BLAST ® » blastp suite » RID-17ND4E1C014

BLAST Results

Job title: AAA63298.1 cystatin C [Mus musculus domesticus]

|			
RID	17ND4E1C014 (Expires on 12-15 23:09 pm)		
Query ID	lcl|Query_133253	**Database Name**	nr
Description	AAA63298.1 cystatin C [Mus musculus domesticus]	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	140	**Program**	BLASTP 2.8.1+

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.

Distribution of the top 100 Blast Hits on 100 subject sequences
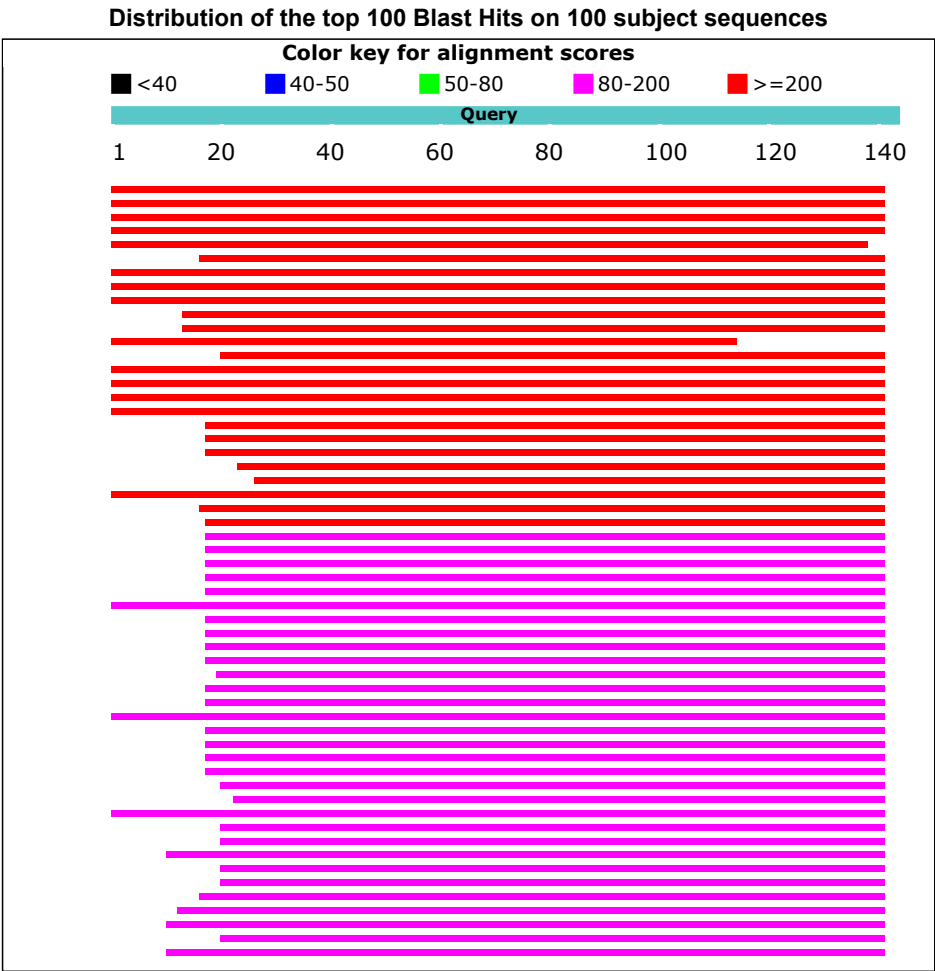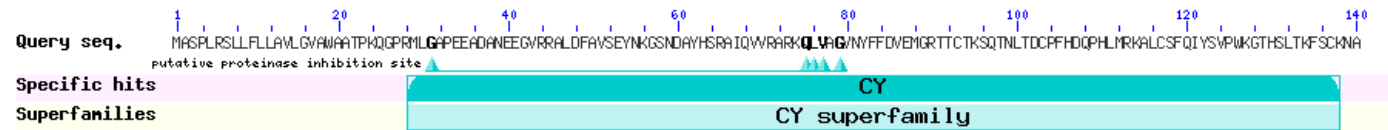
Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
cystatin C [Mus musculus domesticus]	297	297	100%	5e-102	100%	AAA63298.1
hypothetical protein [Escherichia coli]	293	293	100%	2e-100	99%	WP_108998154.1
cystatin C precursor [Mus musculus]	291	291	100%	1e-99	98%	AAG40283.1
cystatin C isoform g- protein precursor [synthetic construct]	289	289	100%	6e-99	97%	AAG40285.1
unnamed protein product [Mus musculus]	287	287	97%	4e-98	99%	BAE32071.1
cystatin-C [Mus pahari]	260	260	88%	1e-87	97%	XP_021049644.1
cystatin-C [Mus caroli]	260	260	100%	2e-87	95%	XP_021010243.1
cystatin C isoform i- protein precursor [synthetic construct]	259	259	100%	3e-87	90%	AAG40284.1
cystatin-C precursor [Rattus norvegicus]	243	243	100%	1e-80	87%	NP_036969.1
unnamed protein product [Rattus norvegicus]	242	242	90%	1e-80	87%	CAA34831.1
cystatin C	241	241	90%	4e-80	87%	1604194A
cystatin C, isoform CRA_b [Mus musculus]	235	235	80%	5e-78	98%	EDL28551.1
cystatin C	228	228	85%	6e-75	87%	1613154A
PREDICTED: cystatin-C [Peromyscus maniculatus bairdii]	222	222	100%	2e-72	80%	XP_006984562.1
cystatin-C [Microtus ochrogaster]	219	219	100%	2e-71	77%	XP_005365528.1
PREDICTED: cystatin-C-like [Nannospalax galili]	216	216	100%	7e-70	71%	XP_008828244.1
PREDICTED: cystatin-C [Cricetulus griseus]	214	214	100%	4e-69	76%	XP_003500011.1
cystatin-C-like [Urocitellus parryii]	210	210	87%	2e-67	76%	XP_026248839.1
PREDICTED: cystatin-C-like [Marmota marmota marmota]	209	209	87%	3e-67	76%	XP_015339072.1
cystatin-C-like [Ictidomys tridecemlineatus]	209	209	87%	3e-67	76%	XP_005334652.1
cystatin-C-like [Mesocricetus auratus]	208	208	83%	5e-67	77%	XP_005072652.1
PREDICTED: cystatin-C [Jaculus jaculus]	208	208	81%	9e-67	80%	XP_004668779.2
PREDICTED: cystatin-C [Saimiri boliviensis boliviensis]	201	201	100%	6e-64	67%	XP_003942971.1
ompA - cystatin C fusion preprotein (AA -21 to 120) [synthetic construct]	200	200	88%	1e-63	71%	CAA31253.1
cystatin-C [Piliocolobus tephrosceles]	200	200	87%	1e-63	72%	XP_026305175.1
cystatin-C [Aotus nancymaae]	199	199	87%	3e-63	73%	XP_012293971.1
PREDICTED: cystatin-C [Rhinopithecus bieti]	198	198	87%	5e-63	72%	XP_017703337.1
PREDICTED: cystatin-C [Colobus angolensis palliatus]	198	198	87%	6e-63	72%	XP_011807579.1
RecName: Full=Cystatin-C; AltName: Full=Cystatin-3; Flags: Precursor	198	198	87%	7e-63	72%	O19093.1
PREDICTED: cystatin-C [Callithrix jacchus]	198	198	87%	7e-63	73%	XP_002747560.1
PREDICTED: cystatin-C-like [Echinops telfairi]	197	197	100%	1e-62	64%	XP_004715357.1
cystatin-C [Loxodonta africana]	197	197	87%	1e-62	72%	XP_003411668.1
Cystatin-3 [Macaca fascicularis]	197	197	87%	2e-62	71%	EHH65608.1
cystatin-C precursor [Macaca mulatta]	197	197	87%	2e-62	71%	NP_001028096.1
PREDICTED: cystatin-C [Rhinopithecus roxellana]	197	197	87%	2e-62	71%	XP_010381300.1
PREDICTED: cystatin-C [Cebus capucinus imitator]	197	197	86%	3e-62	73%	XP_017396941.1
cystatin C [Homo sapiens]	196	196	87%	6e-62	70%	AAA52164.1
Homo sapiens cystatin C (amyloid angiopathy and cerebral hemorrhage) [synthetic construct]	196	196	87%	7e-62	70%	AAP36501.1
PREDICTED: cystatin-C-like [Panthera pardus]	196	196	100%	7e-62	65%	XP_019317889.1
cystatin-C precursor [Homo sapiens]	196	196	87%	7e-62	70%	NP_000090.1
cystatin C [synthetic construct]	196	196	87%	7e-62	70%	AAX36984.1
cystatin-C [Theropithecus gelada]	195	195	87%	9e-62	70%	XP_025256115.1
PREDICTED: cystatin-C [Nomascus leucogenys]	195	195	87%	9e-62	70%	XP_003280894.1
Chain A, Human Cystatin C; Dimeric Form With 3d Domain Swapping	194	194	85%	1e-61	71%	1G96_A
cystatin-C-like [Cavia porcellus]	195	195	84%	1e-61	74%	XP_003476451.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
CST3 [Meriones unguiculatus]	194	194	100%	1e-61	70%	AKI32217.1
Chain A, Crystal Structure Of L68v Mutant Of Human Cystatin C	194	194	85%	2e-61	71%	3PS8_A
Chain A, Crystal Structure Of V57p Mutant Of Human Cystatin C	191	191	85%	1e-60	70%	3S67_A
Cystatin-C [Fukomys damarensis]	192	192	92%	1e-60	68%	KFO21831.1
Chain A, Hinge-Loop Mutation Can Be Used To Control 3d Domain Swapping And Amyloidogenesis Of Human Cystatin C	191	191	85%	1e-60	70%	3NX0_A
Chain A, Crystal structure of V57D mutant of human cystatin C	191	191	85%	1e-60	70%	3SVA_A
cystatin-C [Heterocephalus glaber]	192	192	88%	2e-60	71%	XP_004874841.1
PREDICTED: cystatin-C-like [Orycteropus afer afer]	192	192	91%	2e-60	67%	XP_007954438.1
PREDICTED: cystatin-C isoform X2 [Fukomys damarensis]	193	193	92%	2e-60	68%	XP_010606531.1
Chain A, Crystal structure of monomeric human cystatin C stabilized against aggregation	189	189	85%	8e-60	70%	3GAX_A
PREDICTED: cystatin-C isoform X1 [Fukomys damarensis]	193	193	92%	1e-59	68%	XP_010606529.1
cystatin-C-like [Meriones unguiculatus]	187	187	100%	1e-58	70%	XP_021512271.1
cystatin C, isoform CRA_a [Rattus norvegicus]	187	187	96%	1e-58	76%	EDL95078.1
cystatin-C-like [Puma concolor]	187	187	100%	2e-58	65%	XP_025788311.1
PREDICTED: cystatin-C [Chinchilla lanigera]	188	188	86%	2e-58	69%	XP_005381032.1
Chain A, N-Truncated Human Cystatin C; Dimeric Form With 3D Domain Swapping	185	185	78%	3e-58	75%	1R4C_A
cystatin-C precursor [Felis catus]	186	186	80%	5e-58	74%	NP_001171901.1
PREDICTED: cystatin-C-like [Dipodomys ordii]	185	185	81%	1e-57	73%	XP_012882572.1
PREDICTED: cystatin-C-like [Eptesicus fuscus]	184	184	81%	3e-57	72%	XP_008139370.1
PREDICTED: cystatin-C-like [Erinaceus europaeus]	184	184	89%	3e-57	63%	XP_007535280.2
PREDICTED: cystatin-C [Ursus maritimus]	183	183	80%	6e-57	73%	XP_008705330.1
cystatin-C [Bubalus bubalis]	183	183	97%	6e-57	61%	XP_006062856.1
cystatin-C-like [Myotis lucifugus]	182	182	81%	2e-56	71%	XP_006097998.1
PREDICTED: cystatin-C-like [Rousettus aegyptiacus]	182	182	80%	2e-56	72%	XP_015977454.1
cystatin-C-like [Octodon degus]	181	181	84%	3e-56	69%	XP_004635633.1
cystatin-C [Pan paniscus]	179	179	75%	9e-56	75%	XP_024782633.1
PREDICTED: cystatin-C isoform X2 [Ailuropoda melanoleuca]	180	180	80%	1e-55	72%	XP_011216395.1
PREDICTED: LOW QUALITY PROTEIN: cystatin-C [Capra hircus]	179	179	87%	2e-55	68%	XP_013824066.2
cystatin-C [Odocoileus virginianus texanus]	179	179	87%	2e-55	68%	XP_020733832.1
PREDICTED: cystatin-C [Odobenus rosmarus divergens]	179	179	80%	2e-55	71%	XP_004405155.1
PREDICTED: cystatin-C [Chrysochloris asiatica]	179	179	81%	3e-55	68%	XP_006860726.1
cystatin-C [Microcebus murinus]	179	179	80%	3e-55	72%	XP_012594646.1
cystatin C precursor [Ovis aries]	179	179	85%	3e-55	68%	NP_001267642.1
cystatin-C-like [Ursus arctos horribilis]	178	178	80%	4e-55	71%	XP_026345084.1
LOW QUALITY PROTEIN: cystatin-C-like [Carlito syrichta]	181	181	87%	7e-55	68%	XP_021570310.1
cystatin-C-like [Callorhinus ursinus]	177	177	84%	2e-54	67%	XP_025732762.1
cystatin-C precursor [Oryctolagus cuniculus]	177	177	87%	2e-54	66%	NP_001076175.1
cystatin-C-like [Desmodus rotundus]	176	176	81%	4e-54	70%	XP_024432708.1
PREDICTED: cystatin-C-like [Hipposideros armiger]	176	176	81%	6e-54	68%	XP_019489439.1
cystatin-C precursor [Castor fiber]	176	176	85%	6e-54	66%	AKZ42319.1
cystatin-C-like [Castor canadensis]	176	176	85%	6e-54	66%	XP_020040744.1
PREDICTED: cystatin-C isoform X1 [Ailuropoda melanoleuca]	176	176	80%	6e-54	71%	XP_019649429.1
cystatin-C-like [Otolemur garnettii]	175	175	80%	6e-54	68%	XP_003801217.1
PREDICTED: cystatin-C [Rhinolophus sinicus]	175	175	86%	8e-54	68%	XP_019574234.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: cystatin-C-like [Leptonychotes weddellii]	175	175	85%	1e-53	67%	XP_006742996.1
PREDICTED: cystatin-C [Propithecus coquereli]	175	175	80%	1e-53	71%	XP_012508572.1
cystatin-C-like [Otolemur garnettii]	174	174	80%	1e-53	67%	XP_003803686.1
cystatin-C [Dasypus novemcinctus]	174	174	84%	2e-53	64%	XP_004465363.1
cystatin-C-like [Canis lupus familiaris]	174	174	80%	3e-53	68%	XP_003639869.1
cystatin-C-like [Vulpes vulpes]	172	172	75%	1e-52	71%	XP_025872198.1
cystatin-C precursor [Sus scrofa]	168	168	87%	4e-51	62%	NP_001038067.1
PREDICTED: cystatin-C-like [Elephantulus edwardii]	168	168	92%	4e-51	59%	XP_006888641.1
PREDICTED: cystatin-C-like [Elephantulus edwardii]	168	168	83%	6e-51	62%	XP_006902528.1
PREDICTED: cystatin-C [Lipotes vexillifer]	167	167	82%	1e-50	64%	XP_007451511.1
PREDICTED: cystatin C isoform X1 [Ovis aries]	166	166	85%	2e-50	65%	XP_014954914.1

Alignments

cystatin C [Mus musculus domesticus]
Sequence ID: **AAA63298.1** Length: 140 Number of Matches: 1
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
297 bits(760)	5e-102()	Compositional matrix adjust.	140/140(100%)	140/140(100%)	0/140(0%)	

Features:

```
Query    1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
              MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND
Sbjct    1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60

Query   61    AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ    120
              AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ
Sbjct   61    AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ    120

Query  121    IYSVPWKGTHSLTKFSCKNA    140
              IYSVPWKGTHSLTKFSCKNA
Sbjct  121    IYSVPWKGTHSLTKFSCKNA    140
```

hypothetical protein [Escherichia coli]
Sequence ID: **WP_108998154.1** Length: 140 Number of Matches: 1

See 15 more title(s)
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
293 bits(749)	2e-100()	Compositional matrix adjust.	138/140(99%)	138/140(98%)	0/140(0%)	

Features:

```
Query    1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
              MASPLRSLLFLLAVL VAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND
Sbjct    1    MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60

Query   61    AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ    120
              AYHSRAIQVVRARKQLVAGVNYF DVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ
Sbjct   61    AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ    120

Query  121    IYSVPWKGTHSLTKFSCKNA    140
              IYSVPWKGTHSLTKFSCKNA
Sbjct  121    IYSVPWKGTHSLTKFSCKNA    140
```

cystatin C precursor [Mus musculus]
Sequence ID: **AAG40283.1** Length: 140 Number of Matches: 1
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
291 bits(744)	1e-99()	Compositional matrix adjust.	137/140(98%)	137/140(97%)	0/140(0%)	

Features:

```
Query    1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
              MASPLRSLLFLLAVL VAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND
Sbjct    1    MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60

Query   61    AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ    120
              AYHSRAIQVVRARKQLVAGVNYF DVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ
Sbjct   61    AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ    120
```

```
Query  121  IYSVPWKGTHSLTKFSCKNA    140
            IYSVPWKGTHSLT FSCKNA
Sbjct  121  IYSVPWKGTHSLTNFSCKNA    140
```

cystatin C isoform g- protein precursor [synthetic construct]
Sequence ID: **AAG40285.1** Length: 140 Number of Matches: 1
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
289 bits(740)	6e-99()	Compositional matrix adjust.	136/140(97%)	137/140(97%)	0/140(0%)	

Features:

```
Query    1  MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
            MASPLRSLLFLLAVL VAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND
Sbjct    1  MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60

Query   61  AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
            AYHSRAIQVVRARKQLVAGVNYF DVEMGRTTCTKSQT+LTDCPFHDQPHLMRKALCSFQ
Sbjct   61  AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTDLTDCPFHDQPHLMRKALCSFQ   120

Query  121  IYSVPWKGTHSLTKFSCKNA    140
            IYSVPWKGTHSLT FSCKNA
Sbjct  121  IYSVPWKGTHSLTNFSCKNA    140
```

unnamed protein product, partial [Mus musculus]
Sequence ID: **BAE32071.1** Length: 137 Number of Matches: 1
Range 1: 1 to 137

Score	Expect	Method	Identities	Positives	Gaps	Frame
287 bits(734)	4e-98()	Compositional matrix adjust.	135/137(99%)	135/137(98%)	0/137(0%)	

Features:

```
Query    1  MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
            MASPLRSLLFLLAVL VAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND
Sbjct    1  MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60

Query   61  AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
            AYHSRAIQVVRARKQLVAGVNYF DVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ
Sbjct   61  AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120

Query  121  IYSVPWKGTHSLTKFSC    137
            IYSVPWKGTHSLTKFSC
Sbjct  121  IYSVPWKGTHSLTKFSC    137
```

cystatin-C [Mus pahari]
Sequence ID: **XP_021049644.1** Length: 140 Number of Matches: 1
Range 1: 17 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
260 bits(665)	1e-87()	Compositional matrix adjust.	120/124(97%)	122/124(98%)	0/124(0%)	

Features:

```
Query   17  VAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRARKQL    76
            V WAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKG+NDAYHSRAIQVVRARKQL
Sbjct   17  VTWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGNNDAYHSRAIQVVRARKQL    76

Query   77  VAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLTKFS   136
            VAGVNY+ DVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLTKFS
Sbjct   77  VAGVNYYLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLTKFS   136

Query  137  CKNA    140
            CKNA
Sbjct  137  CKNA    140
```

cystatin-C [Mus caroli]
Sequence ID: **XP_021010243.1** Length: 140 Number of Matches: 1
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
260 bits(664)	2e-87()	Compositional matrix adjust.	133/140(95%)	135/140(96%)	0/140(0%)	

Features:

```
Query    1  MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
            MASPLRS+L LLAVL VAWAATPKQGPRMLGAPEEAD NEEGVRRALDFAVSEYNKG+ND
Sbjct    1  MASPLRSMLLLLAVLAVAWAATPKQGPRMLGAPEEADVNEEGVRRALDFAVSEYNKGNND    60

Query   61  AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
            AYHSRAIQVVRARKQLVAGVNY  DVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ
Sbjct   61  AYHSRAIQVVRARKQLVAGVNYLLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120

Query  121  IYSVPWKGTHSLTKFSCKNA    140
```

```
                 IYSVPWKGTHSLTKFSCKNA
Sbjct  121   IYSVPWKGTHSLTKFSCKNA   140
```

cystatin C isoform i- protein precursor [synthetic construct]
Sequence ID: **AAG40284.1** Length: 129 Number of Matches: 1
Range 1: 1 to 129

Score	Expect	Method	Identities	Positives	Gaps	Frame
259 bits(662)	3e-87()	Compositional matrix adjust.	126/140(90%)	126/140(90%)	11/140(7%)	

Features:

```
Query    1   MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
             MASPLRSLLFLLAVL VAWAA            PEEADANEEGVRRALDFAVSEYNKGSND
Sbjct    1   MASPLRSLLFLLAVLAVAWAA-----------PEEADANEEGVRRALDFAVSEYNKGSND    49

Query   61   AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
             AYHSRAIQVVRARKQLVAGVNYF DVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ
Sbjct   50   AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   109

Query  121   IYSVPWKGTHSLTKFSCKNA   140
             IYSVPWKGTHSLT FSCKNA
Sbjct  110   IYSVPWKGTHSLTNFSCKNA   129
```

cystatin-C precursor [Rattus norvegicus]
Sequence ID: **NP_036969.1** Length: 140 Number of Matches: 1

   See 3 more title(s)
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
243 bits(620)	1e-80()	Compositional matrix adjust.	122/140(87%)	132/140(94%)	0/140(0%)	

Features:

```
Query    1   MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
             MASPLRSL+ LLAVL VAWA T +  PR+LGAP+EADA+EEGV+RALDFAVSEYNKGSND
Sbjct    1   MASPLRSLMLLLAVLAVAWAGTSRPPPRLLGAPQEADASEEGVQRALDFAVSEYNKGSND    60

Query   61   AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
             AYHSRAIQVVRARKQLVAG+NY+ DVEMGRTTCTKSQTNLT+CPFHDQPHLMRKALCSFQ
Sbjct   61   AYHSRAIQVVRARKQLVAGINYYLDVEMGRTTCTKSQTNLTNCPFHDQPHLMRKALCSFQ   120

Query  121   IYSVPWKGTHSLTKFSCKNA   140
             IYSVPWKGTH+LTK SCKNA
Sbjct  121   IYSVPWKGTHTLTKSSCKNA   140
```

unnamed protein product, partial [Rattus norvegicus]
Sequence ID: **CAA34831.1** Length: 127 Number of Matches: 1
Range 1: 1 to 127

Score	Expect	Method	Identities	Positives	Gaps	Frame
242 bits(618)	1e-80()	Compositional matrix adjust.	111/127(87%)	120/127(94%)	0/127(0%)	

Features:

```
Query   14   VLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRAR    73
             VL VAWA T +  PR+LGAP+EADA+EEGV+RALDFAVSEYNKGSNDAYHSRAIQVVRAR
Sbjct    1   VLAVAWAGTSRPPPRLLGAPQEADASEEGVQRALDFAVSEYNKGSNDAYHSRAIQVVRAR    60

Query   74   KQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLT   133
             KQLVAG+NY+ DVEMGRTTCTKSQTNLT+CPFHDQPHLMRKALCSFQIYSVPWKGTH+LT
Sbjct   61   KQLVAGINYYLDVEMGRTTCTKSQTNLTNCPFHDQPHLMRKALCSFQIYSVPWKGTHTLT   120

Query  134   KFSCKNA   140
             K SCKNA
Sbjct  121   KSSCKNA   127
```

cystatin C
Sequence ID: **prf||1604194A** Length: 127 Number of Matches: 1
Range 1: 1 to 127

Score	Expect	Method	Identities	Positives	Gaps	Frame
241 bits(615)	4e-80()	Compositional matrix adjust.	110/127(87%)	120/127(94%)	0/127(0%)	

Features:

```
Query   14   VLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRAR    73
             VL VAWA T +  PR+LGAP+EADA+EEGV+RALDFAVSEYNKGSNDAYHSRAIQVVRAR
Sbjct    1   VLAVAWAGTSRPPPRLLGAPQEADASEEGVQRALDFAVSEYNKGSNDAYHSRAIQVVRAR    60

Query   74   KQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLT   133
             KQLVAG+NY+ DVEMGRTTCTKSQTNLT+CPFHDQPHL+RKALCSFQIYSVPWKGTH+LT
Sbjct   61   KQLVAGINYYLDVEMGRTTCTKSQTNLTNCPFHDQPHLLRKALCSFQIYSVPWKGTHTLT   120

Query  134   KFSCKNA   140
```

```
                       K SCKNA
Sbjct   121   KSSCKNA   127
```

cystatin C, isoform CRA_b [Mus musculus]
Sequence ID: **EDL28551.1** Length: 116 Number of Matches: 1
Range 1: 1 to 113

Score	Expect	Method	Identities	Positives	Gaps	Frame
235 bits(600)	5e-78()	Compositional matrix adjust.	111/113(98%)	111/113(98%)	0/113(0%)	

Features:

```
Query   1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND   60
             MASPLRSLLFLLAVL VAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND
Sbjct   1    MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND   60

Query   61   AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMR   113
             AYHSRAIQVVRARKQLVAGVNYF DVEMGRTTCTKSQTNLTDCPFHDQPHLMR
Sbjct   61   AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMR   113
```

cystatin C
Sequence ID: **prf||1613154A** Length: 120 Number of Matches: 1
Range 1: 1 to 120

Score	Expect	Method	Identities	Positives	Gaps	Frame
228 bits(580)	6e-75()	Compositional matrix adjust.	104/120(87%)	114/120(95%)	0/120(0%)	

Features:

```
Query   21   ATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRARKQLVAGV   80
              T +   PR+LGAP+EADA+EEGV+RALDFAVSEYNKGSNDAY+SRAIQVVRARKQLVAG+
Sbjct   1    GTSRPPPRLLGAPQEADASEEGVQRALDFAVSEYNKGSNDAYNSRAIQVVRARKQLVAGI   60

Query   81   NYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLTKFSCKNA   140
             NY+ DVEMGRTTCTKSQTNLT+CPFHDQPHLMRKALCSFQIYSVPWKGTH+LTK SCKNA
Sbjct   61   NYYLDVEMGRTTCTKSQTNLTNCPFHDQPHLMRKALCSFQIYSVPWKGTHTLTKSSCKNA   120
```

PREDICTED: cystatin-C [Peromyscus maniculatus bairdii]
Sequence ID: **XP_006984562.1** Length: 140 Number of Matches: 1
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
222 bits(565)	2e-72()	Compositional matrix adjust.	112/140(80%)	124/140(88%)	0/140(0%)	

Features:

```
Query   1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND   60
             MAS LR  L LLA+L VA A  PKQG R+LG  +EAD +EEGV+RALDFA+SEYNKGSND
Sbjct   1    MASSLRVPLLLLALLAVASATAPKQGRRLLGGLQEADVHEEGVQRALDFAISEYNKGSND   60

Query   61   AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
             AYHSRAIQVVRARKQ+VAGVNY+ DVE+GRTTCTKSQ NL DCPFHDQPHLMRKALC+FQ
Sbjct   61   AYHSRAIQVVRARKQIVAGVNYYLDVEVGRTTCTKSQPNLADCPFHDQPHLMRKALCTFQ   120

Query   121  IYSVPWKGTHSLTKFSCKNA   140
             IYSVPW+GTHSLTK SCK+A
Sbjct   121  IYSVPWQGTHSLTKSSCKDA   140
```

cystatin-C [Microtus ochrogaster]
Sequence ID: **XP_005365528.1** Length: 140 Number of Matches: 1
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
219 bits(559)	2e-71()	Compositional matrix adjust.	108/140(77%)	125/140(89%)	0/140(0%)	

Features:

```
Query   1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND   60
             MASPLR+ L L+AVL +A AATPKQ PR+LG  +EA+ NEEGV+RA+DFA+SEYNKGSND
Sbjct   1    MASPLRAPLLLMAVLALASAATPKQSPRLLGGLQEANVNEEGVQRAVDFAISEYNKGSND   60

Query   61   AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
             AYHSRA+QV+RARKQ+VAGVNY+ DV +GRTTCTKSQ NL +CPFHDQPHLMRK LCSFQ
Sbjct   61   AYHSRAMQVLRARKQIVAGVNYYLDVMVGRTTCTKSQPNLAECPFHDQPHLMRKTLCSFQ   120

Query   121  IYSVPWKGTHSLTKFSCKNA   140
             IY+VPW+GTHSLTK SCK A
Sbjct   121  IYTVPWEGTHSLTKSSCKTA   140
```

PREDICTED: cystatin-C-like [Nannospalax galili]
Sequence ID: **XP_008828244.1** Length: 147 Number of Matches: 1

Range 1: 1 to 147

Score	Expect	Method	Identities	Positives	Gaps	Frame
216 bits(550)	7e-70()	Compositional matrix adjust.	104/147(71%)	119/147(80%)	7/147(4%)	

Features:

```
Query    1    MASPLRS-------LLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSE    53
              MASP R+         +L ++  +  A   +P+QG R LG   EEAD NEEGV+RA+DFAVSE
Sbjct    1    MASPRRAPLLLLLTVLAMVLAVSSAAGGSPRQGKRKLGGLEEADVNEEGVQRAVDFAVSE    60

Query    54   YNKGSNDAYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMR   113
              YNK SNDAYHSRAIQV+ ARKQ+VAG+NY+ +VE+GRTTCTKSQ NL DCPFHDQPHLMR
Sbjct    61   YNKASNDAYHSRAIQVLSARKQIVAGINYYVEVELGRTTCTKSQPNLADCPFHDQPHLMR   120

Query    114  KALCSFQIYSVPWKGTHSLTKFSCKNA    140
              KALCSFQIYSVPWKGTHSLTK SCK A
Sbjct    121  KALCSFQIYSVPWKGTHSLTKSSCKIA    147
```

PREDICTED: cystatin-C [Cricetulus griseus]
Sequence ID: **XP_003500011.1** Length: 140 Number of Matches: 1

See 3 more title(s)
Range 1: 1 to 140

Score	Expect	Method	Identities	Positives	Gaps	Frame
214 bits(544)	4e-69()	Compositional matrix adjust.	106/140(76%)	123/140(87%)	0/140(0%)	

Features:

```
Query    1    MASPLRSLLFLLAVLGVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND    60
              MASPLR+ L LLA+L VA AA  KQGPR+LG  +EA    EEGV++ALDFA+SEYNKGSND
Sbjct    1    MASPLRTPLLLLAILAVASAANTKQGPRLLGGLQEAKVEEEGVKQALDFAISEYNKGSND    60

Query    61   AYHSRAIQVVRARKQLVAGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ   120
              AYHSRA++VVRARKQ+VAG+NY+ DV +GRTTCTKSQ NLTDCPFHDQPHLMRK LCSFQ
Sbjct    61   AYHSRALEVVRARKQMVAGINYYLDVMVGRTTCTKSQPNLTDCPFHDQPHLMRKTLCSFQ   120

Query    121  IYSVPWKGTHSLTKFSCKNA    140
              IY+VPW+GT +LTK SCK+A
Sbjct    121  IYTVPWQGTQTLTKSSCKSA    140
```

cystatin-C-like [Urocitellus parryii]
Sequence ID: **XP_026248839.1** Length: 146 Number of Matches: 1
Range 1: 24 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
210 bits(534)	2e-67()	Compositional matrix adjust.	94/123(76%)	108/123(87%)	0/123(0%)	

Features:

```
Query    18   AWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRARKQLV    77
              A  A+P+  PR+LG  EEAD NEEGVRRA+DFAVSEYNKGSNDAYHSRA++VVRARKQ+V
Sbjct    24   ATGASPRHSPRLLGGLEEADVNEEGVRRAVDFAVSEYNKGSNDAYHSRAMKVVRARKQIV    83

Query    78   AGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLTKFSC   137
              +GVNYF DVEMGRTTCTK+Q  L DCPFH++PHL RKALCSFQIY+VPW GT S+TK SC
Sbjct    84   SGVNYFLDVEMGRTTCTKTQAYLADCPFHEEPHLKRKALCSFQIYTVPWLGTISMTKSSC   143

Query    138  KNA    140
              +NA
Sbjct    144  QNA    146
```

PREDICTED: cystatin-C-like [Marmota marmota marmota]
Sequence ID: **XP_015339072.1** Length: 146 Number of Matches: 1
Range 1: 24 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
209 bits(532)	3e-67()	Compositional matrix adjust.	94/123(76%)	108/123(87%)	0/123(0%)	

Features:

```
Query    18   AWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRARKQLV    77
              A  A+P+  PR+LG  EEAD NEEGVRRA+DFAVSEYNKGSNDAYHSRA++VVRARKQ+V
Sbjct    24   ATGASPRLSPRLLGGLEEADVNEEGVRRAVDFAVSEYNKGSNDAYHSRAMKVVRARKQIV    83

Query    78   AGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLTKFSC   137
              +GVNYF DVEMGRTTCTK+Q  L DCPFH++PHL RKALCSFQIY+VPW GT S+TK SC
Sbjct    84   SGVNYFLDVEMGRTTCTKTQAYLADCPFHEEPHLKRKALCSFQIYTVPWLGTISMTKSSC   143

Query    138  KNA    140
              +NA
Sbjct    144  QNA    146
```

cystatin-C-like [Ictidomys tridecemlineatus]
Sequence ID: **XP_005334652.1** Length: 146 Number of Matches: 1

Range 1: 24 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
209 bits(532)	3e-67()	Compositional matrix adjust.	94/123(76%)	107/123(86%)	0/123(0%)	

Features:

```
Query   18   AWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRARKQLV   77
             A  A+P+   PR+LG   EEAD NEEGVRRALDFAVSEYNKGSNDAYHSRA++VVRARKQ+V
Sbjct   24   ATGASPRHSPRLLGGLEEADVNEEGVRRALDFAVSEYNKGSNDAYHSRAMKVVRARKQIV   83

Query   78   AGVNYFFDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQIYSVPWKGTHSLTKFSC   137
             +GVNY   DVEMGRTTCTK+Q  L DCPFH++PHL RKALCSFQIY+VPW GT S+TK SC
Sbjct   84   SGVNYLLDVEMGRTTCTKTQAYLADCPFHEEPHLKRKALCSFQIYTVPWLGTISMTKSSC   143

Query   138  KNA   140
             +NA
Sbjct   144  QNA   146
```

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