5' mRNA sequence</a>	269	269	64%	8e-86	50.98%	<a href="#">DW654327.1</a>
<a href="#">ypa1-10-B05 Yellow perch ovarian library 1 Perca flavescens cDNA, mRNA sequence</a>	213	213	64%	2e-64	46.64%	<a href="#">GO653330.1</a>

**Alignment of choice:** a cDNA clone from *Osmerus mordax* (rainbow smelt), with accession number EL540986.1.**E-value and other alignment stats:** E-value = 3e-74, score = 238, query coverage = 67%, percent identity = 49.62%.

**EST\_omor\_rgc\_4939 omorrgc mixed\_tissue Osmerus mordax cDNA Osmerus mordax cDNA clone omor\_rgc\_505\_235\_rev 5', mRNA sequence**  
Sequence ID: [EL540986.1](#) Length: 907 Number of Matches: 1

Range 1: 184 to 906 [GenBank](#) [Graphics](#)

▼ Next Match

▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
238 bits(607)	3e-74	Compositional matrix adjust.	134/266(50%)	171/266(64%)	26/266(9%)	+1
Query 1	MEEPQSDPSVEPPLSQETFS	DLWKLLPENNVLSPLPSQAMDD	LMLSPDDIEQWFTEDPGP	60		
Sbjct 184	MDEPVGNESIT--FSQESFHYLW-----	NLMAGQPTETENCLMEAPLFDEEDLFEEP--	333			
Query 61	DEaprmpeaappvapapapapt	paapapapSWPLSSSVPSQKTYQGS	YGFRLGFLHSGTAK	120		
Sbjct 334	-----TIPAPQAPCHSSDSGSSLTSTVPSTTDYPGSLNFS	LKFQQSSTAK	468			
Query 121	SVTCTYSPALNKMFCQLAKTC	CPVQLWVDSTPPPGTRVRAMAIYKQSQHMT	EVVRRCPHHE	180		
Sbjct 469	SVTCTYSP LNK+FCQLAKTC	VPQ+ V+ PPPG +RA+A+YK+S+ + +VVRRC	PHHE	648		
Query 181	RCS-DSDGLAPPQH	LIRVEGNLRVEYLD	DRNTFRHSVVVPYEPPEVGS	DC	TTIHYNYMCN	239
Sbjct 649	RTTENNEGPAPAGHLV	RVEGNNQARYLADNHTGRHSVLVPYEP	PQVGS	DI	TVLFNYMCN	828
Query 240	SSCMGGMNRRPILTIITLEDSSGNLL	265				
Sbjct 829	SSCMGGMN RPILTIITLE	G LL				

Est\_omor\_rgc\_4939 omorrgc mixed\_tissue Osmerus mordax cDNA Osmerus mordax cDNA clone omor\_rgc\_505\_235\_rev 5', mRNA sequence

Sequence ID: EL540986.1|Length: 907|Number of Matches: 1|Range 1: 184 to 906

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
238 bits(607)	3e-74	Compositional matrix adjust.	134/266(50%)	171/266(64%)	26/266(9%)	+1
Query 1	MEEPQSDPSVEPPLSQETFS	DLWKLLPENNVLSPLPSQAMDD	LMLSPDDIEQWFTEDPGP	60		
	M+EP + S+ SQE+F LW N+++ P++ + LM +P E+ E+P					
Sbjct 184	MDEPVGNESIT--FSQESFHYLW-----	NLMAGQPTETENCLMEAPLFDEEDLFEEP--	333			
Query 61	DEaprmpeaappvapapapapt	paapapapSWPLSSSVPSQKTYQGS	YGFRLGFLHSGTAK	120		
	AP + L+S+VPS Y GS F L F S TAK					
Sbjct 334	-----TIPAPQAPCHSSDSGSSLTSTVPSTTDYPGSLNFS	LKFQQSSTAK	468			
Query 121	SVTCTYSPALNKMFCQLAKTC	CPVQLWVDSTPPPGTRVRAMAIYKQSQHMT	EVVRRCPHHE	180		
	SVTCTYSP LNK+FCQLAKTC	VPQ+ V+ PPPG +RA+A+YK+S+ + +VVRRC	PHHE			
Sbjct 469	SVTCTYSP LNK+FCQLAKTC	VPQ+ V+ PPPG +RA+A+YK+S+ + +VVRRC	PHHE	648		
Query 181	RCS-DSDGLAPPQH	LIRVEGNLRVEYLD	DRNTFRHSVVVPYEPPEVGS	DC	TTIHYNYMCN	239
	R + +++G AP HL+RVEGN + YL D +T RHSV+VPYEP	P+VGSD TT+ +NYMCN				
Sbjct 649	RTTENNEGPAPAGHLV	RVEGNNQARYLADNHTGRHSVLVPYEP	PQVGS	DI	TVLFNYMCN	828
Query 240	SSCMGGMNRRPILTIITLEDSSGNLL	265				
	SSCMGGMN RPILTIITLE	G LL				
Sbjct 829	SSCMGGMNRPILTIITLETQEGQLL	906				

[Q3]

**Protein sequence of choice matches subject above:**

> *Osmerus mordax* protein

MDEPVGNESITFSQESFHYLWNLMAGQPTETENCLMEAPLFDEEDLFEEPTIPAPQAPCHSSDSGSSLTSTVPSTTDYPGSLNFSL  
KFQQSSTAKSVTCTYSPELNKLFCQLAKTCVPQMVVEQAPPPGALLRAVAVYKKSVDVADVVRCPHHERTTENNEGPAPAGHLVR  
VEGNNQARYLADNHTGRHSVLVPYEPFQVGSDIITVLFNYMCNSSCMGMNRPILTIITLETQEGQLL

**Name:** *Osmerus mordax* protein

**Species:** *Osmerus mordax*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii;  
Neopterygii; Teleostei; Stomiatii; Osmeriformes; Osmeridae; Osmerus.

[Q4]

Standard Protein BLAST

BLASTP programs search protein databases using a protein query. [more...](#) [Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

From:  To:

Or, upload file:  No file chosen

Job Title:

☐ Align two or more sequences

Choose Search Set

Database:

Organism:  ☐ exclude

Exclude: ☐ Models (XM/XP) ☐ Non-redundant RefSeq proteins (WP) ☐ Uncultured/environmental sample sequences

Program Selection

Algorithm: ☐ Quick BLASTP (Accelerated protein-protein BLAST) ☒ blastp (protein-protein BLAST) ☐ PSI-BLAST (Position-Specific Iterated BLAST) ☐ PHI-BLAST (Pattern Hit Initiated BLAST) ☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Search database nr using Blastp (protein-protein BLAST)

☐ Show results in a new window

BLAST results will be displayed in a new format by default. You can always switch back to the Traditional Results page.

**Blastp output list with identities & E value:**

[Edit Search](#) [Save Search](#) [Search Summary](#) [How to read this report?](#) [BLAST Help Videos](#) [Back to Traditional Results Page](#)

Job Title: Protein Sequence

RID: [DE3TK58U01R](#) Search expires on 06-04 10:47 am [Download All](#)

Program: BLASTP [Citation](#)

Database: nr [See details](#)

Query ID: lcl|Query\_59915

Description: None

Molecule type: amino acid

Query Length: 241

Other reports: [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

Filter Results

Organism: only top 20 will appear ☐ exclude

Type common name, binomial, taxid or group name

[Add organism](#)

Percent Identity:  to  E value:  to  Query Coverage:  to

Descriptions ☒ Graphic Summary ☐ Alignments ☐ Taxonomy

Sequences producing significant alignments

Download Manage Columns Show 100

☒ select all 100 sequences selected

[GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> cellular tumor antigen p53 isoform X1 [Tachysurus fulvidraco]	275	275	68%	4e-88	78.18%	XP_027035235.1
<input checked="" type="checkbox"/> P53 [Tachysurus fulvidraco]	275	275	68%	5e-88	78.18%	AEB72290.1
<input checked="" type="checkbox"/> tumor suppressor p53 [Danio rerio]	271	271	71%	2e-86	74.57%	AAO85406.1
<input checked="" type="checkbox"/> cellular tumor antigen p53 isoform 3 [Danio rerio]	271	271	71%	2e-86	74.57%	NP_001315516.1

**Top alignment shown with alignment statistics:**

cellular tumor antigen p53 isoform X1 [Tachysurus fulvidraco]

Sequence ID: [XP\\_027035235.1](#) Length: 378 Number of Matches: 1

Range 1: 79 to 243 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
275 bits(703)	4e-88	Compositional matrix adjust.	129/165(78%)	146/165(88%)	0/165(0%)
Query 77	DYPGSLNFSLFQQSSTAKSVTCTYSPELNKLFQQLAKTCPVQMVVEQAPPPGALLRAVA				136
Sbjct 79	DYPG NF+L FQ+SSTAKSVTCTYSPELNKLFQQLAKTCPV M V +PP G++LRA A				138
Query 137	DYPGLHNFTLHFQKSSTAKSVTCTYSPELNKLFQQLAKTCPVLMVAVSFSPPHGSLVRATA				196
Sbjct 139	VYKSKDVADVRRCPHHERTTENNEGPAPAGHLVRVEGNNQARYLADNHTGRHSVLVPY				198
Query 197	VYK+S+ VADVRRCPHHER+ +NNEGPAP GHL+RVEGN++A Y D +T RHSV+VPY				241
Sbjct 199	VYKRSEHVADVRRCPHHERSNDNNEGPAPPGHLLRVEGNSRAVYHEDLNTQRHSVVVPY				243

**Results indicates a “novel” gene found:** The percent identity of the top hit is not 100%, so my protein should be “novel.”

[Q5]

### Trimmed and labeled sequences for alignment:

```
> Human_p53
TYQGSYGFRLGLFHSHTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGRVTRAMAIYKQSQHMTVEVRRCPHHERCSDSDG
LAPPQHILIRVEGNLRVEYLDNRNTRFRHSVVVPYEPPEVGSDCITTHYNMNCSSCMGGMNRRPILTIITLETQEGQLL

> Osmerus_mordax protein
DYPGSLNFSLFQQSSTAKSVTCTYSPELNKLFQQLAKTCPVQMVVEQAPPPGALLRAVAVYKSKDVADVRRCPHHERTTENNE
GPAPAGHLVRVEGNNQARYLADNHTGRHSVLVPYEPPEVGSDCITTVLFNYMNCSSCMGGMNRRPILTIITLETQEGQLL

>Yellow_catfish XP_027035235.1 cellular tumor antigen p53 isoform X1 [Tachysurus
fulvidraco]
DYPGLHNFTLHFQKSSTAKSVTCTYSPELNKLFQQLAKTCPVLMVAVSFSPPHGSLVRATAVYKRSEHVADVRRCPHHERSNDNNE
GPAPPGLHLLRVEGNSRAVYHEDLNTQRHSVVVPYEPPEVGSSECTTVLYNYMNCSSCMGGMNRRPILTIITLETQDQQLL

>Zebrafish AA085406.1 tumor suppressor p53 [Danio rerio]
DYPGDHGFRLRFPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDVAPPQGSVVRATAIYKKSEHVAEVVRRCPHHERTPDGDN
LAPAGHLIRVEGNQRANYREDNITLRHSVFVPYEPQLGAEWTTVLLNYMNCSSCMGGMNRRPILTIITLETQEGQLL

>Brown_bullhead QGQ62196.1:80-244 tumor protein 53 [Ameiurus nebulosus]
DYPGLHDFTLHFQESSTAKSVTCTYSPGLNKLFCQLAKTCPVLMVAVSSSPPPGSLVRATAVYKRSEHVAEVVRRCPHHERSNDSSD
GPAPPGLHLLRVEGNSRAVYQEDGNTQRHSVVVPYEPPEVGSQCTTVLYNYMNCSSCMGGMNRRPILTIITLETQNGHLL

>Wuchang_bream QBM00765.1:59-230 tumor antigen p53 [Megalobrama amblycephala]
DYPGEHGFKLQFPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDIAPPQGSLLRATAIYKKSEHVAEVVRRCPHHERTPDTDG
LAPAAHLIRVEGNLRATYKEDDSTRHSVVVPYEPQLGAGFTTVLYNYMNCSSCMGGMNRRPILTIITLETQDQQLL

>Channel_catfish NP_001187005.1:77-241 cellular tumor antigen p53 [Ictalurus
punctatus]
DYPGLNFTLHFQESSGTSVTCTYSPDLNKLFCQLAKTCPVLMVAVSSSPPPGSLVRATAVYKRSEHVAEVVRRCPHHERSNDSSD
GPAPPGLHLLRVEGNSRAVYQEDGNTQAHSVVVPYEPPEVGSQSTTVLYNYMNCSSCMGGMNRRPILTIITLETQDGHLL

>Grass_carp ANP93608.1:59-230 tumor antigen p53 [Ctenopharyngodon idella]
DYPGEHGFKLQFPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDVAPPQGSVLRATAIYKKSEHVAEVVRRCPHHERTPDTDG
LAPAAHLIRVEGNLRATYKEDDSTRHSVVVPYEPQLGAGFTTVLYNYMNCSSCMGGMNRRPILTIITLETQDQQLL

>West_African_lungfish QC084573.1:180-355 tumor protein suppressor 53 [Protopterus
annectens]
DYPGECFQLVFQESGTSVTCTYSPDLNKLFCQLAKTCPVQIKVESTPEVGAIIRATAVYKKSEHVAEVVRRCPHHERSTEHKD
GLVPPSHLIRVEGNSQAQYLEDNSTRQSVIVPYEKPQVGSDCCTTVLYNYMNCSSCMGGMNRRPILTIITLETQDQQLL

> Rainbow_trout NP_00118164.1:7-254 cellular tumor antigen p53 [Oncorhynchus mykiss]
```

DYPGALGFQRLFLQSSTAKSVTCTYSPDLNKLFCQLAKTCPVQIVVDHPPPPGAVVRALAIYKKLSDVADVVRRCPHHQSTSENNE  
GPAPRGHLVRVEGNQRSEYMEDGNTLRHSVLVPYEPFQVGSECTTVLYNFMCSNCSMGMNRRPILTIITLETQEGQLL

### CLUSTAL multiple sequence alignment by MUSCLE (3.8):

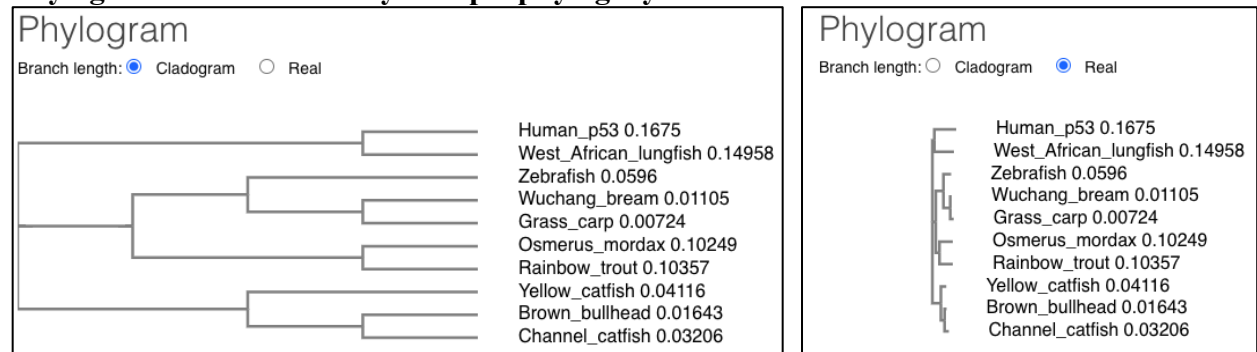
Human_p53	TYQGSYGFRGLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGRTRVRAMA
West_African_lungfish	DYPGECSFQLVFQESGTAKSVTYTYSPTLNKLYCQLAKTCPVQIKVESTPEVGAIIRATA
Zebrafish	DYPGDHGFRLRFPPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDVAPPQGSVVRATA
Wuchang_bream	DYPGEHGFKLQFPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDIAPPQGSLLRATA
Grass_carp	DYPGEHGFKLQFPQSGTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVDVAPPQGSVLRATA
Yellow_catfish	DYPGLHNFTLHFQKSSTAKSVTCTYSPDLNKLFCQLAKTCPVLMVAVSFSPPHGSVLRATA
Brown_bullhead	DYPGLHDFTLHFQESSTAKSVTCTYSPGLNKLFCQLAKTCPVLMVAVSSPPPGSVLRATA
Channel_catfish	DYPGLLNFTLHFQESSGTAKSVTCTYSPDLNKLFCQLAKTCPVLMVAVSSPPPGSVLRATA
Osmerus_mordax	DYPGSLNFKLQFQSSSTAKSVTCTYSPDLNKLFCQLAKTCPVQMVVEQAPPPGALLRAVA
Rainbow_trout	DYPGALGFQRLFLQSSTAKSVTCTYSPDLNKLFCQLAKTCPVQIVVDHPPPPGAVVRALA
	* * . * * * . : * * * * * * * * : * * . * * : * * *

Human_p53	IYKQSQHMTVEVVRCPHHERCSD-SDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPY
West_African_lungfish	VYKKSEHVADVVKRCPPHHERSTEHKDGVLPPSHLIRVEGNSQAQYLEDNTRRQSVIVPY
Zebrafish	IYKKSEHVAEVVRCPHHERTPD-GDNLAPAGHLIRVEGNQRANYREDNITLRHSVFPY
Wuchang_bream	IYKKSEHVAEVVRCPHHERTPD-TDGLAPAAHLIRVEGNLRATYKEDDSTRHSVVVPY
Grass_carp	IYKKSEHVAEVVRCPHHERTPD-TDGLAPAAHLIRVEGNLRATYKEDDSTRHSVVVPY
Yellow_catfish	VYKRSEHVADVVRCPHHERSNDNNEGPAAPPGLLRVEGNSRAVYHEDLNTQRHSVVVPY
Brown_bullhead	VYKRSEHVAEVVRCPHHERSNDSDGPAPPGLLRVEGNSRAVYQEDGNTQRHSVVVPY
Channel_catfish	VYKRSEHVAEVVRCPHHERSNDSDGPAPPGLLRVEGNSRAVYQEDGNTQAHSVVVPY
Osmerus_mordax	VYKSKDVADVVRCPHHERTTENNEGPAAGHLVRVEGNNQARYLADNHTGRHSVLVPY
Rainbow_trout	IYKKLSDVADVVRCPHHERSTSENNEGPAPRGHLVRVEGNQRSEYMEDGNTLRHSVLVPY
	: * * . . : : * * . * * * * : : : . . * * * : * * * * . * * * * : * * . * * *

Human_p53	EPPEVGSDDCTTIHYNMCSNCSMGMNRRPILTIITLEDSSGNLL
West_African_lungfish	EKPQVGSDDCTTVLYNYMCSNCSMGMNRRPILTIITLESKDGLL
Zebrafish	EAPQLGAEWTTVLLNYMCSNCSMGMNRRPILTIITLETQEGQLL
Wuchang_bream	EAPQLGAGFTTVLYNYMCSNCSMGMNRRPILTIITLETQDQQL
Grass_carp	EAPQLGAGFTTVLYNYMCSNCSMGMNRRPILTIITLETQDQQL
Yellow_catfish	EPPQVGSECTTVLYNYMCSNCSMGMNRRPILTIITLETQDQQL
Brown_bullhead	EPPQVGSQCTTVLYNYMCSNCSMGMNRRPILTIITLETQNGHLL
Channel_catfish	EPPQVGSQCTTVLYNYMCSNCSMGMNRRPILTIITLETQDGHLL
Osmerus_mordax	EPPQVGSDDITTVLFNYMCSNCSMGMNRRPILTIITLETQEGQLL
Rainbow_trout	EPPQVGSECTTVLYNFMCSNCSMGMNRRPILTIITLETQEGQLL
	* * : : * : * : * * * * * * * * * * * * * * * * . . : : *

[Q6]

### Phylogenetic tree created by “simple phylogeny” from EBI:



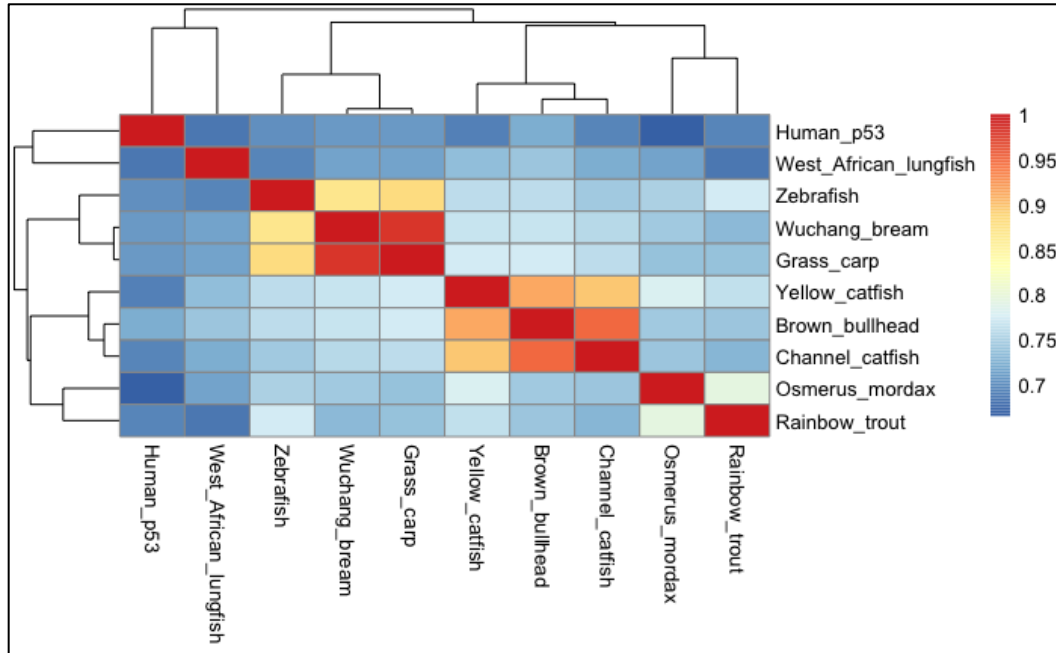
[Q7]

### Sequence identity based heatmap:

```

'''{r}
aln <- read.fasta("https://www.ebi.ac.uk/Tools/services/rest/muscle/result/muscle-I20200603-060439-0837-58473667-
-plm/aln.fasta")
ide <- seqidentity(aln)
pheatmap(ide)
'''

```



[Q8]

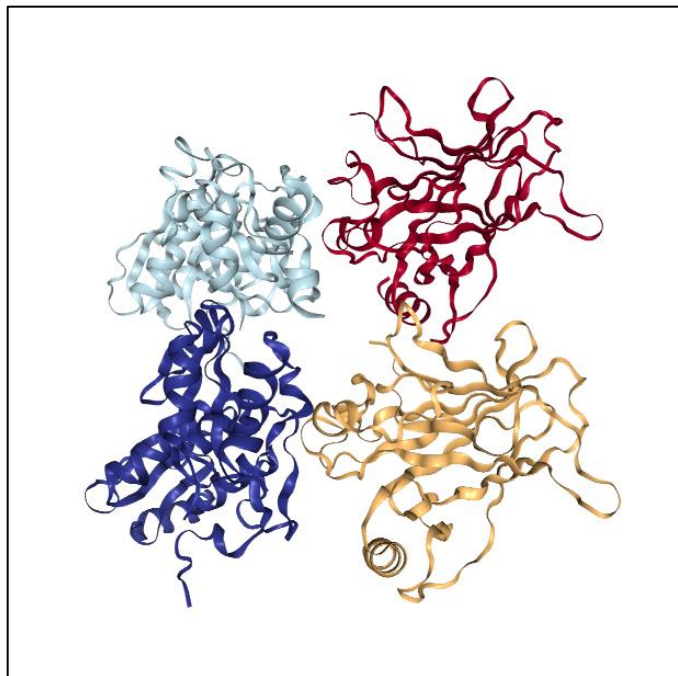
**PDB identifiers from multiple species:**

Structure ID	Technique	Resolution	Source	E value	Identity
1KZY_A	x-ray diffraction	2.5	<i>Homo sapiens</i>	3e-99	71.43%
1HU8_A	x-ray diffraction	2.7	<i>Mus musculus</i>	3e-90	70.81%
4D1L_A	x-ray diffraction	1.97	<i>Danio rerio</i>	2e-15	66.67%

[Q9]

The structure of Chain A, which is colored by red in the figure, can be similar to the *Osmerus mordax* protein studied in this project, given there is a high percent of identity.





[Q10]

**CHEMBL search:**

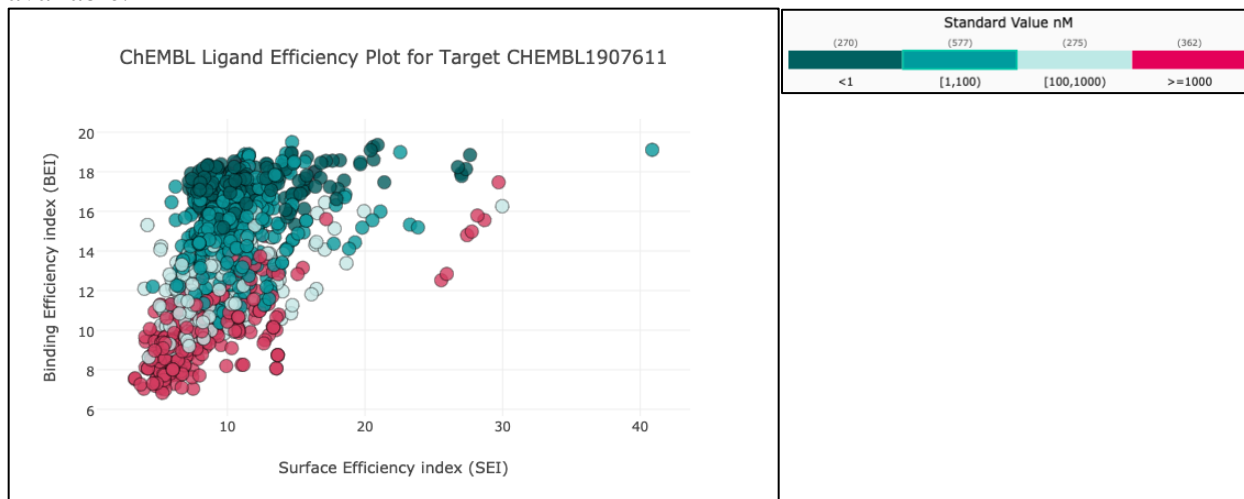
The top hit (CHEMBL3885544) showed a binding assay and no functional assay. There is no ligand efficiency data found.

The binding assay (CHEMBL3778681) tested peptidyl-prolyl cis-trans isomerase D and observed an “inhibition of Flag-tagged p53/GST-tagged PPID (unknown origin) expressed in *Escherichia coli*,” suggesting it inhibition effect on p53.

[https://www.ebi.ac.uk/chembl/target\\_report\\_card/CHEMBL3885544/](https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3885544/)

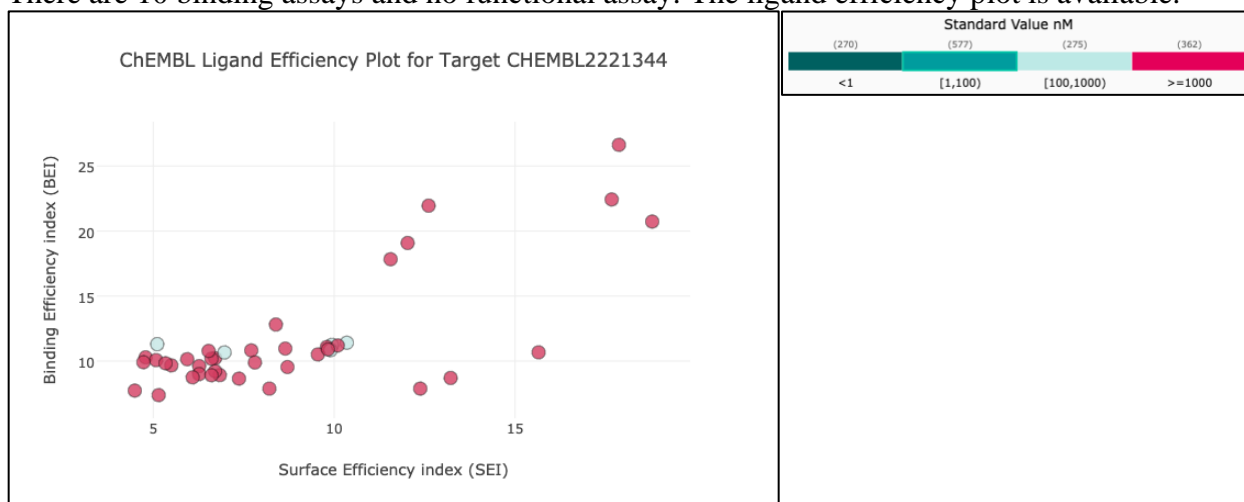
[https://www.ebi.ac.uk/chembl/assay\\_report\\_card/CHEMBL3778681/](https://www.ebi.ac.uk/chembl/assay_report_card/CHEMBL3778681/)

The second hit (CHEMBL1907611) is a protein-protein interaction between p53 and oncoprotein MDM2. There are 147 binding assays and 1 functional assay. The ligand efficiency plot is also available.



[https://www.ebi.ac.uk/chembl/target\\_report\\_card/CHEMBL1907611/](https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1907611/)

The third hit (CHEMBL2221344) is a protein-protein interaction between p53 and MDM4. There are 10 binding assays and no functional assay. The ligand efficiency plot is available.



[https://www.ebi.ac.uk/chembl/target\\_report\\_card/CHEMBL2221344/](https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2221344/)