DSDR | DATA SHARING FOR DEMOGRAPHIC RESEARCH

ICPSR 27031

National Longitudinal Study of Adolescent Health (Add Health), 1994-2008: DNA [Restricted Use]

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Codebook for Wave IV DNA

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Variable Description and Frequencies

Note: Frequencies displayed for the variables are not weighted. They are purely descriptive and may not be representative of the study population. Please review any sampling or weighting information available with the study.

Summary statistics (minimum, maximum, mean, median, and standard deviation) may not be available for every variable in the codebook. Conversely, a listing of frequencies in table format may not be present for every variable in the codebook either. However, all variables in the dataset are present and display sufficient information about each variable. These decisions are made intentionally and are at the discretion of the archive producing this codebook.

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Wave IV DNA

AID	RESPONDENT IDENTIFIER

Location: 1-8 (width: 8; decimal: 0)

Variable Type: character

Based upon 15701 valid cases out of 15701 total cases.

DAT1A	DOPAMINE TRANSPORTER-DAT1-ALLELE A

Location: 9-14 (width: 6; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	558	3.6 %
0	No result for DAT1 - allele A	348	2.2 %
10R	-	8870	56.5 %
11R	-	4	0.0 %
3R	-	39	0.2 %
7R	-	53	0.3 %
8R	-	181	1.2 %
9R	-	5648	36.0 %

Based upon 15701 valid cases out of 15701 total cases.

DAT1B	DOPAMINE TRANSPORTER-DAT1-ALLELE B

Location: 15-17 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	558	3.6 %
0	No result for DAT1 - allele B	348	2.2 %
10R	-	13717	87.4 %
11R	-	224	1.4 %
13R	-	3	0.0 %
7R	-	1	0.0 %
8R	-	11	0.1 %
9R	-	839	5.3 %

Based upon 15701 valid cases out of 15701 total cases.

DAT1_FLG	DOPAMINE TRANSPORTER-DAT1 FLAG

Location: 18-18 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Label*	*Unweighted Frequency*	*%*
1	Genotype value from Wave III data	114	0.7 %
. (M)	-	15587	99.3 %

Based upon 114 valid cases out of 15701 total cases.

- Mean: 1.00
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 1.00
- Standard Deviation: 0.00

DRD4A DOPAMINE RECEPTOR-DRD4-ALLELE A

Location: 19-23 (width: 5; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	558	3.6 %
0	No results for DRD4 - allele A	333	2.1 %
2R	-	2369	15.1 %
3.39R	-	15	0.1 %
3R	-	855	5.4 %
4R	-	10654	67.9 %
5R	-	124	0.8 %
6R	-	62	0.4 %
7R	-	723	4.6 %
8R	-	8	0.1 %

Based upon 15701 valid cases out of 15701 total cases.

DRD4B DOPAMINE RECEPTOR-DRD4-ALLELE B

Location: 24-26 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	558	3.6 %
0	No results for DRD4 - allele B	333	2.1 %
10R	-	14	0.1 %
2R	-	172	1.1 %
3R	-	101	0.6 %

Value	*Label*	*Unweighted Frequency*	*%*
4R	-	8307	52.9 %
5R	-	404	2.6 %
6R	-	251	1.6 %
7R	-	5161	32.9 %
8R	-	379	2.4 %
9R	-	21	0.1 %

Based upon 15701 valid cases out of 15701 total cases.

DRD4_FLG — DOPAMINE RECEPTOR-DRD4 FLAG

Location: 27-27 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Label*	*Unweighted Frequency*	*%*
1	Genotype value from Wave III data	110	0.7 %
. (M)	-	15591	99.3 %

Based upon 110 valid cases out of 15701 total cases.

- Mean: 1.00
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 1.00
- Standard Deviation: 0.00

HTTLPRA — SEROTONIN TRANSPORTER-5HTTLPR-ALLELE A

Location: 28-30 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	558	3.6 %
0	No results for 5HTTLPR - allele A	186	1.2 %
14R	-	9733	62.0 %
16R	-	5220	33.2 %
18R	-	2	0.0 %
20R	-	1	0.0 %
22R	-	1	0.0 %

Based upon 15701 valid cases out of 15701 total cases.

HTTLPRB — SEROTONIN TRANSPORTER-5HTTLPR-ALLELE B

Location: 31-33 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	558	3.6 %
0	No results for 5HTTLPR - allele B	186	1.2 %
14R	-	2858	18.2 %
16R	-	11987	76.3 %
17R	-	1	0.0 %
18R	-	15	0.1 %
19R	-	2	0.0 %
20R	-	83	0.5 %
22R	-	11	0.1 %

Based upon 15701 valid cases out of 15701 total cases.

HTTLPR_F — SEROTONIN TRANSPORTER-5HTTLPR FLAG

Location: 34-34 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Label*	*Unweighted Frequency*	*%*
1	Genotype value from Wave III data	91	0.6 %
. (M)	-	15610	99.4 %

Based upon 91 valid cases out of 15701 total cases.

- Mean: 1.00
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 1.00
- Standard Deviation: 0.00

MAOA_VA — MONOAMINE OXIDASE A-uVNTR-ALLELE A

Location: 35-40 (width: 6; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	558	3.6 %
0	No results for MAOA_V - allele A*	323	2.1 %
2.5R	-	1	0.0 %
2R	-	308	2.0 %
3.5R	-	182	1.2 %
3R	-	7491	47.7 %

Value	Label	Unweighted Frequency	%
4R	-	6766	43.1 %
5R	-	72	0.5 %

Based upon 15701 valid cases out of 15701 total cases.

MAOA_VB — MONOAMINE OXIDASE A-uVNTR-ALLELE B

Location: 41-46 (width: 6; decimal: 0)

Variable Type: character

Value	Label	Unweighted Frequency	%
	-	558	3.6 %
0	No results for MAOA_V - allele B*	7247	46.2 %
2R	-	5	0.0 %
3.5R	-	65	0.4 %
3R	-	1280	8.2 %
4R	-	6391	40.7 %
5R	-	155	1.0 %

Based upon 15701 valid cases out of 15701 total cases.

MAOA_FLG — MONOAMINE OXIDASE A-uVNTR FLAG

Location: 47-47 (width: 1; decimal: 0)

Variable Type: numeric

Value	Label	Unweighted Frequency	%
1	Genotype value from Wave III data	107	0.7 %
. (M)	-	15594	99.3 %

Based upon 107 valid cases out of 15701 total cases.

- Mean: 1.00
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 1.00
- Standard Deviation: 0.00

LALGSA — LaLgS-ALLELE A

Location: 48-50 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	594	3.8 %
0	No result for LaLgS - allele A	274	1.7 %
18R	-	2	0.0 %
20R	-	1	0.0 %
L-A	-	4980	31.7 %
L-G	-	203	1.3 %
S	-	9646	61.4 %
S-G	-	1	0.0 %

Based upon 15701 valid cases out of 15701 total cases.

LALGSB **LaLgS-ALLELE B**

Location: 51-53 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	594	3.8 %
0	No result for LaLgS - allele B	274	1.7 %
17R	-	1	0.0 %
18R	-	15	0.1 %
19R	-	2	0.0 %
20R	-	83	0.5 %
22R	-	10	0.1 %
L-A	-	9080	57.8 %
L-G	-	2808	17.9 %
S	-	2834	18.0 %

Based upon 15701 valid cases out of 15701 total cases.

TRIA **TRIALLELIC SNP IN 5HTTLPR(rs25531)-A**

Location: 54-56 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	594	3.8 %
0	No result for TRIALLELIC ACTIVITY BINS - allele A	274	1.7 %
L'	-	4983	31.7 %
S'	-	9850	62.7 %

Based upon 15701 valid cases out of 15701 total cases.

TRIB **TRIALLELIC SNP IN 5HTTLPR(rs25531)-B**

Location: 57-59 (width: 3; decimal: 0)

Variable Type: character

Value	*Label*	*Unweighted Frequency*	*%*
	-	594	3.8 %
0	No result for TRIALLELIC ACTIVITY BINS - allele B	274	1.7 %
L'	-	9191	58.5 %
S'	-	5642	35.9 %

Based upon 15701 valid cases out of 15701 total cases.