

## **Appendix C**

### **ClustalW alignments and**

### **Blast search results**

## NOP56 protein alignment

CLUSTAL W (1.81) Multiple Sequence Alignments

Sequence format is Pearson  
Sequence 1: Arabidopsis-T6H22 522 aa  
Sequence 2: Cicer arietinum 454 aa  
Sequence 3: Schizosaccharomyces 497 aa  
Sequence 4: Homo sapiens 602 aa  
Sequence 5: D.subobscura 503 aa  
Sequence 6: Saccharomyces 504 aa  
Sequence 7: S acidocaldarius 412 aa

### Pairwise alignments

Sequences (2:3) Aligned. Score: 51  
Sequences (1:2) Aligned. Score: 71  
Sequences (3:4) Aligned. Score: 51  
Sequences (4:5) Aligned. Score: 58  
Sequences (2:4) Aligned. Score: 57  
Sequences (1:3) Aligned. Score: 55  
Sequences (3:5) Aligned. Score: 51  
Sequences (4:6) Aligned. Score: 49  
Sequences (2:5) Aligned. Score: 52  
Sequences (4:7) Aligned. Score: 27  
Sequences (1:4) Aligned. Score: 51  
Sequences (3:6) Aligned. Score: 58  
Sequences (2:6) Aligned. Score: 48  
Sequences (5:6) Aligned. Score: 49  
Sequences (2:7) Aligned. Score: 29  
Sequences (3:7) Aligned. Score: 26  
Sequences (1:5) Aligned. Score: 52  
Sequences (5:7) Aligned. Score: 27  
Sequences (6:7) Aligned. Score: 28  
Sequences (1:6) Aligned. Score: 49  
Sequences (1:7) Aligned. Score: 32

### CLUSTAL W (1.81) multiple sequence alignment

```
Arabidopsis-T6H22      -----MAMYVIYESSSGYGLFEVHG-LDEIGQNTTEAVRTSVSDLSRFGRVVQLTAFHP 52
Cicer arietinum      -----
Schizosaccharomyces  -----MA--DYLLYESATGYSLFDVVG-ADQIAAKTKEVQLSLQDISKFGKVVQLRSFIP 52
Saccharomyces        -----MAPIEYLLFEPEPTGYAVFKVKLQDDIGSRLKEVQEQINDFGAFTKLIELVSFAP 55
Homo                  MAGRGAMVLLHVLFEHAVGYALVALKE-VEEISLLQPQVEESVNLNLGKFHSIVRLVAFCP 59
D.subobscura         -----MSILYCLYEHAAGFSVFSVKE-FEEVSMFLPQVESSVTDFAKFNSIVKLAGFAP 53
Sulfolobus           -----MKIYLVEHAIGSFG-YDESGKLIDFVP 26

Arabidopsis-T6H22      FESALDALNQVNAVSEGVMTDELRSFLELNLPKVKEGKKPKFSLGLAEPKLGSHIFEATK 112
Cicer arietinum      -----TDELRTVLETNLPKVKEGKKPKFSLGVAESKLGSIHDVTK 41
Schizosaccharomyces  FKNAHALENANDISEGLVNDFLKNFLELNLPKAS--KKKKVSLGVQDKNLATSIKSEID 110
Saccharomyces        FKGAAEALLENANDISEGLVSESLKAILDLNLPKASS-KKKNITLAI SDKNLGPSIKKEEFP 114
Homo                  FASSQVALENANAVSEGVVHEDLRLLETHLP-SK---KKKVLLGVGDPKIGAAIQEELG 115
D.subobscura         FKTAIAALENINAISEGIVPQDLLHFLDDFFAKLK--KKKCTLGIADAKLGAATEAIG 110
Sulfolobus           NS-----KDIGKVTEALIENEKGTPLPSAIELIN--KLKPDQVVVENDAIEVPALQKLG 78
                        : * : . : : : . : .
```



Arabidopsis-T6H22	-----GGEETDDGHSTKKK	514
Cicer arietinum	-----PSVDEGANGDSSKKK	444
Schizosaccharomyces	-----KKK	493
Saccharomyces	-----KKK	501
Homo	TAGSTSI PKRKKSTPKEETVNDPEEAGHR SRSKK RKF SKEEPVSSGPEEAVGKSSSKK	592
D.subobscura	-----KKK	494
Sulfolobus	-----	

Arabidopsis-T6H22	KKKSKSAE--	522
Cicer arietinum	KKKSKRMDVD	454
Schizosaccharomyces	KKSH-----	497
Saccharomyces	SKD-----	504
Homo	KKFKASQED	602
D.subobscura	NKNKEAVQA-	503
Sulfolobus	-----	

## NOP58 protein alignment

CLUSTAL W (1.81) Multiple Sequence Alignments

```
Sequence format is Pearson
Sequence 1: Arabidopsis-F108          533 aa
Sequence 2: Arabidopsis-T12H1       533 aa
Sequence 3: PeaSARBP1               560 aa
Sequence 4: PeaSARBP2               550 aa
Sequence 5: Oryza                   485 aa
Sequence 6: Homo                     529 aa
Sequence 7: Rattus                   534 aa
Sequence 8: D melanogaster           510 aa
Sequence 9: Schizosaccharomyces     508 aa
Sequence 10: Saccharomyces           504 aa
```

### Pairwise alignments

```
Sequences (1:2) Aligned. Score: 82
Sequences (4:5) Aligned. Score: 75
Sequences (3:4) Aligned. Score: 86
Sequences (2:3) Aligned. Score: 73
Sequences (1:3) Aligned. Score: 74
Sequences (3:5) Aligned. Score: 77
Sequences (4:6) Aligned. Score: 55
Sequences (2:4) Aligned. Score: 73
Sequences (1:4) Aligned. Score: 73
Sequences (2:5) Aligned. Score: 74
Sequences (3:6) Aligned. Score: 56
Sequences (4:7) Aligned. Score: 55
Sequences (1:5) Aligned. Score: 74
Sequences (2:6) Aligned. Score: 55
Sequences (3:7) Aligned. Score: 55
Sequences (4:8) Aligned. Score: 52
Sequences (1:6) Aligned. Score: 52
Sequences (2:7) Aligned. Score: 55
Sequences (3:8) Aligned. Score: 53
Sequences (4:9) Aligned. Score: 53
Sequences (1:7) Aligned. Score: 54
Sequences (2:8) Aligned. Score: 52
Sequences (3:9) Aligned. Score: 54
Sequences (4:10) Aligned. Score: 40
Sequences (1:8) Aligned. Score: 52
Sequences (2:9) Aligned. Score: 52
Sequences (3:10) Aligned. Score: 41
Sequences (5:6) Aligned. Score: 54
Sequences (1:9) Aligned. Score: 54
Sequences (2:10) Aligned. Score: 40
Sequences (6:7) Aligned. Score: 95
Sequences (5:7) Aligned. Score: 56
Sequences (1:10) Aligned. Score: 41
Sequences (7:8) Aligned. Score: 61
Sequences (6:8) Aligned. Score: 60
Sequences (8:9) Aligned. Score: 50
Sequences (5:8) Aligned. Score: 53
Sequences (7:9) Aligned. Score: 48
Sequences (6:9) Aligned. Score: 49
Sequences (8:10) Aligned. Score: 37
Sequences (5:9) Aligned. Score: 52
Sequences (7:10) Aligned. Score: 37
Sequences (6:10) Aligned. Score: 38
Sequences (9:10) Aligned. Score: 39
Sequences (5:10) Aligned. Score: 39
```

CLUSTAL W (1.81) multiple sequence alignment

```
Homo          ----MLVLFETSVDGYAIFKVLNE--KKLQEVDSLWKEFETPEKANKIVKLKHFEKFDQTA 54
Rattus        ----MLVLFETSVDGYAIFKVLNE--KKLQEVDSLWKEFETPEKANKIVKLKHFEKFDQTA 54
D melanogaster ----MFVLYETPAGYAIKLLDE--KKLEQVDNLYQEFETPEKANKLLKLKHFEKFDNTT 54
Arabidopsis-F108 ----MLILFETPGGFAIFKVLNE--GKLSNVEDLGNEFSTAKLARKMVKLVAFDKFDNTA 54
Arabidopsis-T12H1 ----MVLVLYETAAGFALFKVKDE--GKMANVEDLCKEFDTPDSARKMVKLKAFKFDNTS 55
```

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PeaSARBP1      ---MLVLFETPAGFALFKVLNE--GKLVSEVDLSLDFSTADAARKVVVKLKFASKFENTA 54
PeaSARBP2      ---MLLFFETAAGFALFKVLDE--GKLSKVEDLQQSFSSADTARKVVVKLKFASKFENTS 54
Oryza          ---MLVLFETPAGFALFKVLDE--GKLDKVEDLWKEFTTSDSARKVVVELKAFNKFENTS 54
Schizosaccharomyces ---MFILTTETAAGYAI FKAKD--KLLKRRDALIEDLKSPEGASNLKQSFAPKFESTV 53
Saccharomyces  MAPIEYLLFEEPTGYAVFKVKLQQDDIGSRLLKEVQEQINDFGAFTKLIELVSPAPFKGAA 60
                : * * . * : * : * . . : . : : : * * * * * :

Homo           EALAAFTALMEGKINKQLKKVLKK-IVKEAHE---PLAVADAKLGGVIKEK--LNLSCI 107
Rattus         EALAAFTALMEGKINKQLKKVLKK-IVKEAHE---PLAVADAKLGGVIKEK--LNLSCI 107
D melanogaster EALAAATAAVEGKVAKPLKKTLLKLLVDDVQS---SLLVADAKLGTAIKDK--LSVQCV 108
Arabidopsis-F108 EALEAVAKLLEGTSPSKGLRKFLLKA---NCVGE---TLAVADSKLGNIIKEK--LKIVCV 105
Arabidopsis-T12H1 EALEAVAKLLEGAPSKGLRKFLLKA---NCQGE---TLAVADSKLGNIIKEK--LKIDCI 106
PeaSARBP1      EALEAASCLIDGKTSKGLRKFLLRA---HCDE---ILAVADSKLGNIIKEK--LKIDCV 105
PeaSARBP2      EALKSANLLIDGKASKDLRKFLLSV---HCQNE---TLGVADTKLASIKEK--LQIDCV 105
Oryza          DALSAATLIIDSKPTKGLRKFLLQK---HCEGE---TLAVADSKLGNAIKEK--LKIDCL 105
Schizosaccharomyces DALDNVSALVEGKVSLLSLEGL-LSDSKSS---TLVVADPKLGNAINKPLGFEFII 108
Saccharomyces  EALENANDISEGLVSESLKAILDLNLPKASSKKKNITLAI SDKNLGPSTKEEF-PYVDCI 119
                : ** . : . * * . . . * : * : * . * : . :

Homo           HSPVVNELMRGIRSQMDGLIPGVEPREMAAMCLGLAHSLSRYRLKFSADKVDTMIVQAIS 167
Rattus         HSPVVNELMRGIRSQMDGLIPGVEPREMAAMCLGLAHSLSRYRLKFSADKVDTMIVQAIS 167
D melanogaster CNTGVQVELMRCIRQQADSLGGLPKREMTAMALGLAHSLSRYLKFSPDKIDTMIVQAOQ 168
Arabidopsis-F108 HNAVMEMLLRGIRSQDELISGLGDQDLGPMGLSHSLARYLKFSSDKVDTMIIQAIG 165
Arabidopsis-T12H1 HNAVMEMLLRGIRSQDELISGLGDQDLAPMSLGLSHSLARYLKFSSDKVDTMIIQAIG 166
PeaSARBP1      HNAVMEMLMRGVRVYQLTELSGLAVQDMAPMSLGLSHSLARYLKFSSDKVDTMIVQAIG 165
PeaSARBP2      HNVGVMELMRGVRVYQLTELSGLAVQDMAPMSLGLSHSLARYLKFSSDKVDTMIVQAIG 165
Oryza          HNSAVMEMLMRRLRNQLTELSGLGAQDLGPMGLSHSLARYLKFSSDKVDTMIIQAIG 165
Schizosaccharomyces SDSVQDLYRGI REHLSLSLGLAPSDDL NAMS LGLSHSLSRHKLKFS PDKVDTMIVQAIA 168
Saccharomyces  SNELAQDLIRGVR LHGEKLFKGLQSGDLERAQLGLGHAYSRAKVKFSVQKNDNHIIQAIA 179
                . . : * * : * : * : * : : : * * * . * : * : * * * : * * : * * :

Homo           LDDLDKELNNYIMRCREWYGWHFPELGIISDNLT YCKCLQKVGDRK---NYASAKLSE 224
Rattus         LDDLDKELNNYIMRCREWYGWHFPELGIISDNLT YCKCLQKVGDRK---NYASATLSE 224
D melanogaster LDDLDKELNNYMMRAREWYGWHFPELGIITDNIAFVKTIKLVGTRD---NMATSDLS 225
Arabidopsis-F108 LDDLDKELNTYAMRVREWYGWHFPELAKIVQDNILYAKAVKLMGNRI---NAAKLDSE 222
Arabidopsis-T12H1 LDDLDKELNTYAMRVREWYGWHFPELAKIISDNILYAKSVKLMGNRV---NAAKLDSE 223
PeaSARBP1      LDDLDKELNTYAMRVREWYGWHFPELTKIQDNIQYARSVKLMGDRI---NAAKLDSE 222
PeaSARBP2      LDDLDKELNTYAMRVREWYGWHFPELTKIILDNIQYAKAVKLMGDRI---NAAKLDSE 222
Oryza          LDDLDKELNTYAMRVREWYGWHFPELTKIVADNIQYAKVVKMMGDRI---NAESLDFSE 222
Schizosaccharomyces LDDLDKELNTYAMRVREWYGWHFPEMGI IQDNLAYARVIKAMGRT---KCESLDFSD 225
Saccharomyces  LLDQLDKDINTFAMRVREWYGWHFPELAKLV PDNYTF AKLVLF IKDKASLNDDSLHDLAA 239
                *** : *** : * : * : * : * : * : * : * : * : * : * : * : * : * : * :

Homo           LLP--EEVEAEVKAAAEISMGTEVSEEDICNIIHLCTQVIEISEYRTQLYEYLQNRMMAI 282
Rattus         FLS--EEVEAEVKAAAEISMGTEVSEEDICNIIHLCTQVIEISEYRTQLYEYLQNRMMAI 282
D melanogaster ILP--EDVEEKVKEAAEISMGTEI SEEDV LNIQCLCDEIISINDYRTHLYDYLKARMMAM 283
Arabidopsis-F108 ILA--DEIEAELKEAAVISMGT EVSDDL LLI RELCDQVLSLAEYRAQLYDYLKSRMNTI 280
Arabidopsis-T12H1 ILA--DEIEADLKAAVISMGT EVSDDL LLI RELCDQVLSLSEYRAQLYDYLKSRMNTI 281
PeaSARBP1      ILT--EEVEAEVKAAVISMGT EIGELDSLNI RELCDQVLSLSEYRAQLYDYLKSRMNTI 280
PeaSARBP2      ILS--EEVEAEVKEASVISMGT EIVTLDLENIREL CDQVLSLSEYRAQLYDYLKSRMNTI 280
Oryza          ILS--DEVEAQLKEAAVISMGT EVELDLNIREL CDQVLSLSEYRAQLYDYLRSMNTI 281
Schizosaccharomyces ILP--EEIEATLKSAAEISMGT EIT EEDLDNI VMLADQVLELASYRAQLSEYLRNRMQAI 283
Saccharomyces  LLNEDSGIAQRVIDNARISMGTQD ISETDMENVCVFAQRVASLADYRRQLYDYLCEKMHVT 299
                : * . : : : * * * : : * : : : . : : * * : * * : * : * :

```



Query: gij11878185 NOP58-like protein F108 [Arabidopsis thaliana]

Lineage: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis  
 COG1498 assigned by Cognitor (7 best hits)

Hits   
  Clustal Tree   
  Taxonomy Report   
  3D Structures   
  JDD Search   
  GList

139 BLAST hits to 41 unique species Sort by taxonomy proximity

11 Archaea   
  4 Bacteria   
  84 Metazoa   
  Fungi   
  23 Plants   
  Viruses   
  Other Eukaryotae

Keep only  Cut-Off

533 aa

SCORE	F	P	ACCESSION	GI	PROTEIN DESCRIPTION
2224	19		6729016	2191188	similar to S. cerevisiae SIK1P (FID:g984964) [Arabi
2155	19		AAB61073	3132696	SAR DNA-binding protein-1 [Pisum sativum]
2002	14		AAC16330	3132698	SAR DNA-binding protein-2 [Pisum sativum]
1956	14		AAC16331	3288883	SAR DNA binding protein [Oryza sativa]
1819	11		BAA31260	4680298	nucleolar protein NOP5/NOP58 [Homo sapiens]
1401	3		AAD27610	6180063	Nopp140 associated protein [Rattus norvegicus]
1394	3		AAF05769	10728627	nop5 gene product [Drosophila melanogaster]
1327	3		AAF52455	6433838	DNop5 protein [Drosophila melanogaster]
1317	3		CAB60723	3219757	unknown [Rattus sp.]
1313	3		AAC23535	5912090	hypothetical protein [Homo sapiens]
1298	3		CAB55989	6912023	similar to yeast nucleolar protein Nop5p involved i
1255	3		CAB72231	2996194	SIK similar protein [Mus musculus]
1233	3		AAC08435	2191189	similar to S. cerevisiae SIK1P (PID:g984964) [Arabi
1227	19		AAB61074	2804491	contains similarity to S. cerevisiae Prp31p (GB:U31
1217	3		AAB97597	940841	orf 06108 [Saccharomyces cerevisiae]
1169	3		CAA62165	6841462	HSPC120 [Homo sapiens]
1093	3		AAF29084	6056371	nucleolar protein [Arabidopsis thaliana]
982	19		AAF02835	544506	Sik1p [Saccharomyces cerevisiae]
928	3		AAB67431		



909	BAB02430	11994428	nucleolar protein [Arabidopsis thaliana]
888	CAA72789	2230878	hNop56 [Homo sapiens]
885	XP_009574	11421205	nucleolar protein (KKE/D repeat) [Homo sapiens]
868	BAB26511	12844818	putative [Mus musculus]
867	CAB92783	8218021	nucleolar protein [Drosophila subobscura]
857	AAF55992	7300850	CG13849 gene product [Drosophila melanogaster]
844	CAA10127	3860319	nucleolar protein [Cicer arietinum]
843	CAA22814	4160346	probable involvement in pre-rRNA processing; putati
764	Q21276	2833309	HYPOTHETICAL 54.5 KD PROTEIN K07C5.4 IN CHROMOSOME
674	BAB27647	12847633	putative [Mus musculus]
614	CAC26989	12580672	putative SAR DNA-binding protein-1 [Guillardia thet
500	AAF69253	7769122	NOP56 homolog [Sulfolobus acidocaldarius]
461	AAB98689	1591409	conserved hypothetical protein [Methanococcus janna
453	CAC23263	12312401	pre-mRNA splicing protein [Sulfolobus solfataricus]
449	BAA81210	5105898	423aa long hypothetical nucleolar protein [Pyrococcus horikos
446	BAA29121	3256438	404aa long hypothetical protein [Pyrococcus abyssi]
433	CAB48984	5457493	hypothetical protein [Pyrococcus abyssi]
376	AAB85703	2622324	pre-mRNA splicing protein PRP31 [Methanothermobacte
330	AAG48270	12060857	serologically defined breast cancer antigen NY-BR-9
324	AAF49655	7294306	CG6876 gene product [Drosophila melanogaster]
322	CAB43677	4914604	hypothetical protein [Homo sapiens]
315	CAC00186	9558060	probable sar DNA-binding protein-1 [Leishmania majo
271	AAF60425	7331737	contains similarity to Saccharomyces cerevisiae p1c-
271	AAC24050	3249066	Similar to S. cerevisiae SIK1P protein gb 984964.
271	CAA17928	2959374	splicing factor required for vegetative and meioti
254	CAA76147	2808688	orf169 [Methanosarcina mazei]
238	CAB62868	8248751	conserved hypothetical protein, MAL4P2.27 [Plasmodi
225	AAG19551	10580709	archaeal nucleolar protein homolog; Nop56/58 [Halob
210	CAC12367	10640589	nucleolar protein Nop56 related protein [Thermoplas
187	AAB89168	2648446	conserved hypothetical protein [Archaeoglobus fulgi
184	CAB82665	7329671	putative protein [Arabidopsis thaliana]
173	CAA97094	1323135	ORF YGR091w [Saccharomyces cerevisiae]
170	AAA74984	969101	Prp3lp [Saccharomyces cerevisiae]
145	CAC26930	3329623	F36H12.3 gene product [Caenorhabditis elegans]
138	CAB07640	3878632	Similarity to Human DNA topoisomerase I (SW:P11387)
136	AAC25885	1699079	similar to C. elegans UNC-89 (EMBL:G1160355) and ti
134	S65469	2133452	DNA topoisomerase (EC 5.99.1.2) - Caenorhabditis el
134	CAA65537	1934847	DNA topoisomerase; DNA topoisomerase I [Caenorhabdi
129	BAB11589	10178144	gene id:MPO12.6-unknown protein [Arabidopsis thalia
128	AAB42334	1825739	t23B3.5 gene product [Caenorhabditis elegans]

<u>126</u>	<u>3</u>	<u>AAB40347</u>	<u>11117968</u>	<u>CARS-Cyp [Homo sapiens]</u>
<u>126</u>	<u>3</u>	<u>S43604</u>	<u>630724</u>	<u>R07E5.1 protein (clone R07E5) - Caenorhabditis eleg</u>
<u>125</u>	<u>3</u>	<u>CAB04326</u>	<u>3876805</u>	<u>contains similarity to Pfam domain: PF00533 (BRCA1</u>
<u>124</u>	<u>3</u>	<u>AAC04447</u>	<u>2911882</u>	<u>W09G12.7 gene product [Caenorhabditis elegans]</u>
<u>124</u>	<u>3</u>	<u>CAA80456</u>	<u>396151</u>	<u>cylacin [Bos taurus]</u>
<u>124</u>	<u>3</u>	<u>CAA80457</u>	<u>396105</u>	<u>cylacin [Homo sapiens]</u>
<u>122</u>	<u>3</u>	<u>CAA44805</u>	<u>64937</u>	<u>nucleolin [Xenopus laevis]</u>
<u>119</u>	<u>1</u>	<u>AAC95573</u>	<u>4019275</u>	<u>orf 48 [Ateline herpesvirus 3]</u>
<u>119</u>	<u>3</u>	<u>AAC64862</u>	<u>2258455</u>	<u>centromere-binding factor 5 [Kluyveromyces lactis]</u>
<u>118</u>	<u>3</u>	<u>AAF47885</u>	<u>7292482</u>	<u>CG1326 gene product [Drosophila melanogaster]</u>
<u>118</u>	<u>3</u>	<u>CAA38647</u>	<u>63165</u>	<u>CAP-23 protein [Gallus gallus]</u>
<u>116</u>	<u>3</u>	<u>AAC00191</u>	<u>2828710</u>	<u>matrin cyclophilin [Rattus norvegicus]</u>
<u>115</u>	<u>3</u>	<u>CAB11112</u>	<u>4725982</u>	<u>predicted using hexExon; MAL3P3.12 (PFC0385c), Seri</u>
<u>115</u>	<u>2</u>	<u>AAC34964</u>	<u>3560497</u>	<u>ElpB2 [Borrelia burgdorferi]</u>
<u>115</u>	<u>3</u>	<u>CAA87454</u>	<u>854353</u>	<u>neurofilament protein M [Oryctolagus cuniculus]</u>
<u>115</u>	<u>3</u>	<u>CAA86752</u>	<u>758587</u>	<u>human cylacin II [Homo sapiens]</u>
<u>115</u>	<u>3</u>	<u>CAA86753</u>	<u>757754</u>	<u>cylacin II [Bos taurus]</u>
<u>115</u>	<u>3</u>	<u>AAA37761</u>	<u>418022</u>	<u>histone H1 [Mus musculus]</u>
<u>115</u>	<u>3</u>	<u>A43427</u>	<u>284667</u>	<u>neurofilament triplet H1 protein - rabbit (fragment</u>
<u>114</u>	<u>3</u>	<u>AAF13722</u>	<u>6470331</u>	<u>neurofilament protein [Homo sapiens]</u>
<u>114</u>	<u>3</u>	<u>AAB47593</u>	<u>4850185</u>	<u>C16A3.8 gene product [Caenorhabditis elegans]</u>
<u>114</u>	<u>3</u>	<u>BAA74868</u>	<u>4240179</u>	<u>K1AA0845 protein [Homo sapiens]</u>
<u>114</u>	<u>3</u>	<u>QFHUH</u>	<u>71549</u>	<u>neurofilament triplet H protein - human</u>
<u>113</u>	<u>11</u>	<u>AAG46137</u>	<u>12039350</u>	<u>putative centromere/microtubule binding protein [Or</u>
<u>112</u>	<u>3</u>	<u>CAA86428</u>	<u>3877386</u>	<u>alternatively spliced, the alternatively spliced re</u>
<u>112</u>	<u>3</u>	<u>CAA86427</u>	<u>3877385</u>	<u>cDNA EST yk227g6.5 comes from this gene-cDNA EST yk</u>
<u>112</u>	<u>3</u>	<u>CAA86426</u>	<u>3877384</u>	<u>cDNA EST yk171f11.3 comes from this gene-cDNA EST y</u>
<u>112</u>	<u>3</u>	<u>CAA86425</u>	<u>3877383</u>	<u>cDNA EST yk171f11.5 comes from this gene-cDNA EST y</u>
<u>112</u>	<u>3</u>	<u>S51364</u>	<u>2133632</u>	<u>sperm tail-specific protein mst101(2) - fruit fly</u>
<u>112</u>	<u>3</u>	<u>CAA51876</u>	<u>313202</u>	<u>mst101(2) [Drosophila hydei]</u>
<u>111</u>	<u>3</u>	<u>BAB23689</u>	<u>12836514</u>	<u>putative [Mus musculus]</u>
<u>111</u>	<u>19</u>	<u>BAA97183</u>	<u>8809632</u>	<u>RNA helicase [Arabidopsis thaliana]</u>
<u>111</u>	<u>19</u>	<u>CAA68194</u>	<u>1488521</u>	<u>RNA helicase [Arabidopsis thaliana]</u>
<u>111</u>	<u>3</u>	<u>AAA28192</u>	<u>289753</u>	<u>homology with nucleolin protein; putative [Caenorha</u>
<u>109</u>	<u>19</u>	<u>AAC18800</u>	<u>3176677</u>	<u>Similar to S. cerevisiae SIK1P protein, A_TM021B04.</u>
<u>108</u>	<u>3</u>	<u>CAA83229</u>	<u>463250</u>	<u>Neurofilament protein, high molecular weight subuni</u>
<u>108</u>	<u>3</u>	<u>A43778</u>	<u>110743</u>	<u>neurofilament triplet H protein - mouse</u>
<u>108</u>	<u>3</u>	<u>QFM5H</u>	<u>71550</u>	<u>neurofilament triplet H protein - mouse</u>
<u>107</u>	<u>3</u>	<u>XP_002501</u>	<u>12728621</u>	<u>Clk-associated RS-cyclophilin [Homo sapiens]</u>
<u>107</u>	<u>3</u>	<u>AAF54409</u>	<u>7299212</u>	<u>CG8273 gene product [Drosophila melanogaster]</u>

107	3	CAB65108	6688177	DIPB protein [Homo sapiens]
107	3	AA554132	2088675	C. elegans UNC-89 (GB:U33058) (NID:g1160355) [Caeno
107	3	AA000542	1160355	UNC-89 [Caenorhabditis elegans]
107	3	AAA57153	601931	neurofilament-H [Oryctolagus cuniculus]
107	3	B43427	284668	neurofilament protein H form H2 (repetitive region)
107	3	AA29732	160603	acidic phosphoprotein [Plasmodium chabaudi]
106	3	AAC18442	3172248	topoisomerase I [Cryptococcus neoformans var. grubi
105	19	AAG51793	12323660	cytosolic factor, putative; 12503-14597 [Arabidopsi
105	3	AAF47596	7292185	CG1017 gene product [Drosophila melanogaster]
105	3	CAB63306	6580235	predicted using GeneFinder-cDNA EST yk69h12.3 comes
105	3	AA933453	861278	C17G10.6 [Caenorhabditis elegans]
104	3	AAH00755	12653923	Similar to hepatoma-derived growth factor, related
104	3	AAF51175	7295875	Rrp1 gene product [Drosophila melanogaster]
104	19	AA39661	5103831	ESTs gb H37032, gb R6425, gb Z34651, gb N37268, gb
104	19	CAB43859	4938501	putative protein [Arabidopsis thaliana]
104	3	F27864	133504	RECOMBINATION REPAIR PROTEIN 1 (DNA-(APURINIC OR AP
103	3	AAF46594	7291160	PPP4R2r gene product [Drosophila melanogaster]
103	3	P41891	6226864	GAR2 PROTEIN
103	3	CAA88179	663262	gar2 [Schizosaccharomyces pombe]
102	19	AAG52578	12325271	hypothetical protein; 39633-44904 [Arabidopsis thal
102	3	AAG48509	12232320	hUPF2 [Homo sapiens]
101	2	AAF73814	8163709	surface protein PspC [Streptococcus pneumoniae]
101	2	AAF73788	8163661	surface protein PspC [Streptococcus pneumoniae]
101	19	CAB38930	4490727	putative protein [Arabidopsis thaliana]
101	3	AAA36966	387050	nucleolin, C23 [Cricetulus griseus]
101	3	P08199	128842	NUCLEOLIN (PROTEIN C23)
101	3	A27441	90209	nucleolin - Chinese hamster
100	3	BAB28490	12849811	putative [Mus musculus]
100	3	AAH02181	12805417	Unknown (protein for MGC:7354) [Mus musculus]
100	3	AA56625	5929884	nucleolin-related protein NRP [Rattus norvegicus]
100	14	AAC49447	1480457	latex allergen [Hevea brasiliensis]



942	3	AAB67431	544506	Sik1p [Saccharomyces cerevisiae]
930	19	BAB02430	11994428	nucleolar protein [Arabidopsis thaliana]
911	3	CAA72789	2230878	hNop56 [Homo sapiens]
907	3	XP_009574	11421205	nucleolar protein (KKE/D repeat) [Homo sapiens]
900	3	BAB26511	12844818	putative [Mus musculus]
895	3	CAB92783	8218021	nucleolar protein [Drosophila subobscura]
864	3	CAA22814	4160346	probable involvement in pre rRNA processing; putati
851	14	CAA10127	3860319	nucleolar protein [Cicer arietinum]
823	3	AAF55992	7300850	CG13849 gene product [Drosophila melanogaster]
789	3	Q21276	2833309	HYPOTHETICAL 54.5 KD PROTEIN K07C5.4 IN CHROMOSOME
697	3	BAB27647	12847633	putative [Mus musculus]
611	3	CAC26989	12580672	putative SAR DNA-binding protein-1 [Guillardia thet
492	2	AAF69253	7769122	NOP56 homolog [Sulfolobus acidocaldarius]
469	2	AAB98689	1591409	conserved hypothetical protein [Methanococcus janna
444	2	BAA81210	5105898	423aa long hypothetical nucleolar protein NOP5 [Aer
434	2	CAB48984	3256438	404aa long hypothetical protein [Pyrococcus horikos
369	2	AAB85703	5457493	hypothetical protein [Pyrococcus abyssii]
343	3	AAG48270	2622324	pre-mRNA splicing protein PRP31 [Methanothermobacte
337	3	AAF49655	12060857	serologically defined breast cancer antigen NY-BR-9
335	3	CAB43677	7294306	CG6876 gene product [Drosophila melanogaster]
314	3	CAC00186	4914604	hypothetical protein [Homo sapiens]
285	3	AAF60425	9558060	probable sar DNA-binding protein-1 [Leishmania majo
279	3	CAA17928	7331737	contains similarity to Saccharomyces cerevisiae pre-
270	19	AAC24050	2959374	splicing factor required for vegetative and meioti
260	2	CAA76147	3249066	Similar to S. cerevisiae SIK1P protein gb 984964.
251	3	CAB62868	2808688	orf169 [Methanosarcina mazei]
234	2	AAG19551	8248751	conserved hypothetical protein, MAL4P2.27 [Plasmodi
195	2	CAC12367	10580709	archaeal nucleolar protein homolog; Nop56/58 [Halob
193	3	AAA74984	10640589	nucleolar protein Nop56 related protein [Thermoplas
190	19	CAB82665	969101	Prp31p [Saccharomyces cerevisiae]
183	3	CAA97094	7329671	putative protein [Arabidopsis thaliana]
167	2	AAB89168	1323135	ORF YGR091w [Saccharomyces cerevisiae]
150	3	AAF59460	2648446	conserved hypothetical protein [Archaeoglobus fulgi
149	3	AAC26930	7322701	contains similarity to TR:Q10466 [Caenorhabditis el
141	3	AAF36065	3329623	F36H12.3 gene product [Caenorhabditis elegans]
140	3	AAG14291	7105679	Hypothetical protein Y76B12C.4 [Caenorhabditis eleg
137	2	AAF73814	10180804	glutamic acid-rich protein [Plasmodium falciparum]
137	2	AAF73788	8163709	surface protein PspC [Streptococcus pneumoniae]
136	3	AAF57445	8163661	surface protein PspC [Streptococcus pneumoniae]
			7302356	CG11180 gene product [Drosophila melanogaster]

132	19	BAB11589	10178144	gene_id:MPO12.6-unknown protein [Arabidopsis thaliana]
131	3	BAB23689	12836514	putative [Mus musculus]
130	3	AAD55361	5901659	XNP-1 [Caenorhabditis elegans]
130	3	AAC24256	3253105	strong similarity to the SNF2/RAD54 family of helicases
130	3	B43427	284668	neurofilament protein H form H2 (repetitive region)
129	3	AAA57153	601931	neurofilament-H [Oryctolagus cuniculus]
128	3	CAA86753	757754	cylicin II [Bos taurus]
127	2	AAF73812	8163705	surface protein PspC [Streptococcus pneumoniae]
126	2	AAF73798	8163680	surface protein PspC [Streptococcus pneumoniae]
126	2	AAF73790	8163664	surface protein PspC [Streptococcus pneumoniae]
126	3	AAB53878	1703550	weak similarity human to LINE-1 reverse transcriptase
125	2	AAF73811	8163703	surface protein PspC [Streptococcus pneumoniae]
125	2	AAF73807	8163695	surface protein PspC [Streptococcus pneumoniae]
125	2	AAF73786	8163657	surface protein PspC [Streptococcus pneumoniae]
124	3	AAC25885	1699079	similar to C. elegans UNC-89 (EMBL:G1160355) and tRNA
123	2	AAF73792	8163668	surface protein PspC [Streptococcus pneumoniae]
123	2	AAF73781	8163648	surface protein PspC [Streptococcus pneumoniae]
123	2	AAF73780	8163646	surface protein PspC [Streptococcus pneumoniae]
123	3	CAA38647	63165	CAP-23 protein [Gallus gallus]
122	2	AAC34964	3560497	ElpB2 [Borrelia burgdorferi]
120	2	AAF73796	8163676	surface protein PspC [Streptococcus pneumoniae]
118	3	AAF51535	10727421	spen gene product [alt 1] [Drosophila melanogaster]
118	3	AAF51534	10727420	spen gene product [alt 2] [Drosophila melanogaster]
118	3	AAF48098	7292701	CG1905 gene product [Drosophila melanogaster]
118	3	AAF34661	6979936	split ends long isoform [Drosophila melanogaster]
117	3	O97159	13124018	CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN MI-2 HOMO
116	19	BAB10448	10177036	emb CAB62360.1~gene_id:MLE2.18~strong similarity to
116	2	AAF73779	8163644	surface protein PspC [Streptococcus pneumoniae]
115	3	AAF82247	8979462	junction isoform 1 [Homo sapiens]
115	3	AAF82246	8979460	junction [Homo sapiens]
115	2	AAF73799	8163682	surface protein PspC [Streptococcus pneumoniae]
115	2	AAF73797	8163678	surface protein PspC [Streptococcus pneumoniae]
114	3	AAF57130	10726888	CG15561 gene product [Drosophila melanogaster]
114	2	AAF73810	8163701	surface protein PspC [Streptococcus pneumoniae]
113	19	BAB09233	9758600	gene_id:MDF20.10~pir T08929~similar to unknown protein
113	3	AAF43448	7243779	RNA polymerase I transcription termination factor 1
113	2	AAF40845	7225628	conserved hypothetical protein [Neisseria meningitidis]
113	3	AAB04133	1438951	cutinase negative acting protein [Fusarium solani f. sp. phaseolae]
112	2	AAF73822	8163720	surface protein PspC [Streptococcus pneumoniae]
112	3	CAA86428	3877386	alternatively spliced, the alternatively spliced re

<u>112</u>	<u>3</u>	<u>CAA86427</u>	<u>3877385</u>	<u>CDNA EST yk227g6.5</u>	<u>comes from this gene-cDNA EST yk</u>
<u>112</u>	<u>3</u>	<u>CAA86426</u>	<u>3877384</u>	<u>CDNA EST yk171f11.3</u>	<u>comes from this gene-cDNA EST y</u>
<u>112</u>	<u>3</u>	<u>CAA86425</u>	<u>3877383</u>	<u>CDNA EST yk171f11.5</u>	<u>comes from this gene-cDNA EST y</u>
<u>110</u>	<u>3</u>	<u>BAB31699</u>	<u>12859577</u>	<u>putative [Mus musculus]</u>	
<u>110</u>	<u>19</u>	<u>AAF24557</u>	<u>10764865</u>	<u>FK23.4 [Arabidopsis thaliana]</u>	
<u>110</u>	<u>2</u>	<u>AAF13459</u>	<u>6469853</u>	<u>unknown [Streptococcus pneumoniae]</u>	
<u>110</u>	<u>19</u>	<u>AAC18800</u>	<u>3176677</u>	<u>Similar to S. cerevisiae SIKIP protein, A_TM021B04.</u>	
<u>110</u>	<u>3</u>	<u>CAB09575</u>	<u>2315159</u>	<u>caldesmon [Bos taurus]</u>	
<u>110</u>	<u>3</u>	<u>S43604</u>	<u>630724</u>	<u>R07E5.1 protein (clone R07E5) - Caenorhabditis eleg</u>	
<u>109</u>	<u>3</u>	<u>AAF75554</u>	<u>8468621</u>	<u>mature parasite-infected erythrocyte surface antige</u>	
<u>109</u>	<u>3</u>	<u>AAC00191</u>	<u>2828710</u>	<u>matrin cyclophilin [Rattus norvegicus]</u>	
<u>109</u>	<u>3</u>	<u>CAA53418</u>	<u>433643</u>	<u>D738; glutenin, high molecular weight chain homolog</u>	
<u>108</u>	<u>3</u>	<u>AAF54511</u>	<u>10726425</u>	<u>CG3996 gene product [Drosophila melanogaster]</u>	
<u>108</u>	<u>3</u>	<u>AAF51175</u>	<u>7295875</u>	<u>Rp1 gene product [Drosophila melanogaster]</u>	
<u>108</u>	<u>3</u>	<u>BAA91162</u>	<u>7020518</u>	<u>unnamed protein product [Homo sapiens]</u>	
<u>108</u>	<u>3</u>	<u>A40988</u>	<u>105148</u>	<u>54K arginine-rich nuclear protein - human</u>	
<u>107</u>	<u>19</u>	<u>BAB03174</u>	<u>11994784</u>	<u>gene_id:T19N8.6-unknown protein [Arabidopsis thalia</u>	

Query: gij11878189 NOP56-like protein [Arabidopsis thaliana]

Matching gi: 6056371

Lineage: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis  
 COG1498 assigned by Cognitor (7 best hits)

All   
  Common Tree   
  Taxonomy Report   
  3D structures   
  CDD Search   
  GI list

154 BLAST hits to 38 unique species Sort by taxonomy proximity

11 Archaea   
 2 Bacteria   
 80 Metazoa   
 20 Fungi   
 14 Plants   
 0 Viruses   
 27 Other Eukaryotae

Keep only  Cut-Off

522 aa	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
	2171	19	BAB02430	11994428	nucleolar protein [Arabidopsis thaliana]
	1655	14	CAA10127	3860319	nucleolar protein [Cicer arietinum]
	1420	3	CAA22814	4160346	probable involvement in pre rRNA processing; putati
	1351	3	CAA72789	2230878	hNop56 [Homo sapiens]
	1344	3	XP_009574	11421205	nucleolar protein (KKE/D repeat) [Homo sapiens]
	1342	3	BAB26511	12844818	putative [Mus musculus]
	1307	3	CAB92783	8218021	nucleolar protein [Drosophila subobscura]
	1280	3	AAF55992	7300850	CG13849 gene product [Drosophila melanogaster]
	1258	3	AAB67431	544506	Sik1p [Saccharomyces cerevisiae]
	1172	3	Q21276	2833309	HYPOTHETICAL 54.5 KD PROTEIN K07C5.4 IN CHROMOSOME
	982	19	AAG40836	11878185	NOP58-like protein F108 [Arabidopsis thaliana]
	977	19	6729016		
	975	14	AAC16331	3132698	SAR DNA-binding protein-2 [Pisum sativum]
	951	3	CAB72231	6912023	similar to yeast nucleolar protein Nop5p involved i
	942	14	AAC16330	3132696	SAR DNA-binding protein-1 [Pisum sativum]
	934	3	BAB27647	12847633	putative [Mus musculus]
	896	11	BAA31260	3288883	SAR DNA binding protein [Oryza sativa]
	894	3	AAD27610	4680298	nucleolar protein NOP5/NOP58 [Homo sapiens]



888	3	AAF05769	6180063	Nopp140 associated protein [Rattus norvegicus]
876	3	AAF52455	10728627	nop5 gene product [Drosophila melanogaster]
871	3	CAB60723	6433838	DNop5 protein [Drosophila melanogaster]
870	19	AAB61073	2191188	similar to S. cerevisiae SIK1P (PID:g984964) [Arabi
869	3	CAA62165	940841	orf 06108 [Saccharomyces cerevisiae]
847	3	AAC23535	3219757	unknown [Rattus sp.]
825	3	AAB97597	2804491	contains similarity to S. cerevisiae Prp31p (GB:U31
811	3	CAB55989	5912090	hypothetical protein [Homo sapiens]
756	3	AAC08435	2996194	SIK similar protein [Mus musculus]
743	3	AAF29084	6841462	HSPC120 [Homo sapiens]
636	19	AAB61074	2191189	similar to S. cerevisiae SIK1P (PID:g984964) [Arabi
528	2	AAF69253	7769122	NOP56 homolog [Sulfolobus acidocaldarius]
526	2	CAC23263	12312401	pre-mRNA splicing protein [Sulfolobus solfataricus]
516	2	BAA81210	5105898	423aa long hypothetical nucleolar protein NOP5 [Aer
502	2	BAA29121	3256438	404aa long hypothetical protein [Pyrococcus horikos
493	2	CAB48984	5457493	hypothetical protein [Pyrococcus abyssi]
491	3	CAC26989	12580672	putative SAR DNA-binding protein-1 [Guillardia thet
468	2	AAB98689	1591409	conserved hypothetical protein [Methanococcus janna
386	2	AAB85703	2622324	pre-mRNA splicing protein PRP31 [Methanothermobacte
293	3	CAB43677	4914604	hypothetical protein [Homo sapiens]
286	3	CAC00186	9558060	probable sar DNA-binding protein-1 [Leishmania majo
278	3	AAG48270	12060857	serologically defined breast cancer antigen NY-BR-9
275	2	CAA76147	2808688	orf169 [Methanosarcina mazei]
259	3	AAF49655	7294306	CG6876 gene product [Drosophila melanogaster]
252	3	CAA17928	2959374	splicing factor required for vegetative and meioti
242	2	AAB89168	2648446	conserved hypothetical protein [Archaeoglobus fulgi
236	2	CAC12367	10640589	nucleolar protein Nop56 related protein [Thermoplas
233	2	AAG19551	10580709	archaeal nucleolar protein homolog; Nop56/58 [Halob
224	3	AAF60425	7331737	contains similarity to Saccharomyces cerevisiae pre-
203	3	CAB62868	8248751	conserved hypothetical protein, MAL4P2.27 [Plasmodi
197	19	AAC24050	3249066	Similar to S. cerevisiae SIK1P protein gb 984964.
171	19	CAB82665	7329671	putative protein [Arabidopsis thaliana]
171	3	CAA97094	1323135	ORF YGR091w [Saccharomyces cerevisiae]
171	3	AAA74984	969101	Prp31p [Saccharomyces cerevisiae]
148	2	AAC07794	2984268	initiation factor IF-2 [Aquifex aeolicus]
145	11	AAG46137	12039350	putative centromere/microtubule binding protein [Or
144	3	CAA04133	2292986	cyclic nucleotide-gated channel beta subunit [Rattu
143	3	CAA82046	2980817	ORF YKL201c [Saccharomyces cerevisiae]
143	3	BAA11676	1752736	gene required for phosphorylation of oligosaccharide
143	3	S38038	539218	hypothetical protein YKL201c - yeast [Saccharomyces

<u>140</u>	<u>3</u>	<u>AAC26930</u>	<u>3329623</u>	<u>F36H12.3</u>	<u>gene product [Caenorhabditis elegans]</u>
<u>139</u>	<u>3</u>	<u>CAA93085</u>	<u>3878378</u>	<u>predicted using Genefinder</u>	<u>[Caenorhabditis elegans]</u>
<u>137</u>	<u>3</u>	<u>AAB42258</u>	<u>1825636</u>	<u>ZK354.3</u>	<u>gene product [Caenorhabditis elegans]</u>
<u>136</u>	<u>3</u>	<u>AAC17524</u>	<u>3158469</u>	<u>C35E7.9</u>	<u>gene product [Caenorhabditis elegans]</u>
<u>134</u>	<u>3</u>	<u>AAD55361</u>	<u>5901659</u>	<u>XNP-1</u>	<u>[Caenorhabditis elegans]</u>
<u>134</u>	<u>3</u>	<u>AAC24256</u>	<u>3253105</u>	<u>strong similarity to the SNF2/RAD54</u>	<u>family of helic</u>
<u>131</u>	<u>3</u>	<u>AAC14193</u>	<u>2642493</u>	<u>DNA topoisomerase I</u>	<u>[Physarum polycephalum]</u>
<u>129</u>	<u>19</u>	<u>AAD25853</u>	<u>4587683</u>	<u>hypothetical protein</u>	<u>[Arabidopsis thaliana]</u>
<u>129</u>	<u>3</u>	<u>AA83358</u>	<u>1118176</u>	<u>Contains similarity to Pfam domain: PF00385</u>	<u>(chromo</u>
<u>127</u>	<u>3</u>	<u>AAG22857</u>	<u>11496167</u>	<u>RPGR-interacting protein</u>	<u>[Mus musculus]</u>
<u>127</u>	<u>3</u>	<u>CAB02877</u>	<u>3875441</u>	<u>predicted using Genefinder</u>	<u>[Caenorhabditis elegans]</u>
<u>127</u>	<u>3</u>	<u>A33430</u>	<u>104684</u>	<u>h-caldesmon - chicken</u>	
<u>126</u>	<u>3</u>	<u>AAC71942</u>	<u>3845272</u>	<u>hypothetical protein</u>	<u>[Plasmodium falciparum]</u>
<u>126</u>	<u>3</u>	<u>AAC36357</u>	<u>3641350</u>	<u>neurofilament-M subunit</u>	<u>[Bos taurus]</u>
<u>126</u>	<u>3</u>	<u>AAA80106</u>	<u>632549</u>	<u>NF-180</u>	<u>[Petromyzo marinus]</u>
<u>125</u>	<u>3</u>	<u>CAA61769</u>	<u>1050441</u>	<u>240K protein of rod photoreceptor cng-channel</u>	<u>[Bos</u>
<u>123</u>	<u>3</u>	<u>S65469</u>	<u>2133452</u>	<u>DNA topoisomerase (EC 5.99.1.2) - Caenorhabditis el</u>	
<u>123</u>	<u>3</u>	<u>AAC25849</u>	<u>1255424</u>	<u>C33G8.3</u>	<u>gene product [Caenorhabditis elegans]</u>
<u>122</u>	<u>3</u>	<u>CAB44357</u>	<u>5002645</u>	<u>IF2 protein</u>	<u>[Homo sapiens]</u>
<u>122</u>	<u>3</u>	<u>AAD16006</u>	<u>4322304</u>	<u>translation initiation factor IF2</u>	<u>[Homo sapiens]</u>
<u>122</u>	<u>3</u>	<u>BAA34461</u>	<u>3882203</u>	<u>KIAA0741 protein</u>	<u>[Homo sapiens]</u>
<u>121</u>	<u>3</u>	<u>AAF75554</u>	<u>8468621</u>	<u>mature parasite-infected erythrocyte surface antige</u>	
<u>121</u>	<u>3</u>	<u>S78045</u>	<u>7494167</u>	<u>erythrocyte membrane-associated antigen (clone pPF</u>	
<u>121</u>	<u>3</u>	<u>AAF49848</u>	<u>7294506</u>	<u>CG11274</u>	<u>gene product [Drosophila melanogaster]</u>
<u>121</u>	<u>3</u>	<u>AAD47903</u>	<u>5714396</u>	<u>unconventional myosin heavy chain MyoM</u>	<u>[Dictyosteli</u>
<u>121</u>	<u>3</u>	<u>CAB07639</u>	<u>3878631</u>	<u>Similarity to Human DNA topoisomerase I (SW:P11387)</u>	
<u>121</u>	<u>3</u>	<u>AAC64862</u>	<u>2258455</u>	<u>centromere-binding factor 5</u>	<u>[Kluyveromyces lactis]</u>
<u>120</u>	<u>3</u>	<u>AAF57445</u>	<u>7302356</u>	<u>CG11180</u>	<u>gene product [Drosophila melanogaster]</u>
<u>120</u>	<u>3</u>	<u>AAC13303</u>	<u>3044185</u>	<u>mature parasite-infected erythrocyte surface antige</u>	
<u>120</u>	<u>3</u>	<u>AAB53390</u>	<u>2062611</u>	<u>middle molecular weight neurofilament protein NF-M</u>	<u>(</u>
<u>120</u>	<u>3</u>	<u>AAB53389</u>	<u>2062609</u>	<u>middle molecular weight neurofilament protein NF-M</u>	<u>(</u>
<u>120</u>	<u>3</u>	<u>AAA57153</u>	<u>601931</u>	<u>neurofilament-H</u>	<u>[Oryctolagus cuniculus]</u>
<u>120</u>	<u>3</u>	<u>A40437</u>	<u>108693</u>	<u>glutamic acid-rich protein, retinal - bovine</u>	
<u>119</u>	<u>3</u>	<u>AAF51175</u>	<u>7295875</u>	<u>Rrp1</u>	<u>gene product [Drosophila melanogaster]</u>
<u>119</u>	<u>3</u>	<u>AAC71938</u>	<u>3845266</u>	<u>hypothetical protein</u>	<u>[Plasmodium falciparum]</u>
<u>119</u>	<u>3</u>	<u>AAC06245</u>	<u>2981173</u>	<u>neurofilament medium subunit</u>	<u>[Serinus canaria]</u>
<u>119</u>	<u>3</u>	<u>P02547</u>	<u>1709259</u>	<u>NEUROFILAMENT TRIPLET L PROTEIN</u>	<u>(68 KDA NEUROFILAME</u>
<u>119</u>	<u>3</u>	<u>A45605</u>	<u>323126</u>	<u>mature-parasite-infected erythrocyte surface antige</u>	