

[BLAST®](#) » [blastp suite](#) » RID-M935M1FT01R

BLAST Results

Job title: sp|O14920|IKKB_HUMAN Inhibitor of nuclear...

RID [M935M1FT01R](#) (Expires on 06-18 09:58 am)

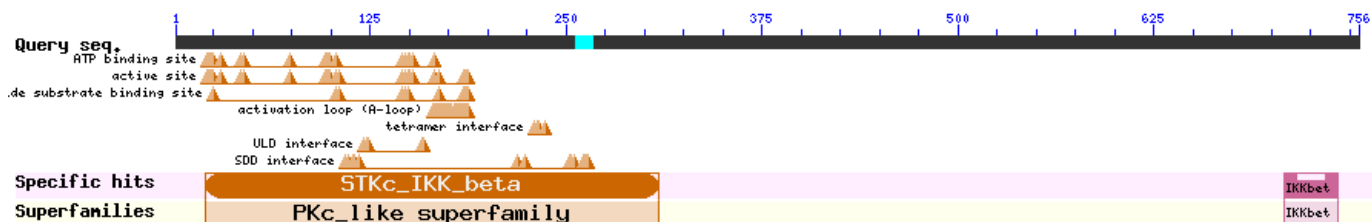
Query ID Icl|Query_307256
Description sp|O14920|IKKB_HUMAN Inhibitor of nuclear factor kappa-B kinase subunit beta OS=Homo sapiens GN=IKKB PE=1 SV=1

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

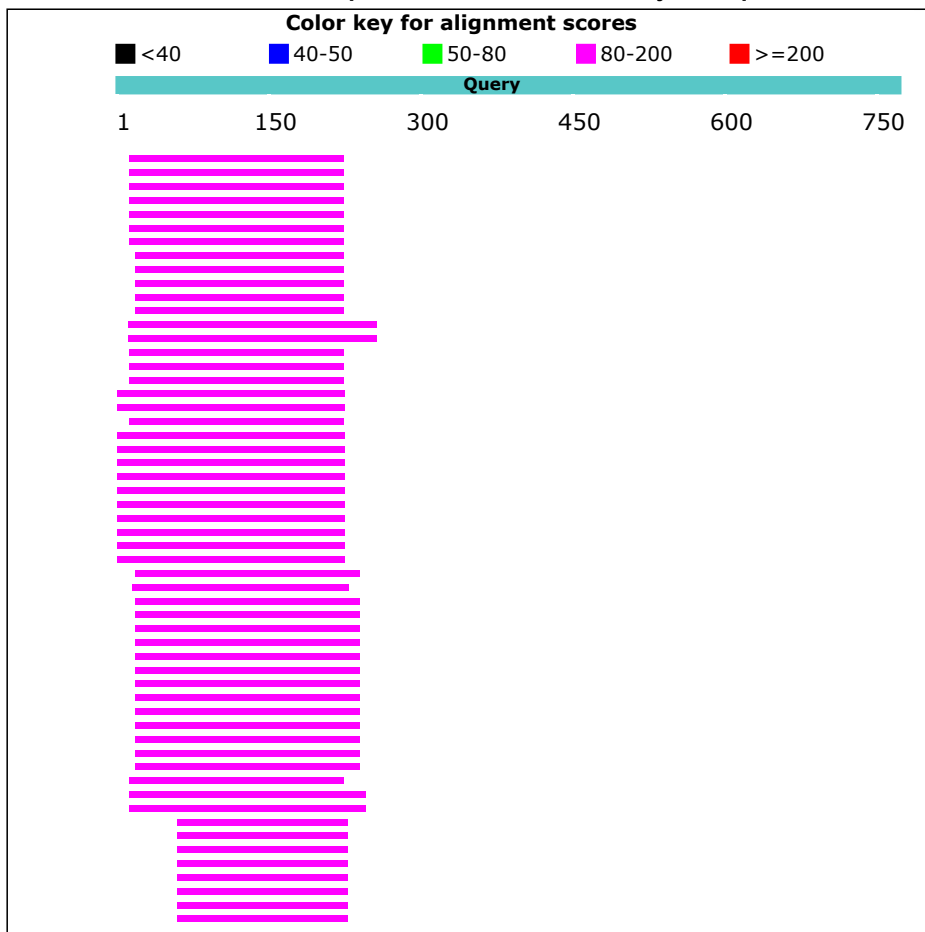
Molecule type amino acid
Query Length 756

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
CAMK/CDPK protein kinase [Plasmodium falciparum 7G8]	120	120	27%	4e-28	34%	EUR75227.1
CAMK/CDPK protein kinase [Plasmodium falciparum FCH/4]	120	120	27%	4e-28	34%	ETW31702.1
CAMK/CDPK protein kinase [Plasmodium falciparum Tanzania (2000708)]	119	119	27%	5e-28	34%	ETW37897.1
CAMK/CDPK protein kinase [Plasmodium falciparum UGT5.1]	119	119	27%	6e-28	34%	EWC77883.1
RecName: Full=Calcium-dependent protein kinase 2; AltName: Full=PfCDPK2	120	120	27%	6e-28	34%	O15865.3
Chain A, Crystal Structure Of Plasmodium Falciparum Cdpk2 Complexed With Inhibitor Staurosporine	120	120	27%	6e-28	34%	4MVF_A
calcium-dependent protein kinase [Plasmodium falciparum 3D7]	120	120	27%	8e-28	34%	XP_966095.1
hypothetical protein PFDG_04193 [Plasmodium falciparum Dd2]	112	112	26%	2e-25	35%	KOB87759.1
CAMK/CDPK protein kinase [Plasmodium falciparum Santa Lucia]	112	112	26%	6e-25	35%	EUT80064.1
calcium-dependent protein kinase, putative [Plasmodium falciparum 3D7]	111	111	26%	6e-25	35%	XP_001350105.1
CAMK/CDPK protein kinase [Plasmodium falciparum MaliPS096_E11]	110	110	26%	8e-25	35%	ETW46239.1
CAMK/CDPK protein kinase [Plasmodium falciparum IGH-CR14]	110	110	26%	1e-24	35%	KNG78610.1
hypothetical protein PFHG_03252 [Plasmodium falciparum HB3]	105	105	32%	3e-24	29%	KOB61520.1
protein kinase [Plasmodium falciparum 3D7]	105	105	32%	4e-24	29%	XP_002808785.1
CAMK/CAMKL protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	106	106	27%	6e-24	33%	ETW17165.1
serine/threonine protein kinase [Plasmodium falciparum 3D7]	105	105	27%	7e-24	33%	XP_001349887.1
CAMK protein kinase [Plasmodium falciparum Tanzania (2000708)]	108	108	27%	9e-24	33%	ETW35934.1
hypothetical protein PFHG_04713 [Plasmodium falciparum HB3]	108	108	29%	1e-23	32%	KOB62953.1
CAMK protein kinase [Plasmodium falciparum CAMP/Malaysia]	108	108	29%	2e-23	32%	ETW60594.1
serine/threonine protein kinase [Plasmodium falciparum UGT5.1]	101	101	27%	2e-23	31%	EWC77408.1
CAMK protein kinase [Plasmodium falciparum Palo Alto/Uganda]	108	108	29%	2e-23	32%	ETW52862.1
CAMK protein kinase [Plasmodium falciparum NF135/5.C10]	108	108	29%	2e-23	32%	ETW41998.1
CAMK protein kinase [Plasmodium falciparum NF54]	108	108	29%	2e-23	32%	EWC87970.1
CAMK protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	108	108	29%	2e-23	32%	ETW15465.1
CAMK protein kinase [Plasmodium falciparum Santa Lucia]	108	108	29%	2e-23	32%	EUT84242.1
CAMK protein kinase [Plasmodium falciparum 7G8]	108	108	29%	2e-23	32%	EUR70174.1
CAMK protein kinase [Plasmodium falciparum FCH/4]	108	108	29%	2e-23	32%	ETW30369.1
CAMK protein kinase [Plasmodium falciparum UGT5.1]	108	108	29%	2e-23	32%	EWC75892.1
CAMK protein kinase [Plasmodium falciparum MaliPS096_E11]	108	108	29%	2e-23	32%	ETW46031.1
calcium-dependent protein kinase, putative [Plasmodium falciparum 3D7]	108	108	29%	3e-23	32%	XP_001347913.1
protein kinase B-like protein [Plasmodium falciparum]	104	104	28%	4e-23	35%	AAT06260.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
AUR protein kinase [Plasmodium falciparum Santa Lucia]	101	101	27%	6e-23	32%	EUT92261.1
AGC/AKT protein kinase [Plasmodium falciparum NF54]	105	105	28%	7e-23	35%	EWC87207.1
AGC/AKT protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	104	104	28%	1e-22	34%	ETW17322.1
rac-beta serine/threonine protein kinase, PfPKB [Plasmodium falciparum 3D7]	105	105	28%	1e-22	35%	XP_001350854.1
AGC/AKT protein kinase [Plasmodium falciparum FCH/4]	104	104	28%	1e-22	34%	ETW29796.1
AGC/AKT protein kinase [Plasmodium falciparum MaliPS096_E11]	104	104	28%	1e-22	34%	ETW47985.1
AGC/AKT protein kinase [Plasmodium falciparum Santa Lucia]	105	105	28%	1e-22	34%	EUT81964.1
AGC/AKT protein kinase [Plasmodium falciparum IGH-CR14]	105	105	28%	1e-22	34%	KNG78024.1
AGC/AKT protein kinase [Plasmodium falciparum 7G8]	105	105	28%	1e-22	34%	EUR67523.1
AGC/AKT protein kinase [Plasmodium falciparum Tanzania (2000708)]	105	105	28%	2e-22	34%	ETW35153.1
serine/threonine protein kinase [Plasmodium falciparum UGT5.1]	105	105	28%	2e-22	34%	EWC75111.1
AGC/AKT protein kinase [Plasmodium falciparum CAMP/Malaysia]	105	105	28%	2e-22	34%	ETW59940.1
AGC/AKT protein kinase [Plasmodium falciparum NF135/5.C10]	105	105	28%	2e-22	34%	ETW41314.1
AGC/AKT protein kinase [Plasmodium falciparum Palo Alto/Uganda]	104	104	28%	2e-22	34%	ETW56107.1
calcium/calmodulin-dependent protein kinase, putative [Plasmodium falciparum 3D7]	99.4	99.4	27%	3e-22	32%	XP_001348401.2
NIMA-related protein kinase [Plasmodium falciparum]	101	101	30%	4e-22	31%	CAB76949.1
NEK protein kinase [Plasmodium falciparum Tanzania (2000708)]	102	102	30%	5e-22	31%	ETW32733.1
CAMK/CDPK protein kinase [Plasmodium falciparum RAJ116]	103	103	21%	5e-22	35%	KNC35220.1
hypothetical protein PFHG_03763 [Plasmodium falciparum HB3]	103	103	21%	6e-22	35%	KOB62013.1
CAMK/CDPK protein kinase [Plasmodium falciparum MaliPS096_E11]	103	103	21%	6e-22	35%	ETW48768.1
CAMK/CDPK protein kinase [Plasmodium falciparum NF135/5.C10]	103	103	21%	6e-22	35%	ETW41995.1
CAMK/CDPK protein kinase [Plasmodium falciparum Palo Alto/Uganda]	103	103	21%	6e-22	35%	ETW52859.1
CAMK/CDPK protein kinase [Plasmodium falciparum UGT5.1]	103	103	21%	7e-22	35%	EWC75970.1
CAMK/CDPK protein kinase [Plasmodium falciparum 7G8]	103	103	21%	7e-22	35%	EUR70171.1
CAMK/CDPK protein kinase [Plasmodium falciparum Tanzania (2000708)]	103	103	21%	7e-22	35%	ETW35931.1
CAMK/CDPK protein kinase [Plasmodium falciparum NF54]	103	103	21%	7e-22	35%	EWC87967.1
CAMK/CDPK protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	103	103	21%	7e-22	35%	ETW15469.1
CAMK/CDPK protein kinase [Plasmodium falciparum CAMP/Malaysia]	103	103	21%	7e-22	35%	ETW60591.1
CAMK/CDPK protein kinase [Plasmodium falciparum FCH/4]	103	103	21%	7e-22	35%	ETW30364.1
calcium-dependent protein kinase, putative [Plasmodium falciparum 3D7]	103	103	21%	7e-22	35%	XP_001347910.1
CAMK/CDPK protein kinase [Plasmodium falciparum IGH-CR14]	103	103	21%	7e-22	35%	KNG76578.1
other/NEK protein kinase [Plasmodium falciparum RAJ116]	102	102	30%	7e-22	31%	KNC35171.1
hypothetical protein PFDG_03020 [Plasmodium falciparum Dd2]	97.8	97.8	26%	9e-22	31%	KOB88610.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
CAMK/CDPK protein kinase [Plasmodium falciparum RAJ116]	100	100	24%	1e-21	34%	KNC37045.1
AUR protein kinase [Plasmodium falciparum NF54]	102	102	27%	2e-21	32%	EWC90792.1
AUR protein kinase [Plasmodium falciparum UGT5.1]	101	101	27%	2e-21	32%	EWC78760.1
AUR protein kinase [Plasmodium falciparum CAMP/Malaysia]	101	101	27%	2e-21	32%	ETW63718.1
AUR protein kinase [Plasmodium falciparum MaliPS096_E11]	101	101	27%	2e-21	32%	ETW51515.1
CAMK/CDPK protein kinase [Plasmodium falciparum FCH/4]	97.8	97.8	26%	3e-21	29%	ETW28056.1
NEK protein kinase [Plasmodium falciparum FCH/4]	100	100	27%	4e-21	32%	ETW29991.1
NEK protein kinase [Plasmodium falciparum UGT5.1]	100	100	30%	5e-21	31%	EWC75333.1
NEK protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	100	100	30%	5e-21	31%	ETW17530.1
other/AUR protein kinase [Plasmodium falciparum RAJ116]	100	100	27%	6e-21	32%	KNC35815.1
NEK protein kinase [Plasmodium falciparum 7G8]	100	100	30%	6e-21	31%	EUR68017.1
NEK protein kinase [Plasmodium falciparum Palo Alto/Uganda]	100	100	30%	6e-21	31%	ETW55970.1
NEK protein kinase [Plasmodium falciparum MaliPS096_E11]	100	100	30%	6e-21	31%	ETW48124.1
NEK protein kinase [Plasmodium falciparum Santa Lucia]	100	100	30%	6e-21	31%	EUT82563.1
NEK protein kinase [Plasmodium falciparum NF54]	100	100	30%	6e-21	31%	EWC89159.1
NEK protein kinase [Plasmodium falciparum NF135/5.C10]	100	100	30%	6e-21	31%	ETW41443.1
NEK protein kinase [Plasmodium falciparum CAMP/Malaysia]	100	100	30%	6e-21	31%	ETW60316.1
NIMA-related protein kinase, Pfnk-1 [Plasmodium falciparum 3D7]	100	100	30%	7e-21	31%	XP_001350680.1
other/NEK protein kinase [Plasmodium falciparum IGH-CR14]	100	100	30%	7e-21	31%	KNG75858.1
hypothetical protein PFHG_00994 [Plasmodium falciparum HB3]	100	100	30%	7e-21	31%	KOB59238.1
hypothetical protein PFDG_01891 [Plasmodium falciparum Dd2]	100	100	30%	7e-21	31%	KOB88360.1
CAMK/CDPK protein kinase [Plasmodium falciparum Tanzania (2000708)]	97.8	97.8	26%	8e-21	29%	ETW33296.1
calcium-dependent protein kinase 4 [Plasmodium falciparum HB3]	98.6	98.6	26%	8e-21	29%	KOB61436.1
calcium-dependent protein kinase 4 [Plasmodium falciparum 3D7]	98.6	98.6	26%	8e-21	29%	XP_001349078.1
AUR protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	100	100	27%	9e-21	32%	ETW20705.1
AUR protein kinase [Plasmodium falciparum FCH/4]	100	100	27%	9e-21	32%	ETW32420.1
Chain A, Apo Crystal Structure Of Cdk4 From Plasmodium Falciparum, Pf3d7_0717500	98.6	98.6	26%	9e-21	29%	4RGJ_A
Chain A, Crystal Structure Of Cdk4 From Plasmodium Falciparum, Pf3d7_0717500	98.6	98.6	26%	9e-21	29%	4QOX_A
CAMK/CDPK protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	98.2	98.2	26%	9e-21	29%	ETW20766.1
AUR protein kinase [Plasmodium falciparum NF135/5.C10]	100	100	27%	1e-20	32%	ETW45173.1
calcium-dependent protein kinase 1 [Plasmodium falciparum HB3]	98.6	98.6	26%	1e-20	29%	KOB60918.1
CAMK/CDPK protein kinase [Plasmodium falciparum IGH-CR14]	98.2	98.2	26%	1e-20	29%	KNG74640.1
hypothetical protein PFHG_01091 [Plasmodium falciparum HB3]	99.8	99.8	27%	1e-20	32%	KOB59334.1
Calcium-dependent protein kinase 1 [Plasmodium falciparum 3D7]	98.2	98.2	26%	1e-20	29%	XP_001349680.1
serine/threonine protein kinase, putative [Plasmodium falciparum 3D7]	99.8	99.8	27%	1e-20	32%	XP_001351166.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
CAMK/CDPK protein kinase [Plasmodium falciparum NF135/5.C10]	98.2	98.2	26%	1e-20	29%	ETW45429.1

Alignments

CAMK/CDPK protein kinase [Plasmodium falciparum 7G8]

Sequence ID: **EUR75227.1** Length: 436 Number of Matches: 1

See 1 more title(s)

Range 1: 72 to 268

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(300)	4e-28()	Compositional matrix adjust.	70/208(34%)	110/208(52%)	11/208(5%)	
Features:						
Query	15	WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVV				74
Sbjct	72	+ + E+LG G +G V + ++ T + AIK+ +++ +N R+ EI+IM++L HPN+V YIIDEKLGQGTGCVYKGDVKNQLYAIKEEKD-RLKNINRFFQEIEIMKKLDHPNIV				130
Query	75	AARDVPEGMQLAPNDLPLAMEYCQGGDLRKYLNQFENCCGLREGAILTLLSDIASALR				134
Sbjct	131	+ E ++ L ME C G R+ + E T++ I SA+ KLYETYEN-----DNYIYLIMELCSG---RELFDSSIENGSTFKNAATIMKQIFSAIF				181
Query	135	YLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLECTSFVGTLOYLAPPELL				194
Sbjct	182	YLH I+HRDLKPEN + Q + + KIID G +K L G T+ GT Y+AP++L YLHSLNIVHRDLKPENFLFQSENKDSLLKIIDFGLSKNLGTGEFTTTKAGTPYYVAPQVL				241
Query	195	EQQKYTVTVDYNSFGTLAFECITGFRPF		222		
Sbjct	242	+ KY D WS G + + + G+ PF D-GKYDKKCDIWSSGVIMYTLCCGYPPF		268		

CAMK/CDPK protein kinase [Plasmodium falciparum FCH/4]

Sequence ID: **ETW31702.1** Length: 440 Number of Matches: 1

Range 1: 72 to 268

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(300)	4e-28()	Compositional matrix adjust.	70/208(34%)	110/208(52%)	11/208(5%)	
Features:						
Query	15	WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVV				74
Sbjct	72	+ + E+LG G +G V + ++ T + AIK+ +++ +N R+ EI+IM++L HPN+V YIIDEKLGQGTGCVYKGDVKNQLYAIKEEKD-RLKNINRFFQEIEIMKKLDHPNIV				130
Query	75	AARDVPEGMQLAPNDLPLAMEYCQGGDLRKYLNQFENCCGLREGAILTLLSDIASALR				134
Sbjct	131	+ E ++ L ME C G R+ + E T++ I SA+ KLYETYEN-----DNYIYLIMELCSG---RELFDSSIENGSTFKNAATIMKQIFSAIF				181
Query	135	YLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLECTSFVGTLOYLAPPELL				194
Sbjct	182	YLH I+HRDLKPEN + Q + + KIID G +K L G T+ GT Y+AP++L YLHSLNIVHRDLKPENFLFQSENKDSLLKIIDFGLSKNLGTGEFTTTKAGTPYYVAPQVL				241
Query	195	EQQKYTVTVDYNSFGTLAFECITGFRPF		222		
Sbjct	242	+ KY D WS G + + + G+ PF D-GKYDKKCDIWSSGVIMYTLCCGYPPF		268		

CAMK/CDPK protein kinase [Plasmodium falciparum Tanzania (2000708)]

Sequence ID: **ETW37897.1** Length: 452 Number of Matches: 1

Range 1: 72 to 268

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(299)	5e-28()	Compositional matrix adjust.	70/208(34%)	110/208(52%)	11/208(5%)	
Features:						
Query	15	WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVV				74
Sbjct	72	+ + E+LG G +G V + ++ T + AIK+ +++ +N R+ EI+IM++L HPN+V YIIDEKLGQGTGCVYKGDVKNQLYAIKEEKD-RLKNINRFFQEIEIMKKLDHPNIV				130
Query	75	AARDVPEGMQLAPNDLPLAMEYCQGGDLRKYLNQFENCCGLREGAILTLLSDIASALR				134
Sbjct	131	+ E ++ L ME C G R+ + E T++ I SA+ KLYETYEN-----DNYIYLIMELCSG---RELFDSSIENGSTFKNAATIMKQIFSAIF				181
Query	135	YLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLECTSFVGTLOYLAPPELL				194
Sbjct	182	YLH I+HRDLKPEN + Q + + KIID G +K L G T+ GT Y+AP++L YLHSLNIVHRDLKPENFLFQSENKDSLLKIIDFGLSKNLGTGEFTTTKAGTPYYVAPQVL				241
Query	195	EQQKYTVTVDYNSFGTLAFECITGFRPF		222		
Sbjct	242	+ KY D WS G + + + G+ PF D-GKYDKKCDIWSSGVIMYTLCCGYPPF		268		

CAMK/CDPK protein kinase [Plasmodium falciparum UGT5.1]

Sequence ID: **EWC77883.1** Length: 447 Number of Matches: 1

Range 1: 83 to 279

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(299)	6e-28()	Compositional matrix adjust.	70/208(34%)	110/208(52%)	11/208(5%)	
Features:						
Query	15	WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVV				74
Sbjct	83	++ E+LG G +G V + ++ T + AIK+ +++ +N R+ EI+IM++L HPN+V YIIDEKLGQGTYGCVYKIDKVTNQLYAIKKEEKD-RLKNINRFFQEIEIMKKLDHPNIV				141
Query	75	AARDVPEGMQNLAPNDLPLAMEYCOGGDLRKYLNQFENCCGLREGAILTLLSDIASALR				134
Sbjct	142	+ E ++ L ME C G R+ + E T++ I SA+ KLYETYEN-----DNYIYLIMELCSG---RELFDSSIENGSTFKNAATIMKQIFSAIF				192
Query	135	YLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLECTSFVGTLOQLAPELL				194
Sbjct	193	YLH I+HRDLKPEN + Q + + KIID G +K L G T+ GT Y+AP++L YLHSLNIVHRDLKPENFLFQSENKDSLLKIIDFGLSKNLGTGEFTTTKAGTPYYVAPQVL				252
Query	195	EQQKYTVTVDYWSFGTLAFECITGFRPF	222			
Sbjct	253	+ KY D WS G + + + G+ PF D-GKYDKKCDIWSSGVIMYTLCCGYPPF	279			

RecName: Full=Calcium-dependent protein kinase 2; AltName: Full=PfCDPK2

Sequence ID: **O15865.3** Length: 513 Number of Matches: 1**See 2 more title(s)**

range 1: 72 to 268

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(301)	6e-28()	Compositional matrix adjust.	70/208(34%)	110/208(52%)	11/208(5%)	
Features:						
Query	15	WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVV				74
Sbjct	72	++ E+LG G +G V + ++ T + AIK+ +++ +N R+ EI+IM++L HPN+V YIIDEKLGQGTYGCVYKIDKVTNQLYAIKKEEKD-RLKNINRFFQEIEIMKKLDHPNIV				130
Query	75	AARDVPEGMQNLAPNDLPLAMEYCOGGDLRKYLNQFENCCGLREGAILTLLSDIASALR				134
Sbjct	131	+ E ++ L ME C G R+ + E T++ I SA+ KLYETYEN-----DNYIYLIMELCSG---RELFDSSIENGSTFKNAATIMKQIFSAIF				181
Query	135	YLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLECTSFVGTLOQLAPELL				194
Sbjct	182	YLH I+HRDLKPEN + Q + + KIID G +K L G T+ GT Y+AP++L YLHSLNIVHRDLKPENFLFQSENKDSLLKIIDFGLSKNLGTGEFTTTKAGTPYYVAPQVL				241
Query	195	EQQKYTVTVDYWSFGTLAFECITGFRPF	222			
Sbjct	242	+ KY D WS G + + + G+ PF D-GKYDKKCDIWSSGVIMYTLCCGYPPF	268			

Chain A, Crystal Structure Of Plasmodium Falciparum Cdpk2 Complexed With Inhibitor Staurosporine

Sequence ID: **4MVF_A** Length: 506 Number of Matches: 1

Range 1: 59 to 255

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(301)	6e-28()	Compositional matrix adjust.	70/208(34%)	110/208(52%)	11/208(5%)	
Features:						
Query	15	WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVV				74
Sbjct	59	++ E+LG G +G V + ++ T + AIK+ +++ +N R+ EI+IM++L HPN+V YIIDEKLGQGTYGCVYKIDKVTNQLYAIKKEEKD-RLKNINRFFQEIEIMKKLDHPNIV				117
Query	75	AARDVPEGMQNLAPNDLPLAMEYCOGGDLRKYLNQFENCCGLREGAILTLLSDIASALR				134
Sbjct	118	+ E ++ L ME C G R+ + E T++ I SA+ KLYETYEN-----DNYIYLIMELCSG---RELFDSSIENGSTFKNAATIMKQIFSAIF				168
Query	135	YLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLECTSFVGTLOQLAPELL				194
Sbjct	169	YLH I+HRDLKPEN + Q + + KIID G +K L G T+ GT Y+AP++L YLHSLNIVHRDLKPENFLFQSENKDSLLKIIDFGLSKNLGTGEFTTTKAGTPYYVAPQVL				228
Query	195	EQQKYTVTVDYWSFGTLAFECITGFRPF	222			
Sbjct	229	+ KY D WS G + + + G+ PF D-GKYDKKCDIWSSGVIMYTLCCGYPPF	255			

calcium-dependent protein kinase [Plasmodium falciparum 3D7]

Sequence ID: **XP_966095.1** Length: 509 Number of Matches: 1**See 8 more title(s)**

range 1: 72 to 268

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(300)	8e-28()	Compositional matrix adjust.	70/208(34%)	110/208(52%)	11/208(5%)	
Features:						

```

Query 15  WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVV 74
+ + E+LG G +G V + ++ T + AIK+ +++ +N R+ EI+IM++L HPN+V
Sbjct 72  YIIDEKLGQGTGVCYKGDVKNQLYAIKEEKD -RLKNINRFFQEIEIMKLDHPNIV 130

Query 75  AARDVPEGMQNLAPNDLPLAMEYCQGGDLRKYLNQFENCGLREGAILTLLSDIASALR 134
+ E + L ME C G R+ + E T++ I SA+
Sbjct 131  KLYETYEN-----DNYIYLIMELCSG---RELFDSSIENGSTFKNAATIMKQIFSAIF 181

Query 135  YLHENRITHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCLTSFVGTLOYLAPELL 194
YLH I+HRDLKPEN + Q + + KIID G +K L G T+ GT Y+AP++L
Sbjct 182  YLHSLNIVHRDLKPENLFDQSENKDSLLKIIDFGLSKNLGTGEFTTTKAGTPYYVAPQVL 241

Query 195  EQQKYTVTVDYWSFGTLAFECITGFRPF 222
+ KY D WS G + + + G+ PF
Sbjct 242  D-GKYDKKCDIWSSGVIMYTLCCGYPPF 268
    
```

hypothetical protein PFDG_04193 [Plasmodium falciparum Dd2]

Sequence ID: **KOB87759.1** Length: 478 Number of Matches: 1
Range 1: 130 to 321

Score	Expect	Method	Identities	Positives	Gaps	Frame
112 bits(280)	2e-25()	Compositional matrix adjust.	71/203(35%)	107/203(52%)	11/203(5%)	
Features:						
Query 20	RLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVVAARDV	79				
Sbjct 130	+LG G +GNV++ ++ TG+Q AIK ++ N ER EI IM+++ HPN++ +V KLGKGSYGNVVKAVSKRTGQRAIKI -IEKKKIHNIERLKRILIMKQMDHPNIIKLYEV	188				
Query 80	PEGMQNLAPNDLPLAMEYCQGGDLRKYLNQFENCGLREGAILTLLSDIASALRYLHEN	139				
Sbjct 189	E + L L +E C GG+L + ++ E ++ I SAL Y H YEDNEKL-----YLVLELCDGGELFDKIVKYG---SFSEYAYKIMKQIFSALYCHSK	239				
Query 140	RIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCLTSFVGTLOYLAPELLEQQKY	199				
Sbjct 240	I+HRDLKPENI+ + +IID G+A + S VGT Y+APE+L + KY NIMHRDLKPENILYVDNTEDSPIQIIDWGFASKCMNNHNLKSVVGTPTYIAPAIL -RGKY	298				
Query 200	TVTVDYWSFGTLAFECITGFRPF 222					
Sbjct 299	D WS G + + + G+ PF DKRCDIWSSGVIMYILLCCGYPPF 321	321				

CAMK/CDPK protein kinase [Plasmodium falciparum Santa Lucia]

Sequence ID: **EUT80064.1** Length: 568 Number of Matches: 1

See 1 more title(s)

Range 1: 130 to 321

Score	Expect	Method	Identities	Positives	Gaps	Frame
112 bits(279)	6e-25()	Compositional matrix adjust.	71/203(35%)	107/203(52%)	11/203(5%)	
Features:						
Query 20	RLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVVAARDV	79				
Sbjct 130	+LG G +GNV++ ++ TG+Q AIK ++ N ER EI IM+++ HPN++ +V KLGKGSYGNVVKAVSKRTGQRAIKI -IEKKKIHNIERLKRILIMKQMDHPNIIKLYEV	188				
Query 80	PEGMQNLAPNDLPLAMEYCQGGDLRKYLNQFENCGLREGAILTLLSDIASALRYLHEN	139				
Sbjct 189	E + L L +E C GG+L + ++ E ++ I SAL Y H YEDNEKL-----YLVLELCDGGELFDKIVKYG---SFSEYAYKIMKQIFSALYCHSK	239				
Query 140	RIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCLTSFVGTLOYLAPELLEQQKY	199				
Sbjct 240	I+HRDLKPENI+ + +IID G+A + S VGT Y+APE+L + KY NIMHRDLKPENILYVDNTEDSPIQIIDWGFASKCMNNHNLKSVVGTPTYIAPAIL -RGKY	298				
Query 200	TVTVDYWSFGTLAFECITGFRPF 222					
Sbjct 299	D WS G + + + G+ PF DKRCDIWSSGVIMYILLCCGYPPF 321	321				

calcium-dependent protein kinase, putative [Plasmodium falciparum 3D7]

Sequence ID: **XP_001350105.1** Length: 568 Number of Matches: 1

See 10 more title(s)

Range 1: 130 to 321

Score	Expect	Method	Identities	Positives	Gaps	Frame
111 bits(278)	6e-25()	Compositional matrix adjust.	71/203(35%)	107/203(52%)	11/203(5%)	
Features:						
Query 20	RLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCLEIQIMRRLTHPNVVAARDV	79				
Sbjct 130	+LG G +GNV++ ++ TG+Q AIK ++ N ER EI IM+++ HPN++ +V KLGKGSYGNVVKAVSKRTGQRAIKI -IEKKKIHNIERLKRILIMKQMDHPNIIKLYEV	188				
Query 80	PEGMQNLAPNDLPLAMEYCQGGDLRKYLNQFENCGLREGAILTLLSDIASALRYLHEN	139				
Sbjct 189	E + L L +E C GG+L + ++ E ++ I SAL Y H YEDNEKL-----YLVLELCDGGELFDKIVKYG---SFSEYAYKIMKQIFSALYCHSK	239				
Query 140	RIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCLTSFVGTLOYLAPELLEQQKY	199				
Sbjct 240	I+HRDLKPENI+ + +IID G+A + S VGT Y+APE+L + KY NIMHRDLKPENILYVDNTEDSPIQIIDWGFASKCMNNHNLKSVVGTPTYIAPAIL -RGKY	298				
Query 200	TVTVDYWSFGTLAFECITGFRPF 222					
	D WS G + + + G+ PF					

Sbjct 299 DKRCDIWSSGVIMYILLCGYPPF 321

CAMK/CDPK protein kinase, partial [Plasmodium falciparum MaliPS096_E11]

Sequence ID: **ETW46239.1** Length: 503 Number of Matches: 1

Range 1: 65 to 256

Score	Expect	Method	Identities	Positives	Gaps	Frame
110 bits(276)	8e-25()	Compositional matrix adjust.	71/203(35%)	106/203(52%)	11/203(5%)	
Features:						
Query 20	RLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCL	EIQIMRRLTHPNVVAARDV	79			
	+LG G +GNV++ ++ TG+Q AIK ++ N ER EI IM+++ HPN++ +V					
Sbjct 65	KLGGKSYGNVVKAVSKRTGQRAIKI-IEKKIHNIERLKR	EILMKQMDHPNIIKLYEV	123			
Query 80	PEGMQLAPNDLPLAMEYCOGGDLRKYLNQFENCCLREGAIL	TLLSDIASALRYLHEN	139			
	E + L L + E C GG+L ++ E ++ I SAL Y H					
Sbjct 124	YEDNEKL-----YLVLELCDGGEL---FDKIVKYG	SFSEYEAYKIMKQIFSALYYCHSK	174			
Query 140	RIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGS	SLCTS FVGT LQYLAPELLEQOKY	199			
	I+HRDLKPENI+ + +IID G+A + S VGT Y+APE+L + KY					
Sbjct 175	NIMHRDLKPENILYVDNTEDSPIQIIDWGFASKMNNH	NLKS VVGTPPYIAPEIL -RGKY	233			
Query 200	TVTVDYWSFGTLAFECITGFRPF	222				
	D WS G + + + G+ PF					
Sbjct 234	DKRCDIWSSGVIMYILLCGYPPF	256				

CAMK/CDPK protein kinase [Plasmodium falciparum IGH-CR14]

Sequence ID: **KNG78610.1** Length: 540 Number of Matches: 1

Range 1: 102 to 293

Score	Expect	Method	Identities	Positives	Gaps	Frame
110 bits(276)	1e-24()	Compositional matrix adjust.	71/203(35%)	106/203(52%)	11/203(5%)	
Features:						
Query 20	RLGTGGFGNVIRWHNQETGEQIAIKQCRQELSPRNRERWCL	EIQIMRRLTHPNVVAARDV	79			
	+LG G +GNV++ ++ TG+Q AIK ++ N ER EI IM+++ HPN++ +V					
Sbjct 102	KLGGKSYGNVVKAVSKRTGQRAIKI-IEKKIHNIERLKR	EILMKQMDHPNIIKLYEV	160			
Query 80	PEGMQLAPNDLPLAMEYCOGGDLRKYLNQFENCCLREGAIL	TLLSDIASALRYLHEN	139			
	E + L L + E C GG+L ++ E ++ I SAL Y H					
Sbjct 161	YEDNEKL-----YLVLELCDGGEL---FDKIVKYG	SFSEYEAYKIMKQIFSALYYCHSK	211			
Query 140	RIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGS	SLCTS FVGT LQYLAPELLEQOKY	199			
	I+HRDLKPENI+ + +IID G+A + S VGT Y+APE+L + KY					
Sbjct 212	NIMHRDLKPENILYVDNTEDSPIQIIDWGFASKMNNH	NLKS VVGTPPYIAPEIL -RGKY	270			
Query 200	TVTVDYWSFGTLAFECITGFRPF	222				
	D WS G + + + G+ PF					
Sbjct 271	DKRCDIWSSGVIMYILLCGYPPF	293				

hypothetical protein PFHG_03252 [Plasmodium falciparum HB3]

Sequence ID: **KOB61520.1** Length: 310 Number of Matches: 1

Range 1: 2 to 238

Score	Expect	Method	Identities	Positives	Gaps	Frame
105 bits(263)	3e-24()	Compositional matrix adjust.	74/251(29%)	128/251(50%)	23/251(9%)	
Features:						
Query 13	GAWEMKERLGTGGFGNVI---RWHNQETGEQIAIKQCRQEL	SPRNRERWCL-EIQIMRR	67			
	+E +G G +GN I R ++ + I I O O+ +R CL E++++ +					
Sbjct 2	NKYEKIRDIGKGNYGNTILVRDRKNDHYVMKIINISQMSQ	-----EKRQCLKEVELLSK	56			
Query 68	LTHPNVVAARDVPEGMQLAPNDLPLAMEYCOGGDLRKYLNQ	FENCCLREGAILTLL	126			
	L HP +V +++ D + M++C+GGDL Y+ N+ + ++E IL L					
Sbjct 57	LNHPFIVKY-----IESYIEGDTLRIVMKHKCGGDL	YHYIQNKKKQNTPIKEKRILIWL	110			
Query 127	SDIASALRYLHENRIIHRDLKPENIVLQQGEQRLIHKIIDL	GYAKELDQG-SLCTS FVGT	185			
	+ I +AL+++LH N I+HRD+K NI++ ++R+ ++ D G +K L+ + +GT					
Sbjct 111	TQILTALKFLHSNHILHRDMKSLNILI-DSDKRV--RLCDF	GISKVLENTLDYANTLIGT	167			
Query 186	LQYLAPELLEQOKYTVTVDYWSFGTLAFECITGFRPFLPN	WQPVQWHSKVRQKSEVDI--	243			
	YL+PEL + +KY+ D W+ G L +E T PF O +R D+					
Sbjct 168	PYYLSPELCKDKKYSWPSDVWATGLIYELATFRTPFHST	KGIQQLCYNIRYAPIPLPN	227			
Query 244	VSEDLNGTVK	254				
	+ S++LN K					
Sbjct 228	IYSKELNNIYK	238				

protein kinase [Plasmodium falciparum 3D7]

Sequence ID: **XP_002808785.1** Length: 310 Number of Matches: 1**See 5 more title(s)**

Range 1: 2 to 238

Score	Expect	Method	Identities	Positives	Gaps	Frame
105 bits(262)	4e-24()	Compositional matrix adjust.	74/251(29%)	128/251(50%)	23/251(9%)	
Features:						
Query	13	GAWEMKERLGTGGFGNVI---RWHNQETGEQIAIKQCRQELSPRNRERWCL-EIQIMRR	67			
Sbjct	2	NKYEKIRDIGKGNVNTILVDRDRKNDHYVMKIINISQMSQK-----EKRQCLKEVELLSK	56			
Query	68	LTHPNVVAARDVPEGMQNLAPNDLPLLAMEYCGGDLRKYL-NQFENCCGLREGAILTL	126			
Sbjct	57	LNHPFIVKY-----IESYIEGDTLRIVMKHCKGGDLHYIQNKKQNTPIKEKRILWL	110			
Query	127	SDIASALRYLHENRIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQG-SLCTSFVGT	185			
Sbjct	111	TQILTALKFLHSNHILHRDMKSLNILLI-DSDKRV--RLCDFGISKVLENTLDYANTLIGT	167			
Query	186	LQYLAPELLEQQKYTVTVDYWSFGTLAFECITGFRPFLPNWQPVQHSKVRQKSEVDI--	243			
Sbjct	168	PYYLSPELCKDKKYSWPSDVWATGCLIVELATFRTPFHSTKGIQQLCYNIRYAPIPDLPN	227			
Query	244	WSEDLNGTVK 254				
Sbjct	228	IYSKELNNIYK 238				

CAMK/CAMKL protein kinase [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]

Sequence ID: **ETW17165.1** Length: 367 Number of Matches: 1

See 7 more title(s)

Range 1: 107 to 309

Score	Expect	Method	Identities	Positives	Gaps	Frame
106 bits(264)	6e-24()	Compositional matrix adjust.	71/214(33%)	109/214(50%)	17/214(7%)	
Features:						
Query	15	WEMKERLGTGGFGNVIHRWHNQETGEQIAIKQCRQE--LSPRNRERWCL-EIQIMRRLTHPN	72			
Sbjct	107	YIVEKRIGSGGFGIVFQGVHIQTKQKVALKFIKSNFLDVTDVHRVFIETQLRGLIHNN	166			
Query	73	VVAARDVPEGMQNLAPNDLPLLAMEYCGGDLRKYL-NQFENCCGLREGAILTLSDIAS	131			
Sbjct	167	IIMYDVNH-FQNYV-----CLIMEYAINGLKKNYIKNKFNGFLSEKEAHDLF--QIVK	218			
Query	132	ALRYLHENRIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLSCTSFVGTLOYLAP	191			
Sbjct	219	GYYCHSKHIVHRDLKLENILL---DEKMTCKIADFGLSDFVNVQNIKTEAGTKAYIAP	275			
Query	192	ELLEQQKYTVTV---DYWSFGTLAFECITGFRPF 222				
Sbjct	276	EIIIFNQITINYSVFKLDIWSLGIILFIMTQGFAPF 309				

serine/threonine protein kinase [Plasmodium falciparum 3D7]

Sequence ID: **XP_001349887.1** Length: 367 Number of Matches: 1

See 7 more title(s)

Range 1: 107 to 309

Score	Expect	Method	Identities	Positives	Gaps	Frame
105 bits(263)	7e-24()	Compositional matrix adjust.	71/214(33%)	109/214(50%)	17/214(7%)	
Features:						
Query	15	WEMKERLGTGGFGNVIHRWHNQETGEQIAIKQCRQE--LSPRNRERWCL-EIQIMRRLTHPN	72			
Sbjct	107	YIVEKRIGSGGFGIVFQGVHIQTKQKVALKFIKSNFLDVTDVHRVFIETQLRGLIHNN	166			
Query	73	VVAARDVPEGMQNLAPNDLPLLAMEYCGGDLRKYL-NQFENCCGLREGAILTLSDIAS	131			
Sbjct	167	IIMYDVNH-FQNYV-----CLIMEYAINGLKKNYIKNKFNGFLSEKEAHDLF--QIVK	218			
Query	132	ALRYLHENRIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSLSCTSFVGTLOYLAP	191			
Sbjct	219	GYYCHSKHIVHRDLKLENILL---DEKMTCKIADFGLSDFVNVQNIKTEAGTKAYIAP	275			
Query	192	ELLEQQKYTVTV---DYWSFGTLAFECITGFRPF 222				
Sbjct	276	EIIIFNQITINYSVFKLDIWSLGIILFIMTQGFAPF 309				

CAMK protein kinase [Plasmodium falciparum Tanzania (2000708)]

Sequence ID: **ETW35934.1** Length: 655 Number of Matches: 1

Range 1: 211 to 410

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(270)	9e-24()	Compositional matrix adjust.	69/209(33%)	105/209(50%)	10/209(4%)	
Features:						
Query	15	WEMKERLGTGGFGNVIHRWHNQETGEQIAIKQCRQELSPRNRERWCL-EIQIMRRLTHPNV	73			
Sbjct	211	YELHEQLGQGFSTVYRINKQTNSEFAIKVIDKRSVSIYEKELLRSEISILRLLRHPNV	270			

```

Query 74  VAARDVPEGMQNLAPNDLPLAMEYCGGDLRKYLNQFENCCLREGAILTLLSDIASAL 133
+ +++ + L ++ME +GG+L +L + I+T L +
Sbjct 271  IYLKEIINTKETL-----YISMELVKGGELYDFLLAETRLSEIHANKIITQL---IKTV 321

Query 134  RYLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCTSFVGTLOYLAPEL 193
YLH IHRD+KPENI+L + K+ D G + L GTL Y+APE+
Sbjct 322  AYLRHRCGIIHRDIKPENILLTDKSRDAQIKLDFGLSTLCAPNELLKEPCGTLAYVAPEV 381

Query 194  LEQOKYTVTVDYWSFGTLAFECITGFRPF 222
+ O Y VD WS G + + ++G PF
Sbjct 382  ITLQGYNHKVDAWSIGIILYLLLSGKLPF 410
    
```

hypothetical protein PFHG_04713 [Plasmodium falciparum HB3]

Sequence ID: **KOB62953.1** Length: 1361 Number of Matches: 1
 Range 1: 905 to 1116

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(271)	1e-23()	Compositional matrix adjust.	70/221(32%)	108/221(48%)	10/221(4%)	

Features:

```

Query 3  WPSPLTTQTCGAWEMKERLGTGGFGNVIRWHNQETGEQIAIKQC-RQELSPRNRERWCLE 61
+S + +E+ E+LG G F V R N++T + AIK ++ +S +E E
Sbjct 905  YSSTKQNTLYNLYELHEQLGQGFSTVYRGINKQTNSEFAIKVIDKRSVSIYEKELLRSE 964

Query 62  IQIMRRLTHPNVVAARDVPEGMQNLAPNDLPLAMEYCGGDLRKYLNQFENCCLREGA 121
I I+R L HPNV+ +++ + L ++ME +GG+L +L +
Sbjct 965  ISILRLLRHPNVVILYKEIINTKETL-----YISMELVKGGELYDFLLAETRLSEIHANK 1018

Query 122  ILTLLSDIASALRYLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCT 181
I+T L + YLH IHRD+KPENI+L + K+ D G + L
Sbjct 1019  IITQL---IKTVAYLRHRCGIIHRDIKPENILLTDKSRDAQIKLDFGLSTLCAPNELLKE 1075

Query 182  FVGTLOYLAPELLEQOKYTVTVDYWSFGTLAFECITGFRPF 222
GTL Y+APE++ O Y VD WS G + + ++G PF
Sbjct 1076  PCGTLAYVAPEVITLQGYNHKVDAWSIGIILYLLLSGKLPF 1116
    
```

CAMK protein kinase [Plasmodium falciparum CAMP/Malaysia]

Sequence ID: **ETW60594.1** Length: 1993 Number of Matches: 1
 Range 1: 1537 to 1748

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(271)	2e-23()	Compositional matrix adjust.	70/221(32%)	108/221(48%)	10/221(4%)	

Features:

```

Query 3  WPSPLTTQTCGAWEMKERLGTGGFGNVIRWHNQETGEQIAIKQC-RQELSPRNRERWCLE 61
+S + +E+ E+LG G F V R N++T + AIK ++ +S +E E
Sbjct 1537  YSSTKQNTLYNLYELHEQLGQGFSTVYRGINKQTNSEFAIKVIDKRSVSIYEKELLRSE 1596

Query 62  IQIMRRLTHPNVVAARDVPEGMQNLAPNDLPLAMEYCGGDLRKYLNQFENCCLREGA 121
I I+R L HPNV+ +++ + L ++ME +GG+L +L +
Sbjct 1597  ISILRLLRHPNVVILYKEIINTKETL-----YISMELVKGGELYDFLLAETRLSEIHANK 1650

Query 122  ILTLLSDIASALRYLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCT 181
I+T L + YLH IHRD+KPENI+L + K+ D G + L
Sbjct 1651  IITQL---IKTVAYLRHRCGIIHRDIKPENILLTDKSRDAQIKLDFGLSTLCAPNELLKE 1707

Query 182  FVGTLOYLAPELLEQOKYTVTVDYWSFGTLAFECITGFRPF 222
GTL Y+APE++ O Y VD WS G + + ++G PF
Sbjct 1708  PCGTLAYVAPEVITLQGYNHKVDAWSIGIILYLLLSGKLPF 1748
    
```

serine/threonine protein kinase [Plasmodium falciparum UGT5.1]

Sequence ID: **EWC77408.1** Length: 224 Number of Matches: 1
 Range 1: 4 to 204

Score	Expect	Method	Identities	Positives	Gaps	Frame
101 bits(251)	2e-23()	Composition-based stats.	67/215(31%)	117/215(54%)	21/215(9%)	

Features:

```

Query 15  WEMKERLGTGGFGNVI----RWHNQETGEQIAIKQCROELSPRNRERWCL-EIQIMRRL 69
+E +G G +GN I R ++ + I I O O+ +R CL E++++ +L
Sbjct 4  YEKIRDIGKGNVNTILVRDRKNDHYVMKIINISQMSQK-----EKRQCLKEVELLSKLN 58

Query 70  HPNVVAARDVPEGMQNLAPNDLPLAMEYCGGDLRKYLNQFENCCLREGAILTLLSD 128
HP +V + +++ D + M++C+GGDL Y+ N+ + ++E IL L+
Sbjct 59  HPPFIV-----KYIESYIEGDTLRIVMKHCKGGDLYHYIQNKKKQNTPIKEKRILWLTQ 112

Query 129  IASALRYLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYAKELDQGSCTSFVGTLO 187
I +AL++LH N I+HRD+K NI++ ++R+ ++ D G +K L+ + +GT
Sbjct 113  ILTALKFLHSNHILHRDMKSLNILIDS-DKRV--RLCDFGISKVLENTLDYANTLIGTPY 169

Query 188  YLAPELLEQOKYTVTVDYWSFGTLAFECITGFRPF 222
YL+PEL + +KY+ D W+ G L +E T PF
Sbjct 170  YLSPELCKDKKYSWPSDVWATGCLIEYELATFRTPF 204
    
```



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