

Страменопилы

(финальная презентация)

	Название	Идентификатор	Длина генома	Число генов
Екатерина Гришина	<i>Aureococcus anophagefferens</i>	GCF_000186865.1	56.7 Mb	11522
Полина Шайдурова	<i>Phytophthora sojae</i>	GCF_000149755.1	82.6 Mb	28142
Илья Герман	<i>Blastocystis hominis</i>	GCF_000151665.1	18.8 Mb	6020
Ян Аникиев	<i>Nannochloropsis gaditana</i>	GCF_000240725.1	34 Mb	3465
Михаил Сизов	<i>Aphanomyces invadans</i>	GCF_000520115.1	71.4 Mb	15416
Ульяна Ключникова	<i>Aphanomyces astaci</i>	GCF_000520075.1	75.8 Mb	19 584
Георгий Караваев	<i>Thalassiosira pseudonana</i>	GCF_000149405.2	32.4 Mb	11771
Денис Михайлов	<i>Phytophthora nicotianae</i>	GCF_000247585.1	82.4 Mb	23240
Егор Попов	<i>Phaeodactylum tricornutum</i>	GCF_000150955.2	27.5 Mb	10398

Число G квадруплексов

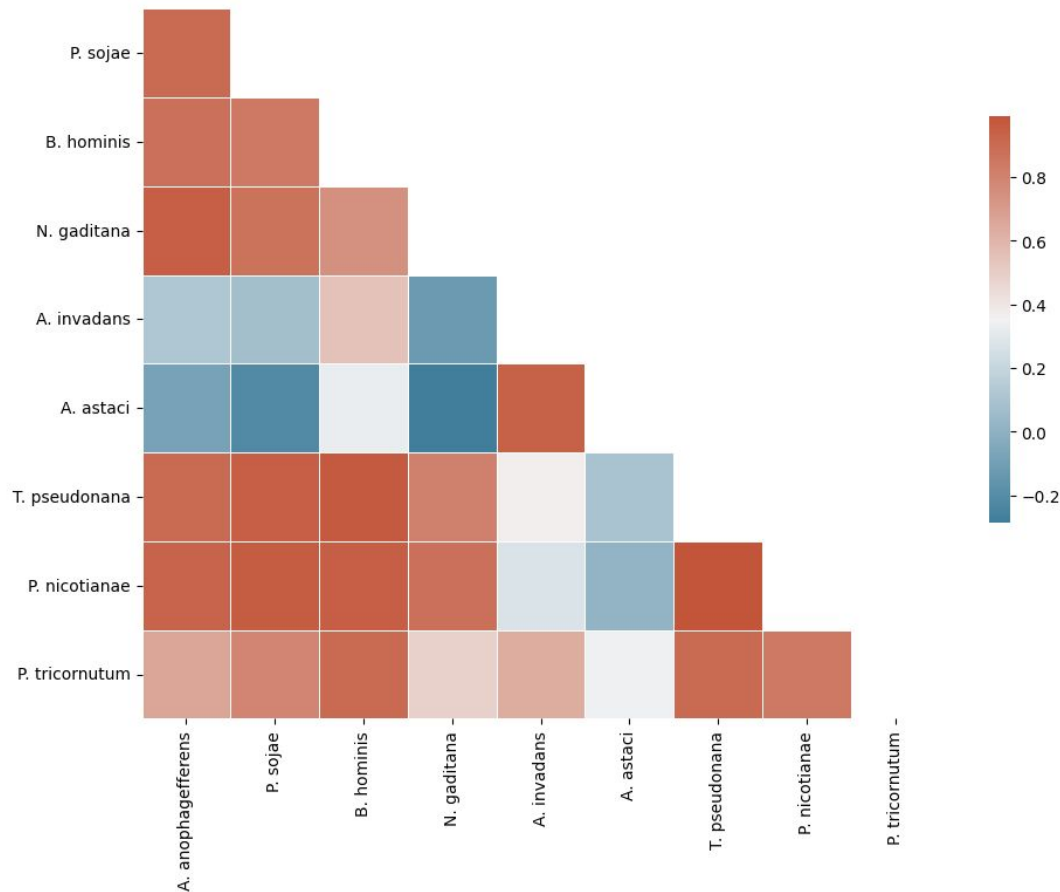
	Всего	Экзоны	Интроны	Промотеры	Downstream	Межгенники
A. anophagefferens	415	101	73	105	33	256
P. sojae	2426	530	256	1100	402	1693
B. hominis	105	42	8	34	9	59
N. gaditana	18495	1908	1550	1756	573	15349
A. invadans	33	31	1	14	3	8
A. astaci	170	127	11	22	2	8
T. pseudonana	1197	393	60	474	131	769
P. nicotianae	41	12	1	14	5	28
P. tricornutum	45	21	0	25	4	25

Доля G квадруплексов

	Экзоны	Интроны	Промотеры	Downstream	Межгенники
A. anophagefferens	0.24	0.18	0.25	0.08	0.62
P. sojae	0.22	0.11	0.45	0.17	0.70
B. hominis	0.4	0.08	0.32	0.09	0.56
N. gaditana	0.1	0.08	0.09	0.03	0.83
A. invadans	0.94	0.03	0.42	0.01	0.24
A. astaci	0.75	0.06	0.13	0.02	0.05
T. pseudonana	0.33	0.05	0.39	0.11	0.64
P. nicotianae	0.29	0.02	0.34	0.12	0.68
P. tricornutum	0.47	0.0	0.56	0.09	0.56

G-Quadruplex fractions

A. anophagefferens -



Видим, что почти все организмы коррелируют по долям квадруплексов, кроме A. invadans и A. astaci, представителей одного рода

Число Z-ДНК (ZDNABERT)

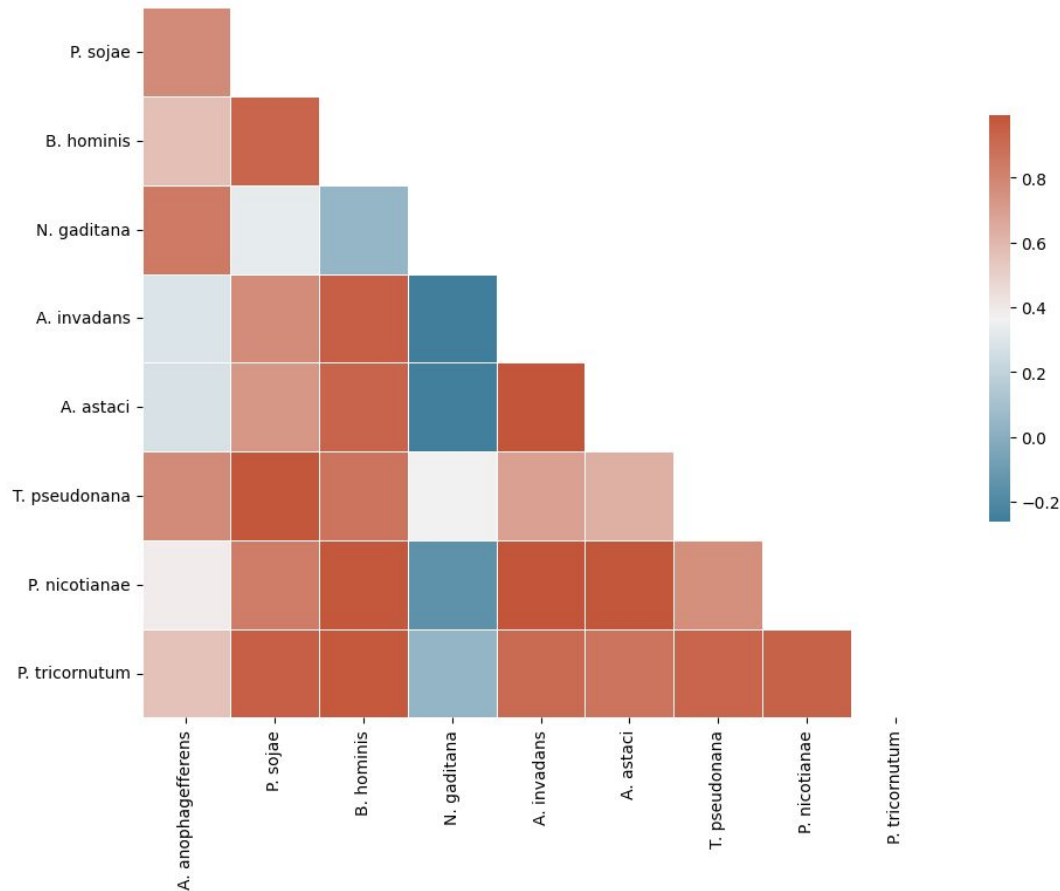
	Всего	Экзоны	Интроны	Промотеры	Downstream	Межгенники
A. anophagefferens	19737	7074	1500	4006	777	11408
P. sojae	104869	57326	7219	38401	6715	42806
B. hominis	1178	836	49	336	48	328
N. gaditana	30287	4262	970	2775	599	25249
A. invadans	2717	3538	303	989	174	351
A. astaci	5661	4306	189	846	109	211
T. pseudonana	3132	1618	197	1306	281	1362
P. nicotianae	2084	2273	77	792	144	467
P. tricornutum	1113	741	46	471	105	340

Доля Z-ДНК (ZDNABERT)

	Экзоны	Интроны	Промотеры	Downstream	Межгенники
A. anophagefferens	0.36	0.08	0.20	0.04	0.58
P. sojae	0.55	0.07	0.37	0.06	0.41
B. hominis	0.71	0.04	0.29	0.04	0.28
N. gaditana	0.14	0.03	0.09	0.02	0.83
A. invadans	1.3	0.11	0.36	0.06	0.13
A. astaci	0.76	0.03	0.15	0.02	0.04
T. pseudonana	0.51	0.06	0.42	0.09	0.43
P. nicotianae	1.09	0.04	0.38	0.07	0.22
P. tricornutum	0.67	0.04	0.42	0.09	0.31

ZDNABERT fractions

A. anophagefferens -



Здесь хорошо коррелируют все, кроме A. anophagefferens и N. gaditana, оомицет и водоросль (живущие в воде)

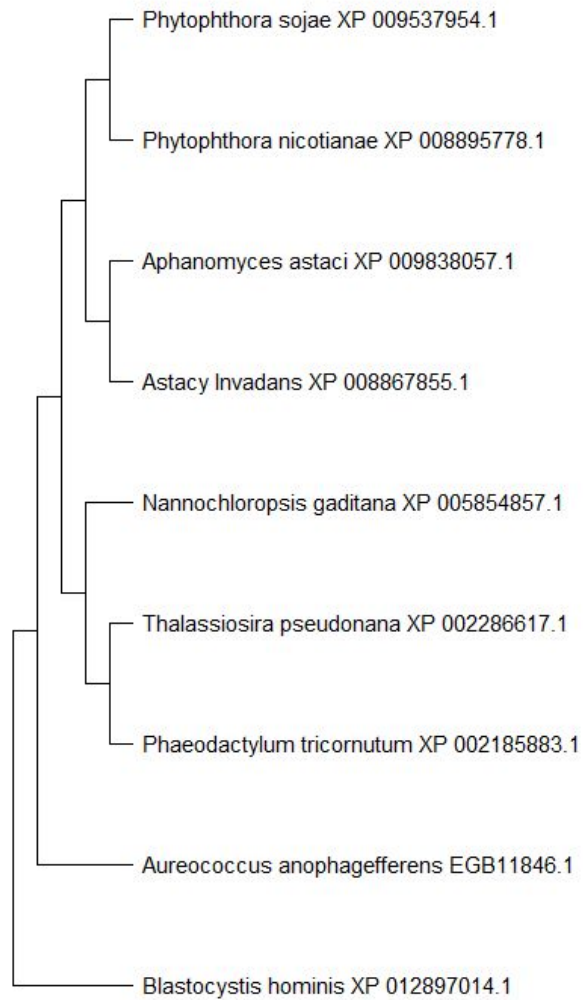
Параметры

- Выравнивая строились при помощи **ClustalW** со стандартными параметрами
- Деревья строились при помощи **Minimum Evolution Tree** со стандартными параметрами
- Параметры для ZHUNT были взяты с прошлого года, то есть запуск команды выглядел так: **!./zhunt3 12 8 12 genomic.fna** и порог был равен **300**
- Параметры для ZDNABERT были стандартными, то есть:

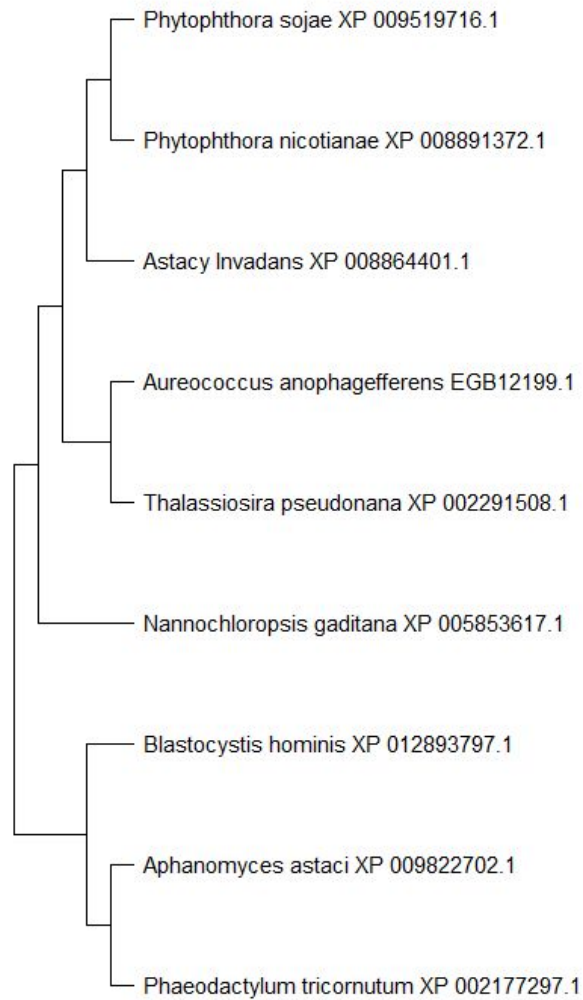
model = 'HG kouzine'
model_confidence_threshold = 0.5
minimum_sequence_length = 10

Pfam Domain	HGNC approved symbol	Function
PF00004	ATAD2	Chromatin remodeling
PF00012	HSPA1A	Histone modification write cofactor
PF00022	ACTB	Chromatin remodeling, Histone modification read
PF00063	MYO1C	Chromatin remodeling cofactor
PF00069	AURKA	Histone modification write

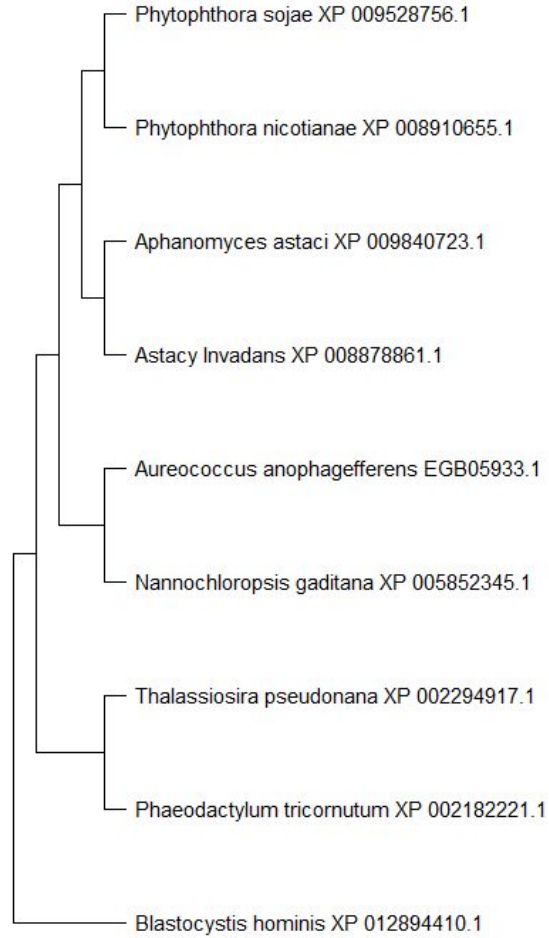
Gene PF00004



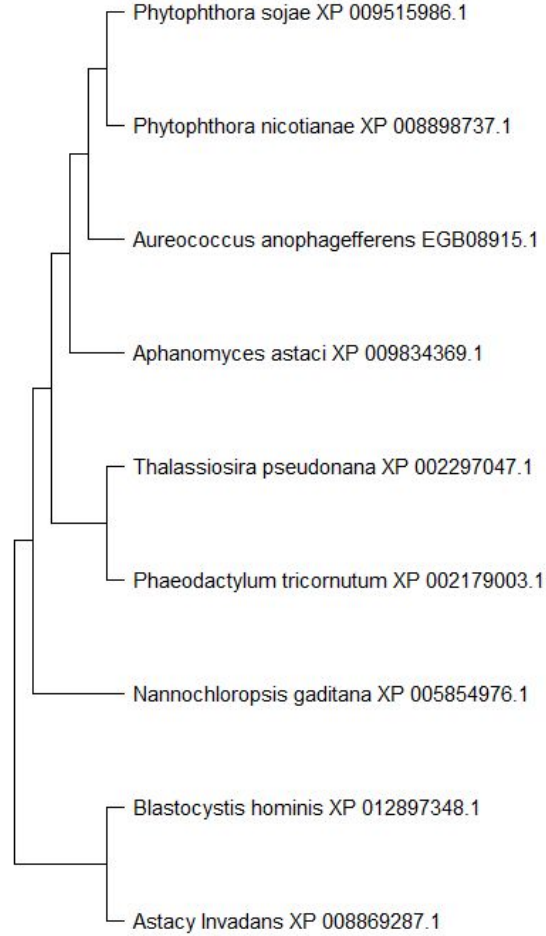
Gene PF0012



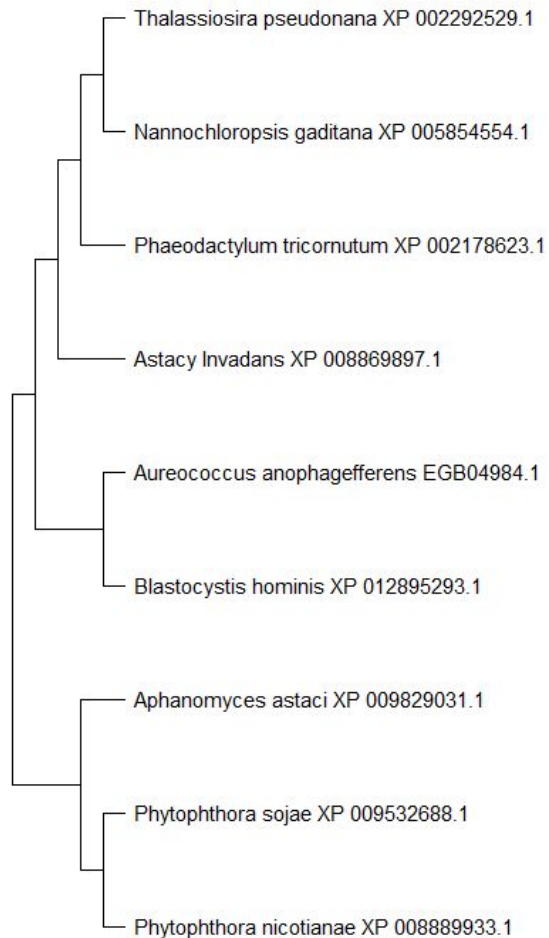
Gene PF0022



Gene PF0063



Gene PF0069



Фитофторы и Aphanomyces часто попадают в одну кладу (патогены). Aureococcus рядом с Blastocystis (паразиты). И оставшиеся 3 водоросли группируются часто в одну кладу.

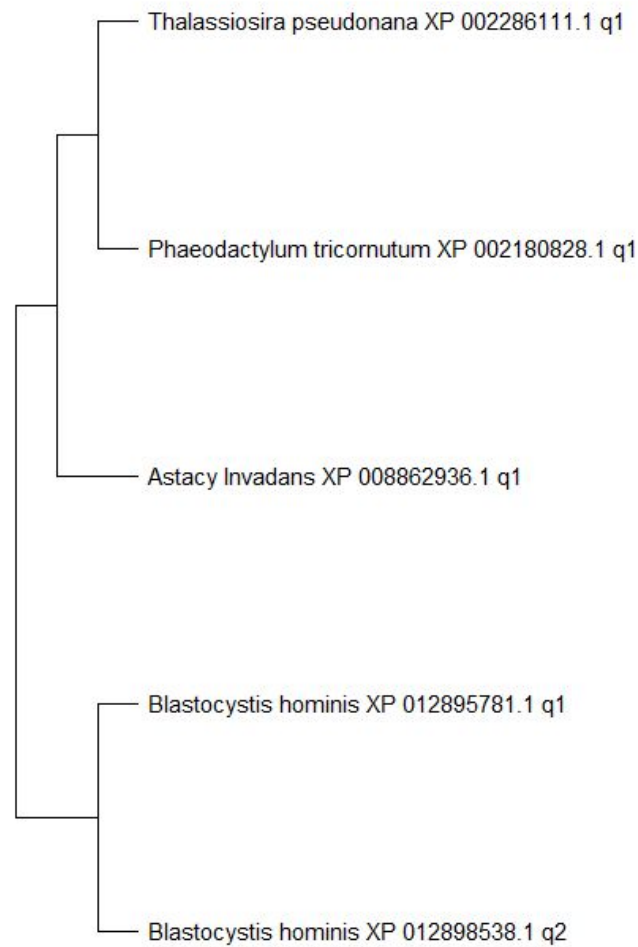
GQ PF00022 (Chromatin remodeling cofactor)

1. <i>Thalassiosira pseudonana</i> XP 002286111.1 q1	G G G G T T G G G G G T - G G T G G G A G G A G G G G - -
2. <i>Blastocystis hominis</i> XP 012895781.1 q1	C C C A C C G G T C C C A C G G G A C C C A C G G G A C C C
3. <i>Blastocystis hominis</i> XP 012898538.1 q2	- - C C C C G T T T C C C C T T - - C C C G C T A G C C C -
4. <i>Astacy Invadans</i> XP 008862936.1 q1	- G G G G T G G T G G - - G G T G G G C G G G G G G - - -
5. <i>Phaeodactylum tricornutum</i> XP 002180828.1 q1	- G G G A T G G G G A T T C G T C G G G G G G T G G G - - -

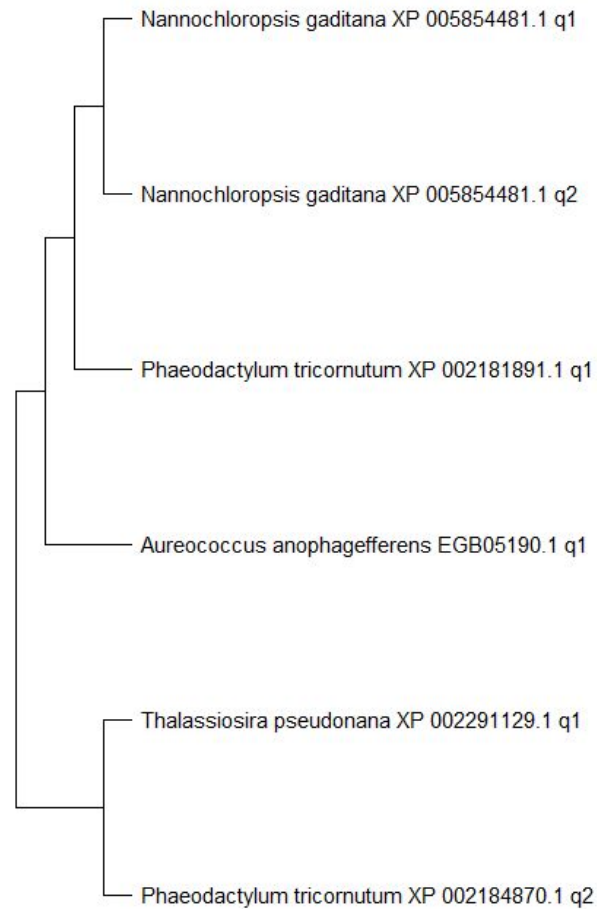
GQ PF00118

[illegible]

GQ PF00022



GQ PF00118



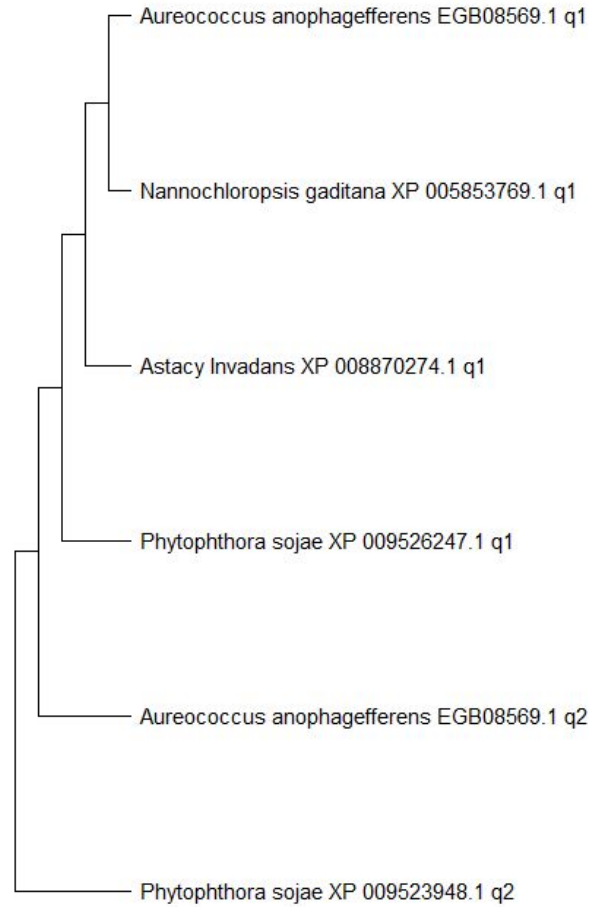
GQ PF00171

1. Aureococcus anophagefferens EGB08569.1 q1	- -	G G G G G G G C G G C G G G T C G C G G G G C G G G C G G G
2. Aureococcus anophagefferens EGB08569.1 q2	G G G C C T G G G C G A C C T G G G G C T G C G C C G G G G	- -
3. Phytophthora sojae XP 009526247.1 q1	- -	G G G A G G G T C G C C G G G C G C T G G G G G - - - - -
4. Phytophthora sojae XP 009523948.1 q2	- - -	C - - - - -
5. Astacy Invadans XP 008870274.1 q1	-	G G G G G G G G C G G T G G G G - G C A G G G G G - - - - -
6. Nannochloropsis gaditana XP 005853769.1 q1	-	G G G A T A A G G G A T G G G T C G A G G G - - - - -

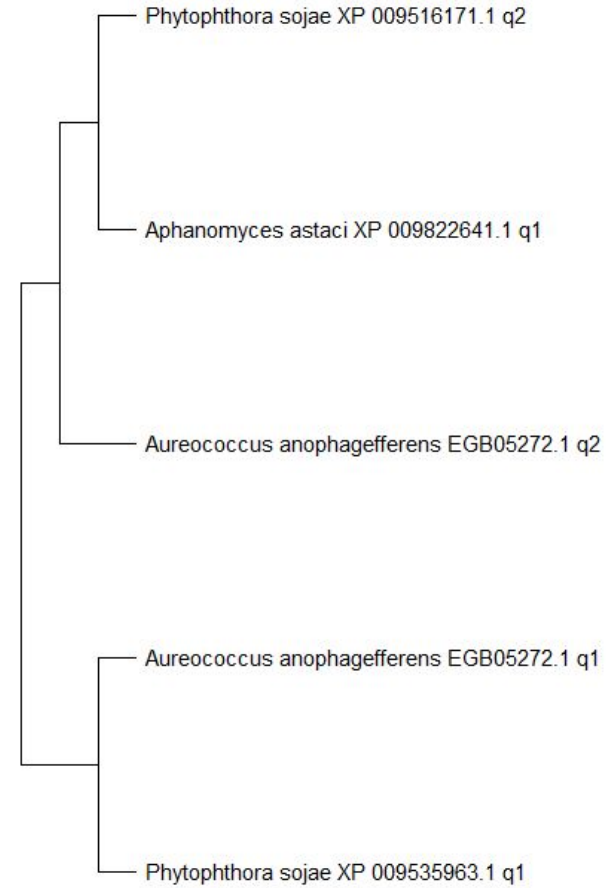
GQ PF00224 (Histone modification write cofactor)

1. Aureococcus anophagefferens EGB05272.1 q1	- - -	G G G C T A C C T G G G A G C G G G C A G C C C G G G
2. Aureococcus anophagefferens EGB05272.1 q2	C C C A G G C C G C C C A G A C G C C C G C G G A G C C C	-
3. Phytophthora sojae XP 009535963.1 q1	- - - -	G G G T A A A G G G G A T T T A G G G A T C A G G G
4. Phytophthora sojae XP 009516171.1 q2	-	C C C T G A T C C C T A A A C C C C C T T T A C C C - - -
5. Aphanomyces astaci XP 009822641.1 q1	- - - - -	C C C C C T C C C C C C C T C C C C - - -

GQ PF00171

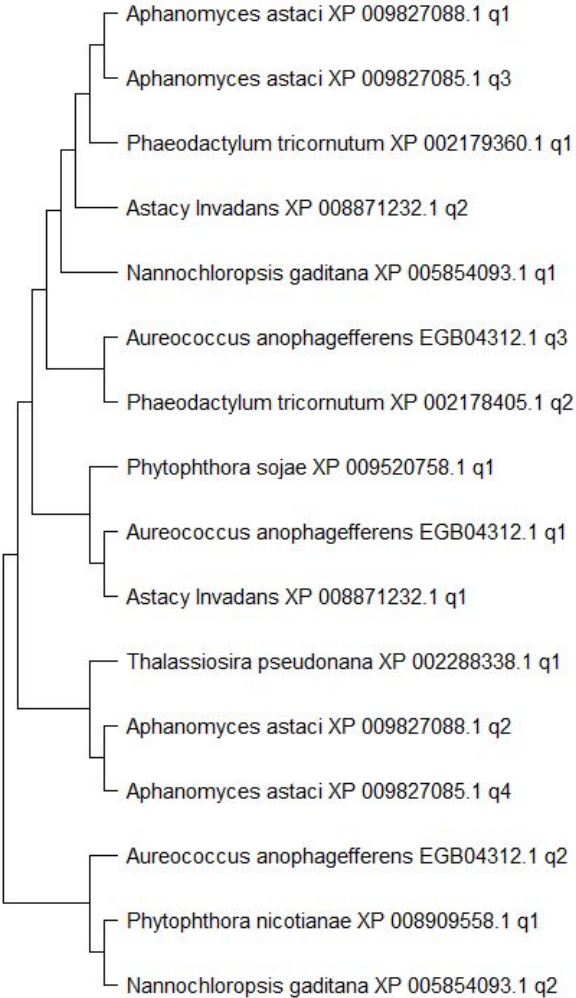


GQ PF00224



ZDNA PF06068 (Chromatin remodeling, modification write)

1. Aureococcus anophagefferens EGB04312.1 q1	-	-	-	G	G	G	C	T	C	G	C	G	C	G	C	G	A	C	-	-	-	-	-
2. Aureococcus anophagefferens EGB04312.1 q2	-	-	-	G	A	T	G	G	C	G	C	G	C	G	C	G	C	C	C	A	A	-	-
3. Aureococcus anophagefferens EGB04312.1 q3	-	-	-	-	-	-	G	G	G	C	G	C	G	T	A	C	A	G	-	-	-	-	-
4. Thalassiosira pseudonana XP 002288338.1 q1	-	-	-	-	-	-	G	T	G	T	G	T	G	T	G	T	G	-	-	-	-	-	-
5. Phytophthora sojae XP 009520758.1 q1	-	-	-	A	A	G	C	A	T	G	C	G	C	G	C	T	G	-	-	-	-	-	-
6. Aphanomyces astaci XP 009827088.1 q1	-	-	-	-	-	-	C	T	C	G	C	A	C	G	T	G	C	A	A	-	-	-	-
7. Aphanomyces astaci XP 009827088.1 q2	-	-	-	-	-	-	G	G	T	G	C	G	C	A	G	G	T	G	C	A	T	-	-
8. Aphanomyces astaci XP 009827085.1 q3	-	-	-	-	-	-	C	T	C	G	C	A	C	G	T	G	C	A	A	-	-	-	-
9. Aphanomyces astaci XP 009827085.1 q4	-	-	-	-	-	-	G	G	T	G	C	G	C	A	G	G	T	G	C	A	T	-	-
10. Astacy Invadans XP 008871232.1 q1	-	-	-	A	G	G	C	G	G	G	T	G	C	G	C	G	A	C	C	-	-	-	-
11. Astacy Invadans XP 008871232.1 q2	-	-	-	G	C	C	A	T	G	C	G	C	A	T	G	C	A	G	-	-	-	-	-
12. Phaeodactylum tricornutum XP 002179360.1 q	-	-	-	-	-	-	T	C	G	C	G	C	A	C	A	T	G	G	C	-	-	-	-
13. Phaeodactylum tricornutum XP 002178405.1 q	-	-	-	A	C	G	G	G	C	G	T	G	T	G	T	G	G	A	-	-	-	-	-
14. Phytophthora nicotianae XP 008909558.1 q1	-	-	-	-	-	-	G	C	T	G	C	G	C	G	C	T	T	G	C	G	C	A	-
15. Nannochloropsis gaditana XP 005854093.1 q1	A	A	A	A	G	C	G	C	G	T	G	C	G	C	A	C	G	G	G	T	G	T	-
16. Nannochloropsis gaditana XP 005854093.1 q2	-	-	-	-	-	-	-	-	-	C	T	G	C	G	C	A	C	G	C	T	T	-	-



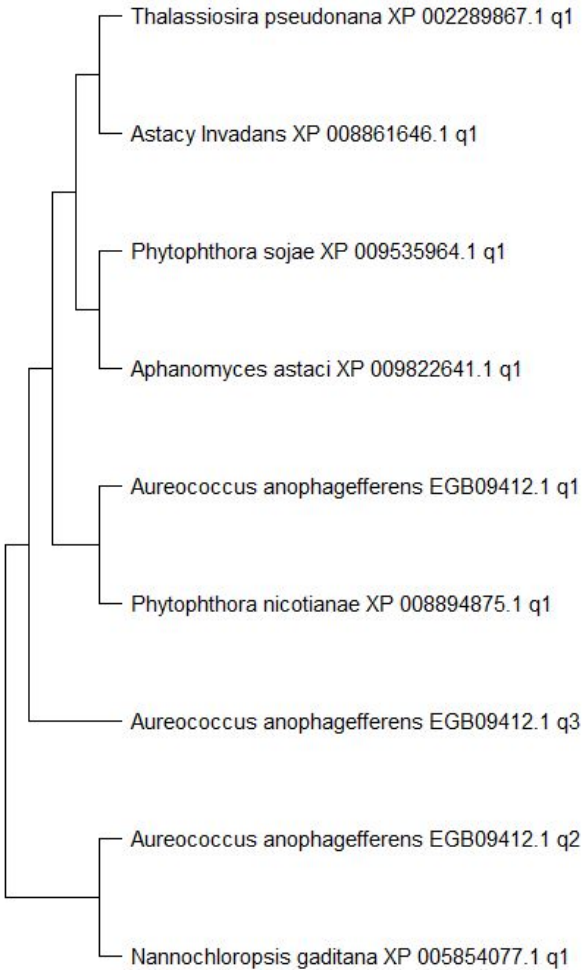
A phylogenetic tree illustrating the evolutionary relationships between various species and their corresponding protein sequences. The tree is rooted on the left and branches out to the right. The species names are followed by their protein sequence identifiers and quality scores.

- Aureococcus anophagefferens EGB11573.1 q4
- Astacy Invadans XP 008866643.1 q2
- Blastocystis hominis XP 012895690.1 q1
- Phytophthora sojae XP 009528478.1 q3
- Phytophthora nicotianae XP 008900994.1 q2
- Thalassiosira pseudonana XP 002295557.1 q1
- Phytophthora sojae XP 009534723.1 q1
- Astacy Invadans XP 008866643.1 q1
- Phytophthora nicotianae XP 008900994.1 q1
- Aureococcus anophagefferens EGB11573.1 q1
- Aphanomyces astaci XP 009832078.1 q1
- Aphanomyces astaci XP 009832078.1 q2
- Aureococcus anophagefferens EGB11573.1 q3
- Aureococcus anophagefferens EGB11573.1 q5
- Phytophthora sojae XP 009528478.1 q4
- Phytophthora sojae XP 009528478.1 q2
- Aureococcus anophagefferens EGB11573.1 q2
- Blastocystis hominis XP 012895690.1 q2

Aureococcus anophagefferens EGB11573.1 q2
Blastocystis hominis XP 012895690.1 q2

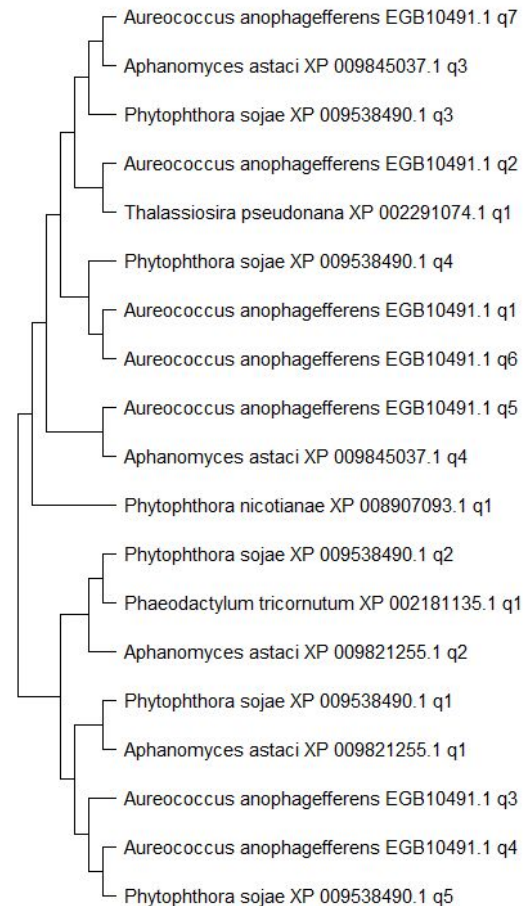
ZDNA PF00224

1. Aureococcus anophagefferens EGB09412.1 q1	-	-	-	-	-	-	C	G	A	C	G	C	G	C	C	C	G	T	C	G	-
2. Aureococcus anophagefferens EGB09412.1 q2	A	T	C	G	C	A	T	G	C	G	C	C	G	G	T	G	C	G	C	G	-
3. Aureococcus anophagefferens EGB09412.1 q3	G	C	G	G	G	C	G	C	G	G	C	G	G	G	C	G	C	G	G	G	-
4. Thalassiosira pseudonana XP 002289867.1 q1	-	-	-	-	-	-	A	G	G	G	C	A	C	G	T	G	C	G	G	C	-
5. Phytophthora sojae XP 009535964.1 q1	-	-	-	-	-	-	G	A	A	A	G	C	G	C	G	C	A	C	T	G	-
6. Aphanomyces astaci XP 009822641.1 q1	-	-	-	-	-	-	C	G	A	A	G	T	G	C	G	C	G	C	T	G	G
7. Astacy Invadans XP 008861646.1 q1	-	-	-	-	-	-	C	T	G	G	G	T	G	C	G	C	A	C	G	A	C
8. Phytophthora nicotianae XP 008894875.1 q1	-	-	-	-	-	-	-	C	G	G	C	G	C	A	C	A	C	A	C	C	T
9. Nannochloropsis gaditana XP 005854077.1 q1	-	-	-	A	T	T	C	A	C	G	C	G	C	G	C	C	C	G	T	G	T



ZDNA PF00136

1. Aureococcus anophagefferens EGB10491.1 q1	- - - - - CCGCCTGCGCGTCCGG
2. Aureococcus anophagefferens EGB10491.1 q2	- - CCATCGCGCGGATT
3. Aureococcus anophagefferens EGB10491.1 q3	- - CCGAGCACGCCTCGCGG
4. Aureococcus anophagefferens EGB10491.1 q4	CAGCGCGCGACGCGCGGTAGCGGCAGCGCGCGTTCGGCGGGCGCG
5. Aureococcus anophagefferens EGB10491.1 q5	- - GTCTCGCGCGCGCAGGAACGCGCA
6. Aureococcus anophagefferens EGB10491.1 q6	- TCCTGCCCTGCGGCGACCG
7. Aureococcus anophagefferens EGB10491.1 q7	- ACCAACACGCGAACC
8. Thalassiosira pseudonana XP_002291074.1 q1	- CTATGCACGCGA
9. Phytophthora sojae XP_009538490.1 q1	- CGGCGGCGCGCGTGCCACGA
10. Phytophthora sojae XP_009538490.1 q2	- CGGCGCGTGCTCGTGG
11. Phytophthora sojae XP_009538490.1 q3	- CTTGCGACGTCG
12. Phytophthora sojae XP_009538490.1 q4	- CGTGCCTGCGCGTGTG
13. Phytophthora sojae XP_009538490.1 q5	- GAGCGGTA-CGGC
14. Aphanomyces astaci XP_009821255.1 q1	- GGC GCCGTGCTCGTGTAAC
15. Aphanomyces astaci XP_009821255.1 q2	- CGCGGTGTGCCCGT
16. Aphanomyces astaci XP_009845037.1 q3	G T G C A C T C G C G C G C A C G G G C G A A C
17. Aphanomyces astaci XP_009845037.1 q4	- CCGACGCGACGCT
18. Phaeodactylum tricornutum XP_002181135.1 q	- TT CGCGCGCGACTT
19. Phytophthora nicotianae XP_008907093.1 q1	- - GAGTGTGCGCATATA



ZDNA PF00183

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