

accession number	length	intron	isolate name	repository strain #	Sequence type
U07400	2282		CDC:0981:V006	ATCC 50494	T1
GQ924681	2275		OSU 08-001		T1
GQ924682	2274		OSU 08-002		T1
AY702998	2078		CDC:V327		T1
DQ992193	2320		EFW9		T2
DQ992190	2304		EFW16		T2
DQ992186	2302		EFW3		T2
DQ992187	2302		EFW11		T2
DQ992188	2302		EFW12		T2
DQ992189	2302		EFW15		T2
CDFA01	2289		"healyi" genome (putative <i>A. palestinensis</i> Reich)	ATCC 30870	T2
U07411	2288		Reich	ATCC 30870	T2
L09599	2286		Reich [AC-014]	ATCC 30870 CCAP 1547/1	T2
AM408800	2280		EI5	ATCC PRA-223	T2
AF019050	2238		GE3a	ATCC 50252	T2
DQ992192	2236		EFW7		T2
AB425949	2252		SE2 6F		T2/6A
AY026244	2244		CCAP 1501/3b	ATCC 30872	T2/6A
AY173011	2314		KA/MSG27		T2/6B
AB425945	2246		OB3b 3A		T2/6B
AB425955	2246		E 5C		T2/6B
JQ669661	2256		OSU09-006		T2/6C
AF019051	2239		OX-1	CCAP 1501/3c	T2/6C
HM159368	2236		WR		T2/6C
AM408799	2277		EI4	ATCC PRA-224	T2/6C

S81337	2294	488	H37 (TIO:H37)	ATCC 50702	T3
U07412	2294	518	S-7	ATCC 30731	T3
no acc	2293	488	H38		T3
no acc	2293	488	H39		T3
AF019053	2249		Sawyer 205-1	ATCC 50435	T3
AF019052	2239		Panola Mountain	ATCC 30487	T3
AF005996	2294		KA/E1		T4A
EF140629	2286		KA/E28		T4A
KF318460	2265		Acanthamoeba sp. 1 FRC-2013		T4A
AF019054	2249		Jin-E5	ATCC 50710	T4A
AF019055	2246		Liu-E1	ATCC 50709	T4A
AY026251	2243		U/E8R		T4A
AY026250	2237		U/E8X		T4A
no acc	2250		KA/WP2		T4A
GQ889265	2241		OSU-08-016 CDCV600		T4A
AY173004	2311		KA/MSG4		T4A
AY173015	2308	967	KA/MSS7		T4A
AY173013	2306	969	KA/MSS2		T4A
AY173014	2297	959	KA/MSS6		T4A
AF349045	2285	957	KA/E4		T4A
AY148954	2276	960	KA/E5		T4A
AY173010	2315		KA/MSG26		T4A
CDFJ01	2304		"pearcii" genome (putative A. sp. problematic)		T4A
U07408	2293		Galka	ATCC 50496	T4A
no acc	2308		GALKA (allele 2)	BCM:1282:324 ATCC 50496	T4A
EF140628	2284		KA/E27		T4A
AF352390	2255		UWC12	ATCC PRA-4	T4A
no acc	2250		KA/LP1		T4A
no acc	2250		KA/WP1		T4A
no acc	2250		KA/WP11		T4A
no acc	2246		KA/WP3		T4A
AF260725	2245		5SU		T4A
AF260719	2244		36KL		T4A
EU683884	2222		CRIB59-49R2		T4A

KF433824	2188		Uncultured Acacanthamoeba AG-P1B	T4A
KF433819	2132		Uncultured Acacanthamoeba AG-122	T4A
AY703025	2002		OSU:02-031	T4A
AF251938	2245		9GU	ATCC PRA-108
U07407	2287		Garcia	ATCC 50371
AY026243	2239		ATCC 30461	ATCC 30461
no acc	2304		Jones	ATCC 30461
U07406	2280		Haas	ATCC 50368
AY148956	2286		KA/E8	T4A
AF005997	2285		KA/E3	T4A
JQ271664	2285		ACANT	T4A
JQ271667	2284		CANZ	T4A
AY026749	2243		U/E10	T4A
AF349044	2298		KA/E6	T4A
CDFN01	2298		quina (isolate Vil3) genome	ATCC 50241
AY703023	2028		quina clone Vil3	ATCC 50241
EF140633	2280	982	KA/E21	T4A
no acc	2250		KA/LP2	T4A
U07413	2290		Castellani AC30	ATCC 50374
KF318462	2256		A. castellanii strain ATCC 30011	ATCC 30011
AF260724	2239		4CL	ATCC PRA-107
AF352387	2235		UWC6	ATCC PRA-1
AF352388	2235		UWE2	ATCC PRA-8
AM941721	2224		UWC1	ATCC PRA-219
AM408797	2145		EI2	ATCC PRA-226
AY702992	2294		CDC:V168	ATCC 50659
EF140626	2280		KA/E25	T4A
AY702999	2237		CDC:V328	T4A
AY703002	2237		CDC:V382	T4A
AY703004	2237		CDC:V390	T4A
AY173008	2306		KA/MSG16	T4A
AY176047	2308	1275	KA/MSG23	T4A
no acc	2250		KA/LP3	T4A
no acc	2250		KA/LP4	T4A
no acc	2250		KA/LP5	T4A

no acc	2250	KA/WK1		T4A
no acc	2250	KA/WK2		T4A
no acc	2250	KA/WK4		T4A
no acc	2250	KA/WP5		T4A
no acc	2250	KA/WP6		T4A
no acc	2250	KA/WP7		T4A
no acc	2250	KA/WP10		T4A
no acc	2250	KA/WP13		T4A
KR780555	2171	AM19		T4A
KR780556	2171	AM101		T4A
U07403	2282	CDC:0786:V042	ATCC 50493	T4A
JQ271663	2274	4482SL		T4A
AF019056	2237	HC-2	ATCC 50725	T4A
AY703024	2237	OSU:02-013 Hicks OHSU		T4A
AF260718	2235	312-2		T4A
AY965873	2169	AND32		T4A
AF260720	2242	7AR		T4A
CDFB01	2353	lugdenensis (isolate L3a) genome	ATCC 50240	T4A
AF005995	2292	L3a	ATCC 50240	T4A
AF316545	2293	KA/E12		T4A
AF005998	2292	KA/E2		T4A
no acc	2291	H31 (AcPHL/7b)		T4A
U07410	2282	Rawdon	ATCC 50497	T4A
no acc	2282	TIO:H30 allele 1	ATCC 50726	T4A
no acc	2282	H30 (AcPHL/7a)		T4A
EF140627	2276	KA/E26		T4A
AY703018	2237	CDC:VE67/H7		T4A
no acc	2237	KA/WP4		T4A
no acc	2236	KA/WP8		T4A
no acc	2236	KA/WP12		T4A
KR780546	2172	A-T4-1-57		T4A
KR780547	2172	A-T4-1-89		T4A
KR780551	2171	AM-4H		T4A
KR780552	2171	AM-5H		T4A
KR780553	2171	A-T4-3-62		T4A

KR780554	2171	A-T4-3-146		T4A
KR780548	2170	A-T4-2-58		T4A
KR780549	2170	A-T4-2-60		T4A
KR780550	2170	A-T4-2-104		T4A
AY173003	2300	KA/MSG3		T4A
AY173012	2304	KA/MSG29		T4A
AY173007	2301	KA/MSG15		T4A
GU320592	2280	COHH 55		T4A
GU320594	2280	COHH 57		T4A
no acc	2291	H32		T4A
EF140638	2285	KA/E22		T4A
EF429130	2243	PAT05		T4A
GU320586	2281	COHH 26		T4A
EF554328	2236	Neff	ATCC 30010	T4A
AY148960	2283	KA/E14		T4A
KT185626	2282	A. castellanii BCP-EM3VF21-1		T4A
no acc	2250	KA/WK3		T4A
KF318461	2245	Acanthamoeba sp. 2 FRC-2013		T4A
AY148959	2280	KA/E13		T4A
EF140630	2248	KA/E29		T4A
DQ013363	2244	A. polyphaga pond		T4A
AY148961	2276	KA/E15		T4A
AY148962	2276	KA/E16		T4A
no acc	2306	Kamph		T4A
no acc	2305	JAC/E2		T4A
no acc	2297	JAC/E3		T4A
no acc	2297	JAC/E4		T4A
no acc	2297	JAC/9E		T4A
AY703019	2244	CDC:VEPV94-3		T4B
AF019057	2245	Diamond	ATCC 50724	T4B
AF019058	2244	Vazaldua CEI:M95:5:27	ATCC 50723	T4B
AY026249	2239	U/E7 clone 2		T4B
GU808307	2238	Ac E12a		T4B
GU808285	2236	Ac E4b		T4B

GU808308	2236	Ac E12b		T4B
GU808309	2236	Ac E12c		T4B
GU808319	2236	Ac PT3		T4B
AY026247	2233	U/E7 clone 1		T4B
AY694140	2245	L1060/96		T4B
AY552093	2141	OSU03-002		T4B
AY552094	2141	OSU03-003		T4B
AY552095	2141	OSU03-004		T4B
AY552096	2141	OSU03-005		T4B
EF140632	2242	KA/E20		T4B
AY026748	2237	U/E5		T4B
GU808329	2236	Ac PCN20		T4B
GU808283	2235	Ac E3		T4B
AF132135	2233	HN-3	ATCC 30173	T4B
AY148958	2283	KA/E11		T4B
GU808304	2240	Ac E10b		T4B
AY026246	2239	U/E6		T4B
GU808303	2236	Ac E10a		T4B
GU808305	2236	Ac E10c		T4B
GU808326	2236	Ac PCN18a		T4B
GU808327	2236	Ac PCN18b		T4B
GU808328	2236	Ac PCN18c		T4B
U07404	2290	CDC:0688:V125	ATCC 50498	T4B
U07405	2284	CDC:0180:1	ATCC 50491	T4B
AY702983	2245	CDC:V017	ATCC 50656	T4B
AF285277	2243	KO99		T4B
GU808296	2236	Ac E7a		T4B
GU808297	2235	Ac E7b		T4B
GU808284	2240	Ac E4a		T4B
GU808287	2240	Ac E4d		T4B
GU808288	2240	Ac E4e		T4B
AY173000	2310	KA/MSS8-1		T4B
AY694139	2245	L773/96		T4B
AY694142	2193	L1002/99		T4B
AY148957	2288	KA/E10		T4B

GU320589	2272	COHH 43		T4B
CDFK01	2304	"A. polyphaga (CCAP 1501/3b)" genome	ATCC 50872?	T4B
no acc	2300	KA/PE1		T4B
CDFL01	2283	castellanii (isolate Ma) genome	ATCC 50370	T4B
U07414	2278	Ma	ATCC 50370	T4B
U07415	2276	JAC/S2	ATCC 50372	T4B
U07402	2273	CDC:0885:V029	ATCC 50495	T4B
GU320583	2271	Dighton Bridge		T4B
AF260721	2231	1BU	ATCC PRA-105	T4B
AB425952	2229	Mbc 3E		T4B
AF260723	2228	3ST	ATCC PRA-114	T4B
AY026248	2225	U/Oft1		T4B
no acc	2290	JAC/E7		T4B
no acc	2290	JAC/473U		T4B
no acc	2289	Bitzer (Ac/PHL/6)	(Ac/PHL/6)	T4B
AF316546	2333	KA/E9		T4C
AY148963	2287	KA/E17		T4C
EF140625	2287	KA/E23		T4C
JX423610	2251	OSU07-103-MEEI0184		T4C
GU808323	2240	Ac P12b		T4C
GU808321	2239	Ac P12 CSF		T4C
GU808322	2238	Ac P12a		T4C
U07401	2227	CDC:0184:V014	ATCC 50492	T4C
GU808286	2238	Ac E4c		T4C
U07409	2298	Fernandez	ATCC 50369	T4C
AF352389	2259	TUMSJ-226	ATCC PRA-10	T4C
GU808317	2244	Ac F2		T4C
GU808312	2243	Ac F1a		T4C
GU808316	2243	Ac F1e		T4C
AY694138	2250	L565/97		T4C
AY694143	2250	L1629/99		T4C
GU808325	2241	Ac P12d		T4C
GU808324	2240	Ac P12c		T4C
JX423611	2251	OSU10-025-ITSON-AK1		T4C

AY026747	2244	U/E3		T4C
GU808313	2248	Ac F1b		T4C
GU808315	2248	Ac F1d		T4C
GU808314	2247	Ac F1c		T4C
GU808289	2246	Ac E5a		T4C
GU808290	2245	Ac E5b		T4C
KF433822	2145	Uncultured <i>Acacanthamoeba</i> AG-RB1		T4C
AY351646	2247	AA2	ATCC 50238	T4D
AY351645	2227	AA1	ATCC 50251	T4D
DQ992185	2255	EFW4		T4D
DQ992182	2249	EFW6		T4D
DQ992183	2249	EFW8		T4D
DQ992179	2247	EFW1		T4D
DQ992180	2247	EFW10		T4D
DQ992181	2246	EFW14		T4D
AF019062	2243	Nagington	ATCC 30873 CCAP:1501/3d	T4D
EF205325	2227	ACLCCOF-001		T4D
DQ992184	2181	EFW2		T4D
AY694141	2241	L749/98		T4D
AY694144	2241	L98/00		T4D
AY173005	2314	KA/MSG10		T4D
AY173009	2314	KA/MSG18		T4D
CDFE01	2300	mauritaniensis (isolate 1652) genome	ATCC 50253	T4D
AY351647	2224	mauritaniensis 1652	ATCC 50253	T4D
JQ271666	2282	ALC2A		T4D
AY173002	2312	KA/MSG1		T4D
U07417	2278	Oak Ridge [AC-023]	ATCC 30884	T4D
CDFC01	2302	rhysodes (isolate Singh) genome	ATCC 30973	T4D
no acc	2245	OSU-Singh	ATCC 30973	T4D
AY351644	2243	Singh	ATCC 30973	T4D
DQ103890	2241	MZOR		T4D
AM408803	2230	5a2	ATCC PRA-228	T4D
JQ271665	2284	ALC10		T4D
AM408802	2283	EIDS3	ATCC PRA-221	T4D

FJ807647	2274	DWDS		T4D
DQ264391	2255	FA03		T4D
EF429131	2248	PAT06		T4D
DQ185606	2249	PS		T4D
no acc	2265	KA/WP9		T4D
AB425948	2249	SM6 6A		T4E
AY148964	2295	KA/E18		T4E
EF140639	2292	KA/E24		T4E
AF260722	2252	2HH	ATCC PRA-113	T4E
AF019060	2224	2AX1	ATCC 50727	T4E
AY173001	2322	KA/MSS8-2		T4E
AY148955	2294	KA/E7		T4E
AF019059	2256	Rodriguez	ATCC 50711	T4E
HM363628	2286	GERF3		T4E
AF019061	2253	Page-23	ATCC 30871 CCAP:1501/3a	T4E
EF140631	2250	KA/E19		T4E
CDFD01	2292	"palestinesis" genome (putative <i>A. triangularis</i> (isolate SH621))	ATCC 50254	T4F
AF316547	2308	SH621	ATCC 50254	T4F
AF346662	2181	<i>triangularis</i> SH621	ATCC 50254	T4F
GU808294	2230	Ac E6d		T4F
GU808292	2228	Ac E6b		T4F
GU808291	2173	Ac E6a		T4F
AF366580	2251	TUMSJ-321		T4F
GU808298	2231	Ac E8a		T4F
GU808318	2231	Ac F3		T4F
GU808299	2228	Ac E8b		T4F
GU808300	2228	Ac E8c		T4F
GU808293	2228	Ac E6c		T4F
GU808295	2228	Ac E6e		T4F
GU808306	2228	Ac E11		T4F
AEYA01002259	2304	Neff	ATCC 30010	T4-Neff
M13435	2303	Neff	ATCC 30010	T4-Neff

AF114438	2301		40AB	ATCC PRA-106	T4-Neff
U07416	2299		Neff OS4-7B/Neff	ATCC 50373	T4-Neff
AM408801	2290		E16	ATCC PRA-222	T4-Neff
GU001160	2287		Neff		T4-Neff
AM408796	2287		E11	ATCC PRA-227	T4-Neff
AY173006	2370		KA/MSG12		T5
AF352391	2338	652	TUMSJ-341	ATCC PRA-11	T5
CDFG01	2295	663	lenticulata (isolate PD2S) genome	ATCC 30841	T5
U94741	2294	656	lenticulata PD2S	ATCC 30841	T5
U94740	2294	679	lenticulata 25/1	ATCC 50707	T5
U94738	2294	642	lenticulata NJSP-3-2	ATCC 50429	T5
U94735	2294	641	lenticulata E18-2	ATCC 50690	T5
U94736	2294	640	lenticulata 118	ATCC 50706	T5
U94737	2294	636	lenticulata 53-2	ATCC 50691	T5
U94739	2293	699	lenticulata Jc-1	ATCC 50428	T5
U94733	2293		lenticulata 68-2	ATCC 50427	T5
U94731	2292		lenticulata 7327	ATCC 50705	T5
U94734	2291	721	lenticulata 407-3a	ATCC 50692	T5
U94730	2291		lenticulata 45	ATCC 50703	T5
U94732	2291		lenticulata 72/2	ATCC 50704	T5
AY172999	2314		KA/MSS1		T6
AY033896	2289		CDC-149	ATCC 50243	T6
AF019063	2249		2802	ATCC 50708 [CCAP:1501/3c]	T6
AB425954	2247		E 5F		T6
AB425956	2246		E 5E		T6
AF251939	2244		11DS	ATCC PRA-112	T6
CDFH01	2784		A. astronyxis genome	ATCC 30137	T7
AF019064	2682		A. astronyxis (Ray&Hayes)	ATCC 30137	T7
DQ992178	2666		EFW5		T7

AF019065	2517	OC-15C	ATCC 30867	T8
AF019066	2572	(Comandon & de Fonbrune)	ATCC 30135	T9
GU808280	2569	Ac E2a		T9
DQ185605	2582	PJ		T9
DQ185607	2579	PSH		T9
GU808281	2572	Ac E2b		T9
AY026242	2559	ATCC30901	ATCC 30901	T9
GU808282	2559	Ac E2c		T9
CDFF01	2354	culbertsoni (strain A1) genome	ATCC 30171	T10
AF019067	2292	Lilly A-1 [AC-001]	ATCC 30171	T10
DQ499151	2289	CDC V409C		T10
GU808320	2280	Ac P4		T10
AF333608	2415	PN14		T11
AF251937	2242	4RE	ATCC PRA-115	T11
AF019068	2242	BH-2	ATCC 30730	T11
GU808311	2242	Ac E13		T11
no acc	2241	Oregon OHSUAK		T11
AF019069	2236	RB:F:1	ATCC 50388	T11
KR780557	2178	A-T11-1-72		T11
KR780558	2178	A-T11-1-145		T11
KF433820	2116	Uncultured Acacanthamoeba AG-1244		T11
AF019070	2323	CDC1283:V013	ATCC 30866	T12
EU686716	2262	Acanthamoeba sp. 38.I		T12
AF132134	2257	UWC9	ATCC PRA-3	T13
AF132136	2253	UWET39	ATCC PRA-9	T13
AY102615	2239	TUMK-23		T13
KF928950	2198	Tib1		T13

AF333607	2377	PN15	114
AF333609	2377	PN13	114

NO T15 SEQUENCES

AY026245	2217	U/HC1	T16
GQ380408	2157	Acanthamoeba sp. cvX	T16

GU808277	2581	Ac E1a	T17
GU808301	2574	Ac E9a	T17
GU808302	2574	Ac E9b	T17
GU808279	2570	Ac E1c	T17
GU808278	2556	Ac E1b	T17

KC822466	2639	CDC:V621 clone 6	T18
KC822461	2633	CDC:V621 clone 1	T18
KC822469	2630	CDC:V621 clone 9	T18
KC822462	2629	CDC:V621 clone 2	T18
KC822463	2629	CDC:V621 clone 3	T18
KC822464	2629	CDC:V621 clone 4	T18
KC822465	2629	CDC:V621 clone 5	T18
KC822467	2629	CDC:V621 clone 7	T18
KC822468	2628	CDC:V621 clone 8	T18
KC822470	2628	CDC:V621 clone 10	T18
SRX2460089	2651	PB30/40	ATCC PRA-287 T18

KJ413084	2301	USP-AWW-A68	T19
KP711387	2288	Acanthamoeba micheli strain BRO-2	T19

DQ451161	2244	OSU 04-020 clone 2	T20
DQ451163	2238	OSU 04-023 clone 3	T20
KR780563	2131	AM-1H	T20
KR780560	2130	AM-2H	T20
KR780561	2130	A-T16-1-50	T20
KR780562	2130	A-T16-1-66	T20
KR780564	2130	A-T16-2-51	T20
KR780564	2130	AM-3H	T20
KR780566	2130	A-T16-2-86	T20
KR780567	2130	A-T16-2-136	T20
KR780568	2130	A-T16-2-144	T20
KR780569	2129	AM22	T20
KR780559	2119	AM38	T20
CDEZ01	2241	"royreba" genome - true identity unknown	T21
KX840327	2248	Acanthamoeba pyriformis isolate CR15	T22
EF023500	2019	Eimeriidae Amb 18S 1092	T99
EF023541	2019	Eimeriidae Amb 18S 1143	T99
EF023659	2019	Eimeriidae Amb 18S 911	T99
EF023745	2019	Eimeriidae Amb 18S 1183	T99
EF023774	2019	Eimeriidae Amb 18S 1215	T99
EF023782	2019	Acanthamoeba Amb 18S 1223	T99