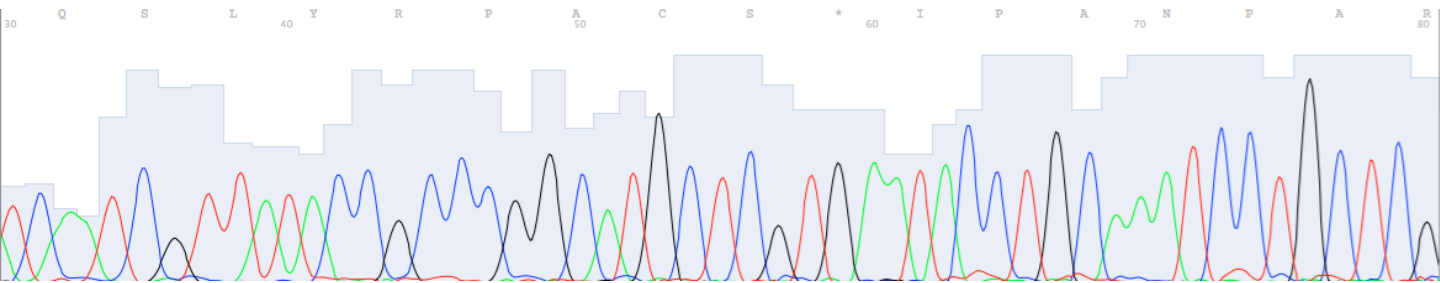
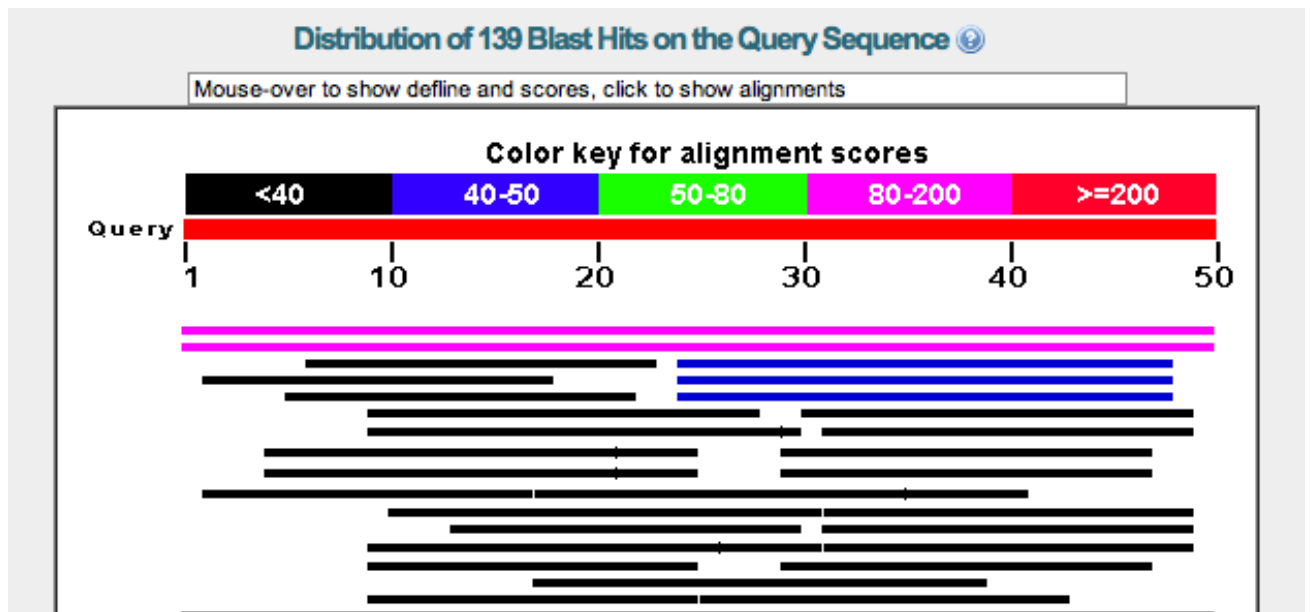


Use the following data to construct your sequence.

Blue = C, Red = T, Green = A, Black = G



Below is the BLAST analysis of your sequence.



Descriptions

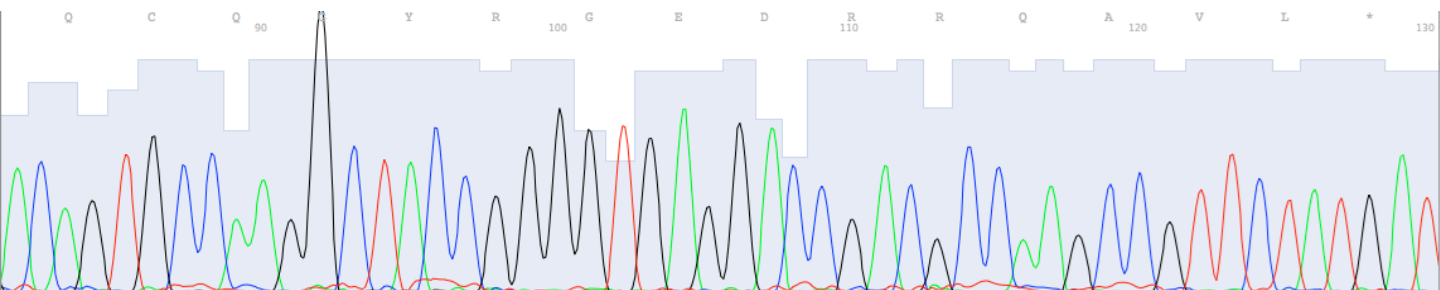
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [B](#) PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
qii327374765 CP002585.1	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421,	99.6	317	100%	1e-18	100%	
qii359757955 CP003150.1	<i>Pseudomonas fluorescens</i> F113, complete genome	83.8	208	100%	7e-14	100%	
qii288945675 CP001924.1	<i>Dehalococcoides</i> sp. GT, complete genome	40.1	40.1	48%	1.0	96%	
qii146269600 CP000688.1	<i>Dehalococcoides</i> sp. BAV1, complete genome	40.1	40.1	48%	1.0	96%	
qii73659672 AJ965256.1	<i>Dehalococcoides</i> sp. CBDB1 complete genome	40.1	40.1	48%	1.0	96%	
qii374843763 F0082843.1	<i>Nocardia cyriacigeorgica</i> GUH-2 chromosome complete genom	38.2	68.4	38%	4.0	100%	
qii145301903 CP000667.1	<i>Salinispora tropica</i> CNB-440, complete genome	38.2	70.4	42%	4.0	100%	
qii22038511 AC113378.2	Homo sapiens chromosome 5 clone RP11-278A18, complete se	38.2	38.2	38%	4.0	100%	
qii354795750 JN960251.1	<i>Mus musculus</i> targeted non-conditional, lacZ-tagged mutant al	36.2	36.2	36%	16	100%	
qii354791434 JN955935.1	<i>Mus musculus</i> targeted KO-first, conditional ready, lacZ-tagger	36.2	36.2	36%	16	100%	

Use the following data to construct your sequence.

Blue = C, Red = T, Green = A, Black = G

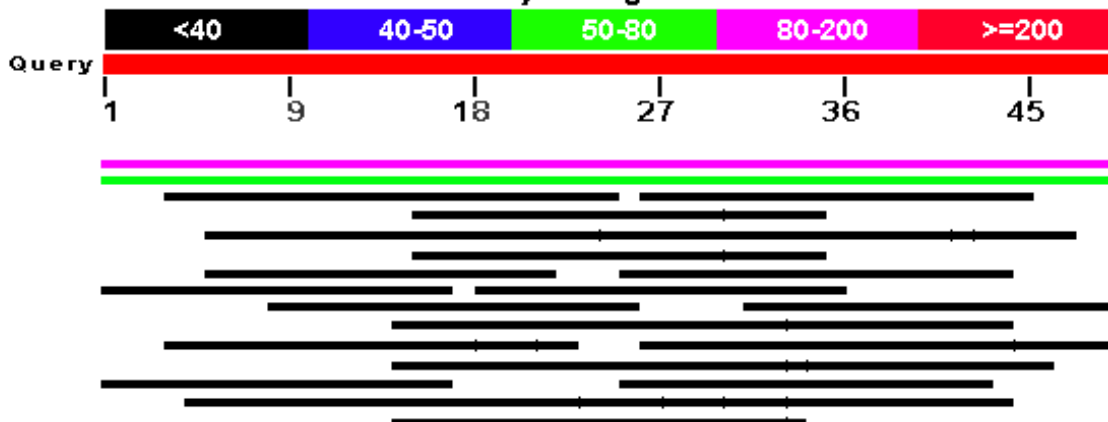


Below is the BLAST analysis of your sequence.

Distribution of 205 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments

Color key for alignment scores



Descriptions

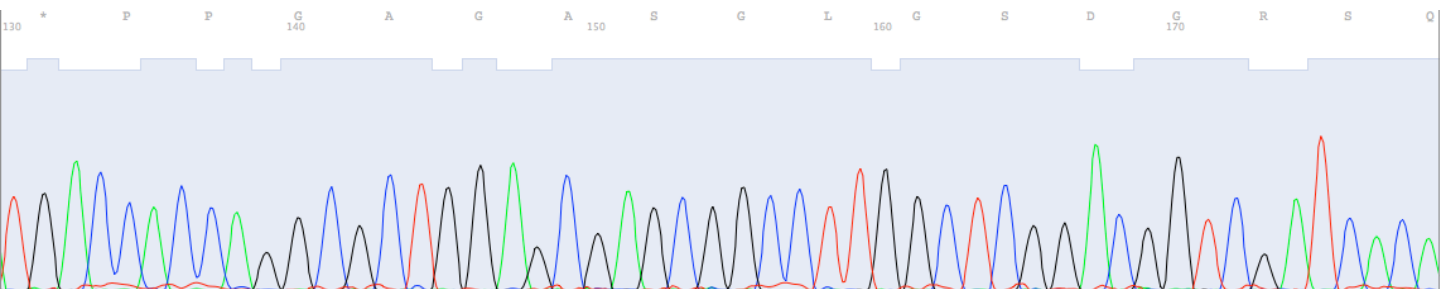
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Sequences producing significant alignments:

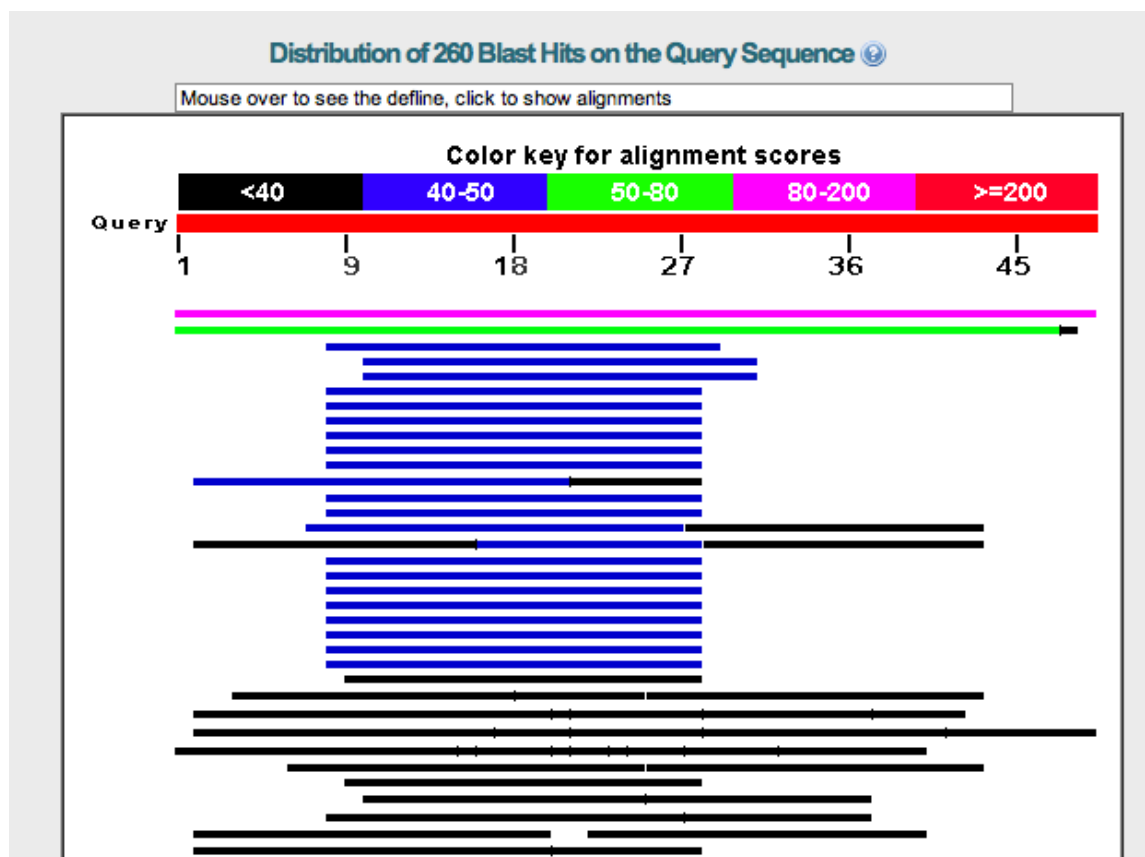
Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
gi 327374765 CP002585.1	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421,	97.6	158	100%	5e-18	100%	
gi 359757955 CP003150.1	<i>Pseudomonas fluorescens</i> F113, complete genome	58.0	58.0	100%	4e-06	90%	
gi 390421916 CP003274.1	<i>Alistipes finegoldii</i> DSM 17242, complete genome	38.2	38.2	38%	3.8	100%	
gi 383508497 CP003252.1	<i>Thermus thermophilus</i> JL-18, complete genome	38.2	68.4	40%	3.8	100%	
gi 381356398 AP012279.1	<i>Bradyrhizobium</i> sp. S23321 DNA, complete genome	38.2	191	85%	3.8	100%	
gi 333965676 CP002777.1	<i>Thermus thermophilus</i> SG0.5JP17-16, complete genome	38.2	68.4	40%	3.8	100%	
gi 262083393 CP001802.1	<i>Gordonia bronchialis</i> DSM 43247, complete genome	38.2	38.2	38%	3.8	100%	
gi 402798256 CP003788.1	<i>Nocardioopsis alba</i> ATCC BAA-2165, complete genome	36.2	36.2	36%	15	100%	
gi 357155363 XM_003577048.1	PREDICTED: <i>Brachypodium distachyon</i> scarecrow-like protein 1	36.2	36.2	36%	15	100%	G
gi 333484608 CP002329.1	<i>Mycobacterium</i> sp. JDM601, complete genome	36.2	66.4	61%	15	100%	

Use the following data to construct your sequence.

Blue = C, Red = T, Green = A, Black = G



Below is the BLAST analysis of your sequence.



Descriptions

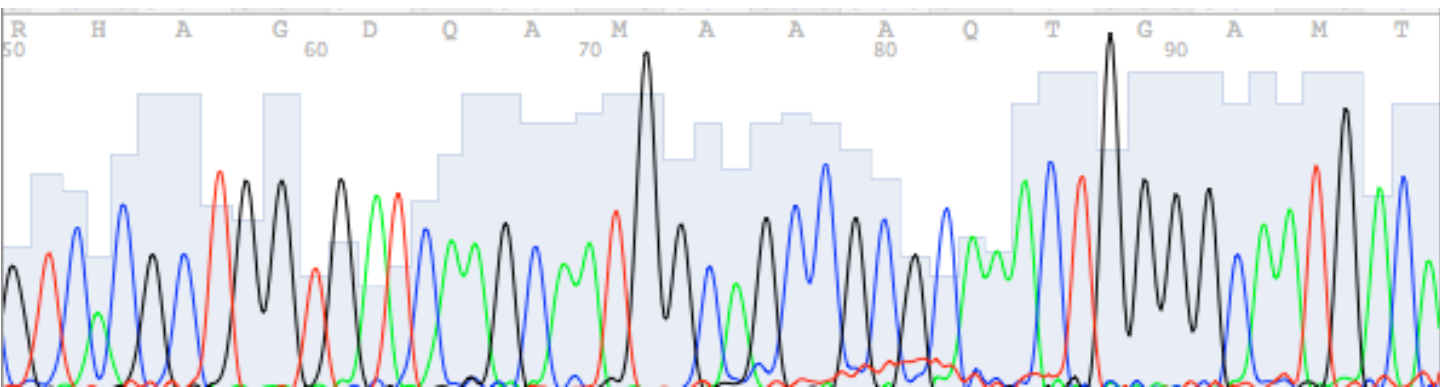
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Sequences producing significant alignments:

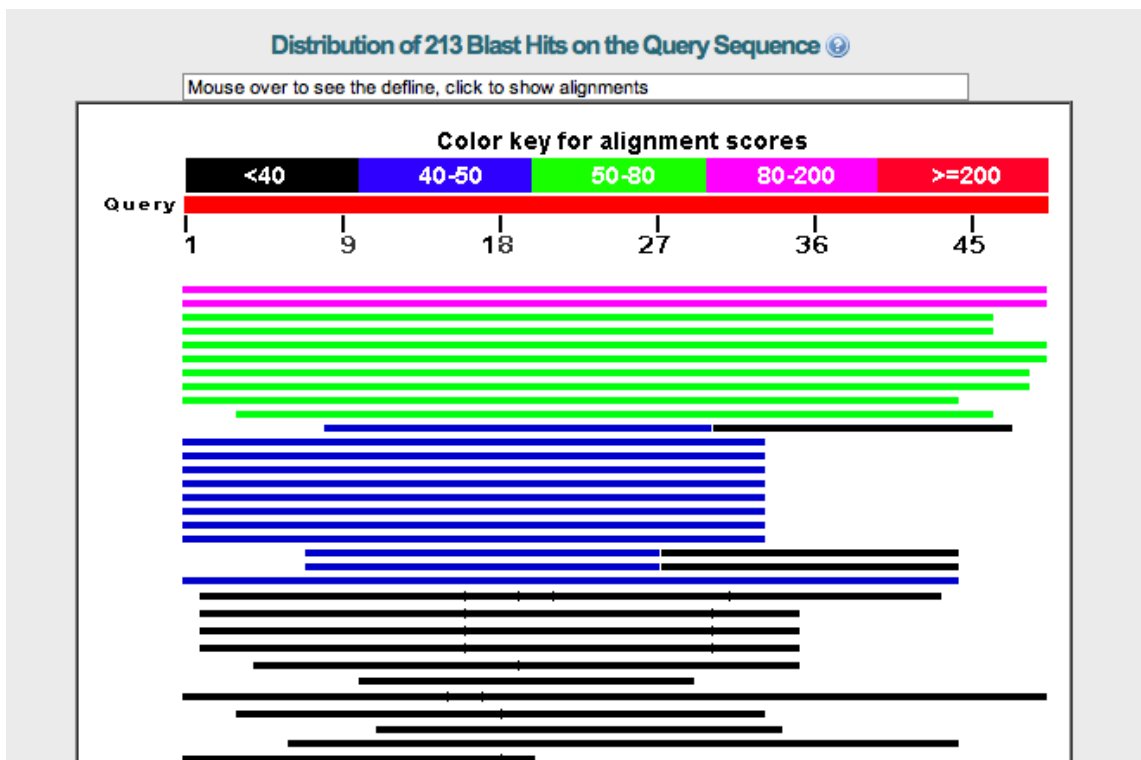
Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
qi 327374765 CP002585.1	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421	97.6	278	100%	5e-18	100%	
qi 359757955 CP003150.1	<i>Pseudomonas fluorescens</i> F113, complete genome	61.9	122	97%	3e-07	100%	
qi 403300134 XR_167683.1	PREDICTED: <i>Saimiri boliviensis</i> boliviensis ciliary rootlet coiled-coil, rootletin (42.1	42.1	42%	0.25	100%	
qi 359393185 JN248522.1	Uncultured bacterium clone MALINA_OTU32_430 photosyntheti	42.1	42.1	42%	0.25	100%	
qi 359393173 JN248516.1	Uncultured bacterium clone MALINA_OTU32_343 photosyntheti	42.1	42.1	42%	0.25	100%	
qi 402853120 XM_003891200.1	PREDICTED: <i>Papio anubis</i> ciliary rootlet coiled-coil, rootletin (40.1	40.1	40%	0.97	100%	
qi 397486792 XM_003814459.1	PREDICTED: <i>Pan paniscus</i> ciliary rootlet coiled-coil, rootletin (40.1	40.1	40%	0.97	100%	G
qi 392996994 AC244231.3	Homo sapiens BAC clone CH17-471H1 from chromosome 1, cc	40.1	40.1	40%	0.97	100%	
qi 381214411 AC245745.3	Homo sapiens BAC clone CH17-304K16 from chromosome 1, c	40.1	40.1	40%	0.97	100%	
qi 332266293 XR_123362.1	PREDICTED: <i>Nomascus leucogenys</i> rootletin-like (LOC1005830	40.1	40.1	40%	0.97	100%	GM

Use the following data to construct your sequence.

Blue = C, Red = T, Green = A, Black = G



Below is the BLAST analysis of your sequence.



Descriptions

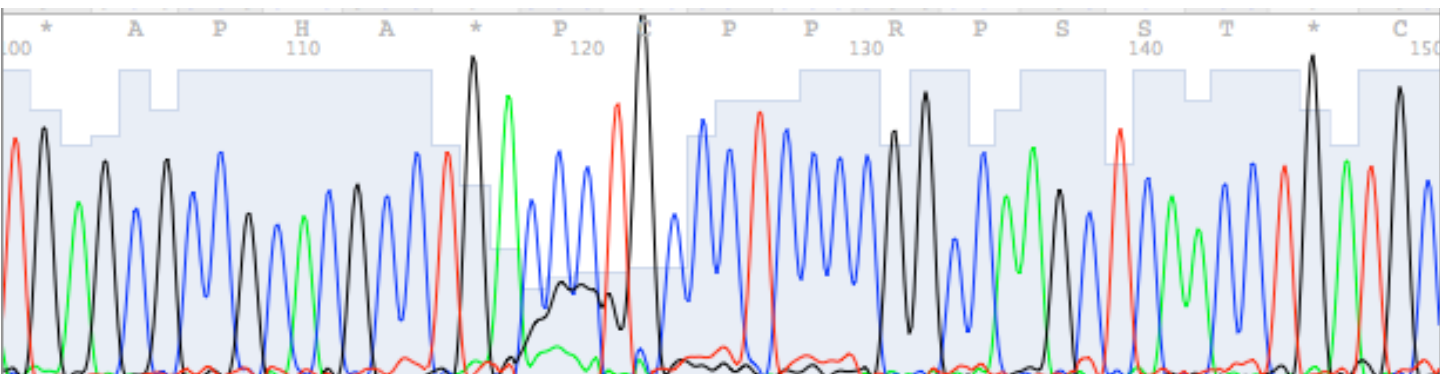
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Sequences producing significant alignments:

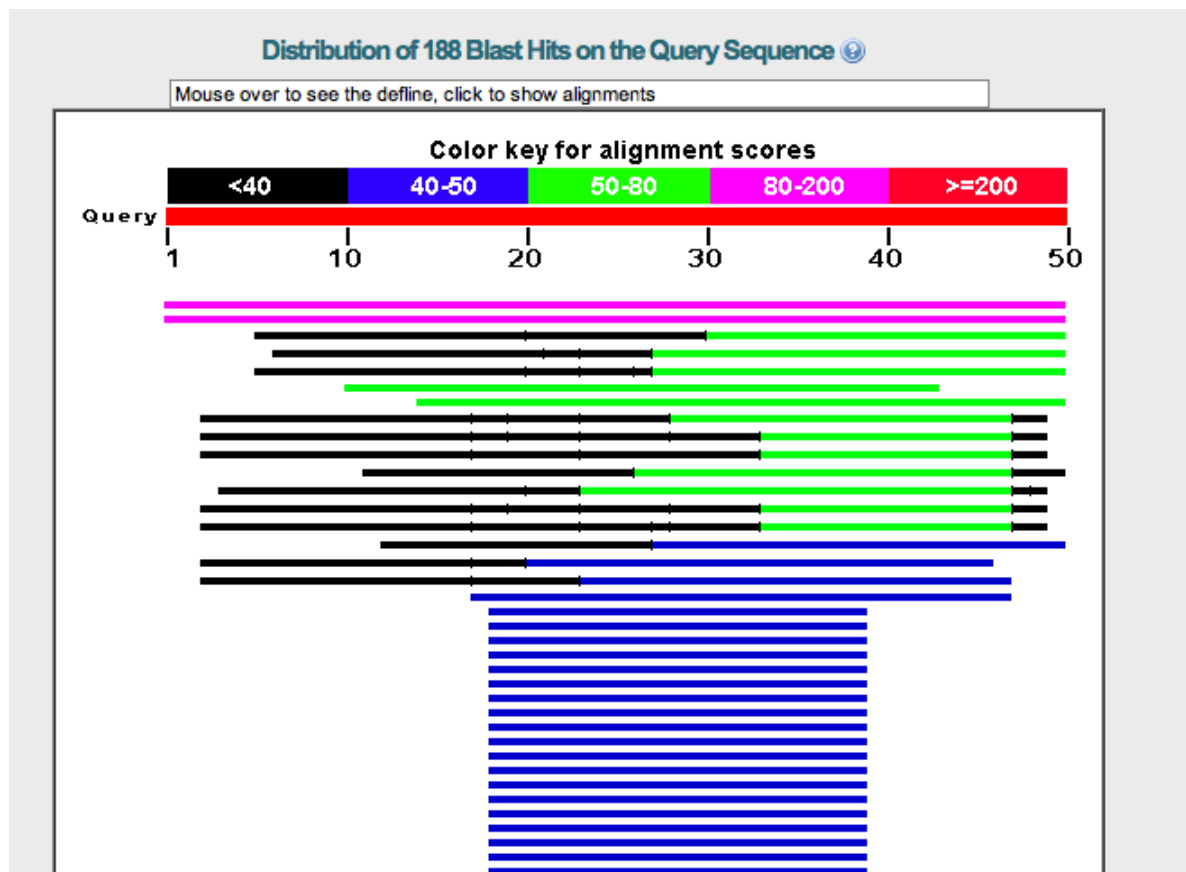
Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
qi 327374765 CP002585.1	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421,	97.6	190	100%	5e-18	100%	
qi 359757955 CP003150.1	<i>Pseudomonas fluorescens</i> F113, complete genome	89.7	156	100%	1e-15	100%	
qi 387159426 CP003041.1	<i>Pseudomonas fluorescens</i> A506, complete genome	67.9	160	93%	4e-09	100%	
qi 229359445 IAM181176.4	<i>Pseudomonas fluorescens</i> SBW25 complete genome	67.9	188	93%	4e-09	100%	
qi 71553748 CP000058.1	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A, complete geno	65.9	96.1	100%	2e-08	100%	
qi 28856110 AE016853.1	<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000, complete geno	65.9	156	100%	2e-08	100%	
qi 68342549 CP000076.1	<i>Pseudomonas protegens</i> Pf-5, complete genome	63.9	126	97%	7e-08	100%	
qi 63253978 CP000075.1	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a, complete genome	63.9	94.2	97%	7e-08	100%	
qi 323388126 HM752578.1	<i>Pseudomonas fluorescens</i> strain BBc6R8 T3SS gene cluster, coi	56.0	56.0	89%	2e-05	91%	
qi 253992019 CP000094.2	<i>Pseudomonas fluorescens</i> Pf0-1, complete genome	54.0	174	87%	6e-05	100%	

Use the following data to construct your sequence.

Blue = C, Red = T, Green = A, Black = G



Below is the BLAST analysis of your sequence.



Descriptions

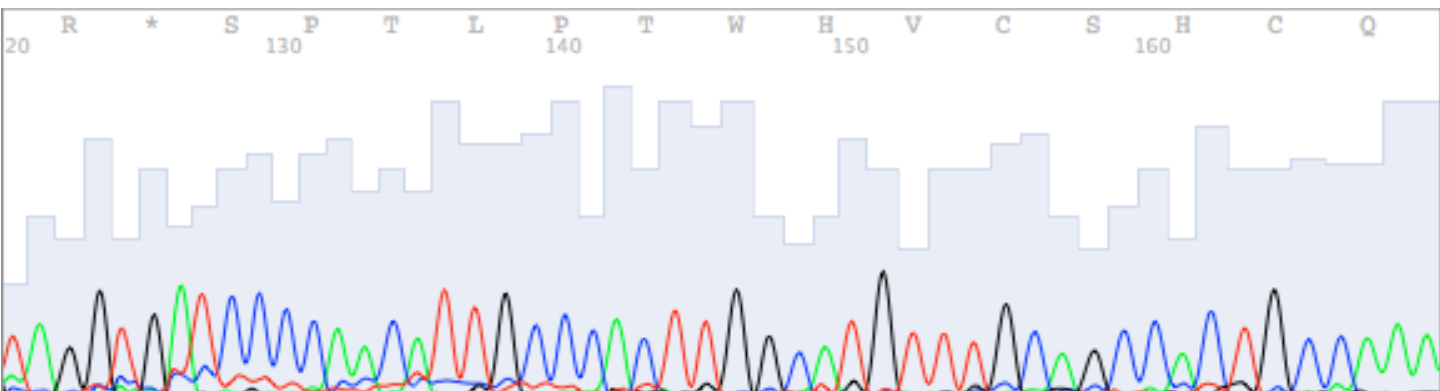
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Sequences producing significant alignments:

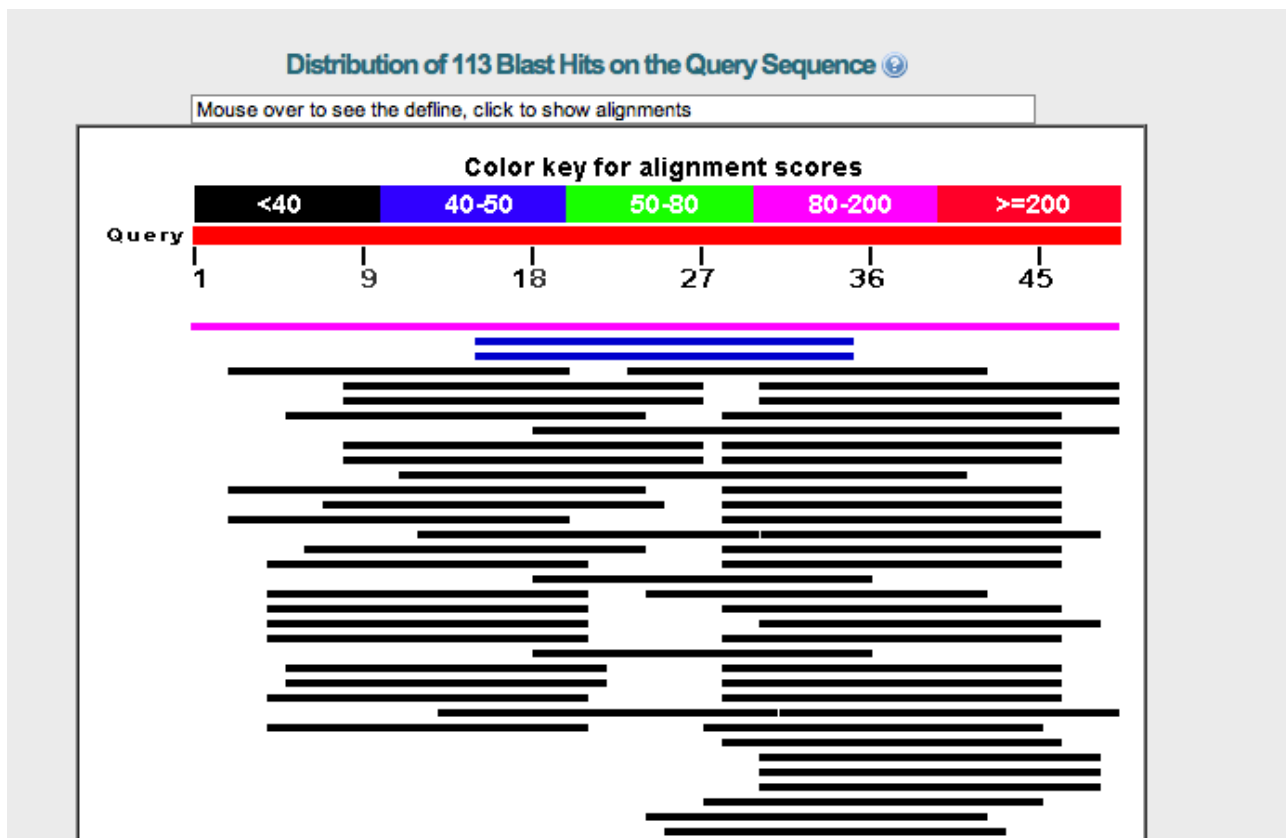
Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
gi 327374765 CP002585.1	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421, c	99.6	222	100%	1e-18	100%	
gi 359757955 CP003150.1	<i>Pseudomonas fluorescens</i> F113, complete genome	91.7	220	100%	3e-16	100%	
gi 387159426 CP003041.1	<i>Pseudomonas fluorescens</i> A506, complete genome	69.9	283	90%	1e-09	100%	
gi 68342549 CP000076.1	<i>Pseudomonas protegens</i> Pf-5, complete genome	63.9	339	88%	7e-08	100%	
gi 229359445 AM181176.4	<i>Pseudomonas fluorescens</i> SBW25 complete genome	61.9	341	90%	3e-07	100%	
gi 323388126 HM752578.1	<i>Pseudomonas fluorescens</i> strain BBc6R8 T3SS gene cluster, com	58.0	58.0	66%	4e-06	97%	
gi 145573243 CP000680.1	<i>Pseudomonas mendocina</i> ymp, complete genome	56.0	118	72%	2e-05	100%	
gi 397329500 CP003734.1	<i>Pseudomonas putida</i> DOT-T1E, complete genome	52.0	265	94%	3e-04	100%	
gi 388557647 CP003588.1	<i>Pseudomonas putida</i> ND6, complete genome	52.0	267	94%	3e-04	100%	
gi 313496345 CP002290.1	<i>Pseudomonas putida</i> BIRD-1, complete genome	52.0	205	94%	3e-04	100%	

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Blue = C, Red = T, Green = A, Black = G



Below is the BLAST analysis of your sequence.



Descriptions

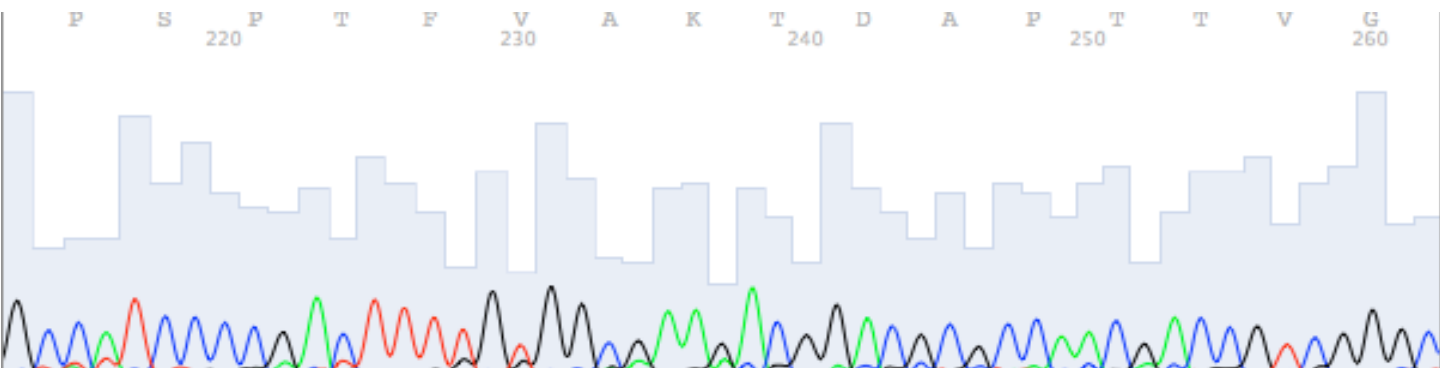
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [B](#) PubChem BioAssay

Sequences producing significant alignments:

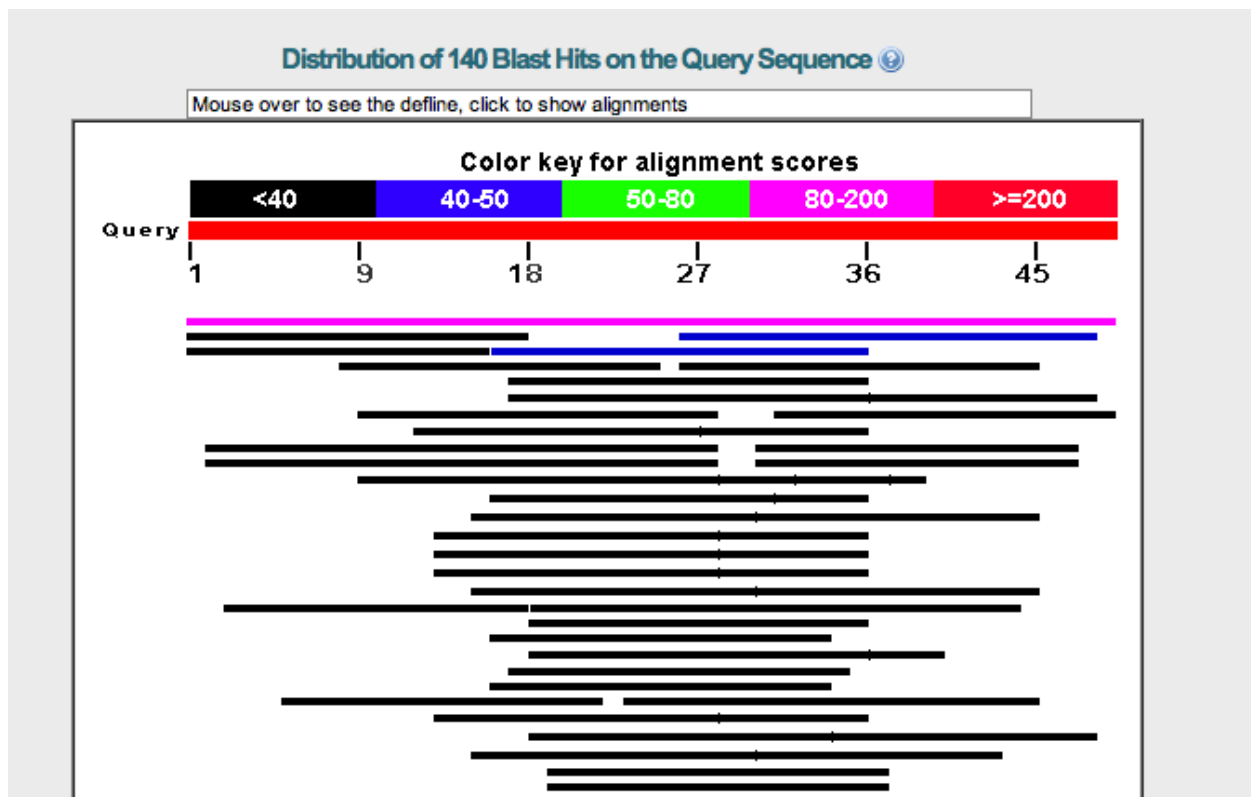
Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
gi 327374765 CP002585.1	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421,	97.6	158	100%	5e-18	100%	
gi 51101130 AC120877.15	<i>Mus musculus</i> chromosome 6, clone RP24-548D19, complete s	40.1	40.1	40%	0.97	100%	
gi 74039096 AC159332.11	<i>Mus musculus</i> 6 BAC RP23-413D8 (Roswell Park Cancer Institu	40.1	40.1	40%	0.97	100%	
gi 387853393 CP002961.1	<i>Emticia oligotrophica</i> DSM 17448, complete genome	38.2	38.2	38%	3.8	100%	
gi 363737092 XM_422647.3	PREDICTED: <i>Gallus gallus</i> thrombospondin-type laminin G dom	38.2	38.2	38%	3.8	100%	GM
gi 333747798 CP002736.1	<i>Desulfotomaculum carboxydivorans</i> CO-1-SRB, complete geno	38.2	38.2	38%	3.8	100%	
gi 326925740 XM_003209020.1	PREDICTED: <i>Meleagris gallopavo</i> protein TSPEAR-like (LOC100	38.2	38.2	38%	3.8	100%	GM
gi 227481098 AM712908.1	<i>Ceratophyllum demersum</i> chloroplast, complete genome	38.2	76.3	38%	3.8	100%	
gi 148508422 EF614270.1	<i>Ceratophyllum demersum</i> chloroplast, complete genome	38.2	76.3	38%	3.8	100%	
gi 156040422 XM_001587148.1	<i>Sclerotinia sclerotiorum</i> 1980 hypothetical protein (SS1G_1222	38.2	38.2	38%	3.8	100%	G

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Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
gi 327374765 CP002585.1	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421,	97.6	129	100%	5e-18	100%	
gi 403643428 CP002907.1	<i>Gordonia</i> sp. KTR9, complete genome	44.1	44.1	44%	0.062	100%	
gi 282154984 AP011532.1	<i>Methanocella paludicola</i> SANA E DNA, complete genome	40.1	40.1	40%	0.97	100%	
gi 374852043 AP011706.1	Uncultured planctomycete DNA, fosmid clone: JFF022_C11	38.2	38.2	38%	3.8	100%	
gi 336261049 XM_003345268.1	<i>Sordaria macrospora</i> k-hell hypothetical protein (SMAC_04549)	38.2	38.2	38%	3.8	100%	G
gi 295429362 CP002008.1	<i>Caulobacter segnis</i> ATCC 21756, complete genome	38.2	68.4	63%	3.8	100%	
gi 258564892 XM_002583145.1	<i>Uncinocarpus reesii</i> 1704 conserved hypothetical protein, mRNA	38.2	38.2	38%	3.8	100%	G
gi 239794502 AP010904.1	<i>Desulfovibrio magneticus</i> RS-1 DNA, complete genome	38.2	68.4	48%	3.8	100%	
gi 145350002 XM_001419377.1	<i>Ostreococcus lucimarinus</i> CCE9901 predicted protein (OSTLU_3	38.2	38.2	55%	3.8	93%	G
gi 144579271 CP000588.1	<i>Ostreococcus lucimarinus</i> CCE9901 chromosome 8, complete se	38.2	38.2	55%	3.8	93%	G M