# GWA Studies Reveal Important Transporter Polymorphisms As Biomarkers for Pharmacokinetics and Pharmacodynamics

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Speakers: Kate M. Hillgren, PhD (Eli Lilly and Co.)

Kathy Giacomini, PhD (UCSF)



# **ASCPT 2016 ANNUAL MEETING**

MARCH 8-12, 2016 HILTON BAYFRONT, SAN DIEGO, CA

# Transporter Databases

Databases and Web Address	Content						
SLC Tables http://www.bioparadigms.org/slc/intro.htm	Brief information about all genes in the SLC superfamily: substrates, link to review article.						
Transporter Classification  Database  http://www.tcdb.org	Structure, sequence and annotation about the transporters						
UCSF-FDA Transportal http://dbts.ucsf.edu/fdatransportal	Transporter-mediated Drug-Drug Interaction database						
UCSF-PMT Pharmacogenomics of Membrane Transporter http://pharmacogenetics.ucsf.edu	Genetic variation of ABC and SLC transporters from PMT sequencing and 1000 Genome. Also expression data from GTEx						
Human Transporter Database http://htd.cbi.pku.edu.cn/index.php	Collected data from various databases including SNPs: NCBI, HapMap, PharmGKB etc.						

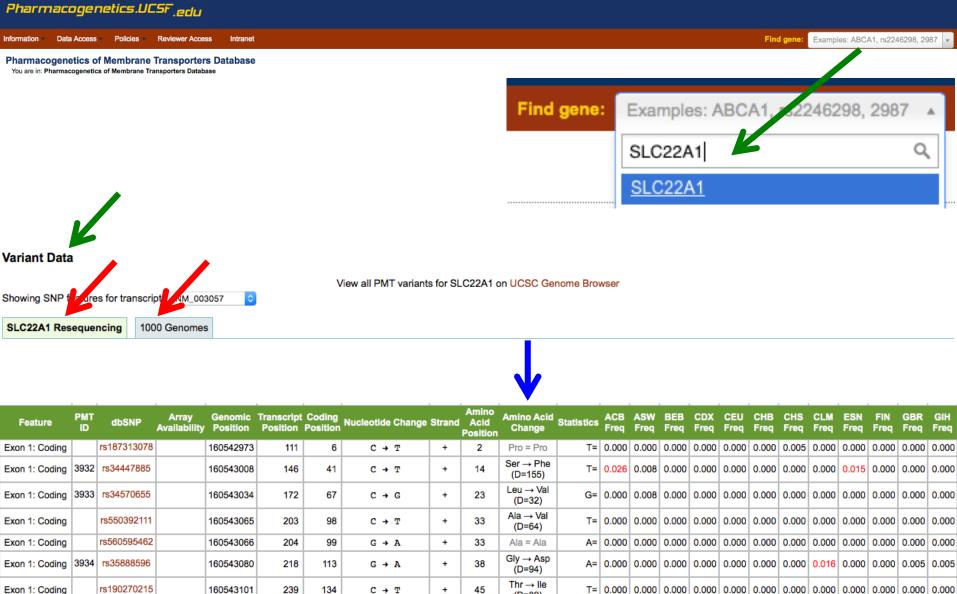
# Scenario 1: You have a new drug X in Phase I Clinical Trial

- It is a substrate of OCT1 and its drug concentrations were affected by OCT1 inhibitor in drug-drug interaction study.
- Consider doing a genetic study in Phase I clinical trial.
- Which SNP(s) should you genotype?
- Are there clinical association of the SNPs with phenotype?

http://pharmacogenetics.ucsf.edu

Pharmacogenetics.UCSF\_edu

Information • Data Access



(D=89)

Ser = Ser  $Arg \rightarrow Cys$ 

(D=180)  $Arg \rightarrow His$ 

(D=29) Pro → Leu

(D=98) Ala → Val 0.295 | 0.186 | 0.312 | 0.197 | 0.408 | 0.410

T= | 0.016 | 0.016 | 0.017 | 0.000 | 0.081 | 0.000 | 0.000 | 0.037 | 0.000 | 0.061

0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 | 0.000 | 0.000 | 0.000

T= 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.005 0.000 0.000 0.000 0.000 0.000

T= | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |

0.245 | 0.348 | 0.172 | 0.148 | 0.228

0.060 0.015

0.000 0.000

52

61

61

79

80

+

+

261

286

287

341

344

160543123

160543148

160543149

160543203

160543206

156

181

182

236

239

T → C

 $C \rightarrow T$ 

 $G \rightarrow A$ 

 $C \rightarrow T$ 

 $C \rightarrow T$ 

3935

Exon 1: Coding

rs1867351

rs145649236

rs200409072

rs145740120

3936 rs12208357

F	eature	PMT ID	dbSN	NP A	Array vailability	Genom Position	nic Tran	nscript ( sition F	Coding	Nucleotic	ie Chang	e Strand	Amino Acid Positio	AMII	o Acid ange	Statistics	ACB Freq	ASW Freq			CEU Freq	CHB Freq	CHS Freq				GBR Freq	GIH Freq
Exon	1: Codin	g	rs18731	3078		1605429	973	111	6	C ·	→ T	+	2	_	= Pro	T=	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000
Exon	1: Codin	g 3932	rs34447	7885		1605430	800	146	41	c ·	→ T	+	14		→ Phe :155)	T=	0.026	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.000	0.000	0.000
Exon	1: Codin	g 3933	rs34570	0655		1605430	034	172	67	C ·	→ G	+	23		→ Val =32)	G=	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
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Ex	on 1:	Codi	ng		rs18	731	in			160	5429	73		111		Mi	nh		T			+		2		Pro	= P	ro
Exc	on 1:	Codi	ng 3	3932	rs34	447		delli omb		160	5430	08	•	146		Cit Vie	y, etna	m	т			+		14		Ser - (D=	→ P =155	
	enga 6 su			ngla	idesi	h (	(94 sub	ject	s)	160	5430	34		172		(99 su	) bjed	cts)	G			+		23		Leu (D:	→ \ =32)	
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		Freq	Freq	Freq			Freq			Freq			Freq	Freq	Freq	Freq	Freq					req	Freq	Fred				Freq
T=	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.00	0.00	0.0	00 0	0.000	0.000	0.00	0.0	00 0.0	000	0.000
T=	0.026	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.000	0.000	0.000	0.018	0.005	0.000	0.000	0.000	0.02	0.01	8 0.0	08 0	0.006	0.000	0.00	5 0.0	00 0.0	000	0.014
G=	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.00	5 0.00	0.0	00 0	0.000	0.000	0.00	0.0	00 0.0	000	0.000
T=	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.00	0.00	0.0	00 0	0.000	0.000	0.00	0.0	00 0.	000	0.000
A=	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.00	0.00	0.0	00 0	0.000	0.000	0.00	0.0	00 0.	000	0.000
A=	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016	0.000	0.000	0.005	0.005	0.000	0.009	0.000	0.000	0.000	0.00	5 0.00	0.0	00 0	0.000	0.000	0.02	4 0.0	00 0.	009	0.000
T=	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.00	0.00	0.0	00 0	0.000	0.000	0.00	0.0	00 0.	000	0.000
C=	0.391	0.295	0.186	0.312	0.197	0.408	0.410	0.245	0.348	0.172	0.148	0.228	0.283	0.196	0.186	0.466	0.348	0.32	8 0.37	6 0.3	91 0	0.341	0.161	0.22	1 0.2	40 0.	206	0.269

Promoter

Exon 1:

Coding

Exon 1:

Coding

3932

P D

rs6899549

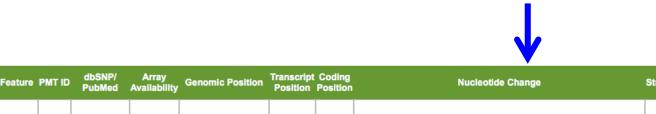
rs34447885

5 pubs

rs34570655

Ι





-44

146

172

160462757 NCBI36

160542819 GRCh37

160462809 NCBI36

160543008 GRCh37

160462998 NCBI36

160543034 GRCh37

160463024 NCBI36

Charries Co.	View all PMT variants for SLC22A1 on UCSC Genome Browse	r
Showing Shatures for transcript: NM_003057	•	
SLC22A1 Resequencing 1000 Genomes		
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	script Coding Nucleotide Change S	Amino Amino Acid Statistics AA CA AS ME PA Strand Acid Change Statistics Freq Freq Freq Freq Freq Position

SLC2	2A1 R	Resequenc	cing 1	1000 Genomes												
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Feature	PMT ID	dbSNP/ PubMed	Array Availability	Genomic Position	Transcript Position	Coding Position	Nucleotide Change	Strand	Amino Acid Position	Amino Acid Change	Statistics	AA Freq	CA Freq	AS Freq	ME Freq	PA Freq
Promoter	3160 PD	rs60541448		160542739 GRCh37 160462729 NCBI36	-124	-229	$\texttt{GCTTAGACCCCACTGACTCGCTCCC} \ \textbf{G} \ \textbf{A} \ \texttt{GGCAAAGCAAACGATTTGATCAGAT}$	+			n= G/G= G/A= A/A= A=	134 67 0 0 0.000	134 67 0 0 0.000	130 65 0 0 0.000	U	n/a 0.000
Promoter	3161	rs58812592		160542767 GRCh37	-96	-201	$\texttt{CAAAGCAAACGATTTGATCAGATGG} \ \textbf{C} \ \ \textbf{G} \ \texttt{CACGTGCATTCTTCCTTTTCCTGAA}$	+			n= C/C= C/G=	134 66 1	134 67 0	130 65 0	136 68 0	n/a

-149 CCAGCACCATAGGGTAAAAGATTAT T → C TCTACTTGGTTGCCTTCCAGATGTT

41 GACATTCTGGAGCAGGTTGGGGAGT C → T TGGCTGGTTCCAGAAGCAAGCCTTC

67 TGGCTGGTTCCAGAAGCAAGCCTTC C → G TCATCTTATGCCTGCTGTCGGCTGC

0.000

n/a

0.000

7

0

14

G/G=

T/T=

T/C=

C/C=

C/C=

C/T=

T/T=

T=

n=

C/C=

C/G=

G/G=

Ser → Phe

(D=155)

Leu → Val

(D=32)

14

23

C=

G= | 0.007 | 0.000 | 0.000 | 0.000

134

67

0

0

192

96

0

0

97

0

0

0.052 | 0.000 | 0.000 | 0.000

130

65

30

0

0

60

30

0 0.005 | 0.000 | 0.000 | 0.000 | 0.000

0.031 | 0.000 | 0.000 | 0.000 | 0.000

0

136

68

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18

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134

61

196

198

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4

5

Showi	Showing SN Catures for transcript: NM_003057 🛊															
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							<b>↓</b>									
Feature	PMT ID	dbSNP/ PubMed	Array Availability	, Genomic Position	Transcript Position	Coding Position	Nucleotide Change	Strand	Amino Acid Position	Amino Acid Change	Statistics	AA Freq	CA Freq	AS Freq	ME Freq	PA Freq
Promoter	3160 P D	rs60541448		160542739 GRCh37 160462729 NCBI36	-124	-229	$\texttt{GCTTAGACCCCACTGACTCGCTCCC} \ \ \textbf{A} \ \ \texttt{GGCAAAGCAAACGATTTGATCAGAT}$				n= G/G= G/A= A/A=	134 67 0 0	134 67 0 0	130 65 0 0	ó	n/a 0.000

Information Data	Access Police	cies   Reviewer Access	Intranet							Find gen	e: Examples	· ABCA1_rs224	6298, 2987
Pharmacogene	Pharmacogenetics of Membrane Transporters Database												
You are in: Pharmac	rs12208357	7   16054314 16046343	8 GRCh37	286 181 Reduced			ctgtggctggagccctgc n transfected cells. PMi			→ Cys =180) C	/C= 99 /T= 0 /T= 0 T= 0.000	83 30 14 0 0 0 0.072 0.000	1 0
Exon 1: Coding	3936 ₽	rs12208357 19 pubs	61	Arg → Cys (D=180)	CCCGCGGGCGAGG	CCTTC C -> T T	TGGCCAGTGCAGGCGCTA	rgaagt +		→ Phe =22) C	n= 198 /C= 97 /T= 2 /T= 0 T= 0.010	194 60 97 30 0 0 0 0 0.000 0.000	9 7
Exon 1: Coding	3937 P D	rs35546288		ed metformin ar 346.						+	61		→ Cys =180)
Exon 2: Coding	3938	rs683369 9 pubs	CCTGGGG	GCCCGCGGGCGAC	GGCCTTC	С → Тт	TGGCCAGTGC	AGGGGGTA Statistics	ΔΔ	+ CA Freq	85 AS Freq		→ Phe =22) PA Freq
			AGTCCTG	GTTTGAATGCGG(	GCTTCTT	61	Arg → Cys (D=180)	n= C/C= C/T= T/T= T=	198 99 0	3 194 9 83 0 14	60 30 0	18 8 1 0	14 7 0 0 0.000
						85	Leu → Phe (D=22)	n= C/C= C/T= T/T= T=	198 97 2	3 194 7 97 2 0	60 30 0 0 0.000	18 9 0 0 0.000	14 7 0 0 0.000
						160	Phe → Leu (D=22)	n= C/C= C/G= G/G= G=	99 1	88 1 11 0 1	60 29 1 0 0.017	9 1 0	14 7 0 0 0.000

# Scenario 2: You want to know other drug response phenotypes associated with *SLCO1B1* variant

GRASP: Genome-Wide Repository of Associations Between SNPs and Phenotypes

https://grasp.nhlbi.nih.gov/Overview.aspx





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Monday, March 07, 2016

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submit results in

publications

GWAS-L mailing list to find

#### Genetics & Genomics Programs

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Methods & Resources

Comparison to Other GWAS Catalogs

Updates & DB Information

Glossary

# GRASP: Genome-Wide Repository of Associations Between SNPs and Phenotypes

#### Overview

GRASP includes all available genetic association results from papers, their supplements and webbased content meeting the following guidelines:

- All associations with P<0.05 from GWAS defined as >= 25,000 markers tested for 1 or more traits.
- Study exclusion criteria: CNV-only studies, replication/follow-up studies testing <25K markers, non-human only studies, article not in English, gene-environment or gene-gene GWAS where single SNP main effects are not given, linkage only studies, aCGH/LOH only studies, heterozygosity/homozygosity (genome-wide or long run) studies, studies only presenting gene-based or pathway-based results, simulation-only studies, studies which we judge as redundant with prior studies since they do not provide significant inclusion of new samples or exposure of new results (e.g., many methodological papers on the WTCCC and FHS GWAS).</li>
- More detailed methods and resources used in constructing the catalog are described at the "Methods & Resources" page.

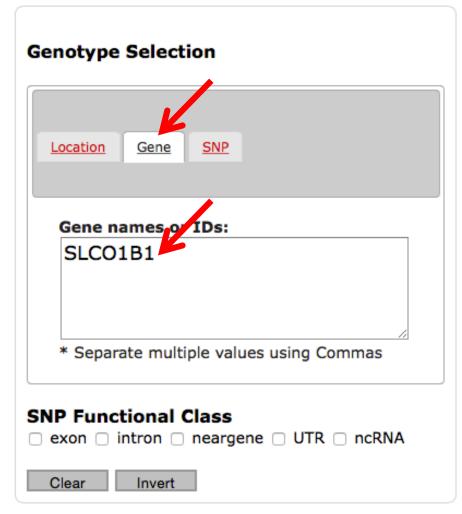
### **SEARCH**

Genetics & Genomics Programs GRASP Search - v2.0.0.0

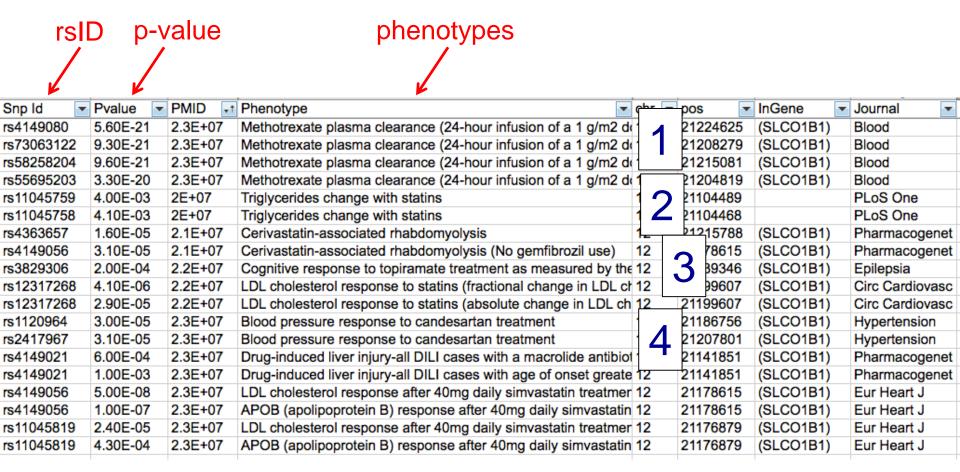
GRASP Over new

The GRASP search tool searches genome-wide association study (GWAS) catalog data housed at the National Center for Biotechnology Information (NCBI). By accessing and using this catalog you agree to comply with the complete terms of use.

Phenotype S	Selection
Category:	Drug response 🗘
Trait:	[Any]
P-Value <	1 x 10 -



## Export the file to excel to view the results



Methotrexate plasma clearance Response to statins (TG, LDL)

Blood presegrencespeothiseer injury

# Q & A

 What other information that you would like to know about transporter polymorphisms that are not covered here?

 What are the transporter databases that you use often and like to share with the group?