

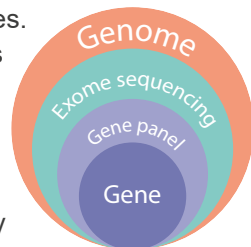


Whole Exome Sequencing in genetic diseases

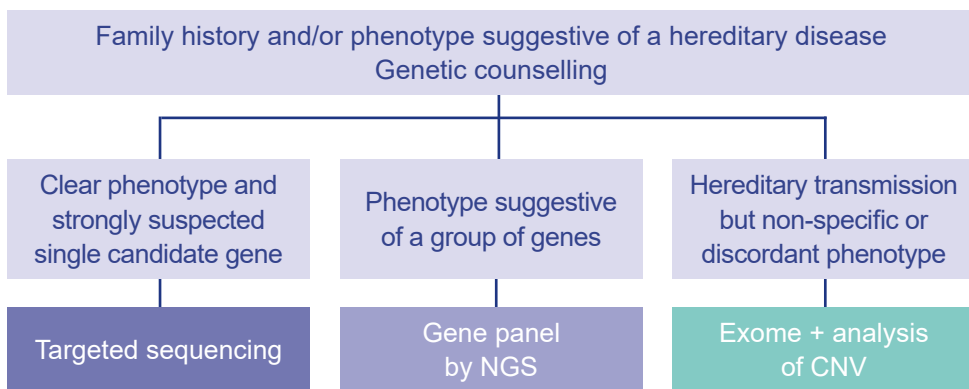
**The clinical / clinical pathology partnership
that benefits patients**

Whole Exome Sequencing (“WES”) in diagnostic practice

The term “genetic disease” embraces a wide range of pathologies. The identification of causal variants facilitates clinical diagnosis and prognosis, patient management, genetic counselling and, in some cases, the adjustment of therapeutic care to individual patient needs.



The conventional step-by-step sequencing approach (gene by gene or panel by panel), which sometimes follows complex decision trees, is gradually being replaced by **“Whole Exome Sequencing” as a first-tier technique, in an increasing number of indications¹⁻².**



Whole Exome Sequencing makes it possible to sequence, in a single step, all of the coding regions of the human genome (containing more than 85% of pathogenic mutations) **at an affordable price.**

As a first-tier technique, WES provides:



time-saving compared to carrying out a series of gene panels,



a diagnostic test for patients where the clinical examination does not enable the clinician to identify the gene/panel of genes to be tested.



retrophenotyping in atypical clinical pictures,



an improved diagnostic yield compared to the gene panel.

The “Whole Exome” test by Eurofins Biomnis

6 weeks

In the laboratory

- A dedicated team of clinical pathologists, technicians and bioinformatics specialists
- Continuous biopathological support, from the implementation of the test to the interpretation of the results.

Sequencing

- ~98% 30X*
- > 99% sensitivity**

At the end of the analytical process

- An interpretation of an average of 30,000 variants in consultation with the clinician
- Provision of raw data (fastQ, VCF, BAM and quality report) via a secure interface
- Report with detailed results within an optimised period of 6 weeks

Why Eurofins Biomnis?



- Specialised medical pathology laboratory
- ISO 15189 accreditation (CAP standard equivalent)
- Authorisation to perform constitutional genetics tests
- Certified clinical pathologists
- Expertise in sequencing techniques in diagnostic practice

The clinical/clinical pathology partnership that benefits patients

One of the challenges of exome sequencing is the interpretation of variants.

To actively involve partner clinicians and clinical pathologists in the interpretation of data, Eurofins Biomnis provides access to **SeqOne**, a secure bioinformatics platform.

*target Refseq + 2 base pairs

**data calculated from SNV's from NIST reference samples, for 40 million pairs of reads generated.

SeqOne, for optimal diagnostic performance

Thanks to this platform, a **joint interpretation with Eurofins Biomnis or an autonomous interpretation** is possible. This ensures **optimal diagnostic performance** (laboratory experience and literature³).

ACMG	VEB	Gene	Transcript	NA Mutation	AA Mutation	Impact	Effect	Transmission	Databases	Pop freq	Sample Freq
✓	✓	SLC25A22	NM_024698.5	c.813_B1del	p.A272Q/ter144	High	frameshift variant	[AR]	dbvar, clinvar, omim	N/A	2/3 66.67%
✓	✓	SLC25A22	NM_024698.5	c.813G>A	p.R273K	Moderate	missense variant	[AR]	dbvar, clinvar, omim	41 x10 ⁻⁴	2/3 66.67%
✓	✓	COLN	NM_002538.3	c.1037+1G>A		High	splice donor variant	[AR]	dbvar, clinvar, omim	27 x10 ⁻⁵	2/3 66.67%
✓	✓	MOPH1	NM_024596.3	c.1544A>G	p.K313R	Moderate	missense variant	[AR]	dbvar, clinvar, omim	N/A	2/3 66.67%
✓	✓	POLG	NM_002693.2	c.147C>G	p.P168	Moderate	missense variant	[Ho, AR][AR][AR][AR]	dbvar, clinvar, omim	N/A	1/3 33.33%
✓	✓	SFT2	NM_013284.3	c.662G>A	p.V228	Moderate	missense variant	[AR]	dbvar, clinvar, omim	55 x10 ⁻⁵	2/3 66.67%
✓	✓	ALMS1	NM_015126.4	c.1039T>C	p.Q345P	Moderate	missense variant	[AR]	omim	N/A	2/3 66.67%
✓	✓	PCNT	NM_006031.5	c.3091C>G	p.R1031G	Moderate	missense variant	[AR]	dbvar, clinvar, omim	12 x10 ⁻⁵	2/3 66.67%
✓	✓	BCAP31	NM_02139441.1	c.45+1_45+2..		High	splice donor variant	[KLR]	omim	N/A	1/3 33.33%
✓	✓	CEP55	NM_018131.4	c.256C>T	p.R85Ter	High	stop gained	N/A	dbvar, clinvar, omim	28 x10 ⁻⁴	2/3 66.67%
✓	✓	ADAMTS2	NM_014244.4	c.345G>T	p.T113I	Moderate	missense variant	[AR]	dbvar, clinvar, omim	45 x10 ⁻⁴	1/3 33.33%

The data is accessible and available to the clinician at all times, which allows:

- reanalysis, when if required;
- use of data for research.

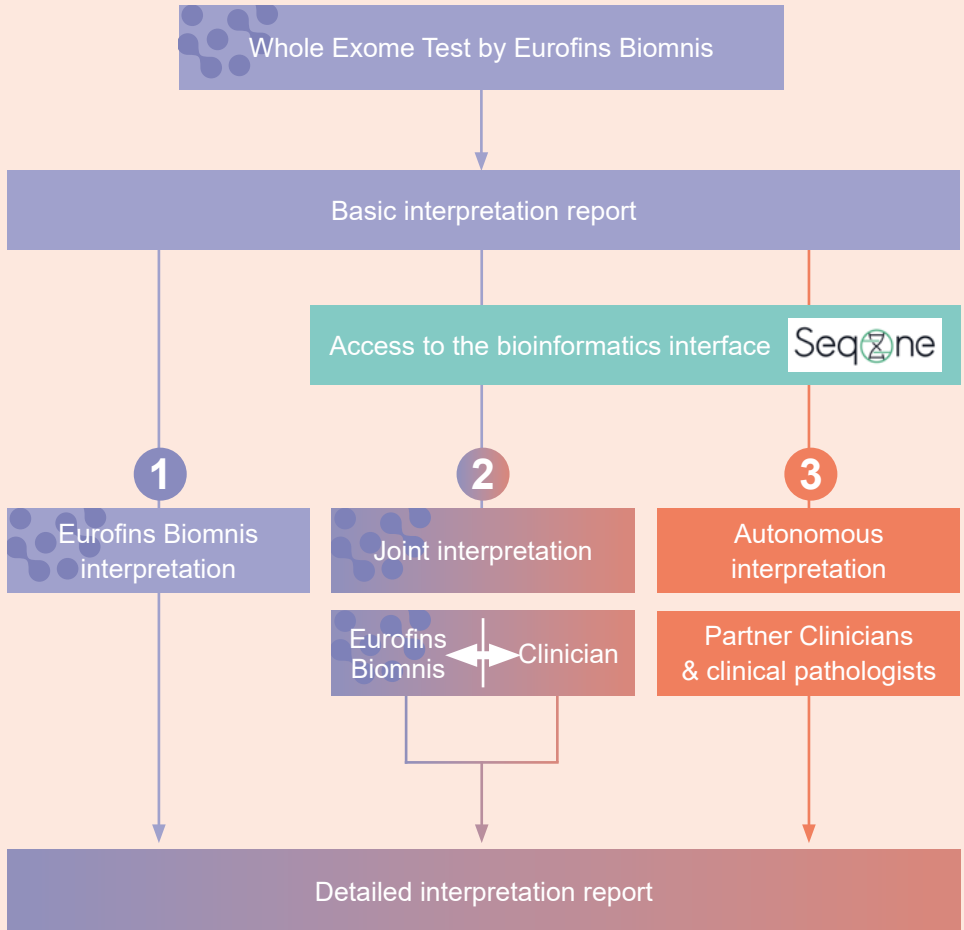
Why SeqOne?

- **Simplicity of interpretation:** intuitive platform and possibility of joint interpretation
- **Search for pathogenic variants:** prioritisation of pathogenic variants by AI and by phenotype, automated ACMG score calculation and detailed investigation with specific databases.
- **Customised features:** solo or trio analysis, OMIM pro version database and private annotation management
- **Safety and Quality:** coverage control, health data host (HDS), and CE IVD certification
- **Training and assistance:** support in the handling of the tool and ongoing operational support.



Sequence your exomes with Eurofins Biomnis

3 interpretation options/solutions



References

1. Exome sequencing has higher diagnostic yield compared to simulated disease-specific panels in children with suspected monogenic disorders. Oliver James Dillon et al. European Society of Human Genetics, Feb 18, 2018.
2. Meta-analysis and multidisciplinary consensus statement: exome sequencing is a first-tier clinical diagnostic test for individuals with neurodevelopmental disorders. Srivastava S et al. Genet Med. 2019 Nov;21(11):2413-2421. doi: 10.1038/s41436-019-0554-6. Epub 2019 Jun 11.
3. Paediatric genomics: diagnosing rare disease in children. Wright CF et al. Nat Rev Genet. 2018 May;19(5):253-268. doi: 10.1038/nrg.2017.116. Epub 2018 Feb 5.



Practical details

Whole Exome Sequencing & Access to the interpretation interface		
Interpretation level	Detailed report	Basic report
Turnaround	<ul style="list-style-type: none">6 weeks for a negative resultExtended deadline if additional examinations necessary	4 weeks
Indications	<ul style="list-style-type: none">intellectual disability, neurodevelopmental disorders,syndrome-based disorders,clinical pictures which do not directly suggest a specific gene test or gene panel, or negative result for these primary tests,organ damage (kidney, heart, etc.).	
Sample	Solo: 5 mL EDTA whole blood or DNA sample Duo/Trio: 5mL EDTA whole blood or DNA sample from relative	
Conservation & transport	Room temperature	
Technique	Exome sequencing + bioinformatics pipeline	
Required documents	B34-INTGB Test request form available on www.eurofins-biomnis.com > Test guide > Analysis code EXOME	
Price	Contact us	
Complementary test	Study of relative persons by Sanger sequencing: 5 mL EDTA whole blood or DNA sample from relative	

For more information:

Eurofins Biomnis

International Division

17/19 avenue Tony Garnier

BP 7322 - 69357 LYON Cedex 07 - FRANCE

E-mail: international@eurofins-biomnis.com

www.eurofins-biomnis.com



Biomnis