

BLAST® » blastp suite » RID-5K8J5GW1013

BLAST Results

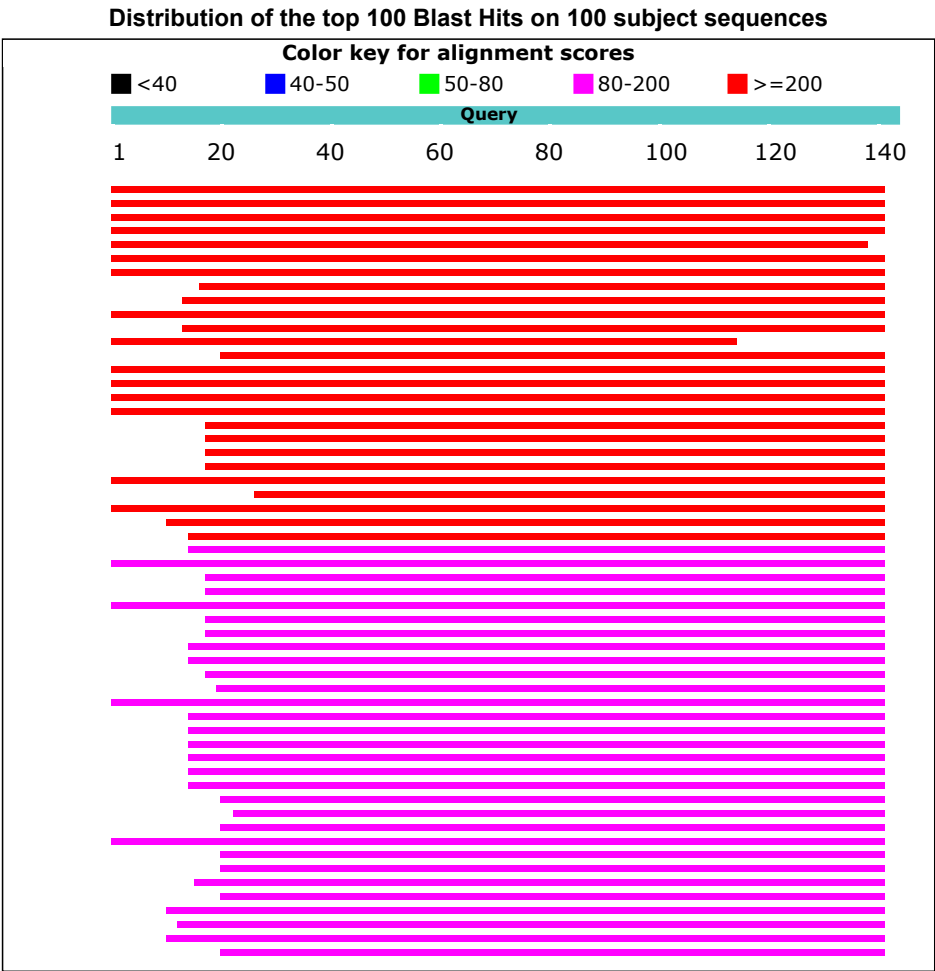
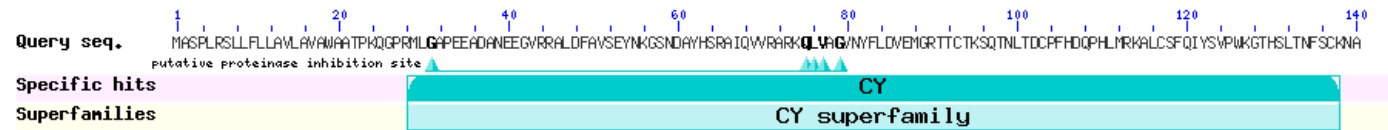
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Job title: AAG40283.1 cystatin C precursor [Mus musculus]

RID	5K8J5GW1013 (Expires on 02-06 21:48 pm)	Database Name	nr
Query ID	Idl Query_197252	Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Description	AAG40283.1 cystatin C precursor [Mus musculus]	Program	BLASTP 2.8.1+
Molecule type	amino acid		
Query Length	140		

Graphic Summary

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



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
cystatin C precursor [Mus musculus]	296	296	100%	8e-102	100%	AAG40283.1
cystatin C isoform g- protein precursor [synthetic construct]	294	294	100%	6e-101	99%	AAG40285.1
hypothetical protein [Escherichia coli]	294	294	100%	7e-101	99%	WP_108998154.1
cystatin C [Mus musculus domesticus]	291	291	100%	1e-99	98%	AAA63298.1
unnamed protein product [Mus musculus]	288	288	97%	1e-98	99%	BAE32071.1
cystatin-C [Mus caroli]	286	286	100%	7e-98	96%	XP_021010243.1
cystatin C isoform i- protein precursor [synthetic construct]	264	264	100%	3e-89	92%	AAG40284.1
cystatin-C [Mus pahari]	260	260	88%	2e-87	97%	XP_021049644.1
unnamed protein product [Rattus norvegicus]	243	243	90%	4e-81	88%	CAA34831.1
cystatin-C precursor [Rattus norvegicus]	243	243	100%	1e-80	88%	NP_036969.1
cystatin C	242	242	90%	2e-80	87%	1604194A
cystatin C, isoform CRA_b [Mus musculus]	238	238	80%	5e-79	100%	EDL28551.1
cystatin C	228	228	85%	8e-75	87%	1613154A
PREDICTED: cystatin-C [Peromyscus maniculatus bairdii]	222	222	100%	2e-72	81%	XP_006984562.1
cystatin-C [Microtus ochrogaster]	219	219	100%	2e-71	78%	XP_005365528.1
PREDICTED: cystatin-C-like [Nannospalax galili]	216	216	100%	9e-70	70%	XP_008828244.1
cystatin-C [Cricetulus griseus]	214	214	100%	3e-69	76%	XP_003500011.1
cystatin-C-like [Urocyon parryi]	210	210	87%	2e-67	76%	XP_026248839.1
cystatin-C-like [Marmota flaviventris]	209	209	87%	2e-67	76%	XP_027811610.1
PREDICTED: cystatin-C-like [Marmota marmota marmota]	209	209	87%	4e-67	76%	XP_015339072.1
cystatin-C-like [Ictidomys tridecemlineatus]	209	209	87%	4e-67	76%	XP_005334652.1
cystatin-C-like [Mesocricetus auratus]	208	208	100%	6e-67	74%	XP_005072652.1
PREDICTED: cystatin-C [Jaculus jaculus]	207	207	81%	2e-66	79%	XP_004668779.2
PREDICTED: cystatin-C [Saimiri boliviensis boliviensis]	201	201	100%	5e-64	67%	XP_003942971.1
ompA - cystatin C fusion preprotein (AA -21 to 120) [synthetic construct]	200	200	92%	9e-64	68%	CAA31253.1
cystatin-C [Piliocolobus tephrosceles]	200	200	90%	2e-63	71%	XP_026305175.1
cystatin-C [Aotus nancymaeae]	199	199	90%	4e-63	71%	XP_012293971.1
PREDICTED: cystatin-C-like [Echinops telfairi]	198	198	100%	5e-63	65%	XP_004715357.1
PREDICTED: cystatin-C [Rhinopithecus bieti]	198	198	87%	7e-63	72%	XP_017703337.1
PREDICTED: cystatin-C [Colobus angolensis palliatus]	198	198	87%	7e-63	72%	XP_011807579.1
PREDICTED: cystatin-C [Callithrix jacchus]	198	198	100%	7e-63	66%	XP_002747560.1
RecName: Full=Cystatin-C; AltName: Full=Cystatin-3; Flags: Precursor	198	198	87%	9e-63	72%	O19093.1
cystatin-C [Loxodonta africana]	197	197	87%	1e-62	72%	XP_003411668.1
Cystatin-3 [Macaca fascicularis]	197	197	90%	2e-62	69%	EHH65608.1
cystatin-C precursor [Macaca mulatta]	197	197	90%	2e-62	69%	NP_001028096.1
PREDICTED: cystatin-C [Rhinopithecus roxellana]	197	197	87%	2e-62	71%	XP_010381300.1
PREDICTED: cystatin-C [Cebus capucinus imitator]	196	196	86%	4e-62	73%	XP_017396941.1
CST3 [Meriones unguiculatus]	196	196	100%	5e-62	71%	AKI32217.1
cystatin C [Homo sapiens]	196	196	90%	6e-62	68%	AAA52164.1
Homo sapiens cystatin C (amyloid angiopathy and cerebral hemorrhage) [synthetic construct]	196	196	90%	6e-62	68%	AAP36501.1
cystatin C [synthetic construct]	196	196	90%	7e-62	68%	AAX36984.1
cystatin-C precursor [Homo sapiens]	196	196	90%	7e-62	68%	NP_000090.1
cystatin-C [Theropithecus gelada]	195	195	90%	9e-62	68%	XP_025256115.1
PREDICTED: cystatin-C [Nomascus leucogenys]	195	195	90%	1e-61	68%	XP_003280894.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
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
Chain A, Crystal Structure Of L68v Mutant Of Human Cystatin C	194	194	85%	2e-61	71%	3PS8_A
PREDICTED: cystatin-C-like [Panthera pardus]	194	194	100%	4e-61	65%	XP_019317889.1
Chain A, Crystal Structure Of V57p Mutant Of Human Cystatin C	191	191	85%	1e-60	70%	3S67_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	89%	1e-60	70%	XP_004874841.1
Chain A, Hinge-Loop Mutation Can Be Used To Control 3d Domain Swapping And Amyloidogenesis Of Human Cystatin C	191	191	85%	2e-60	70%	3NX0_A
Cystatin-C [Fukomys damarensis]	192	192	92%	2e-60	68%	KFO21831.1
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%	3e-60	68%	XP_010606531.1
Chain A, Crystal structure of monomeric human cystatin C stabilized against aggregation	189	189	85%	9e-60	70%	3GAX_A
cystatin C, isoform CRA_a [Rattus norvegicus]	190	190	96%	1e-59	77%	EDL95078.1
PREDICTED: cystatin-C isoform X1 [Fukomys damarensis]	192	192	92%	2e-59	68%	XP_010606529.1
cystatin-C-like [Meriones unguiculatus]	188	188	100%	4e-59	72%	XP_021512271.1
cystatin-C-like [Puma concolor]	187	187	100%	2e-58	66%	XP_025788311.1
PREDICTED: cystatin-C [Chinchilla lanigera]	188	188	86%	3e-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]	185	185	80%	9e-58	74%	NP_001171901.1
PREDICTED: cystatin-C-like [Dipodomys ordii]	184	184	81%	2e-57	73%	XP_012882572.1
cystatin-C [Bubalus bubalis]	184	184	97%	3e-57	62%	XP_006062856.1
PREDICTED: cystatin-C-like [Eptesicus fuscus]	183	183	81%	5e-57	72%	XP_008139370.1
PREDICTED: cystatin-C-like [Erinaceus europaeus]	183	183	87%	8e-57	64%	XP_007535280.2
PREDICTED: cystatin-C [Ursus maritimus]	182	182	80%	1e-56	73%	XP_008705330.1
cystatin-C-like [Myotis lucifugus]	181	181	81%	3e-56	71%	XP_006097998.1
cystatin-C-like [Octodon degus]	181	181	84%	3e-56	69%	XP_004635633.1
PREDICTED: cystatin-C-like [Rousettus aegyptiacus]	182	182	80%	3e-56	72%	XP_015977454.1
cystatin-C [Pan paniscus]	179	179	75%	1e-55	75%	XP_024782633.1
cystatin-C [Odocoileus virginianus texanus]	179	179	87%	2e-55	68%	XP_020733832.1
PREDICTED: cystatin-C isoform X2 [Ailuropoda melanoleuca]	179	179	80%	2e-55	72%	XP_011216395.1
PREDICTED: LOW QUALITY PROTEIN: cystatin-C [Capra hircus]	179	179	87%	2e-55	68%	XP_013824066.2
PREDICTED: cystatin-C [Odobenus rosmarus divergens]	179	179	80%	4e-55	71%	XP_004405155.1
PREDICTED: cystatin-C [Chrysochloris asiatica]	178	178	81%	4e-55	68%	XP_006860726.1
cystatin C precursor [Ovis aries]	178	178	85%	4e-55	68%	NP_001267642.1
cystatin-C-like [Ursus arctos horribilis]	177	177	80%	8e-55	71%	XP_026345084.1
LOW QUALITY PROTEIN: cystatin-C-like [Carlito syrichta]	181	181	90%	9e-55	66%	XP_021570310.1
cystatin-C-like [Callorhinus ursinus]	177	177	100%	2e-54	62%	XP_025732762.1
cystatin-C precursor [Oryctolagus cuniculus]	176	176	87%	3e-54	66%	NP_001076175.1
cystatin-C-like [Desmodus rotundus]	176	176	81%	6e-54	70%	XP_024432708.1
PREDICTED: cystatin-C-like [Hipposideros armiger]	175	175	81%	7e-54	68%	XP_019489439.1
cystatin-C-like [Otlemur garnettii]	175	175	80%	8e-54	68%	XP_003801217.1
PREDICTED: cystatin-C isoform X1 [Ailuropoda melanoleuca]	175	175	80%	1e-53	71%	XP_019649429.1
cystatin-C precursor [Castor fiber]	175	175	85%	1e-53	66%	AKZ42319.1
cystatin-C-like [Castor canadensis]	175	175	85%	1e-53	66%	XP_020040744.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: cystatin-C [Rhinolophus sinicus]	175	175	86%	1e-53	68%	XP_019574234.1
cystatin-C [Microcebus murinus]	175	175	80%	1e-53	71%	XP_012594646.1
PREDICTED: cystatin-C-like [Leptonychotes weddellii]	174	174	85%	2e-53	67%	XP_006742996.1
cystatin-C-like [Otolemur garnettii]	174	174	80%	2e-53	67%	XP_003803686.1
PREDICTED: cystatin-C [Propithecus coquereli]	174	174	80%	2e-53	71%	XP_012508572.1
cystatin-C-like [Canis lupus familiaris]	174	174	80%	4e-53	68%	XP_003639869.1
cystatin-C [Dasypus novemcinctus]	173	173	84%	5e-53	64%	XP_004465363.1
cystatin-C-like [Vulpes vulpes]	172	172	75%	2e-52	71%	XP_025872198.1
PREDICTED: cystatin-C [Lipotes vexillifer]	171	171	82%	4e-52	65%	XP_007451511.1
PREDICTED: cystatin-C-like [Elephantulus edwardii]	168	168	92%	6e-51	59%	XP_006888641.1
cystatin-C precursor [Sus scrofa]	168	168	87%	6e-51	62%	NP_001038067.1
PREDICTED: cystatin-C-like [Elephantulus edwardii]	168	168	83%	7e-51	62%	XP_006902528.1

Alignments

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
296 bits(758) 8e-102() Compositional matrix adjust. 140/140(100%) 140/140(100%) 0/140(0%)						
Features:						
Query	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND				60
Sbjct	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND				60
Query	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ				120
Sbjct	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ				120
Query	121	IYSVPWKGTHSLTNFSCKNA	140			
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
294 bits(753) 6e-101() Compositional matrix adjust. 139/140(99%) 140/140(100%) 0/140(0%)						
Features:						
Query	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND				60
Sbjct	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND				60
Query	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ				120
Sbjct	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ				120
Query	121	IYSVPWKGTHSLTNFSCKNA	140			
Sbjct	121	IYSVPWKGTHSLTNFSCKNA	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
294 bits(752) 7e-101() Compositional matrix adjust. 139/140(99%) 139/140(99%) 0/140(0%)						
Features:						
Query	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND	60			
Sbjct	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANEEGVRRALDFAVSEYNKGSND	60			
Query	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGRTTCTKSQTNLTDCPFHDQPHLMRKALCSFQ	120			

Sbjct	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGR	TCTKSQTNLTDCPFHDQPHLMRKALCSFQ	120
Query	121	IYSVPWKGTHSLTNFSC	KNA 140	
Sbjct	121	IYSVPWKGTHSLT	FSC	KNA 140

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
291 bits(744)	1e-99()	Compositional matrix adjust.	137/140(98%)	137/140(97%)	0/140(0%)	

Features:

Query	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANE	EGVRRALDFAVSEYNKGSND	60
Sbjct	1	MASPLRSLLFLLAVL VAWAATPKQGPRMLGAPEEADANE	EGVRRALDFAVSEYNKGSND	60
Query	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGR	TCTKSQTNLTDCPFHDQPHLMRKALCSFQ	120
Sbjct	61	AYHSRAIQVVRARKQLVAGVNYF	DVEMGR	TCTKSQTNLTDCPFHDQPHLMRKALCSFQ 120
Query	121	IYSVPWKGTHSLTNFSC	KNA 140	
Sbjct	121	IYSVPWKGTHSLT	FSC	KNA 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
288 bits(737)	1e-98()	Compositional matrix adjust.	136/137(99%)	136/137(99%)	0/137(0%)	

Features:

Query	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANE	EGVRRALDFAVSEYNKGSND	60
Sbjct	1	MASPLRSLLFLLAVLAVAWAATPKQGPRMLGAPEEADANE	EGVRRALDFAVSEYNKGSND	60
Query	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGR	TCTKSQTNLTDCPFHDQPHLMRKALCSFQ	120
Sbjct	61	AYHSRAIQVVRARKQLVAGVNYFLDVEMGR	TCTKSQTNLTDCPFHDQPHLMRKALCSFQ	120
Query	121	IYSVPWKGTHSLTNFSC	137	
Sbjct	121	IYSVPWKGTHSLT	FSC	137

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