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BLAST Results

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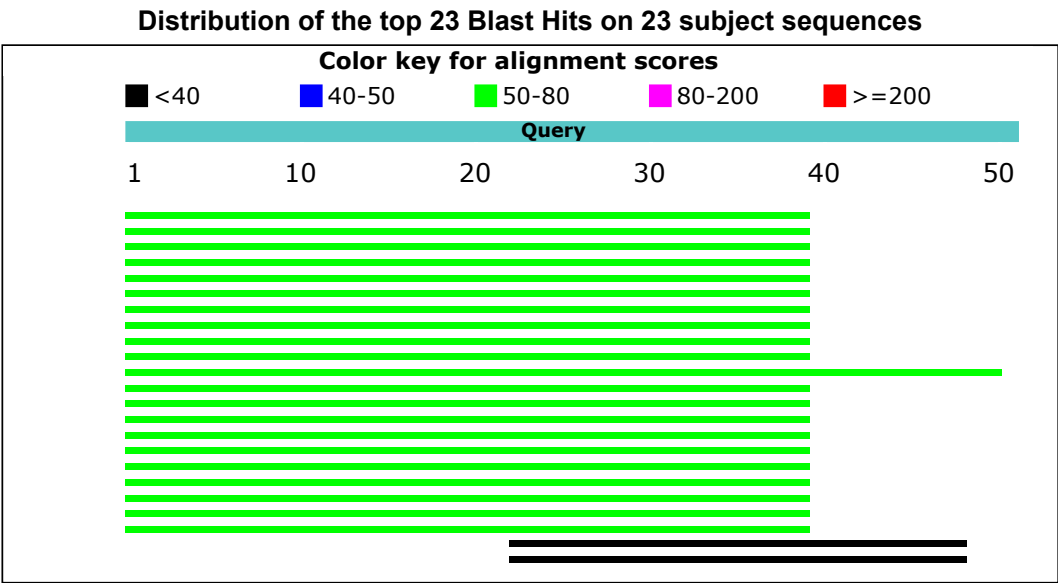
Job title: 2 sequences (Sequentie 1)

RID [DBFJ4AW6015](#) (Expires on 04-18 17:28 pm)

Query ID Icl|Query_93344
Description Sequentie 2
Molecule type amino acid
Query Length 50

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.8.0+

Graphic Summary



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein PFMALIP_05733 [Plasmodium falciparum MaliPS096_E11]	62.4	62.4	78%	5e-10	79%	ETW46202.1
hypothetical protein PFMALIP_05988 [Plasmodium falciparum MaliPS096_E11]	62.4	62.4	78%	5e-10	79%	ETW45945.1
hypothetical protein C923_01680 [Plasmodium falciparum UGT5.1]	62.0	62.0	78%	7e-10	79%	EWC77650.1
erythrocyte membrane protein 1 [Plasmodium falciparum]	62.0	62.0	78%	8e-10	82%	AAQ73931.1
hypothetical protein PFFVO_01919 [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	61.6	61.6	78%	8e-10	82%	ETW19344.1
hypothetical protein PFUGPA_00643 [Plasmodium falciparum Palo Alto/Uganda]	61.2	61.2	78%	1e-09	79%	ETW57363.1
erythrocyte membrane protein 1 [Plasmodium falciparum RAJ116]	61.2	61.2	78%	1e-09	82%	KNC35020.1
hypothetical protein PFMC_01263 [Plasmodium falciparum CAMP/Malaysia]	60.8	60.8	78%	2e-09	79%	ETW62864.1
erythrocyte membrane protein 1 [Plasmodium falciparum]	60.8	60.8	78%	2e-09	79%	AAQ73929.1
erythrocyte membrane protein 1, PfEMP1 [Plasmodium falciparum 3D7]	60.5	60.5	78%	2e-09	79%	XP_965999.1
erythrocyte membrane protein 1, PfEMP1, putative [Plasmodium sp. gorilla clade G1]	58.9	58.9	100%	8e-09	58%	SOS79565.1
hypothetical protein PFNF54_01300 [Plasmodium falciparum NF54]	58.9	58.9	78%	9e-09	74%	EWC89893.1
hypothetical protein C923_02755 [Plasmodium falciparum UGT5.1]	58.2	58.2	78%	2e-08	74%	EWC76588.1
hypothetical protein PFMALIP_05730 [Plasmodium falciparum MaliPS096_E11]	57.8	57.8	78%	2e-08	74%	ETW46205.1
hypothetical protein PFTANZ_03630 [Plasmodium falciparum Tanzania (2000708)]	57.8	57.8	78%	2e-08	74%	ETW35677.1
erythrocyte membrane protein 1, PfEMP1 [Plasmodium falciparum 3D7]	56.2	56.2	78%	7e-08	74%	XP_001352240.1
hypothetical protein PFNF54_02678 [Plasmodium falciparum NF54]	56.2	56.2	78%	8e-08	74%	EWC88543.1
hypothetical protein PFNF54_00006 [Plasmodium falciparum NF54]	55.5	55.5	78%	1e-07	74%	EWC91185.1
erythrocyte membrane protein 1, PfEMP1 [Plasmodium falciparum 3D7]	55.5	55.5	78%	1e-07	74%	XP_001350938.1
hypothetical protein PFNF135_02415 [Plasmodium falciparum NF135/5.C10]	54.7	54.7	78%	2e-07	74%	ETW42940.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein C923_02743 [Plasmodium falciparum UGT5.1]	54.7	54.7	78%	3e-07	72%	EWC76600.1
hypothetical protein ASC73_20450 [Phenylobacterium sp. Root1277]	35.0	35.0	52%	2.2	54%	KQW65551.1
MULTISPECIES: amidohydrolase [Phenylobacterium]	35.0	35.0	52%	2.3	54%	WP_082531874.1

Alignments

hypothetical protein PFMALIP_05733, partial [Plasmodium falciparum MaliPS096_E11]

Sequence ID: **ETW46202.1** Length: 994 Number of Matches: 1

Range 1: 357 to 395

Score	Expect	Method	Identities	Positives	Gaps	Frame
62.4 bits(150)	5e-10()	Compositional matrix adjust.	31/39(79%)	35/39(89%)	0/39(0%)	

Features:

```

Query 1    FKELVAKAKNEFEKLSMKWKELWIKLSTNITKONSSAPE 39
          FKELV+K KNEF+K SMK+ EL+IK STNITKONSSAPE
Sbjct 357  FKELVSKWKNEFDKQSMKYMELYIKASTNITKONSSAPE 395

```

hypothetical protein PFMALIP_05988 [Plasmodium falciparum MaliPS096_E11]

Sequence ID: **ETW45945.1** Length: 2694 Number of Matches: 1

Range 1: 1841 to 1879

Score	Expect	Method	Identities	Positives	Gaps	Frame
62.4 bits(150)	5e-10()	Compositional matrix adjust.	31/39(79%)	35/39(89%)	0/39(0%)	

Features:

```

Query 1    FKELVAKAKNEFEKLSMKWKELWIKLSTNITKONSSAPE 39
          FKELV+K KNEF+K SMK+ EL+IK STNITKONSSAPE
Sbjct 1841  FKELVSKWKNEFDKQSMKYMELYIKASTNITKONSSAPE 1879

```

hypothetical protein C923_01680, partial [Plasmodium falciparum UGT5.1]

Sequence ID: **EWC77650.1** Length: 424 Number of Matches: 1

Range 1: 362 to 400

Score	Expect	Method	Identities	Positives	Gaps	Frame
62.0 bits(149)	7e-10()	Composition-based stats.	31/39(79%)	36/39(92%)	0/39(0%)	

Features:

```

Query 1    FKELVAKAKNEFEKLSMKWKELWIKLSTNITKONSSAPE 39
          FKELV+K KNEF+K SMK+KEL+IK STNITKONSS+PE
Sbjct 362  FKELVSKWKNEFDKQSMKYKELYIKASTNITKONSSSPE 400

```

erythrocyte membrane protein 1 [Plasmodium falciparum]

Sequence ID: **AAQ73931.1** Length: 1324 Number of Matches: 1

Range 1: 361 to 399

Score	Expect	Method	Identities	Positives	Gaps	Frame
62.0 bits(149)	8e-10()	Composition-based stats.	32/39(82%)	36/39(92%)	0/39(0%)	

Features:

```


Query 1    FKELVAKAKNEFEKLSMKWKELWIKLSTNITKONSSAPE 39
          FKELV+K KNEF+K SMK+KEL+IK STNITKONSSAPE
Sbjct 361  FKELVSKWKNEFDKQSMKYKELYIKASTNITKONSSAPE 399

```

hypothetical protein PFFVO_01919 [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]
Sequence ID: **ETW19344.1** Length: 1324 Number of Matches: 1
Range 1: 361 to 399

Score	Expect	Method	Identities	Positives	Gaps	Frame
61.6 bits(148)	8e-10()	Composition-based stats.	32/39(82%)	36/39(92%)	0/39(0%)	
Features:						
Query	1	FKELVAKAKNEFEKLSMKWKELWIKLSTNITKQNSSAPE		39		
		FKELV+K KNEF+K SMK+KEL+IK STNITKQNSSAPE				
Sbjct	361	FKELVSKWKNEFDKQSMKYKELYIKASTNITKQNSSAPE		399		

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