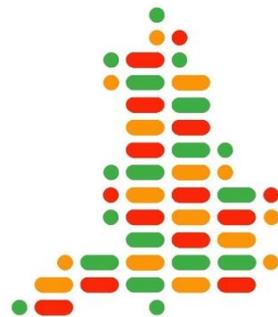




A Reviewers' Guide To PanelApp Australia



PanelApp Release 3.0.2

Reviewers' Guide V1.

Created: 24.11.19

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Adapted for use by PanelApp Australia by A/Prof Zornitza Stark

Reviewing Panels in PanelApp

- Expert review of the gene panels is sought to enable a community consensus to be reached on which genes should appear on a diagnostic-grade panel for each disorder and to keep content current in light of new gene discoveries.
- We request that reviewers have expertise in a disease area relevant to the panel they are reviewing.
- Reviewers can be based anywhere in the world, and can have an academic, clinical or diagnostic laboratory background.
- This guide highlights the key **Review** functions of PanelApp, in a series of how-to steps. The guide can be used alongside the current PanelApp handbook, which details how to browse PanelApp and leave reviews.

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Creating a PanelApp Reviewer Account, and Logging in

Use the top **PanelApp Toolbar** to Register as a Reviewer:



PanelApp Panels Genes and Entities Activity [Log in](#)

PanelApp Australia

A crowdsourcing tool to allow gene panels to be shared, downloaded, viewed and evaluated by the Scientific Community

Home

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Welcome to PanelApp Australia



1. You can log in and register to be a reviewer using your Google account. Your account details will not be displayed when you review genes and panels

<https://panelapp.gha.umccr.org>

Finding your panel or gene of interest in PanelApp

Use the top **PanelApp Toolbar** to log in to your reviewer account, and search for your panel or gene of interest:



2. To leave a review on a gene, search PanelApp for a panel or gene
Refer to the PanelApp handbook for more details on searching.



1. Log in to your Reviewer account
You can browse PanelApp without logging in, but need to create a Reviewer account to leave ratings and comments.

PanelApp Australia
A crowdsourcing tool to allow gene panels to be shared, downloaded, viewed and evaluated by the Scientific Community

- Home
- News
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Welcome to PanelApp Australia



Finding a panel to review:

PanelApp

Panels

Genes and Entities

Activity

rebecca_reviewer

Log out

293 panels

Clicking on **Panels** in the top Toolbar will list all panels. Type in the **Filter panels** box to find your panel of interest.

Compare two panels

Panel ↓	Evaluated genes	Reviewers	Actions
<input type="text" value="limb"/>			3 panels
VACTERL-like phenotypes Level 3: Limb disorders Level 2: Dysmorphic and congenital abnormality Relevant disorders: Version 1.22		reviewers	Download
Limb girdle muscular dystrophy Level 3: Neuromuscular disorders Level 2: Neurology and neurodevelopmental dis Version 1.12	11 of 17	3 reviewers	Download
Limb disorders Version 1.2			

Filter the list by typing in key words

Click on a panel name to:

- 1) View the panel description.
- 2) View the panel type.
- 3) View Genes on the panel, and their current ratings.
- 4) Select a gene on the panel to review.

Each panel is versioned.

Each change to a panel increases the minor version incrementally (e.g. Version 1.11 to Version 1.12. Note that Version 1.12 of a gene panel is more recent than Version 1.2.

An overview of information captured on a PanelApp panel

217 Entities
215 reviewed, 114 green

List ↑	Entity	Reviews	Mode of inheritance	Details
	Filter Entities			217 Entities
Green	ARHGAP31	3 reviews Add review 1 green	MONOALLELIC, autosomal or pseudoautosomal, NOT imprinted	Sources <ul style="list-style-type: none"> Emory Genetics Laboratory Expert Review Green Expert list Illumina TruGenome Clinical Sequencing Services London South East RGC GSTT Radboud University Medical Center, Nijmegen UKGTN Viapath Phenotypes <ul style="list-style-type: none"> Adams-Oliver syndrome 1, 100300 Tags
Green	ARSE	2 reviews Add review 1 green	X-LINKED: hemizygous mutation in males, biallelic mutations in females	Sources <ul style="list-style-type: none"> Expert Review Green London South East RGC GSTT Radboud University Medical Center, Nijmegen UKGTN Viapath Phenotypes <ul style="list-style-type: none"> CDPXL Chondrodysplasia punctata, X-linked recessive, 302950 X-linked recessive chondrodysplasia punctata CHONDRODYSPLASIA PUNCTATA 1, X-LINKED Tags
Green	BHLHA9	3 reviews Add review 1 green	BIALLELIC, autosomal or pseudoautosomal	Sources <ul style="list-style-type: none"> Expert Review Green Expert list London South East RGC GSTT Viapath Victorian Clinical Genetics Services Phenotypes <ul style="list-style-type: none"> Syndactyly, mesoaxial synostotic, with phalangeal reduction, 009432 Polydactyly Tags

Click on a gene symbol to see further gene details, and **provide a review.**

Panels / Limb disorders / ARSE

Genes in panel

↑ Prev Next ↓

● ARHGAP31 3

● ARSE 2

● BHLHA9 3

● BMPR1B 2

● BRCA2 0

● BRIP1 0

● DLX5 3

● DOCK6 2

● DVL1 3

● EBP 1

● EOGT 2

● ERCC4 4

● ESCO2 3

● FAM58A 4

● FANCA 2

● FANCB 4

● FANCC 2

● FANCD2 2

● FANCE 2

● FANCF 2

● FANCG 2

● FANCI 2

● FANCL 2

● FGD1 2

● FGF10 3

● FGF16 2

● FGFR1 2

● FGFR2 3

● FGFR3 3

● FIG4 3

● FLNA 4

● FRAS1 1

● FREM2 1

Limb disorders

Gene: ARSE

Green List (high evidence)

ARSE (arylsulfatase E (chondrodysplasia punctata 1))

EnsemblGenIds (GRCh38): ENSG00000157399

EnsemblGenIds (GRCh37): ENSG00000157399

OMIM: 300180, Gene2Phenotype

ARSE is in 6 panels

Reviews (2)

Details

History

Review gene

Rating: ⓘ

Provide rating

Mode of Inheritance: ⓘ

Provide a mode of inheritance

Mode of pathogenicity: ⓘ

Provide exceptions to loss-of-function

Publications (PMID: 1234;4321):

Publications (PMID: 1234;4321)

Phenotypes (separate using a semi-colon -;):

Phenotypes (separate using a semi-colon -;)

Current diagnostic: ⓘ

 Current diagnostic

Comments:

Comments

Submit review

2 reviews

Sarah Leigh (Genomics England Curator)

Comment on phenotypes: Chondrodysplasia punctata, X-linked recessive 302950

13 Jul 2016, 7:38 a.m.

Once you have clicked on a gene symbol, you can provide a review using the Reviews tab.

Further gene and curation information can be found in the Details and History tabs, respectively.

Existing reviews for the gene (where present) can be viewed at the bottom of the Reviews tab.

Understanding Gene Ratings in PanelApp

Understanding PanelApp Gene Ratings:



STOP: not enough evidence for this gene-disease; this gene should not be used for genome interpretation.

PAUSE: moderate evidence for this gene-disease association, and should not yet be used for genome interpretation.

GO: high level of evidence for this gene-disease association, demonstrates confidence that this gene should be used for genome interpretation.

- Reviewers are asked to rate genes according to this traffic light system.
- Green genes on Version 1+ panels will reflect this evidence system and can be used for genome interpretation.

Genes on a panel are classified according to a traffic light system. Genes are rated in terms of the level of evidence to support their association with the phenotypes covered by the gene panel in question.

For rare disease, the criteria for assessing the evidence were developed from a combination of the ClinGen DEFINITIVE and DDG2P CONFIRMED gene evidence levels (set out in full on the next slide). In summary:

- A diagnostic-grade (**Green**) rating on a panel requires evidence from **2-3 unrelated families where there is strong additional functional data** OR from 3 or more unrelated families.
- Genes that do not meet these criteria are rated as **Amber** (borderline) or **Red** (low level of evidence), and are not used for diagnostic testing.

PanelApp Criteria for Diagnostic Grade 'Green' Genes for Rare Diseases:



A. There are plausible disease-causing variants¹ within, affecting or encompassing an interpretable functional region of this gene² identified in multiple (3 or more) unrelated cases/families with the phenotype³.

OR

B. There are plausible disease-causing variants¹ within, affecting or encompassing cis-regulatory elements convincingly affecting the expression of a single gene identified in multiple (3 or more) unrelated cases/families with the phenotype³.

OR

C. As definitions A or B but in 2 or 3 unrelated cases/families with the phenotype, with the addition of convincing bioinformatic or functional evidence of causation e.g. known inborn error of metabolism with mutation in orthologous gene which is known to have the relevant deficient enzymatic activity in other species; existence of an animal model which recapitulates the human phenotype.

AND

D. Evidence indicates that disease-causing variants follow a Mendelian pattern of causation appropriate for reporting in a diagnostic setting⁴.

AND

E. No convincing evidence exists or has emerged that contradicts the role of the gene in the specified phenotype.

¹Plausible disease-causing variants: Recurrent de novo variants convincingly affecting gene function. Rare, fully-penetrant variants - relevant genotype never, or very rarely, seen in controls.

²Interpretable functional region: ORF in protein coding genes miRNA stem or loop.

³Phenotype: the rare disease category, as described in the eligibility statement.

⁴Intermediate penetrance genes should not be included.



Adapted from references: PMID:28552198 and PMID: 25529582

Leaving a Review in PanelApp

When reviewing a gene please **rate** whether there is sufficient evidence for the gene to be on a diagnostic panel.

You can also **add the following fields** when reviewing, although they are not compulsory, they are useful when a curator is collating the reviews.

- Mode of inheritance
- Mode of pathogenicity
- Publications
- Phenotypes
- Free-text comments

Genes in panel	
↑ Prev	Next ↓
● ARHGAP31	3
● ARSE	2
● BHLHA9	3
● BMPR1B	2
● BRCA2	0
● BRIP1	0
● DLX5	3
● DOCK6	2
● DVL1	3
● EBP	1
● EOGT	2
● ERCC4	0
● ESCO2	0
● FAM58A	4
● FANCA	0
● FANCB	0
● FANCC	0
● FANCD2	0
● FANCE	0
● FANCF	0

Limb disorders

Gene: ARSE

Green List (high evidence)

ARSE (arylsulfatase E (chondrodysplasia punctata 1))

EnsemblGenIds (GRCh38): [ENSG00000157399](#)

EnsemblGenIds (GRCh37): [ENSG00000157399](#)

OMIM: [300180](#), [Gene2Phenotype](#)

ARSE is in [6 panels](#)

Reviews (2) Details History

Review gene

Rating: ?

Provide rating

Rating: ?

Provide rating

Provide rating

Green List (high evidence)

Red List (low evidence)

I don't know

Current diagnostic: ?

Current diagnostic

Provide a rating for a gene by selecting an option from the drop-down menu:

- **Green List (high evidence)**: variants in this gene are diagnostically-reportable.
- **I don't know**: moderate evidence if there is some supportive evidence, but not sufficient for a Green/diagnostic rating, or you are uncertain of the evidence level.
- **Red List (low evidence)**: variants in this gene are not diagnostically reportable.

See slides 13-14 for guidelines on PanelApp gene ratings.

Genes in panel

↑ Prev Next ↓

● ARHGAP31 3

● ARSE 2

● BHLHA9 3

● BMPR1B 2

● BRCA2 0

● BRIP1 0

● DLX5 3

● DOCK6 2

● DVL1 3

● EBP 1

● EOGT 2

● ERCC4 0

● ESCO2 0

● FAM58A 4

● FANCA 0

● FANCB 0

● FANCC 0

● FANCD2 0

● FANCE 0

● FANCF 0

Gene: ARSE

Green List (high evidence)

ARSE (arylsulfatase E (chondrodysplasia punctata 1))

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 EnsemblGenIds (GRCh37): [ENSG00000157399](#)

 OMIM: [300180](#), [Gene2Phenotype](#)

ARSE is in 6 panels

Reviews (2)

Details

History

Review gene

Rating: ⓘ

Provide rating

Mode of Inheritance: ⓘ

Provide a mode of inheritance

Mode of Inheritance: ⓘ

Provide a mode of inheritance

Provide a mode of inheritance

MONOALLELIC, autosomal or pseudoautosomal, NOT imprinted

MONOALLELIC, autosomal or pseudoautosomal, maternally imprinted (paternal allele expressed)

MONOALLELIC, autosomal or pseudoautosomal, paternally imprinted (maternal allele expressed)

MONOALLELIC, autosomal or pseudoautosomal, imprinted status unknown

BIALLELIC, autosomal or pseudoautosomal

BOTH monoallelic and biallelic, autosomal or pseudoautosomal

BOTH monoallelic and biallelic (but BIALLELIC mutations cause a more SEVERE disease form), autosomal or pseudoautosomal

X-LINKED: hemizygous mutation in males, biallelic mutations in females

X-LINKED: hemizygous mutation in males, monoallelic mutations in females may cause disease (may be less severe, later onset than males)

MITOCHONDRIAL

Unknown

Other - please specify in evaluation comments

- Select a mode of inheritance for the gene-disease association from the drop-down menu.
- If the mode of inheritance you want is not within the drop-down menu, select 'Other' and provide details in the comments box.
- If known, please provide information regarding imprinting by selecting either the maternally imprinted or paternally imprinted mode of inheritance, and leaving details in the comments box.

Definitions for each mode of inheritance term can be found by clicking on the question-mark pop-up icon.

Gene: ARSE

Green List (high evidence)

ARSE (arylsulfatase E (chondrodysplasia punctata 1))

EnsemblGenIds (GRCh38): ENSG00000157399

EnsemblGenIds (GRCh37): ENSG00000157399

OMIM: 300180, Gene2Phenotype

ARSE is in 6 panels

Reviews (2) Details History

Review gene

Rating: ⓘ

Provide rating

Mode of Inheritance: ⓘ

Provide a mode of inheritance

Mode of pathogenicity: ⓘ

Provide exceptions to loss-of-function

Mode of pathogenicity: ⓘ

Provide exceptions to loss-of-function

Provide exceptions to loss-of-function

Loss-of-function variants (as defined in pop up message) DO NOT cause this phenotype - please provide details in the comments

Other - please provide details in the comments

- If loss-of-function variants do not cause the disease phenotype, please select an option in the mode of pathogenicity dropdown menu.
- If providing exceptions to loss-of-function, please leave a free-text comment to explain your selection (e.g. detailing literature or clinical evidence).

Genes in panel

↑ Prev Next ↓

● ARHGAP31 3

● **ARSE** 2

● BHLHA9 3

● BMPR1B 2

● BRCA2 0

● BRIP1 0

● DLX5 3

● DOCK6 2

● DVL1 3

● EBP 1

● EOGT 2

● ERCC4 0

● ESCO2 0

● FAM58A 4

● FANCA 0

● FANCB 0

● FANCC 0

● FANCD2 0

● FANCE 0

● FANCF 0



In PanelApp, we classify loss-of-function (high impact) variants as those with the sequence ontology (SO) terms:

- transcript_ablation
- splice_acceptor_variant
- splice_donor_variant
- stop_gained
- frameshift_variant
- stop_lost
- Initiator_codon_variant



Genes in panel	
↑ Prev	Next ↓
● ARHGAP31	3
● ARSE	2
● BHLHA9	3
● BMPR1B	2
● BRCA2	0
● BRIP1	0
● DLX5	3
● DOCK6	2
● DVL1	3
● EBP	1
● EOGT	2
● ERCC4	0
● ESCO2	0
● FAM58A	4
● FANCA	0
● FANCB	0
● FANCC	0
● FANCD2	0
● FANCE	0
● FANCF	0

Limb disorders

Gene: ARSE

Green List (high evidence)

ARSE (arylsulfatase E (chondrodysplasia punctata 1))

EnsemblGenIds (GRCh38): [ENSG00000157399](#)

EnsemblGenIds (GRCh37): [ENSG00000157399](#)

OMIM: [300180](#), [Gene2Phenotype](#)

ARSE is in 6 panels

Reviews (2) Details History

Review gene

Rating: ?

Provide rating

Mode of Inheritance: ?

Provide a mode of inheritance

Mode of pathogenicity: ?

Provide exceptions to loss-of-function

Publications (PMID: 1234;4321):

Publications (PMID: 1234;4321)

Phenotypes (separate using a semi-colon - ;):

Phenotypes (separate using a semi-colon - ;)

Current diagnostic: ?

Current diagnostic

Add any relevant publications.

- Please provide PubMed IDs separated by a semi-colon: E.g. PMID:123456;9876545
- Include publications that provide supporting evidence for your given rating, or publications refuting the gene-disorder association.
- Where the paper doesn't have a PubMed identifier, add in the publication as free text, and these will be subsequently updated by a curator.

Add in phenotypes.

- Separate phenotypes with a semi colon.
- Include relevant identifiers where possible (e.g. OMIM disease IDs and HPO terms). You can also use free text.

E.g. Alport syndrome, 301050; Hearing Loss

● DOCK6	2
● DVL1	3
● EBP	1
● EOGT	2
● ERCC4	4
● ESCO2	3
● FAM58A	4
● FANCA	2
● FANCB	4
● FANCC	2
● FANCD2	2
● FANCE	2
● FANCF	2
● FANCG	2
● FANCI	2
● FANCL	2
● FGD1	2
● FGF10	3
● FGF16	2
● FGFR1	2
● FGFR2	3
● FGFR3	2

Review gene

Rating: ⓘ
 Provide rating

Mode of Inheritance: ⓘ
 Provide a mode of inheritance

Mode of pathogenicity: ⓘ
 Provide exceptions to loss-of-function

Publications (PMID: 1234;4321):
 Publications (PMID: 1234;4321)

Phenotypes (separate using a semi-colon - ;):
 Phenotypes (separate using a semi-colon - ;)

Current diagnostic: ⓘ
 Current diagnostic

Comments:
 Comments

If submitting the gene evaluation on behalf of a clinical laboratory, indicate whether variants in the gene are reported as part of your current diagnostic practice by checking the **Current diagnostic** box.

Provide justifications in the comments box to support your gene rating, particularly when changing the existing rating for a gene.
Comments will be publically visible.

Click **Submit review** when finished.

Adding Genes to a PanelApp Panel

Adding a gene to a Panel:

Red Ready 🔒	ZFYVE26	2 reviews Add review 1 red	BIALLELIC, autosomal or pseudoautosomal	Sources <ul style="list-style-type: none"> Expert Review Red Phenotypes <ul style="list-style-type: none"> Autosomal recessive spastic paraplegia 15 (#270700) complex form of the disease including ataxia. Pyle et al. (2015), Brain, 138, pp.276-283. Implicated in undiagnosed ataxia.
Red Ready 🔒	ZNF592	2 reviews Add review	BIALLELIC, autosomal or pseudoautosomal	Sources <ul style="list-style-type: none"> Radboud University Medical Center, Nijmegen UKGTN Expert Review Red Phenotypes <ul style="list-style-type: none"> Spinocerebellar ataxia, autosomal recessive 5
<div style="border: 1px solid #ccc; padding: 5px; display: flex; justify-content: space-between;"> + Add a Gene to this panel + Add a STR to this panel + Add a Region to this panel </div>				



If any genes are missing from a panel, you can add them using the tool bar below the Entities list:

+ Add a Gene to this panel

+ Add a STR to this panel

+ Add a Region to this panel

Add gene to panel

Gene symbol:

Source:

Mode of pathogenicity: ⓘ
Provide exceptions to loss-of-function

Mode of inheritance: ⓘ
Provide a mode of inheritance

Penetrance:

Publications (PMID: 1234;4321):
Publications (PMID: 1234;4321)

Phenotypes (separate using a semi-colon - ;):
Phenotypes (separate using a semi-colon - ;)

Tags:

Rating: ⓘ
Provide rating

Current diagnostic: ⓘ
 Current diagnostic

Comments:
Comments

Start typing an HGNC Gene symbol into the top box to select your gene to add to a panel.

You must include a source of information for the gene:disease association. E.g. literature/Expert list.

You must provide a **Mode of inheritance** for the gene-disease association.

You can also add a **Mode of pathogenicity, Publications and Phenotypes**.

If penetrance is not complete, please denote using the drop down menu in the **Penetrance** field, and provide a comment.

Select a gene **rating** here.

The **Comments** box can be used to leave free-text information about the gene:disorder association and why the gene was added to the panel.

Comments will be publically visible.

Click **Add gene** when finished. Your gene will be added to the panel as **Grey**. A curator will then curate the evidence and adjust the rating to Green, Amber or Red.

View or Edit your Evaluations

How to view or edit your Reviews:

PanelApp

Panels

Genes and Entities

Activity

rebecca_reviewer

Log out

1. From the PanelApp homepage, click on your username in the top right hand corner to view your user information and a list of your evaluations.

2. Click on the gene symbol to make changes to your evaluation, or click on the panel name to view the entire gene panel.

View Changes to Panels and new reviews

How to view updates or new reviews in PanelApp:

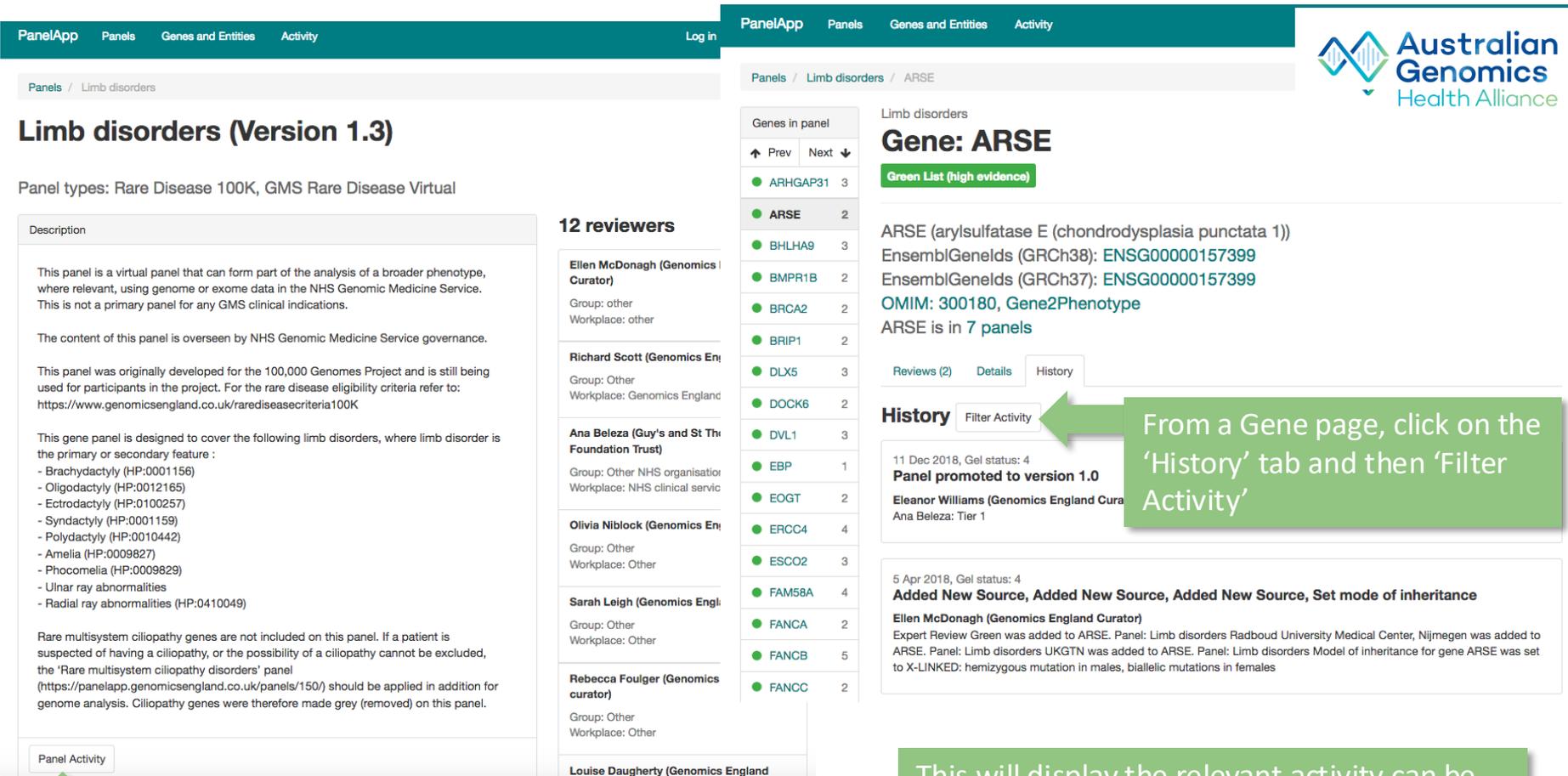
From the PanelApp homepage, click on the 'Activity' page

This will display activity for all panels in PanelApp and can be filtered for date, panel name, version, gene activity type, name of Reviewer or Curator

Activity ▾

Date	Panel	Item	Activity
Filter activities			3000 actions
24 Nov 2019	Early onset Parkinson disease_MelbourneGenomics_VCGS v0.2	PDE8B	Zornitza Stark Marked gene: PDE8B as ready
24 Nov 2019	Early onset Parkinson disease_MelbourneGenomics_VCGS v0.2	PDE8B	Zornitza Stark Gene: pde8b has been classified as Green List (High Evidence).
24 Nov 2019	Early onset Parkinson disease_MelbourneGenomics_VCGS v0.2	PDE8B	Zornitza Stark Classified gene: PDE8B as Green List (high evidence)
24 Nov 2019	Early onset Parkinson disease_MelbourneGenomics_VCGS v0.2	PDE8B	Zornitza Stark Gene: pde8b has been classified as Green List (High Evidence).
24 Nov 2019	Early onset Parkinson disease_MelbourneGenomics_VCGS v0.1	PDE8B	Zornitza Stark gene: PDE8B was added gene: PDE8B was added to Early onset Parkinson disease_MelbourneGenomics_VCGS. Sources: Expert Review Mode of inheritance for gene: PDE8B was set to MONOALLELIC, autosomal or pseudoautosomal, NOT imprinted

How to view updates on individual Panel or Gene pages:



PanelApp Panels Genes and Entities Activity Log in

Panels / Limb disorders

Limb disorders (Version 1.3)

Panel types: Rare Disease 100K, GMS Rare Disease Virtual

12 reviewers

- Ellen McDonagh (Genomics Curator)
- Richard Scott (Genomics England)
- Ana Beleza (Guy's and St Thomas Foundation Trust)
- Olivia Niblock (Genomics England)
- Sarah Leigh (Genomics England)
- Rebecca Foulger (Genomics curator)
- Louise Daugherty (Genomics England)

Gene: ARSE
Green List (high evidence)

ARSE (arylsulfatase E (chondrodysplasia punctata 1))
EnsemblGenIds (GRCh38): ENSG00000157399
EnsemblGenIds (GRCh37): ENSG00000157399
OMIM: 300180, Gene2Phenotype
ARSE is in 7 panels

History (2) Details History

History Filter Activity

- 11 Dec 2018, Gel status: 4
Panel promoted to version 1.0
Eleanor Williams (Genomics England Curator)
Ana Beleza: Tier 1
- 5 Apr 2018, Gel status: 4
Added New Source, Added New Source, Added New Source, Set mode of inheritance
Ellen McDonagh (Genomics England Curator)
Expert Review Green was added to ARSE. Panel: Limb disorders Radboud University Medical Center, Nijmegen was added to ARSE. Panel: Limb disorders UKGTN was added to ARSE. Panel: Limb disorders Model of inheritance for gene ARSE was set to X-LINKED: hemizygous mutation in males, biallelic mutations in females

From a Panel page, click on 'Panel Activity'

From a Gene page, click on the 'History' tab and then 'Filter Activity'

This will display the relevant activity can be filtered for date, version, activity type, name of Reviewer or Curator

Additional Notes for Reviewers

- Your evaluations and comments will be tagged with your name and affiliation, and are public. Your name and affiliation will appear in the list of reviewers at the top of the panel.
- The date you made your review will appear, along with the version of the panel you reviewed.
- You can make multiple comments for each gene, and edit or delete them individually.
- Changes to the rating, mode of inheritance, mode of pathogenicity and current diagnostic practice by a curator will overwrite your initial evaluation.
- Publications and phenotypes will be saved in the evaluation tool and can be added to.
- When you have reviewed a gene, you can see your review under the review tab along with any reviews from other experts.
- For your reviewed genes, a tick will appear in front of the gene in the Genes in panel list. A tick together with **You reviewed** text will also be added to the Reviewed column on the main panel page.

Acknowledgements



- **We are extremely grateful to the Genomics England PanelApp team** for making PanelApp open source, helping us deploy an Australian instance and for sharing documentation and expertise
- **In particular, we would like to thank:** Ellen McDonagh, Rebecca Foulger, Antonio Rueda-Martin, Oleg Gerasimenko and Augusto Rendon
- **We are also very grateful to the Australian Genomics Program 2 team** who deployed the Australian instance: Oliver Hoffman, Victor San Kho Lin and Roman Valls

<https://panelapp.gha.umccr.org>