

"Research paper: Growth and primary metabolism of lettuce seedlings (*Lactuca sativa* L.) are promoted by an innovative Iron-Based Fenton composted amendment.
Amalia Piro, Daniela Oliva, Dante Matteo Nisticò, Ilaria Lania, Maria Rita Basile, Giuseppe Chidichimo, Silvia Mazzuca"

Supplementary table 6a. KEGG enrichment analysis of DAPs in roots of *Lactuca sativa* seedlings after treatment with FCA

Query	KO	Definition
sp O64989 C90B1_ARATH (513)	K09587	CYP90B, DWF4; steroid 22S-hydroxylase [EC:1.14.14.178]
sp Q3MV14 DSE1_ARATH (386)	K24770	DSE1, ALT2, EMB2757; protein decreased size exclusion limit 1
sp Q6F3F1 METK4_ATRNU (396)	K00789	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]
sp Q9SCY2 FKB13_ARATH (208)	K01802	E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]
sp Q8RXG3 M2K5_ARATH (348)	K13413	MKK4_5; mitogen-activated protein kinase kinase 4/5 [EC:2.7.12.2]
sp Q9XIF2 MTR4_ARATH (988)	K12598	MTR4, SKIV2L2; ATP-dependent RNA helicase DOB1 [EC:3.6.4.13]
sp Q9FX68 ZWIP6_ARATH (302)		
sp Q8RWH9 NUP58_ARATH (513)	K14307	NUPL1, NUP49; nucleoporin p58/p45
sp Q9SLK2 ALIS3_ARATH (349)		
sp Q5K4R0 MAD47_ORYSJ (250)		
sp Q9FME5 COBL5_ARATH (204)		
sp Q96552 METK2_CATRO (393)	K00789	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]
sp Q9LNQ1 TI231_ARATH (187)	K17794	TIM23; mitochondrial import inner membrane translocase subunit TIM23
sp Q8GYT9 SIS3_ARATH (358)	K16284	SIS3; E3 ubiquitin-protein ligase SIS3 [EC:2.3.2.27]
sp Q9CA93 BAC2_ARATH (296)	K15109	SLC25A20_29, CACT, CACL, CRC1; solute carrier family 25 (mitochondrial carnitine/acylcarnitine transporter), member 20/29
sp Q38841 AGL12_ARATH (211)		
sp Q84WW2 6PGL3_ARATH (325)	K01057	PGLS, pgl, devB; 6-phosphogluconolactonase [EC:3.1.1.31]
sp Q6NKU9 TI223_ARATH (214)	K17790	TIM22; mitochondrial import inner membrane translocase subunit TIM22
sp Q9SJQ1 PXC1_ARATH (672)		
sp Q5H8A6 CASTO_LOTJA (853)	K21866	POLLUX, DMI1, CASTOR; ion channel POLLUX/CASTOR
sp O23254 GLYC4_ARATH (471)	K00600	glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1]

sp Q96551 METK1_CATRO (393)	K007 89	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]
sp P13868 CALM1_SOLTU (149)	K021 83	CALM; calmodulin
sp Q9STE8 TC753_ARATH (818)		
sp Q9LIK0 PKP1_ARATH (596)	K008 73	PK, pyk; pyruvate kinase [EC:2.7.1.40]
sp Q8L7W2 NUDT8_ARATH (369)		
sp Q94A28 ACO2M_ARATH (995)	K016 81	ACO, acnA; aconitate hydratase [EC:4.2.1.3]
sp Q67Z52 TBCB_ARATH (243)	K172 62	TBCB, CKAP1, ALF1; tubulin-specific chaperone B
sp O24520 HBL1_ARATH (160)		
sp Q9ZT81 CSPLK_ARATH (164)		
sp Q37001 1A15_ARATH (470)	K017 62	ACS; 1-aminocyclopropane-1-carboxylate synthase [EC:4.4.1.14]
sp Q9LE81 IRE_ARATH (1168)		
sp Q9AVJ9 MXMT1_COFAR (378)	K214 82	BAMT; benzoate O-methyltransferase [EC:2.1.1.273]
sp Q5W7C1 STAR2_ORYSJ (285)	K020 69	STAR2, fetB; UDP-glucose/iron transport system permease protein
sp Q9S7Z3 PCS1_ARATH (485)	K059 41	E2.3.2.15; glutathione gamma-glutamylcysteinyltransferase [EC:2.3.2.15]
	K255 87	E3.4.17.25; glutathione-S-conjugate glycine hydrolase [EC:3.4.17.25]
sp Q9LSF6 VTH21_ARATH (219)	K227 36	VIT; vacuolar iron transporter family protein
sp Q766Z3 REV3_ARATH (1890)	K023 50	REV3L, POLZ; DNA polymerase zeta [EC:2.7.7.7]
sp Q8S8S1 PEX16_ARATH (367)	K133 35	PEX16; peroxin-16
sp O24379 LOX12_SOLTU (861)	K157 18	LOX1_5; linoleate 9S-lipoxygenase [EC:1.13.11.58]
sp B9G5Y5 AB25G_ORYSJ (1004)		
sp O49485 SERA1_ARATH (603)	K000 58	serA, PHGDH; D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase [EC:1.1.1.95 1.1.1.399]
sp Q8RXE1 GAUT5_ARATH (610)	K136 48	GAUT; alpha-1,4-galacturonosyltransferase [EC:2.4.1.43]
sp O23180 PLP5_ARATH (414)		
sp Q0WQG8 GTG2_ARATH (467)		
sp P43281 METK2_SOLLC (393)	K007 89	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]
sp Q8LDP4 CP19D_ARATH (201)	K018 02	E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]

sp P22221 PPDK_FLATR (953)	K01006	ppdK; pyruvate, orthophosphate dikinase [EC:2.7.9.1]
sp O04089 ZIP4_ARATH (374)	K14709	SLC39A1_2_3, ZIP1_2_3; solute carrier family 39 (zinc transporter), member 1/2/3
sp Q9LZW4 CIPKE_ARATH (442)		
sp Q7XZR1 METK1_ATRNU (396)	K00789	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]
sp Q652K1 SGR_ORYSJ (274)	K22013	SGR, SGRL; magnesium dechelataase [EC:4.99.1.10]
sp Q9LDM2 CER7L_ARATH (307)	K03678	RRP45, EXOSC9; exosome complex component RRP45
sp Q10MI0 SRL2_ORYSJ (988)	K21842	EFR3; protein EFR3
sp Q9LMA7 CXE1_ARATH (318)		
sp Q9AST8 ROSY1_ARATH (160)		
sp Q9CAU2 SCP5_ARATH (438)	K16296	SCPL-I; serine carboxypeptidase-like clade I [EC:3.4.16.-]
sp Q5GHF7 IPT_HUMLU (329)	K10760	IPT; adenylate dimethylallyltransferase (cytokinin synthase) [EC:2.5.1.27 2.5.1.112]
sp Q9SEZ1 ZHD11_ARATH (242)		
sp Q9LW00 MBD11_ARATH (254)		
sp H6WS93 PDR1_PETAX (1452)	K08711	PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR
sp Q9LFS4 NIK1_ARATH (638)		
sp Q6XMI3 BSMT1_ARATH (379)	K21483	SAMT; salicylate 1-O-methyltransferase [EC:2.1.1.274]
sp Q0WQF4 VP53A_ARATH (828)	K20299	VPS53; vacuolar protein sorting-associated protein 53
sp Q9SN68 RAF2B_ARATH (200)	K07889	RAB5C; Ras-related protein Rab-5C
sp Q949P1 ABAH1_ARATH (467)	K09843	CYP707A; (+)-abscisic acid 8'-hydroxylase [EC:1.14.14.137]
sp O65530 PEK14_ARATH (731)		
sp Q06611 PIP12_ARATH (286)	K09872	PIP; aquaporin PIP
sp Q69XJ0 SPX1_ORYSJ (295)		
sp Q9ZWS9 ARR3_ARATH (231)	K14492	ARR-A; two-component response regulator ARR-A family
sp Q9FUY7 C79F2_ARATH (537)		
sp Q94C74 GLYM2_ARATH (517)	K00600	glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1]
sp O82345 BAG6_ARATH (1043)		

sp P17784 ALFC1_ORYSJ (358)	K016 23	ALDO; fructose-bisphosphate aldolase, class I [EC:4.1.2.13]
sp Q06197 IDHC_SOYBN (413)	K000 31	IDH1, IDH2, icd; isocitrate dehydrogenase [EC:1.1.1.42]
sp P53392 SUT2_STYHA (662)	K174 70	SULTR1; sulfate transporter 1, high-affinity
sp Q7XHW5 C14B1_ORYSJ (534)	K206 61	CYP714A1; cytochrome P450 family 714 subfamily A1
sp Q0WT24 STOP2_ARATH (373)		
sp Q6ZIB5 PIN5C_ORYSJ (370)	K139 47	PIN; auxin efflux carrier family protein
sp Q8S341 PPA7_ARATH (328)	K143 79	ACP5; tartrate-resistant acid phosphatase type 5 [EC:3.1.3.2]
sp Q1H595 LSM2_ARATH (93)	K126 21	LSM2; U6 snRNA-associated Sm-like protein LSM2
sp Q84S07 NIP33_ORYSJ (278)	K098 74	NIP; aquaporin NIP
sp Q94A57 PHL2_ARATH (295)		
sp Q852M4 PLAT3_ORYSJ (749)	K013 01	NAALAD; N-acetylated-alpha-linked acidic dipeptidase [EC:3.4.17.21]
sp Q8S397 NHX4_ARATH (529)		
sp Q9SXF8 PIP13_ORYSJ (288)	K098 72	PIP; aquaporin PIP
sp A8MRY9 UGNT1_ARATH (344)	K152 81	SLC35D1_2_3; solute carrier family 35, member D1/2/3
sp Q37145 ACA1_ARATH (1020)	K015 37	ATP2C; P-type Ca ²⁺ transporter type 2C [EC:7.2.2.10]
sp A0A1D6HQ92 YCED1_MAI ZE (293)		
sp Q0D9R7 ARFS_ORYSJ (1161)		
sp Q9SFU3 PPA15_ARATH (532)	K223 90	ACP7; acid phosphatase type 7
sp Q9XFR0 KCO3_ARATH (260)	K053 89	KCNKF; potassium channel subfamily K, other eukaryote
sp P04770 GLNA1_PHAVU (356)	K019 15	glNA, GLUL; glutamine synthetase [EC:6.3.1.2]
sp Q93Z81 CAX3_ARATH (459)	K073 00	chaA, CAX; Ca ²⁺ :H ⁺ antiporter
sp Q50LH3 C7192_ESCCA (495)	K097 54	CYP98A, C3'H; 5-O-(4-coumaroyl)-D-quinic acid 3'-monooxygenase [EC:1.14.14.96]
sp Q94A16 CP21C_ARATH (230)		
sp Q94FA5 METK4_BRAJU (390)	K007 89	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]
sp Q945Q1 CYT1_ARATH (101)		
sp Q8H0V4 DUF7_ARATH (722)		

sp Q8GVE8 CAPP4_ARATH (1032)	K01595	ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
sp Q9FMF5 RPT3_ARATH (746)		
sp P43282 METK3_SOLLC (390)	K00789	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]
sp Q40872 AG_PANGI (242)	K09264	K09264; MADS-box transcription factor, plant
sp Q9FMS7 OFP10_ARATH (196)		
sp Q08062 MDHC_MAIZE (332)	K00025	MDH1; malate dehydrogenase [EC:1.1.1.37]
sp O81001 GRF1_ARATH (530)		
sp Q8GXJ4 GLR34_ARATH (959)	K05387	GRIP; glutamate receptor, ionotropic, plant
sp Q9FFN7 DGK2_ARATH (712)	K00901	dgkA, DGK; diacylglycerol kinase (ATP) [EC:2.7.1.107]
sp Q7XSQ9 PIP12_ORYSJ (288)	K09872	PIP; aquaporin PIP
tr L0GDQ5 L0GDQ5_WHEAT (262)	K06630	YWHAE; 14-3-3 protein epsilon
tr A0A0U2WTZ1 A0A0U2WTZ1_PRUAV (290)	K09872	PIP; aquaporin PIP
sp Q96293 ACT8_ARATH (377)	K10355	ACTF; actin, other eukaryote
tr A0A178WDV5 A0A178WDV5_ARATH (377)	K10355	ACTF; actin, other eukaryote
tr A0A140JW78 A0A140JW78_9GENT (304)	K09422	MYBP; transcription factor MYB, plant
sp Q9LHJ9 P2C38_ARATH (385)	K01102	PDP; pyruvate dehydrogenase phosphatase [EC:3.1.3.43]
tr B9DH70 B9DH70_ARATH (337)		
tr B6TD48 B6TD48_MAIZE (307)	K00472	P4HA; prolyl 4-hydroxylase [EC:1.14.11.2]
tr A5YM78 A5YM78_CICAR (261)	K06630	YWHAE; 14-3-3 protein epsilon
tr Q0WTE4 Q0WTE4_ARATH (186)	K08515	VAMP7; vesicle-associated membrane protein 7
tr Q705X3 Q705X3_MEDTR (233)	K12462	ARHGDI, RHOGDI; Rho GDP-dissociation inhibitor
tr Q7Y0W8 Q7Y0W8_LUPAL (412)	K00031	IDH1, IDH2, icd; isocitrate dehydrogenase [EC:1.1.1.42]
tr Q9XGB4 Q9XGB4_TRIRP (298)	K01183	E3.2.1.14; chitinase [EC:3.2.1.14]
tr A0A2K8GLT3 A0A2K8GLT3_LUPAL (487)	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
tr F8WL60 F8WL60_RHISY (297)	K10355	ACTF; actin, other eukaryote
tr A0A1U8YLW4 A0A1U8YLW4_VIGUN (289)	K09872	PIP; aquaporin PIP

tr A0A076V5N5 A0A076V5N5_9APIA (509)	K00938	E2.7.4.2, mvaK2; phosphomevalonate kinase [EC:2.7.4.2]
tr B2L2W9 B2L2W9_9SOLA (260)	K08081	TR1; tropinone reductase I [EC:1.1.1.206]
tr A0A1U8YLV7 A0A1U8YLV7_VIGUN (289)	K09872	PIP; aquaporin PIP
tr Q9SAZ6 Q9SAZ6_MAIZE (960)	K01595	ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
tr I3NN78 I3NN78_SOLLC (310)		
tr V5RDW6 V5RDW6_CUCSA (292)	K09872	PIP; aquaporin PIP
tr L7NJI5 L7NJI5_GOSBA (267)	K01183	E3.2.1.14; chitinase [EC:3.2.1.14]
tr C0Z2S6 C0Z2S6_ARATH (325)	K13260	CYP81E; isoflavone/4'-methoxyisoflavone 2'-hydroxylase [EC:1.14.14.90 1.14.14.89]
tr B2ZUU2 B2ZUU2_LOTJA (516)		
tr A0A2Z5EMU8 A0A2Z5EMU8_ORYSI (568)		
tr A0A0D5W5Q1 A0A0D5W5Q1_9ROSI (287)	K09872	PIP; aquaporin PIP
tr M4M6J9 M4M6J9_TRIRP (182)		
sp Q42908 PMGI_MESCR (559)	K15633	gpml; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]
sp P14654 GLN12_ORYSJ (357)	K01915	glnA, GLUL; glutamine synthetase [EC:6.3.1.2]
tr C5G5Y5 C5G5Y5_PHAAN (301)	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]
tr O22339 O22339_MEDSA (290)	K09872	PIP; aquaporin PIP
tr Q3T1V7 Q3T1V7_9LILI (517)	K20000	MATK; maturase K
sp Q42899 GLNA1_LOTJA (356)	K01915	glnA, GLUL; glutamine synthetase [EC:6.3.1.2]
tr B6SM21 B6SM21_MAIZE (330)	K08064	NFYA, HAP2; nuclear transcription factor Y, alpha
sp Q10M12 40C1_ORYSJ (348)		
tr M1EY53 M1EY53_9ROSI (281)	K09872	PIP; aquaporin PIP
sp P42895 ENO2_MAIZE (446)	K01689	ENO, eno; enolase [EC:4.2.1.11]
tr Q41730 Q41730_MAIZE (169)		
tr Q1H8M9 Q1H8M9_BETVU (290)		
tr H2BPE1 H2BPE1_9MONI (427)	K02112	ATPF1B, atpD; F-type H ⁺ /Na ⁺ -transporting ATPase subunit beta [EC:7.1.2.2 7.2.2.1]
tr A0A804J464 A0A804J464_MUSAM (386)	K05605	HIBCH; 3-hydroxyisobutyryl-CoA hydrolase [EC:3.1.2.4]

tr I1SUZ0 I1SUZ0_CICAR (261)	K06630	YWHAE; 14-3-3 protein epsilon
tr T1R3E6 T1R3E6_DATGL (187)		
tr A0A075EC73 A0A075EC73_ASTME (571)	K00021	HMGCR; hydroxymethylglutaryl-CoA reductase (NADPH) [EC:1.1.1.34]
tr A0A2H4RK81 A0A2H4RK81_9ERIC (1223)		
tr Q5KTN5 Q5KTN5_TOBAC (260)	K06630	YWHAE; 14-3-3 protein epsilon
tr L0GED8 L0GED8_WHEAT (261)	K06630	YWHAE; 14-3-3 protein epsilon
tr L7X5Z3 L7X5Z3_GOSHI (246)		
XP_009387221.1 (277)	K08150	SLC2A13, ITR; MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13
XP_018677474.1 (264)	K13066	COMT; caffeic acid 3-O-methyltransferase / acetylserotonin O-methyltransferase [EC:2.1.1.68 2.1.1.4]
XP_018673750.1 (335)	K13356	FAR; alcohol-forming fatty acyl-CoA reductase [EC:1.2.1.84]

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Supplementary table 6b. KEGG enrichment analysis of DAPs in leaves of *Lactuca sativa* seedlings after treatment with FCA

Query	KO	Definition
tr A0A2J6KJN7 A0A2J6KJN7_LACSA (496)	K02112	ATPF1B, atpD; F-type H ⁺ /Na ⁺ -transporting ATPase subunit beta [EC:7.1.2.2 7.2.2.1]
tr A0A2J6KR38 A0A2J6KR38_LACSA (484)	K01601	rbcl, cbbL; ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39]
tr A0A2J6K870 A0A2J6K870_LACSA (648)	K02132	ATPeF1A, ATP5A1, ATP1; F-type H ⁺ -transporting ATPase subunit alpha
tr A0A2J6KSN5 A0A2J6KSN5_LACSA (609)		
tr A0A2J6KR44 A0A2J6KR44_LACSA (329)	K02716	psbO; photosystem II oxygen-evolving enhancer protein 1
tr A0A2J6KNE7 A0A2J6KNE7_LACSA (949)	K08675	PRSS15, PIM1; ATP-dependent Lon protease [EC:3.4.21.53]
tr A0A2J6KM75 A0A2J6KM75_LACSA (377)	K00847	E2.7.1.4, scrK; fructokinase [EC:2.7.1.4]
tr A0A2J6KKS5 A0A2J6KKS5_LACSA (955)	K01535	PMA1, PMA2; H ⁺ -transporting ATPase [EC:7.1.2.1]
tr A0A2J6KC04 A0A2J6KC04_LACSA (328)	K00025	MDH1; malate dehydrogenase [EC:1.1.1.37]
tr A0A2J6JYJ9 A0A2J6JYJ9_LACSA (221)	K02995	RP-S8e, RPS8; small subunit ribosomal protein S8e

tr A0A2J6M0L9 A0A2J6M0L9_LACSA (647)	K03283	HSPA1s; heat shock 70kDa protein 1/2/6/8
tr A0A2J6LQR8 A0A2J6LQR8_LACSA (450)	K07374	TUBA; tubulin alpha
tr A0A2J6K4N9 A0A2J6K4N9_LACSA (233)	K02934	RP-L6e, RPL6; large subunit ribosomal protein L6e
tr A0A2J6K1M5 A0A2J6K1M5_LACSA (1252)		
tr A0A2J6K1D0 A0A2J6K1D0_LACSA (813)		
tr A0A2J6JZ15 A0A2J6JZ15_LACSA (382)		
tr A0A2J6JZ00 A0A2J6JZ00_LACSA (471)		
tr A0A2J6K6R8 A0A2J6K6R8_LACSA (431)	K11340	ACTL6A, INO80K; actin-like protein 6A
tr A0A2J6JYV6 A0A2J6JYV6_LACSA (843)	K03234	EEF2; elongation factor 2
tr A0A2J6LKC2 A0A2J6LKC2_LACSA (190)	K11254	H4; histone H4
tr A0A2J6JPA2 A0A2J6JPA2_LACSA (203)	K12876	RBM8A, Y14; RNA-binding protein 8A
tr A0A2J6MF89 A0A2J6MF89_LACSA (99)	K02692	psaD; photosystem I subunit II
tr A0A2J6JN28 A0A2J6JN28_LACSA (777)	K19984	EXOC5, SEC10; exocyst complex component 5
tr A0A2J6K212 A0A2J6K212_LACSA (266)	K08912	LHCB1; light-harvesting complex II chlorophyll a/b binding protein 1
tr A0A2J6JGN9 A0A2J6JGN9_LACSA (1409)	K15601	KDM3; [histone H3]-dimethyl-L-lysine9 demethylase [EC:1.14.11.65]
tr A0A2J6M6Y2 A0A2J6M6Y2_LACSA (218)	K03564	BCP, PRXQ, DOT5; thioredoxin-dependent peroxiredoxin [EC:1.11.1.24]
tr A0A2J6M0G5 A0A2J6M0G5_LACSA (523)		
tr A0A2J6MHG7 A0A2J6MHG7_LACSA (464)	K01369	LGMN; legumain [EC:3.4.22.34]
tr A0A2J6LS26 A0A2J6LS26_LACSA (1150)	K03021	RPC2, POLR3B; DNA-directed RNA polymerase III subunit RPC2 [EC:2.7.7.6]
tr A0A2J6KRH0 A0A2J6KRH0_LACSA (403)	K02930	RP-L4e, RPL4; large subunit ribosomal protein L4e
tr A0A2J6MHA8 A0A2J6MHA8_LACSA (957)	K10405	KIFC1; kinesin family member C1
tr A0A2J6LNZ7 A0A2J6LNZ7_LACSA (437)	K01438	argE; acetylornithine deacetylase [EC:3.5.1.16]
tr A0A2J6LI76 A0A2J6LI76_LACSA (623)	K02145	ATPeV1A, ATP6A; V-type H ⁺ -transporting ATPase subunit A [EC:7.1.2.2]
tr A0A2J6LHJ7 A0A2J6LHJ7_LACSA (389)	K00218	por; protochlorophyllide reductase [EC:1.3.1.33]
tr A0A2J6K7V0 A0A2J6K7V0_LACSA (477)		
tr A0A2J6MJP6 A0A2J6MJP6_LACSA (635)	K08991	MUS81; crossover junction endonuclease MUS81 [EC:3.1.22.-]
tr A0A2J6LDW8 A0A2J6LDW8_LACSA (249)	K02991	RP-S6e, RPS6; small subunit ribosomal protein S6e

tr A0A2J6LC77 A0A2J6LC77_LACSA (1974)	K02349	POLQ; DNA polymerase theta [EC:2.7.7.7]
tr A0A2J6LC09 A0A2J6LC09_LACSA (622)	K17681	ATAD3A_B; ATPase family AAA domain-containing protein 3A/B
tr A0A2J6LBI7 A0A2J6LBI7_LACSA (404)	K01623	ALDO; fructose-bisphosphate aldolase, class I [EC:4.1.2.13]
tr A0A2J6LBG3 A0A2J6LBG3_LACSA (894)	K03696	clpC; ATP-dependent Clp protease ATP-binding subunit ClpC
tr A0A2J6JY99 A0A2J6JY99_LACSA (249)	K08909	LHCA3; light-harvesting complex I chlorophyll a/b binding protein 3
tr A0A2J6JLK0 A0A2J6JLK0_LACSA (449)	K03231	EEF1A; elongation factor 1-alpha
tr A0A2J6L776 A0A2J6L776_LACSA (511)	K18757	LARP1; la-related protein 1
tr A0A2J6L5J6 A0A2J6L5J6_LACSA (1093)	K11838	USP7, UBP15; ubiquitin carboxyl-terminal hydrolase 7 [EC:3.4.19.12]
tr A0A2J6L1L3 A0A2J6L1L3_LACSA (177)	K01602	rbcS, cbbS; ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]
tr A0A2J6L042 A0A2J6L042_LACSA (479)		
tr A0A2J6KTT7 A0A2J6KTT7_LACSA (552)	K02147	ATPeV1B, ATP6B; V-type H ⁺ -transporting ATPase subunit B
tr A0A2J6MCD9 A0A2J6MCD9_LACSA (508)	K02111	ATPF1A, atpA; F-type H ⁺ /Na ⁺ -transporting ATPase subunit alpha [EC:7.1.2.2 7.2.2.1]