Supplementary material

Table S1. Gene ID of more than 80% similarity.

Sequence ID of v2019	Sequence ID of v2021	Identity%
Gb_01884 (GbMADS08)	GWHPBAVD001372 (GbMADS32)	90
Gb_12581 (GbMADS26)	GWHPBAVD001363 (GbMADS30)	88.525
Gb_12581 (GbMADS26)	GWHPBAVD001372 (GbMADS32)	88.525
Gb_12586 (GbMADS21)	GWHPBAVD004734 (GbMADS42)	100
Gb_15398 (GbMADS23)	GWHPBAVD006355 (GbMADS43)	99.639
Gb_16301 (GbMADS20)	GWHPBAVD021902 (GbMADS41)	99.103
Gb_21526 (GbMADS22)	GWHPBAVD009168 (GbMADS46)	100
Gb_28587 (GbMADS12)	GWHPBAVD009827 (GbMADS34)	100
Gb_30604 (GbMADS06)	GWHPBAVD018550 (GbMADS38)	81.667
Gb_31417 (GbMADS01)	GWHPBAVD000173 (GbMADS27)	100
Gb_33168 (GbMADS14)	GWHPBAVD012282 (GbMADS37)	100
Gb_36364 (GbMADS05)	GWHPBAVD001358 (GbMADS29)	100
Gb_39109 (GbMADS10)	GWHPBAVD018550 (GbMADS38)	80.328
Gb_41549 (GbMADS03)	GWHPBAVD001364 (GbMADS31)	100
Gb_41550 (GbMADS04)	GWHPBAVD001364 (GbMADS31)	96.667

Table S2. Primer sequence of GbMADS genes.

Gene ID	F	R
GAPDH	GGTGCCAAAAAGGTGGTCAT	CAACAACGAACATGGGAGCAT
GbMADS01	GCAAAATATTGTTCCGCCTAGT	TGTCTTGAGGTGTTGAATGGTG
GbMADS03	CCCTGCCTACGGTGTAAATG	CAATGTGTAGAGTCGGTTCGC
GbMADS04	TCCAGAACCCTGCGTGAAC	CCGATGGTCCCAAGAATGA
GbMADS05	TCGGAAAAAGGAAAGGCTGC	AGGTCCATTATCGTCGGTAGG
GbMADS06	TGGCTGACCTGGAGAGAAAAC	TGCCTCTTTCTCAACCGTATCT
GbMADS07	CAACGCAATGCCACTGAACT	TTCATCATAGACATTTCCCCCA
GbMADS08	ACCACTCCATCATACAAGCCTG	CACGGACTTCAAAAAACTACGG
GbMADS09	ACCAGACTGCAACGTCCATG	CCACTGGCTTGAATCCGAG
GbMADS10	CTCAGAAGTGGAGATTTTGCGT	TTTCTGGTCGGCAGTTTATGTC
GbMADS11	GTCTAGTGCCATCGCAGGAA	GTCTACCAAGGGAGGAGGAAGT
GbMADS12	GAGCGTTCTTTACACAGGCATT	CGAAAAGTTGGTGCTACAGGTG
GbMADS14	AAGAGCAGGGCAAGATGAATAA	TCCGTCTCCAAAAGCCTGTT
GbMADS16	GAAGCGCGAGAAGAAGAGTGA	CGCAGGAGAGAAGACGATAAAA
GbMADS17	CCGTGATTTGGACAGCAGC	CGTGGCAGAAATGACGATGA
GbMADS18	AGTCAGTTGCGACAGAGGGTAA	GCCGAGAAGACGATGAGAGC
GbMADS19	TCCAAATCAAGCGGATAGACA	CCAACTTCGGCATCACAGAG
GbMADS20	AGACACTTGATGGGGGACGC	CGAGAATCAAATCCAGGCAA
GbMADS21	AGCAGTAAAAAGCACCGAGAG	GGCAAAAGGTTCCCCGAT
GbMADS23	TTTTACAGCCCTTAGAGCCAGC	TCTCACTTTTCACCATTGCCAT
GbMADS26	GTAGGACTGGTTTTATGCGGC	AGACCGAAGAAACAAATGGCT
GbMADS28	ATTCAACGAGCAGGCAGGTC	TGTTTGCCAGTGCTGGAAAA
GbMADS33	TGGGAGATGGCATTGATTTTG	GCAGGGCATCATCCTTAAAGTAT
GbMADS35	AAGCAGTGGTAGCAGCATAAAGC	TGTGTTGAGGTCTTCACCCATC
GbMADS36	CTTTACCAAATGCTTGCTGAACAC	AAGTTTGGTTGGCTTGGCTG
GbMADS39	GCGGCTGTCCGAGTTTGATA	GGTCAGGTCTTCACCCAACAT
GbMADS40	AGAGTCCTCAAGCCTGGTGAA	TCCTCCGCTAGAGAAGACGATA
GbMADS44	CAGGTACGGTCTGGTTGGGT	GGCTGCATCTTCGATTTTCA

Gene ID	F	R
GbMADS45	ATGATGGGTGAACAGATTACGG	GTCGCTCGGTTGTTGGTAAG

Table S3. *GbMADS* genes information homologous to MADS in *Arabidopsis thaliana*.

Query Gene	String Id	Identity	Bitscore
Gb_01884 (GbMADS08)	AGL20	46.2	139
Gb_03068 (GbMADS19)	AGL16	77.3	100.1
Gb_03807 (GbMADS17)	AGL16	63.2	89
Gb_05128 (GbMADS18)	AGL24	40.8	146
Gb_05359 (GbMADS13)	AGL86	31.6	68.6
Gb_12581 (GbMADS26)	AGL6	78	94.7
Gb_12586 (GbMADS21)	AGL61	41.7	109.8
Gb_12778 (GbMADS15)	AGL14	75.3	126.7
Gb_15398 (GbMADS23)	PI	42	172.9
Gb_16301 (GbMADS20)	AG	61.7	266.9
Gb_19178 (GbMADS09)	AGL6	45.6	139.8
Gb_19258 (GbMADS16)	AGL61	36.2	91.7
Gb_21526 (GbMADS22)	AT1G72350	47.5	60.1
Gb_28587 (GbMADS12)	AGL8	45.9	136
Gb_30604 (GbMADS06)	AGL6	49.4	147.5
Gb_31417 (GbMADS01)	AGL104	45.3	180.3
Gb_33168 (GbMADS14)	AGL80	30.8	87
Gb_36364 (GbMADS05)	AGL2	56.2	214.5
Gb_37613 (GbMADS25)	AGL62	39.3	92.8
Gb_38365 (GbMADS02)	AGL6	77.4	96.7
Gb_38883 (GbMADS11)	AT5G26630	37.6	96.7
Gb_38922 (GbMADS07)	AGL6	77.4	98.2
Gb_39109 (GbMADS10)	AGL6	49	142.9
Gb_40092 (GbMADS24)	AGL62	39.3	92.8
Gb_41549 (GbMADS03)	AGL4	52.1	208.8
Gb_41550 (GbMADS04)	3-Sep	85.7	108.2
GWHPBAVD000173 (GbMADS27)	AGL104	45.3	180.3
GWHPBAVD000308 (GbMADS28)	AGL44	85	104.4
GWHPBAVD001358 (GbMADS29)	AGL2	56.2	214.9
GWHPBAVD001363 (GbMADS30)	AGL6	78	93.6
GWHPBAVD001364 (GbMADS31)	AGL4	52.1	208.8
GWHPBAVD001372 (GbMADS32)	AGL6	78	96.3
GWHPBAVD001859 (GbMADS33)	AGL80	31	98.6
GWHPBAVD004734 (GbMADS42)	AGL61	41.7	109.8
GWHPBAVD006355 (GbMADS43)	PI	42	173.3
GWHPBAVD006759 (GbMADS44)	AGL21	69.5	89.7
GWHPBAVD008845 (GbMADS45)	AGL15	44.5	164.1
GWHPBAVD009168 (GbMADS46)	AGL13	42.9	71.2
GWHPBAVD009827 (GbMADS34)	AGL8	45.9	136
GWHPBAVD009828 (GbMADS35)	AP1	48.7	135.2
GWHPBAVD009829 (GbMADS36)	AGL6	42.3	142.9
GWHPBAVD012282 (GbMADS37)	AGL80	30.8	87
GWHPBAVD018550 (GbMADS38)	AGL6	95.1	116.3
GWHPBAVD019150 (GbMADS39)	TT16	53.4	168.7
GWHPBAVD021889 (GbMADS40)	SHP1	72.2	104.4

	GWHPBAVD021902 (GbMADS41)	AG	61.7	261.9

Table S4. Expression of GbMADS genes.

|	Female Flower	Male Flower	Early Seed	Development Seed	Mature Seed	Root	Stem	Leaf
GbMADS21	122.1	2413.1	79.6	32.1	5.5	17.2	84.4	65.2
GbMADS14	56.8	17198.6	120.4	667.8	226.2	532.5	44.5	377.4
GbMADS11	0.1	81.8	28.5	4.9	31.0	0.1	0.1	0.1
GbMADS33	2.5	52.3	15.8	3.4	32.4	0.1	0.1	0.1
GbMADS16	0.1	2043.3	0.1	0.1	0.1	0.1	0.1	0.1
GbMADS01	0.1	651.1	2.1	15.2	2432.7	0.1	0.1	0.1
GbMADS17	505.5	9.1	10.3	7.7	0.1	0.1	227.3	0.1
GbMADS07	32.3	40.6	56.8	67.3	4.4	0.1	4837.3	6.2
GbMADS08	22047.6	7049.6	4921.9	2015.1	93.4	8.5	14.1	0.1
GbMADS18	4865.4	87.0	2595.3	946.6	80.9	10.9	6848.9	824.1
GbMADS19	8.0	0.1	3.5	6.7	1.6	667.8	44.8	14.5
GbMADS26	191.1	233.9	206.7	219.8	34.5	41.8	0.1	0.1
GbMADS23	272.8	273.1	54.1	27.8	2.3	29.0	48.9	64.1
GbMADS20	40.2	4471.9	17743.5	5634.2	990.3	27.5	21.0	6.6
GbMADS09	713.3	327.8	25.6	13.9	5.3	0.1	0.1	0.1
GbMADS12	49.0	58.9	1.2	3.0	0.1	1.0	0.1	2.7
GbMADS06	8220.4	1964.6	848.2	1045.5	163.3	226.0	328.2	1924.1
GbMADS05	10453.3	6251.6	8769.8	4683.4	217.0	2001.2	98.5	1570.1
GbMADS10	1948.8	643.6	74.8	15.3	264.1	1102.6	1073.7	2309.4
GbMADS03	4765.2	2702.4	1205.2	885.3	352.5	9855.2	0.1	0.1
GbMADS04	26.2	11.5	13.5	11.9	0.1	13.2	0.1	0.1
GbMADS36	39.2	64.1	41.3	63.6	30.8	97.2	158.5	65.8
GbMADS44	52.4	0.1	0.1	0.1	0.1	42.7	65.3	0.1
GbMADS28	20.0	0.1	0.1	0.1	0.1	2452.4	17.6	0.1
GbMADS45	4.3	720.7	1.6	98.4	48.7	78.2	191.6	144.7
GbMADS35	458.8	29.7	3.6	0.1	0.1	0.1	6.9	9.5
GbMADS36	0.1	9280.6	46.7	4.3	2.9	0.1	0.1	0.1
GbMADS39	0.1	90.7	208.7	12707.0	50.4	0.1	0.1	0.1
GbMADS40	5.3	0.1	0.1	0.1	0.1	113.2	0.1	0.1

version 2019
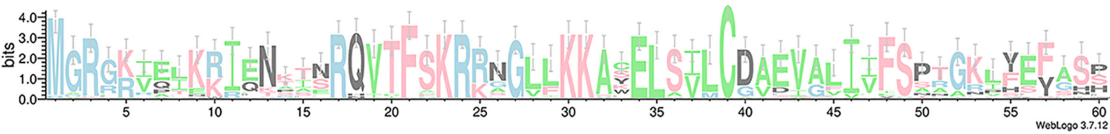
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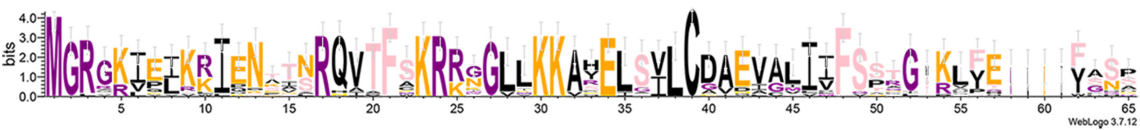
Figure S1. Weblogo of GbMADS domain.
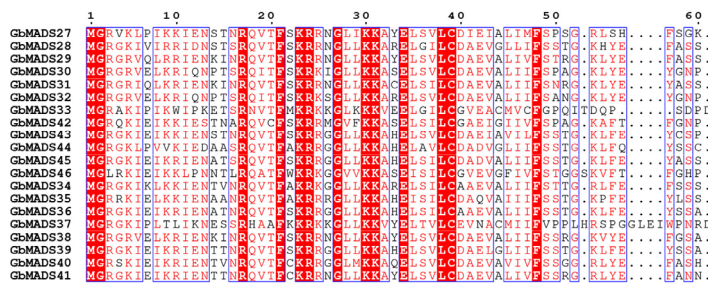
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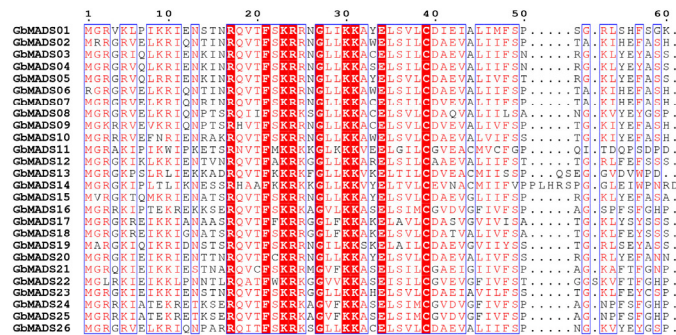
version 2021

Figure S2. GbMADS domain sequence alignment.

S1. GbMADS protein sequences of v2019 genome.

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SENEQLHKTLRHMMGEDVNSLSTDELHSLEQTLEIASSRVRTKKNQYLVQ
QIDKLRKKERFLNEHNNHLYALLVENQASMRDSSTSCQHREQPTAQAFRV
QPSQPNLQDREHDEHHDLRLGFSYFLG
>GbMADS24
MGRRKIATEKRETKSERQVTFSKRKAGVFKKASELSIMCGVDVGFIVFSP
AGNPFSFGHPSVDHLVHKLLRLDPLPPPPAPENFQLHLTQHASLQERYQR
EKVLNKALKLRDNSQPARGQFWWEDDTKNLNPAELKAKYHALKLFKSKLE
LRIAKLRANDGIARPATTDETAGVNNQESDRDRGIEMEAPLLLFETQSKS
NEGEGAATTYDQSCVKQQTTSEPPLVNMTSSCTSAADFIQYQLLHTPPVE
HHNFFQPAMNTDISDQYSSPPGPSSSSWNRTEYGYVGQIPGPAQPQPAFP
PALLPPPPSPLPLLPPPPHIPLPPPPSPPTFANNQN
>GbMADS25
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EKVLNKALKLRDNSQPARGQFWWEDDTKNLNPAELKAKYHALKLFKSKLE
LRIAKLRANDGIARPATTDETAGVNNQESDRDRGIEMEAPLLLFETQSKS
NEGEVGATTYDQSCVKQQTTSEPPLVNMTSSCTSAADFIQYQLLHTPPVE
HHNFFQPAMNTDISDQYSSPPGPSSSSWNRTEYGYVGQIPGPAQPQPAFP
PALLPPPPSPLPLLPPPPHIPLPPPPSPPTFANNQN
>GbMADS26
MGRGRVELKRIQNPARRQITFSKRKSGLLKKACELSVLCDAEVALIIFSP
NGKVYEYGSPRQEELTSGVELDAVWSKGATHVNTLNENSYRSRTGFMRQK
NVYTLISPLRASKKAICFFGLN

S2. GbMADS protein sequences of v2021 genome.

>GbMADS27
MGRVKLPIKKIENSTNRQVTFSKRRNGLIKKAYELSVLCDIEIALIMFSPSGRLSHFSGKNSRIED
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VRLRKQQLEHNQMAVAFNDANLQFYIQTQNGLPN
GTDTSQNHLYNSWMPQGDPHTSVQNFMEHENSNAMLAMREAQCMAKCLQNGTVFPALQDA
TGMQLPNESASTQPYIPTSHMQFDYTLTDNNNNEHAEQAD
IAAAFDYGSDAMASVHWQTSYGSMTPIVTNQQYPLTKGIMQNIVPPSMSIYQQDGSSSQGTHH
STPQDNAGMDASFQNGYVTGQVDLKFLVELIIVMNFG
EDGAISYRKRIIEDFSSMALPLPKERKELDWIAQACEYCVLKYKFFEAGSD
>GbMADS28
MGRGKIVIRRIDNSTSRQVTFSKRRNGLLKKARELGILCDAEVGLLIFSSTGKHYEFASSRFNVL
CS
>GbMADS29
MGRGRVQLRRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIVFSTRGKLYEFASSSMNK
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ELLQQSQRHLLGEDLGPLSVKELQQLERQLEIALNHVRSRKSQVMMDLIDELRKKERLLQEVN
KSLHKKLSESEGRNATHDMRHPTDDNGPWNPSVNGGY
ALPSTQQNTNLHPVDCEPTLQIGYQSVPRESIEPPQEQTHNQPQDNYTGWWV
>GbMADS30
MGRGRVELKRIQNPTSRQITFSKRKIGLLKKASELSVLCDAEVALIIFSPAGKLYEYGNPR
>GbMADS31
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QILQQSQRHLLGEDLGMLSLKELHQLEHQVEVALKHLRSRKTQIMLDQIDDLRKKERMLQEVN
KSLHKKFLEADGQNACNFGQFSRPWDSAVGNPAYGVN
EPDSHVQPAHREPTLHIGYREAAHPVSTVHRQKQSANHYTQDWMV
>GbMADS32
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>GbMADS33
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GMPKALQVIDRYKSLSKEEQDKKKLDNSSFLEQRIKK
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VENTMQVPLTELESIARQSMEGTAPQMMFPYNLMPCH
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KPIGSSSNNNNNMDQKMVNTDSMAEDRITGVTGYSM
MNKSFPLMGDYEHVQSSAIAGNCSQWRCAVTPLSCCSVHTDSIHNSLYSFPQHYMNPYGQTAN
QQTQASCEPQHHQSWLNELIDLQNIQQKLLGDGIDFA
RNNARLPPPLVDRSGTDQDYKLKNLQDLETLQKMKPEYFKDDALQ
>GbMADS42
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NRSLTAMETLQKPQQSVYYDRESPQVHQIQQTLPSF
PLTSGVQSQLVQWDQESGPNTMGHWNSQEPYNSIGTSFHGPTDAKYSLVQFNPAMQDASFVS
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>GbMADS43
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ILFSSTGKLFEYCSPRSSIKTVIDRYQRVSGARLWDTQHQNLFSEMAMVKSENEQLHKTLRHM
MGEDVNSLSTDELHSLEQTLEIASSRVRTRKNQYLVQ
QIDKLRKKERFLNEHNNHLYALLVENQASMRDSSTSCQHREQPTAQAFRVQPSQPNLQDREHD
EHHDLRLGFSYFLG
>GbMADS44
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DVGLIIFSSTGKLFQYSSCK
>GbMADS45
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ESLHKQLEEVQKSLPTTERQIAAYLEFQPLESRDFSAK
HVVTRPVAVHNPSFEDSEPSDTSLHLG
>GbMADS46
MGLRKIEIKKLPNNTLRQATFWKRKGGVVKKASEISILCGVEVGFIVFSTGGSKVFTFGHPSLRH
LIHRLHNRPPPPFDNQKLQADLEILEGNYNAFEVR
VKGERAMNTTLKRANKRVQSLCSENKVDFWWAEDTKDFGIAQSKRFYYALKLLKTNIQRRM
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>GbMADS34
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LKRYLCISGKRLWDHQHLISEMATIKKENERLRNALKHVMGNDLNSLSIHELQHLEQSLEIAKT
RVRTRKNQHILEEMESLRKKERSLHRHYNLLTRILA
RHDGPETVHMTPVAPTFRAQPIQPNLQDIVNQETDLQLGISCAQQTQIPLNTDLTLS
>GbMADS35
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LERYQRSTSAWLLDIAHQQLLYDMTRIKNENER
LQNSLRHMMGEDLNTLSTNELHHLEQNLEIATTRVRARKDQLLRQQLEKLTKKLAGHHFPVR
GPVNTYSLYCEGGGPNPLHMTSQHPALAFCPQPSQPNL
QSKEHQQSDLRLGFNCARHQC
>GbMADS36
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RVFCPYCTSGENIFQHLFCEMTRIKNENERLQTA
MRHMMGEDINSLSTNELHQLEQNLEIAGTRVRTRKNQQMAQQLDKLRKKERFLHQHNNRLY
QMLAEHHEAPMGESSNGYTAFCQQGSNIVHMTPAAPGFR
VQPSQPNLQDNGYQQPDLQLGNDKLSNSFALIIL
>GbMADS37
MGRGKIPLTLIKNESSRHAAFKKRKKGLLKKVYELTVLCEVNACMIIFVPPLHRSPGGLEIWPNR
DEAMEVITRYRDLPQYEQEQGKMNNLSFLQQQNIN
LDKEFKKKWIQNRLLETENVYPSWDPRLDNYTVEELQDLVSFVNSKMSEVLDQIQSRENNIQS
MDGNQPLPEASNNESLQQNNFSSCTHQGLCPDIEACI
NRLFEEQFP
>GbMADS38
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>GbMADS39
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IIERYQKVSGARLSEFDNQHLFCEMTRIKNENEK
LQTSIRHMLGEDLTSLTMTELHHLEQQLEVAANRVRTRKNQLMLQQLDNLRRKERLLEEQNSH
LCRLLAEHQAAVEGVVAEPMIDFGVFCQSEARNPLHL
TAQSMQGFRLQPTQPNLQESGMQRPALQLWY
>GbMADS40
MTTHTCNYKVNALLDNHDRLSFGKQPHQQGCYVVEKRIKAFEDSRHPPSYPRFSGYKYISLLVI
EIHRVLKPGEAIRPDLIVLRHNRVLCSRPGGLSAES
IRIMGRSKIEIKRIENTVNRQVTFCKRRGGLMKKAQELSVLCDAEVAVIVFSSGGRLYEFASHGY
CPSLQISLYLLVRSCFILQVS
>GbMADS41
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IDILQNANRHLMGDALTSLSVKELKQLEIRLERGISRVRSKKNEMLLEEIEIMQRREHILLAENQF
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HASIMDAHHYAQQDQTALQLGSSRPNWLE