



## CRISPR Gene Panels

Focused and affordable screens based on the award-winning Sanger Whole Genome Arrayed Library

### Description

Panels are derived using expert-curated databases, gene ontology (GO) terms, PubMed identifiers (PMID), research supported gene pathway and druggable genome sources. Then, they are mapped to the Sanger Whole Genome Arrayed CRISPR KO Library. The resulting collection is a budget-friendly and time-saving option for researchers answering critical questions in health and disease.

### Two Convenient Formats

#### Expanded Discovery

The most comprehensive screening panels; includes the maximum amount of non-redundant genes in a defined research category

#### Core Essential

Increased stringency to emphasize higher confidence targets while maintaining rich, curated content. High-value and cost effective



# CRISPR Gene Panels

Gene Panel Name	Expanded Discovery		Core Essential	
	# of Genes	# of Clones	# of Genes	# of Clones
Human Druggable	8564	17128	967	1934
Tumor Suppressor	1989	3978	446	892
Transcription Factors	1909	3818	607	1214
Cancer Cell Biology	1875	3750	524	1048
Cell Surface Proteins	1914	3828	781	1562
Epigenetics	1751	3502	655	1310
Cell Cycle	1682	3364	508	1017
Kinase	1470	2940	715	1430
GPCR	1094	2188	554	1108
Apoptosis	1065	2130	178	356
Cell Adhesion	969	1938	296	592
Cytokine&Cytokine Receptor	807	1614	223	446
Ubiquitin Ligases	647	1294	202	404
Ubiquitin Enzymes	596	1192	287	574
Membrane Trafficking	639	1278	254	508
Ion Channel	615	1230	383	766
DNA Repair	533	1066	258	516
Proteases	528	1056	210	410
Phosphatase	406	812	219	438
B Cell Activation	318	636	42	84
T Cell Activation	211	422	35	70
Helicase	146	292	91	182
JAKSTAT	183	366	128	256
Ubiquitin Proteases	100	200	72	144
Nuclear Hormone Receptors	56	112	40	80

## Sources

KEGG Database  
 Gene Panel Specific Databases: (eg. KinBase)  
 Evidence based GO terms  
 Manual Curation using PMIDs  
 Reactome Database  
 Druggable Genome Database from Washington University in St. Louis

## References:

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3. Griffith M, Griffith OL, Coffman AC, Weible J V., Mcmichael JF, Spies NC, et al. *DGIdb: Mining the druggable genome*. Nat Methods. 2013
4. Cotto C, Wagner A, et al. *DGIdb 3.0: a redesign and expansion of the drug-gene interaction database*. Nucleic Acids Research, 2017
5. Hopkins AL, Groom CR. *The druggable genome*. Nat Rev Drug Discov. 2002

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