ClinGen KCNQ1 Variant Curation Expert Panel						
Start Date	Your Name	Do you work for a laboratory that offers fee-for-service testing related to the work of your Expert Panel?	Have you made substantial contributions to the literature implicating a gene:disease relationship that relates to the work of your Expert Panel?		Do you have any other existing or planned independent curation efforts that will potentially overlap with the scope of your ClinGen work? If so, please describe:	Please disclose any other relevant conflicts of interest (e.g. patents, intellectual property ownership, or paid consultancies related to any variants or genes associated with the work of your Expert Panel):
	Open-Ended Response	Response	Response	If yes, please list the genes:	Open-Ended Response	Open-Ended Response
2019-04-15 8:18:52	Emanuela Abiusi	No	No		no	nothing to disclose
2019-04-12 3:27:10	Hennie Bikker	Yes	No		no	none
2019-04-11 17:21:00	Jennifer Semotok	Yes	No		No	Not applicable
2019-01-29 16:56:58	Marco Perez	No	No		No	No other relevant conflicts of interest.
2018-12-19 9:29:02	Wojciech Zareba	No	Yes	long QT syndrome	No	
2018-09-13 15:58:46	James Ware	No	No		- I am part of the Transforming Genomic Medicine Initiative (TGMI), which is collaborating with ClinGen on harmonisation of terms for curation of genes, variants, mechanisms & inheritance modes (under the banner of the Gene Curation Coalition). - We have developed CardioClassifier (already published) - a decision support tool for variant interpretation. This has involved some curation to determine which genes should be included, which molecular mechanisms are relevant, and curation of variants. These are not being promoted as final, and our goal is to align with ClinGen outputs as the consensus curations come online.	I hold a patent related to technology to support variant interpretation. I have consultancy agreements with Third Rock Ventures & Myokardia (but not directly connected to the work of this EP).
2018-08-30 18:37:04	michael gollob	No	No		no	none
2018-06-21 17:16:35	valeria novelli	No				
2018-06-15 10:54:54	Michael J. Ackerman, MD, PhD	No	Yes	For LQTS - CAV3, CACNA1C, SNTA1, AKAP9, CALM3, TRDN	Yes, continuing with variant resolution and gene discovery/GUS resolution, etc. Paper submitted on RYR2 variants etc.	Consultant - Invitae
2018-06-14 14:51:17	John Garcia	Yes	No		Invitae is constantly curating gene-disease relationships and interpreting variants. However, we use non-ACMG criteria	full-time employee of Invitae, which does diagnostic testing that includes these genes
2018-05-11 15:07:52	Melanie Care	No	No		No	N/A
2018-03-03 15:29:03	Ray Hershberger	No	Yes	first discovery papers for PSEN1, PSEN2, BAG3 in DCM.	ongoing discovery work in DCM; do not anticipate conflicts.	none of the above.
2018-03-02 17:15:17	Amy Sturm	No	No		No	
2018-03-02 13:13:33	Arthur Wilde	No	Yes	Our lab has not specifically been involved in describing new genes but we have contributed significantly to genotype-phenotype relationships in LQTS	no	co-owner of a patent on the 3" UTR variants in KCNQ1 as potential modifiers of the LQT1 phenotype.