

Cytochrome C

Sequences :

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>NP_061820.1 cytochrome c [Homo sapiens]
MGDVEKGKKIFIMKCSQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGYSYTAANKNKGIWGEDTLMLEYL
NPKKYIPGTMIFVGIKKKEERADLIAYLKATNE

>NP_001124639.1 cytochrome c [Pongo abelii]
MGDVEKGKKIFIMKCSQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGYSYTAANKNKGIWGEDTLMLEYL
NPKKYIPGTMIFVGIKKKEERADLIAYLKATNE

>NP_031834.1 cytochrome c, somatic [Mus musculus]
MGDVEKGKKIFVQKCAQCHTVEKGGKHKTGPNLHGLFGRKTGQAAGFSYTDANKNKGITWGEDTLMLEYL
NPKKYIPGTMIFAGIKKKSERVDLIAYLKDATSK

>NP_001072946.1 cytochrome c [Gallus gallus]
MGDIEKGKKIFVQKCSQCHTVEKGGKHKTGPNLHGLFGRKTGQAEGFSYTDANKNKGITWGEDTLMLEYL
NPKKYIPGTMIFAGIKKKSERVDLIAYLKDATSK

>NP_001085462.1 cytochrome c, somatic A [Xenopus laevis]
MGDAEKGKKIFIQKCAQCHTVEKTGKHKTGPNLWGLFGRKTGQAAGFSYTDANKSKGIVWGEDTLFEYLE
NPKKYIPGTMIFAGIKKKNERLDLIAYLKSTSE

>XP_014028790.1 cytochrome c [Salmo salar]
MGDIAGKKKAFVQKCAQCHTVEGGKHKVGPNLWGLFGRKTGQAEGYSYTDANKSKGIWETDTLMTYLE
NPKKYIPGTMIFAGIKKKGERADLIAYLKSATS

>XP_032813079.1 cytochrome c, somatic-like [Petromyzon marinus]
MADVEKGKKVVFVQKCSQCHTVEGGKHKTGPNLWGLFGRKTGQAPGYSYTDANKSKGITWEEDTLVYYLE
NPKKYIPGTMIFAGIKKKDERNNLIAYLKSTSD

>XP_019613432.1 PREDICTED: cytochrome c, testis-specific [Branchiostoma belcheri]
MADAVKNGNPEKGKKVVFVQKCAQCHTVEAGGKHKTGPNLNLGLFGRKTGQAAGFSYTDANKNKGITWAEDT
LWIYLENPKKYIPGTMIFAGLKKKGERADLISYLKESTSS

>NP_001285984.1 cytochrome c proximal, isoform B [Drosophila melanogaster]
MGVPAGDVEKGKKLFVQRCAQCHTVEAGGKHKVGPNLHGLIGRKTGQAAGFAYTDANKAKGITWNEDTLF
EYLENPKKYIPGTMIFAGLKKPNERGDLIAYLKSATK

>XP_001635381.1 cytochrome c [Nematostella vectensis]
MGDATKGAQVFKTKAQCHTVEAGGKHKTGPNLHGLFGRKTGQAEGFSYTTANQNKGITWGEDTLMVYLE
NPKKYIPGTMVIFAGIKKKNERLDLIAYLKQETS

>XP_004209990.1 cytochrome c [Hydra vulgaris]
MGAEEKIPTGDATKGAQVFKQCAQCHVIDQSGKHKTGPNLYGLIGRKTGQAAGFSYTTANQNKGITWNKD
TLMWYLENPSKYIPGTMVIFAGIKKKQERADLIAYLEEECKK

>XP_003388937.1 PREDICTED: cytochrome c-like [Amphimedon queenslandica]
MRSFLLQRTLDSVVTEKGVVTGYHCISLKAEKEKALQRRSILQLLGKMSIPQGDPAAGAKIFKQRCACQ
HTTEAGGKHKTGPNLHGLFGRKTGQAAGFTYTTQANKSKGITWGEDTLFVYLEAPKKYIPGTMVIFAGLKK
PQERADLIAHLKEATK
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Alignment

XP_003388937.1[A.queenslandica]	MRSFLQRTLDVVTKEGVVVTGYHCISLKAAEEKEKALQRRSILQLLGKMSIPQGD	60
XP_004209990.1[H.vulgaris]	-----MGAEKIPTGDATKGA	15
NP_001285984.1[D.melanogaster]	-----MGVPAGDVEKGG	12
XP_019613432.1[B.belcheri]	-----MADAVKNGNPEKGG	14
XP_001635381.1[N.vectensis]	-----MGDATKGA	8
XP_032813079.1[P.marinus]	-----MGDVEKGG	8
XP_014028790.1[S.salar]	-----MGDIAKGG	8
NP_001085462.1[X.laervis]	-----MGDAEKGG	8
NP_061820.1[H.sapiens]	-----MGDVEKGG	8
NP_001124639.1[P.abelii]	-----MGDVEKGG	8
NP_031834.1[M.musculus]	-----MGDVEKGG	8
NP_001072946.1[G.gallus]	-----MGDIEKGG	8
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XP_003388937.1[A.queenslandica]	KIFKQRCACQCHTTEAGGKHKGTGPNLHGLFGRKTGQAPGFTYTQANKSKGITWGEDTLFVY	120
XP_004209990.1[H.vulgaris]	KVFQKRCACQCHVIDQSGKHKGTGPNLYGLIGRKTGQAPGFSYTDANKQNGITWNKDTLMVY	75
NP_001285984.1[D.melanogaster]	KLFVQRCACQCHTVEAGGKHKVGPNLHGLIGRKTGQAGFAYTDANKKAGITWNEDTLFEY	72
XP_019613432.1[B.belcheri]	KVFVQKCAQCHTVEAGGKHKGTGPNLHGLFGRKTGQAPGFSYTDANKKAGITWAEDTLMIY	74
XP_001635381.1[N.vectensis]	KVFPTKCAQCHTVEAGGKHKGTGPNLHGLFGRKTGQAGGFSYTDANKNGKITWGEDTLMVY	68
XP_032813079.1[P.marinus]	KVFVKCSQCHTVEAGGKHKGTGPNLHGLFGRKTGQAPGFSYTDANKSKGITWEEDTLVYV	68
XP_014028790.1[S.salar]	KAFVQKCAQCHTVENGGKHKVGPNLHGLFGRKTGQAGGFSYTDANKSKGIITWEDTLMTY	68
NP_001085462.1[X.laervis]	KIFIQKCAQCHTVEKTGKHKGTGPNLHGLFGRKTGQAPGFSYTDANKSKGIWGEDTLFEY	68
NP_061820.1[H.sapiens]	KIFIMKCSQCHTVEKGGKHKGTGPNLHGLFGRKTGQAPGFSYTDANKNGKITWGEDTLMEY	68
NP_001124639.1[P.abelii]	KIFIMKCSQCHTVEKGGKHKGTGPNLHGLFGRKTGQAPGFSYTDANKNGKITWGEDTLMEY	68
NP_031834.1[M.musculus]	KIFVOKCAQCHTVEKGGKHKGTGPNLHGLFGRKTGQAGGFSYTDANKNGKITWGEDTLMEY	68
NP_001072946.1[G.gallus]	KIFVOKCSQCHTVEKGGKHKGTGPNLHGLFGRKTGQAGGFSYTDANKNGKITWGEDTLMEY	68
	* * :*:***. : ****.*** **;***** *:*** **: *** * *** *	
XP_003388937.1[A.queenslandica]	LEAPKKYIPGTRMVFAGLKKPQERADLIAHLKEATK-	156
XP_004209990.1[H.vulgaris]	LENPSKYIPGTRMVFAGIKKKQERADLIALEECECK	112
NP_001285984.1[D.melanogaster]	LENPKKYIPGTRMVFAGLKKPNERGDLIAYLKSATK-	108
XP_019613432.1[B.belcheri]	LENPKKYIPGTRMVFAGLKKKGERADLIAYLKESTSS	111
XP_001635381.1[N.vectensis]	LENPKKYIPGTRMVFAGIKKKNERLDLIAYLKQETSS	104
XP_032813079.1[P.marinus]	LENPKKYIPGTRMIFAGIKKKDERNNLIAYLKSTSD	105
XP_014028790.1[S.salar]	LENPKKYIPGTRMIFAGIKKKGERADLIAYLKSTSS-	104
NP_001085462.1[X.laervis]	LENPKKYIPGTRMIFAGIKKKNERLDLIAYLKSTSE	105
NP_061820.1[H.sapiens]	LENPKKYIPGTRMIFVGIKKKEERADLIAYLKKATNE	105
NP_001124639.1[P.abelii]	LENPKKYIPGTRMIFVGIKKKEERADLIAYLKKATNE	105
NP_031834.1[M.musculus]	LENPKKYIPGTRMIFAGIKKKGERADLIAYLKKATNE	105
NP_001072946.1[G.gallus]	LENPKKYIPGTRMIFAGIKKKSERVDLIAYLKDATSK	105
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Percent identity matrix:

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#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_003388937.1[A.queenslandica] 100.00 72.97 77.78 73.64 77.88 72.12 73.08 75.96 74.04 74.04 77.88 75.96
2: XP_004209990.1[H.vulgaris] 72.97 100.00 68.52 69.37 77.88 67.62 67.31 69.52 66.67 66.67 70.48 69.52
3: NP_001285984.1[D.melanogaster] 77.78 68.52 100.00 76.85 75.96 76.92 78.85 79.81 76.92 76.92 84.62 81.73
4: XP_019613432.1[B.belcheri] 73.64 69.37 76.85 100.00 80.77 80.95 79.81 80.95 77.14 77.14 83.81 81.90
5: XP_001635381.1[N.vectensis] 77.88 77.88 75.96 80.77 100.00 78.85 78.85 82.69 79.81 79.81 83.65 84.62
6: XP_032813079.1[P.marinus] 72.12 67.62 76.92 80.95 78.85 100.00 83.65 84.76 81.90 81.90 83.81 83.81
7: XP_014028790.1[S.salar] 73.08 67.31 78.85 79.81 78.85 83.65 100.00 82.69 81.73 81.73 85.58 85.58
8: NP_001085462.1[X.laevis] 75.96 69.52 79.81 80.95 82.69 84.76 82.69 100.00 85.71 85.71 88.57 86.67
9: NP_061820.1[H.sapiens] 74.04 66.67 76.92 77.14 79.81 81.90 81.73 85.71 100.00 100.00 91.43 87.62
10: NP_001124639.1[P.abelii] 74.04 66.67 76.92 77.14 79.81 81.90 81.73 85.71 100.00 100.00 91.43 87.62
11: NP_031834.1[M.musculus] 77.88 70.48 84.62 83.81 83.65 83.81 85.58 88.57 91.43 91.43 100.00 92.38
12: NP_001072946.1[G.gallus] 75.96 69.52 81.73 81.90 84.62 83.81 85.58 86.67 87.62 87.62 92.38 100.00
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