



# ProtPathDB v 1.0

*A Database for Pathogen and Parasite Proteases*



5 Taxa comprising 23 species

5 Catalytic Classes

locBLAST

Displays the graph and statistics related to proteases

Allows the user to have access to direct links to other web resources

Gene ID /Text Search

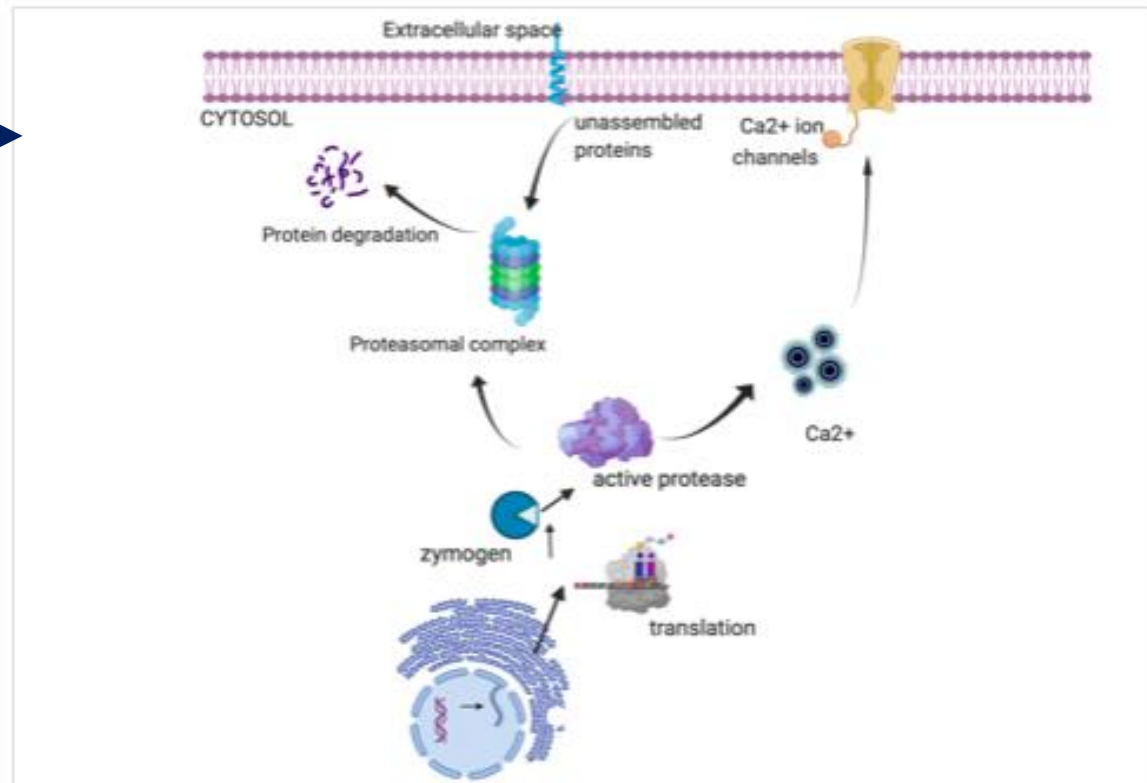
Home Taxonomy ▾ Class ▾ Tools ▾ Statistics Other Links Contact Acknowledgement Help

Search

Proteases are known to regulate multiple aspects of protein's life viz., protein's fate, localization, and activity, modulation of protein-protein interactions, creation of new bioactive molecules, contribution to the processing of cellular information, and in the generation, transduction, and amplification of molecular signals. Any alterations in the essential roles of proteases subjects to multiple pathological conditions such as cancer, neurodegenerative disorders, and inflammatory and cardiovascular diseases. Proteases cleave peptide bonds being N-terminal (for aminopeptidases), internal (for endopeptidases), and C-terminal (for carboxypeptidases). Carbonyl group of the substrate peptide bond is polarized by all the proteases stabilizing the oxyanion hole oxygen, which leads to the increased susceptibility of carbon to be attacked by an activated nucleophile. This is accomplished by four ways, and hence receives the names of four catalytic classes: aspartic proteases, cysteine proteases, metalloproteases, serine proteases. The modern system provides the five groups of classification of proteases- aspartic, cysteine, metallo, serine, and threonine.

**Description of Proteases and their Classification**

**Role of different protease in various functional biological pathways**



ProtPathDB - local NCBI BLAST

Program: [BLASTP 2]

Database: [Protein Database (ABC\_N)]

Enter sequence below in FASTA format (copy)

Or load it from disk

Output: [Graphical Overview] Plain Text

Algorithm Parameters: [Default] Advanced

Advanced Options

Maximum Target Sequences: [50]

Expect Threshold: [10.0]

Word Size: [3]

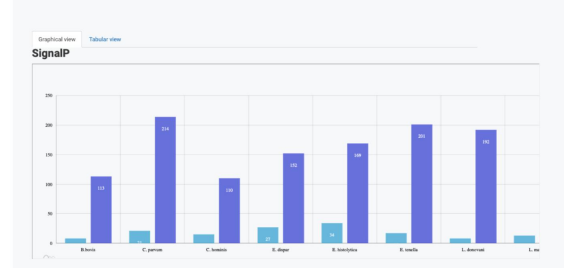
Matrix: [BLOSUM62]

Gap Costs: [Extension: 11, Existence: 7]

Filter Low Complexity Regions

Mask for Lookup Table Only

Reset Clear Sequence Search



| Organism       | Secondary signal peptides (SP) | Count |
|----------------|--------------------------------|-------|
| Abaco          | 8                              | 103   |
| C. parvum      | 21                             | 234   |
| C. hominis     | 15                             | 110   |
| E. dispar      | 27                             | 152   |
| E. histolytica | 24                             | 169   |
| E. maeili      | 17                             | 201   |
| L. donovani    | 8                              | 182   |
| L. major       | 13                             | 207   |
| L. mexicana    | 15                             | 203   |
| N. caninum     | 17                             | 193   |

- >MEROPS
- >CDD
- >Eupath
- >MPMP
- >InterProScan
- >KEGG
- >Gene Ontology (Amigo 2)
- >PlasmoGEM
- >NCBI
- >BIOGRID

## ProtPathDB v 1.0

A Database for Pathogen and Parasite Proteases

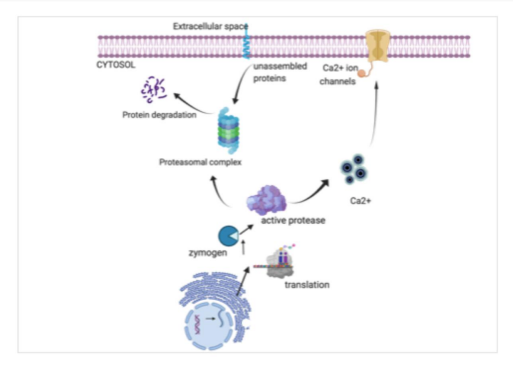


Home Taxonomy Class Tools Statistics Other Links Contact Acknowledgement Help

Search

Proteases are known to regulate multiple aspects of protein's life viz., protein's fate, localization, and activity, modulation of protein-protein interactions, creation of new bioactive molecules, contribution to the processing of cellular information, and in the generation, transduction, and amplification of molecular signals. Any alterations in the essential roles of proteases subjects to multiple pathological conditions such as cancer, neurodegenerative disorders, and inflammatory and cardiovascular diseases. Proteases cleave peptide bonds being N-terminal (for aminopeptidases), internal (for endopeptidases), and C-terminal (for carboxypeptidases). Carbonyl group of the substrate peptide bond is polarized by all the proteases stabilizing the oxyanion hole oxygen, which leads to the increased susceptibility of carbon to be attacked by an activated nucleophile. This is accomplished by four ways, and hence receives the names of four catalytic classes: aspartic proteases, cysteine proteases, metalloproteases, serine proteases. The modern system provides the five groups of classification of proteases- aspartic, cysteine, metallo, serine, and threonine.

- Apicomplexa
  - Cryptosporidium parvum
  - Cryptosporidium hominis
- Amoebozoa
  - Theileria annulata
- Fungi
  - Babesia bovis
  - Eimeria tenella
- Heterolobosea
  - Neospora caninum
- Kinetoplastida
  - Toxoplasma gondii
  - Plasmodium vivax
  - Plasmodium knowlesi
  - Plasmodium chabaudi
  - Plasmodium falciparum
  - Plasmodium yoelli
  - Plasmodium berghei
  - Plasmodium cynomolgi



- Aspartate
- Cysteine
- Serine
- Metalloprotease
- Threonine
- Others

**Aspartate**

Aspartic proteases/acidic proteases are the endopeptidases which requires aspartic acid residues for their catalysis and usually function in acid solutions. Due to their functioning in acid environment the functioning of aspartic proteases are limited to certain locations. The catalytic site consists of two aspartic acid residues at positions 32 and 215. Two aspartic residues which mediate the nucleophilic attack on the peptide bond by activating the water molecule (James, 2004). Aspartic proteases exhibit maximal activity at 3 to 4, an isoelectric point in the range of pH 3 to 4.5 and molecular masses are in the range of 30 to 45 kDa (Rao et al., 1998). The active-site aspartic acid residue is situated within the motif Asp-Xaa-Gly, in which Xaa can be Ser or Thr. The aspartic proteases are inhibited by pepstatin, along with being sensitive to diazotone compounds such as diazocetyl-DL-norleucine methyl ester (DAN) and 1,2-epoxy-3-(p-nitrophenoxy)propane (EPNP) in the presence of copper ions (Rao et al., 1998).

ProtPathDB Data Table

Export Basic

| Gene_ID   | Product_Description   | Organism                       | Ortholog_Group |
|-----------|---|--------------------------------|----------------|
| cgd1_1080 | Alpha beta hydrolase  | Cryptosporidium parvum Iowa II | OG6_106560     |
| cgd1_1100 | X-Pro dipeptidyl-peptidase  | Cryptosporidium parvum Iowa II | OG6_124529     |
| cgd1_1170 | Ubiquitin carboxyl-terminal hydrolase   | Cryptosporidium parvum Iowa II | OG6_102753     |
| cgd1_1270 | PPPDE peptidase/PUB domain containing protein   | Cryptosporidium parvum Iowa II | OG6_102579     |
| cgd1_1680 | Insulinase like protease  | Cryptosporidium parvum Iowa II | OG6_158720     |
| cgd1_220  | Glycosylphosphatidylinositol transamidase   | Cryptosporidium parvum Iowa II | OG6_101767     |
| cgd1_2240 | Aspartic peptidase A1 family protein  | Cryptosporidium parvum Iowa II | OG6_107443     |
| cgd1_2490 | Proteasome subunit beta type  | Cryptosporidium parvum Iowa II | OG6_101631     |
| cgd1_2700 | Methionine aminopeptidase   | Cryptosporidium parvum Iowa II | OG6_100342     |
| cgd1_2870 | Hemimethylated DNA-binding/Glucosidase II beta subunit-like domain containing protein | Cryptosporidium parvum Iowa II | OG6_153953     |

Showing 1 to 10 of 148 rows 10 rows per page

ProtPathDB Data Table

Export Basic

| GeneID         | Product_Description                         | Transcript_Product_Description              |
|----------------|---|---|
| BBOV_II007340  | erythrocyte membrane-associated antigen     | erythrocyte membrane-associated antigen     |
| BBOV_II007410  | erythrocyte membrane-associated antigen     | erythrocyte membrane-associated antigen     |
| BBOV_II007480  | 26S proteasome regulatory subunit, putative | 26S proteasome regulatory subunit, putative |
| BBOV_III001640 | aspartyl protease family protein            | aspartyl protease family protein            |
| BBOV_III003510 | eukaryotic aspartyl protease family protein | eukaryotic aspartyl protease family protein |
| BBOV_III010190 | conserved hypothetical protein              | conserved hypothetical protein              |
| BBOV_IV007890  | aspartyl protease, putative                 | aspartyl protease, putative                 |
| BBOV_IV009660  | aspartyl protease, putative                 | aspartyl protease, putative                 |
| BBOV_IV010360  | aspartyl protease, putative                 | aspartyl protease, putative                 |
| cgd1_2240      | Aspartic peptidase A1 family protein        | Aspartic peptidase A1 family protein        |

Showing 1 to 10 of 213 rows 10 rows per page



# ProtPathDB v 1.0

*A Database for Pathogen and Parasite Proteases*



## cgd1\_1080 | Alpha beta hydrolase

> ID's → UniProt\_ID: 096162

> GEO Functions

> Subcellular Localization

> Sequence

> Domains

> Structure

> Post Translational Modifications

> Protein-Protein Interaction

> Literature

Computed\_GO\_Component\_IDs: GO:0005739  
 Computed\_GO\_Components: mitochondrion  
 Computed\_GO\_Function\_IDs: GO:0008234  
 Computed\_GO\_Functions: cysteine-type peptidase activity  
 {Computed\_GO\_Process\_IDs: GO:0006508  
 Computed\_GO\_Processes: proteolysis  
 Curated\_GO\_Component\_IDs:  
 Curated\_GO\_Components:  
 Curated\_GO\_Function\_IDs: GO:0008234  
 Curated\_GO\_Functions: cysteine-type peptidase activity  
 Curated\_GO\_Processes: proteolysis

> Targetp

> Signalp

> Mitoprot

> Targetp

Search     

| <input type="checkbox"/> _ID           | Prediction | OTHER    | SP       | mTP      | CS_Position |
|--|------------|----------|----------|----------|-------------|
| <input type="checkbox"/> PF3D7_0207300 | OTHER      | 0.695151 | 0.051355 | 0.253494 |             |

Showing 1 to 1 of 1 rows



## cgd1\_1080 | Alpha beta hydrolase

- > ID's
- > GEO Functions
- > Subcellular Localization
- > Sequence
- > Domains
- > Structure
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- > Protein-Protein Interaction
- > Literature

- > Targetp
- > Signalp
- > Mitoprot

### > Signalp

| gene_id       | prediction | SPSecSPI | OTHER    |
|---------------|------------|----------|----------|
| PF3D7_0207300 | OTHER      | 0.075951 | 0.924049 |

Showing 1 to 1 of 1 rows

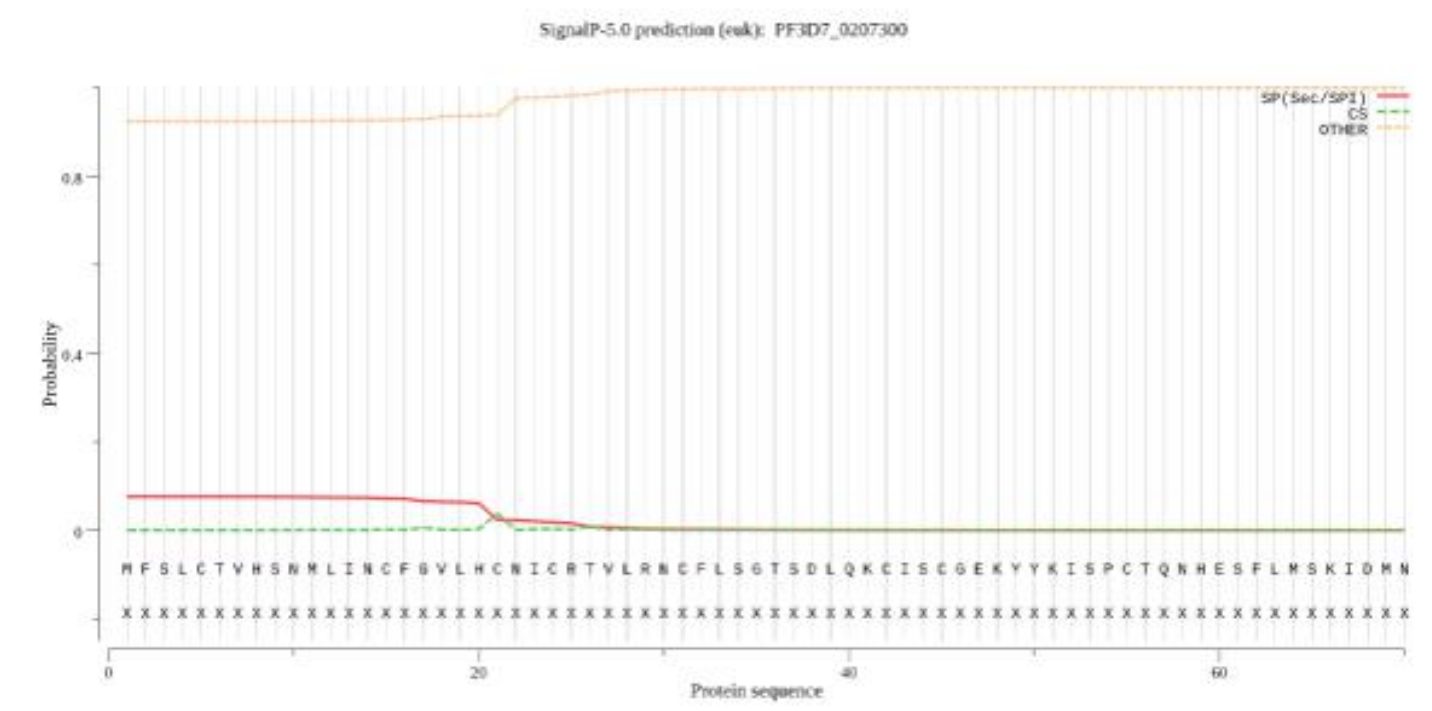
#### Fasta :-

```

>PF3D7_0207300 MFSLCTVHSNMLINCFBVLHLCNICRTVLRNCFLSGTSDLQKCI SCGEKYYKISPCTQNHE SFLMSKIDMNTFVELKDHEEVTDEKMKNLITKII EIAIDRHTLGLHDFSSVSDEYKEKI KMLCMF
NPNQWVKDRAGFKDDDKPSVGIIPERKIFKPYDIKTLKSSLYASSTNCDRQFCDRFSDSN ECEHRIRVNLNQGKCGNCWVFASSVIAAYRCRKG LFGAEP SIKYYVTLCKNKHLMDIDNNP FGHYNDNICEGGHL SYY
LMDRIYAGYIYHGYFKVSFKDYVVSNRNDLNI IKDYIIQQGSV FVSM EVDKLTFDHD GTKVMMSCEDNDSPDHALVLIGYDYIKTNGKKSSY WLLRNSWGS HWGDKGNFKLDMYGP NNCNGKVL YNAFPLLL
SNDNDRNYINPYNKNDNNYPY NKPHYNDKENDAYYEKND DYNNAHIRRNTIRFKKRIIK YSLYARIGNTVYKRTIFSKRKDEYKEPYSCLRTFSFEKDSDTKCRSNCEKYIDKCKHNSS IGECLIQHSPNYKCVYCGM

```

[Download Fasta](#)





## cgd1\_1080 | Alpha beta hydrolase

- > ID's
- > GEO Functions
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- > Structure
- > Post Translational Modifications
- > Protein-Protein Interaction
- > Literature

- > Targetp
- > Signalp
- > Mitoprot

### > Mitoprot

MitoProt II - v1.101

File : /home/rajan/sadaf/4480\_mitoprot/test/PF3D7\_0207300.fa  
 Sequence name : PF3D7\_0207300  
 Sequence length : 679

#### VALUES OF COMPUTED PARAMETERS

Coef20 : 4.231  
 CoefTot : -0.186  
 ChDiff : 6  
 ZoneTo : 37  
 KR : 2  
 DE : 0  
 CleavSite : 0

#### HYDROPHOBIC SCALE USED

|          | GES    | KD     | GVH1   | ECS    |
|----------|--------|--------|--------|--------|
| H17      | 1.194  | 1.371  | 0.133  | 0.455  |
| MesoH    | -0.676 | 0.115  | -0.340 | 0.129  |
| MuHd_075 | 35.369 | 29.665 | 8.949  | 10.236 |
| MuHd_095 | 39.117 | 25.350 | 10.510 | 9.735  |
| MuHd_100 | 36.382 | 21.237 | 8.788  | 9.316  |
| MuHd_105 | 24.792 | 13.800 | 8.825  | 6.341  |
| Hmax_075 | 20.400 | 18.667 | 5.794  | 8.100  |
| Hmax_095 | 18.200 | 20.900 | 5.225  | 6.291  |
| Hmax_100 | 18.200 | 20.900 | 4.733  | 6.900  |
| Hmax_105 | 13.700 | 17.033 | 7.096  | 6.043  |

| CLASS | NOT-MITO | MITO(/CHLORO) |
|-------|----------|---------------|
| DFM   | 0.1999   | 0.8001        |
| DFMC  | 0.3285   | 0.6715        |

This protein is probably imported in mitochondria.  
 f(Cys) = 0.1001, f(Arg) = 0.0541, CMi = 0.74919



cgd1\_1080 | Alpha beta hydrolase

> **Sequence**

> **ID's**

> **GEO Functions**

> **Subcellular Localization**

> **Sequence**

> **Nucleotide sequence**

> **Protein sequence**

> **Domains**

> **Structure**

> **Post Translational Modifications**

> **Protein-Protein Interaction**

> **Literature**

> **Nucleotide sequence**

**Fasta :-**

```
>PF3D7_0207300 ATGTTTTCCCTGTGTACAGTACATTCAAATATGTTAATTAATTGCTTTGGAGTTCTACAT TGTAATATATGCCGCACAGTATTAAGAAATTG
AAATGTATTTTCATGTGGAGAGAAGTATTACAAAATTAGTCCTTGTACACAAAACCATGAA AGCTTTTTGATGTCCAAAATAGATATGAATAACACATTTGTGGA
AGGCATACGTTGGGTTTACACGATTTTAGTAGTGTTAGCGATGAATATAAAGAGAAAATA AAAATGTTATGTATGTTTTCTAACTATAAAGATAACTATGAAAAT
GAAGAAAATAATATGGAACATATGAAAGATTTATTAAGAATCCAGCTTTATGTTTAAAA AATCCTAATCAATGGGTTAAAGATAGAGCAGGTTTTAAAGATGA
TTATATGCCTCTAGCACAAATTGTGACAGGCAATTTTGTGATCGTTTTTCTGATTCAAAT GAATGTGAGCATAGAATTAGGGTTCTCAATCAAGGAAAATGTGG
TCAATAAAATATGTAACATTATGTAATAAATAACACTTAATGGATATCGACAATAATCCC TTTGGTCATTATAATGATAACATATGTAAGAGGGTGGTCATCTT
ACAGGATCGGAATGTCCTGATAATAAGGAGACATGGAGTAATATATGGAAAGGTGTAAT TTGATGGATAGGATATATGCAGGATATATATATCATGGGTATTTT
CAACAAGGATCTGTATTTGTTTCTATGGAAGTAACAGATAAATTAACATTTGATCATGAT GGGACAAAAGTTATGATGAGTTGTGAAGATAATGATAGTCCGGA
AATAGTTGGGGATCACATTGGGGTGATAAGGGGAATTTTAAATTAGATATGTATGGTCCC AATAATTGTAATGGTAAAGTATTATATAATGCCTTTCTTTACTT
AGACAATCGGATTTAATCAAATAGAAATAGAAATAATTATCCACAATATGATAAAAAC AGTAATGATAATGATCGAAATTATTAATCCATATAATAAGAATC
GATTATAAATGCACATATTAGGAGAAATACAATTCGTTTCAAGAAAAGAATTATCAAG TATTCTTTATATGCAAGAATTGGAAACACTGTATATAAGAGGACT
GATACTAAGTGCCGTAGTAATTGTGAGAAGTACATTGATAAATGTAACATAATTCTTCT ATAGGAGAATGCTTAATACAACATTCTCCAAATTATAAATGTGTA
```

[Download Fasta](#)

> **Protein sequence**

**Fasta :-**

```
MFSLCTVHSNMLINCFVGLHLCNICRTVLRNCFSLGTSDLQKISCCEKYYKISPCTQNH E SFLMSKIDMNNTFVELKDHEEVTDEKMKNLITKIIAIDRHTLGLHDF
NPNQWVKDRAGFKDDDKPSVGIIPERKIFKPYDIKTLKSSLYASSTNCDRQFCDRFSDSN ECEHRIRVLNQGKCGNCWVFASSVIAAYRCRKGGLGFAEPSIKYVTLG
LMDRIYAGYIYHGYFKVSFKDYVVSNRNTNDLINIIKDYIIQQGSVFSMEVTDKLTDFHD GTKVMMSCEDNDSPDHALVLIYGYDIKTNGKKSSYWLLRNSWGSW
SNDNDRNYINPYNKNDNNYPYKPHYNDKENDAYYEKNDYNNNAHIRRNTIRFKRIK YSLYARIGNTVYKRTIFSKRKDEYKEPYSCLRFTFSFEKSDTKCRSNC
```



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*A Database for Pathogen and Parasite Proteases*



## cgd1\_1080 | Alpha beta hydrolase

> [ID's](#)

> [GEO Functions](#)

> [Subcellular Localization](#)

> [Sequence](#)

> [Domains](#) → [Papain-like](#)

> [Structure](#) →

Title: active site

> [Post Translational Modifications](#) Coordinates: Q251,C257,H436,N461

> [Protein-Protein Interaction](#)

> [Literature](#)



# ProtPathDB v 1.0

A Database for Pathogen and Parasite Proteases



Home Taxonomy Class Tools Statistics Other Links Contact Acknowledgement Help

Search



PF3D7\_0207500 | serine repeat antigen 6

> ID's

> GEO Functions

> Subcellular Localization

> Sequence

> Domains

> Structure

title: active site  
coordinates: Q638,C644,I681,D,N635  
pdb/PF3D7\_0207500/PF3D7\_0207500.pdb  
pdb/PF3D7\_0207500/PF3D7\_0207500\_site1.pdb  
pdb/PF3D7\_0207500/PF3D7\_0207500\_site2.pdb  
pdb/PF3D7\_0207500/PF3D7\_0207500\_site3.pdb  
pdb/PF3D7\_0207500/PF3D7\_0207500\_site4.pdb  
pdb/PF3D7\_0207500/PF3D7\_0207500\_site5.pdb

> Post Translational Modifications

> Protein-Protein Interaction

> Literature



## Sitemap

Search



| <input type="checkbox"/>            | Gene_ID              | SiteScore | size | Dscore | volume  | exposure | enclosure | contact | phobic | philic | balance | don  |
|-------------------------------------|----------------------|-----------|------|--------|---------|----------|-----------|---------|--------|--------|---------|------|
| <input type="checkbox"/>            | PF3D7_0207500_site_1 | 1.031     | 93   | 0.849  | 232.897 | 0.551    | 0.784     | 1.059   | 0.192  | 1.518  | 0.118   | 0.54 |
| <input checked="" type="checkbox"/> | PF3D7_0207500_site_2 | 0.683     | 83   | 0.832  | 200.312 | 0.656    | 0.62      | 0.849   | 0.113  | 1.218  | 0.033   | 0.62 |
| <input type="checkbox"/>            | PF3D7_0207500_site_3 | 0.79      | 67   | 0.69   | 146.461 | 0.697    | 0.583     | 0.833   | 0.046  | 1.317  | 0.035   | 0.75 |
| <input type="checkbox"/>            | PF3D7_0207500_site_5 | 0.714     | 40   | 0.593  | 104.272 | 0.608    | 0.673     | 0.923   | 0.11   | 1.243  | 0.099   | 1.26 |
| <input type="checkbox"/>            | PF3D7_0207500_site_4 | 0.713     | 48   | 0.592  | 106.673 | 0.655    | 0.606     | 0.843   | 0.091  | 1.295  | 0.07    | 0.54 |

Showing 1 to 5 of 5 rows





# ProtPathDB v 1.0

A Database for Pathogen and Parasite Proteases



## cgd1\_1080 | Alpha beta hydrolase

- > ID's
- > GEO Functions
- > Subcellular Localization
- > Sequence
- > Domains
- > Structure
- > Post Translational Modifications →
- > Protein-Protein Interaction
- > Literature

### > N\_Linked Glycosylation

No Results

### > O\_Linked Glycosylation

No Results

### > Phosphorylation

| <input type="checkbox"/> | ID            | Site  | Peptide   | Score | Method | ID            | Site  | Peptide   |
|--------------------------|---------------|-------|-----------|-------|--------|---------------|-------|-----------|
| <input type="checkbox"/> | PF3D7_0207300 | 378 S | YFKVSFKDY | 0.996 | unsp   | PF3D7_0207300 | 427 S | KVMMSCEDN |

Showing 1 to 1 of 1 rows



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*A Database for Pathogen and Parasite Proteases*



## cgd1\_1080 | Alpha beta hydrolase

- > **ID's**
  - > **GEO Functions**
  - > **Subcellular Localization**
  - > **Sequence**
  - > **Domains**
  - > **Structure**
  - > **Post Translational Modifications**
  - > **Protein-Protein Interaction** → **> PubMed**
  - > **Literature** → **> Google Scholar**
- > String**  
PF02\_0069;PFB0325c



Search

teases are known to reg...  
Blas  
cessing of cellular inform...  
cancer, neurodegenerative disorders, a...  
carboxypeptidases). Carbonyl group c...  
an activated nucleophile. This is accor...  
tem provides the five groups of classifi...

ProtPathDB - local NCBI BLAST

CHOOSE PROGRAM TO USE AND DATABASE TO SEARCH

Program: BlastP

← Compares Protein Query v...

Database: Protein Database (ABC\_N)

Enter sequence below in FASTA format (DEMO)

[Empty text input box for FASTA format sequence]

Or load it from disk

Choose File no file selected

Output:  Graphical Overview  Plain Text

Algorithm Parameters:  Default  Advanced

Reset Clear Sequence Search

Advanced Options

Maximum Target Sequences: 50

Expect Threshold: 10.0

Word Size: 6



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*A Database for Pathogen and Parasite Proteases*

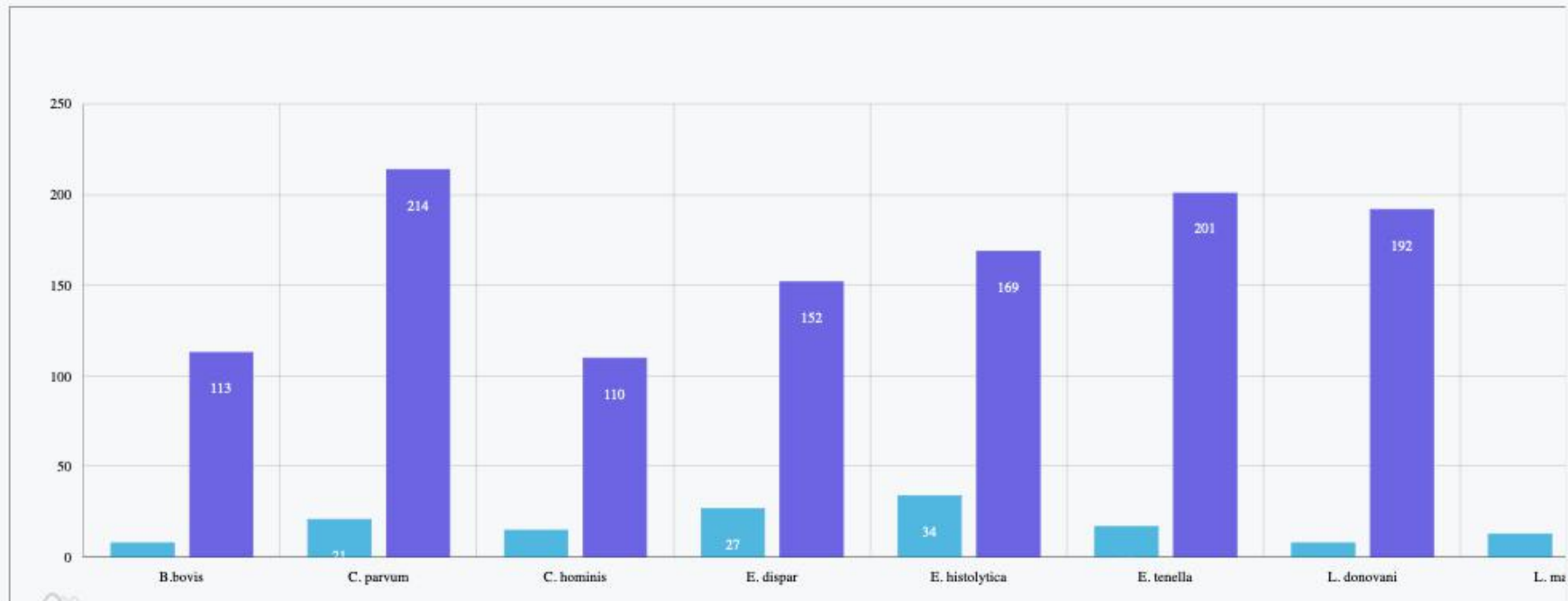


Displays the graph and statistics

- Home
- Taxonomy ▾
- Class ▾
- Tools ▾
- Statistics ▾
- Other Links
- Contact
- Acknowledgement
- Help

Graphical view  Tabular view

## SignalP



Graphical view  Tabular view

## SignalP

Export

| Species       | Secretory signal peptides (SP) | Other |
|---------------|--------------------------------|-------|
| B.bovis       | 8                              | 113   |
| C.parvum      | 21                             | 214   |
| C.hominis     | 15                             | 110   |
| E.dispar      | 27                             | 152   |
| E.histolytica | 34                             | 169   |
| E.tenella     | 17                             | 201   |
| L.donovani    | 8                              | 192   |
| L.major       | 13                             | 207   |
| L.mexicana    | 15                             | 203   |
| N.canninum    | 17                             | 193   |



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[>MEROPS](#)

[>CDD](#)

[>Eupath](#)

[>MPMP](#)

[>InterProScan](#)

[>KEGG](#)

[>Gene Ontology \(Amigo 2\)](#)

[>PlasmoGEM](#)

[>NCBI](#)

[>BIOGRID](#)



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**Allows the user to contact the team in case any help is required**

Home Taxonomy ▾ Class ▾ Tools ▾ Statistics Other Links **Contact** Acknowledgement Help

Search

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