

Find a Gene Project

Jaewon Kim

PID: A16675101

Email: [jak001@ucsd.edu](mailto:jak001@ucsd.edu)

[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 it's 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: major intrinsically disordered NOTCH2-binding receptor 1-like (MINAR2)

Accession: NP\_001244237.1

Species: Homo Sapiens

Function: MINAR2 prevents cancer development and activate cell defense system by negatively regulating following:

- Angiogenesis
- Cell growth
- Cell population proliferation
- Neuron projection development
- Protein ubiquitination
- TOR signaling

[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).

Blast method: tblastn

Database searched: Expressed sequence tags (est)

Limited organism: Humans (9606)

The screenshot shows the NCBI BLAST search interface for the tblastn method. The browser address bar shows the URL `blast.ncbi.nlm.nih.gov/Blast.cgi`. The page title is "Translated BLAST: tblastn". The search parameters are as follows:

- Enter Query Sequence:** The "Enter accession number(s), gi(s), or FASTA sequence(s)" field contains "NP\_001244237.1". The "Query subrange" fields "From" and "To" are empty.
- Or, upload file:** The "파일 선택" (Select file) button is highlighted.
- Job Title:** The field contains "NP\_001244237:major intrinsically disordered...".
- Choose Search Set:**
  - Database:** "Expressed sequence tags (est)" is selected.
  - Organism:** "humans (taxid:9606)" is selected. The "exclude" checkbox is unchecked.
  - Exclude:** The "Models (XM/XP)" checkbox is unchecked. The "Uncultured/environmental sample sequences" checkbox is unchecked.
  - Limit to:** The "Sequences from type material" checkbox is unchecked.
  - Entrez Query:** The field is empty.
- BLAST:** The "Search database est using Tblastn (search translated nucleotide databases using a protein query)" checkbox is checked. The "Show results in a new window" checkbox is unchecked.

A note at the bottom states: "Note: Parameter values that differ from the default are highlighted in yellow and marked with + sign". The "Algorithm parameters" section is expanded, showing a plus sign and the text "Algorithm parameters".

Also include the output of that BLAST search in your document. If appropriate, change the font to Courier size 10 so that the results are displayed neatly. You can also screen capture a BLAST output (e.g. alt print screen on a PC or on a MAC press `⌘-shift-4`. The pointer becomes a bulls eye. Select the area you wish to capture and release. The image is saved as a file called Screen Shot [].png in your Desktop directory). It is not necessary to print out all of the blast results if there are many pages.

Find\_A\_Gene\_Project\_Example x major intrinsically disordered x NCBI BlastNP\_001244237.m... x EMBOSS Transeq - EMBL EBI x NCBI BlastDR731264.1.6 MG... x +

blast.ncbi.nlm.nih.gov/Blast.cgi

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

**Information** Your search is limited to records that include: humans (taxid:9606)

Job Title **NP\_001244237:major intrinsically disordered...**

RID [X6E0A2VU016](#) Search expires on 02-20 18:14 pm [Download All](#)

Program **TBLASTN** [Citation](#)

Database **est** [See details](#)

Query ID [NP\\_001244237.1](#)

Description **major intrinsically disordered NOTCH2-binding receptor 1-...**

Molecule type **amino acid**

Query Length **190**

Other reports [?](#)

**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

[Filter](#) [Reset](#)

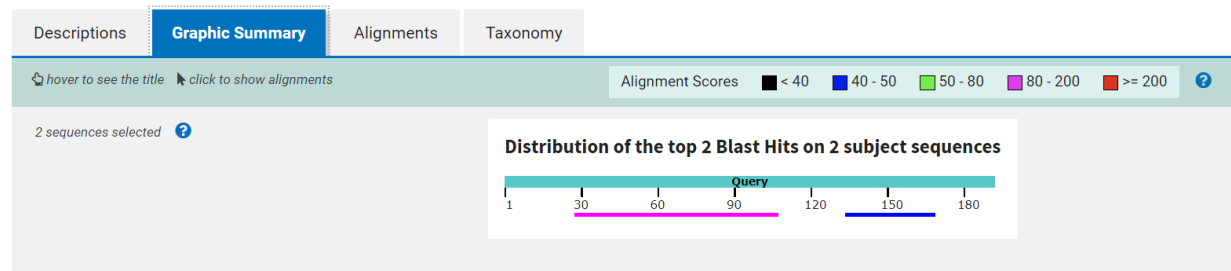
**Descriptions** [Graphic Summary](#) [Alignments](#) [Taxonomy](#)

**Sequences producing significant alignments** [Download](#) [Select columns](#) [Show](#) 100 [?](#)

☒ select all 2 sequences selected [GenBank](#) [Graphics](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	MGC7.2.1.1.H04.R.1 NIH_MGC_331 Homo sapiens cDNA clone MGC7.2.1.1.H04 mRNA sequence	Homo sapiens	147	147	41%	1e-44	92.41%	230	DR731264.1
<input checked="" type="checkbox"/>	DKFZp680E21247_r1.686 (synonym: hloc3) Homo sapiens cDNA clone DKFZp680E21247.5 mRNA sequence	Homo sapiens	49.3	49.3	18%	3e-05	48.57%	674	BX485465.1

[Feedback](#)



Chosen match- top match (highlighted with red box in the screenshot above)

Accession: DR731264.1

Name: MGC7.2.1.1.H04.R.1 NIH\_MGC\_331 Homo sapiens cDNA clone MGC7.2.1.1.H04, mRNA sequence

Species: Homo sapiens

Total/Max score: 147, 147

Query cover, E-value, percent identity: 41%, 1e-44, 92.41% (other scores in screenshot above and below)

[Download](#)
[GenBank](#)
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[Descriptions](#)

**MGC7.2.1.1.H04.R.1 NIH\_MGC\_331 Homo sapiens cDNA clone MGC7.2.1.1.H04, mRNA sequence**

Sequence ID: [DR731264.1](#) Length: 239 Number of Matches: 1

---

Range 1: 3 to 239
[GenBank](#)
[Graphics](#)

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

Score

Expect

Method

Identities

Positives

Gaps

Frame

147 bits(372)
1e-44
Compositional matrix adjust.
73/79(92%)
74/79(93%)
0/79(0%)
-1

Query

28

ALLQASLVRFPGGNYPAAQHWQNLVYSQREKKNIAAQRIRGSSADSLVTADSPPPSMSSV

87

+L QASLVRFPGGNYPAA HWQNLVYSQREKKNIAAQRIR SADSLVTADSPPPSMSSV

Sbjct

239

SLSQASLVRFPGGNYPAA\*HWQNLVYSQREKKNIAAQRIRFFSADSLVTADSPPPSMSSV

60

Query

88

MKNNPLYGDLSEEEAMEER

106

MKNNPLY DLSLEEAMEER

Sbjct

59

MKNNPLYSDLSLEEAMEER

3

Related Information

[Gene](#) - associated gene details

## Alignment details:

Query: major intrinsically disordered NOTCH2-binding receptor 1-like [Homo sapiens]

Query ID: NP\_001244237.1 Length: 190

>MGC7.2.1.1.H04.R.1 NIH\_MGC\_331 Homo sapiens cDNA clone MGC7.2.1.1.H04, mRNA sequence

Sequence ID: DR731264.1 Length: 239

Range 1: 3 to 239

Score:147 bits(372), Expect:1e-44, Method: Compositional matrix adjust.

Identities:73/79(92%), Positives:74/79(93%), Gaps:0/79(0%)

Query 28 ALLQASLVRFPGGNYPAAQHWQNLVYSQREKKNIAAQRIRGSSADSLVTADSPPPSMSSV 87

+L QASLVRFPGGNYPAA HWQNLVYSQREKKNIAAQRIR SADSLVTADSPPPSMSSV

Subject 239 SLSQASLVRFPGGNYPAA\*HWQNLVYSQREKKNIAAQRIRFFSADSLVTADSPPPSMSSV 60

Query 88 MKNNPLYGDLSEEEAMEER 106

MKNNPLY DLSLEEAMEER

Subject 59 MKNNPLYSDLSLEEAMEER 3

On the BLAST results, clearly indicate a match that represents a protein sequence, encoded from some DNA sequence, that is homologous to your query protein. I need to be able to inspect the pairwise alignment you have selected, including the E value and score. It should be labeled a "genomic clone" or "mRNA sequence", etc. - but include no functional annotation.

In general, [Q2] is the most difficult for students because it requires you to have a “feel” for how to interpret BLAST results. You need to distinguish between a perfect match to your query (i.e. a sequence that is not “novel”), a near match (something that might be “novel”, depending on the results of [Q4]), and a non-homologous result. If you are having trouble finding a novel gene try restricting your search to an organism that is poorly annotated.

[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.

EMBOSS Transeq result:

```
>DR731264.1_1 MGC7.2.1.1.1.H04.R.1 NIH_MGC_331 Homo sapiens cDNA clone  
MGC7.2.1.1.1.H04, mRNA sequence
```

```
FLSSIASSKLRLS*SGLFFITDDMDGGGLSAVTRLSALKNLIR*AAIFFFSLCE*TRFCQ  
CYAAG*FPPGNLTRLA*ERX
```

```
>DR731264.1_2 MGC7.2.1.1.1.H04.R.1 NIH_MGC_331 Homo sapiens cDNA clone  
MGC7.2.1.1.1.H04, mRNA sequence
```

```
FFLP*LPPNLGHYRVGYSS*LMTWMVGGYQQ*QGCLH*KT*FVEQQYSSFPSVSRQGFAS  
VMQQDNFHPETSPGWPERGX
```

```
>DR731264.1_3 MGC7.2.1.1.1.H04.R.1 NIH_MGC_331 Homo sapiens cDNA clone  
MGC7.2.1.1.1.H04, mRNA sequence
```

```
SFFHSFLQT*VTIEWVILHN**HGWWGAISSDKAVCTEKPNSLSSNILLFPL*VDKVLPV  
LCSRIISTRKPHQAGLREG
```

```
>DR731264.1_4 MGC7.2.1.1.1.H04.R.1 NIH_MGC_331 Homo sapiens cDNA clone  
MGC7.2.1.1.1.H04, mRNA sequence
```

```
PLSQPGEVSGWKLSCCITLAKPCLLTEGKEEYCCSTN*VFQCRQPCHC**PPTIHVISY  
EE*PTL**PKFGGSYGRKK
```

```
>DR731264.1_5 MGC7.2.1.1.1.H04.R.1 NIH_MGC_331 Homo sapiens cDNA clone  
MGC7.2.1.1.1.H04, mRNA sequence
```

```
PSLRPAW*GFRVEIILLHNTGKTLSTHRGKRRILLNLGFSVQTALSLLIAPHHPCQHL  
*RITHSIVT*VWRKLWKKEKX
```

```
>DR731264.1_6 MGC7.2.1.1.1.H04.R.1 NIH_MGC_331 Homo sapiens cDNA clone  
MGC7.2.1.1.1.H04, mRNA sequence
```

```
SLSQASLVRFPGGNYPA*HWQNLVYSQREKNIAAQIRFFSADSLVTADSPPPSMSSV  
MKNNPLYSDLSEEEAMEERX
```

Chosen sequence for blastp was highlighted in red. Green is sequences that returned no result when blastp was done.

Here, tell me the name of the novel protein, and the species from which it derives. It is very unlikely (but still definitely possible) that you will find a novel gene from an organism such as *S. cerevisiae*, human or mouse, because those genomes have already been thoroughly annotated. It is more likely that you will discover a new gene in a genome that is currently being sequenced, such as bacteria or plants or protozoa.

Protein name: Homo sapiens major intrinsically disordered NOTCH2-binding receptor (MINAR)

Species: Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria;  
Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

[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.

- If there is a match with 100% amino acid identity to a protein in the database, from the same species, then your protein is NOT novel (even if the match is to a protein with a name such as “unknown”). Someone has already found and annotated this sequence, and assigned it an accession number.
- If the top match reported has less than 100% identity, then it is likely that your protein is novel, and you have succeeded.
- If there is a match with 100% identity, but to a different species than the one you started with, then you have likely succeeded in finding a novel gene.
- If there are no database matches to the original query from [Q1], this indicates that you have partially succeeded: yes, you may have found a new gene, but no, it is not actually homologous to the original query. You should probably start over.

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) [Query subrange](#)

clone MGC7.2.1.1.H04, mRNA sequence  
SLSQASLVRFPGGNYPAA\*HWQNLVYSQREKKNIAAQRIRFFSADSLVTADS  
PPPSMSV  
MKNNPLYSDLSLEEAMEERX

From   
To

Or, upload file   [?](#)

Job Title   
[Enter a descriptive title for your BLAST search](#)

☐ Align two or more sequences [?](#)

**Choose Search Set**

Databases ☒ Standard databases (nr etc.): [Now](#) ☐ Experimental databases [Try experimental clustered nr database](#) [For more info see What is clustered nr?](#)

Compare ☐ Select to compare standard and experimental database [?](#)

**Standard**

Database  [?](#)

Organism [Optional](#)  ☐ exclude [Add organism](#)  
[Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown](#) [?](#)

Exclude [Optional](#) ☐ 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)  
[Choose a BLAST algorithm](#) [?](#)

None of blastp result had 100% identity, and <95% identity with low E-value indicates that the results are likely to be a novel protein. The top match was “major intrinsically disordered NOTCH2-binding receptor 1-like” from Homo sapiens, where there total score/max score/query coverage/e-value/percent identity are 148/148/96%/5e-32/92.41, respectively. Alignment detail is shown in the screenshot below.

\*Result wasn’t filtered just for Homo sapiens as top hit was the only result from corresponding species.




**Job Title** DR731264.1\_6 MGC7.2.1.1.1.H04.R.1 NIH\_MGC\_331...  
**RID** [X6F3P1SZ016](#) Search expires on 02-20 18:33 pm [Download All](#)   
**Program** BLASTP [Citation](#)   
**Database** nr [See details](#)   
**Query ID** lcl|Query\_11709707  
**Description** DR731264.1\_6 MGC7.2.1.1.1.H04.R.1 NIH\_MGC\_331 Hom ...  
**Molecule type** amino acid  
**Query Length** 80  
**Other reports** [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#) 

## Filter Results

**Organism** only top 20 will appear ☐ exclude  
  
[+ Add organism](#)




**Percent Identity**  to   
**E value**  to   
**Query Coverage**  to

Compare these results against the new Clustered nr database 

**BLAST**

[Descriptions](#)
[Graphic Summary](#)
[Alignments](#)
[Taxonomy](#)

## Sequences producing significant alignments

[Download](#) 
[Select columns](#) 
Show  

☒ select all 100 sequences selected

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Homo sapiens]	<a href="#">Homo sapiens</a>	148	148	98%	5e-43	92.41%	190	<a href="#">NP_001244237.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Pan paniscus]	<a href="#">Pan paniscus</a>	147	147	98%	2e-42	91.14%	190	<a href="#">XP_003829382.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Pan troglodytes]	<a href="#">Pan troglodytes</a>	147	147	98%	2e-42	91.14%	190	<a href="#">XP_003950663.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Pongo abelii]	<a href="#">Pongo abelii</a>	146	146	98%	3e-42	91.14%	190	<a href="#">XP_002815898.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Rhinopithecus roxellana]	<a href="#">Rhinopithecus roxellana</a>	145	145	98%	5e-42	91.14%	190	<a href="#">XP_010379869.2</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Gorilla gorilla gorilla]	<a href="#">Gorilla gorilla gorilla</a>	145	145	98%	9e-42	89.87%	190	<a href="#">XP_004042492.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Nomascus leucogenys]	<a href="#">Nomascus leucogenys</a>	145	145	95%	1e-41	93.42%	190	<a href="#">XP_004087485.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Ptilocolobus lephrosceles]	<a href="#">Ptilocolobus lephrosceles</a>	144	144	98%	2e-41	89.87%	190	<a href="#">XP_023050104.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Trachypithecus francoisi]	<a href="#">Trachypithecus francoisi</a>	144	144	98%	2e-41	89.87%	190	<a href="#">XP_033037245.1</a>
<input checked="" type="checkbox"/>	PREDICTED: UPF0258 protein KIAA1024-like homolog isoform X3 [Cercopithecus atys]	<a href="#">Cercopithecus atys</a>	144	144	98%	2e-41	89.87%	190	<a href="#">XP_011945527.1</a>
<input checked="" type="checkbox"/>	PREDICTED: UPF0258 protein KIAA1024-like homolog [Mandrillus leucophaeus]	<a href="#">Mandrillus leucophaeus</a>	144	144	98%	3e-41	89.87%	190	<a href="#">XP_011836578.1</a>
<input checked="" type="checkbox"/>	UPF0258 protein KIAA1024-like homolog isoform X2 [Macaca nemestrina]	<a href="#">Macaca nemestrina</a>	142	142	98%	6e-41	87.34%	162	<a href="#">XP_024644098.1</a>
<input checked="" type="checkbox"/>	PREDICTED: UPF0258 protein KIAA1024-like homolog [Colobus angolensis palliatus]	<a href="#">Colobus angolensis palliatus</a>	143	143	98%	7e-41	88.61%	190	<a href="#">XP_011797493.1</a>
<input checked="" type="checkbox"/>	UPF0258 protein KIAA1024-like homolog [Theropithecus gelada]	<a href="#">Theropithecus gelada</a>	142	142	98%	9e-41	88.61%	190	<a href="#">XP_025245224.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Chlorocebus sabaeus]	<a href="#">Chlorocebus sabaeus</a>	142	142	98%	1e-40	88.61%	190	<a href="#">XP_008012506.2</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Macaca mulatta]	<a href="#">Macaca mulatta</a>	142	142	98%	1e-40	87.34%	190	<a href="#">NP_001180990.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Symphalangus syndactylus]	<a href="#">Symphalangus syndactylus</a>	142	142	95%	1e-40	92.11%	190	<a href="#">XP_055155282.1</a>
<input checked="" type="checkbox"/>	UPF0258 protein KIAA1024-like homolog isoform X1 [Macaca nemestrina]	<a href="#">Macaca nemestrina</a>	142	142	98%	1e-40	87.34%	190	<a href="#">XP_011715000.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Hylobates moloch]	<a href="#">Hylobates moloch</a>	142	142	95%	2e-40	90.79%	190	<a href="#">XP_032012416.1</a>
<input checked="" type="checkbox"/>	PREDICTED: UPF0258 protein KIAA1024-like homolog [Rhinopithecus bieti]	<a href="#">Rhinopithecus bieti</a>	141	141	98%	4e-40	88.61%	190	<a href="#">XP_017730223.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Sapajus apella]	<a href="#">Sapajus apella</a>	139	139	98%	2e-39	86.08%	190	<a href="#">XP_032117284.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Callithrix jacchus]	<a href="#">Callithrix jacchus</a>	137	137	98%	9e-39	84.81%	190	<a href="#">XP_002744678.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Cebus imitator]	<a href="#">Cebus imitator</a>	133	133	98%	4e-37	83.54%	190	<a href="#">XP_017387650.1</a>
<input checked="" type="checkbox"/>	PREDICTED: UPF0258 protein KIAA1024-like homolog isoform X2 [Cercopithecus atys]	<a href="#">Cercopithecus atys</a>	133	133	98%	5e-37	72.45%	193	<a href="#">XP_011945526.1</a>
<input checked="" type="checkbox"/>	UPF0258 protein [Sciurus carolinensis]	<a href="#">Sciurus carolinensis</a>	133	133	98%	6e-37	82.28%	194	<a href="#">MBZ3891378.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Sciurus carolinensis]	<a href="#">Sciurus carolinensis</a>	133	133	98%	6e-37	82.28%	194	<a href="#">XP_047412257.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Saimiri boliviensis boliviensis]	<a href="#">Saimiri boliviensis boliviensis</a>	132	132	98%	8e-37	82.28%	190	<a href="#">XP_003920680.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Mesopodion densirostris]	<a href="#">Mesopodion densirostris</a>	132	132	98%	1e-36	78.48%	190	<a href="#">XP_059948605.1</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Physeter catodon]	<a href="#">Physeter catodon</a>	132	132	98%	1e-36	78.48%	190	<a href="#">XP_007122371.2</a>
<input checked="" type="checkbox"/>	major intrinsically disordered NOTCH2-binding receptor 1-like [Balaenoptera musculus]	<a href="#">Balaenoptera musculus</a>	132	132	98%	2e-36	78.48%	190	<a href="#">XP_036701798.1</a>
<input checked="" type="checkbox"/>	PREDICTED: UPF0258 protein KIAA1024-like homolog isoform X1 [Cercopithecus atys]	<a href="#">Cercopithecus atys</a>	132	132	98%	2e-36	72.45%	209	<a href="#">XP_011945525.1</a>

major intrinsically disordered NOTCH2-binding receptor 1-like [Homo sapiens]

Sequence ID: [NP\\_001244237.1](#) Length: 190 Number of Matches: 1

[See 4 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 28 to 106 [GenPept](#) [Graphics](#)

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

Score	Expect	Method	Identities	Positives	Gaps
148 bits(374)	5e-43	Compositional matrix adjust.	73/79(92%)	74/79(93%)	0/79(0%)
Query 1	SLSQASLYRFPGGNYPAA*HWQONLYYSQREKKNIAAQRIRFFSADSLYTADSPPPSMSSV				60
	+L QASLYRFPGGNYPAA HWQONLYYSQREKKNIAAQRIR SADSLYTADSPPPSMSSV				
Sbjct 28	ALLQASLYRFPGGNYPAAQHWWQONLYYSQREKKNIAAQRIRGSSADSLYTADSPPPSMSSV				87
Query 61	MKNNPLYSDLSEEEAMEER 79				
	MKNNPLY DLSLEEAMEER				
Sbjct 88	MKNNPLYGDLSEEEAMEER 106				

Related Information

[Gene](#) - associated gene details  
[AlphaFold Structure](#) - 3D structure displays  
[Genome Data Viewer](#) - aligned genomic context  
[Identical Proteins](#) - Identical proteins to NP\_001244237.1