

Supplement to: O. V. Sergeeva, D. O. Bredikhin, M. V. Nesterchuk, M. V. Serebryakova, P. V. Sergiev, and O. A. Dontsova, Possible Role of *Escherichia coli* Protein YbgI (ISSN 0006-2979, *Biochemistry (Moscow)*, 2018, Vol. 83, No. 3, pp. 270-280)

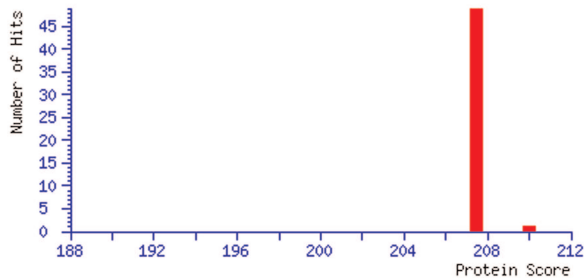
MATRIX SCIENCE Mascot Search Results

User :
 Email :
 Search title :
 Database : NCBIInr 20131103 (34061736 sequences; 11899143971 residues)
 Timestamp : 13 Nov 2013 at 08:00:58 GMT
 Top Score : 210 for [gi|491275550](#), glutamine-fructose-6-phosphate transaminase, partial [Shigella flexneri]

	NCBIInr	Decov
Protein hits above identity threshold	50	0
Highest scoring protein hit	210	69

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 88 are significant ($p < 0.05$).



Accession	Mass	Score	Description
1. gi 491275550	64887	210	glutamine-fructose-6-phosphate transaminase, partial [Shigella flexneri]
2. gi 353251646	66690	207	Chain A, C1a Mutant Of E. Coli Glms In Complex With Glucose-6p And Glutamate
3. gi 17942686	66694	207	Chain A, Glucosamine 6-Phosphate Synthase With Glucose 6-Phosphate
4. gi 118138642	66722	207	Chain A, E. Coli Glucosamine-6-p Synthase In Complex With Glucose-6p And 5-oxo-1-norleucine
5. gi 16131597	66853	207	L-glutamine:D-fructose-6-phosphate aminotransferase [Escherichia coli str. K-12 substr. MG1655]
6. gi 24115032	66825	207	glucosamine--fructose-6-phosphate aminotransferase [Shigella flexneri 2a str. 301]
7. gi 187733589	66883	207	glucosamine--fructose-6-phosphate aminotransferase [Shigella boydii CDC 3083-94]
8. gi 110644070	66795	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli 536]
9. gi 446256229	66807	207	glucosamine--fructose-6-phosphate aminotransferase [Shigella dysenteriae]
10. gi 15833925	66844	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli O157:H7 str. Sakai]
11. gi 43268	66825	207	unnamed protein product [Escherichia coli]
12. gi 73671334	66865	207	GlmS variant [Escherichia coli LW1655F+]
13. gi 117626002	66807	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli APEC O1]
14. gi 218556300	66867	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli IAI1]
15. gi 218560804	66807	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli S88]
16. gi 218692017	66841	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli ED1a]
17. gi 446256243	66823	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli]
18. gi 446256236	66851	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli]
19. gi 446256238	66779	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia]
20. gi 446256235	66856	207	glucosamine--fructose-6-phosphate aminotransferase [Shigella boydii]
21. gi 446256234	66853	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli]
22. gi 446256248	66853	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli]
23. gi 446256250	66837	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli]
24. gi 26250472	66737	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli CFT073]
25. gi 15804329	66867	207	glucosamine--fructose-6-phosphate aminotransferase [Escherichia coli O157:H7 str. EDL933]
26. gi 82546110	66857	207	glucosamine--fructose-6-phosphate aminotransferase [Shigella boydii Sb227]
27. gi 82779079	66863	207	glucosamine--fructose-6-phosphate aminotransferase [Shigella dysenteriae Sd197]
28. gi 290577	66833	207	glutamine amidotransferase [Escherichia coli]
29. gi 485801761	66867	207	glutamine-fructose-6-phosphate transaminase [Escherichia coli]
30. gi 487413051	66924	207	glucosamine-fructose-6-phosphate aminotransferase [isomerizing] [Escherichia coli]
31. gi 485749535	66825	207	glutamine-fructose-6-phosphate transaminase [Escherichia coli]
32. gi 487499164	66849	207	glutamine-fructose-6-phosphate transaminase [Escherichia coli]

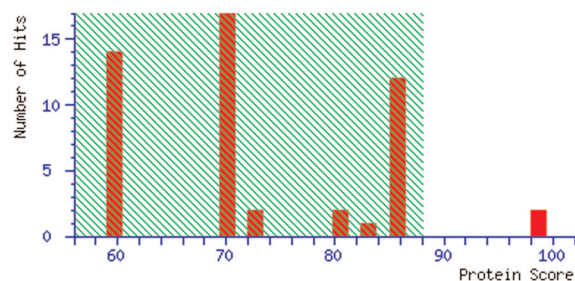
MATRIX SCIENCE Mascot Search Results

User :
 Email :
 Search title :
 Database : NCBIInr 20131103 (34061736 sequences; 11899143971 residues)
 Timestamp : 13 Nov 2013 at 08:02:47 GMT
 Top Score : 99 for **gi|187733584**, 16S rRNA pseudouridylylate synthase A [Shigella boydii CDC 3083-94]

	NCBIInr	Decoy
Protein hits above identity threshold	2	0
Highest scoring protein hit	99	68

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 88 are significant ($p < 0.05$).



Index

Accession	Mass	Score	Description
1. gi 187733584	25875	99	16S rRNA pseudouridylylate synthase A [Shigella boydii CDC 3083-94]
2. gi 447157596	25875	99	16S rRNA pseudouridylylate synthase [Escherichia coli]
3. gi 15802739	25849	85	16S rRNA pseudouridylylate synthase A [Escherichia coli O157:H7 str. EDL933]
4. gi 218554753	25861	85	16S rRNA pseudouridylylate synthase A [Escherichia coli IAI1]
5. gi 491132470	25848	85	16S rRNA pseudouridylylate synthase [Shigella boydii]
6. gi 386624880	25877	85	16S rRNA pseudouridylylate synthase A [Escherichia coli O7:K1 str. CE10]
7. gi 447157602	25836	85	16S rRNA pseudouridylylate synthase [Escherichia]
8. gi 485747967	25809	85	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
9. gi 487518802	25807	85	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
10. gi 487585887	25807	85	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
11. gi 486297027	25835	85	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
12. gi 487361570	25835	85	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
13. gi 510915965	25879	85	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
14. gi 545268909	25909	85	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
15. gi 519082428	27148	84	16S rRNA pseudouridylylate synthase [Escherichia coli]
16. gi 347357888	29680	81	16S rRNA pseudouridylylate synthase A [Escherichia coli CFT073]
17. gi 485689455	30252	80	16S rRNA pseudouridylylate synthase [Escherichia coli]
18. gi 545261749	25835	72	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
19. gi 485687270	23267	72	16S rRNA pseudouridylylate synthase A, partial [Escherichia coli]
20. gi 447157590	25835	71	16S rRNA pseudouridylylate synthase [Escherichia coli]
21. gi 447157591	25835	71	16S rRNA pseudouridylylate synthase [Escherichia coli]
22. gi 74312704	25819	71	16S rRNA pseudouridylylate synthase A [Shigella sonnei Ss046]
23. gi 485878556	25863	71	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
24. gi 545268013	25848	71	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
25. gi 20664188	26050	71	Chain A, Structure Of RsaA
26. gi 447157598	25877	71	16S rRNA pseudouridylylate synthase [Escherichia coli]
27. gi 487490496	25879	71	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
28. gi 485795082	25862	71	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
29. gi 485770421	25848	71	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
30. gi 487582822	25807	70	ribosomal small subunit pseudouridine synthase A [Escherichia coli]
31. gi 519081283	26735	70	16S rRNA pseudouridylylate synthase [Escherichia coli]
32. gi 218690332	25879	69	16S rRNA pseudouridylylate synthase A [Escherichia coli ED1a]
33. gi 485718745	25863	69	16S rRNA pseudouridylylate synthase [Escherichia coli]
34. gi 447157593	25830	69	16S rRNA pseudouridylylate synthase [Shigella flexneri]

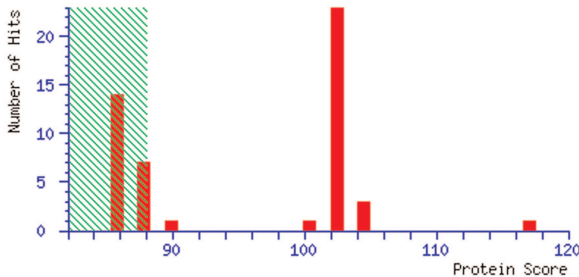
MATRIX SCIENCE Mascot Search Results

User :
 Email :
 Search title :
 Database : NCBIInr 20131103 (34061736 sequences; 11899143971 residues)
 Timestamp : 13 Nov 2013 at 08:04:50 GMT
 Top Score : 117 for [gi|485703777](#), ribose-phosphate pyrophosphokinase [Escherichia coli]

	NCBIInr	Decoy
Protein hits above identity threshold	29	0
Highest scoring protein hit	117	69

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 88 are significant ($p < 0.05$).



Index

Accession	Mass	Score	Description
1. gi 485703777	34861	117	ribose-phosphate pyrophosphokinase [Escherichia coli]
2. gi 446519410	33721	104	ribose-phosphate pyrophosphokinase, partial [Salmonella enterica]
3. gi 224583731	33852	104	ribose-phosphate pyrophosphokinase [Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594]
4. gi 386705100	33854	104	Ribose-phosphate pyrophosphokinase [Escherichia coli P12b]
5. gi 491182863	33872	103	ribose-phosphate pyrophosphokinase [Shigella dysenteriae]
6. gi 16760673	34195	103	ribose-phosphate pyrophosphokinase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]
7. gi 485652116	34223	103	ribose-phosphate pyrophosphokinase [Escherichia coli]
8. gi 486143377	34223	103	ribose-phosphate pyrophosphokinase [Escherichia]
9. gi 491277224	34227	103	ribose-phosphate pyrophosphokinase [Shigella flexneri]
10. gi 15830966	34197	103	ribose-phosphate pyrophosphokinase [Escherichia coli O157:H7 str. Sakai]
11. gi 187731868	34213	103	ribose-phosphate pyrophosphokinase [Shigella boydii CDC 3083-94]
12. gi 86516950	34183	103	PrsA [Shigella boydii]
13. gi 86516964	34199	103	PrsA [Shigella boydii]
14. gi 86517026	34257	103	PrsA [Escherichia coli]
15. gi 86516956	34139	103	PrsA [Shigella boydii]
16. gi 147379	34209	103	phosphoribosylpyrophosphate synthetase (gtg start codon; EC 2.7.6.1) [Escherichia coli]
17. gi 487386280	34184	103	ribose-phosphate pyrophosphokinase [Escherichia coli]
18. gi 487138526	34155	103	ribose-phosphate pyrophosphokinase [Escherichia coli]
19. gi 157145528	34845	103	ribose-phosphate pyrophosphokinase [Citrobacter koseri ATCC BAA-895]
20. gi 447038205	34847	103	ribose-phosphate pyrophosphokinase [Escherichia]
21. gi 493873811	34859	103	ribose-phosphate pyrophosphokinase [Yokenella regensburgei]
22. gi 205352552	34225	103	ribose-phosphate pyrophosphokinase [Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91]
23. gi 491170111	34215	102	ribose-phosphate pyrophosphokinase [Shigella dysenteriae]
24. gi 26247530	36626	102	ribose-phosphate pyrophosphokinase [Escherichia coli CFT073]
25. gi 62180344	36624	102	ribose-phosphate pyrophosphokinase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
26. gi 447042128	36658	102	ribose-phosphate pyrophosphokinase [Salmonella enterica]
27. gi 447042143	36654	102	ribose-phosphate pyrophosphokinase [Salmonella enterica]
28. gi 487383714	35613	101	Ribose-phosphate pyrophosphokinase [Salmonella enterica]
29. gi 554923369	29031	90	ribose-phosphate pyrophosphokinase, partial [Salmonella enterica]
30. gi 491240277	33824	88	ribose-phosphate pyrophosphokinase [Shigella flexneri]
31. gi 490194741	33850	88	ribose-phosphate pyrophosphokinase [Escherichia coli]
32. gi 487369334	34121	87	ribose-phosphate pyrophosphokinase [Escherichia coli]
33. gi 493611631	34175	87	ribose-phosphate pyrophosphokinase [Salmonella enterica]
34. gi 30062731	34167	87	ribose-phosphate pyrophosphokinase [Shigella flexneri 2a str. 2457T]

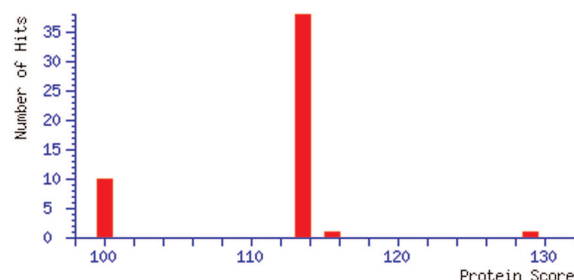
MATRIX SCIENCE Mascot Search Results

User :
 Email :
 Search title :
 Database : NCBIInr 20131103 (34061736 sequences; 11899143971 residues)
 Timestamp : 13 Nov 2013 at 08:06:38 GMT
 Top Score : 129 for [gi|485791866](#), P-protein [Escherichia coli]

	NCBIInr	Decoy
Protein hits above identity threshold	50	0
Highest scoring protein hit	129	67

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 88 are significant ($p < 0.05$).



Index

Accession	Mass	Score	Description
1. gi 485791866	43042	129	P-protein [Escherichia coli]
2. gi 486039041	42476	115	P-protein, partial [Escherichia coli]
3. gi 485813730	42943	114	P-protein [Escherichia coli]
4. gi 26248962	43027	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
5. gi 15832716	43084	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
6. gi 443618652	43100	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
7. gi 170681627	43057	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
8. gi 218690717	43043	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
9. gi 387613243	42985	114	P-protein [includes: chorismate mutase; prephenate dehydratase]
10. gi 254547525	43080	114	chorismate mutase p-prephenate dehydratase [Escherichia coli]
11. gi 446122236	43041	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
12. gi 386620196	43085	114	Chorismate mutase I / Prephenate dehydratase [Escherichia coli]
13. gi 446122235	43013	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
14. gi 446122266	43114	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
15. gi 446122238	42932	114	bifunctional chorismate mutase/prephenate dehydratase [Shigella flexneri]
16. gi 446122270	43027	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
17. gi 446122241	43045	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
18. gi 446122254	43067	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
19. gi 446122278	43110	114	bifunctional chorismate mutase/prephenate dehydratase [Shigella flexneri]
20. gi 446122248	43098	114	bifunctional chorismate mutase/prephenate dehydratase [Shigella flexneri]
21. gi 446122268	43128	114	bifunctional chorismate mutase/prephenate dehydratase [Shigella flexneri]
22. gi 446122252	42997	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
23. gi 15803121	43067	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
24. gi 82777952	42889	114	bifunctional chorismate mutase/prephenate dehydratase [Shigella flexneri]
25. gi 486191345	43127	114	P-protein [Escherichia coli]
26. gi 446122267	43083	114	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli]
27. gi 487427427	43080	114	P-protein [Escherichia coli]
28. gi 487447371	43044	114	P-protein [Escherichia coli]
29. gi 487465026	43042	114	P-protein [Escherichia coli]
30. gi 490054935	43058	114	P-protein [Escherichia coli]
31. gi 485770556	42943	114	P-protein [Escherichia coli]
32. gi 485857517	42955	114	P-protein [Escherichia coli]