

# ASSIGNMENT

## BIOINFORMATICS BASED TOOLS FOR ANALYSIS OF PROTEOMICS DATA

### Expasy Server

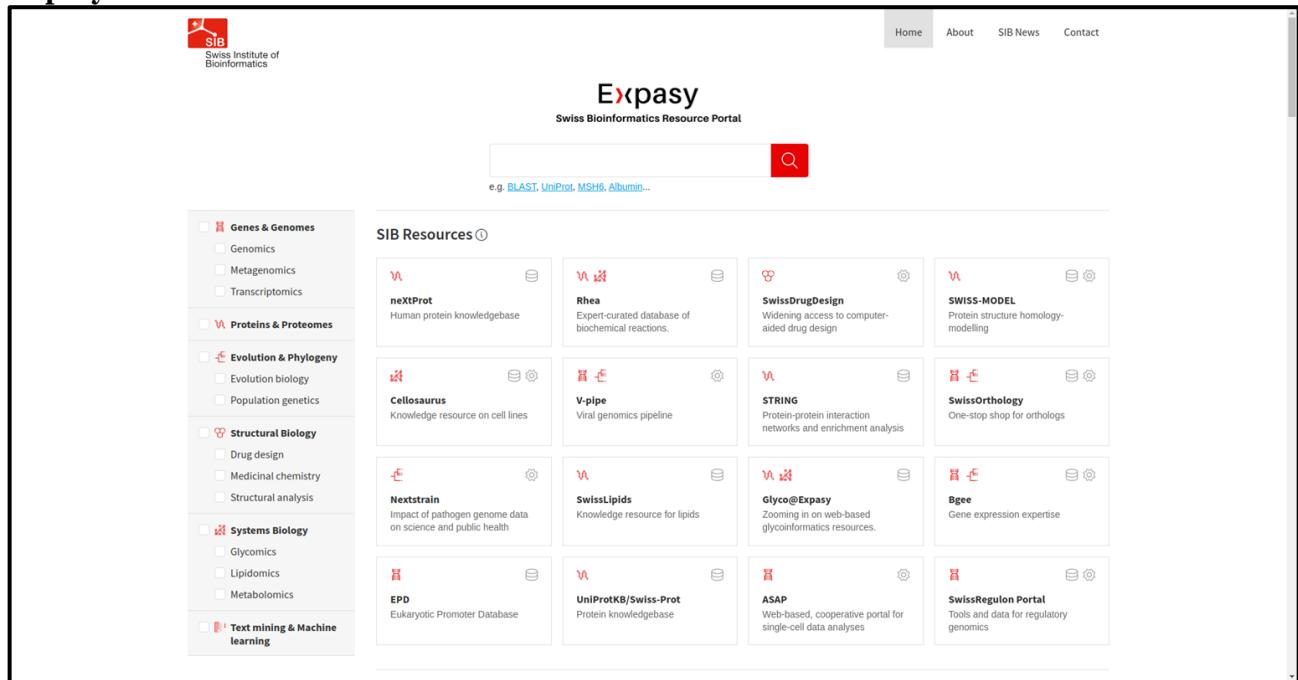


Fig1. Homepage of Expasy Server

### 1. Compute pI/MW

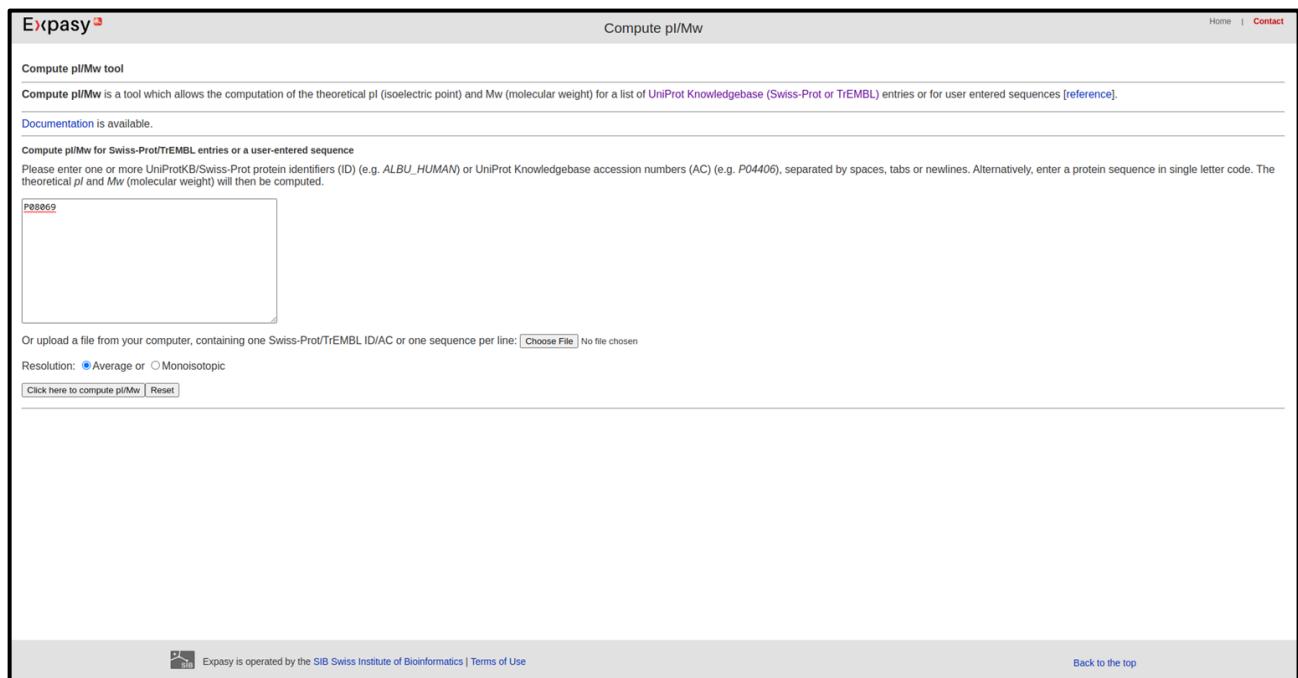


Fig2. Homepage of Compute pI/MW tool

ExPasy 

Compute pi/Mw tool

Compute pi/Mw is a tool which allows the computation of the theoretical pi (isoelectric point) and Mw (molecular weight) for a list of UniProt Knowledgebase (Swiss-Prot or TrEMBL) entries or for user entered sequences [reference].

Documentation is available.

Compute pi/Mw for Swiss-Prot/TrEMBL entries or a user-entered sequence

Please enter one or more UniProtKB/Swiss-Prot protein identifiers (ID) (e.g. ALBU\_HUMAN) or UniProt Knowledgebase accession numbers (AC) (e.g. P04406), separated by spaces, tabs or newlines. Alternatively, enter a protein sequence in single letter code. The theoretical pi and Mw (molecular weight) will then be computed.

P08069

Or upload a file from your computer, containing one Swiss-Prot/TrEMBL ID/AC or one sequence per line:  No file chosen

Resolution:  Average or  Monoisotopic

[Click here to compute pi/Mw](#) | [Reset](#)

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Fig3. Website of Compute pi/MW Accession number : P08069

ExPasy 

Compute pi/Mw

Selection of endpoints on the sequence

**IGF1R\_HUMAN (P08069)**  
Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) (Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain)  
Homo sapiens (Human)

Please select one of the following features by clicking on a pair of endpoints, and the computation will be carried out for the corresponding sequence fragment. By default, the complete sequence is used.

Note: Only the features corresponding to subsequences of at least 5 residues are highlighted.

FT	SIGNAL	1-38
FT	CHAIN	<b>31-736</b> Insulin-like growth factor 1 receptor alpha chain
FT	CHAIN	<b>741-1367</b> Insulin-like growth factor 1 receptor beta chain
FT	TOPO_DOM	741-935 Extracellular
FT	TRANSMEM	936-959 Helical
FT	TOPO_DOM	968-1367 Cytoplasmic
FT	DOMAIN	491-609 Fibronectin type-III 1
FT	DOMAIN	610-768 Fibronectin type-III 2
FT	DOMAIN	794-848 Fibronectin type-III 3
FT	DOMAIN	834-927 Fibronectin type-III 4
FT	DOMAIN	999-1274 Protein kinase
FT	NP_BIND	1005-1013 ATP
FT	REGION	1288-1367 Disordered
FT	MOTIF	977-980 IRS1- and SHC1-binding
FT	STRAND	37-41
FT	STRAND	43-49
FT	STRAND	53-57
FT	STRAND	59-65
FT	STRAND	68-70
FT	STRAND	88-83
FT	STRAND	85-92
FT	STRAND	96-98
FT	STRAND	115-121
FT	STRAND	133-144
FT	STRAND	152-154
FT	HELIX	157-168
FT	HELIX	164-166
FT	STRAND	168-171
FT	HELIX	175-178
FT	TURN	183-186
FT	STRAND	184-199
FT	STRAND	201-203
FT	STRAND	205-209
FT	HELIX	217-219
FT	STRAND	222-224
FT	HELIX	226-228
FT	STRAND	239-241
FT	STRAND	247-255
FT	STRAND	257-263
FT	STRAND	269-271
FT	TURN	272-274

Fig4. Result of query

Expasy 

Compute pi/Mw [Home](#) [Contact](#)

Compute pi/Mw

**IGF1R\_HUMAN (P08069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain]  
Homo sapiens (Human)

The parameters have been computed for the following feature:

FT CHAIN 31 736 Insulin-like growth factor 1 receptor alpha chain

Considered sequence fragment:

1	11	21	31	41	51
5					
61	ILLISKAEDY	PSYRFPKLTIV	ITTEVYLLLFRV	AGLESIGLDF	PNLTVTRQWK
121	EMTHLKOIGL	YLNBNTRGA	IRIEKADLIC	YLSTVINSLI	LFVINVALVIF
181	LCPGTMEKWP	MCKETTINNE	YNRWCWITNR	COOMCPSTCG	KRACTENNEC
241	APDNDTACVA	CRHYYAGVC	VPACPPTNRY	FEGRWCVDNE	CHPECLGSCS
301	GECMQECPSS	FIIRNGGSQSM	CIPCEGCPCK	VCEEEKTKTKT	IDSVTSAQM
361	361	LNINRGRNNE	ASELENFMG	IEVTVYKNI	RSHALVLSL
421	421	481	481	481	481
541	541	541	541	541	541
601	601	601	601	601	601
661	661	661	661	661	661
721	721	721	721	721	721

> Fasta

Molecular weight (Da): 80410.51 (average mass), 80358.31 (monoisotopic mass)

Theoretical pi: 5.93

Fig5. Feature Chain

**Expsy<sup>3</sup>** [Home](#) [Contact](#)

Compute pi/Mw

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**Compute pi/Mw tool**

Compute pi/Mw is a tool which allows the computation of the theoretical pi (isoelectric point) and Mw (molecular weight) for a list of [UniProt Knowledgebase \(Swiss-Prot or TrEMBL\)](#) entries or for user entered sequences [\[reference\]](#).

---

**Documentation** is available.

---

**Compute pi/Mw for Swiss-Prot/TrEMBL entries or a user-entered sequence**

Please enter one or more UniProtKB/Swiss-Prot protein identifiers (ID) (e.g. *ALBU\_HUMAN*) or UniProt Knowledgebase accession numbers (AC) (e.g. *P04406*), separated by spaces, tabs or newlines. Alternatively, enter a protein sequence in single letter code. The theoretical *pi* and *Mw* (molecular weight) will then be computed.

Or upload a file from your computer, containing one Swiss-Prot/TrEMBL ID/AC or one sequence per line:  No file chosen

Resolution:  Average or  Monoisotopic

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Fig6. Random unknown sequence entered to search for pI and MW

ExPasy 

Compute pi/Mw

Theoretical pi/Mw (average) for the user-entered sequence:

18  
LKPWTQYAVY

Theoretical pi/Mw: 8.50 / 1268.48

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Fig7. Result page for random unknown sequence

ExPasy 

Compute pi/Mw

**IGF1R\_HUMAN (P08069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain]  
Homo sapiens (Human)  
The parameters have been computed for the following feature:

FT DOMAIN 491 609 Fibronectin type-III 1

Considered sequence fragment:

```

 481      491      501      511      521      531
 |          |          |          |          |          |
 481 DVLHFTSTTT SKNRRIIWH RYRPPDYRDL ISFTVYYKEA PFKNVTEYDG 540
 541 QDAGCSNSWN MVVDVLPPNK DVEPGILLHG LKPWTQYAVY VKAVTLMVE NDHIRGAKSE 600
 601 ILYIRTNAS
  
```

[» Fasta](#)

Molecular weight (Da): 13723.52 (average mass), 13714.91 (monoisotopic mass)  
Theoretical pi: 6.45

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Fig8. Feature Domain

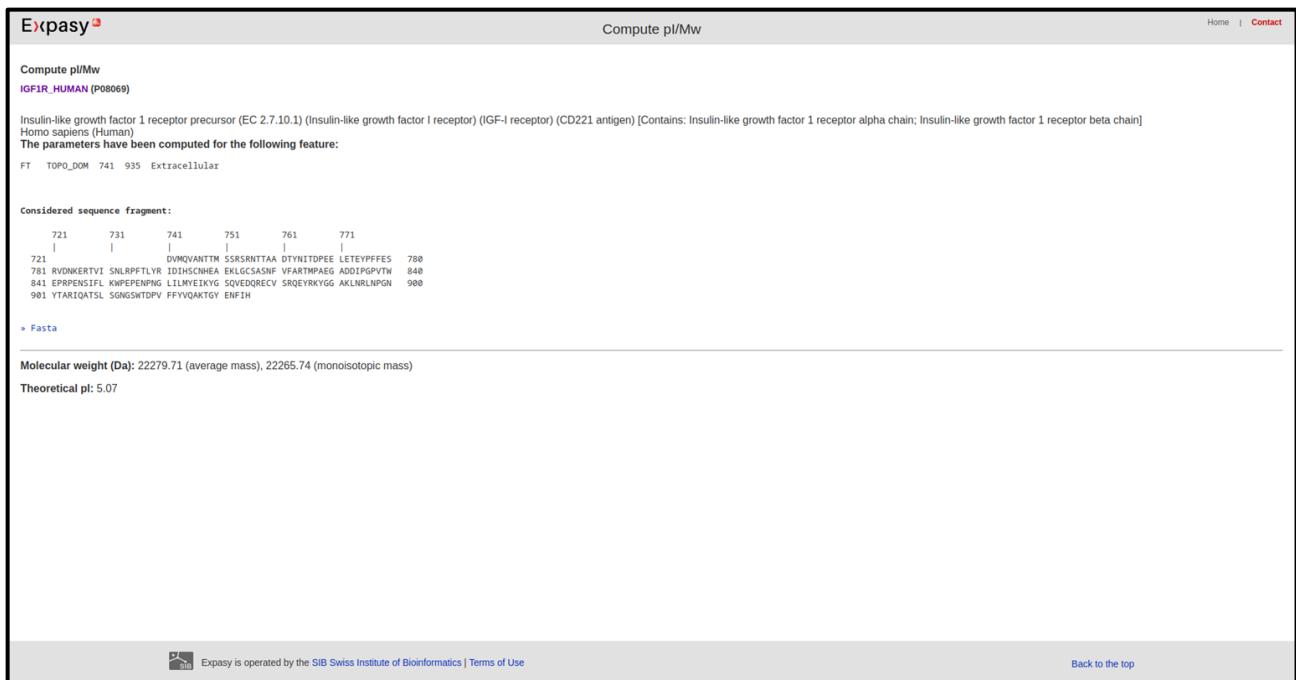


Fig9. Feature TOPODOM

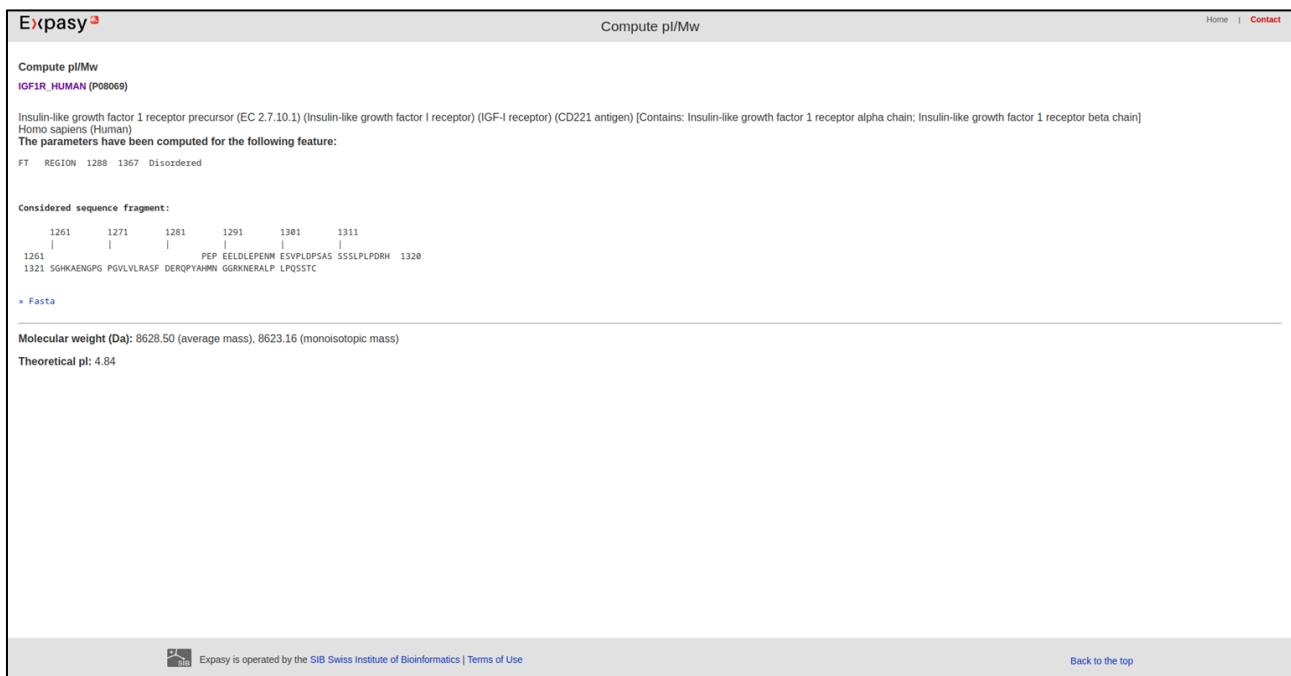
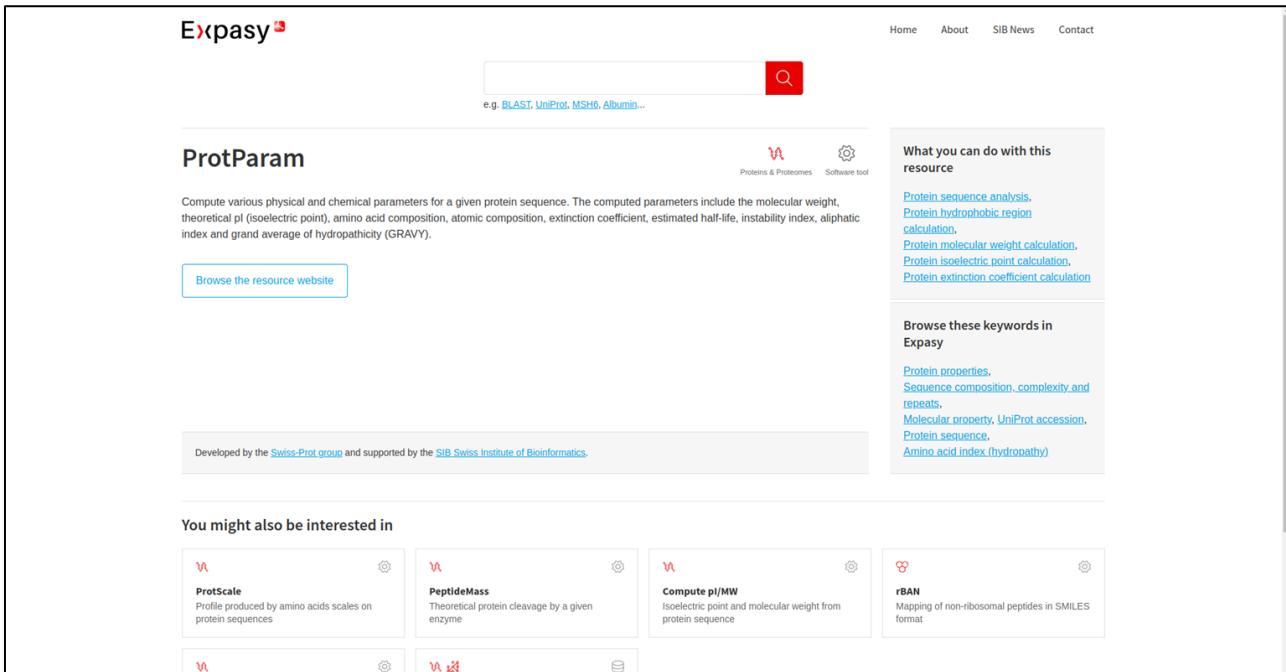


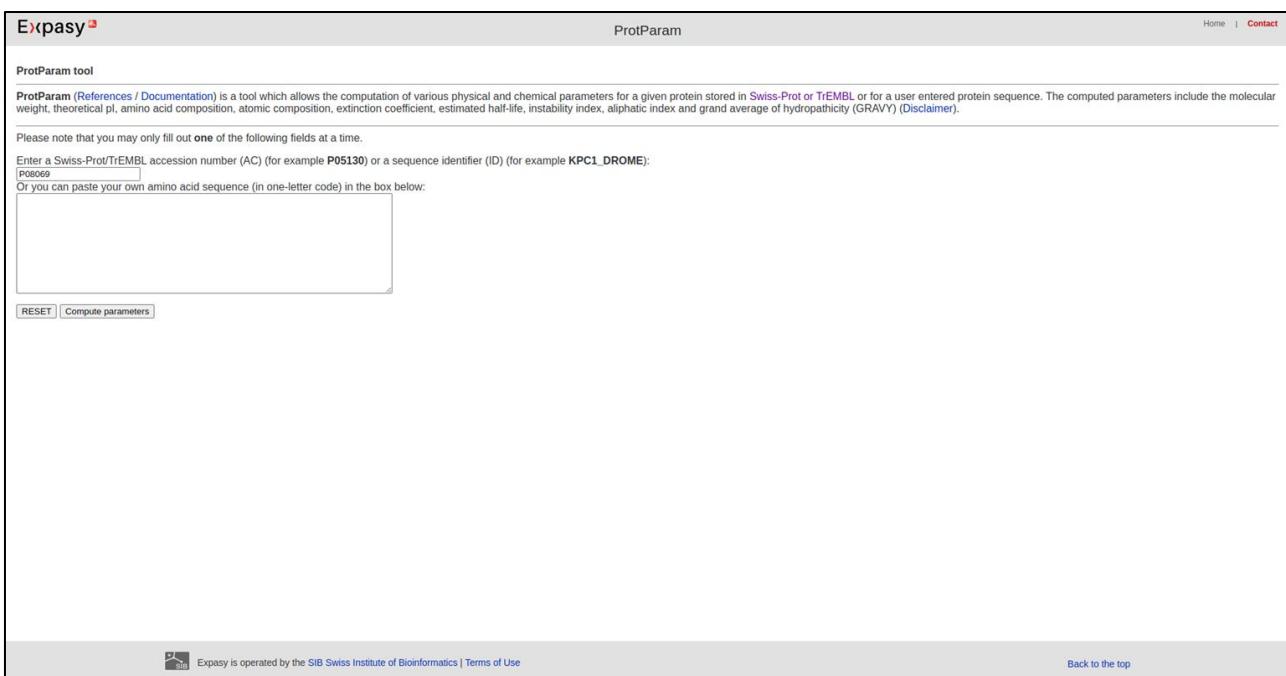
Fig10. Feature Region

## 2. ProtParam:



The screenshot shows the ProtParam tool on the ExPasy website. At the top, there is a search bar with the placeholder "e.g. BLAST, UniProt, MSH6, Albumin...". Below the search bar, the "ProtParam" tool is highlighted. A sub-header "What you can do with this resource" lists several protein analysis tools: Protein sequence analysis, Protein hydrophobic region calculation, Protein molecular weight calculation, Protein isoelectric point calculation, and Protein extinction coefficient calculation. Another section, "Browse these keywords in ExPasy", lists: Protein properties, Sequence composition, complexity and repeats, Molecular property, UniProt accession, Protein sequence, and Amino acid index (hydropathy). At the bottom left, a note states: "Developed by the Swiss-Prot group and supported by the SIB Swiss Institute of Bioinformatics." A "Browse the resource website" button is also present.

Fig11. Homepage of ProtParam



The screenshot shows the ProtParam tool interface. At the top, the "ProtParam" tool is selected. The main area contains a text input field for "Enter a Swiss-Prot/TrEMBL accession number (AC) (for example P05130) or a sequence identifier (ID) (for example KPC1\_DROME):" with the value "P08069" entered. Below this, a note says "Or you can paste your own amino acid sequence (in one-letter code) in the box below." A large text input area is provided for this purpose. At the bottom of the form are "RESET" and "Compute parameters" buttons. The footer includes the SIB logo, a note that ExPasy is operated by the SIB Swiss Institute of Bioinformatics | Terms of Use, and a "Back to the top" link.

Fig12. Website of ProtParam [Accession number: P08069]

ExPasy  ProtParam

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**ProtParam**

Selection of endpoints on the sequence

**IGF1R\_HUMAN (P08069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain] Homo sapiens (Human)

Please select one of the following features by clicking on a pair of endpoints, and the computation will be carried out for the corresponding sequence fragment. By default, the complete sequence is used.

Note: Only the features corresponding to subsequences of at least 5 residues are highlighted.

FT	SIGNAL	1-30
FT	CHAIN	31-736 Insulin-like growth factor 1 receptor alpha chain
FT	CHAIN	741-1367 Insulin-like growth factor 1 receptor beta chain
FT	TOPO_DOM	1-1367 Membrane
FT	TOPO_DOM	936-959 Helical
FT	TOPO_DOM	960-1367 Cytoplasmic
FT	DOMAIN	491-689 Fibronectin type-III 1
FT	DOMAIN	610-788 Fibronectin type-III 2
FT	DOMAIN	735-828 Fibronectin type-III 3
FT	DOMAIN	834-927 Fibronectin type-III 4
FT	DOMAIN	999-1021 Protein kinase
FT	NP_BIND	1805-1813 ATP
FT	REGION	1388-1367 Disordered
FT	MOTIF	977-988 IRS1- and SHC1-binding
FT	STRAND	37-41
FT	HELIX	43-49
FT	STRAND	53-57
FT	STRAND	59-65
FT	STRAND	68-79
FT	STRAND	88-83
FT	STRAND	85-92
FT	HELIX	96-98
FT	STRAND	115-121
FT	STRAND	138-144
FT	STRAND	152-154
FT	HELIX	156-169
FT	HELIX	164-166
FT	STRAND	168-171
FT	HELIX	175-178
FT	TURN	183-188
FT	STRAND	194-199
FT	STRAND	201-205
FT	STRAND	206-209
FT	HELIX	217-219
FT	STRAND	222-224
FT	HELIX	226-228
FT	STRAND	235-241
FT	STRAND	247-255
FT	STRAND	257-265
FT	STRAND	266-271
FT	TURN	273-275

Fig13. Result Page of Query

ExPasy  ProtParam

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ProtParam

**IGF1R\_HUMAN (P08069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain]  
Homo sapiens (Human)

**The parameters have been computed for the following feature:**

FT CHAIN 31 736 Insulin-like growth factor 1 receptor alpha chain

**Considered sequence fragment:**

1	11	21	31	41	51	
1			ELCPSDIDH	NOVQKLE	NTCTVLSVGH	60
61	ILLISKADEDY	RSYRFPKPLY	ITVELLFLPQ	AGLCEGSDLPF	PHVITRQKQ	LYHIVALIF
121	EMTNKLQIGL	YHLVNNTIGA	TR1RKRNDL	CL	YLTVDVHSLL	LDASHVNIV
181	LCPGTMHEKP	MECKTTTINNE	YVNCRHTNC	COMKPCSTCG	KRATCENNEC	CHPECLGSCS
241	APNDNTACVA	CHRYYYAGVC	VPACPPNTYR	FEGRCRVDRD	FCANL1SAES	DS6EGFVHD
301	GECMQECPGS	FTRNQGSSMY	C1PCEGCPCKV	VCEEEKTKT	IDSVTSAQ	QGCTIFKGNL
361	361 LINIRGRNNIE	ASELENFMGL	IEVVTGTVKL	RHSALVLSL	FLKNLRLIG	EQELEGQNYSF
421	YVLDMLNQ	LWEDVQV	IKAGQIAFAF	NQCLVSEIY	RMEEVITRKG	RQSKGDNTR
481	681 YDQGKQDQ	QDQFQDQF	QDQFQDQF	QDQFQDQF	QDQFQDQF	QDQFQDQF
541	QDQFQDQF	QDQFQDQF	QDQFQDQF	QDQFQDQF	QDQFQDQF	QDQFQDQF
601	601 ILYIRTHASV	PSPLDVLSA	SNSSQSLVK	WNPFLSPGN	LSVYIIRMRQ	QDQDGLYRH
661	661 NVCSDKQIPI	RYKAYGDI	EVTEVNPKTE	VCGGEKGPC	ACPKTEAERQ	AEKEEAEYRK
721	721 VFNFLHNSI	FVPRPE				

**Fasta**

```
Warning: All computation results shown below do not take into account  
any annotated post-translational modification.  
References and documentation are available.
```

---

Number of amino acids: 706

Molecular weight: 80410.51

Theoretical pI: 5.93

Amino acid composition: [CSV format](#)

Ala (A)	32	4.5%
Arg (R)	38	5.4%
Asn (N)	58	7.1%

Fig 14. Feature: Chain

Amino acid composition: [CSV format](#)

Ala (A)	32	4.5%
Arg (R)	38	5.4%
Asn (N)	39	5.1%
Asp (D)	24	4.0%
Cys (C)	36	5.1%
Gln (Q)	19	2.7%
Glu (E)	54	7.6%
Gly (G)	43	6.1%
His (H)	13	1.8%
Ile (I)	47	6.7%
Leu (L)	57	8.1%
Lys (K)	41	5.8%
Met (M)	12	1.7%
Phe (F)	21	3.0%
Pro (P)	37	5.2%
Ser (S)	40	6.2%
Thr (T)	40	5.7%
Trp (W)	11	1.6%
Tyr (Y)	37	5.2%
Val (V)	40	5.7%
Py1 (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 88  
 Total number of positively charged residues (Arg + Lys): 79

Atomic composition:

Carbon	C	3547
Hydrogen	H	5513
Nitrogen	N	967
Oxygen	O	1073
Sulfur	S	48

Formula: C3547H5513N967O1073S48  
 Total number of atoms: 11148

Extinction coefficients:

Extinction coefficients are in units of  $M^{-1} \text{ cm}^{-1}$ , at 280 nm measured in water.

Ext. coefficient	117880
Abs 0.1% (=1 g/l)	1.466, assuming all pairs of Cys residues form cystines

Ext. coefficient 115630  
 Abs 0.1% (=1 g/l) 1.438, assuming all Cys residues are reduced

Estimated half-life:

Fig15. Feature Chain (cont)

Total number of negatively charged residues (Asp + Glu): 88  
 Total number of positively charged residues (Arg + Lys): 79

Atomic composition:

Carbon	C	3547
Hydrogen	H	5513
Nitrogen	N	967
Oxygen	O	1073
Sulfur	S	48

Formula: C3547H5513N967O1073S48  
 Total number of atoms: 11148

Extinction coefficients:

Extinction coefficients are in units of  $M^{-1} \text{ cm}^{-1}$ , at 280 nm measured in water.

Ext. coefficient	117880
Abs 0.1% (=1 g/l)	1.466, assuming all pairs of Cys residues form cystines

Ext. coefficient 115630  
 Abs 0.1% (=1 g/l) 1.438, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is E (Glu).

The estimated half-life is: 1 hours (mammalian reticulocytes, in vitro).  
 30 min (yeast, in vivo).  
 >10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 49.64  
 This classifies the protein as unstable.

Aliphatic index: 78.41  
 Grand average of hydropathicity (GRAVY): -0.417

Fig16. Feature Chain (cont)

ExPasy  ProtParam

ProtParam

**IGF1R\_HUMAN (P00069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain]  
Homo sapiens (Human)

The parameters have been computed for the following feature:

FT STRAND 37 41

Considered sequence fragment:

```

  1      11      21      31      41      51
  |      |      |      |      |      |
  1      IDIR N
  
```

[» Fasta](#)

Warning: All computation results shown below do **not** take into account any annotated post-translational modification.  
References and documentation are available.

---

Number of amino acids: 5

Molecular weight: 629.71

Theoretical pI: 5.84

Amino acid composition: [CSV format](#)

Amino Acid	Count	Percentage
Ala (A)	0	0.0%
Arg (R)	1	20.0%
Asn (N)	1	20.0%
Asp (D)	0	0.0%
Cys (C)	0	0.0%
Gln (Q)	0	0.0%
Glu (E)	0	0.0%
Gly (G)	0	0.0%
His (H)	0	0.0%
Ile (I)	2	40.0%
Leu (L)	0	0.0%
Lys (K)	0	0.0%
Met (M)	0	0.0%
Phe (F)	0	0.0%
Pro (P)	0	0.0%
Ser (S)	0	0.0%

Fig17. Feature Strand

Total number of negatively charged residues (Asp + Glu): 1  
Total number of positively charged residues (Arg + Lys): 1

Atomic composition:

Element	Count	Percentage
Carbon	C	26
Hydrogen	H	47
Nitrogen	N	9
Oxygen	O	9
Sulfur	S	0

Formula:  $C_{26}H_{47}N_9O_9$   
Total number of atoms: 91

Extinction coefficients:

As there are no Trp, Tyr or Cys in the region considered, your protein should not be visible by UV spectrophotometry.

Estimated half-life:

The N-terminal of the sequence considered is I (Ile).  
The estimated half-life is: 20 hours (mammalian reticulocytes, in vitro).  
30 min (yeast, in vivo).  
>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 32.68.  
This classifies the protein as stable.

Aliphatic index: 156.00  
Grand average of hydropathicity (GRAVY): -0.500

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Fig18. Feature Strand (cont)

**ExPasy**  ProtParam

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ProtParam

**IGF1R\_HUMAN (P08069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain]  
Homo sapiens (Human)

The parameters have been computed for the following feature:

FT DOMAIN 491 609 Fibronectin type-III 1

Considered sequence fragment:

```

 481   |   491   |   501   |   511   |   521   |   531
 481   DVLHFHTSTTT SKNRLLIIMH RVRPPDYL ISFTVVYKKA PFKWVTEYDG 540
 541 QDAGGSNSNN MVOVOLPPNK DVEPGILLHG LKPWTQYAVV VKAVTLLTWE NDHIGRAKSE 600
 601 ILVIRTNAS
  
```

[» Fasta](#)

Warning: All computation results shown below do **not** take into account any annotated post-translational modification.  
References and documentation are available.

---

Number of amino acids: 119

Molecular weight: 13723.52

Theoretical pI: 6.45

Amino acid composition: [CSV format](#)

Amino Acid	Percentage
Ala (A)	5.8%
Arg (R)	5.0%
Asn (N)	5.9%
Asp (D)	7.6%
Cys (C)	0.8%
Gln (Q)	1.7%
Glu (E)	4.2%
Gly (G)	4.2%
His (H)	3.4%
Ile (I)	6.7%
Leu (L)	6.7%
Lys (K)	5.9%
Met (M)	1.7%
Phe (F)	2.5%
Pro (P)	5.9%
Ser (S)	5.9%
Thr (T)	9.2%
Trp (W)	2.5%
Tyr (Y)	6.7%
Val (V)	8.4%
Py1 (O)	0.0%
Sec (U)	0.0%
(B)	0.0%
(Z)	0.0%
(X)	0.0%

Total number of negatively charged residues (Asp + Glu): 14  
Total number of positively charged residues (Arg + Lys): 13

Atomic composition:

Element	Quantity
Carbon	628
Hydrogen	948
Nitrogen	164
Oxygen	183
Sulfur	3

Formula: C<sub>628</sub>H<sub>948</sub>N<sub>164</sub>O<sub>183</sub>S<sub>3</sub>  
Total number of atoms: 1918

Extinction coefficients:

Extinction coefficients are in units of M<sup>-1</sup> cm<sup>-1</sup>, at 280 nm measured in water.

Ext. coefficient 28420  
Abs 0.1% (=1 g/l) 2.071, assuming all pairs of Cys residues form cystines

Ext. coefficient 28200  
Abs 0.1% (=1 g/l) 2.071, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is D (Asp).

The estimated half-life is: 1.1 hours (mammalian reticulocytes, in vitro).  
3 min (yeast, in vivo).  
>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 27.01  
This classifies the protein as stable.

Fig19. Feature Domain

Lys (K) 7 5.9%  
Met (M) 2 1.7%  
Phe (F) 3 2.5%  
Pro (P) 7 5.9%  
Ser (S) 7 5.9%  
Thr (T) 11 9.2%  
Trp (W) 2 2.5%  
Tyr (Y) 8 6.7%  
Val (V) 10 8.4%  
Py1 (O) 0 0.0%  
Sec (U) 0 0.0%

(B) 0 0.0%  
(Z) 0 0.0%  
(X) 0 0.0%

Total number of negatively charged residues (Asp + Glu): 14  
Total number of positively charged residues (Arg + Lys): 13

Atomic composition:

Element	Quantity
Carbon	628
Hydrogen	948
Nitrogen	164
Oxygen	183
Sulfur	3

Formula: C<sub>628</sub>H<sub>948</sub>N<sub>164</sub>O<sub>183</sub>S<sub>3</sub>  
Total number of atoms: 1918

Extinction coefficients:

Extinction coefficients are in units of M<sup>-1</sup> cm<sup>-1</sup>, at 280 nm measured in water.

Ext. coefficient 28420  
Abs 0.1% (=1 g/l) 2.071, assuming all pairs of Cys residues form cystines

Ext. coefficient 28200  
Abs 0.1% (=1 g/l) 2.071, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is D (Asp).

The estimated half-life is: 1.1 hours (mammalian reticulocytes, in vitro).  
3 min (yeast, in vivo).  
>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 27.01  
This classifies the protein as stable.

Fig20. Feature Domain

ExPasy  ProtParam

ProtParam

**IGF1R\_HUMAN (P08069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain]  
Homo sapiens (Human)

The parameters have been computed for the following feature:

FT HELIX 43 49

Considered sequence fragment:

```

  1      11     21      31      41      51
  |      |      |      |      |      |
  1      YQQLKRL
  
```

[» Fasta](#)

Warning: All computation results shown below do **not** take into account any annotated post-translational modification.  
[References](#) and [documentation](#) are available.

---

Number of amino acids: 7

Molecular weight: 948.13

Theoretical pI: 9.99

Amino acid composition: [CSV format](#)

Ala (A)	0	0.0%
Arg (R)	1	14.3%
Asn (N)	0	0.0%
Asp (D)	0	0.0%
Cys (C)	0	0.0%
Gln (Q)	2	28.6%
Glu (E)	0	0.0%
Gly (G)	0	0.0%
His (H)	0	0.0%
Ile (I)	0	0.0%
Leu (L)	2	28.6%
Lys (K)	1	14.3%
Met (M)	0	0.0%
Phe (F)	0	0.0%
Pro (P)	0	0.0%
Ser (S)	0	0.0%
Thr (T)	0	0.0%
Trp (W)	0	0.0%
Tyr (Y)	1	14.3%
Val (V)	0	0.0%
Py1 (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 0  
Total number of positively charged residues (Arg + Lys): 2

Atomic composition:

Carbon	C	43
Hydrogen	H	73
Nitrogen	N	13
Oxygen	O	11
Sulfur	S	0

Formula:  $C_{43}H_{73}N_{13}O_{11}$   
Total number of atoms: 140

Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of  $M^{-1} \text{cm}^{-1}$ , at 280 nm measured in water.

Ext. coefficient 1490  
Abs 0.1% (=1 g/l) 1.572

Estimated half-life:

The N-terminal of the sequence considered is Y (Tyr).

The estimated half-life is: 2.8 hours (mammalian reticulocytes, *in vitro*).  
10 min (yeast, *in vivo*).  
2 min (*Escherichia coli*, *in vivo*).

Instability index:

The instability index (II) is computed to be 70.53  
This classifies the protein as unstable.

Fig21. Feature Helix

Leu (L) 2 28.6%  
Lys (K) 1 14.3%  
Met (M) 0 0.0%  
Phe (F) 0 0.0%  
Pro (P) 0 0.0%  
Ser (S) 0 0.0%  
Thr (T) 0 0.0%  
Trp (W) 0 0.0%  
Tyr (Y) 1 14.3%  
Val (V) 0 0.0%  
Py1 (O) 0 0.0%  
Sec (U) 0 0.0%

(B) 0 0.0%  
(Z) 0 0.0%  
(X) 0 0.0%

Total number of negatively charged residues (Asp + Glu): 0  
Total number of positively charged residues (Arg + Lys): 2

Atomic composition:

Carbon	C	43
Hydrogen	H	73
Nitrogen	N	13
Oxygen	O	11
Sulfur	S	0

Formula:  $C_{43}H_{73}N_{13}O_{11}$   
Total number of atoms: 140

Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of  $M^{-1} \text{cm}^{-1}$ , at 280 nm measured in water.

Ext. coefficient 1490  
Abs 0.1% (=1 g/l) 1.572

Estimated half-life:

The N-terminal of the sequence considered is Y (Tyr).

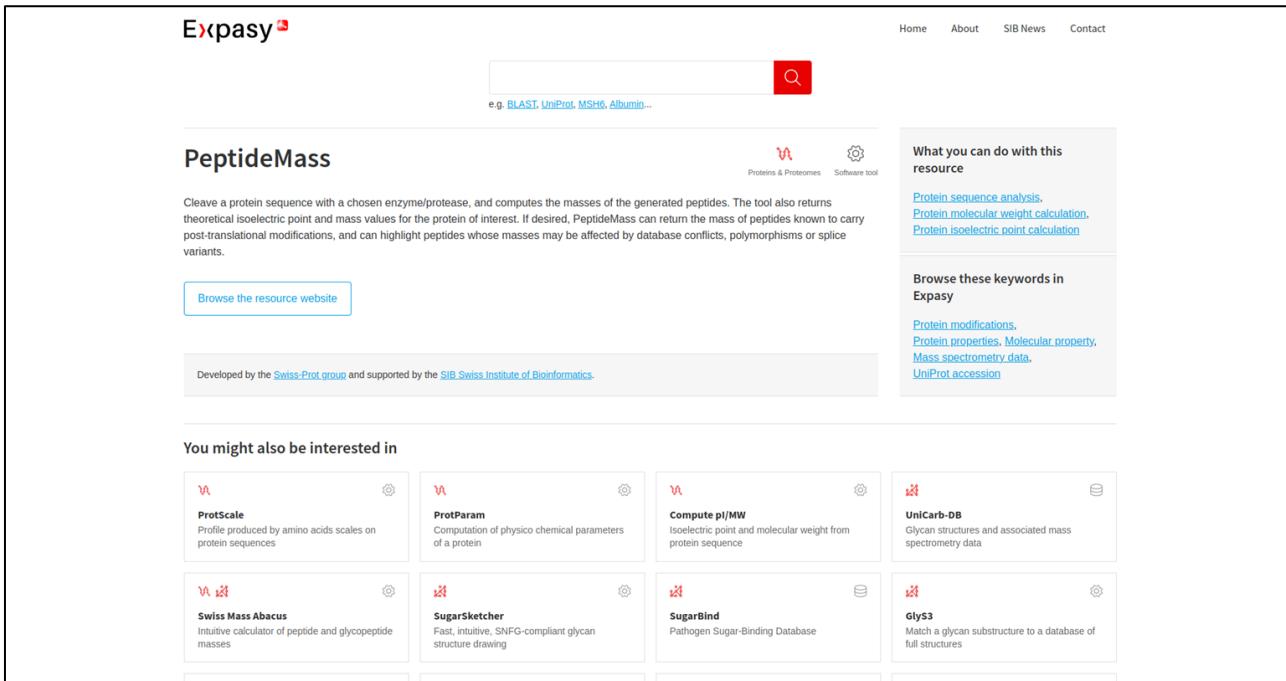
The estimated half-life is: 2.8 hours (mammalian reticulocytes, *in vitro*).  
10 min (yeast, *in vivo*).  
2 min (*Escherichia coli*, *in vivo*).

Instability index:

The instability index (II) is computed to be 70.53  
This classifies the protein as unstable.

Fig22. Feature Helix

### 3. PeptideMass:



ExPasy 

Home About SIB News Contact

e.g. BLAST, UniProt, MSH6, Albumin...

**PeptideMass**

Cleave a protein sequence with a chosen enzyme/protease, and computes the masses of the generated peptides. The tool also returns theoretical isoelectric point and mass values for the protein of interest. If desired, PeptideMass can return the mass of peptides known to carry post-translational modifications, and can highlight peptides whose masses may be affected by database conflicts, polymorphisms or splice variants.

[Browse the resource website](#)

Developed by the [Swiss-Prot group](#) and supported by the [SIB Swiss Institute of Bioinformatics](#).

**What you can do with this resource**

[Protein sequence analysis](#), [Protein molecular weight calculation](#), [Protein isoelectric point calculation](#)

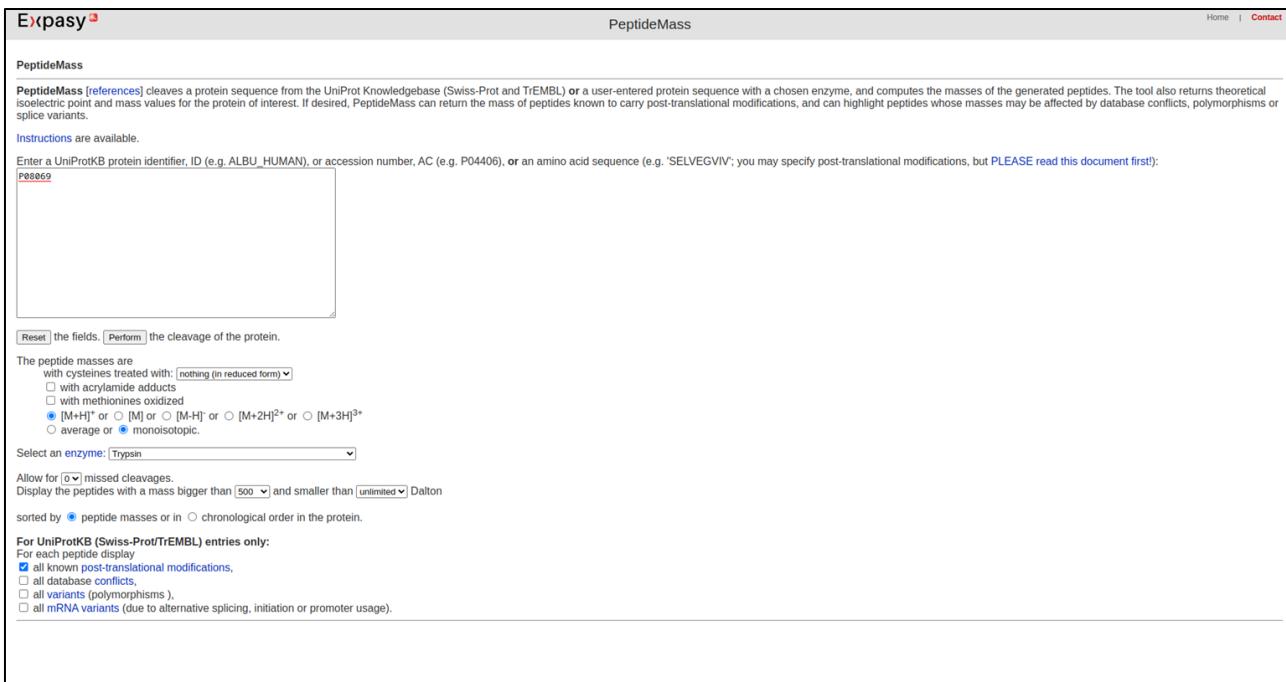
**Browse these keywords in ExPasy**

[Protein modifications](#), [Protein properties, Molecular property](#), [Mass spectrometry data](#), [UniProt accession](#)

**You might also be interested in**

 <b>ProtScale</b> Profile produced by amino acids scales on protein sequences	 <b>ProtParam</b> Computation of physico chemical parameters of a protein	 <b>Compute pI/MW</b> Isoelectric point and molecular weight from protein sequence	 <b>UniCarb-DB</b> Glycan structures and associated mass spectrometry data
 <b>Swiss Mass Abacus</b> Intuitive calculator of peptide and glycopeptide masses	 <b>SugarSketcher</b> Fast, intuitive, SNFG-compliant glycan structure drawing	 <b>SugarBind</b> Pathogen Sugar-Binding Database	 <b>Gly53</b> Match a glycan substructure to a database of full structures

Fig23. Homepage of peptidemass



ExPasy 

PeptideMass

Home | Contact

**PeptideMass**

PeptideMass [\[references\]](#) cleaves a protein sequence from the UniProt Knowledgebase (Swiss-Prot and TrEMBL) or a user-entered protein sequence with a chosen enzyme, and computes the masses of the generated peptides. The tool also returns theoretical isoelectric point and mass values for the protein of interest. If desired, PeptideMass can return the mass of peptides known to carry post-translational modifications, and can highlight peptides whose masses may be affected by database conflicts, polymorphisms or splice variants.

Instructions are available.

Enter a UniProtKB protein identifier, ID (e.g. ALBU\_HUMAN), or accession number, AC (e.g. P04406), or an amino acid sequence (e.g. 'SELVEGVIV'; you may specify post-translational modifications, but PLEASE read this document first):

P08069

the cleavage of the protein.

The peptide masses are  
with cysteines treated with:   with acrylamide adducts  with methionine oxidized   $[M+H]^+$  or   $[M]$  or   $[M-H]^-$  or   $[M+2H]^{2+}$  or   $[M+3H]^{3+}$   average or  monoisotopic.

Select an enzyme:

Allow for  missed cleavages.  
Display the peptides with a mass bigger than  and smaller than  Dalton  
sorted by  peptide masses or  chronological order in the protein.

For UniProtKB (Swiss-Prot/TrEMBL) entries only:  
For each peptide display  
 all known post-translational modifications,  all database conflicts,  all variants (polymorphisms),  all mRNA variants (due to alternative splicing, initiation or promoter usage).

Fig24. Website of PeptideMass (P08069)

**ExPasy**  PeptideMass

PeptideMass

The entered protein is: P08069

The selected enzyme is: Trypsin

Maximum number of missed cleavages (MC): 0

All cysteines in reduced form.

Methionines have not been oxidized.

Displaying peptides with a mass bigger than 500 Dalton.

Using monoisotopic masses of the occurring amino acid residues and giving peptide masses as [M+H]<sup>+</sup>.

---

You have selected **IGF1R\_HUMAN** (P08069) from UniProtKB/Swiss-Prot.

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain] Signal in positions 1-30 has been removed.

- Chain Insulin-like growth factor 1 receptor alpha chain at positions **31 - 736** [Theoretical pI: 5.93 / Mw (average mass): 80410.51 / Mw (monoisotopic mass): 80358.31]

mass	position	MC	modifications	peptide sequence
3835.6350	407-437	0		LILGEEQLEGNYSFVYVLNDQ NLQLQLWDWDHR
3693.5600	280-313	0		DFCANILSAESSDSEGFIH DCECMQECPSGFIIR
3422.7300	146-176	0		NADLCYLSTVTDWSILDAVS NNYIVGNKPKK
3116.1399	223-252	0		ACTENNECCHPECLGSCSAP DNNDTACVACR
2968.2723	534-560	0		NVTEYDQDAGCSNSWNMVD VDLPPNK
2527.3613	606-630	0		TNASVPSIPLDVLVSAANSSS QLIVK
2526.3754	561-582	0		DVEPGILLGKLPWTQYAVV VK
2497.2642	367-389	0		GNNIAELENFMGLIEVVTG YV
2073.9309	253-270	0		HYYAGAVCVPACPPNTYR
2058.1303	49-66	0		LENCTVIEGYLHILLISK
1999.7938	177-194	0		ECGDLCPGTMEKEPMCEK
1990.0181	631-647	0		WNPPSLPNGLNSYIIVR
1979.0346	111-126	0		LFYNALVIFEMTNLK
1944.9966	721-736	0		VFENFLHNSIFVPRPE
1942.9612	340-357	0		TIDSVTSQMLQGCTIFK
1914.0694	90-107	0		VAGLESGLDFPNLTVIR
1813.8272	486-502	0		ASCESDVLHFTSTTTSK
1813.7376	314-330	0		NGSQSMYCIPECEGCPK
1793.8439	673-688	0		YADGTTIDIEEVTEPNPK
1498.7682	583-595	0		AVTLMVENDHIR
1480.8773	78-89	0		LTVITEYLLFR
1328.7528	302-403	0		HSIAIVVSLSELK

Fig25. Result Page of Query

5

**ExPasy**  PeptideCutter

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PeptideCutter

PeptideCutter predicts potential substrate cleavage sites, cleaved by proteases or chemicals in a given protein sequence. The tool returns the query sequence with the possible cleavage sites mapped on it and/or a table of cleavage site positions.

[Browse the resource website](#)

e.g. [BLAST](#), [UniProt](#), [MSH6](#), [Albumin](#)...

Developed by the [Swiss-Prot group](#) and supported by the [SIB Swiss Institute of Bioinformatics](#).

**What you can do with this resource**

[Protein sequence analysis](#), [Protein sequence cleavage](#)

**Browse these keywords in ExPasy**

[Enzymes](#), [Mass spectrometry data](#), [UniProt accession](#), [Proteolytic digest](#), [Protein sequence](#)

**You might also be interested in**

 <a href="#">MetaNetX</a> Metabolic network repository & analysis	 <a href="#">GlycoDigest</a> In silico digestion of glycans by exoglycosidases	 <a href="#">SwissLipids</a> Knowledge resource for lipids	 <a href="#">Rhea</a> Expert-curated database of biochemical reactions
 <a href="#">Biochemical Pathways</a> Roche Biochemical Pathways	 <a href="#">ENZYME</a> Enzyme nomenclature database	 <a href="#">Rhea SPARQL endpoint</a> SPARQL access to the Rhea DB	 <a href="#">HMO-Glycologue</a> Simulator of Human Milk Oligosaccharide synthesis

Fig26. Homepage of PeptideCutter

**ExPasy**<sup>3</sup> PeptideCutter

PeptideCutter

PeptideCutter [references / documentation] predicts potential cleavage sites cleaved by proteases or chemicals in a given protein sequence. PeptideCutter returns the query sequence with the possible cleavage sites mapped on it and /or a table of cleavage site positions.

Enter a UniProtKB (Swiss-Prot or TrEMBL) protein identifier, ID (e.g. ALBU\_HUMAN), or accession number, AC (e.g. P04406), or an amino acid sequence (e.g. 'SERVELAT'): P08069

the cleavage of the protein.  the fields.

**Please, select**

all available enzymes and chemicals  
 only the following selection of **enzymes and chemicals**

Arg-C proteinase  
 BNPS-Skatole  
 Caspase3  
 Caspase6  
 Caspase9  
 Chymotrypsin-high specificity (C-term to [FYW], not before P)  
 Clostripain (Clostridiopeptidase B)  
 Factor Xa  
 GranzymeB  
 LysC  
 Neutrophil elastase  
 Pepsin (pH1.3)  
 Proteinase K  
 Thermolysin

Asp-N endopeptidase  
 Caspase1  
 Caspase4  
 Caspase7  
 Caspase10  
 Chymotrypsin-low specificity (C-term to [FYWML], not before P)  
 CNBr  
 Formic acid  
 Hydroxylamine  
 LysN  
 Pepsin (pH>2)  
 Staphylococcal peptidase I  
 Thrombin

Asp-N endopeptidase + N-terminal Glu  
 Caspase2  
 Caspase5  
 Caspase8  
 Enterokinase  
 Glutamyl endopeptidase  
 Iodosobenzoic acid  
 NTCB (2-nitro-5-thiocyanobenzoic acid)  
 Proline-endopeptidase  
 Tobacco etch virus protease  
 Trypsin

for the following enzymes an additional, more **sophisticated model** can be applied that attributes a probability of cleavage to each site :

Chymotrypsin -  
Trypsin -

Fig27. Website of PeptideCutter (P08069)

**Please, select**

all available enzymes and chemicals  
 only the following selection of **enzymes and chemicals**

Arg-C proteinase  
 BNPS-Skatole  
 Caspase3  
 Caspase6  
 Caspase9  
 Chymotrypsin-high specificity (C-term to [FYW], not before P)  
 Clostripain (Clostridiopeptidase B)  
 Factor Xa  
 GranzymeB  
 LysC  
 Neutrophil elastase  
 Pepsin (pH1.3)  
 Proteinase K  
 Thermolysin

Asp-N endopeptidase  
 Caspase1  
 Caspase4  
 Caspase7  
 Caspase10  
 Chymotrypsin-low specificity (C-term to [FYWML], not before P)  
 CNBr  
 Formic acid  
 Hydroxylamine  
 LysN  
 Pepsin (pH>2)  
 Staphylococcal peptidase I  
 Thrombin

Asp-N endopeptidase + N-terminal Glu  
 Caspase2  
 Caspase5  
 Caspase8  
 Enterokinase  
 Glutamyl endopeptidase  
 Iodosobenzoic acid  
 NTCB (2-nitro-5-thiocyanobenzoic acid)  
 Proline-endopeptidase  
 Tobacco etch virus protease  
 Trypsin

for the following enzymes an additional, more **sophisticated model** can be applied that attributes a probability of cleavage to each site :

Chymotrypsin -  
Trypsin -

Please enter the lowest cleavage probability that you would like to be displayed:  %

**Please indicate the way you would like the cleavage sites to be displayed**

Map of cleavage sites. Please select the number of amino acid within one block:    
 Table of sites, sorted alphabetically by enzyme and chemical name  
 Table of sites, sorted sequentially by amino acid number

**Please indicate which enzymes to include in the display**

All enzymes and chemicals  
 Enzymes and chemicals cleaving exactly  times  
 Enzymes and chemicals cleaving at least  times, and at most  times

Fig28. Different options of enzymes and chemicals available

ExPasy  PeptideCutter

Home | Contact

**PeptideCutter**

You have selected the protein **IGF1R\_HUMAN (P00009)** from UniProtKB/Swiss-Prot :

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain]

The sequence to investigate:

```

 18      28      38      48      58      68
MKSGGGGSP TSLWGLLFLS AALSINPTSG EICGGPGIDIR NDYQQQLKRLE NCTVIEGYLH

 78      88      98      108     118      128
ILLISKAEDY RSRFPKLTIV ITEYLLLFRV AGLESGLDF PNLTIVRGWK LFVNVALVIF

138      148      158      168      178      188
EMTNLKGIDL YNLNRNTRGA IRIEKNADLC YLSTVOWSLI LDASVNVIVI GNKPKKEGDO

198      208      218      228      238      248
LCPGTMEEKP MCEKTTINNE YNYRCWTTRN CQKMCPSCTG KRACTENNEC CHPECLGSCS

258      268      278      288      298      308
APONDITACVA CRHYYYAGYC VPACCPNTYR FEGWICVORD FCANILSAES SDSEGFVHIO

318      328      338      348      358      368
GECMQECP5G FIRNGSQSMY CIPCEGCPFK VCEEEKKTKT IDSVTSQML QGCTIFKGNL

378      388      398      408      418      428
LINIRRNNI ASELENFMGL IEVTGIVYKI RSHALVLSL FLKNLRLILG EEQLEGNYSF

438      448      458      468      478      488
YVLDDQNLQW LDWHDHRNLK IAKGKMYYAF NPKLKVSEIY RMEETGTTKG RDSKGDNTR

498      508      518      528      538      548
NNGERASCES DVLHFTSTTT SKNRRIITWH RYRPPDVYRDL ISFTVYYKEA PFKNVTEYDG

558      568      578      588      598      608
QDAGGSNSINN MVDVDPPLPPG DVEPGILLNG LKPTWQYAVV VKAVTLTMVE NDHIGRKAKE

618      628      638      648      658      668
IYIYRTNASV PSLPLOVLSA SNSSSQLIYK WHPPLPLPQHNG LSYIYIVRNQH QPQGQYLRYH

678      688      698      708      718      728
NYCSKDKIPI RKYADQTIDI EEVTEPNKTE VCGGEGKGPC CACPTEAEKO AEKEEAEYRK

738      748      758      768      778      788
VFENFLHNSI FVPVRERKRR DVMQVANTM SSRSRNTAA DTYNITDPEE LETEYPPFES

798      808      818      828      838      848
RVDKIKRTVI SNLRPFTLYR IDIHSNHEA EKLGCSASNF VFAARTMPAEQ ADDPGPVTH

858      868      878      888      898      908
EPRPENISFL KWPPEPNPQ LILMYEIKYG SQQEDQRECV SRQEYRKYGG AKLNRLNPGN

```

Fig29. Result page of Query

1288 1288 1298 1308 1318 1328  
EIISSIKEEM EPGFREVFSV YSEENKLPEP EELDLEPENK ESVPLDPASAS 555PLPLDORH

1338 1348 1358 1368  
SGHKAENGPG PGVLVLRASF DERQPYAHMN GGRKNERALP LPQ5STC

The sequence is 1367 amino acids long.

**Available enzymes:**  
The enzyme(s) that you have chosen:

- Arg-C proteinase
- Arg-N endopeptidase
- Asp-N endopeptidase + N-terminal Glu
- BNPS-Skatole
- Caspase1
- Caspase2
- Caspase3
- Caspase4
- Caspase5
- Caspase6
- Caspase7
- Caspase8
- Caspase9
- Caspase10
- Chymotrypsin-high specificity (C-term to [FYW], not before P)
- Chymotrypsin-low specificity (C-term to [FYWML], not before P)
- Clostrypain
- CGP-96376
- Enterokinase
- GranzymeB
- Factor Xa
- Formic acid
- Glutamyl endopeptidase
- Hydroxylamine
- Iodoacetamide
- LysC
- LysN
- NTCB (2-nitro-5-thiocyanobenzoic acid)
- Pepsin (pH1.3)
- Pepsin (pH>2)
- Proline-endopeptidase [•]
- Proteinase K
- Staphylococcal peptidase I
- Tobacco etch virus protease
- Thermolysin
- Thrombin
- Trypsin

[•] NOTE: Proline-endopeptidase was reported to cleave only substrates whose sequences do not exceed 30 amino acids. An unusual beta-propeller domain regulates proteolysis: see [Fulop et al., 1998](#).

These enzymes cleave the sequence:  
You have chosen to display all possible cleaving enzymes.

Name of enzyme	No. of	Positions of cleavage sites

Fig30. Enzymes selected while performing

Hydroxylamine	8	314 482 638 859 913 969 1327 1350
Iodosobenzoic acid	21	14 26 109 157 206 274 432 434 509 549 574 631 648 840 852 916 992 1178 1196 1203 1249
LysC	69	2 47 66 77 110 126 145 173 176 189 194 213 221 330 336 337 339 357 389 403 442 445 453 469 474 502 528 533 560 572 582 598 630 665 667 672 688 696 704 709 713 720 738 785 812 851 868 887 892 927 961 998 1019 1022 1033 1058 1111 1130 1168 1171 1185 1233 1254 1267 1324 1354
LysN	69	1 46 65 76 109 125 144 172 175 188 193 212 220 329 335 336 338 356 388 402 441 444 452 468 473 501 527 532 559 571 581 597 629 664 666 671 687 695 703 708 712 719 737 784 811 850 867 886 891 926 960 997 1018 1022 1032 1054 1087 1110 1129 1149 1167 1170 1184 1232 1253 1266 1285 1323 1353
NTCB (2-nitro-5-thiocyanobenzoic acid)	44	32 51 149 177 181 191 204 210 214 218 223 229 230 234 238 247 250 259 263 275 281 302 306 320 323 327 331 352 454 487 543 662 691 699 699 701 805 814 878 1058 1140 1236 1247 1366
Pepsin (pH1.3)	234	12 13 15 16 17 18 19 22 23 24 45 46 58 59 61 63 75 78 84 85 86 87 88 92 93 95 96 98 100 103 110 111 116 117 119 120 124 125 130 132 133 148 149 151 152 153 158 160 161 180 235 236 271 269 285 286 295 296 310 311 340 353 358 363 367 373 374 375 376 377 378 379 380 386 387 395 398 399 400 401 402 404 407 409 413 414 417 418 419 420 421 422 423 427 428 430 431 432 433 434 446 448 449 454 459 460 492 493 494 495 508 509 517 519 522 525 526 527 531 537 538 548 549 556 567 568 570 573 576 577 579 580 585 586 601 587 588 589 590 591 592 593 594 595 596 597 598 599 601 602 603 604 605 606 607 608 610 613 615 617 618 620 627 628 631 641 644 645 646 648 585 586 591 592 593 594 595 596 597 598 599 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 639 643 649 850 851 852 863 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 915 916 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1047 1048 1056 1065 1076 1086 1087 1088 1091 1093 1109 1124 1125 1130 1131 1146 1147 1151 1154 1161 1166 1167 1172 1177 1181 1188 1190 1191 1192 1195 1196 1197 1198 1201 1202 1203 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1221 1222 1224 1225 1227 1230 1231 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1274 1278 1279 1280 1281 1283 1284 1287 1289 1291 1292 1293 1295 1296 1298 1301 1303 1305 1309 1314 1316 1325 1326
Pepsin (pH>2)	344	12 13 14 15 16 17 18 19 22 23 24 26 45 57 59 61 63 75 78 83 85 86 87 88 92 93 95 96 98 100 103 108 110 111 113 114 115 116 117 119 120 124 125 129 130 131 132 133 148 149 150 151 152 156 157 158 159 160 161 167 168 180 200 201 202 203 205 235 236 252 261 268 269 271 273 274 280 285 295 296 310 311 319 320 353 356 360 361 373 374 375 376 377 378 379 380 386 387 395 398 399 400 401 402 404 407 409 413 414 417 418 419 420 421 422 423 427 428 430 431 432 433 434 446 448 449 454 459 460 492 493 494 495 508 509 517 519 522 525 526 527 531 537 538 548 549 556 567 568 570 573 576 577 579 580 585 586 601 863 864 865 868 869 885 887 892 893 900 901 909 910 915 916 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 944 945 946 947 948 951 954 955 956 957 958 967 971 972 973 980 981 986 991 992 1004 1009 1010 1013 1014 1047 1048 1056 1065 1076 1086 1087 1088 1091 1093 1109 1124 1125 1130 1131 1146 1147 1151 1154 1161 1166 1167 1172 1177 1181 1188 1190 1191 1192 1195 1196 1197 1198 1201 1202 1203 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1221 1222 1224 1225 1227 1230 1231 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1274 1278 1279 1280 1281 1283 1284 1287 1289 1291 1292 1293 1295 1296 1298 1301 1303 1305 1309 1314 1316 1325 1326
Proline-endopeptidase [?]	9	190 233 573 735 795 844 1096 1234 1257
Proteinase K	661	11 13 14 16 17 18 19 22 23 24 36 45 57 59 61 63 75 78 83 85 86 87 88 92 93 95 96 98 100 103 108 110 111 113 114 115 116 117 119 120 124 125 129 130 131 132 133 148 149 150 151 152 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 311 312 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 399 400 401 402 403 404 405 406 407 408 413 414 417 418 419 420 421 422 423 427 428 430 431 432 433 434 446 448 449 454 459 460 492 493 494 495 508 509 517 519 522 525 526 527 531 532 533 534 535 536 537 538 548 549 556 567 568 570 573 576 577 579 580 585 586 601 863 864 865 868 869 885 887 892 893 900 901 909 910 915 916 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 944 945 946 947 948 951 952 953 954 955 956 957 958 967 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 999 1000 1001 1012 1016 1017 1020 1021 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1108 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1274 1278 1279 1280 1281 1283 1284 1287 1289 1291 1292 1293 1295 1296 1298 1301 1303 1305 1309 1314 1316 1325 1326
Staphylococcal peptidase I	102	829 841 845 854 856 866 878 884 931 979 993 997 1001 1014 1015 1025 1027 1037 1043 1046 1050 1056 1080 1204 1099 1114 1145 1162 1182 1204 1210 1219 1221 1261 1268 1271 1276 1283 1289 1290 1291 1292 1293 1295 1296 1298 1301 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1399 1400 1399 1401 1402 1403 1404 1405 1406 1407 1408 1409 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1499 1500 1499 1501 1502 1503 1504 1505 1506 1507 1508 1509 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1569 1570 1571 1572 1573 1574 1575 1575 1576 1577 1578 1579 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1589 1590 1591 1592 1593 1594 1595 1596 1597 1597 1598 1599 1599 1599 1600 1599 1601 1602 1603 1604 1605 1606 1607 1608 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1618 1619 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1668 1669 1669 1670 1671 1672 1673 1674 1675 1675 1676 1677 1678 1678 1679 1679 1680 1680 1681 1682 1682 1683 1683 1684 1684 1685 1685 1686 1686 1687 1687 1688 1688 1689 1689 1690 1690 1691 1691 1692 1692 1693 1693 1694 1694 1695 1695 1696 1696 1697 1697 1698 1698 1699 1699 1699 1699 1700 1699 1701 1701 1702 1702 1703 1703 1704 1704 1705 1705 1706 1706 1707 1707 1708 1708 1709 1709 1710 1710 1711 1711 1712 1712 1713 1713 1714 1714 1715 1715 1716 1716 1717 1717 1718 1718 1719 1719 1720 1720 1721 1721 1722 1722 1723 1723 1724 1724 1725 1725 1726 1726 1727 1727 1728 1728 1729 1729 1730 1730 1731 1731 1732 1732 1733 1733 1734 1734 1735 1735 1736 1736 1737 1737 1738 1738 1739 1739 1740 1740 1741 1741 1742 1742 1743 1743 1744 1744 1745 1745 1746 1746 1747 1747 1748 1748 1749 1749 1750 1750 1751 1751 1752 1752 1753 1753 1754 1754 1755 1755 1756 1756 1757 1757 1758 1758 1759 1759 1760 1760 1761 1761 1762 1762 1763 1763 1764 1764 1765 1765 1766 1766 1767 1767 1768 1768 1769 1769 1770 1770 1771 1771 1772 1772 1773 1773 1774 1774 1775 1775 1776 1776 1777 1777 1778 1778 1779 1779 1780 1780 1781 1781 1782 1782 1783 1783 1784 1784 1785 1785 1786 1786 1787 1787 1788 1788 1789 1789 1790 1790 1791 1791 1792 1792 1793 1793 1794 1794 1795 1795 1796 1796 1797 1797 1798 1798 1799 1799 1800 1800 1801 1801 1802 1802

Fig34. Selected enzymes that do not cut

## 5. ProtScale:

Fig35. Homepage of protscale

ExPasy  ProtScale

ProtScale

ProtScale [Reference / Documentation] allows you to compute and represent the profile produced by an amino acid scale on a selected protein.

An amino acid scale is defined by a numerical value assigned to each type of amino acid. The most frequently used scales are the hydrophobicity or hydrophilicity scales and the secondary structure conformational parameters scales, but many other scales exist which are based on different chemical and physical properties of the amino acids. This program provides 57 predefined scales entered from the literature.

Enter a UniProtKB/Swiss-Prot or UniProtKB/T/EMBL accession number (AC) (e.g. P05130) or a sequence identifier (ID) (e.g. KPC1\_DROME):

Or you can paste your own sequence in the box below:  
P08069

Please choose an amino acid scale from the following list. To display information about a scale (author, reference, amino acid scale values) you can click on its name.

Molecular weight  
 Bulkiness  
 Polarity / Grantham  
 Recognition factors  
 Hphob. OMH / Sweet et al.  
 Hphob. / Kyte & Doolittle  
 Hphob. / Abraham & Leo  
 Hphob. / Bull & Breese  
 Hphob. / Guy  
 Hphob. / Miyazawa et al.  
 Hphob. / Roseman  
 Hphob. / Wolfenden et al.  
 Hphob. / HPLC / Wilson & al  
 Hphob. / HPLC pH3.4 / Cowan  
 Hphob. / RF mobility  
 HPLC / TFA retention  
 HPLC / retention pH 2.1  
 % buried residues  
 Hphob. / Chothia  
 Ratio hetero end/side  
 Average flexibility  
 beta-sheet / Chou & Fasman  
 alpha-helix / Deleage & Roux  
 beta-turn / Deleage & Roux  
 alpha-helix / Levitt  
 beta-turn / Levitt  
 Antiparallel beta-strand  
 A.A. composition  
 Relative mutability  
 Number of codon(s)  
 Polarity / Zimmerman  
 Refractivity  
 Hphob. / Eisenberg et al.  
 Hphob. / Hopp & Woods  
 Hphob. / Manavalan et al.  
 Hphob. / Black  
 Hphob. / Fauchere et al.  
 Hphob. / Janin  
 Hphob. / Rao & Argos  
 Hphob. / Tanford  
 Hphob. / Welling & al  
 Hphob. / HPLC / Parker & al  
 Hphob. / HPLC pH7.5 / Cowan  
 HPLC / HFBA retention  
 Transmembrane tendency  
 HPLC / retention pH 7.4  
 % accessible residues  
 Hphob. / Rose & al  
 Average area buried  
 alpha-helix / Chou & Fasman  
 beta-turn / Chou & Fasman  
 beta-sheet / Deleage & Roux  
 Coil / Deleage & Roux  
 beta-sheet / Levitt  
 Total beta-strand  
 Parallel beta-strand  
 A.A. comp. in Swiss-Prot

Fig36. Homepage of ProtScale (P08069)

Please choose an amino acid scale from the following list. To display information about a scale (author, reference, amino acid scale values) you can click on its name.

Molecular weight  
 Bulkiness  
 Polarity / Grantham  
 Recognition factors  
 Hphob. OMH / Sweet et al.  
 Hphob. / Kyte & Doolittle  
 Hphob. / Abraham & Leo  
 Hphob. / Bull & Breese  
 Hphob. / Guy  
 Hphob. / Miyazawa et al.  
 Hphob. / Roseman  
 Hphob. / Wolfenden et al.  
 Hphob. / HPLC / Wilson & al  
 Hphob. / HPLC pH3.4 / Cowan  
 Hphob. / RF mobility  
 HPLC / TFA retention  
 HPLC / retention pH 2.1  
 % buried residues  
 Hphob. / Chothia  
 Ratio hetero end/side  
 Average flexibility  
 beta-sheet / Chou & Fasman  
 alpha-helix / Deleage & Roux  
 beta-turn / Deleage & Roux  
 alpha-helix / Levitt  
 beta-turn / Levitt  
 Antiparallel beta-strand  
 A.A. composition  
 Relative mutability  
 Number of codon(s)  
 Polarity / Zimmerman  
 Refractivity  
 Hphob. / Eisenberg et al.  
 Hphob. / Hopp & Woods  
 Hphob. / Manavalan et al.  
 Hphob. / Black  
 Hphob. / Fauchere et al.  
 Hphob. / Janin  
 Hphob. / Rao & Argos  
 Hphob. / Tanford  
 Hphob. / Welling & al  
 Hphob. / HPLC / Parker & al  
 Hphob. / HPLC pH7.5 / Cowan  
 HPLC / HFBA retention  
 Transmembrane tendency  
 HPLC / retention pH 7.4  
 % accessible residues  
 Hphob. / Rose & al  
 Average area buried  
 alpha-helix / Chou & Fasman  
 beta-turn / Chou & Fasman  
 beta-sheet / Deleage & Roux  
 Coil / Deleage & Roux  
 beta-sheet / Levitt  
 Total beta-strand  
 Parallel beta-strand  
 A.A. comp. in Swiss-Prot

Window size:  Relative weight of the window edges compared to the window center (in %):   
 Weight variation model (if the relative weight at the edges is < 100%):  linear  exponential  
 Do you want to normalize the scale from 0 to 1?  yes  no

If you need more information about how to set these parameters, please click [here](#).

Fig37. List of different amico acid scales

ExPasy  ProtScale

ProtScale

Selection of endpoints on the sequence

**IGF1R\_HUMAN (P08069)**

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain] Homo sapiens (Human)

Please select one of the following features by clicking on a pair of endpoints, and the computation will be carried out for the corresponding sequence fragment. By default, the complete sequence is used.

Note: Only the features corresponding to subsequences of at least 18 residues are highlighted.

FT	SIGNAL	1-30
FT	CHAIN	31-736 Insulin-like growth factor 1 receptor alpha chain
FT	CHAIN	741-1367 Insulin-like growth factor 1 receptor beta chain
FT	TOPO_DOM	1-1365 Intracellular
FT	TOPO_DOM	936-959 Helical
FT	TOPO_DOM	960-1367 Cytoplasmic
FT	DOMAIN	491-609 Fibronectin type-III 1
FT	DOMAIN	610-708 Fibronectin type-III 2
FT	DOMAIN	735-828 Fibronectin type-III 3
FT	DOMAIN	834-927 Fibronectin type-III 4
FT	DOMAIN	928-1000 Tyrosine kinase
FT	NP_BIND	1085-1813 ATP
FT	REGION	1288-1367 Disordered
FT	MOTIF	977-980 IRS1- and SHC1-binding
FT	STRAND	37-41
FT	HELIX	43-49
FT	STRAND	53-57
FT	STRAND	69-75
FT	STRAND	68-78
FT	STRAND	80-83
FT	STRAND	85-92
FT	HELIX	96-98
FT	STRAND	115-121
FT	STRAND	138-144
FT	STRAND	152-154
FT	HELIX	160
FT	HELIX	164-166
FT	STRAND	168-171
FT	HELIX	175-178
FT	TURN	183-188
FT	STRAND	194-199
FT	STRAND	281-283
FT	STRAND	300-309
FT	HELIX	217-219
FT	STRAND	222-224
FT	HELIX	226-228
FT	STRAND	235-241
FT	STRAND	247-255
FT	STRAND	257-263
FT	STRAND	269-271
FT	TURB	279

Fig38. Result page of query

Expsys

ProtScale

Home | Contact

ProtScale

IGF1R\_HUMAN (P08069)

Insulin-like growth factor 1 receptor precursor (EC 2.7.10.1) (Insulin-like growth factor I receptor) (IGF-I receptor) (CD221 antigen) [Contains: Insulin-like growth factor 1 receptor alpha chain; Insulin-like growth factor 1 receptor beta chain] Homo sapiens (Human)

The parameters have been computed for the following feature:

FT CHAIN 31 736 Insulin-like growth factor 1 receptor alpha chain

Considered sequence fragment:

1	11	21	31	41	51	
1						
1			ELIGPGRDIER	PPQKQLE	NTCTVEGH	60
61	ILLTISKEDY	EVYRFPKPLTV	IETVLLFRRV	PLVQEGDIE	PLVYTRKQD	120
121	ERTNLKQDQL	YKRNTRIGA	TRIEKHLADL	YLTSTVWHLI	LDVAVRNHIV	180
181	LCPGTMKEKP	MKCTTINNE	YINRCRHTTIN	YVACMPSTCG	KRATCENNEC	240
241	APNDOTACAA	CRHYYAVG	YPAACPNTYR	FEGRWCVDR	FCANLSAES	300
301	GECMQECPSS	FRINGSSQSM	CPICEGCP	YCEEEKKTKT	IDSVTSAQML	360
361	LINTRRQNT	ASELENFMQI	IEVYTGQVYK	RHSHALVLSL	FLKNLRLLG	420
421	YLDNQNLOQ	LHDDHHRNLT	IKAKGKMFYA	NPKLCVSEIY	RMEEVGTGKG	480
481	NNHRRASCES	DWVQHRRR	SKNRRITLHN	YRPPVYDRL	ISVTYVHEA	540
541	ILYRHTNQH	YDQVDPKQ	YDQVDPKQ	YDQVDPKQ	YDQVDPKQ	600
601	ILYRHTNQH	YDQVDPKQ	YDQVDPKQ	YDQVDPKQ	YDQVDPKQ	660
661	NYCSKDKIPI	PSIPFLVLSA	INSSQSLVW	WPPSPLNHN	LSVTYVHQQR	720
721	YFENFLINSI	PPVPRP				

» Fasta

SEQUENCE LENGTH: 786

Using the scale **Hphys** / **Kyte & Doolittle**, the individual values for the 20 amino acids are:

Ala:	1.000	Arg:	-4.508	Asn:	-3.500	Asp:	-3.500	Cys:	2.500	Gln:	-3.500
Glu:	-3.500	Gly:	-0.400	His:	-3.200	Ile:	4.500	Leu:	3.500	Lys:	-3.900
Met:	1.900	Phe:	2.800	Pro:	-1.600	Seu:	-0.800	Thr:	-0.700	Tip:	-0.900
Tyr:	-1.300	Val:	4.200								

Weights for window positions 1...9, using linear weight variation model:

1	2	3	4	5	6	7	8	9	
1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
edge					center				edge

Fig39. Feature Chain

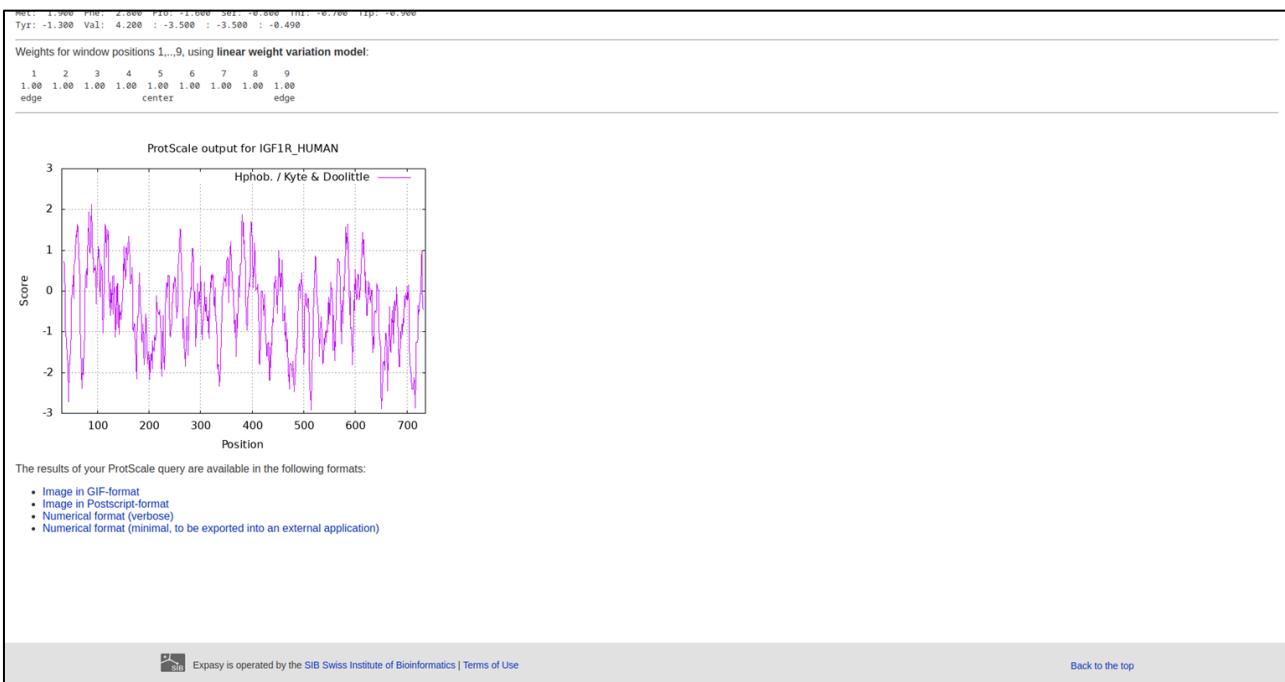


Fig40. Scale Hphob /Kyle & Doolittle

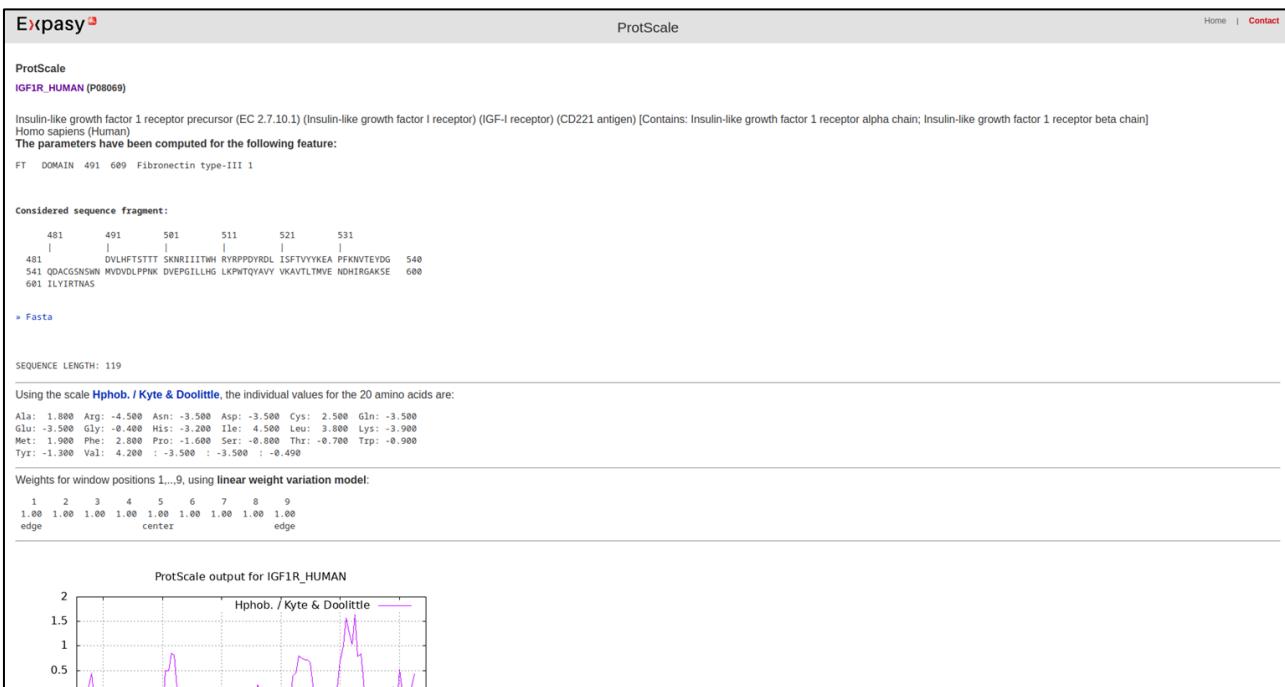


Fig41. Feature Domain

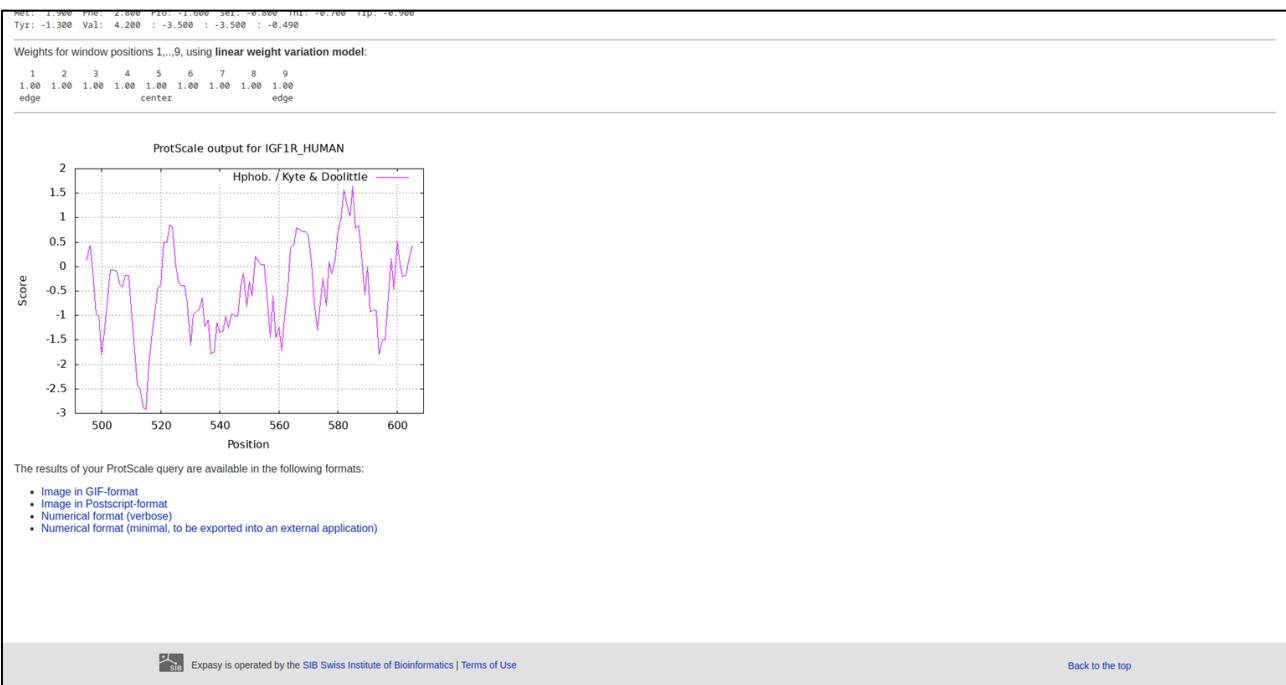


Fig42. Scale Hphob Kyte & doolittle

## References:

### Expasy Server:

1. <https://www.expasy.org/>

### Compute pI/MW:

2. <https://www.expasy.org/resources/compute-pi-mw>
3. [https://web.expasy.org/compute\\_pi/](https://web.expasy.org/compute_pi/)
4. [https://web.expasy.org/cgi-bin/compute\\_pi/pi\\_tool](https://web.expasy.org/cgi-bin/compute_pi/pi_tool)
5. [https://web.expasy.org/cgi-bin/compute\\_pi/pi\\_tool1?P08069@25-152@average](https://web.expasy.org/cgi-bin/compute_pi/pi_tool1?P08069@25-152@average)
6. [https://web.expasy.org/cgi-bin/compute\\_pi/pi\\_tool](https://web.expasy.org/cgi-bin/compute_pi/pi_tool)
7. [https://web.expasy.org/cgi-bin/compute\\_pi/pi\\_tool1?P08069@26-149@average](https://web.expasy.org/cgi-bin/compute_pi/pi_tool1?P08069@26-149@average)
8. [https://web.expasy.org/cgi-bin/compute\\_pi/pi\\_tool1?P08069@87-93@average](https://web.expasy.org/cgi-bin/compute_pi/pi_tool1?P08069@87-93@average)
9. [https://web.expasy.org/cgi-bin/compute\\_pi/pi\\_tool1?P08069@130-135@average](https://web.expasy.org/cgi-bin/compute_pi/pi_tool1?P08069@130-135@average)

### ProtParam:

10. <https://www.expasy.org/resources/protparam>
11. <https://web.expasy.org/protparam/>
12. <https://web.expasy.org/cgi-bin/protparam/protparam>
13. <https://web.expasy.org/cgi-bin/protparam/protparam1?P08069@25-152@>
14. <https://web.expasy.org/cgi-bin/protparam/protparam1?P08069@51-58@>
15. <https://web.expasy.org/cgi-bin/protparam/protparam1?P08069@26-149@>
16. <https://web.expasy.org/cgi-bin/protparam/protparam1?P08069@130-135@>

### PeptideMass:

17. <https://www.expasy.org/resources/peptidemass>
18. [https://web.expasy.org/peptide\\_mass/](https://web.expasy.org/peptide_mass/)
19. [https://web.expasy.org/cgi-bin/peptide\\_mass/peptide-mass.pl](https://web.expasy.org/cgi-bin/peptide_mass/peptide-mass.pl)

### PeptideCutter:

20. <https://www.expasy.org/resources/peptidecutter>
21. [https://web.expasy.org/peptide\\_cutter/](https://web.expasy.org/peptide_cutter/)
22. [https://web.expasy.org/peptide\\_cutter/peptidecutter\\_enzymes.html#Tryps](https://web.expasy.org/peptide_cutter/peptidecutter_enzymes.html#Tryps)

### ProtScale:

23. <https://www.expasy.org/resources/protscale>
24. <https://web.expasy.org/protscale/>
25. <https://web.expasy.org/cgi-bin/protscale/protscale.pl?1>
26. <https://web.expasy.org/cgi-bin/protscale/protscale.pl?P08069@25-152@Hphob.--Kyte--&--Doolittle 7 100 linear no>

27. [https://web.expasy.org/cgi-bin/protscale/protscale.pl?P08069@26-149@Hphob.--/--Kyte--&--Doolittle\\_7\\_100\\_linear\\_no](https://web.expasy.org/cgi-bin/protscale/protscale.pl?P08069@26-149@Hphob.--/--Kyte--&--Doolittle_7_100_linear_no)