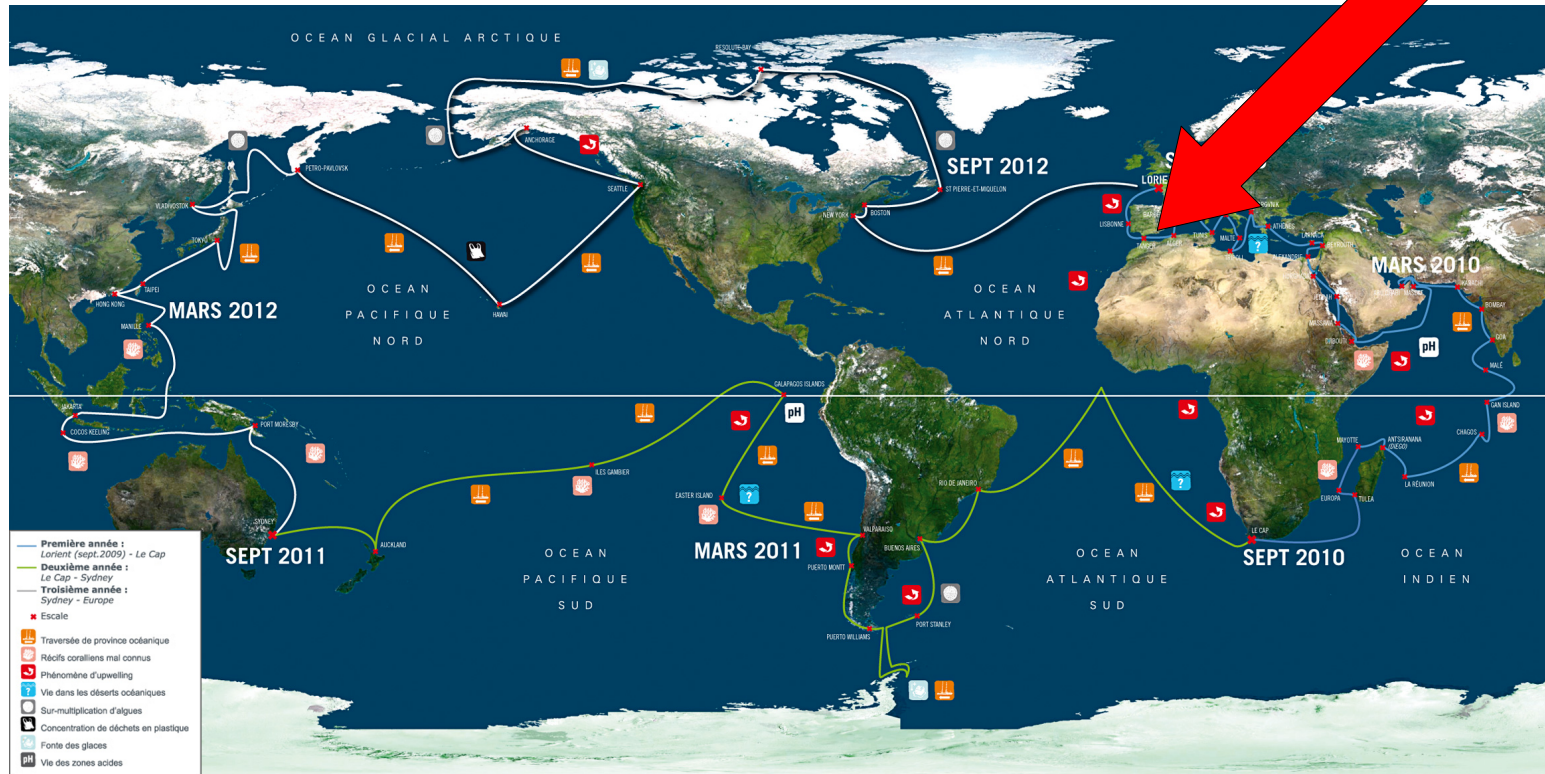


Analyse et classification de la séquence d'ADN TARA 7S_3634040



Présentation de la séquence d'ADN

Tanger

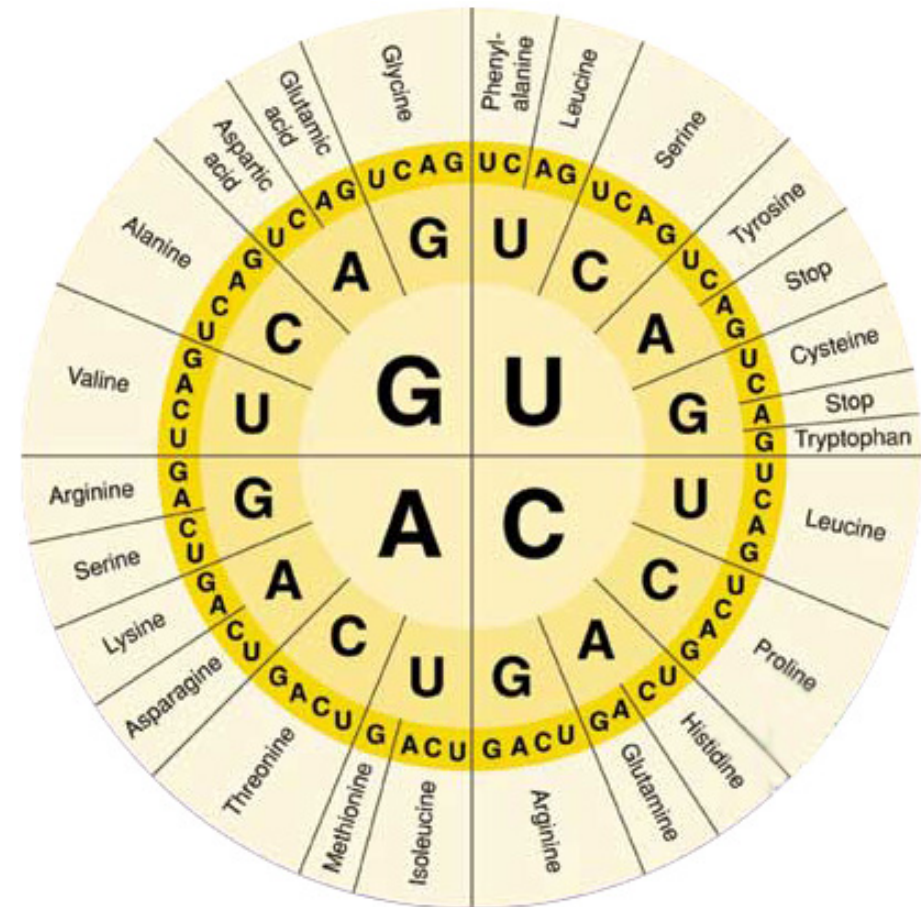
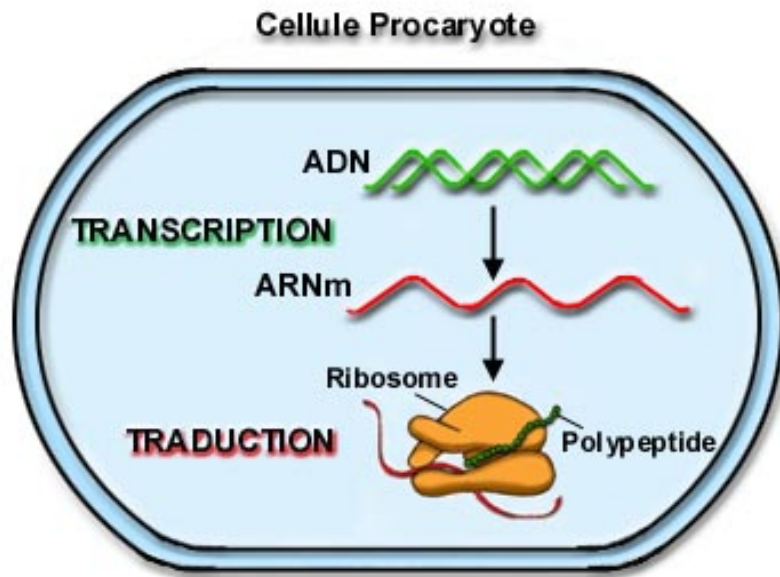


TARA7S_3634040 ADN génomique (Tanger-Alger, station 7 [SRF])

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Transcription et traduction

Utilisation d'Open Reading Frame (ORF)



Code génétique universel

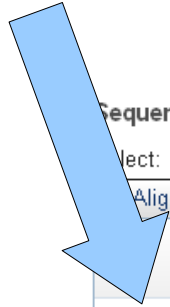
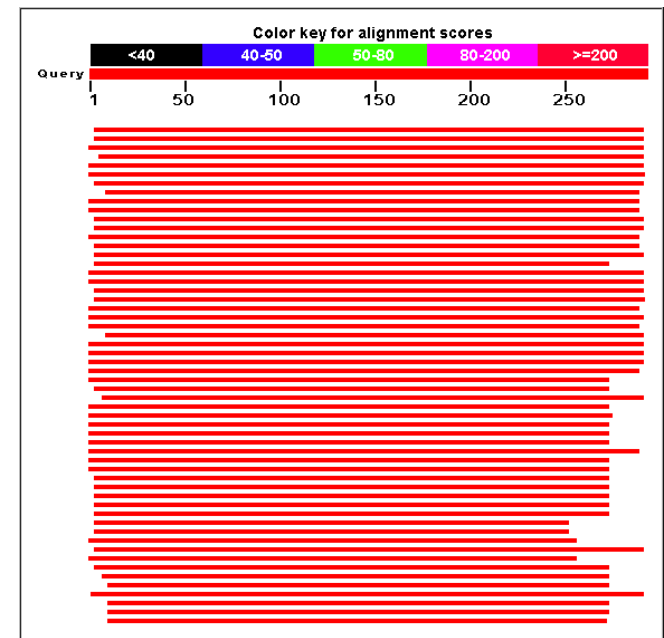
Séquence de 292 acides aminés

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BLAST_P

Basic Local Alignment Search Tool

« FAD-linked oxidase » présente chez une **gammaprotéobactérie**.



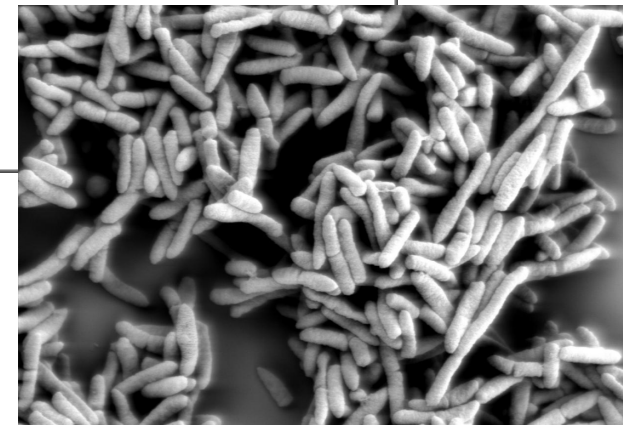
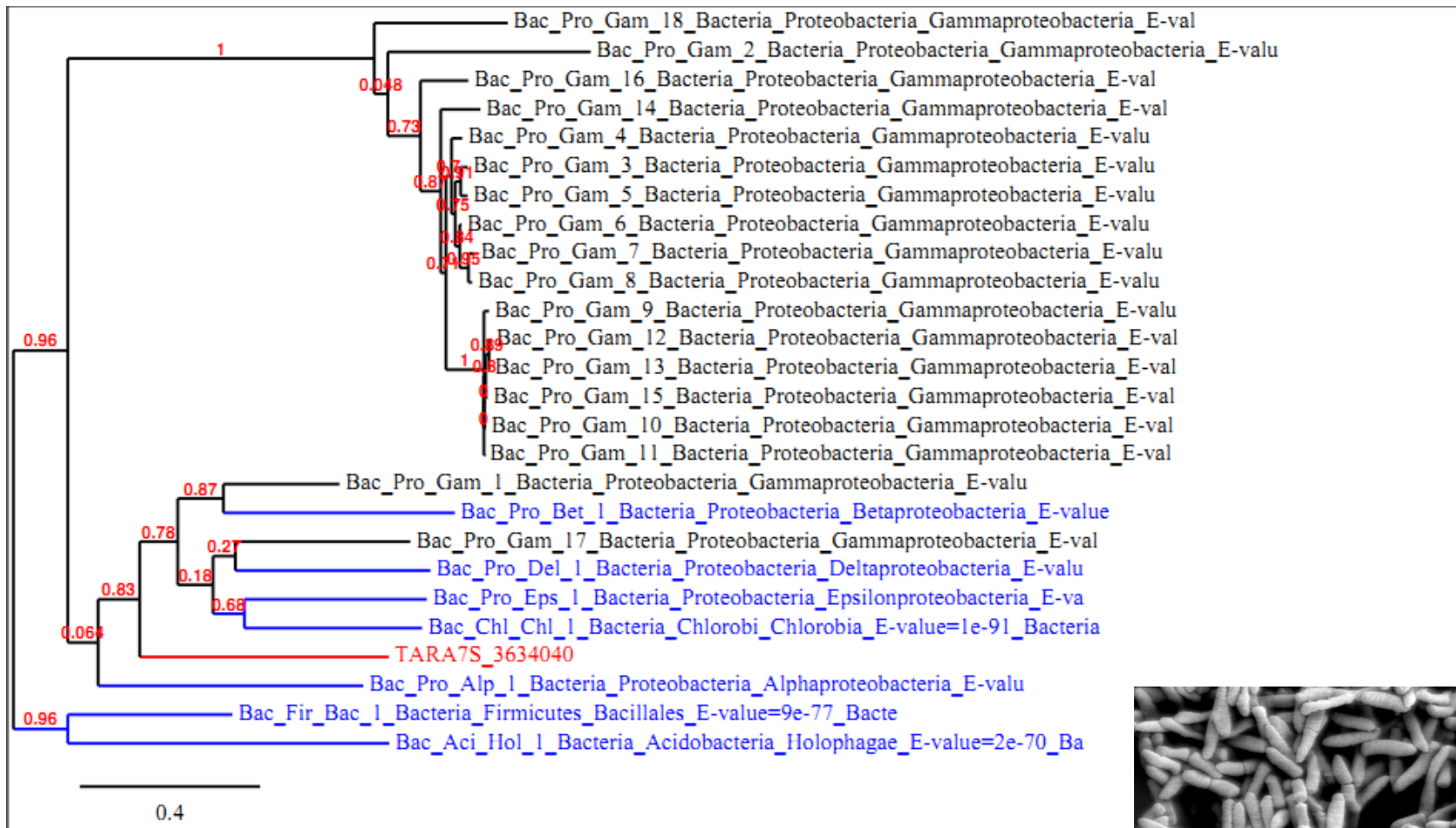
Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

Description	E value	Max ident
<input type="checkbox"/> FAD linked oxidase domain-containing protein [Pseudomonas aeruginosa VRFP01] >qb EME12322.1 FAD linked oxidase domain-containing protein [Pseudor	3e-111	54%
<input type="checkbox"/> FAD linked oxidase domain-containing protein [Pseudomonas aeruginosa PA7] >qb ABR82404.1 FAD linked oxidase domain protein [Pseudomonas aeruginos	4e-111	55%
<input type="checkbox"/> hypothetical protein CT0170 [Chlorobium tepidum TLS] >qb AAM71418.1 conserved hypothetical protein [Chlorobium tepidum TLS]	1e-106	55%
<input type="checkbox"/> FAD linked oxidase domain protein [Vibrio parahaemolyticus AN-5034] >ref ZP_12107637.1 oxidoreductase, FAD-binding, putative [Vibrio parahaemolyticus 103	2e-99	51%
<input type="checkbox"/> oxidoreductase, FAD-binding [Methylococcus capsulatus str. Bath] >qb AAU91361.1 putative oxidoreductase, FAD-binding [Methylococcus capsulatus str. Bath]	3e-93	49%
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<input type="checkbox"/> FAD linked oxidase-like protein [Sulfurimonas denitrificans DSM 1251] >qb ABB44496.1 FAD linked oxidase-like protein [Sulfurimonas denitrificans DSM 1251]	2e-89	48%
<input type="checkbox"/> FAD linked oxidase domain-containing protein [Syntrophobacter fumaroxidans MPOB] >qb ABK15844.1 FAD linked oxidase domain protein [Syntrophobacter fum	4e-89	48%
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<input type="checkbox"/> FAD linked oxidase domain protein [Burkholderia graminis C4D1M] >qb EDT11557.1 FAD linked oxidase domain protein [Burkholderia graminis C4D1M]	1e-80	47%

Phylogénie de la séquence peptidique étudiée



Les autres séquences

Séquence d'ADN TARA23S_3634010

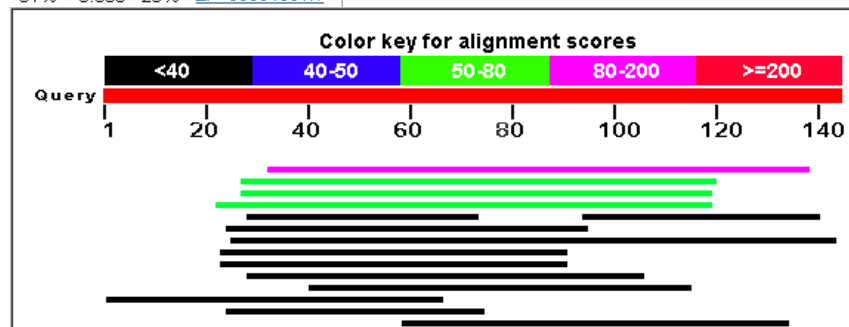
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Transcription/Traduction

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BLASTp

Description	Max score	Total score	Query cover	E value	Max ident	Accession
hypothetical protein GB2207_09866 [gamma proteobacterium HTCC2207] > qblEAS48108.1 hypothetical protein GB2207_09866 [marine	157	157	73%	6e-47	67%	ZP_01223549.1
hypothetical protein GPB2148_3139 [marine gamma proteobacterium HTCC2148] > qblEEB80323.1 hypothetical protein GPB2148_3139	60.5	60.5	64%	1e-09	37%	ZP_05093350.1
possible transmembrane protein [marine gamma proteobacterium HTCC2143] > qblEAW31244.1 possible transmembrane protein [mari	58.9	58.9	63%	5e-09	38%	ZP_01617062.1
hypothetical protein PrubA2_16796 [Pseudoalteromonas rubra ATCC 29570]	53.9	53.9	67%	3e-07	34%	ZP_10295183.1
hypothetical protein OAN307_c45140 [Octadecabacter antarcticus 307] > qblAGI69871.1 hypothetical protein OAN307_c45140 [Octadecab	39.3	39.3	31%	0.048	40%	YP_007706505.1
hypothetical protein [Candidatus Puniceispirillum marinum IMCC1322] > qblADE40669.1 possible transmembrane protein [Candidatus P	38.9	38.9	48%	0.064	27%	YP_003552753.1
hypothetical protein GPB2148_1859 [marine gamma proteobacterium HTCC2148] > qblEEB79211.1 hypothetical protein GPB2148_1859	38.9	38.9	81%	0.068	25%	ZP_05094631.1
hypothetical protein OAN307_c18560 [Octadecabacter antarcticus 307] > qblAGI67510.1 hypothetical protein OAN307_c18560 [Octadecab	38.9	38.9				
hypothetical protein OAN307_c11030 [Octadecabacter antarcticus 307] > qblAGI66808.1 hypothetical protein OAN307_c11030 [Octadecab	38.5	38.5				
hypothetical protein HIMB100_00012280 [SAR116 cluster alpha proteobacterium HIMB100] > qblEHI48875.1 hypothetical protein HIMB100	35.8	35.8				
methyltransferase [Oxalobacter formigenes OXCC13] > qblEEE029540.1 methyltransferase [Oxalobacter formigenes OXCC13]	35.8	35.8				
periplasmic binding protein [Stackebrandtia nassauensis DSM 44728] > qblADD44155.1 periplasmic binding protein [Stackebrandtia nas	35.4	35.4				
predicted protein [Arabidopsis thaliana]	35.0	35.0				
hypothetical protein HIMB59_00011640 [alpha proteobacterium HIMB59] > qblAFS49346.1 hypothetical protein HIMB59_00011640 [alpha r	33.1	33.1				
ABC transporter permease [Acholeplasma laidlawii PG-8A] > qblABX81335.1 ABC-type transport system, permease component [Acholepl	34.7	34.7				



Remerciements

Pascal Hingamp, Laboratoire Informatique Génomique et Structurale, Université Aix Marseille pour son aide précieuse et la mise à disposition du website www.annotathon.org

Merçi *de votre attention*

