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**BLAST®** » **blastn suite** » results for RID-Z54VYXC8016

Job Title	<a href="#">Nucleotide Sequence ...</a>
RID	<a href="#">Z54VYXC8016</a> Search expires on 03-15 14:04 pm
Program	BLASTN
Database	nt
Query ID	lcl Query_7079913
Description	<a href="#">None ...</a>
Molecule type	dna
Query Length	956

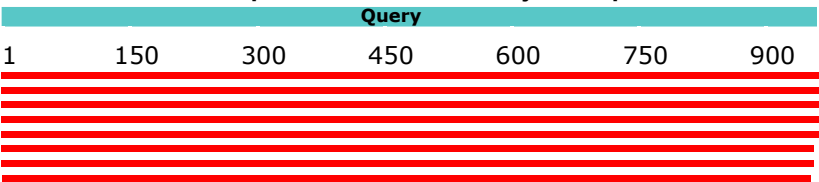
Descriptions



Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<a href="#">Aspergillus fumigatus Af293 lipase/esterase, putative (AFUA_8G01050), partial mRNA</a>	<a href="#">Aspergillus fumigatus Af293</a>	1725	1725	100%	0.0	99.17%	972	<a href="#">XM_742008.1</a>
<a href="#">Aspergillus fumigatus Af293 lipase/esterase gene, complete cds</a>	<a href="#">Aspergillus fumigatus Af293</a>	1703	1703	100%	0.0	98.75%	972	<a href="#">HQ231780.1</a>
<a href="#">Aspergillus fumigatus isolate Afir964 chromosome 8</a>	<a href="#">Aspergillus fumigatus</a>	1635	1635	100%	0.0	97.41%	1743900	<a href="#">CP084982.1</a>
<a href="#">Aspergillus fumigatus strain Afir974 chromosome 8</a>	<a href="#">Aspergillus fumigatus</a>	1635	1635	100%	0.0	97.41%	1792146	<a href="#">CP084973.1</a>
<a href="#">Aspergillus fumigatus CEA10 chromosome 8</a>	<a href="#">Aspergillus fumigatus</a>	1631	1631	100%	0.0	97.40%	1949143	<a href="#">CP097570.1</a>
<a href="#">Aspergillus fischeri NRRL 181 alpha/beta hydrolase fold protein (NFIA_094490), partial mRNA</a>	<a href="#">Aspergillus fischeri NRRL 181</a>	1384	1384	99%	0.0	92.98%	972	<a href="#">XM_001261725.1</a>
<a href="#">Aspergillus udagawae uncharacterized protein (Aud_005463), partial mRNA</a>	<a href="#">Aspergillus udagawae</a>	1301	1301	99%	0.0	91.40%	972	<a href="#">XM_043290393.1</a>
<a href="#">Aspergillus thermomutatus uncharacterized protein (CDV56_104905), partial mRNA</a>	<a href="#">Aspergillus thermomutatus</a>	1033	1033	98%	0.0	86.42%	972	<a href="#">XM_026758524.1</a>

Graphic Summary

Distribution of the top 8 Blast Hits on 8 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

Aspergillus fumigatus Af293 lipase/esterase, putative (AFUA\_8G01050), partial mRNA  
Sequence ID: XM\_742008.1 Length: 972 Number of Matches: 1  
Range 1: 1 to 960

Score	Expect	Identities	Gaps	Strand	Frame
1725 bits(934)	0.0()	953/961(99%)	6/961(0%)	Plus/Plus	
Query 1	ATGGCTTCTCCAATTCTGCGATCACC	GATTACTTCGGACCTCGCCAACGTAACACCCGAT	60		
Sbjct 1	ATGGCTTCTCCAATTCTGCGATCACC	GATTACTTCGGACCTCGCCAACGTAACACCCGAT	60		
Query 61	TGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGGAATCACTTGAACCAATC	120			
Sbjct 61	TGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGGAATCACTTGAACCAATC	120			
Query 121	TTCACCTTGGAGAAATATCATCCGAGGGAAAGAGAACATCATCTCTACGAGGAACTGGAC	180			
Sbjct 121	TTCACCTTGGAGAAATATCATCCGAGGGAAAGAGAACATCATCTCTACGAGGAACTGGAC	180			
Query 181	ATCCCAGGCCCCGAGGACCGATGCGGGCCACCATCTTCGCCCCAAGCACCAAACCCAC	240			
Sbjct 181	ATCCCAGGCCCCGAGGACCGATGCGGGCCACCATCTTCGCCCCAAGCACCAAACCCAC	240			
Query 241	CCTATCGATGAAATCCCTGGTATCCTACACATCCACGGCGGGGCGCTCGCCACGGGAAAC	300			



Sbjct	241	CCTATCGATGAAATCCCTGGTATCCTACACATCCACGGCGGGGCGCTCGCCACGGGAAAC	300
Query	301	CGCTTCCTGGGCTTACCATGCTCGACTGGGTCGAGTCCCT-GGTGCCGTCTGCCTGACG	359
Sbjct	301	CGCTTCCTGGGCTTACCATGCTCGACTGGGTCGAGTCCCTCGGTGCCGTCTGCCTGACG	360
Query	360	GCCGAGTACCGTCTCGCCCCGGAACATCACCAGCCCGCCAGCTGGAAGACAGCTACGCC	419
Sbjct	361	GCCGAGTACCGTCTCGCCCCGGAACATCACCAGCCCGCCAGCTGGAAGACAGCTACGCC	420
Query	420	G-GCTGCAGTGGATGAGCGACCACGCCGCCGAGCTGGGCTTCAACCCGCGCAAGCTGGTT	478
Sbjct	421	GCGCTGCAGTGGATGAGCGACCACGCCGCCGAGCTGGGCTTCAACCCGCGCAAGCTGGTT	480
Query	479	GTCTGCGGTAGCTCGGCGGGGGCAATCTCACGGCGGGGTCACCTTACTCGCGGGGAC	538
Sbjct	481	GTCTGCGGTAGCTCGGCGGGGGCAATCTCACGGCGGGGTCACCTTACTCGCGGGGAC	540
Query	539	CGCTCGGGCCCGCAAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGGCATG	598
Sbjct	541	CGCTCGGGCCCGCAAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGGCATG	600
Query	599	GACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGCCGCC	658
Sbjct	601	GACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGCCGCC	660
Query	659	GTGTTGGCTAATTATGCGTTTGCGAGAGGCGCGAGCACGCGGATATGTATACTGTGCCG	718
Sbjct	661	GTGTTGGCTAATTATGCGTTTGCGAGAGGCGCGAGCACGCGGATATGTATACTGTGCCG	720
Query	719	ATGCGCGCGACGAATTT-GCGGGCTTGCCCCGACGTTTATCGATGTGGGTGAGGCGGA	777
Sbjct	721	ATGCGCGCGACGAATTTGCG-GGGCTTGCCCCGACGTTTATCGATGTGGGTGAGGCGGA	779
Query	778	TGTGTTTCGTATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCTCGAC	837
Sbjct	780	TGTGTTTCGTATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCTCGAC	839
Query	838	TGAGTTGCATCTGTGG-CGGGCAGTTGGCATWGGTTTGATGTCTTTGTTCTGATGCTCC	896
Sbjct	840	TGAGTTGCATCTGTGGCCGGGCAGTTGGCATGGGTTTGATGTCTTTGTTCTGATGCTCC	899
Query	897	CATTAGTCGGCGGGCGAGGGCTGCT-GGTTGGAATGGCTTCGGAAGTTGTTAAGTGTGCC	955
Sbjct	900	CATTAGTCGGCGGGCGAGGGCTGCTCGGTTGGAATGGCTTCGGAAGTTGTTAAGTGTGCC	959
Query	956	T	956
Sbjct	960	T	960

**Aspergillus fumigatus Af293 lipase/esterase gene, complete cds**

Sequence ID: HQ231780.1 Length: 972 Number of Matches: 1

Range 1: 1 to 960

	Score	Expect	Identities	Gaps	Strand	Frame
	1703 bits(922)	0.0()	949/961(99%)	6/961(0%)	Plus/Plus	
Query	1	ATGGGTTTCTCCAATTCTGCGATCACC	GATTACTTCGGACCTCGCCAACGTAACACCCGAT	60		
Sbjct	1	ATGGGTTTCTCCAATTCTGCGATCACC	GATTACTTCGGACCTCGCCAACGTAACACCCGAT	60		
Query	61	TTGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGCAATCACTTGAACCAATC	120			
Sbjct	61	TTGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGCAATCACTTGTACCAATC	120			
Query	121	TTCACCTTGGAGAATATCATCCGAGGGAAAGAGAACATCATCTCTACGAGGAAGTGGAC	180			
Sbjct	121	TTCACCTTGGAGAATATCATCCGAGGGAAAGAGAACATCATCTCTACGAGGAAGTGGAC	180			
Query	181	ATCCCAGGCCCCGAGGACCGATGCGGGCCACCATCTTCCGCCCAAGCACCAAACCCAC	240			
Sbjct	181	ATCCCAGGCCCCGAGGACCGATGCGGGCCACCATCTTCCGCCCAAGCACCAAACCCAC	240			
Query	241	CCTATCGATGAAATCCCTGGTATCCTACACATCCACGGCGGGGCGCTCGCCACGGGAAAC	300			
Sbjct	241	CCCATCGATGAAATCCCTGGTATCCTACACATCCACGGCGGGGCGCTCGCCACGGGAAAC	300			
Query	301	CGCTTCCTGGGCTTACCATGCTCGACTGGGTCGAGTCCCT-GGTGCCGTCTGCCTGACG	359			
Sbjct	301	CGCTTCCTGGGCTTACCATGCTCGACTGGGTCGAGTCCCTCGGTGCCGTCTGCCTGACG	360			
Query	360	GCCGAGTACCGTCTCGCCCCGGAACATCACCAGCCCGCCAGCTGGAAGACAGCTACGCC	419			
Sbjct	361	GCCGAGTACCGTCTCGCCCCGGAACATCACCAGCCCGCCAGCTGGAAGACAGCTACGCC	420			
Query	420	G-GCTGCAGTGGATGAGCGACCACGCCGCCGAGCTGGGCTTCAACCCGCGCAAGCTGGTT	478			
Sbjct	421	GCGCTGCAGTGGATGAGCGACCACGCCGCCGAGCTGGGCTTCAACCCGCGCAAGCTGGTT	480			
Query	479	GTCTGCGGTAGCTCGGCGGGGGCAATCTCACGGCGGGGTCACCTTACTCGCGGGGAC	538			
Sbjct	481	GTCTGCGGTAGCTCGGCGGGGGCAATCTCACGGCGGGGTCACCTTACTCGCGGGGAC	540			
Query	539	CGCTCGGGCCCGCAAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGGCATG	598			
Sbjct	541	CGCTCGGGCCCGCAAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGGCATG	600			
Query	599	GACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGCCGCC	658			
Sbjct	601	GACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGCCGCC	660			



Query 659 GTGTTGGCTAATTATGCGTTTGGCGAGAGGCGCGAGCACGCGGATATGTATACTGTGCCG 718  
 Sbjct 661 GTGTTGGCTAATTATGCGTTTGGCGAGAGGCGCGAGCACGCGGATATGTATACTGTGCCG 720  
 Query 719 ATGCGCGCGACGAATTT-GCGGGGCTTGCCCCGACGTTTATCGATGTGGGTGAGGCGGA 777  
 Sbjct 721 ATGCGCGCGACGAATTCGCA-GGCTTGCCCCGACGTTTATCGATGTGGGTGAGGCGGA 779  
 Query 778 TGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCTCGAC 837  
 Sbjct 780 TGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCTCGAC 839  
 Query 838 TGAGTTGCATCTGTGG-CGGGCAGTTGGCATWGGTTTGATGTCTTTGTTCTGATGCTCC 896  
 Sbjct 840 TGAGTTGCATGTGTGGCCGGCAGTTGGCATGGGTTTGATGTCTTTGTTCTGATGCTCC 899  
 Query 897 CATTAGTCGGCGGGCGAGGGCTGCT-GGTTGGAATGGCTTCGGAAGTTGTTAAGTGTGCC 955  
 Sbjct 900 CATTAGTCGGCGGGCGAGGGCTGCTCGGTTGGAATGGCTTCGGAAGTTGTTAAGTGTGCC 959  
 Query 956 T 956  
 Sbjct 960 T 960

**Aspergillus fumigatus isolate Afir964 chromosome 8**

Sequence ID: CP084982.1 Length: 1743900 Number of Matches: 1

Range 1: 206231 to 207194

Score	Expect	Identities	Gaps	Strand	Frame
1635 bits(885)	0.0()	940/965(97%)	10/965(1%)	Plus/Plus	
Query 1	ATGGCTTCTCCAATTCTGCGATCACCATTACTTCGGACCTCGCCAACGTAACACCCGAT	60			
Sbjct 206231	ATGGCTTCTCCAATTCTGCGATCACCATTACTTCGGACCTCGCCAACGTAACACCCGAT	206290			
Query 61	TTGGTGGATGTTAGCACTCCGAAAAAATTGAAATCTACCGGAATCACTTGAACCAATC	120			
Sbjct 206291	TTGGTGGATGTTAGCACTCCGAAAAAATTGAAATCTACCGGAATCACTTGAACCAATC	206350			
Query 121	TTCACCTTGGAGAATATCATCCGAGGAAAAGAGAATCATCTCTACGAGGAACCTGGAC	180			
Sbjct 206351	TGCACCTTGGAGAATATCATCCGAGGAAAAGAGAATCATCTCTACGAGGAACCTGGAC	206410			
Query 181	ATCCCAGGCCCCGAGGACCGATGC--G-GG-CCACCATCTTCCGCCCAAGCACCAAAC	236			
Sbjct 206411	ATCCCAGGCCCCGAGGACCGATGCATGCGGACCACCATCTTCCGCCCAAGCACCAAAC	206470			
Query 237	CCACCCATCGATGAAATCCCTGGTATCCTACACATCCACGCGGGGGCTCGCCACGGG	296			
Sbjct 206471	CCACCCATCGATGAAATCCCGGTATCCTACACATCCACGCGGGGGCTTGCCACCGG	206530			
Query 297	AAACCGCTTCTCTGGGTTTACCATGCTCGACTGGGTTCGAGTCCCT-GGTGCCGTCTGCCT	355			
Sbjct 206531	AAACCGCTTCTCTGGGTTTACCATGCTCGACTGGGTTCGAGTCCCTCGGCGCGTCTGCCT	206590			
Query 356	GACGGCCGAGTACCGTCTCGCCCCGGAACATACCAGCCCCAGCTGGAAGACAGCTA	415			
Sbjct 206591	GACGGCCGAGTACCGTCTCGCCCCGAGCATACCAGCCAGCCAGCTAGAAGACAGCTA	206650			
Query 416	CGCCG-GCTGCAGTGGATGAGCGACCACGCCGCGAGCTGGGCTTCAACCCGCGCAAGCT	474			
Sbjct 206651	CGCCGCGCTGCAGTGGATGAGCGACCACGCCGCGAGCTGGGCTTCAACCCGCGCAAGCT	206710			
Query 475	GGTTGTCTGCGGTAGCTCGGCGGGGGCAATCTCACGCGGGGGTCACCTTACTCGCGCG	534			
Sbjct 206711	GGTTGTCTGCGGTAGCTCGGCGGGGGCAATCTCACGCGGGGGTCACCTTACTCGCGCG	206770			
Query 535	GGACCGCTCGGGCCGCAAAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGG	594			
Sbjct 206771	GGACCGCTCGGGCCGCAAAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGG	206830			
Query 595	CATGGACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGC	654			
Sbjct 206831	CATGGACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGC	206890			
Query 655	CGCCGTGTTGGCTAATTATGCGTTTGGCGAGAGGCGCGAGCACGCGGATATGTATACTGT	714			
Sbjct 206891	CGCCGTGTTGGCTAATTATGCGTTTGGCGAGAGGCGCGAGCACGCGGATATGTATACTGT	206950			
Query 715	GCCGATGCGCGCGACGAATTT-GCGGGGCTTGCCCCGACGTTTATCGATGTGGGTGAGG	773			
Sbjct 206951	GCCGATGCGCGCGACGAATTTGCG-GGGCTTGCCCCGACGTTTATCGATGTGGGTGAGG	207009			
Query 774	CGGATGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCT	833			
Sbjct 207010	CGGATGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCT	207069			
Query 834	CGACTGAGTTGCATCTGTGGCG-GGCAGTTGGCATWGGTTTGATGTCTTTGTTCTGATG	892			
Sbjct 207070	CGACTGAGTTGCATCTGTGGCCTGGCAGTTGGCATGGGTTTGATGTCTTTGTTCTGATG	207129			
Query 893	CTCCCATAGTCGGCGGGCGAGGGCTGCT-GGTTGGAATGGCTTCGGAAGTTGTTAAGTG	951			
Sbjct 207130	CTCCCATAGTCGGCGGGCGAGGGCTGCTCGGTTGGAATGGCTTCGGAAGTTGTTAAGTG	207189			
Query 952	TGCCT 956				
Sbjct 207190	TGCCT 207194				



**Aspergillus fumigatus strain Afir974 chromosome 8**

Sequence ID: CP084973.1 Length: 1792146 Number of Matches: 1

Range 1: 247410 to 248373

Score	Expect	Identities	Gaps	Strand	Frame
1635 bits(885)	0.0()	940/965(97%)	10/965(1%)	Plus/Plus	
Query 1	ATGGCTTCTCCAATTCTGCGATCACCATTACTTCGGACCTCGCCAACGTAACACCCGAT				60
Sbjct 247410	ATGGCTTCTCCAATTCTGCGATCACCATTACTTCGGACCTCGCCAACGTAACACCCGAT				247469
Query 61	TTGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGGAATCACTTGAACCAATC				120
Sbjct 247470	TTGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGGAATCACTTGAACCAATC				247529
Query 121	TTCACCTTGGAGAATATCATCCGAGGGAAAAGAGAACATCATCTCTACGAGGAACCTGGAC				180
Sbjct 247530	TGCACCTTGGAGAATATCATCCGAGGGAAAAGAGAACATCATCTCTACGAGGAACCTGGAC				247589
Query 181	ATCCCAGGCCCGCAGGACCGATGC--G-GG-CCACCATCTTCGCCCAAGCACCAAAC				236
Sbjct 247590	ATCCCAGGCCCGCAGGACCGATGCATGCGGACCACCATCTTCGCCCAAGCACCAAAC				247649
Query 237	CCACCCATATCGATGAAATCCCTGGTATCCTACACATCCACGGCGGGGCTCGCCACGGG				296
Sbjct 247650	CCACCCATATCGATGAAATCCCGGTATCCTACACATCCACGGCGGGGCTTGCACCGG				247709
Query 297	AAACCGCTTCTGGGCTTACCATGCTCGACTGGGTCGAGTCCCT-GGTGCCGTCTGCCT				355
Sbjct 247710	AAACCGCTTCTGGGTTTACCATGCTCGACTGGGTCGAGTCCCTCGGCGCGTCTGCCT				247769
Query 356	GACGGCCGAGTACCGTCTCGCCCGGAACATACCAGCCCGCCAGCTGGAAGACAGCTA				415
Sbjct 247770	GACGGCCGAGTACCGTCTCGCCCGGAGCATACCAGCCAGCCAGCTAGAAGACAGCTA				247829
Query 416	CGCCG-GCTGCACTGGATGAGCGACCACGCCCGGAGCTGGGCTTCAACCCGCGCAAGCT				474
Sbjct 247830	CGCCGCGCTGCACTGGATGAGCGACCACGCCCGGAGCTGGGCTTCAACCCGCGCAAGCT				247889
Query 475	GGTTGTCTGCGGTAGCTCGGCGGGGGCAATCTCACGGCGGGGTCACCTTACTCGCGCG				534
Sbjct 247890	GGTTGTCTGCGGTAGCTCGGCGGGGGCAATCTCACGGCGGGGTCACCTTACTCGCGCG				247949
Query 535	GGACCGCTCGGGCCCGCAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGG				594
Sbjct 247950	GGACCGCTCGGGCCCGCAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGG				248009
Query 595	CATGGACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGC				654
Sbjct 248010	CATGGACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGC				248069
Query 655	CGCCGTGTTGGCTAATTATGCGTTTGGCGAGAGGCGCGAGCACGCGGATATGTATACTGT				714
Sbjct 248070	CGCCGTGTTGGCTAATTATGCGTTTGGCGAGAGGCGCGAGCACGAGATATGTATACTGT				248129
Query 715	GCCGATGCGCGCGACGAATTT-GCGGGGCTTGCCCCGACGTTTATCGATGTGGGTGAGG				773
Sbjct 248130	GCCGATGCGCGCGACGAATTTGCG-GGGCTTGCCCCGACGTTTATCGATGTGGGTGAGG				248188
Query 774	CGGATGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCT				833
Sbjct 248189	CGGATGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCT				248248
Query 834	CGACTGAGTTGCATCTGTGGCG-GGCAGTTGGCATWGGTTTGATGTCTTTGTTCTGATG				892
Sbjct 248249	CGACTGAGTTGCATGTGTGGCCTGGCAGTTGGCATGGGTTTGATGTCTTTGTTCTGATG				248308
Query 893	CTCCCATTAGTCGGCGGGCGAGGGCTGCT-GGTTGGAATGGCTTCGGAAGTTGTTAAGTG				951
Sbjct 248309	CTCCCATTAGTCGGCGGGCGAGGGCTGCTCGGTTGGAATGGCTTCGGAAGTTGTTAAGTG				248368
Query 952	TGCTT 956				
Sbjct 248369	TGCTT 248373				

**Aspergillus fumigatus CEA10 chromosome 8**

Sequence ID: CP097570.1 Length: 1949143 Number of Matches: 1

Range 1: 224028 to 224987

Score	Expect	Identities	Gaps	Strand	Frame
1631 bits(883)	0.0()	936/961(97%)	6/961(0%)	Plus/Plus	
Query 1	ATGGCTTCTCCAATTCTGCGATCACCATTACTTCGGACCTCGCCAACGTAACACCCGAT				60
Sbjct 224028	ATGGCTTCTCCAATTCTGCGATCACCATTACTTCGGACCTCGCCAACGTAACACCCGAT				224087
Query 61	TTGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGGAATCACTTGAACCAATC				120
Sbjct 224088	TTGGTGGATGTTAGCACTCCCGAAAAATTGAAATCCTACCGGAATCACTTGAACCAATC				224147
Query 121	TTCACCTTGGAGAATATCATCCGAGGGAAAAGAGAACATCATCTCTACGAGGAACCTGGAC				180
Sbjct 224148	TTCACCTTGGAGAATATCATCCGAGGGAAAAGAGAACATCATCTCTGGGAGGAACCTGGAC				224207



Query	181	ATCCCAGGCCCCGAGGACCGATGCGGGCCACCATCTTCCGCCCCAAGCACAAACCCAC	240
Sbjct	224208	ATCCCAGGCCCCGAGGACCGATGCGGGCCACCATCTTCCGCCCCAAGCACAAACCCAC	224267
Query	241	CCTATCGATGAAATCCCTGGTATCTACACATCCACGGCGGGGGCTCGCCACGGGAAAC	300
Sbjct	224268	CCCATCGATGAAATCCCTGGTATCTACACATCCACGGCGGGGGCTTGCCACCGGAAAC	224327
Query	301	CGCTTCCTGGGCTTACCATGCTCGACTGGGTCGAGTCCCT-GGTGCCGTCTGCCTGACG	359
Sbjct	224328	CGCTTCCTGGGTTTACCATGCTCGACTGGGTCGAGTCCCTCGGCGCGGTCTGCCTGACG	224387
Query	360	GCCGAGTACCGTCTCGCCCCGGAACATACCAGCCCCAGCTGGAAGACAGCTACGCC	419
Sbjct	224388	GCCGAGTACCGTCTCGCCCCGAGCATACCAGCCAGCCAGCTAGAAGACAGCTACGCC	224447
Query	420	G-GCTGCAGTGGATGAGCGACCACGCCGCCGAGCTGGGCTTCAACCCGCGCAAGCTGGTT	478
Sbjct	224448	GCGCTGCAGTGGATGAGCGACCACGCCGCCGAGCTGGGCTTCAACCCGACAAGCTGGTT	224507
Query	479	GTCTGCGGTAGCTCGGCGGGGGCAATCTCACGGCGGGGTACACCTTACTCGCGGGGAC	538
Sbjct	224508	GTCTGCGGAGCTCGGCGGGGGCAATCTCACGGCGGGGTACACCTTACTTGC CGGGGAC	224567
Query	539	CGCTCGGGCCCCGAAATCCGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGGCATG	598
Sbjct	224568	CGCTCGGGCCCCGAAATCTGCGGCCAGGTGTTGATCTATCCGTGGGTTGACGATGGCATG	224627
Query	599	GACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGCCGCC	658
Sbjct	224628	GACTACGTGTCCATGCGGCAGTATGCGGATATTGCGCCTGTGAGGGACGTGGACGCCGCC	224687
Query	659	GTGTTGGCTAATTATGCGTTTGGCGAGAGGCGGAGCACGCGGATATGTATACTGTGCCG	718
Sbjct	224688	GTATTGGCTAATTATGCGTTTGGCGAGAGGCGGAGCACGAGATATGTATACTGTGCCG	224747
Query	719	ATGCGCGCGACGAATTT-GCGGGGCTTGCCCCGACGTTTATCGATGTGGGTGAGGCGGA	777
Sbjct	224748	ATGCGCGCGACGAATTTGCG-GGGCTTGCCCCGACGTTTATCGATGTGGGTGAGGCGGA	224806
Query	778	TGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCTCGAC	837
Sbjct	224807	TGTGTTTCGTGATCAGGATATCGCGTACGCGTCGGCTTTGTGGAAGGATGGTGTCTCGAC	224866
Query	838	TGAGTTGCATCTGTGG-CGGGCAGTTGGCATWGGTTTGATGTCTTTGTTCCCTGATGCTCC	896
Sbjct	224867	TGAGTTGCATGTGTGGCCGGCAGTTGGCATGGGTTTGATGTCTTTGTTCCCTGATGCTCC	224926
Query	897	CATTAGTCGGCGGGCGAGGGCTGCT-GGTTGGAATGGCTTCGGAAGTTGTTAAGTGTGCC	955
Sbjct	224927	CATTAGTCGGCGGGCGAGGGCTGCTCGGTTGGAATGGCTTCGGAAGTTGTTAAGTGTGCC	224986
Query	956	T 956	
Sbjct	224987	T 224987	

Taxonomy

Reports

- Lineage

Organism	Blast Name	Score	Number of Hits	Description
<a href="#">Aspergillus</a>	<a href="#">ascomycete fungi</a>		<a href="#">8</a>	
<a href="#">.Aspergillus subgen. Fumigati</a>	<a href="#">ascomycete fungi</a>		<a href="#">6</a>	
<a href="#">..Aspergillus fumigatus</a>	<a href="#">ascomycete fungi</a>		<a href="#">3</a>	
<a href="#">...Aspergillus fumigatus Af293</a>	<a href="#">ascomycete fungi</a>	1725	<a href="#">2</a>	<a href="#">Aspergillus fumigatus Af293 hits</a>
<a href="#">..Aspergillus fumigatus</a>	<a href="#">ascomycete fungi</a>	1635	<a href="#">3</a>	<a href="#">Aspergillus fumigatus hits</a>
<a href="#">..Aspergillus fischeri NRRL 181</a>	<a href="#">ascomycete fungi</a>	1384	<a href="#">1</a>	<a href="#">Aspergillus fischeri NRRL 181 hits</a>
<a href="#">.Aspergillus udagawae</a>	<a href="#">ascomycete fungi</a>	1301	<a href="#">1</a>	<a href="#">Aspergillus udagawae hits</a>
<a href="#">.Aspergillus thermomutatus</a>	<a href="#">ascomycete fungi</a>	1033	<a href="#">1</a>	<a href="#">Aspergillus thermomutatus hits</a>

- Organism

Description	Score	E value	Accession
Aspergillus fumigatus Af293 [ascomycete fungi ]			
<a href="#">Aspergillus fumigatus Af293 lipase/esterase, putative (AFUA_8G01050), partial mRNA</a>	1725	0.0	<a href="#">XM_742008</a>
<a href="#">Aspergillus fumigatus Af293 lipase/esterase gene, complete cds</a>	1703	0.0	<a href="#">HQ231780</a>
Aspergillus fumigatus [ascomycete fungi ]			
<a href="#">Aspergillus fumigatus isolate Afir964 chromosome 8</a>	1635	0.0	<a href="#">CP084982</a>



Description	Score	E value	Accession
<a href="#">Aspergillus fumigatus strain Afir974 chromosome 8</a>	1635	0.0	<a href="#">CP084973</a>
<a href="#">Aspergillus fumigatus CEA10 chromosome 8</a>	1631	0.0	<a href="#">CP097570</a>
Aspergillus fischeri NRRL 181 [ascomycete fungi ]			
<a href="#">Aspergillus fischeri NRRL 181 alpha/beta hydrolase fold protein (NFIA_094490), partial mRNA</a>	1384	0.0	<a href="#">XM_001261725</a>
Aspergillus udagawae [ascomycete fungi ]			
<a href="#">Aspergillus udagawae uncharacterized protein (Aud_005463), partial mRNA</a>	1301	0.0	<a href="#">XM_043290393</a>
Aspergillus thermomutatus [ascomycete fungi ]			
<a href="#">Aspergillus thermomutatus uncharacterized protein (CDV56_104905), partial mRNA</a>	1033	0.0	<a href="#">XM_026758524</a>

## ◦ Taxonomy

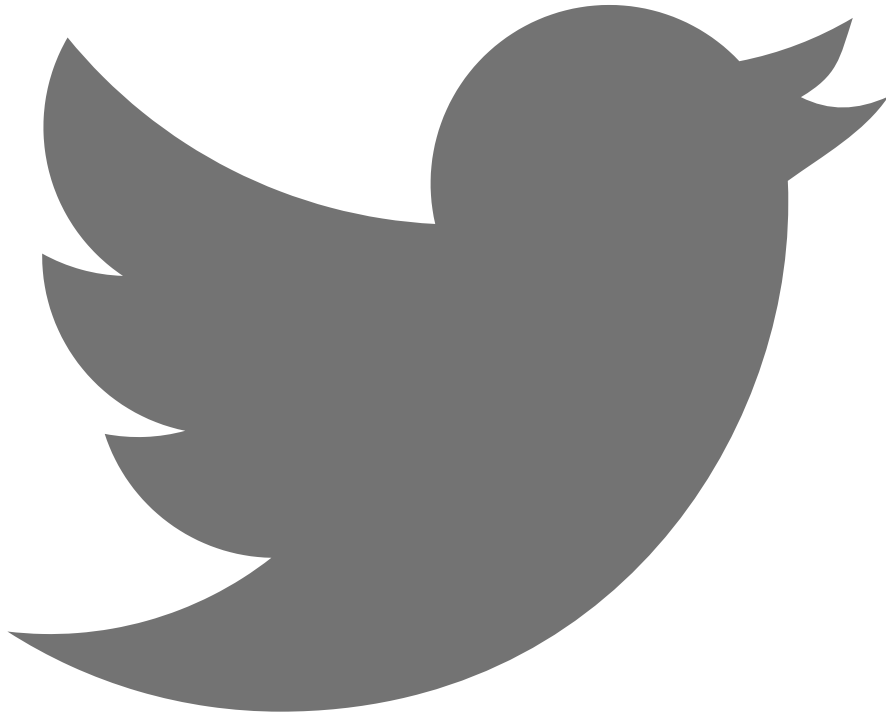
Taxonomy	Number of hits	Number of Organisms	Description
<a href="#">Aspergillus</a>	<a href="#">8</a>	5	
. <a href="#">Aspergillus subgen. Fumigati</a>	<a href="#">6</a>	3	
.. <a href="#">Aspergillus fumigatus</a>	<a href="#">3</a>	2	<a href="#">Aspergillus fumigatus hits</a>
... <a href="#">Aspergillus fumigatus Af293</a>	<a href="#">2</a>	1	<a href="#">Aspergillus fumigatus Af293 hits</a>
.. <a href="#">Aspergillus fischeri NRRL 181</a>	<a href="#">1</a>	1	<a href="#">Aspergillus fischeri NRRL 181 hits</a>
. <a href="#">Aspergillus udagawae</a>	<a href="#">1</a>	1	<a href="#">Aspergillus udagawae hits</a>
. <a href="#">Aspergillus thermomutatus</a>	<a href="#">1</a>	1	<a href="#">Aspergillus thermomutatus hits</a>

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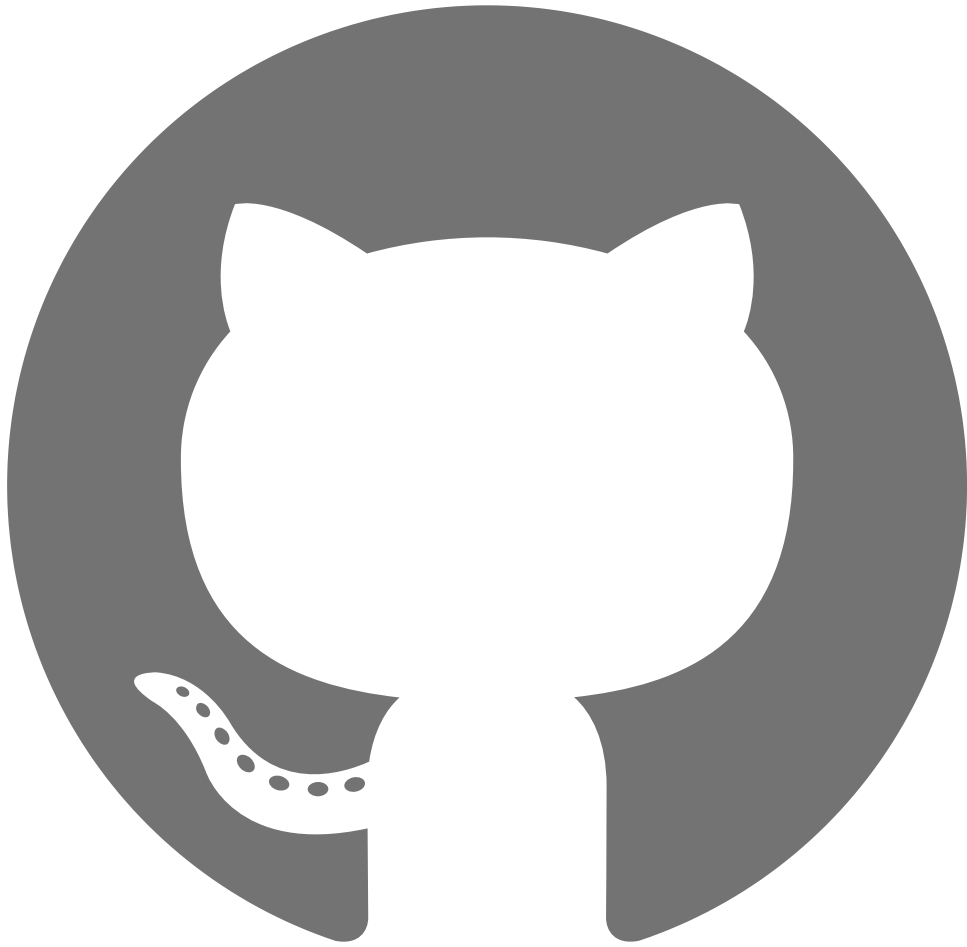














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