

BLAST Results

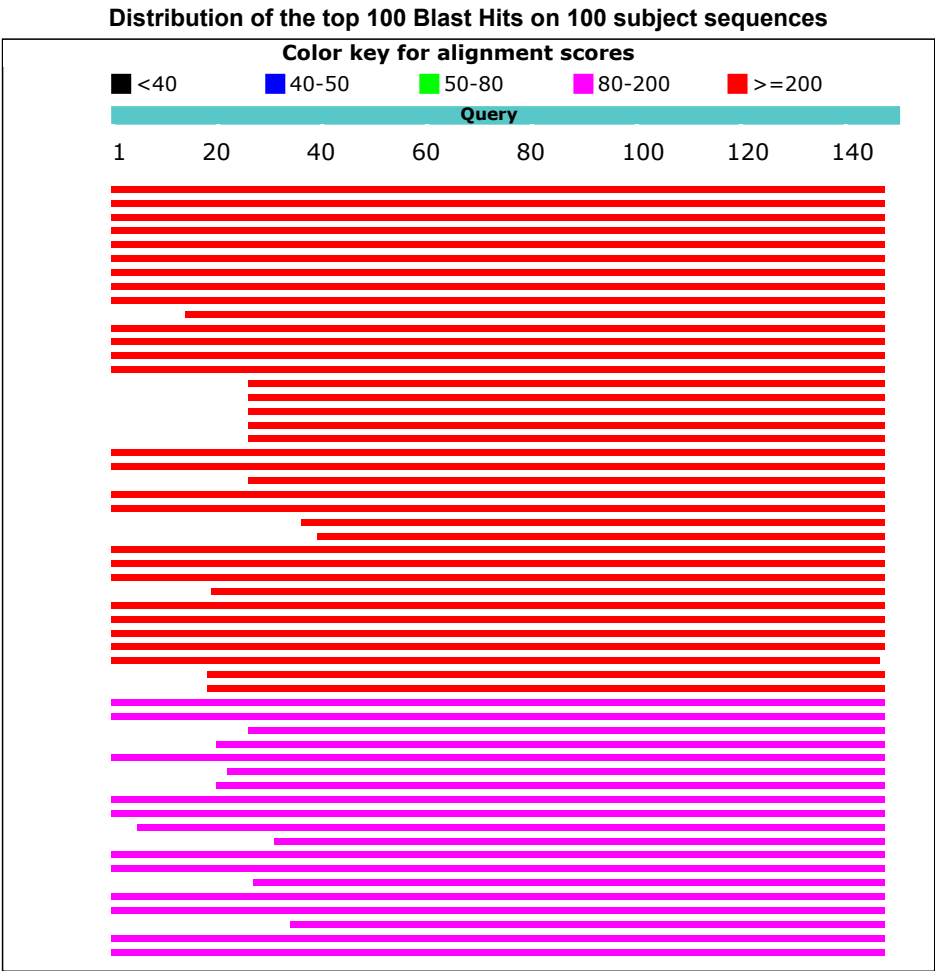
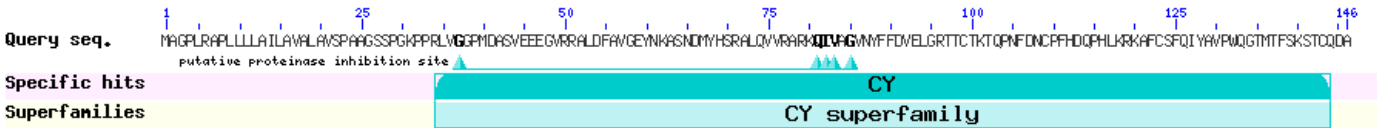
[Questions/comments](#)

Job title: CST3

RID	15KWR5XZ014	(Expires on 12-15 04:31 am)	Database Name	nr
Query ID	Idl Query_304550		Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Description	None		Program	BLASTP 2.8.1+
Molecule type	amino acid			
Query Length	146			

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
Homo sapiens cystatin C (amyloid angiopathy and cerebral hemorrhage) [synthetic construct]	300	300	100%	3e-103	98%	AAP36501.1
cystatin-C precursor [Homo sapiens]	300	300	100%	3e-103	98%	NP_000090.1
cystatin C [synthetic construct]	300	300	100%	3e-103	98%	AAX36984.1
cystatin C [Homo sapiens]	299	299	100%	1e-102	97%	AAA52164.1
cystatin-C [Piliocolobus tephrosceles]	261	261	100%	2e-87	95%	XP_026305175.1
PREDICTED: cystatin-C [Rhinopithecus bieti]	260	260	100%	2e-87	95%	XP_017703337.1
PREDICTED: cystatin-C [Nomascus leucogenys]	260	260	100%	2e-87	95%	XP_003280894.1
Cystatin-3 [Macaca fascicularis]	260	260	100%	3e-87	95%	EHH65608.1
cystatin-C precursor [Macaca mulatta]	260	260	100%	3e-87	95%	NP_001028096.1
ompA - cystatin C fusion preprotein (AA -21 to 120) [synthetic construct]	259	259	90%	6e-87	92%	CAA31253.1
PREDICTED: cystatin-C [Colobus angolensis palliatus]	259	259	100%	7e-87	95%	XP_011807579.1
cystatin-C [Theropithecus gelada]	259	259	100%	1e-86	95%	XP_025256115.1
PREDICTED: cystatin-C [Rhinopithecus roxellana]	256	256	100%	8e-86	94%	XP_010381300.1
PREDICTED: cystatin-C [Saimiri boliviensis boliviensis]	254	254	100%	8e-85	88%	XP_003942971.1
Chain A, Human Cystatin C; Dimeric Form With 3d Domain Swapping	253	253	82%	1e-84	98%	1G96_A
Chain A, Crystal Structure Of L68v Mutant Of Human Cystatin C	251	251	82%	3e-84	97%	3PS8_A
Chain A, Hinge-Loop Mutation Can Be Used To Control 3d Domain Swapping And Amyloidogenesis Of Human Cystatin C	250	250	82%	1e-83	97%	3NX0_A
Chain A, Crystal structure of V57D mutant of human cystatin C	249	249	82%	2e-83	97%	3SVA_A
Chain A, Crystal Structure Of V57p Mutant Of Human Cystatin C	249	249	82%	2e-83	97%	3S67_A
PREDICTED: cystatin-C [Callithrix jacchus]	249	249	100%	5e-83	87%	XP_002747560.1
RecName: Full=Cystatin-C; AltName: Full=Cystatin-3; Flags: Precursor	249	249	100%	7e-83	90%	O19093.1
Chain A, Crystal structure of monomeric human cystatin C stabilized against aggregation	247	247	82%	2e-82	96%	3GAX_A
cystatin-C [Aotus nancymaae]	245	245	100%	2e-81	89%	XP_012293971.1
PREDICTED: cystatin-C [Cebus capucinus imitator]	243	243	100%	2e-80	88%	XP_017396941.1
Chain A, N-Truncated Human Cystatin C; Dimeric Form With 3D Domain Swapping	233	233	75%	7e-77	97%	1R4C_A
cystatin-C [Pan paniscus]	224	224	73%	2e-73	96%	XP_024782633.1
cystatin C [Mus musculus domesticus]	213	213	100%	6e-69	67%	AAA63298.1
PREDICTED: cystatin-C-like [Panthera pardus]	210	210	100%	2e-67	68%	XP_019317889.1
cystatin-C [Loxodonta africana]	207	207	100%	2e-66	72%	XP_003411668.1
LOW QUALITY PROTEIN: cystatin-C-like [Carlito syrichta]	209	209	86%	5e-66	74%	XP_021570310.1
cystatin-C-like [Urocitellus parryii]	205	205	100%	2e-65	71%	XP_026248839.1
cystatin-C-like [Ictidomys tridecemlineatus]	205	205	100%	2e-65	71%	XP_005334652.1
PREDICTED: cystatin-C-like [Marmota marmota]	204	204	100%	3e-65	71%	XP_015339072.1
PREDICTED: cystatin-C-like [Echinops telfairi]	204	204	100%	4e-65	61%	XP_004715357.1
cystatin-C [Bubalus bubalis]	202	202	99%	3e-64	65%	XP_006062856.1
unnamed protein product [Rattus norvegicus]	201	201	87%	5e-64	70%	CAA34831.1
cystatin C	200	200	87%	8e-64	70%	1604194A
PREDICTED: cystatin-C-like [Nannospalax galili]	199	199	100%	5e-63	67%	XP_008828244.1
cystatin-C precursor [Rattus norvegicus]	198	198	100%	8e-63	66%	NP_036969.1
PREDICTED: cystatin-S-like [Gorilla gorilla gorilla]	197	197	82%	1e-62	75%	XP_018872892.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: cystatin-C-like [Orycteropus afer afer]	197	197	86%	1e-62	67%	XP_007954438.1
PREDICTED: cystatin-C [Peromyscus maniculatus bairdii]	197	197	100%	2e-62	69%	XP_006984562.1
PREDICTED: cystatin-C-like [Erinaceus europaeus]	197	197	84%	3e-62	68%	XP_007535280.2
PREDICTED: cystatin-C-like [Eptesicus fuscus]	196	196	86%	5e-62	70%	XP_008139370.1
PREDICTED: cystatin-C [Cricetulus griseus]	196	196	100%	6e-62	68%	XP_003500011.1
cystatin-C-like [Puma concolor]	195	195	100%	2e-61	66%	XP_025788311.1
Cystatin-C [Fukomys damarensis]	194	194	96%	2e-61	64%	KFO21831.1
cystatin C	194	194	78%	2e-61	72%	1613154A
PREDICTED: cystatin-C isoform X2 [Fukomys damarensis]	196	196	100%	3e-61	62%	XP_010606531.1
hypothetical protein [Escherichia coli]	194	194	100%	3e-61	67%	WP_108998154.1
cystatin-C-like [Cavia porcellus]	193	193	81%	5e-61	70%	XP_003476451.1
PREDICTED: cystatin-C [Ursus maritimus]	194	194	100%	5e-61	65%	XP_008705330.1
cystatin-C precursor [Felis catus]	193	193	100%	8e-61	67%	NP_001171901.1
cystatin-C [Microcebus murinus]	193	193	76%	9e-61	75%	XP_012594646.1
cystatin-C [Mus caroli]	192	192	100%	1e-60	67%	XP_021010243.1
PREDICTED: cystatin-C isoform X1 [Fukomys damarensis]	196	196	100%	2e-60	62%	XP_010606529.1
cystatin C precursor [Mus musculus]	192	192	100%	2e-60	66%	AAG40283.1
PREDICTED: cystatin-C [Propithecus coquereli]	192	192	100%	2e-60	71%	XP_012508572.1
unnamed protein product [Mus musculus]	191	191	97%	3e-60	68%	BAE32071.1
PREDICTED: cystatin-C-like [Colobus angolensis palliatus]	191	191	82%	9e-60	90%	XP_011787072.1
cystatin C isoform g- protein precursor [synthetic construct]	190	190	100%	1e-59	66%	AAG40285.1
PREDICTED: cystatin-C [Odobenus rosmarus divergens]	190	190	100%	1e-59	66%	XP_004405155.1
cystatin-C-like [Callorhinus ursinus]	190	190	100%	1e-59	66%	XP_025732762.1
cystatin-C [Mus pahari]	190	190	82%	1e-59	67%	XP_021049644.1
cystatin-C [Heterocephalus glaber]	190	190	85%	1e-59	66%	XP_004874841.1
cystatin-C [Microtus ochrogaster]	190	190	81%	2e-59	68%	XP_005365528.1
cystatin-C-like [Mesocricetus auratus]	189	189	77%	2e-59	71%	XP_005072652.1
cystatin-C-like [Ursus arctos horribilis]	189	189	100%	2e-59	64%	XP_026345084.1
PREDICTED: cystatin-C [Rhinolophus sinicus]	189	189	100%	5e-59	66%	XP_019574234.1
PREDICTED: cystatin-C [Chrysochloris asiatica]	188	188	86%	8e-59	67%	XP_006860726.1
PREDICTED: cystatin-C isoform X2 [Ailuropoda melanoleuca]	188	188	100%	9e-59	66%	XP_011216395.1
cystatin-C-like [Otolemur garnettii]	187	187	100%	2e-58	68%	XP_003803686.1
cystatin-C-like [Canis lupus familiaris]	186	186	99%	6e-58	63%	XP_003639869.1
PREDICTED: cystatin-C-like [Hipposideros armiger]	184	184	100%	3e-57	62%	XP_019489439.1
PREDICTED: cystatin-C [Jaculus jaculus]	184	184	78%	3e-57	68%	XP_004668779.2
cystatin-C-like [Myotis lucifugus]	183	183	82%	6e-57	66%	XP_006097998.1
cystatin-C-like [Otolemur garnettii]	182	182	77%	8e-57	70%	XP_003801217.1
PREDICTED: cystatin-C [Chinchilla lanigera]	184	184	82%	9e-57	65%	XP_005381032.1
PREDICTED: cystatin-C-like [Elephantulus edwardii]	183	183	85%	9e-57	63%	XP_006902528.1
cystatin-C [Odocoileus virginianus texanus]	182	182	84%	1e-56	67%	XP_020733832.1
cystatin-C-like [Vulpes vulpes]	181	181	72%	5e-56	73%	XP_025872198.1
cystatin-C-like [Octodon degus]	181	181	80%	7e-56	67%	XP_004635633.1
PREDICTED: cystatin-C-like [Leptonyctotes weddellii]	181	181	76%	7e-56	69%	XP_006742996.1
PREDICTED: cystatin-C-like [Rousettus aegyptiacus]	181	181	77%	1e-55	70%	XP_015977454.1
cystatin-C-like [Desmodus rotundus]	180	180	100%	1e-55	66%	XP_024432708.1
cystatin C isoform i- protein precursor [synthetic construct]	179	179	73%	1e-55	72%	AAG40284.1
LOW QUALITY PROTEIN: cystatin-C [Trichechus manatus latirostris]	180	180	100%	1e-55	58%	XP_004391263.1
PREDICTED: cystatin-C isoform X1 [Ailuropoda melanoleuca]	180	180	100%	1e-55	62%	XP_019649429.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: LOW QUALITY PROTEIN: cystatin-C [Capra hircus]	179	179	84%	3e-55	65%	XP_013824066.2
cystatin-C precursor [Sus scrofa]	179	179	99%	4e-55	65%	NP_001038067.1
cystatin C precursor [Ovis aries]	177	177	84%	1e-54	65%	NP_001267642.1
PREDICTED: cystatin-C-like [Dipodomys ordii]	177	177	86%	2e-54	61%	XP_012882572.1
cystatin-C [Dasypus novemcinctus]	177	177	82%	2e-54	63%	XP_004465363.1
PREDICTED: cystatin-C-like [Elephantulus edwardii]	176	176	90%	4e-54	58%	XP_006888641.1
cystatin-C precursor [Oryctolagus cuniculus]	175	175	85%	1e-53	63%	NP_001076175.1
cystatin-C-like [Castor canadensis]	175	175	100%	1e-53	61%	XP_020040744.1
cystatin-C-like [Carlito syrichta]	174	174	76%	2e-53	68%	XP_008059411.1
cystatin-C precursor [Castor fiber]	172	172	85%	1e-52	58%	AKZ42319.1
CST3 [Meriones unguiculatus]	171	171	100%	4e-52	61%	AKI32217.1
cystatin-C-like [Meriones unguiculatus]	170	170	100%	1e-51	61%	XP_021512271.1

Alignments

Homo sapiens cystatin C (amyloid angiopathy and cerebral hemorrhage), partial [synthetic construct]
Sequence ID: **AAP36501.1** Length: 147 Number of Matches: 1

See 2 more title(s)
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
300 bits(769)	3e-103()	Compositional matrix adjust.	143/146(98%)	143/146(97%)	0/146(0%)	
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDQPHLKRK	120			
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN D NCPFHDQPHLKRK	120			
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIYAVPWQGTMT SKSTCQDA	146			

cystatin-C precursor [Homo sapiens]
Sequence ID: **NP_000090.1** Length: 146 Number of Matches: 1

See 28 more title(s)
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
300 bits(769)	3e-103()	Compositional matrix adjust.	143/146(98%)	143/146(97%)	0/146(0%)	
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDQPHLKRK	120			
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN D NCPFHDQPHLKRK	120			
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIYAVPWQGTMT SKSTCQDA	146			

cystatin C, partial [synthetic construct]
Sequence ID: **AAX36984.1** Length: 147 Number of Matches: 1
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
300 bits(769)	3e-103()	Compositional matrix adjust.	143/146(98%)	143/146(97%)	0/146(0%)	
Features:						

Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDQPHLKRK	120
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN D NCPFHDQPHLKRK	120
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146
Sbjct	121	AFCSFQIYAVPWQGTMTLSKSTCQDA	146

cystatin C [Homo sapiens]
Sequence ID: **AAA52164.1** Length: 146 Number of Matches: 1
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
299 bits(765) 1e-102() Compositional matrix adjust. 142/146(97%) 142/146(97%) 0/146(0%)						
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY				60
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPA GSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY				60
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDQPHLKRK				120
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN D NCPFHDQPHLKRK				120
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIYAVPWQGTMTLSKSTCQDA	146			

cystatin-C [Piliocolobus tephrosceles]
Sequence ID: **XP_026305175.1** Length: 146 Number of Matches: 1
See 1 more title(s)
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
<hr/>						
261 bits(666)	2e-87()	Compositional matrix adjust.	139/146(95%)	141/146(96%)	0/146(0%)	
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY				60
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPAAG++PGKPPRLVGGPMDASVEEEGVRRALDFAV EY				60
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDQPHLKRK				120
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN D NCPFHDQPHLKRK				120
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIY VPWQGTMT SKSTCQDA	146			

PREDICTED: cystatin-C [Rhinopithecus bieti]
Sequence ID: **XP_017703337.1** Length: 146 Number of Matches: 1
See 1 more title(s)
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
260 bits(665) 2e-87() Compositional matrix adjust. 139/146(95%) 141/146(96%) 0/146(0%)						
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY				60
Sbjct	1	MAGPLRAPLLLLLAILAVALAV+PAAG+SPGKPPRLVGGPMDASVEEEGVRRALDFAV EY				60
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDQPHLKRK				120
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN D NCPFHDQPHLKRK				120
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIY VPWQGTMT SKSTCQDA	146			

PREDICTED: cystatin-C [Nomascus leucogenys]
Sequence ID: **XP_003280894.1** Length: 146 Number of Matches: 1
See 1 more title(s)
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
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260 bits(665) 2e-87() Compositional matrix adjust. 139/146(95%) 141/146(96%) 0/146(0%)

Features:

Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60
		MAGPLRAPLLLLLAILAVALAVSPAAG+SPGKPPRLVGGPMDASVEEEGVRRALDFAV EY	
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPAAGASPGKPPRLVGGPMDASVEEEGVRRALDFAVSEY	60
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRK	120
		N+ASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN DNCP HDQPHLKRRK	
Sbjct	61	NRASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCTKTQPNLDNCPHLDQPHLKRRK	120
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146
		AFCSFQIYAVPWQGTMT SKSTCQDA	
Sbjct	121	AFCSFQIYAVPWQGTMTLSKSTCQDA	146

Cystatin-3 [Macaca fascicularis]

Sequence ID: **EHH65608.1** Length: 146 Number of Matches: 1
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
260 bits(664)	3e-87()	Compositional matrix adjust.	138/146(95%)	140/146(95%)	0/146(0%)	

Features:

Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60
		MAGPLRA LLLLLAILAVALAVSPAAG+SPGKPPRLVGGPMDASVEEEGVRRALDFAV EY	
Sbjct	1	MAGPLRATLLLLLAILAVALAVSPAAGASPGKPPRLVGGPMDASVEEEGVRRALDFAVSEY	60
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRK	120
		NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN DNCPPH+QPHLKRRK	
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCTKTQPNLDNCPFHEQPHLKRRK	120
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146
		AFCSFQIY VPWQGTMT SKSTCQDA	
Sbjct	121	AFCSFQIYTPWQGTMTLSKSTCQDA	146

cystatin-C precursor [Macaca mulatta]

Sequence ID: **NP_001028096.1** Length: 146 Number of Matches: 1

See 10 more title(s)
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
260 bits(664)	3e-87()	Compositional matrix adjust.	139/146(95%)	141/146(96%)	0/146(0%)	

Features:

Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60
		MAGPLRAPLLLLLAILAVALAVSPAAG+SPGKPPRLVGGPMDASVEEEGVRRALDFAV EY	
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPAAGASPGKPPRLVGGPMDASVEEEGVRRALDFAVSEY	60
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRK	120
		NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN DNCPPH+QPHLKRRK	
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCTKTQPNLDNCPFHEQPHLKRRK	120
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146
		AFCSFQIY VPWQGTMT SKSTCQDA	
Sbjct	121	AFCSFQIYTPWQGTMTLSKSTCQDA	146

ompA - cystatin C fusion preprotein (AA -21 to 120) [synthetic construct]

Sequence ID: **CAA31253.1** Length: 141 Number of Matches: 1
Range 1: 8 to 141

Score	Expect	Method	Identities	Positives	Gaps	Frame
259 bits(661)	6e-87()	Compositional matrix adjust.	123/134(92%)	125/134(93%)	2/134(1%)	

Features:

Query	15	LAVALA--VSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRA	72
		+AVALA + A SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRA	
Sbjct	8	IAVALAGFATVAQASSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRA	67
Query	73	LQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRKAFCSFQIYAVPW	132
		LQVVRARKQIVAGVNYF DVELGRTTCTKTQPN DNCPPHDQPHLKRRKAFCSFQIYAVPW	
Sbjct	68	LQVVRARKQIVAGVNYFLDVELGRTTCTKTQPNLDNCPFHDPHLKRRKAFCSFQIYAVPW	127
Query	133	QGTMTFSKSTCQDA	146
		QGTMT SKSTCQDA	
Sbjct	128	QGTMTLSKSTCQDA	141

PREDICTED: cystatin-C [Colobus angolensis palliatus]

Sequence ID: **XP_011807579.1** Length: 146 Number of Matches: 1

See 2 more title(s)
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
259 bits(662)	7e-87()	Compositional matrix adjust.	138/146(95%)	140/146(95%)	0/146(0%)	
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Sbjct	1	M GPLRAPLLLLLAILAVALAV+PAAG+SPGKPPRLVGGPMDASVEEEGVRRALDFAV EY	60			
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRK	120			
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN DNCPPHDPHLKRRK	120			
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIY VPWQGTMT SKSTCQDA	146			

cystatin-C [Theropithecus gelada]
Sequence ID: **XP_025256115.1** Length: 146 Number of Matches: 1

See 1 more title(s)
range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
259 bits(661)	1e-86()	Compositional matrix adjust.	138/146(95%)	140/146(95%)	0/146(0%)	
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Sbjct	1	MAGPLRAPLLLLLAILAVALAVSPAAG+SPGKPPRLVGGPMDASVEEEGVRRALDFAV EY	60			
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRK	120			
Sbjct	61	NKASNDMYHSR LQVVRARKQIVAGVNYF DVELGRTTCTKTQPN DNCPPH+QPHLKRRK	120			
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIY VPWQGTMT SKSTCQDA	146			

PREDICTED: cystatin-C [Rhinopithecus roxellana]
Sequence ID: **XP_010381300.1** Length: 146 Number of Matches: 1

See 1 more title(s)
range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
256 bits(654)	8e-86()	Compositional matrix adjust.	137/146(94%)	139/146(95%)	0/146(0%)	
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Sbjct	1	MAG LRAPLLLLLAILAVALAV+PAAG+SPGKPPRLVGGPMD SVEEEGVRRALDFAV EY	60			
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRK	120			
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVELGRTTCTKTQPN DNCPPHDPHLKRRK	120			
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIY VPWQGTMT SKSTCQDA	146			

PREDICTED: cystatin-C [Saimiri boliviensis boliviensis]
Sequence ID: **XP_003942971.1** Length: 146 Number of Matches: 1
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
254 bits(648)	8e-85()	Compositional matrix adjust.	128/146(88%)	137/146(93%)	0/146(0%)	
Features:						
Query	1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60			
Sbjct	1	MAGPLR+PL LLAILAVALA+SPAAG+SPG+ PRL+GGPMDASVEEEGVRRALDFAV EY	60			
Query	61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRRK	120			
Sbjct	61	NKASNDMYHSRALQVVRARKQIVAGVNYF DVE+GRTTCTK QPN DNCPPH+QPHLKRRK	120			
Query	121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	121	AFCSFQIY+VPWQG MT SKS CQ+A	146			

Chain A, Human Cystatin C; Dimeric Form With 3d Domain Swapping
Sequence ID: **1G96_A** Length: 120 Number of Matches: 1

See 3 more title(s)

Range 1: 1 to 120

Score	Expect	Method	Identities	Positives	Gaps	Frame
253 bits(645)	1e-84()	Compositional matrix adjust.	117/120(98%)	117/120(97%)	0/120(0%)	
Features:						
Query	27	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGV	86			
Sbjct	1	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGV	60			
Query	87	NYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRKAFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	61	NYFLDVELGRTTCTKTQPNLDNCPFHDPHLKRKAFCSFQIYAVPWQGTMTLSKSTCQDA	120			

Chain A, Crystal Structure Of L68v Mutant Of Human Cystatin C

Sequence ID: **3PS8_A** Length: 120 Number of Matches: 1**See 4 more title(s)**

Range 1: 1 to 120

Score	Expect	Method	Identities	Positives	Gaps	Frame
251 bits(641)	3e-84()	Compositional matrix adjust.	116/120(97%)	117/120(97%)	0/120(0%)	
Features:						
Query	27	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGV	86			
Sbjct	1	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGV	60			
Query	87	NYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRKAFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	61	NYF DVE+GRTTCTKTQPN D NCPFHDPHLKRKAFCSFQIYAVPWQGTMT SKSTCQDA	120			

Chain A, Hinge-Loop Mutation Can Be Used To Control 3d Domain Swapping And Amyloidogenesis Of Human Cystatin C

Sequence ID: **3NX0_A** Length: 120 Number of Matches: 1**See 1 more title(s)**

Range 1: 1 to 120

Score	Expect	Method	Identities	Positives	Gaps	Frame
250 bits(638)	1e-83()	Compositional matrix adjust.	116/120(97%)	116/120(96%)	0/120(0%)	
Features:						
Query	27	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGV	86			
Sbjct	1	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQI AGV	60			
Query	87	NYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRKAFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	61	NYF DVELGRTTCTKTQPN D NCPFHDPHLKRKAFCSFQIYAVPWQGTMT SKSTCQDA	120			

Chain A, Crystal structure of V57D mutant of human cystatin C

Sequence ID: **3SVA_A** Length: 120 Number of Matches: 1

Range 1: 1 to 120

Score	Expect	Method	Identities	Positives	Gaps	Frame
249 bits(637)	2e-83()	Compositional matrix adjust.	116/120(97%)	116/120(96%)	0/120(0%)	
Features:						
Query	27	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGV	86			
Sbjct	1	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQI AGV	60			
Query	87	NYFFDVELGRTTCTKTQPNFDNCPFHDPHLKRKAFCSFQIYAVPWQGTMTFSKSTCQDA	146			
Sbjct	61	NYF DVELGRTTCTKTQPN D NCPFHDPHLKRKAFCSFQIYAVPWQGTMT SKSTCQDA	120			

Chain A, Crystal Structure Of V57p Mutant Of Human Cystatin C

Sequence ID: **3S67_A** Length: 120 Number of Matches: 1

Range 1: 1 to 120


Score	Expect	Method	Identities	Positives	Gaps	Frame
249 bits(636)	2e-83()	Compositional matrix adjust.	116/120(97%)	116/120(96%)	0/120(0%)	
Features:						
Query	27	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGV	86			
Sbjct	1	SSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQI AGV	60			

Query 87 NYFFDVELGRTTCTKTQPNFDNCPFHDPHLLKRRKAFCSFQIYAVPWQGTMTFSKSTCQDA 146
Sbjct 61 NYF DVELGRTTCTKTQPN D NCPFHDPHLLKRRKAFCSFQIYAVPWQGTMT SKSTCQDA 120
NYFLDVELGRTTCTKTQPNLDNCPFHDPHLLKRRKAFCSFQIYAVPWQGTMTLSKSTCQDA

PREDICTED: cystatin-C [Callithrix jacchus]
Sequence ID: **XP_002747560.1** Length: 146 Number of Matches: 1
Range 1: 1 to 146

Score	Expect	Method	Identities	Positives	Gaps	Frame
249 bits(637)	5e-83()	Compositional matrix adjust.	127/146(87%)	137/146(93%)	0/146(0%)	
Features:						
Query 1	MAGPLRAPLLLLLAILAVALAVSPAAGSSPGKPPRLVGGPMDASVEEEGVRRALDFAVGEY	60				
Sbjct 1	MAGPLR PLLLLA+LA+ALAVSPAAG+SPG+ PRL+GGPMDASVEEEGVRRALDFAV EY	60				
Query 61	NKASNDMYHSRALQVVRARKQIVAGVNYFFDVELGRTTCTKTQPNFDNCPFHDPHLLKRRK	120				
Sbjct 61	NKASND YHSRALQVVRARKQIVAGVNYF DVE+GRTTCTK QPN D NCPFH+QPHLLKRRK	120				
Query 121	AFCSFQIYAVPWQGTMTFSKSTCQDA	146				
Sbjct 121	AFCSFQIY+VPWQG MT SKS+CQ+A	146				
Sbjct 121	AFCSFQIYSVPWQGLMTLSKSSCQNA	146				

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