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Amaranthus hypochondricus: Noncoding RNA Database

The genus *Amaranthus* is an herbaceous C4 dicotyledonous plant which comprises approximately 70 species relatively having high genetic variability. *Amaranthus* plants are a source of highly nutritious pseudo-cereals, rich in vitamins and minerals and also cultivated as ornamentals (Akubugwo et al., 2007; Hill and Rawate, 1982; Shukla et al., 2006). Thus, *Amaranthus* seeds are also a rich source of gluten-free protein having a composition of amino-acid that are nutritionally balanced (Brenner et al., 2000). Moreover, it has greater ability to withstand the salt and drought stress than crops like wheat, sorghum, cotton and corn through superficial water use efficiency (Jiayi and WS, 1989; Johnson and Henderson, 2002). The grain amaranths have also been noted for their drought tolerance (Brenner 2000), disease and pest resistance, high yield in production. Considering its agronomic and economic importance, attention is being given to the cultivation, conservation, and sustainable utilization of this promising crop.

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User can explore these options for extracting information which are available in the database.

For any information, please contact us through the email id provided in the contact us tab.

31	ahy-mir-750-5p	TACACAAGATCCAACCTTAATT	30.44	23	-41.3	1.044	AH011599-RA	NA	NA
32	ahy-mir1886.3	TATGTCCATCGAAAGATTTTCAT	30.44	23	-41.5	1.041	AH007551-RA	NA	NA
33	ahy-mir096	CTTCGACAACAACCTTCCTCATA	39.14	23	-68.7	1.039	AH000715-RA	UTP:galactose-1-phosphate uridylyltransferases	NA
34	ahy-mir-8379b-5p	AGATGCTGTCAAAGACAGCTG	43.48	23	-62.2	1.037	NA	NA	NA
35	ahy-mir-10143-3p	CCTGCAGGACTTTTGTCCATTG	47.83	23	-83.7	1.036	AH004699-RA	Domain of unknown function (DUF23)	NA
36	ahy-mir-10734	CTTAACATCTTTAGAATTGAGG	30.44	23	-44.7	1.02	AH021488-RA	aspartic proteinase A1	NA
37	ahy-mir-10555	TAAGGAAGCTGCTGCTTATTCT	39.14	23	-58.7	1.014	AH003920-RA	GRAM domain family protein	NA
38	ahy-mir-9237b	ATCAGGTGTTGGTGTCTCACGT	47.83	23	-62.8	1.01	AH018815-RA	AMP deaminase, putative	NA
39	ahy-mir-9993a-3p	AGTCCCATCTCGGTGGGATCGG	60.87	23	-134.4	1.008	AH013636-RA	actin depolymerizing factor 4	NA
40	ahy-mir-7304-3p	ATTTATACAATGGGGTCTCCTT	34.79	23	-55.9	1.004	AH009533-RA	Transducin/WD4NA superfamily protein	repeat-like NA
41	ahy-mir9559-3p	TAGGGAATTTGGATTTGGAAAA	30.44	23	-50.6	1.002	AH014667-RA	hydroxyproline-rich glycoprotein family protein	NA
42	ahy-mir8775	CTCAACCATCAGCTTGAAGTTT	39.14	23	-83	0.987	AH011176-RA	Pentatricopeptide superfamily protein	repeat (PPR) NA
43	ahy-mir-6-3p	TGCTGTTCTTTTTTTCCTTTTC	30.44	23	-44.1	0.979	AH006656-RA	poly(A) polymerase 1	NA
44	ahy-mir-2498a-5p	TATAGCATACTTATGGGAAGTA	30.44	23	-41.4	0.979	AH004686-RA	NA	NA
45	ahy-mir-10314	GTGTATGAACCAAGGCGGAAAT	43.48	23	-60.2	0.975	AH019374-RA	alpha/beta-Hydrolases protein	superfamily NA
46	ahy-mir2936	TTGAGAACAACCTCTCAAGATA	34.79	23	-67.2	0.971	AH003309-RA	NA	NA
47	ahy-mir-8362-3p	CACAAGTATCTTTAAAGTCAGA	30.44	23	-51.1	0.965	AH003925-RA	NA	NA
48	ahy-mir-7132b-5p	TTCGACCAAGTCTGTACAATTG	39.14	23	-53.3	0.634	AH012287-RA	cleavage and polyadenylation specificity factor 16NA	di nucleotide
49	ahy-mir-11619d-5p	CGAAAACGATATATTCTTCATG	30.44	23	-61.8	0.958	AH020514-RA	DWNN domain; a CCHC-type zinc finger	NA
50	ahy-mir4349-3p	GAGTATATAACGTATCCTGATG	34.79	23	-71.5	0.956	AH008075-RA	exostosin family protein	NA

MFE: Minimum free energy; MFEI: Minimum free energy index;



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Some important points on above used scientific abbreviations

- miRNAid : miRNA are nomenclature as per Ambros Rule.
- Sequences : Nucleotide sequences are provided.
- GC%: The highest value is 70.26 followed by 30.43 as lowest value with an average of 37.20.
- miRNA length: The miRNA length lies between 21-25 nucleotides.
- MFE: Minimum free energy.
- MFEI: Minimum free energy index.
- miRNA's target gene: Target gene were retrieved from Phytozome database.
- miRNA's Target Function: Target gene's function were retrieved from Phytozome database.
- Type of SSR: Krait tool was used for SSR identification.

This page display the detail information of incRNA e.g. IncRNAid, Length, CPC index, IRSOM Accuracy score, FPKM value, MFE, type of SSr, IncRNA's target gene and IncRNA's target function

Click on shown menu for IncRNA detail

IncRNA INFORMATION									
S.No.	IncRNA id	Length	CPC index	IRSOM Accuracy Score	FPKM Value	MFE	Type of SSR	IncRNA's Target gene	IncRNA's Target Function
1	Ahy_Inc_0519	289	-1.13207	0.994927	14787.6	101.2	NA	NA	NA
2	Ahy_Inc_0176	397	-1.09396	0.962619	1086.88	160.8	NA	NA	NA
3	Ahy_Inc_2621	287	-1.07418	0.997325	1010.72	96.8	NA	NA	NA
4	Ahy_Inc_2148	380	-1.299	0.986279	838.57	196.9	NA	AH018098-RA	Peptidase C12, ubiquitin carboxyl-terminal hydrolase 1
5	Ahy_Inc_2076	217	-1.0592	0.988083	740.69	194.4	Tri nucleotide	AH018735-RA	MATE efflux family protein
6	Ahy_Inc_0995	230	-1.07993	0.99351	649.99	86.1	NA	AH018624-RA	receptor like protein 50
7	Ahy_Inc_2390	340	-1.16572	0.988106	425.97	632	NA	NA	NA
8	Ahy_Inc_2189	290	-1.14278	0.990963	350.19	209.7	NA	AH018735-RA	MATE efflux family protein
9	Ahy_Inc_1888	224	-1.15843	0.989427	336.05	97	NA	AH022193-RA	Ribosomal protein L13 family protein
10	Ahy_Inc_2280	238	-1.52351	0.990779	292.79	93.8	NA	AH018310-RA	Protein of unknown function (DUF1639)
11	Ahy_Inc_2381	210	-1.17968	0.957129	291.93	128.7	NA	AH018456-RA	DNAJ heat shock N-terminal domain-containing protein
12	Ahy_Inc_2160	753	-1.13204	0.956337	277.52	82.1	NA	AH020681-RA	Inorganic H pyrophosphatase family protein
13	Ahy_Inc_1822	286	-1.07785	0.984981	264.13	116.9	NA	AH018384-RA	C2H2 and C2HC zinc fingers superfamily protein
14	Ahy_Inc_1416	315	-1.07039	0.972505	239.23	202.3	NA	AH018832-RA	ubiquitin activating enzyme 2
15	Ahy_Inc_2084	216	-1.00837	0.992028	238.86	137.2	NA	NA	NA



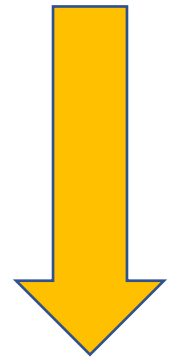
Some important points on above used scientific abbreviations

- lncRNA id: First letter from genus and last two letter from species eg. Ahy_lncRNA_001
- Length: Length is greater than 200 base pair.
- CPC index: coding potential calculator index less than -1.
- IRSOM Accuracy score:
- FPKM value: Expression value of lncRNA
- MFE: Minimum free energy
- Type of SSR: SSR bearing lncRNA
- lncRNA's target gene: Target gene were retrieved from Phytozome database
- lncRNA's target function: Target gene's function were retrieved from Phytozome database

This window displays the Information of circRNA e.g circRNA id, Length, FPKM Value, CPC_Index, Non_Coding Prob, Sponge miRNA and miRNA's Target Function

Click here for circRNA

S.No.	circRNA id	Length	FPKM Value	CPC_index	Non_coding prob	Sponge miRNA	miRNA's Target Function
1	Ah_circ002	7444	2061.34	0.0813656	0.918634	ahy-mir4382	cation/hydrogen exchanger 15
2	Ah_circ003	191	3157.88	0.00594549	0.994054	ahy-mir-2c-3p	Lipase class 3-related protein
3	Ah_circ004	23683	482.08	0.0895304	0.91047	ahy-mir11475	F-box family protein
4	Ah_circ005	146	64460.2	0.0104434	0.989557	NA	NA
5	Ah_circ006	157	152292	0.0102073	0.989793	NA	NA
6	Ah_circ007	295	21070.7	0.036269	0.963731	ahy-mir079	with no lysine (K) kinase 4
7	Ah_circ008	9828	239.14	0.197288	0.802712	ahy-mir5298a	DNA-binding bromodomain-containing protein
8	Ah_circ009	172	136304	0.0661077	0.933892	NA	NA
9	Ah_circ010	7594	56.93	0.202038	0.797962	ahy-mir-10743	O-acetyltransferase family protein
10	Ah_circ011	179	173610	0.012588	0.987412	NA	NA
11	Ah_circ012	198	56016	0.00563652	0.994363	NA	NA
12	Ah_circ013	163	3940.02	0.129681	0.870319	NA	NA
13	Ah_circ014	27121	398.29	0.0473755	0.952624	ahy-mir3712	NA
14	Ah_circ015	10361	1933.47	0.0604998	0.9395	ahy-mir5649b	WHIRLY 2
15	Ah_circ016	2201	1110.03	0.0736799	0.92632	ahy-mir-2704	NAD(P)-binding Rossmann-fold superfamily protein
16	Ah_circ017	7855	3768.69	0.0327066	0.967293	ahy-mir156g-3p	Frigida-like protein
17	Ah_circ018	182	58087	0.00859435	0.991406	NA	NA
18	Ah_circ019	440	131647	0.0000804	0.999992	NA	NA
19	Ah_circ020	138	0	0.170647	0.829353	ahy-mir5298a	DNA-binding bromodomain-containing protein
20	Ah_circ021	9290	6201.66	0.145096	0.854904	ahy-mir073	ARM repeat protein interacting with ABF2
21	Ah_circ022	178	2524.88	0.0699805	0.930019	NA	NA



Some important points on used scientific abbreviations

- circRNA id : First letter from genus and last letter from species eg. Ah_circ001
- Length: Length of circularRNA. It ranges from 138 to 27121 as longest and smallest length respectively.
- FPKM Value: Expression value of circRNA
- CPC_Index: Coding potential calculator
- Non_Coding Prob: it shows the non coding probability of circular RNA.
- Sponge miRNA: Interaction between circular RNA and miRNA.
- miRNA Target Function: Target gene's function were retrieved from Phytozome database

Click here for SSR

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Browse for SSR and thier Primer

Enter SSR type :

Enter Repeat :

1: mono nucleotide 2: di nucleotide 3: tri nucleotide 4: tetra nucleotide 5: penta nucleotide 6: hexa nucleotide

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Activate Windows
Go to Settings to activate Windows.

Enter the no. of SSR type
from 1-6
And enter the repeat and
click for search

After clicking on search button the following page will be opened in which user can view SSR information like SSR_id, Motif, Type, Repeats, SSR length, SSR on Gene and Primer

Total no. records : 215

SSR_id	Motif	Type	Repeats	SSR length	SSR on Gene	Primer
Ahy_SSR0177	CCCAT	6	4	24	0	Primer
Ahy_SSR0178	CCCAT	6	4	24	0	Primer
Ahy_SSR0206	CCCAT	6	4	24	0	Primer
Ahy_SSR0574	GCGGCT	6	4	24	0	Primer
Ahy_SSR0760	TTGGGT	6	4	24	0	Primer
Ahy_SSR0761	TTGGGT	6	4	24	0	Primer
Ahy_SSR0990	GAAGAC	6	4	24	0	Primer
Ahy_SSR1216	TTCCAT	6	4	24	0	Primer
Ahy_SSR1226	TTGGGT	6	4	24	0	Primer
Ahy_SSR1342	TTCCAT	6	4	24	0	Primer
Ahy_SSR1343	TTCCAT	6	4	24	0	Primer
Ahy_SSR1365	TGGATC	6	4	24	0	Primer
Ahy_SSR1366	TGGATC	6	4	24	0	Primer
Ahy_SSR1581	TTCCCA	6	4	24	0	Primer
Ahy_SSR1591	TGGTGC	6	4	24	0	Primer
Ahy_SSR1592	TGGTGC	6	4	24	0	Primer
Ahy_SSR1744	ATTTTA	6	4	24	0	Primer
Ahy_SSR1906	AGAACA	6	4	24	0	Primer
Ahy_SSR2090	GAGGCT	6	4	24	0	Primer
Ahy_SSR2091	GAGGCT	6	4	24	0	Primer
Ahy_SSR2150	AACATG	6	4	24	0	Primer
Ahy_SSR2228	TTTTGA	6	4	24	0	Primer
Ahy_SSR1078	ATTTTG	6	4	24	AATP1	Primer
Ahy_SSR0602	TGCTGT	6	4	24	"ABF2	Primer
Ahy_SSR0689	TGCTGT	6	4	24	"ABF2	Primer
Ahy_SSR0690	TGCTGT	6	4	24	"ABF2	Primer
Ahy_SSR0395	TGGAGG	6	4	24	ABP	Primer
Ahy_SSR0396	TGGAGG	6	4	24	ABP	Primer
Ahy_SSR0403	GAGGTG	6	4	24	ABP	Primer

Click here for
Primer's detail



After clicking on Primer the following page will be opened in which user can view detail information e.g. SSR_id, Forward Primer, TM, GC%, Reverse Primer, TM, GC% and Product Size

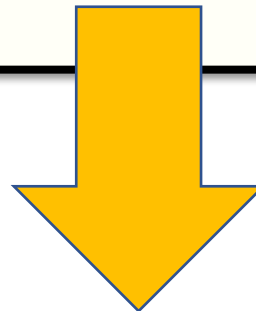
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PRIMER INFORMATION

Total no. records : 1

SSR_id	Forward Primer	TM	GC%	Reverse Primer	TM	GC%	Product Size
Ahy_SSR1531	TCTTTCCTCTATAATCCGCCCC	59.1	50	GTAATGAGAAAAGTAAAACAGGAAACCC	58.92	37.04	147

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Some important points on above used scientific abbreviations

- SSR_id:
- Motif:
- Type: mono, di, tri, tetra, penta and hexa nucleotide SSRs
- Repeats:
- SSR length: Total length of SSRs
- SSR Gene: Presence of SSRs on gene
- Forward Primer
 - TM : Melting Temperature
 - GC%: Total GC content
- Reverse Primer
 - TM: Melting Temperature
 - GC% :GC content
- Product Size : Total size of primer including both forward and reverse primer.

For further information, please contact us

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