

**Dataset Integrity Check (DSIC) for the
TEDDY Data Files**

Reference paper:

Hagopian WA, et al.

*The Environmental Determinants of Diabetes in the Young (TEDDY): genetic criteria and international diabetes risk screening of 421 000 infants
Pediatric Diabetes 2011 May 12. [epub ahead of print]
doi: 10.1111/j.1399-5448.2011.00774.x*

The TEDDY study seeks to identify environmental factors influencing the development of type 1 diabetes (T1D) via an intensive follow-up of children at elevated genetic risk. The study utilized a cost-effective yet accurate screening strategy to identify the high-risk cohort. The TEDDY cohort was identified through newborn screening via human leukocyte antigen (HLA) class II genes based on criteria established with pre-TEDDY data. TEDDY developed separate inclusion criteria for the general population (GP) and first-degree relatives (FDRs) of T1D patients. The FDR eligibility included nine haplogenotypes (*DR3/4*, *DR4/4*, *DR4/8*, *DR3/3*, *DR4/4b*, *DR4/1*, *DR4/13*, *DR4/9*, and *DR3/9*) for broad HLA diversity, while the GP eligibility included only the first four haplogenotypes with *DRB1*0403* as an exclusion allele. Screening for TEDDY has ended and the corresponding screening dataset has been archived at the NIDDK Repository.

As a partial check of the integrity of the archived TEDDY screening dataset, a dataset integrity check (DSIC) was performed to verify that selected published results from the TEDDY study can be reproduced using the archived dataset. The DSIC consists of a small number of analyses performed to duplicate published results reported by Hagopian WA, et al., in *Pediatric Diabetes* in May, 2011. Results of the DSIC are described below.

The intent of this DSIC is to provide confidence that the data distributed by the NIDDK repository is a true copy of the study data. Our intent is *not* to assess the integrity of the statistical analyses reported by study investigators. As with all statistical analyses of complex datasets, complete replication of a set of statistical results should not be expected on a first exercise in secondary analysis. This occurs for a number of reasons including differences in the handling of missing data, restrictions on cases included in samples for a particular analysis, software coding used to define complex variables, etc. Experience suggests that most discrepancies can ordinarily be resolved by consultation with the study data coordinating center (DCC), however this process is labor-intensive for both DCC and Repository staff. We do not attempt to resolve minor or inconsequential discrepancies with published results or discrepancies that involve complex analyses, *unless staff of the NIDDK Repository suspect that the observed discrepancy suggests that the dataset may have been corrupted in storage, transmission, or processing by repository staff.* We do, however, document in the integrity check those instances in which our secondary analyses produced results that were not fully consistent with those reported in the target publication.

Archived Dataset Contents. The DCC submitted a single SAS data file representing the raw data collected from the screening data collection form. The screening file is called `<teddy_screening.sas7bdat>`, dated 8/25/2011. The exact variables on the file are:

- <maskid>: Participant’s masked ID number
- <hla_screen_genotype>: HLA screening genotype result (ineligible infants coded as “Not Eligible”)
- <country>: Country of clinical center
- <anyfamilymemt1d>: indicator for whether the child has any family member with Type 1 diabetes
- <whichfamilymemt1d_father>: indicator for father having Type 1 diabetes
- <whichfamilymemt1d_mother>: indicator for mother having Type 1 diabetes
- <whichfamilymemt1d_sibling>: indicator for sibling having Type 1 diabetes.

DSIC Analysis Methods. For this DSIC, we attempted to replicate as many results as possible using the available screening variables.

First, the archived screening dataset was divided into two subpopulations, based on the variable <anyfamilymemt1d>:

- 1.) infants in the *general population* (GP)
- 2.) infants with a *first degree relative* with diabetes (FDR).¹

Eligible subjects in the two subpopulations were identified by those testing positive for selected haplogenotypes. Infants with an FDR also had to test positive for any of nine haplogenotypes (*DR3/4*, *DR4/4*, *DR4/8*, *DR3/3,DR4/4b*, *DR4/1*, *DR4/13*, *DR4/9*, and *DR3/9*) for broad HLA diversity. Infants in the GP had to test positive for any of the first four haplogenotypes, with *DRB1*0403* as an exclusion allele. In the archived screening dataset, the variable <hla_screen_genotype> was used to determine each participant’s eligibility status.²

Finally, the number screened, the number eligible, and breakdown of haplogenotypes were determined for each subpopulation, stratified by country of clinical center. Results were compared to published numbers.

All statistical analyses were conducted using *SAS version 9.2 (Cary, NC)*.

¹ Per the DCC, all participants for whom <anyfamilymemt1d>='Yes' were considered as part of the FDR group; those with <anyfamilymemt1d>='No' or 'Unknown' were considered as part of the GP group. This was regardless of responses to <whichfamilymemt1d_father>, <whichfamilymemt1d_mother>, <whichfamilymemt1d_sibling>.

² Six participants in the screening dataset were missing their HLA screening result. The DCC confirmed that one of the participants was eligible (maskid=826749), while the other five were not.

DSIC Results. The publication reports that TEDDY screened a total of 414,714 GP infants from September 2004 to February 2010, of whom 19,906 (4.8%) were found to be eligible for follow-up studies. The archived screening dataset, current as of July 2011, indicates that 418,372 GP infants were screened, of whom 20,138 (4.8%) were eligible. The more recent date of the archived data likely explains the small increase in actual numbers (+1%), though the eligibility rate is exactly the same.

The publication reports that TEDDY screened a total of 6333 infants with an FDR, of whom 1,415 (22.3%) were found to be eligible. The archived screening dataset, current as of July 2011, indicates that 6,416 FDR infants were screened, of whom 1,433 (22.3%) were eligible. Again, the more recent date of the archived data likely explains the slight increase in actual numbers (+1%).

Table 1 is a comparison of archived versus published data for subpopulation breakdowns of number screened, number eligible, and percent eligible, by each country of screening. Country breakdowns show that the number of screened and number eligible are very similar between archived and published data. If anything, absolute numbers are slightly higher in archived data (corresponding to higher total numbers as presented above). The only exception is for GP infants screened in Sweden, where the number screened is slightly lower in archived versus published data; the eligibility rate, however, remains exactly the same.

Distributions by haplogenotype are also compared between archived and published data in Table 1. Distributions within each subpopulation are very similar between archived and published data; any differences were in the decimal points. As previously discussed, our analysis indicates that the population under study in archived data is slightly larger than that reported in the publication, which may explain these small differences.

Conclusion. With the replication of selected results, the analysis of archived screening data closely matches published results, allowing for variations from a possible increase in the number screened since publication. We are confident there were no errors in the transmission of the archived screening dataset from the DCC to the Repository.

Table 1: TEDDY human leukocyte antigen screening and eligibility results for GP (Part 1) and FDR (Part 2) newborns, archived versus published data

Part 1. General Population (GP) Infants

Country	Screened (n)				Eligible (n)			Eligible (%)		
	Published	Archived	Diff, Arch - Pub	% Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA*	273627	276809	3182	1%	11675	11871	196	4.3	4.3	0.0
FIN	59754	59876	122	0.2%	3370	3389	19	5.6	5.7	0.1
GER	34218	34570	352	1%	1353	1374	21	4.0	4.0	0.0
SWE	47115	47117	2	0.004%	3508	3504	-4	7.4	7.4	0.0
Total	414714	418372	3658	1%	19906	20138	232	4.8	4.8	0.0

Country	Haplogenotype Percent of Screened GP											
	A (DR 3/4)			B (DR 4/4)			C (DR 4/8)			D (DR 3/3)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA*	1.5-2.0	1.7	n.c.	0.6-1.4	0.9	n.c.	0.4-1.2	0.7	n.c.	0.9-1.0	1.0	n.c.
FIN	1.9	1.9	0.0	1.0	1.0	0.0	1.9	1.9	0.0	0.9	0.9	0.0
GER	1.7	1.7	0.0	0.7	0.7	0.0	0.4	0.4	0.0	1.1	1.1	0.0
SWE	3.2	3.2	0.0	1.6	1.6	0.0	1.0	1.0	0.0	1.7	1.6	-0.1
Total	1.9	1.9	0.0	1.0	1.0	0.0	0.9	0.9	0.0	1.1	1.1	0.0

Country	Haplogenotype Percent of Eligible GP											
	A (DR 3/4)			B (DR 4/4)			C (DR 4/8)			D (DR 3/3)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA*	35.2-44.2	39.7	n.c.	18.0-24.6	20.4	n.c.	11.0-21.3	16.1	n.c.	18.9-26.7	23.8	n.c.
FIN	33.6	33.5	-0.1	17.7	17.6	-0.1	32.7	32.8	0.1	16.0	16.0	0.0
GER	43.8	43.9	0.1	18.8	18.8	0.0	10.6	10.6	0.0	26.9	26.7	-0.2
SWE	42.5	42.6	0.1	21.7	21.7	0.0	13.6	13.6	0.0	22.2	22.2	0.0
Total	39.5	39.5	0.0	20.0	20.0	0.0	18.1	18.1	0.0	22.4	22.4	0.0

* published as 3 clinical centers: COL, GEO, and WAS

Table 1, continued: TEDDY human leukocyte antigen screening and eligibility results for GP (Part 1) and FDR (Part 2) newborns, archived versus published data.

Part 2, First Degree Relative (FDR) infants

Country	Screened (n)				Eligible (n)			Eligible (%)		
	Published	Archived	Diff, Arch - Pub	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA**	2872	2930	58	2%	615	624	9	21.4	21.3	-0.1
FIN	924	928	4	0.4%	288	290	2	31.2	31.3	0.1
GER	1518	1535	17	1%	297	300	3	19.6	19.5	-0.1
SWE	1019	1023	4	0.4%	215	219	4	21.1	21.4	0.3
Total	6333	6416	83	1%	1415	1433	18	22.3	22.3	0.0

Country	Haplogenotype Percent of Eligible FDR											
	A (DR 3/4)			B (DR 4/4)			C (DR 4/8)			D (DR 3/3)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA**	29.5-50.0	35.3	n.c.	0.0-17.1	15.9	n.c.	0.0-12.5	6.7	n.c.	15.7-33.3	16.3	n.c.
FIN	20.8	20.7	-0.1	14.2	14.5	0.3	13.9	14.1	0.2	5.6	5.5	-0.1
GER	31.6	31.7	0.1	15.2	15.0	-0.2	6.7	6.7	0.0	12.8	13.3	0.5
SWE	33.5	33.3	-0.2	20.5	21.0	0.5	7.9	8.2	0.3	11.6	11.9	0.3
Total	31.5	31.3	-0.2	15.6	16.2	0.6	8.5	8.4	-0.1	12.7	12.8	0.1

Country	Haplogenotype Percent of Eligible FDR (continued)											
	E (DR 4/4b)			F (DR 4/1)			G (DR 4/13)			H (DR 4/9)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA**	0.0-1.4	0.8	n.c.	0.0-17.1	15.9	n.c.	0.0-6.2	5.1	n.c.	0.0-1.9	1.1	n.c.
FIN	0.0	0.0	0.0	29.2	28.9	-0.3	5.9	5.9	0.0	6.9	6.9	0.0
GER	0.3	0.3	0.0	22.6	22.3	-0.3	7.1	7.0	-0.1	1.3	1.3	0.0
SWE	0.5	0.5	0.0	16.7	16.4	-0.3	7.0	6.8	-0.2	1.4	1.4	0.0
Total	0.5	0.5	0.0	20.1	20.0	-0.1	6.0	5.9	-0.1	2.4	2.4	0.0

Country	Haplogenotype Percent of Eligible FDR (continued)		
	I (DR 3/9)		Diff, Arch - Pub
	Published	Archived	Diff, Arch - Pub
USA**	0.0-3.8	2.9	n.c.
FIN	3.5	3.4	-0.1
GER	2.4	2.3	-0.1
SWE	0.9	0.5	-0.4
Total	2.6	2.5	-0.1

** Tabulations for USA represent a combination of 5 clinical centers: COL, GEO, WAS, NBD, CHP

References

[1] Hagopian WA, Erlich H, Lernmark Å, Rewers M, Ziegler AG, Simell O, Akolkar B, Vogt Jr R, Blair A, Ilonen J, Krischer J, She J, and the TEDDY Study Group. The Environmental Determinants of Diabetes in the Young (TEDDY): genetic criteria and international diabetes risk screening of 421 000 infants. *Pediatric Diabetes* 2011 May 12. [Epub ahead of print]

Appendices

[1] SAS version 9.2 Log for programming code submitted for the replication of results in *Hagopian WA, et al, Pediatric Diabetes 2011 May 12*

[2] SAS version 9.2 Output for programming code submitted for the replication of results in *Hagopian WA, et al, Pediatric Diabetes 2011 May 12*

Appendix 1

***SAS version 9.2* Log
for programming code submitted
for the replication of results in
Hagopian WA, et al., Pediatric Diabetes 2011 May 12.**

NOTE: Copyright (c) 2002-2008 by SAS Institute Inc., Cary, NC, USA.

NOTE: SAS (r) Proprietary Software 9.2 (TS2M0)
Licensed to RTI INTL MAIN, Site 70006746.

NOTE: This session is executing on the XP_PRO platform.

NOTE: SAS initialization used:
real time 8.62 seconds
cpu time 2.43 seconds

```
1 options ps=55 ls=75 nonumber formchar='|----|+\---+=|~^<>*' mprint  
orientation=portrait;
```

```
2  
3 *****  
4 * TEDDY dsic for submission.sas *  
5 * Purpose: to perform Data Set Integrity Analyses *  
6 * on TEDDY the Screening legacy dataset *  
7 * * *  
8 * * *  
9 * Input: *  
10 * teddy_screening.sas7bdat, submitted by TEDDY study group *  
11 * dated 8/25/2011 *  
12 * * *  
13 * * *  
14 * comparison study paper: *  
15 * Hagopian WA, et al... Pediatric Diabetes 2011 May 12. *  
16 * * *  
17 * Programmed by: S. Tan *  
18 *****;  
19  
20 libname teddy 'C:\Documents and Settings\stan\My  
Documents\DATA\NIDDK\TEDDY\Teddy_DATA';
```

NOTE: Libref TEDDY was successfully assigned as follows:

```
Engine: V9  
Physical Name: C:\Documents and Settings\stan\My  
Documents\DATA\NIDDK\TEDDY\Teddy_DATA
```

```
21  
22 data teddyscreen; set teddy.teddy_screening;  
NOTE: Data file TEDDY.TEDDY_SCREENING.DATA is in a format that is native to another  
host, or the  
file encoding does not match the session encoding. Cross Environment Data  
Access will be  
used, which might require additional CPU resources and might reduce  
performance.
```

```
23  
24 elig=.;  
25 if hla_screen_genotype in ('Not*Eligible','') then elig=0;  
26 /* confirmed in email sent by TEDDY DCC 10/17/11 */  
27 else if hla_screen_genotype^='' then elig=1;  
28 IF MASKID=826749 THEN ELIG=1;  
29 /* mask ID identified in email sent by TEDDY DCC 10/17/11 */  
30  
31 if anyfamilymentld='Yes' then group='T1D';  
32 else if anyfamilymentld in ('No','Unknown') then group='GP';  
33  
34 * general population *;  
35 title GP, eligibility rate;
```

NOTE: There were 424788 observations read from the data set TEDDY.TEDDY_SCREENING.
NOTE: The data set WORK.TEDDYSCREEN has 424788 observations and 9 variables.
NOTE: DATA statement used (Total process time):
real time 11.53 seconds
cpu time 1.76 seconds

```
36 proc freq; tables country*elig/ missing; where group='GP'; run;
```

NOTE: There were 418372 observations read from the data set WORK.TEDDYSCREEN.
WHERE group='GP';
NOTE: PROCEDURE FREQ used (Total process time):
real time 0.85 seconds
cpu time 0.50 seconds

```
37 title GP, haplogenotype distn among all screened;  
38 proc freq; tables country*hla_screen_genotype/ missing; where group='GP'; run;
```

NOTE: There were 418372 observations read from the data set WORK.TEDDYSCREEN.
WHERE group='GP';
NOTE: PROCEDURE FREQ used (Total process time):
real time 0.26 seconds
cpu time 0.26 seconds

```
39 title GP, haplogenotype distn among all eligible;  
40 proc freq; tables country*hla_screen_genotype/ missing; where group='GP' and  
elig=1; run;
```

NOTE: There were 20138 observations read from the data set WORK.TEDDYSCREEN.
WHERE (group='GP') and (elig=1);
NOTE: PROCEDURE FREQ used (Total process time):
real time 0.18 seconds
cpu time 0.17 seconds

```
41  
42 * infants with a relative with T1D *;  
43 title T1D, eligibility rate;  
44 proc freq; tables country*elig/ missing; where group='T1D'; run;
```

NOTE: There were 6416 observations read from the data set WORK.TEDDYSCREEN.
WHERE group='T1D';
NOTE: PROCEDURE FREQ used (Total process time):
real time 0.06 seconds
cpu time 0.04 seconds

```
45 title T1D, haplogenotype distn among all eligible;  
46 proc freq; tables country*hla_screen_genotype/ missing; where group='T1D' and  
elig=1; run;
```

NOTE: There were 1433 observations read from the data set WORK.TEDDYSCREEN.
WHERE (group='T1D') and (elig=1);
NOTE: PROCEDURE FREQ used (Total process time):
real time 0.06 seconds

Appendix 2

***SAS version 9.2* Output
for programming code submitted
for the replication of results in
Hagopian WA, et al., *Pediatric Diabetes* 2011 May 12.**

2011

The FREQ Procedure

Table of country by elig

country(Country of Clinical Center)
 elig

Frequency			
Percent			
Row Pct			
Col Pct	0	1	Total
Finland	56487	3389	59876
	13.50	0.81	14.31
	94.34	5.66	
	14.18	16.83	
Germany	33196	1374	34570
	7.93	0.33	8.26
	96.03	3.97	
	8.34	6.82	
Sweden	43613	3504	47117
	10.42	0.84	11.26
	92.56	7.44	
	10.95	17.40	
US	264938	11871	276809
	63.33	2.84	66.16
	95.71	4.29	
	66.53	58.95	
Total	398234	20138	418372
	95.19	4.81	100.00

The FREQ Procedure

Table of country by hla_screen_genotype

country(Country of Clinical Center)

hla_screen_genotype(HLA screening genotype)

Frequency							Total
Percent							
Row Pct							
Col Pct	DR3*0501	DR4*030X	DR4*030X	DR4*030X	DR4*030X	Not*Elig	
	/0201*DR	/0302*DR	/0302*DR	/0302*DR	/0302*DR	ible	
	3*0501/0	3*0501/0	4*030X/0	8*0401/0			
	201	201	302	402			
Finland	3	543	1136	598	1111	56485	59876
	0.00	0.13	0.27	0.14	0.27	13.50	14.31
	0.01	0.91	1.90	1.00	1.86	94.34	
	50.00	12.03	14.29	14.81	30.51	14.18	
Germany	0	367	603	258	146	33196	34570
	0.00	0.09	0.14	0.06	0.03	7.93	8.26
	0.00	1.06	1.74	0.75	0.42	96.03	
	0.00	8.13	7.59	6.39	4.01	8.34	
Sweden	0	777	1491	761	475	43613	47117
	0.00	0.19	0.36	0.18	0.11	10.42	11.26
	0.00	1.65	3.16	1.62	1.01	92.56	
	0.00	17.22	18.76	18.85	13.05	10.95	
US	3	2825	4717	2420	1909	264935	276809
	0.00	0.68	1.13	0.58	0.46	63.33	66.16
	0.00	1.02	1.70	0.87	0.69	95.71	
	50.00	62.61	59.36	59.95	52.43	66.53	
Total	6	4512	7947	4037	3641	398229	418372
	0.00	1.08	1.90	0.96	0.87	95.19	100.00

The FREQ Procedure

Table of country by hla_screen_genotype

country(Country of Clinical Center)						
hla_screen_genotype(HLA screening genotype)						
Frequency						
Percent						
Row Pct						
Col Pct	DR3*0501	DR4*030X	DR4*030X	DR4*030X	DR4*030X	Total
	/0201*DR	/0302*DR	/0302*DR	/0302*DR	/0302*DR	
	3*0501/0	3*0501/0	4*030X/0	8*0401/0		
	201	201	302	402		
Finland	1	543	1136	598	1111	3389
	0.00	2.70	5.64	2.97	5.52	16.83
	0.03	16.02	33.52	17.65	32.78	
	100.00	12.03	14.29	14.81	30.51	
Germany	0	367	603	258	146	1374
	0.00	1.82	2.99	1.28	0.72	6.82
	0.00	26.71	43.89	18.78	10.63	
	0.00	8.13	7.59	6.39	4.01	
Sweden	0	777	1491	761	475	3504
	0.00	3.86	7.40	3.78	2.36	17.40
	0.00	22.17	42.55	21.72	13.56	
	0.00	17.22	18.76	18.85	13.05	
US	0	2825	4717	2420	1909	11871
	0.00	14.03	23.42	12.02	9.48	58.95
	0.00	23.80	39.74	20.39	16.08	
	0.00	62.61	59.36	59.95	52.43	
Total	1	4512	7947	4037	3641	20138
	0.00	22.41	39.46	20.05	18.08	100.00

The FREQ Procedure

Table of country by elig

country(Country of Clinical Center)
elig

Frequency			Total
Percent			
Row Pct			
Col Pct	0	1	
Finland	638	290	928
	9.94	4.52	14.46
	68.75	31.25	
	12.80	20.24	
Germany	1235	300	1535
	19.25	4.68	23.92
	80.46	19.54	
	24.78	20.94	
Sweden	804	219	1023
	12.53	3.41	15.94
	78.59	21.41	
	16.13	15.28	
US	2306	624	2930
	35.94	9.73	45.67
	78.70	21.30	
	46.28	43.55	
Total	4983	1433	6416
	77.67	22.33	100.00

The FREQ Procedure

Table of country by hla_screen_genotype

country(Country of Clinical Center)	hla_screen_genotype(HLA screening genotype)									
Frequency	DR3*0501	DR3*0501	DR4*030X							
Percent	/0201*DR	/0201*DR	/0302*DR							
Row Pct	3*0501/0	9*030X/0	1*0101/0	13*0102/	3*0501/0	4*030X/0	4*030X/0	8*0401/0	9*030X/0	
Col Pct	201	303	501	0604	201	20X	302	402	303	
Total										
Finland 290	16	10	84	17	60	0	42	41	20	
20.24	1.12	0.70	5.86	1.19	4.19	0.00	2.93	2.86	1.40	
	5.52	3.45	28.97	5.86	20.69	0.00	14.48	14.14	6.90	
	8.70	27.78	29.37	20.00	13.39	0.00	18.10	33.88	58.82	
Germany 300	40	7	67	21	95	1	45	20	4	
20.94	2.79	0.49	4.68	1.47	6.63	0.07	3.14	1.40	0.28	
	13.33	2.33	22.33	7.00	31.67	0.33	15.00	6.67	1.33	
	21.74	19.44	23.43	24.71	21.21	14.29	19.40	16.53	11.76	
Sweden 219	26	1	36	15	73	1	46	18	3	
15.28	1.81	0.07	2.51	1.05	5.09	0.07	3.21	1.26	0.21	
	11.87	0.46	16.44	6.85	33.33	0.46	21.00	8.22	1.37	
	14.13	2.78	12.59	17.65	16.29	14.29	19.83	14.88	8.82	
US 624	102	18	99	32	220	5	99	42	7	
43.55	7.12	1.26	6.91	2.23	15.35	0.35	6.91	2.93	0.49	
	16.35	2.88	15.87	5.13	35.26	0.80	15.87	6.73	1.12	
	55.43	50.00	34.62	37.65	49.11	71.43	42.67	34.71	20.59	
Total 1433	184	36	286	85	448	7	232	121	34	
100.00	12.84	2.51	19.96	5.93	31.26	0.49	16.19	8.44	2.37	