20160204_data_release_notes

Overview of changes in the release of February 4, 2016

Please also see our RSS feed for information about accessing the data, and our release notes for recent changes to ClinVar's web display.

Overview of submissions: 2016

Date	Total Submissions
Jan 01, 2016	172867
Feb 01, 2016	176710

Content

Brief	Explanation
Submission from Invitae	Invitae submitted 5145 variant interpretations, including novel and updated interpretations.
Submission from CHOP	Children's Hospital of Philadelphia submitted 693 novel variant interpretations.
Submission from University of Washington	Cytogenetics and Genomics Laboratory, University of Washington submitted 35 variant interpretations, including novel and updated interpretations.
Submission from HerediLab	HerediLab submitted interpretations for 20 variants in SERPINA1.
Submission from GeneDx	GeneDx submitted 6 novel variant interpretations.
representation of submitted condition in XML	In November 2015, we changed how data is reported the TraitSet in the SCV section of clinvar_public XML. The TraitSet now includes exactly the data that was submitted to ClinVar, e.g. if OMIM 219700 was submitted for the condition, the TraitSet for the SCV includes that data but does not include the name CYSTIC FIBROSIS; CF. Or if the name "cystic fibrosis" was submitted as the condition, then the TraitSet for the SCV includes that name but does not include the OMIM number. The preferred name and all database identifiers for the condition continue to be reported in the TraitSet in the RCV section of clinvar_public XML.
update to tab-delimited report of conflicting interpretations	ClinVar's report of conflicting interpretations is being updated to: ■ report only conflicts in clinical significance, not condition ■ report all pairwise conflicts ■ exclude submissions with a clinical significance of "not provided" ■ include the gene symbol, whether provided by the submitter or calculated by NCBI Both the old and new formats are available for the February 2016 release. After that, only the new format will be provided. Old format: summary_of_conflicting_data.txt New format: summary_of_conflicting_interpretations.txt
measure types for fusion/intrachromosomal breakpoint	The measure type "fusion" (SO:0000287) will be replaced by the more specific term "intrachromosomal breakpoint" (SO:0001874). We are also adding a measure type for "interchromosomal breakpoint" (SO:0001873). These terms will provide greater consistency with data in dbVar.

Overview of submissions: 2015

Date	Total Submissions

Jan 01, 2015	149013
Feb 01, 2015	156999
Mar 01, 2015	162455
Apr 01, 2015	171408
May 01, 2015	172044
Jun 01, 2015	173236
Jul 01, 2015	184506
Aug 01, 2015	154686
Sep 01, 2015	158580
Oct 01, 2015	160538
Nov 01, 2015	170931
Dec 01, 2015	172006

Overview of submissions: 2014

Date	Total Submissions
Jan 01, 2014	68204
Feb 01, 2014	73492
Mar 01, 2014	83343
Apr 01, 2014	111501
May 01, 2014	112349
Jun 01, 2014	117209
Jul 01, 2014	127132
Aug 01, 2014	127557
Sep 1, 2014	143114
Oct 1, 2014	143601
Nov 1, 2014	144117
Dec 1, 2014	148008

Overview of Submissions: 2013

Date	Total Submissions
Apr 05, 2013	30333
May 01, 2013	30386
Jun 01, 2013	39047
Jul 01, 2013	39170
Aug 01, 2013	45901

Sep 01, 2013	50263
Oct 01, 2013	52047
Nov 01, 2013	64750
Dec 01, 2013	64881