NEW ZEALAND DATA SHEET – Galafold® (MIGALASTAT) HARD CAPSULES

1 NAME OF THE MEDICINE

Galafold 123 mg hard capsules

2 QUALITATIVE AND QUANTITATIVE COMPOSITION

Galafold capsule contains 123 mg migalastat equivalent to 150 mg migalastat hydrochloride.

For the full list of excipients, see Section 6.1 List of excipients.

3 PHARMACEUTICAL FORM

Galafold capsule is a size 2 hard capsule (6.4 x 18.0 mm) with an opaque blue cap and opaque white body with "A1001" printed in black.

4 CLINICAL PARTICULARS

4.1 THERAPEUTIC INDICATIONS

Galafold is indicated for long-term treatment of adult and adolescent patients 12 years and older with a confirmed diagnosis of Fabry disease (α-galactosidase A deficiency) and who have an amenable mutation (see the table in Section 5.1 Pharmacodynamic properties, Mechanism of action).

4.2 DOSE AND METHOD OF ADMINISTRATION

Dosage (dose and interval)

Treatment with Galafold should be initiated and supervised by specialist physicians experienced in the diagnosis and treatment of Fabry disease. Galafold is not intended for concomitant use with enzyme replacement therapy (ERT).

The recommended dosage regimen in adults is 123 mg Galafold (1 capsule) taken orally once every other day at the same time of day.

The recommended dosage regimen in adolescents aged 12 years to <18 years and weighing ≥45 kg is 123 mg Galafold (1 capsule) taken orally once every other day at the same time of day.

Galafold should not be taken on 2 consecutive days.

Missed dose

If the usual dosing time is missed, the patient should take the missed dose of Galafold only if it is within 12 hours of the normal time the dose is taken. If more than 12 hours has passed, the patient should resume taking Galafold at the next planned dosing day and time according to the every other day dosing schedule.

Dosage adjustment

Paediatric population

Adolescents aged 12 to <18 years and weighing ≥45 kg

123 mg Galafold (1 capsule) taken once every other day at the same time of the day (see Section 5.2 Pharmacokinetic properties).

Children <12 years

The safety and efficacy of Galafold in children below the age of 12 years have not yet been established. No data are available.

Use in the elderly

No dosage adjustment is required based on age.

Use in renal impairment

Galafold is not recommended for use in patients with Fabry disease who have estimated GFR less than 30 mL/min/1.73 m^2 (see Section 5.2 Pharmacokinetic properties).

Use in hepatic impairment

No dosage adjustment of Galafold is required in patients with hepatic impairment (see Section 5.2 Pharmacokinetic properties).

Method of administration

Galafold exposure is decreased by approximately 40% when taken with food and 60% when taken with coffee (see Section 5.2 Pharmacokinetic Properties). Food and caffeine should not be consumed at least 2 hours before and 2 hours after taking Galafold to give a minimum 4 hours fast.

Water (plain, flavoured, sweetened), fruit juices without pulp, and caffeine-free carbonated beverages can be consumed during the 4-hour fasting period.

Galafold should be taken every other day at the same time of day to ensure optimal benefits to the patient. Capsules must be swallowed whole. The capsules must not be cut, crushed, or chewed (see Section 5.2 Pharmacokinetic properties).

4.3 CONTRAINDICATIONS

Hypersensitivity to the active substance or to any of the excipients (see Section 6.1 List of excipients).

4.4 SPECIAL WARNINGS AND PRECAUTIONS FOR USE

It is advised to periodically monitor (6 months, or at the usual regular intervals according to national practices) renal function, echocardiographic parameters, and biochemical markers in patients initiated on or switched to Galafold. In case of meaningful clinical deterioration, further clinical evaluation or discontinuation of treatment with Galafold should be considered.

Galafold is not indicated for use in patients with non-amenable mutations as efficacy with these mutations has not been demonstrated (see Section 5.1 Pharmacodynamic properties).

Limited data suggest that co-administration of a single dose of Galafold and a standard ERT infusion results in increased exposure to agalsidase up to 5-fold. This study also indicated that agalsidase has no effect on the pharmacokinetics of migalastat. Galafold is not intended for concomitant use with enzyme replacement therapy (see Section 4.5 Interactions with other medicines and other forms of interactions)

Galafold is not recommended in women of childbearing potential not using contraception (see Section 5.1 Pharmacodynamic properties).

Use in renal impairment

No reduction in proteinuria was observed in patients treated with Galafold.

Galafold is not recommended for use in patients with severe renal insufficiency, defined as estimated GFR less than 30 mL/min/1.73 m^2 (see Section 5.2 Pharmacokinetic properties).

Use in the elderly

No dosage adjustment is required based on age (see Section 5.2 Pharmacokinetic properties).

Paediatric use

Galafold is not suitable for adolescents aged 12 years to <18 years and weighing <45 kg (see Section 5.2 Pharmacokinetic Properties). Galafold has not been studied in paediatric subjects below the age of 12 years.

Effects on laboratory tests

No data available.

4.5 INTERACTIONS WITH OTHER MEDICINES AND OTHER FORMS OF INTERACTIONS

Based upon *in vitro* data, migalastat is not an inducer of CYP1A2, 2B6, or 3A4. Furthermore, migalastat is not an inhibitor or a substrate of CYP1A2, 2A6, 2B6, 2C8, 2C9, 2C19, 2D6, 2E1, or 3A4/5. Migalastat is not a substrate for MDR1 or BCRP, nor is it an inhibitor of BCRP, MDR1, or BSEP human efflux transporters. In addition, migalastat is not a substrate for MATE1, MATE2-K, OAT1, OAT3, or OCT2, nor is it an inhibitor of OATP1B1, OATP1B3, OAT1, OAT3, OCT1, OCT2, MATE1, or MATE2-K human uptake transporters. Limited data suggest that co-administration of a single dose of Galafold and a standard ERT infusion results in increased exposure to agalsidase up to 5-fold. Agalsidase has no effect on the pharmacokinetics of migalastat (See Section 4.4 Special warnings and Precautions).

Effect of other drugs on Galafold

Limited data suggest that co-administration of Galafold with caffeine decreases migalastat systemic exposure (AUC and C_{max}) which may reduce Galafold efficacy (see Section 5.2 Pharmacokinetic Properties). Avoid co-administration of Galafold with caffeine at least 2 hours before and 2 hours after taking Galafold (see Section 4.2 Dose and Method of Administration).

4.6 FERTILITY, PREGNANCY AND LACTATION

Effects on fertility

The effects of Galafold on fertility in humans have not been studied. Non-clinical studies suggest no specific hazard for humans on the basis of single- and repeat-dose studies, with the exception of transient but fully reversible infertility in male rats associated with migalastat treatment at ≥2.5 mg/kg/day (≥0.2 times the clinical exposure based on AUC). The infertility associated with migalastat treatment was reported at subclinical relative exposures. Complete reversibility was seen after 4 weeks off-dose. Similar findings have been noted pre-clinically following treatment with other iminosugars. Galafold did not affect fertility in female rats.

Use in pregnancy

Category B3
There are limited data from the use of Galafold in pregnant women. In the rabbit embryo-foetal toxicity study, findings including embryo-foetal death, a reduction in mean foetal weight, retarded ossification, and slightly increased incidences of minor skeletal abnormalities were observed only at doses of ≥300 mg/kg/day (≥240 times the clinical exposure based on AUC), which were associated with maternal toxicity. No Galafold-related embryo-foetal development issues were reported up to 1500 mg/kg/day in rats (>50 times the clinical exposure) or 120 mg/kg/day in rabbits (74 times clinical exposure). Galafold is not recommended during pregnancy.

Use in lactation

It is not known whether Galafold is secreted in human milk. However, migalastat has been shown to be secreted in the milk of lactating rats. Accordingly, a risk of migalastat exposure to the breast-feeding infant cannot be excluded. A decision must be made whether to discontinue breast-feeding or to discontinue Galafold, taking into account the benefit of breast-feeding for the child relative to the benefit of therapy for the mother.

4.7 EFFECTS ON ABILITY TO DRIVE AND USE MACHINES

No specific studies have been conducted to assess the direct effect of Galafold on the ability to drive and use machines.

4.8 ADVERSE EFFECTS (UNDESIRABLE EFFECTS)

Experience from clinical trials

The most common adverse reaction was headache, which was experienced by approximately 10% of patients who received Galafold.

Tabulated list of adverse reactions

Frequencies are defined as: very common (≥1/10), common (≥1/100 to <1/10), uncommon (≥1/1,000 to <1/100), rare (≥1/10,000 to <1/1,000), very rare (<1/10,000), and not known (cannot be estimated from the available data). Within each frequency grouping, adverse reactions are presented in order of decreasing frequency within each System Organ Class.

Table 1: Study AT1001-011 (FACETS*) and AT1001-012 (ATTRACT) Combined, Treatment-Related Treatment-Emergent Adverse Events for Migalastat**

System Organ Class **Preferred Term**	**Frequency of adverse reaction (%)**		
	Very common (≥1/10)	**Common (≥1/100 to <1/10)**	**Uncommon (≥1/1,000 to <1/100)**
Cardiac Disorders			
Palpitations		1.7%	
Ear and Labyrinth Disorders			
Vertigo		2.6%	
Eye Disorders			
Eye pruritus			0.9%
Visual acuity reduced			0.9%
Gastrointestinal Disorders			
Diarrhoea		7.8%	
Nausea		5.2%	
Abdominal pain		2.6%	
Constipation		2.6%	
Dry mouth		2.6%	
Defaecation urgency		1.7%	
Dyspepsia		1.7%	
Abdominal pain upper			0.9%
Change of bowel habit			0.9%
Faecal incontinence			0.9%
Irritable bowel syndrome			0.9%
Vomiting			0.9%
General Disorders and Administration Site Conditions			
Fatigue		2.6%	
Pain		1.7%	
Inflammation			0.9%
Influenza like illness			0.9%
Local swelling			0.9%
Oedema peripheral			0.9%
Pyrexia			0.9%
Hepatobiliary Disorders			
Hepatocellular injury			0.9%
Injury, Poisoning and Procedural Complications			
Incorrect dose administered		2.6%	

System Organ Class Preferred Term	Frequency of adverse reaction (%)		
	Very common (≥1/10)	Common (≥1/100 to <1/10)	Uncommon (≥1/1,000 to <1/100)
Overdose			0.9%
Radiation skin injury			0.9%
Investigations			
Blood creatine phosphokinase increased		2.6%	
Weight increased		2.6%	
Blood bilirubin increased			0.9%
Blood calcium decreased			0.9%
Blood cholesterol increased			0.9%
Blood pressure increased			0.9%
Body temperature increased			0.9%
Liver function test abnormal			0.9%
Weight decreased			0.9%
White blood cell count decreased			0.9%
Metabolism and Nutrition Disorders			
Decreased appetite			0.9%
Hypoglycaemia			0.9%
Musculoskeletal and Connective Tissue Disorders			
Muscle spasms		3.5%	
Myalgia		1.7%	
Pain in extremity		1.7%	
Torticollis		1.7%	
Flank pain			0.9%
Muscle twitching			0.9%
Musculoskeletal chest pain			0.9%
Nervous System Disorders			
Headache	10.4%		
Dizziness		5.2%	
Paraesthesia		5.2%	
Hypoaesthesia		1.7%	
Ataxia			0.9%
Balance disorder			0.9%
Hyperaesthesia			0.9%
Memory impairment			0.9%

System Organ Class Preferred Term	Frequency of adverse reaction (%)		
	Very common (≥1/10)	Common (≥1/100 to <1/10)	Uncommon (≥1/1,000 to <1/100)
Migraine			0.9%
Neuralgia			0.9%
Somnolence			0.9%
Tremor			0.9%
Psychiatric Disorders			
Depression		1.7%	
Insomnia			0.9%
Sleep Disorder			0.9%
Renal and Urinary Disorders			
Proteinuria		1.7%	
Pollakiuria			0.9%
Respiratory, Thoracic and Mediastinal Disorders			
Dyspnoea		1.7%	
Epistaxis		1.7%	
Rhinorrhoea			0.9%
Skin and Subcutaneous Tissue Disorders			
Rash		2.6%	
Pruritus		1.7%	
Erythema			0.9%
Hyperhidrosis			0.9%
Night sweats			0.9%
Psoriasis			0.9%
Vascular Disorders			
Systolic hypertension			0.9%

*FACETS - Fabry AT1001 Chaperone Efficacy, Therapeutics and Safety Study

**ATTRACT - AT1001 Therapy Compared to Enzyme Replacement in Fabry Patients with AT1001-responsive Mutations: a Global Clinical Trial

Note: Pooled database from all patients who received at least one dose of migalastat in AT1001-011 (0 to 24 months) and AT1001-012 (0 to 30 months). Source: Table 2 Tintext 1112 SmPC-TEAE.

Paediatric population

The safety assessment in 21 adolescents (12 to <18 years of age and weighing ≥45 kg) is based on 1-year safety data from the open-label AT1001-020 trial in which subjects received the same dosage regimen as adults (see Section 5.2 Pharmacokinetic Properties). No age-specific differences in adverse reactions were observed between adolescent and adult subjects.

Post-marketing experience

The following adverse reaction has been identified during post approval use of Galafold. Because this reaction is reported voluntarily from a population of uncertain size, it is not always possible to reliably estimate its frequency which is therefore categorized as not known.

Table 2: List of adverse drug reactions from post-marketing data

System Organ Class **Preferred term**	**Frequency of adverse reaction**
Skin and subcutaneous tissue disorders	
Angioedema	Not known

Reporting suspected adverse effects

Reporting suspected adverse reactions after authorization of the medicine is important. It allows continued monitoring of the benefit/risk balance of the medicine.

Healthcare professionals are asked to report any suspected adverse reactions at https://pophealth.my.site.com/carmreportnz/s/.

4.9 OVERDOSE

For advice on the management of overdose, please contact the National Poisons Centre on 0800 POISON (0800 764 766).

In case of overdose, general medical care is recommended. Headache and dizziness were the most common adverse reactions reported at doses of Galafold of up to 1250 mg and 2000 mg, respectively.

5 PHARMACOLOGICAL PROPERTIES

5.1 PHARMACODYNAMIC PROPERTIES

Pharmacotherapeutic group: Various alimentary tract and metabolism products.
ATC Code: A16AX14.

Fabry disease is a progressive X-linked lysosomal storage disorder that affects males and females. Fabry disease-causing mutations in the *GLA* gene result in a deficiency of the lysosomal enzyme α-galactosidase A (α-Gal A) that is required for glycosphingolipid substrate (eg, GL-3, lyso-Gb_3) metabolism. Reduced α-Gal A activity is, therefore, associated with the progressive accumulation of substrate in vulnerable organs and tissues, which leads to the morbidity and mortality associated with Fabry disease.

Mechanism of action

Certain *GLA* mutations can result in the production of abnormally folded and unstable mutant forms of α-Gal A. Migalastat is a pharmacological chaperone that is designed to selectively and reversibly bind with high affinity to the active sites of certain mutant forms of α-Gal A, the genotypes of which are referred to as amenable mutations. Migalastat binding stabilizes these mutant forms of α-Gal A in the endoplasmic reticulum and facilitates their proper trafficking to lysosomes where dissociation of migalastat restores α-Gal A activity, leading to the catabolism of GL-3 and related substrates.

The *GLA* mutations amenable to treatment with Galafold are listed in Table 3. The *GLA* mutations are also accessible by health care providers atwww.galafoldamenabilitytable.co.nz.

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.7C>G	c.C7G	L3V
c.8T>C	c.T8C	L3P
c.[11G>T; 620A>C]	c.G11T/A620C	R4M/Y207S
c.13A>G	c.A13G	N5D
c.15C>G	c.C15G	N5K
c.16C>A	c.C16A	P6T
c.16C>T	c.C16T	P6S
c.17C>A	c.C17A	P6Q
c.17C>G	c.C17G	P6R
c.17C>T	c.C17T	P6L
c.19G>A	c.G19A	E7K
c.20A>T	c.A20T	E7V
c.21A>T	c.A21T	E7D
c.22C>A	c.C22A	L8I
c.23T>A	c.T23A	L8Q
c.23T>C	c.T23C	L8P
c.25C>T	c.C25T	H9Y
c.26A>G	c.A26G	H9R
c.26A>T	c.A26T	H9L
c.27T>A	c.T27A	H9Q
c.28C>A	c.C28A	L10M
c.28C>G	c.C28G	L10V
c.29T>A	c.T29A	L10Q
c.29T>C	c.T29C	L10P
c.29T>G	c.T29G	L10R
c.31G>A	c.G31A	G11S
c.31G>C	c.G31C	G11R
c.31G>T	c.G31T	G11C
c.32G>A	c.G32A	G11D
c.32G>T	c.G32T	G11V
c.34T>A	c.T34A	C12S
c.34T>C	c.T34C	C12R
c.34T>G	c.T34G	C12G
c.35G>A	c.G35A	C12Y
c.37G>A	c.G37A	A13T
c.37G>C	c.G37C	A13P
c.38C>A	c.C38A	A13E

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.38C>G	c.C38G	A13G
c.40C>G	c.C40G	L14V
c.40C>T	c.C40T	L14F
c.41T>A	c.T41A	L14H
c.43G>A	c.G43A	A15T
c.44C>G	c.C44G	A15G
c.49C>A	c.C49A	R17S
c.49C>G	c.C49G	R17G
c.49C>T	c.C49T	R17C
c.50G>A	c.G50A	R17H
c.50G>C	c.G50C	R17P
c.52T>A	c.T52A	F18I
c.53T>G	c.T53G	F18C
c.54C>G	c.C54G	F18L
c.58G>C	c.G58C	A20P
c.59C>A	c.C59A	A20D
c.59C>G	c.C59G	A20G
c.62T>A	c.T62A	L21H
c.64G>A	c.G64A	V22I
c.64G>C	c.G64C	V22L
c.64G>T	c.G64T	V22F
c.65T>C	c.T65C	V22A
c.65T>G	c.T65G	V22G
c.67T>A	c.T67A	S23T
c.67T>C	c.T67C	S23P
c.70T>C or c.70T>A	c.T70C or c.T70A	W24R
c.[70T>A; 1255A>G]	c.T70A/A1255G	W24R/N419D
c.70T>G	c.T70G	W24G
c.71G>C	c.G71C	W24S
c.72G>C or c.72G>T	c.G72C or c.G72T	W24C
c.73G>C	c.G73C	D25H
c.77T>A	c.T77A	I26N
c.79C>A	c.C79A	P27T
c.79C>G	c.C79G	P27A
c.79C>T	c.C79T	P27S
c.80C>T	c.C80T	P27L
c.82G>C	c.G82C	G28R
c.82G>T	c.G82T	G28W
c.83G>A	c.G83A	G28E
c.85G>C	c.G85C	A29P
c.86C>A	c.C86A	A29D

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.86C>G	c.C86G	A29G
c.86C>T	c.C86T	A29V
c.88A>G	c.A88G	R30G
c.94C>A	c.C94A	L32M
c.94C>G	c.C94G	L32V
c.95T>A	c.T95A	L32Q
c.95T>C	c.T95C	L32P
c.95T>G	c.T95G	L32R
c.97G>C	c.G97C	D33H
c.97G>T	c.G97T	D33Y
c.98A>C	c.A98C	D33A
c.98A>G	c.A98G	D33G
c.98A>T	c.A98T	D33V
c.99C>G	c.C99G	D33E
c.100A>C	c.A100C	N34H
c.100A>G	c.A100G	N34D
c.101A>C	c.A101C	N34T
c.101A>G	c.A101G	N34S
c.102T>G or c.102T>A	c.T102G or c.T102A	N34K
c.103G>C or c.103G>A	c.G103C or c.G103A	G35R
c.104G>A	c.G104A	G35E
c.104G>C	c.G104C	G35A
c.104G>T	c.G104T	G35V
c.106T>A	c.T106A	L36M
c.106T>G	c.T106G	L36V
c.107T>C	c.T107C	L36S
c.107T>G	c.T107G	L36W
c.108G>C or c.108G>T	c.G108C or c.G108T	L36F
c.109G>A	c.G109A	A37T
c.109G>T	c.G109T	A37S
c.110C>A	c.C110A	A37E
c.110C>G	c.C110G	A37G
c.110C>T	c.C110T	A37V
c.112A>G	c.A112G	R38G
c.112A>T	c.A112T	R38W
c.113G>T	c.G113T	R38M
c.114G>C	c.G114C	R38S
c.115A>G	c.A115G	T39A
c.115A>T	c.A115T	T39S
c.116C>A	c.C116A	T39K
c.116C>G	c.C116G	T39R

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.116C>T	c.C116T	T39M
c.121A>G	c.A121G	T41A
c.122C>A	c.C122A	T41N
c.122C>G	c.C122G	T41S
c.122C>T	c.C122T	T41I
c.124A>C or c.124A>T	c.A124C or c.A124T	M42L
c.124A>G	c.A124G	M42V
c.125T>A	c.T125A	M42K
c.125T>C	c.T125C	M42T
c.125T>G	c.T125G	M42R
c.126G>A or c.126G>C or c.126G>T	c.G126A or c.G126C or c.G126T	M42I
c.128G>C	c.G128C	G43A
c.133C>A	c.C133A	L45M
c.133C>G	c.C133G	L45V
c.136C>A	c.C136A	H46N
c.136C>G	c.C136G	H46D
c.137A>C	c.A137C	H46P
c.138C>G	c.C138G	H46Q
c.142G>C	c.G142C	E48Q
c.143A>C	c.A143C	E48A
c.149T>A	c.T149A	F50Y
c.151A>G	c.A151G	M51V
c.152T>A	c.T152A	M51K
c.152T>C	c.T152C	M51T
c.152T>G	c.T152G	M51R
c.153G>A or c.153G>T or c.153G>C	c.G153A or c.G153T or c.G153C	M51I
c.157A>C	c.A157C	N53H
c.[157A>C; 158A>T]	c.A157C/A158T	N53L
c.157A>G	c.A157G	N53D
c.157A>T	c.A157T	N53Y
c.158A>C	c.A158C	N53T
c.158A>G	c.A158G	N53S
c.158A>T	c.A158T	N53I
c.159C>G or c.159C>A	c.C159G or c.C159A	N53K
c.160C>G	c.C160G	L54V
c.160C>T	c.C160T	L54F
c.161T>A	c.T161A	L54H
c.161T>C	c.T161C	L54P
c.161T>G	c.T161G	L54R

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.163G>C	c.G163C	D55H
c.163G>T	c.G163T	D55Y
c.164A>C	c.A164C	D55A
c.164A>G	c.A164G	D55G
c.164A>T	c.A164T	D55V
c.[164A>T; 170A>T]	c.A164T/A170T	D55V/Q57L
c.165C>G	c.C165G	D55E
c.167G>A	c.G167A	C56Y
c.167G>T	c.G167T	C56F
c.168C>G	c.C168G	C56W
c.170A>G	c.A170G	Q57R
c.170A>T	c.A170T	Q57L
c.172G>A	c.G172A	E58K
c.175G>A	c.G175A	E59K
c.175G>C	c.G175C	E59Q
c.176A>C	c.A176C	E59A
c.176A>G	c.A176G	E59G
c.176A>T	c.A176T	E59V
c.177G>C	c.G177C	E59D
c.178C>A	c.C178A	P60T
c.178C>G	c.C178G	P60A
c.178C>T	c.C178T	P60S
c.179C>A	c.C179A	P60Q
c.179C>G	c.C179G	P60R
c.179C>T	c.C179T	P60L
c.182A>T	c.A182T	D61V
c.183T>A	c.T183A	D61E
c.184_185insTAG	c.184_185insTAG	S62delinsLA
c.184T>C	c.T184C	S62P
c.184T>G	c.T184G	S62A
c.185C>A	c.C185A	S62Y
c.185C>G	c.C185G	S62C
c.185C>T	c.C185T	S62F
c.190A>C	c.A190C	I64L
c.190A>G	c.A190G	I64V
c.193A>G	c.A193G	S65G
c.193A>T	c.A193T	S65C
c.195T>A	c.T195A	S65R
c.196G>A	c.G196A	E66K
c.197A>G	c.A197G	E66G
c.197A>T	c.A197T	E66V

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.198G>C	c.G198C	E66D
c.199A>C	c.A199C	K67Q
c.199A>G	c.A199G	K67E
c.200A>C	c.A200C	K67T
c.200A>T	c.A200T	K67M
c.201G>C	c.G201C	K67N
c.202C>A	c.C202A	L68I
c.205T>A	c.T205A	F69I
c.206T>A	c.T206A	F69Y
c.207C>A or c.207C>G	c.C207A or c.C207G	F69L
c.208A>T	c.A208T	M70L
c.209T>A	c.T209A	M70K
c.209T>G	c.T209G	M70R
c.210G>C	c.G210C	M70I
c.211G>C	c.G211C	E71Q
c.212A>C	c.A212C	E71A
c.212A>G	c.A212G	E71G
c.212A>T	c.A212T	E71V
c.213G>C	c.G213C	E71D
c.214A>G	c.A214G	M72V
c.214A>T	c.A214T	M72L
c.215T>C	c.T215C	M72T
c.216G>A or c.216G>T or c.216G>C	c.G216A or c.G216T or c.G216C	M72I
c.217G>A	c.G217A	A73T
c.217G>T	c.G217T	A73S
c.218C>T	c.C218T	A73V
c.[218C>T; 525C>G]	c.C218T/C525G	A73V/D175E
c.220G>A	c.G220A	E74K
c.221A>G	c.A221G	E74G
c.221A>T	c.A221T	E74V
c.222G>C	c.G222C	E74D
c.223C>T	c.C223T	L75F
c.224T>C	c.T224C	L75P
c.226A>G	c.A226G	M76V
c.227T>C	c.T227C	M76T
c.229G>A	c.G229A	V77I
c.229G>C	c.G229C	V77L
c.232T>C	c.T232C	S78P
c.233C>T	c.C233T	S78L
c.235G>A	c.G235A	E79K

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.235G>C	c.G235C	E79Q
c.236A>C	c.A236C	E79A
c.236A>G	c.A236G	E79G
c.236A>T	c.A236T	E79V
c.237A>T	c.A237T	E79D
c.238G>A	c.G238A	G80S
c.238G>T	c.G238T	G80C
c.239G>A	c.G239A	G80D
c.239G>C	c.G239C	G80A
c.239G>T	c.G239T	G80V
c.242G>T	c.G242T	W81L
c.244A>G	c.A244G	K82E
c.245A>C	c.A245C	K82T
c.245A>G	c.A245G	K82R
c.245A>T	c.A245T	K82M
c.246G>C	c.G246C	K82N
c.247G>A	c.G247A	D83N
c.248A>C	c.A248C	D83A
c.248A>G	c.A248G	D83G
c.248A>T	c.A248T	D83V
c.249T>A	c.T249A	D83E
c.250G>A	c.G250A	A84T
c.250G>C	c.G250C	A84P
c.250G>T	c.G250T	A84S
c.251C>A	c.C251A	A84E
c.251C>G	c.C251G	A84G
c.251C>T	c.C251T	A84V
c.253G>A	c.G253A	G85S
c.[253G>A; 254G>A]	c.G253A/G254A	G85N
c.[253G>A; 254G>T; 255T>G]	c.G253A/G254T/T255G	G85M
c.253G>C	c.G253C	G85R
c.253G>T	c.G253T	G85C
c.254G>A	c.G254A	G85D
c.254G>C	c.G254C	G85A
c.257A>T	c.A257T	Y86F
c.260A>G	c.A260G	E87G
c.261G>C or c.261G>T	c.G261C or c.G261T	E87D
c.262T>A	c.T262A	Y88N
c.262T>C	c.T262C	Y88H
c.263A>C	c.A263C	Y88S

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.263A>G	c.A263G	Y88C
c.265C>G	c.C265G	L89V
c.265C>T	c.C265T	L89F
c.271A>C	c.A271C	I91L
c.271A>T	c.A271T	I91F
c.272T>C	c.T272C	I91T
c.272T>G	c.T272G	I91S
c.273T>G	c.T273G	I91M
c.286A>G	c.A286G	M96V
c.286A>T	c.A286T	M96L
c.287T>C	c.T287C	M96T
c.288G>A or c.288G>T or c.288G>C	c.G288A or c.G288T or c.G288C	M96I
c.289G>A	c.G289A	A97T
c.289G>C	c.G289C	A97P
c.289G>T	c.G289T	A97S
c.290C>A	c.C290A	A97D
c.290C>T	c.C290T	A97V
c.293C>A	c.C293A	P98H
c.293C>G	c.C293G	P98R
c.293C>T	c.C293T	P98L
c.295C>G	c.C295G	Q99E
c.296A>C	c.A296C	Q99P
c.296A>G	c.A296G	Q99R
c.296A>T	c.A296T	Q99L
c.301G>C	c.G301C	D101H
c.302A>C	c.A302C	D101A
c.302A>G	c.A302G	D101G
c.302A>T	c.A302T	D101V
c.303T>A	c.T303A	D101E
c.304T>A	c.T304A	S102T
c.304T>C	c.T304C	S102P
c.304T>G	c.T304G	S102A
c.305C>T	c.C305T	S102L
c.310G>A	c.G310A	G104S
c.311G>A	c.G311A	G104D
c.311G>C	c.G311C	G104A
c.311G>T	c.G311T	G104V
c.313A>G	c.A313G	R105G
c.314G>A	c.G314A	R105K
c.314G>C	c.G314C	R105T

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.314G>T	c.G314T	R105I
c.316C>A	c.C316A	L106I
c.316C>G	c.C316G	L106V
c.316C>T	c.C316T	L106F
c.317T>A	c.T317A	L106H
c.317T>C	c.T317C	L106P
c.319C>A	c.C319A	Q107K
c.319C>G	c.C319G	Q107E
c.320A>G	c.A320G	Q107R
c.321G>C	c.G321C	Q107H
c.322G>A	c.G322A	A108T
c.323C>A	c.C323A	A108E
c.323C>T	c.C323T	A108V
c.325G>A	c.G325A	D109N
c.325G>C	c.G325C	D109H
c.325G>T	c.G325T	D109Y
c.326A>C	c.A326C	D109A
c.326A>G	c.A326G	D109G
c.327C>G	c.C327G	D109E
c.328C>A	c.C328A	P110T
c.334C>G	c.C334G	R112G
c.335G>A	c.G335A	R112H
c.335G>T	c.G335T	R112L
c.337T>A	c.T337A	F113I
c.337T>C or c.339T>A or c.339T>G	c.T337C or c.T339A or c.T339G	F113L
c.337T>G	c.T337G	F113V
c.338T>A	c.T338A	F113Y
c.341C>T	c.C341T	P114L
c.343C>A	c.C343A	H115N
c.343C>G	c.C343G	H115D
c.346G>C	c.G346C	G116R
c.350T>C	c.T350C	I117T
c.351T>G	c.T351G	I117M
c.352C>T	c.C352T	R118C
c.361G>A	c.G361A	A121T
c.362C>T	c.C362T	A121V
c.367T>A	c.T367A	Y123N
c.367T>G	c.T367G	Y123D
c.368A>C	c.A368C	Y123S
c.368A>G	c.A368G	Y123C

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.368A>T	c.A368T	Y123F
c.370G>A	c.G370A	V124I
c.371T>G	c.T371G	V124G
c.373C>A	c.C373A	H125N
c.373C>G	c.C373G	H125D
c.373C>T	c.C373T	H125Y
c.374A>G	c.A374G	H125R
c.374A>T	c.A374T	H125L
c.376A>G	c.A376G	S126G
c.376A>T	c.A376T	S126C
c.377G>T	c.G377T	S126I
c.379A>G	c.A379G	K127E
c.383G>A	c.G383A	G128E
c.383G>C	c.G383C	G128A
c.385C>G	c.C385G	L129V
c.388A>C	c.A388C	K130Q
c.389A>T	c.A389T	K130M
c.390G>C	c.G390C	K130N
c.391C>G	c.C391G	L131V
c.397A>C	c.A397C	I133L
c.397A>G	c.A397G	I133V
c.397A>T	c.A397T	I133F
c.398T>C	c.T398C	I133T
c.399T>G	c.T399G	I133M
c.[399T>G; 434T>C]	c.T399G/T434C	I133M/F145S
c.403G>A	c.G403A	A135T
c.403G>T	c.G403T	A135S
c.404C>A	c.C404A	A135E
c.404C>G	c.C404G	A135G
c.404C>T	c.C404T	A135V
c.406G>A	c.G406A	D136N
c.407A>C	c.A407C	D136A
c.407A>T	c.A407T	D136V
c.408T>A or c.408T>G	c.T408A or c.T408G	D136E
c.409G>A	c.G409A	V137I
c.409G>C	c.G409C	V137L
c.410T>A	c.T410A	V137D
c.410T>C	c.T410C	V137A
c.410T>G	c.T410G	V137G
c.413G>C	c.G413C	G138A
c.415A>C	c.A415C	N139H

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.415A>T	c.A415T	N139Y
c.416A>G	c.A416G	N139S
c.416A>T	c.A416T	N139I
c.417T>A	c.T417A	N139K
c.418A>C	c.A418C	K140Q
c.418A>G	c.A418G	K140E
c.419A>C	c.A419C	K140T
c.419A>G	c.A419G	K140R
c.419A>T	c.A419T	K140I
c.420A>T	c.A420T	K140N
c.421A>T	c.A421T	T141S
c.427G>A	c.G427A	A143T
c.428C>A	c.C428A	A143E
c.428C>G	c.C428G	A143G
c.428C>T	c.C428T	A143V
c.430G>A	c.G430A	G144S
c.430G>C	c.G430C	G144R
c.430G>T	c.G430T	G144C
c.431G>A	c.G431A	G144D
c.431G>C	c.G431C	G144A
c.431G>T	c.G431T	G144V
c.433T>G	c.T433G	F145V
c.434T>A	c.T434A	F145Y
c.434T>C	c.T434C	F145S
c.434T>G	c.T434G	F145C
c.435C>G	c.C435G	F145L
c.436C>A	c.C436A	P146T
c.436C>G	c.C436G	P146A
c.436C>T	c.C436T	P146S
c.437C>A	c.C437A	P146H
c.437C>G	c.C437G	P146R
c.437C>T	c.C437T	P146L
c.440G>C	c.G440C	G147A
c.442A>G	c.A442G	S148G
c.442A>T	c.A442T	S148C
c.443G>C	c.G443C	S148T
c.446T>G	c.T446G	F149C
c.449G>A	c.G449A	G150E
c.449G>T	c.G449T	G150V
c.451T>G	c.T451G	Y151D
c.452A>C	c.A452C	Y151S

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.452A>G	c.A452G	Y151C
c.454T>A	c.T454A	Y152N
c.454T>C	c.T454C	Y152H
c.454T>G	c.T454G	Y152D
c.455A>C	c.A455C	Y152S
c.455A>G	c.A455G	Y152C
c.455A>T	c.A455T	Y152F
c.457G>A	c.G457A	D153N
c.457G>C	c.G457C	D153H
c.457G>T	c.G457T	D153Y
c.458A>C	c.A458C	D153A
c.458A>T	c.A458T	D153V
c.465T>A or c.465T>G	c.T465A or c.T465G	D155E
c.466G>A	c.G466A	A156T
c.466G>T	c.G466T	A156S
c.467C>G	c.C467G	A156G
c.467C>T	c.C467T	A156V
c.469C>A	c.C469A	Q157K
c.469C>G	c.C469G	Q157E
c.470A>C	c.A470C	Q157P
c.470A>T	c.A470T	Q157L
c.471G>C or c.471G>T	c.G471C or c.G471T	Q157H
c.472A>G	c.A472G	T158A
c.472A>T	c.A472T	T158S
c.473C>A	c.C473A	T158N
c.473C>T	c.C473T	T158I
c.475T>A	c.T475A	F159I
c.475T>G	c.T475G	F159V
c.476T>A	c.T476A	F159Y
c.476T>G	c.T476G	F159C
c.477T>A	c.T477A	F159L
c.478G>A	c.G478A	A160T
c.478G>T	c.G478T	A160S
c.479C>A	c.C479A	A160D
c.479C>G	c.C479G	A160G
c.479C>T	c.C479T	A160V
c.481G>A	c.G481A	D161N
c.481G>C	c.G481C	D161H
c.481G>T	c.G481T	D161Y
c.482A>T	c.A482T	D161V
c.484T>G	c.T484G	W162G

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.485G>C	c.G485C	W162S
c.490G>A	c.G490A	V164I
c.490G>T	c.G490T	V164L
c.491T>C	c.T491C	V164A
c.493G>A	c.G493A	D165N
c.493G>C	c.G493C	D165H
c.494A>C	c.A494C	D165A
c.494A>G	c.A494G	D165G
c.495T>A	c.T495A	D165E
c.496_497delinsTC	c.496_497delinsTC	L166S
c.496C>A	c.C496A	L166M
c.496C>G	c.C496G	L166V
c.[496C>G; 497T>G]	c.C496G/T497G	L166G
c.497T>A	c.T497A	L166Q
c.499C>A	c.C499A	L167I
c.499C>G	c.C499G	L167V
c.505T>A	c.T505A	F169I
c.505T>G	c.T505G	F169V
c.506T>A	c.T506A	F169Y
c.506T>C	c.T506C	F169S
c.506T>G	c.T506G	F169C
c.507T>A	c.T507A	F169L
c.511G>A	c.G511A	G171S
c.512G>C	c.G512C	G171A
c.512G>T	c.G512T	G171V
c.517T>C	c.T517C	Y173H
c.518A>C	c.A518C	Y173S
c.518A>G	c.A518G	Y173C
c.518A>T	c.A518T	Y173F
c.520T>C	c.T520C	C174R
c.520T>G	c.T520G	C174G
c.523G>C	c.G523C	D175H
c.523G>T	c.G523T	D175Y
c.524A>G	c.A524G	D175G
c.524A>T	c.A524T	D175V
c.525C>G or c.525C>A	c.C525G or c.C525A	D175E
c.526A>T	c.A526T	S176C
c.528T>A	c.T528A	S176R
c.529T>A	c.T529A	L177M
c.529T>G	c.T529G	L177V
c.530T>C	c.T530C	L177S

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.530T>G	c.T530G	L177W
c.531G>C	c.G531C	L177F
c.532G>A	c.G532A	E178K
c.532G>C	c.G532C	E178Q
c.533A>C	c.A533C	E178A
c.533A>G	c.A533G	E178G
c.538T>A	c.T538A	L180M
c.538T>G	c.T538G	L180V
c.539T>C	c.T539C	L180S
c.539T>G	c.T539G	L180W
c.540G>C or c.540G>T	c.G540C or c.G540T	L180F
c.541G>A	c.G541A	A181T
c.541G>C	c.G541C	A181P
c.542C>T	c.C542T	A181V
c.544G>T	c.G544T	D182Y
c.545A>C	c.A545C	D182A
c.545A>G	c.A545G	D182G
c.545A>T	c.A545T	D182V
c.546T>A	c.T546A	D182E
c.548G>A	c.G548A	G183D
c.548G>C	c.G548C	G183A
c.550T>A	c.T550A	Y184N
c.550T>C	c.T550C	Y184H
c.551A>C	c.A551C	Y184S
c.551A>G	c.A551G	Y184C
c.551A>T	c.A551T	Y184F
c.553A>C	c.A553C	K185Q
c.553A>G	c.A553G	K185E
c.554A>C	c.A554C	K185T
c.554A>T	c.A554T	K185M
c.555G>C	c.G555C	K185N
c.556C>A	c.C556A	H186N
c.556C>G	c.C556G	H186D
c.556C>T	c.C556T	H186Y
c.557A>T	c.A557T	H186L
c.558C>G	c.C558G	H186Q
c.559_564dup	c.559_564dup	p.M187_S188dup
c.559A>G	c.A559G	M187V
c.559A>T	c.A559T	M187L
c.560T>C	c.T560C	M187T

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.561G>T or c.561G>A or c.561G>C	c.G561T or c.G561A or c.G561C	M187I
c.562T>A	c.T562A	S188T
c.562T>C	c.T562C	S188P
c.562T>G	c.T562G	S188A
c.563C>A	c.C563A	S188Y
c.563C>G	c.C563G	S188C
c.563C>T	c.C563T	S188F
c.565T>G	c.T565G	L189V
c.566T>C	c.T566C	L189S
c.567G>C or c.567G>T	c.G567C or c.G567T	L189F
c.568G>A	c.G568A	A190T
c.568G>T	c.G568T	A190S
c.569C>A	c.C569A	A190D
c.569C>G	c.C569G	A190G
c.569C>T	c.C569T	A190V
c.571C>A	c.C571A	L191M
c.571C>G	c.C571G	L191V
c.572T>A	c.T572A	L191Q
c.574A>C	c.A574C	N192H
c.574A>G	c.A574G	N192D
c.575A>C	c.A575C	N192T
c.575A>G	c.A575G	N192S
c.576T>A	c.T576A	N192K
c.577A>G	c.A577G	R193G
c.577A>T	c.A577T	R193W
c.578G>C	c.G578C	R193T
c.578G>T	c.G578T	R193M
c.[578G>T; 936G>C]	c.G578T/G936C	R193M/Q312H
c.580A>C	c.A580C	T194P
c.580A>G	c.A580G	T194A
c.580A>T or c.581C>G	c.A580T or c.C581G	T194S
c.581C>A	c.C581A	T194N
c.581C>T	c.C581T	T194I
c.583G>A	c.G583A	G195S
c.583G>C	c.G583C	G195R
c.583G>T	c.G583T	G195C
c.584G>T	c.G584T	G195V
c.586A>G	c.A586G	R196G
c.587G>A	c.G587A	R196K
c.587G>C	c.G587C	R196T

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.587G>T	c.G587T	R196I
c.589A>G	c.A589G	S197G
c.589A>T	c.A589T	S197C
c.590G>A	c.G590A	S197N
c.590G>C	c.G590C	S197T
c.590G>T	c.G590T	S197I
c.593T>C	c.T593C	I198T
c.593T>G	c.T593G	I198S
c.594T>G	c.T594G	I198M
c.595G>A	c.G595A	V199M
c.595G>C	c.G595C	V199L
c.596T>A	c.T596A	V199E
c.596T>C	c.T596C	V199A
c.596T>G	c.T596G	V199G
c.598T>A	c.T598A	Y200N
c.599A>C	c.A599C	Y200S
c.599A>G	c.A599G	Y200C
c.601T>A	c.T601A	S201T
c.601T>G	c.T601G	S201A
c.602C>A	c.C602A	S201Y
c.602C>G	c.C602G	S201C
c.602C>T	c.C602T	S201F
c.[602C>T; 937G>T]	c.C602T/G937T	S201F/D313Y
c.607G>C	c.G607C	E203Q
c.608A>C	c.A608C	E203A
c.608A>G	c.A608G	E203G
c.608A>T	c.A608T	E203V
c.609G>C or c.609G>T	c.G609C or c.G609T	E203D
c.610T>G	c.T610G	W204G
c.611G>C	c.G611C	W204S
c.611G>T	c.G611T	W204L
c.613C>A	c.C613A	P205T
c.613C>T	c.C613T	P205S
c.614C>T	c.C614T	P205L
c.616C>A	c.C616A	L206I
c.616C>G	c.C616G	L206V
c.616C>T	c.C616T	L206F
c.617T>A	c.T617A	L206H
c.617T>G	c.T617G	L206R
c.619T>C	c.T619C	Y207H
c.620A>C	c.A620C	Y207S

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.620A>T	c.A620T	Y207F
c.623T>A	c.T623A	M208K
c.623T>G	c.T623G	M208R
c.625T>A	c.T625A	W209R
c.625T>G	c.T625G	W209G
c.627G>C	c.G627C	W209C
c.628C>A	c.C628A	P210T
c.628C>T	c.C628T	P210S
c.629C>A	c.C629A	P210H
c.629C>T	c.C629T	P210L
c.631T>C	c.T631C	F211L
c.631T>G	c.T631G	F211V
c.632T>A	c.T632A	F211Y
c.632T>C	c.T632C	F211S
c.632T>G	c.T632G	F211C
c.635A>C	c.A635C	Q212P
c.636A>T	c.A636T	Q212H
c.637A>C	c.A637C	K213Q
c.637A>G	c.A637G	K213E
c.638A>G	c.A638G	K213R
c.638A>T	c.A638T	K213M
c.640C>A	c.C640A	P214T
c.640C>G	c.C640G	P214A
c.640C>T	c.C640T	P214S
c.641C>A	c.C641A	P214H
c.641C>G	c.C641G	P214R
c.641C>T	c.C641T	P214L
c.643A>C	c.A643C	N215H
c.643A>G	c.A643G	N215D
c.643A>T	c.A643T	N215Y
c.644A>C	c.A644C	N215T
c.644A>G	c.A644G	N215S
c.[644A>G; 937G>T]	c.A644G/G937T	N215S/D313Y
c.644A>T	c.A644T	N215I
c.645T>A	c.T645A	N215K
c.646T>A	c.T646A	Y216N
c.646T>C	c.T646C	Y216H
c.646T>G	c.T646G	Y216D
c.647A>C	c.A647C	Y216S
c.647A>G	c.A647G	Y216C
c.647A>T	c.A647T	Y216F

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.649A>C	c.A649C	T217P
c.649A>G	c.A649G	T217A
c.649A>T	c.A649T	T217S
c.650C>A	c.C650A	T217K
c.650C>G	c.C650G	T217R
c.650C>T	c.C650T	T217I
c.652G>A	c.G652A	E218K
c.652G>C	c.G652C	E218Q
c.653A>C	c.A653C	E218A
c.653A>G	c.A653G	E218G
c.653A>T	c.A653T	E218V
c.654A>T	c.A654T	E218D
c.655A>C	c.A655C	I219L
c.655A>T	c.A655T	I219F
c.656T>A	c.T656A	I219N
c.656T>C	c.T656C	I219T
c.656T>G	c.T656G	I219S
c.657C>G	c.C657G	I219M
c.659G>A	c.G659A	R220Q
c.659G>C	c.G659C	R220P
c.659G>T	c.G659T	R220L
c.661C>A	c.C661A	Q221K
c.661C>G	c.C661G	Q221E
c.662A>C	c.A662C	Q221P
c.662A>G	c.A662G	Q221R
c.662A>T	c.A662T	Q221L
c.663G>C	c.G663C	Q221H
c.664T>A	c.T664A	Y222N
c.664T>C	c.T664C	Y222H
c.664T>G	c.T664G	Y222D
c.665A>C	c.A665C	Y222S
c.665A>G	c.A665G	Y222C
c.670A>C	c.A670C	N224H
c.671A>C	c.A671C	N224T
c.671A>G	c.A671G	N224S
c.673C>G	c.C673G	H225D
c.679C>G	c.C679G	R227G
c.682A>C	c.A682C	N228H
c.682A>G	c.A682G	N228D
c.683A>C	c.A683C	N228T
c.683A>G	c.A683G	N228S

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.683A>T	c.A683T	N228I
c.685T>A	c.T685A	F229I
c.686T>A	c.T686A	F229Y
c.686T>C	c.T686C	F229S
c.687T>A or c.687T>G	c.T687A or c.T687G	F229L
c.688G>C	c.G688C	A230P
c.689C>A	c.C689A	A230D
c.689C>G	c.C689G	A230G
c.689C>T	c.C689T	A230V
c.694A>C	c.A694C	I232L
c.694A>G	c.A694G	I232V
c.695T>C	c.T695C	I232T
c.696T>G	c.T696G	I232M
c.698A>C	c.A698C	D233A
c.698A>G	c.A698G	D233G
c.698A>T	c.A698T	D233V
c.699T>A	c.T699A	D233E
c.703T>A	c.T703A	S235T
c.703T>G	c.T703G	S235A
c.710A>T	c.A710T	K237I
c.712A>G	c.A712G	S238G
c.712A>T	c.A712T	S238C
c.713G>A	c.G713A	S238N
c.713G>C	c.G713C	S238T
c.713G>T	c.G713T	S238I
c.715A>T	c.A715T	I239L
c.716T>C	c.T716C	I239T
c.717A>G	c.A717G	I239M
c.718A>G	c.A718G	K240E
c.719A>G	c.A719G	K240R
c.719A>T	c.A719T	K240M
c.720G>C or c.720G>T	c.G720C or c.G720T	K240N
c.721A>T	c.A721T	S241C
c.722G>C	c.G722C	S241T
c.722G>T	c.G722T	S241I
c.724A>C	c.A724C	I242L
c.724A>G	c.A724G	I242V
c.724A>T	c.A724T	I242F
c.725T>A	c.T725A	I242N
c.725T>C	c.T725C	I242T
c.725T>G	c.T725G	I242S

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.726C>G	c.C726G	I242M
c.727T>A	c.T727A	L243M
c.727T>G	c.T727G	L243V
c.728T>C	c.T728C	L243S
c.728T>G	c.T728G	L243W
c.729G>C or c.729G>T	c.G729C or c.G729T	L243F
c.730G>A	c.G730A	D244N
c.730G>C	c.G730C	D244H
c.730G>T	c.G730T	D244Y
c.731A>C	c.A731C	D244A
c.731A>G	c.A731G	D244G
c.731A>T	c.A731T	D244V
c.732C>G	c.C732G	D244E
c.733T>G	c.T733G	W245G
c.735G>C	c.G735C	W245C
c.736A>G	c.A736G	T246A
c.737C>A	c.C737A	T246K
c.737C>G	c.C737G	T246R
c.737C>T	c.C737T	T246I
c.739T>A	c.T739A	S247T
c.739T>G	c.T739G	S247A
c.740C>A	c.C740A	S247Y
c.740C>G	c.C740G	S247C
c.740C>T	c.C740T	S247F
c.742T>G	c.T742G	F248V
c.743T>A	c.T743A	F248Y
c.743T>G	c.T743G	F248C
c.744T>A	c.T744A	F248L
c.745A>C	c.A745C	N249H
c.745A>G	c.A745G	N249D
c.745A>T	c.A745T	N249Y
c.746A>C	c.A746C	N249T
c.746A>G	c.A746G	N249S
c.746A>T	c.A746T	N249I
c.747C>G or c.747C>A	c.C747G or c.C747A	N249K
c.748C>A	c.C748A	Q250K
c.748C>G	c.C748G	Q250E
c.749A>C	c.A749C	Q250P
c.749A>G	c.A749G	Q250R
c.749A>T	c.A749T	Q250L
c.750G>C	c.G750C	Q250H

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.751G>A	c.G751A	E251K
c.751G>C	c.G751C	E251Q
c.752A>G	c.A752G	E251G
c.752A>T	c.A752T	E251V
c.754A>G	c.A754G	R252G
c.757A>G	c.A757G	I253V
c.757A>T	c.A757T	I253F
c.758T>A	c.T758A	I253N
c.758T>C	c.T758C	I253T
c.758T>G	c.T758G	I253S
c.760-762delGTT or c.761-763del	c.760_762delGTT or c.761_763del	p.V254del
c.760G>T	c.G760T	V254F
c.761T>A	c.T761A	V254D
c.761T>C	c.T761C	V254A
c.761T>G	c.T761G	V254G
c.763G>A	c.G763A	D255N
c.763G>C	c.G763C	D255H
c.763G>T	c.G763T	D255Y
c.764A>C	c.A764C	D255A
c.764A>T	c.A764T	D255V
c.765T>A	c.T765A	D255E
c.766G>C	c.G766C	V256L
c.767T>A	c.T767A	V256D
c.767T>G	c.T767G	V256G
c.769G>A	c.G769A	A257T
c.769G>C	c.G769C	A257P
c.769G>T	c.G769T	A257S
c.770C>G	c.C770G	A257G
c.770C>T	c.C770T	A257V
c.772G>C or c.772G>A	c.G772C or c.G772A	G258R
c.773G>A	c.G773A	G258E
c.773G>T	c.G773T	G258V
c.775C>A	c.C775A	P259T
c.775C>G	c.C775G	P259A
c.775C>T	c.C775T	P259S
c.776C>A	c.C776A	P259Q
c.776C>G	c.C776G	P259R
c.776C>T	c.C776T	P259L
c.778G>T	c.G778T	G260W
c.779G>A	c.G779A	G260E

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.779G>C	c.G779C	G260A
c.781G>A	c.G781A	G261S
c.781G>C	c.G781C	G261R
c.781G>T	c.G781T	G261C
c.782G>C	c.G782C	G261A
c.787A>C	c.A787C	N263H
c.788A>C	c.A788C	N263T
c.788A>G	c.A788G	N263S
c.790G>A	c.G790A	D264N
c.790G>C	c.G790C	D264H
c.790G>T	c.G790T	D264Y
c.793C>G	c.C793G	P265A
c.794C>A	c.C794A	P265Q
c.794C>T	c.C794T	P265L
c.799A>G	c.A799G	M267V
c.799A>T	c.A799T	M267L
c.800T>C	c.T800C	M267T
c.802T>A	c.T802A	L268I
c.804A>T	c.A804T	L268F
c.805G>A	c.G805A	V269M
c.805G>C	c.G805C	V269L
c.806T>C	c.T806C	V269A
c.808A>C	c.A808C	I270L
c.808A>G	c.A808G	I270V
c.809T>C	c.T809C	I270T
c.809T>G	c.T809G	I270S
c.810T>G	c.T810G	I270M
c.811G>A	c.G811A	G271S
c.[811G>A; 937G>T]	c.G811A/G937T	G271S/D313Y
c.812G>A	c.G812A	G271D
c.812G>C	c.G812C	G271A
c.814A>G	c.A814G	N272D
c.818T>A	c.T818A	F273Y
c.823C>A	c.C823A	L275I
c.823C>G	c.C823G	L275V
c.827G>A	c.G827A	S276N
c.827G>C	c.G827C	S276T
c.829T>G	c.T829G	W277G
c.830G>T	c.G830T	W277L
c.831G>T or c.831G>C	c.G831T or c.G831C	W277C
c.832A>T	c.A832T	N278Y

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.833A>T	c.A833T	N278I
c.835C>G	c.C835G	Q279E
c.838C>A	c.C838A	Q280K
c.839A>G	c.A839G	Q280R
c.839A>T	c.A839T	Q280L
c.840A>T or c.840A>C	c.A840T or c.A840C	Q280H
c.841G>C	c.G841C	V281L
c.842T>A	c.T842A	V281E
c.842T>C	c.T842C	V281A
c.842T>G	c.T842G	V281G
c.844A>G	c.A844G	T282A
c.844A>T	c.A844T	T282S
c.845C>T	c.C845T	T282I
c.847C>G	c.C847G	Q283E
c.848A>T	c.A848T	Q283L
c.849G>C	c.G849C	Q283H
c.850A>G	c.A850G	M284V
c.850A>T	c.A850T	M284L
c.851T>C	c.T851C	M284T
c.852G>C	c.G852C	M284I
c.853G>A	c.G853A	A285T
c.854C>G	c.C854G	A285G
c.854C>T	c.C854T	A285V
c.856C>G	c.C856G	L286V
c.856C>T	c.C856T	L286F
c.857T>A	c.T857A	L286H
c.860G>T	c.G860T	W287L
c.862G>C	c.G862C	A288P
c.862G>T	c.G862T	A288S
c.863C>G	c.C863G	A288G
c.863C>T	c.C863T	A288V
c.865A>C	c.A865C	I289L
c.865A>G	c.A865G	I289V
c.866T>C	c.T866C	I289T
c.866T>G	c.T866G	I289S
c.868A>C or c.868A>T	c.A868C or c.A868T	M290L
c.868A>G	c.A868G	M290V
c.869T>C	c.T869C	M290T
c.870G>A or c.870G>C or c.870G>T	c.G870A or c.G870C or c.G870T	M290I
c.871G>A	c.G871A	A291T

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.871G>T	c.G871T	A291S
c.872C>G	c.C872G	A291G
c.874G>T	c.G874T	A292S
c.875C>G	c.C875G	A292G
c.877C>A	c.C877A	P293T
c.880T>A	c.T880A	L294I
c.880T>G	c.T880G	L294V
c.881T>C	c.T881C	L294S
c.882A>T	c.A882T	L294F
c.883T>A	c.T883A	F295I
c.883T>G	c.T883G	F295V
c.884T>A	c.T884A	F295Y
c.884T>C	c.T884C	F295S
c.884T>G	c.T884G	F295C
c.886A>G	c.A886G	M296V
c.886A>T or c.886A>C	c.A886T or c.A886C	M296L
c.887T>C	c.T887C	M296T
c.888G>A or c.888G>T or c.888G>C	c.G888A or c.G888T or c.G888C	M296I
c.889T>A	c.T889A	S297T
c.892A>G	c.A892G	N298D
c.893A>C	c.A893C	N298T
c.893A>G	c.A893G	N298S
c.893A>T	c.A893T	N298I
c.895G>A	c.G895A	D299N
c.895G>C	c.G895C	D299H
c.897C>G or c.897C>A	c.C897G or c.C897A	D299E
c.898C>A	c.C898A	L300I
c.898C>G	c.C898G	L300V
c.898C>T	c.C898T	L300F
c.899T>C	c.T899C	L300P
c.901C>G	c.C901G	R301G
c.902G>A	c.G902A	R301Q
c.902G>C	c.G902C	R301P
c.902G>T	c.G902T	R301L
c.904C>A	c.C904A	H302N
c.904C>G	c.C904G	H302D
c.904C>T	c.C904T	H302Y
c.905A>T	c.A905T	H302L
c.907A>G	c.A907G	I303V
c.907A>T	c.A907T	I303F

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.908T>A	c.T908A	I303N
c.908T>C	c.T908C	I303T
c.908T>G	c.T908G	I303S
c.911G>A	c.G911A	S304N
c.911G>C	c.G911C	S304T
c.911G>T	c.G911T	S304I
c.916C>G	c.C916G	Q306E
c.917A>C	c.A917C	Q306P
c.917A>T	c.A917T	Q306L
c.919G>A	c.G919A	A307T
c.919G>C	c.G919C	A307P
c.919G>T	c.G919T	A307S
c.920C>A	c.C920A	A307D
c.920C>G	c.C920G	A307G
c.920C>T	c.C920T	A307V
c.922A>C	c.A922C	K308Q
c.922A>G	c.A922G	K308E
c.923A>G	c.A923G	K308R
c.923A>T	c.A923T	K308I
c.924A>T or c.924A>C	c.A924T or c.A924C	K308N
c.925G>A	c.G925A	A309T
c.925G>C	c.G925C	A309P
c.926C>A	c.C926A	A309D
c.926C>T	c.C926T	A309V
c.928C>A	c.C928A	L310I
c.928C>G	c.C928G	L310V
c.928C>T	c.C928T	L310F
c.931C>A	c.C931A	L311I
c.931C>G	c.C931G	L311V
c.934C>A	c.C934A	Q312K
c.934C>G	c.C934G	Q312E
c.935A>T	c.A935T	Q312L
c.935A>G	c.A935G	Q312R
c.936G>T or c.936G>C	c.G936T or c.G936C	Q312H
c.937G>T	c.G937T	D313Y
c.[937G>T; 1232G>A]	c.G937T/G1232A	D313Y/G411D
c.938A>G	c.A938G	D313G
c.938A>T	c.A938T	D313V
c.939T>A	c.T939A	D313E
c.940A>G	c.A940G	K314E
c.941A>C	c.A941C	K314T

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.941A>T	c.A941T	K314M
c.942G>C	c.G942C	K314N
c.943G>A	c.G943A	D315N
c.943G>C	c.G943C	D315H
c.943G>T	c.G943T	D315Y
c.944A>C	c.A944C	D315A
c.944A>G	c.A944G	D315G
c.944A>T	c.A944T	D315V
c.946G>A	c.G946A	V316I
c.946G>C	c.G946C	V316L
c.947T>C	c.T947C	V316A
c.947T>G	c.T947G	V316G
c.949A>C	c.A949C	I317L
c.949A>G	c.A949G	I317V
c.950T>C	c.T950C	I317T
c.951T>G	c.T951G	I317M
c.952G>A	c.G952A	A318T
c.952G>C	c.G952C	A318P
c.953C>A	c.C953A	A318D
c.953C>T	c.C953T	A318V
c.955A>T	c.A955T	I319F
c.956T>C	c.T956C	I319T
c.957C>G	c.C957G	I319M
c.958A>C	c.A958C	N320H
c.959A>C	c.A959C	N320T
c.959A>G	c.A959G	N320S
c.959A>T	c.A959T	N320I
c.961C>A	c.C961A	Q321K
c.962A>G	c.A962G	Q321R
c.962A>T	c.A962T	Q321L
c.963G>C or c.963G>T	c.G963C or c.G963T	Q321H
c.964G>A	c.G964A	D322N
c.964G>C	c.G964C	D322H
c.965A>C	c.A965C	D322A
c.965A>T	c.A965T	D322V
c.966C>A or c.966C>G	c.C966A or c.C966G	D322E
c.967C>A	c.C967A	P323T
c.968C>G	c.C968G	P323R
c.970T>G	c.T970G	L324V
c.971T>G	c.T971G	L324W
c.973G>A	c.G973A	G325S

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.973G>C	c.G973C	G325R
c.973G>T	c.G973T	G325C
c.974G>C	c.G974C	G325A
c.974G>T	c.G974T	G325V
c.976A>C	c.A976C	K326Q
c.976A>G	c.A976G	K326E
c.977A>C	c.A977C	K326T
c.977A>G	c.A977G	K326R
c.977A>T	c.A977T	K326M
c.978G>C or c.978G>T	c.G978C or c.G978T	K326N
c.979C>G	c.C979G	Q327E
c.980A>C	c.A980C	Q327P
c.980A>T	c.A980T	Q327L
c.981A>T or c.981A>C	c.A981T or c.A981C	Q327H
c.983G>C	c.G983C	G328A
c.985T>A	c.T985A	Y329N
c.985T>C	c.T985C	Y329H
c.985T>G	c.T985G	Y329D
c.986A>G	c.A986G	Y329C
c.986A>T	c.A986T	Y329F
c.988C>A	c.C988A	Q330K
c.988C>G	c.C988G	Q330E
c.989A>C	c.A989C	Q330P
c.989A>G	c.A989G	Q330R
c.990G>C	c.G990C	Q330H
c.991C>G	c.C991G	L331V
c.992T>A	c.T992A	L331H
c.992T>C	c.T992C	L331P
c.992T>G	c.T992G	L331R
c.994A>G	c.A994G	R332G
c.995G>C	c.G995C	R332T
c.995G>T	c.G995T	R332I
c.996A>T	c.A996T	R332S
c.997C>G	c.C997G	Q333E
c.998A>C	c.A998C	Q333P
c.998A>T	c.A998T	Q333L
c.1000G>C	c.G1000C	G334R
c.1001G>A	c.G1001A	G334E
c.1001G>T	c.G1001T	G334V
c.1003G>T	c.G1003T	D335Y
c.1004A>C	c.A1004C	D335A

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1004A>G	c.A1004G	D335G
c.1004A>T	c.A1004T	D335V
c.1005C>G	c.C1005G	D335E
c.1006A>G	c.A1006G	N336D
c.1006A>T	c.A1006T	N336Y
c.1007A>C	c.A1007C	N336T
c.1007A>G	c.A1007G	N336S
c.1007A>T	c.A1007T	N336I
c.1009T>G	c.T1009G	F337V
c.1010T>A	c.T1010A	F337Y
c.1010T>C	c.T1010C	F337S
c.1010T>G	c.T1010G	F337C
c.1011T>A	c.T1011A	F337L
c.1012G>A	c.G1012A	E338K
c.1013A>C	c.A1013C	E338A
c.1013A>G	c.A1013G	E338G
c.1013A>T	c.A1013T	E338V
c.1014A>T	c.A1014T	E338D
c.1015G>A	c.G1015A	V339M
c.1016T>A	c.T1016A	V339E
c.1016T>C	c.T1016C	V339A
c.1021G>C	c.G1021C	E341Q
c.1022A>C	c.A1022C	E341A
c.1027C>A	c.C1027A	P343T
c.1027C>G	c.C1027G	P343A
c.1027C>T	c.C1027T	P343S
c.1028C>T	c.C1028T	P343L
c.1030C>G	c.C1030G	L344V
c.1030C>T	c.C1030T	L344F
c.1031T>G	c.T1031G	L344R
c.1033T>C	c.T1033C	S345P
c.1036G>T	c.G1036T	G346C
c.1037G>A	c.G1037A	G346D
c.1037G>C	c.G1037C	G346A
c.1037G>T	c.G1037T	G346V
c.1039T>A	c.T1039A	L347I
c.1043C>A	c.C1043A	A348D
c.1046G>C	c.G1046C	W349S
c.1046G>T	c.G1046T	W349L
c.1047G>C	c.G1047C	W349C
c.1048G>A	c.G1048A	A350T

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1048G>T	c.G1048T	A350S
c.1049C>G	c.C1049G	A350G
c.1049C>T	c.C1049T	A350V
c.1052T>A	c.T1052A	V351E
c.1052T>C	c.T1052C	V351A
c.1054G>A	c.G1054A	A352T
c.1054G>T	c.G1054T	A352S
c.1055C>G	c.C1055G	A352G
c.1055C>T	c.C1055T	A352V
c.1057A>T	c.A1057T	M353L
c.1058T>A	c.T1058A	M353K
c.1058T>C	c.T1058C	M353T
c.1061T>A	c.T1061A	I354K
c.1061T>G	c.T1061G	I354R
c.1063A>C	c.A1063C	N355H
c.1063A>G	c.A1063G	N355D
c.1063A>T	c.A1063T	N355Y
c.1064A>G	c.A1064G	N355S
c.1066C>G	c.C1066G	R356G
c.1066C>T	c.C1066T	R356W
c.1067G>A	c.G1067A	R356Q
c.1067G>C	c.G1067C	R356P
c.1067G>T	c.G1067T	R356L
c.1069C>G	c.C1069G	Q357E
c.1072G>C	c.G1072C	E358Q
c.1073A>C	c.A1073C	E358A
c.1073A>G	c.A1073G	E358G
c.1074G>T or c.1074G>C	c.G1074T or c.G1074C	E358D
c.1075A>C	c.A1075C	I359L
c.1075A>G	c.A1075G	I359V
c.1075A>T	c.A1075T	I359F
c.1076T>A	c.T1076A	I359N
c.1076T>C	c.T1076C	I359T
c.1076T>G	c.T1076G	I359S
c.1078G>A	c.G1078A	G360S
c.1078G>C	c.G1078C	G360R
c.1078G>T	c.G1078T	G360C
c.1079G>A	c.G1079A	G360D
c.1079G>C	c.G1079C	G360A
c.1082G>A	c.G1082A	G361E
c.1082G>C	c.G1082C	G361A

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1084C>A	c.C1084A	P362T
c.1084C>G	c.C1084G	P362A
c.1084C>T	c.C1084T	P362S
c.1085C>A	c.C1085A	P362H
c.1085C>G	c.C1085G	P362R
c.1085C>T	c.C1085T	P362L
c.1087C>A	c.C1087A	R363S
c.1087C>G	c.C1087G	R363G
c.1087C>T	c.C1087T	R363C
c.1088G>A	c.G1088A	R363H
c.1088G>T	c.G1088T	R363L
c.1090T>C	c.T1090C	S364P
c.1091C>G	c.C1091G	S364C
c.1093T>A	c.T1093A	Y365N
c.1093T>G	c.T1093G	Y365D
c.1094A>C	c.A1094C	Y365S
c.1094A>T	c.A1094T	Y365F
c.1096A>C	c.A1096C	T366P
c.1096A>T	c.A1096T	T366S
c.1097C>A	c.C1097A	T366N
c.1097C>T	c.C1097T	T366I
c.1099A>C	c.A1099C	I367L
c.1099A>T	c.A1099T	I367F
c.1101C>G	c.C1101G	I367M
c.1102G>A	c.G1102A	A368T
c.1102G>C	c.G1102C	A368P
c.1103C>G	c.C1103G	A368G
c.1105G>A	c.G1105A	V369I
c.1105G>C	c.G1105C	V369L
c.1105G>T	c.G1105T	V369F
c.1106T>C	c.T1106C	V369A
c.1106T>G	c.T1106G	V369G
c.1108G>A	c.G1108A	A370T
c.1108G>C	c.G1108C	A370P
c.1109C>A	c.C1109A	A370D
c.1109C>G	c.C1109G	A370G
c.1109C>T	c.C1109T	A370V
c.1111T>A	c.T1111A	S371T
c.1112C>G	c.C1112G	S371C
c.1117G>A	c.G1117A	G373S
c.1117G>T	c.G1117T	G373C

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1118G>C	c.G1118C	G373A
c.1120A>G	c.A1120G	K374E
c.1121A>C	c.A1121C	K374T
c.1121A>G	c.A1121G	K374R
c.1121A>T	c.A1121T	K374I
c.1123G>C	c.G1123C	G375R
c.1124G>A	c.G1124A	G375E
c.1124G>C	c.G1124C	G375A
c.1126G>A	c.G1126A	V376M
c.1126G>C	c.G1126C	V376L
c.1127T>A	c.T1127A	V376E
c.1127T>G	c.T1127G	V376G
c.1129G>A	c.G1129A	A377T
c.1129G>C	c.G1129C	A377P
c.1129G>T	c.G1129T	A377S
c.1130C>G	c.C1130G	A377G
c.1135A>G	c.A1135G	N379D
c.1136A>C	c.A1136C	N379T
c.1136A>T	c.A1136T	N379I
c.1137T>A	c.T1137A	N379K
c.1138C>A	c.C1138A	P380T
c.1138C>G	c.C1138G	P380A
c.1139C>A	c.C1139A	P380H
c.1139C>G	c.C1139G	P380R
c.1139C>T	c.C1139T	P380L
c.1142C>A	c.C1142A	A381D
c.1147T>A	c.T1147A	F383I
c.1148T>A	c.T1148A	F383Y
c.1148T>G	c.T1148G	F383C
c.1150A>T	c.A1150T	I384F
c.1151T>C	c.T1151C	I384T
c.1152C>G	c.C1152G	I384M
c.1153A>G	c.A1153G	T385A
c.1154C>T	c.C1154T	T385I
c.1156C>A	c.C1156A	Q386K
c.1157A>T	c.A1157T	Q386L
c.1158G>C	c.G1158C	Q386H
c.1159C>A	c.C1159A	L387I
c.1159C>T	c.C1159T	L387F
c.1160T>A	c.T1160A	L387H
c.1160T>G	c.T1160G	L387R

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1162C>A	c.C1162A	L388I
c.1162C>G	c.C1162G	L388V
c.1162C>T	c.C1162T	L388F
c.1163T>A	c.T1163A	L388H
c.1163T>G	c.T1163G	L388R
c.1168G>A	c.G1168A	V390M
c.1171A>C	c.A1171C	K391Q
c.1171A>G	c.A1171G	K391E
c.1172A>C	c.A1172C	K391T
c.1172A>G	c.A1172G	K391R
c.1172A>T	c.A1172T	K391I
c.1173A>T	c.A1173T	K391N
c.1174A>G	c.A1174G	R392G
c.1174A>T	c.A1174T	R392W
c.1175G>A	c.G1175A	R392K
c.1175G>C	c.G1175C	R392T
c.1175G>T	c.G1175T	R392M
c.1177A>C	c.A1177C	K393Q
c.1177A>G	c.A1177G	K393E
c.1178A>C	c.A1178C	K393T
c.1179G>C	c.G1179C	K393N
c.1180C>A	c.C1180A	L394I
c.1181T>A	c.T1181A	L394Q
c.1181T>C	c.T1181C	L394P
c.1181T>G	c.T1181G	L394R
c.1183G>C	c.G1183C	G395R
c.1184G>A	c.G1184A	G395E
c.1184G>C	c.G1184C	G395A
c.1186T>A	c.T1186A	F396I
c.1186T>G	c.T1186G	F396V
c.1187T>G	c.T1187G	F396C
c.1188C>G	c.C1188G	F396L
c.1189T>A	c.T1189A	Y397N
c.1189T>C	c.T1189C	Y397H
c.1190A>C	c.A1190C	Y397S
c.1190A>G	c.A1190G	Y397C
c.1190A>T	c.A1190T	Y397F
c.1192G>A	c.G1192A	E398K
c.1192G>C	c.G1192C	E398Q
c.1193A>G	c.A1193G	E398G
c.1195T>A	c.T1195A	W399R

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1195T>G	c.T1195G	W399G
c.1198A>C	c.A1198C	T400P
c.1198A>G	c.A1198G	T400A
c.1198A>T	c.A1198T	T400S
c.1199C>A	c.C1199A	T400N
c.1199C>T	c.C1199T	T400I
c.1201T>A	c.T1201A	S401T
c.1201T>G	c.T1201G	S401A
c.1202_1203insGACTTC	c.1202_1203insGACTTC	p.T400_S401dup
c.1202C>T	c.C1202T	S401L
c.1204A>G	c.A1204G	R402G
c.1204A>T	c.A1204T	R402W
c.1205G>C	c.G1205C	R402T
c.1205G>T	c.G1205T	R402M
c.1206G>C	c.G1206C	R402S
c.1207T>G	c.T1207G	L403V
c.1208T>C	c.T1208C	L403S
c.1209A>T	c.A1209T	L403F
c.1210A>G	c.A1210G	R404G
c.1211G>A	c.G1211A	R404K
c.1211G>C	c.G1211C	R404T
c.1211G>T	c.G1211T	R404I
c.1212A>T	c.A1212T	R404S
c.1213A>G	c.A1213G	S405G
c.1216C>G	c.C1216G	H406D
c.1217A>T	c.A1217T	H406L
c.1218C>G	c.C1218G	H406Q
c.1219A>T	c.A1219T	I407L
c.1220T>C	c.T1220C	I407T
c.1221A>G	c.A1221G	I407M
c.1222A>C	c.A1222C	N408H
c.1222A>G	c.A1222G	N408D
c.1222A>T	c.A1222T	N408Y
c.1223A>C	c.A1223C	N408T
c.1225C>A	c.C1225A	P409T
c.1225C>G	c.C1225G	P409A
c.1225C>T	c.C1225T	P409S
c.1226C>T	c.C1226T	P409L
c.1228A>G	c.A1228G	T410A
c.1228A>T	c.A1228T	T410S
c.1229C>T	c.C1229T	T410I

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1231G>A	c.G1231A	G411S
c.1231G>T	c.G1231T	G411C
c.1232G>A	c.G1232A	G411D
c.1232G>C	c.G1232C	G411A
c.1232G>T	c.G1232T	G411V
c.1234A>C	c.A1234C	T412P
c.1234A>G	c.A1234G	T412A
c.1234A>T	c.A1234T	T412S
c.1235C>A	c.C1235A	T412N
c.1235C>T	c.C1235T	T412I
c.1237G>A	c.G1237A	V413I
c.1237G>T	c.G1237T	V413F
c.1238T>G	c.T1238G	V413G
c.1240T>G	c.T1240G	L414V
c.1242G>C	c.G1242C	L414F
c.1243C>A	c.C1243A	L415I
c.1244T>A	c.T1244A	L415H
c.1246C>G	c.C1246G	Q416E
c.1247A>T	c.A1247T	Q416L
c.1248G>C	c.G1248C	Q416H
c.1249C>A	c.C1249A	L417I
c.1252G>A	c.G1252A	E418K
c.1252G>C	c.G1252C	E418Q
c.1253A>C	c.A1253C	E418A
c.1253A>G	c.A1253G	E418G
c.1254A>T	c.A1254T	E418D
c.1255A>G	c.A1255G	N419D
c.1255A>T	c.A1255T	N419Y
c.1256A>C	c.A1256C	N419T
c.1256A>G	c.A1256G	N419S
c.1256A>T	c.A1256T	N419I
c.1258A>C	c.A1258C	T420P
c.1258A>T	c.A1258T	T420S
c.1259C>A	c.C1259A	T420K
c.1259C>G	c.C1259G	T420R
c.1261A>G	c.A1261G	M421V
c.1261A>T	c.A1261T	M421L
c.1262T>A	c.T1262A	M421K
c.1262T>C	c.T1262C	M421T
c.1262T>G	c.T1262G	M421R
c.1263G>C	c.G1263C	M421I

Table 3: Galafold (migalastat) Amenability Table[†]

Nucleotide change	Nucleotide change	Protein sequence change
c.1265A>C	c.A1265C	Q422P
c.1267A>T	c.A1267T	M423L
c.1268T>A	c.T1268A	M423K
c.1268T>C	c.T1268C	M423T
c.1269G>C	c.G1269C	M423I
c.1271C>T	c.C1271T	S424L
c.1275A>C	c.A1275C	L425F
c.1279G>A	c.G1279A	D427N
c.1286T>G	c.T1286G	L429R

[†] If a double mutation is present on the same chromosome (males and females), that patient is amenable if the double mutation is present in one entry in Table 3 (eg, D55V/Q57L). If a double mutation is present on different chromosomes (only in females), that patient is amenable if either one of the individual mutations is present in Table 3.

Pharmacodynamic effects

Treatment with Galafold in Phase 2 pharmacodynamic trials generally resulted in increases in endogenous α-Gal A activity in white blood cells (WBCs), as well as in skin and kidney for the majority of patients. In patients with amenable mutations, GL-3 levels tended to decrease in urine and in kidney interstitial capillaries.

Clinical trials

The clinical efficacy and safety of Galafold have been evaluated in two Phase 3 pivotal trials and two open-label extension trials. All patients received the recommended dosage of 123 mg Galafold every other day.

The first Phase 3 trial AT1001-012 (ATTRACT) was an 18-month, randomised, open-label active comparator trial that evaluated the efficacy and safety of Galafold compared to enzyme replacement therapy (ERT) (agalsidase beta, agalsidase alfa) in 52 patients (87% Caucasian, 12% Asian and 2% Other, 22 male and 30 female patients, mean age of 49.0 years) with Fabry disease who were receiving ERT prior to trial entry and who have amenable mutations (ERT-experienced trial). The study was structured in two periods. During the first period (18 months) ERT-experienced patients were randomised to switch from ERT to migalastat or continue with ERT. The second period was an optional 12-month open-label extension (OLE) in which all subjects received migalastat.

The second Phase 3 trial AT1001-011 (FACETS) was a 6-month, randomised, double-blind placebo-controlled trial (through Month 6) with an 18-month open-label period to evaluate the efficacy and safety of Galafold in 50 patients (96% Caucasian and 4% Other, 18 male and 32 female patients, mean age of 43.2 years) with Fabry disease who were naïve to ERT, or had previously been on ERT and had stopped for at least 6 months, and who have amenable mutations (ERT-naïve trial).

The first OLE trial (AT1001-041) included patients from Phase 2 and Phase 3 studies and has completed. The mean extent of exposure to the marketed dose of Galafold 123 mg QOD in patients completing study AT1001-041 was 3.57 (±1.23) years (n=85). The maximum exposure was 5.6 years.

The second OLE trial (AT1001-042) included patients that either transferred from OLE study AT1001-041 or directly from Phase 3 study ATTRACT. The mean (SD) and median extent of exposure to the marketed dose of Galafold 123 mg QOD in patients this study was 32.3 (±12.3) months and 36.75 months (n=82), respectively. The maximum exposure was 51.9 months.

Renal function

In the ERT-experienced trial, renal function remained stable for up to 18 months of treatment with Galafold. Mean annualised rate of change in $eGFR_{CKD-EPI}$ was -0.40 mL/min/1.73 m^2 (95% CI: -2.272, 1.478) in the Galafold group compared to -1.03 mL/min/1.73 m^2 (95% CI: -3.636, 1.575) in the ERT group.

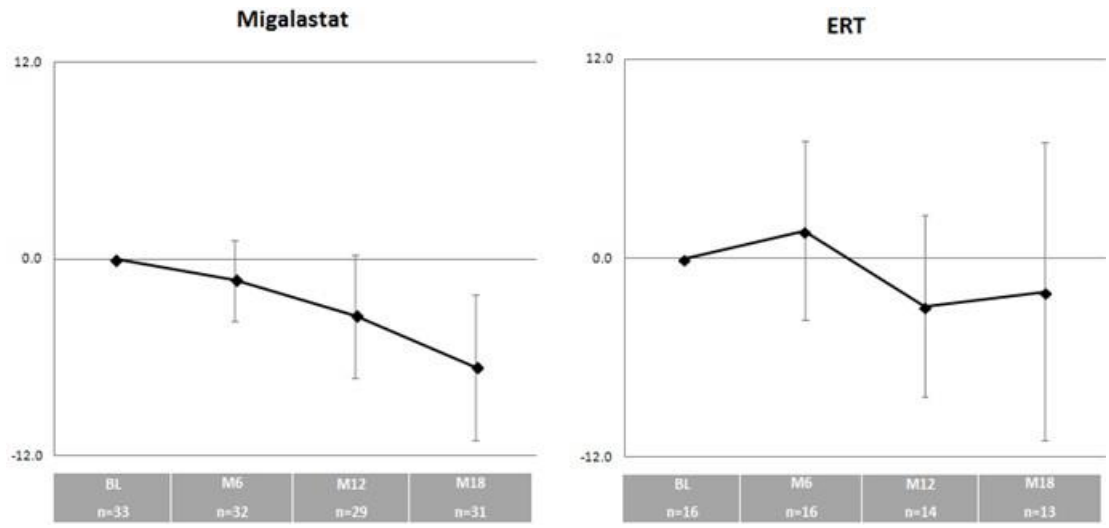
In the ERT-naïve trial and open label extension, renal function remained stable for 3 years of treatment with Galafold. After an average of 36 months of treatment, the mean annualised rate of change in $eGFR_{CKD-EPI}$ was -0.81 mL/min/1.73 m^2 (95% CI: -2.00, 0.37). No clinically significant differences were observed during the initial 6-month placebo-controlled period.

Data for the annualised rate of change for $eGFR_{CKD-EPI}$ was pooled for ERT-naïve subjects and ERT-experienced subjects with amenable mutations and is partly derived from the uncontrolled, open-label extension studies. Whilst acknowledging the study limitations, these results are consistent with stabilisation of renal function up to 8.6 years in annualised rate of change. After a mean duration of 5.2 years, ERT-naïve patients had a mean annualised rate of change from baseline of -1.71 mL/min/1.73 m^2 (CI: -2.83, -0.60; n=47) with a median of -1.06 mL/min/1.73 m^2. After a mean duration of 4.3 years, ERT-experienced patients had a mean annualised rate of change from baseline of -1.78 mL/min/1.73 m^2 (CI: -3.76, 0.20; n=49) with a median of -1.21 mL/min/1.73 m^2.

Left Ventricular Mass Index (LVMi)

In the ERT-experienced trial following 18 months of treatment with migalastat, there was a statistically *significant decrease* in LVMi *(p* <0.05*).* The baseline values were 95.3 g/m^2 for the Galafold arm and 92.9 g/m^2 for the ERT arm and the mean change from baseline in LVMi at Month 18 was -6.6 (95% CI: -11.0, -2.1; n=31) for migalastat and -2.0 (95% CI: -11.0, 7.0; n=13) for ERT (Figure 1).

Figure 1: ATTRACT Study: LVMi Change (Mean and 95% CI) over 18 Months with Migalastat and ERT



In the ERT-naïve trial, Galafold resulted in a statistically significant decrease in LVMi for all patients with amenable mutations (p <0.05); the mean change from baseline in LVMi from Month 18 to 24 was -7.7 (95% CI: -15.4, -0.01; n=27). After follow-up in the open label extension, the mean change from baseline in LVMi from Month 30 to 36 was -17.0 (95% CI: -26.2, -7.9; n=15) (p <0.05) The mean change from baseline in LVMi from Month 18 to 24 in patients with left ventricular hypertrophy at baseline (females with baseline LVMi >95 g/m^2 or males with baseline LVMi >115 g/m^2) was -18.6 (95% CI: -38.2, 1.0; n=8). After follow-up in the open label extension, the mean change from baseline in LVMi in patients with left ventricular hypertrophy at baseline from Month 30 to 36 was -30.0 (95% CI: -57.9, -2.2; n=4). No clinically significant differences in LVMi were observed during the initial 6-month placebo-controlled period.

These results demonstrate that Galafold leads to improvements in cardiac hypertrophy, which is a major risk factor for cardiac complications in Fabry disease.

Data for the mean change in LVMi was pooled for ERT-naïve subjects and ERT-experienced subjects with amenable mutations and is partly derived from the uncontrolled, open-label extension studies. Whilst acknowledging the study limitations and small sample size in this analysis, the mean change in LVMi from AT1001-042 baseline was 1.2 g/m^2 (95% CI: -5.3, 7.7; n=15) and -5.6 g/m^2 (95% CI: -28.5, 17.2; n=4) respectively, and the median change in LVMi from AT1001-042 baseline was 0.41 g/m^2 and 1.02 g/m^2 respectively, for patients treated with Galafold for an average of 2.4 and 2.9 years (up to 4.0 and 4.3 years, respectively).

Disease substrate

In the ERT-naïve trial, Galafold showed statistically significant reductions in plasma lyso-Gb_3 concentrations and kidney interstitial capillary GL-3 inclusions in patients with amenable mutations. Patients randomised to Galafold in Stage 1 demonstrated statistically significant greater reduction (±SEM) in mean interstitial capillary GL-3 deposition (-0.25 ± 0.10; -39%) at Month 6 compared to placebo (+0.07 ± 0.13; +14%) (p=0.008). Patients randomised to placebo in Stage 1 and switched to Galafold at

Month 6 (Stage 2) also demonstrated statistically significant decreases in interstitial capillary GL-3 inclusions at Month 12 (-0.33 ± 0.15; -58%) (p=0.014). Qualitative reductions in GL-3 levels were observed in multiple renal cell types: podocytes, mesangial cells, and glomerular endothelial cells, respectively, over 12 months of treatment with Galafold.

In the ERT-experienced trial, plasma lyso-Gb_3 levels remained low and stable for up to 18 months in patients with amenable mutations switched from ERT to Galafold, and in patients remaining on ERT.

Composite clinical outcomes

In the ERT-experienced trial, analysis of a composite clinical outcome composed of renal, cardiac, and cerebrovascular events, or death, the frequency of events observed in the Galafold treatment group was 29% and was 44% in the ERT group (Table 4).

Table 4: Number (%) of Patients Who Experienced the Composite Clinical Outcome

Component	Galafold (n=34)	ERT (n=18)
Renal	8 (24%)	6 (33%)
Cardiac	2 (6%)	3 (17%)
Cerebrovascular	0 (0%)	1 (6%)
Death	0 (0%)	0 (0%)
Any	10 (29%)	8* (44%)

* 2 ERT-experienced patients each had 1 cardiac and 1 renal event.
Renal events included increased proteinuria and decreased GFR (Galafold and ERT treatment groups); Cardiac events included arrhythmia (Galafold and ERT treatment groups) and cardiac failure (ERT treatment group only); Cerebrovascular event was transient ischemic attack.

Patient-Reported outcome - Gastrointestinal Symptoms Rating Scale

In the ERT-naïve trial, analyses of the Gastrointestinal Symptoms Rating Scale demonstrated that treatment with Galafold was associated with statistically significant (p <0.05) improvements versus placebo from baseline to Month 6 in the diarrhoea domain, and in the reflux domain for patients with symptoms at baseline. During the open-label extension, statistically significant (p <0.05) improvements from baseline were observed in the diarrhoea and indigestion domains, with a trend of improvement in the constipation domain.

Patient-Reported outcome – Short Form-36 (SF-36v2)

After 24 months of treatment with migalastat in the ERT-naïve patients study and 18 months of treatment in the ERT-experienced patients study, no significant changes from baseline were observed in SF-36v2.

Patient-Reported outcome – Brief Pain Inventory (BPI)

Patient's pain scales remained stable when switched from ERT to Galafold.

Paediatric population

In Study AT1001-020, a 1-year, Phase 3b, open-label, uncontrolled, multicentre study, the safety, PK, pharmacodynamic (PD), and efficacy of migalastat treatment was evaluated in 21 adolescent subjects (12 to <18 years of age and weighing ≥45 kg) with

Fabry disease and who have amenable mutations of the gene encoding α-galactosidase A (*GLA*). Subjects were either naïve to ERT or had stopped ERT at least 14 days before screening. The mean number of years since diagnosis of Fabry disease was 9.6 (± 4.25) years and the median years since diagnosis of Fabry disease was 10.70 years (range: 1.6 to 16.9 years) (n=22; 21 actually dosed with migalastat).

The overall mean (SD) and median (range) change from baseline in eGFR was -1.6 (15.4) mL/min/1.73 m^2 and 0.0 (-21, 45) mL/min/1.73 m^2 (n=19), respectively. The overall mean (SD) and median (range) change from baseline for LVMi was -3.9 (13.5) g/m^2 and -4.3 (-29.9, 15.3) g/m^2 (n=18), respectively. LVMi decreased in 10 subjects and increased in 8 subjects, but all subjects remained within normal limits at 12 months. Baseline plasma lyso-Gb_3 median (range) was 4.49 (0.4, 78.8) ng/mL and the overall median (range) change from baseline in plasma lyso-Gb_3 was 0.18 (-65.4, 115.8) (n=19). A reduction in plasma lyso-Gb_3 from baseline was observed in ERT-naïve subjects (median [range] -2.23 [-65.4, 0.1] ng/mL, n=9) and levels remained generally stable in ERT-experienced subjects (median [range] 0.54 [0.2, 115.8] ng/mL, n=10). There were no notable changes in patient reported outcomes. The efficacy results presented in these subjects may reflect factors other than treatment with migalastat hydrochloride.

5.2 PHARMACOKINETIC PROPERTIES

Absorption

The absolute bioavailability (AUC) for a single oral 150 mg migalastat hydrochloride dose was approximately 75%. Following a single oral dose of 150 mg migalastat hydrochloride solution, the time to peak plasma concentration was approximately 3 hours. Plasma migalastat exposure ($AUC_{0-\infty}$) and mean peak migalastat plasma concentration (C_{max}) demonstrated dose-proportional increases at migalastat oral doses from 50 mg to 1250 mg.

Migalastat hydrochloride administered with a high-fat meal, or 1 hour before a high-fat or light meal, or 1 hour after a light meal resulted in significant reductions of 37% to 42% in mean total migalastat exposure ($AUC_{0-\infty}$) and reductions of 15% to 40% in mean peak migalastat plasma concentration (C_{max}) compared with the fasting state.

A single-dose, 6-way crossover pharmacokinetic study was conducted in 20 healthy subjects. Compared to the intake of a single dose of migalastat with water, co-administration of approximately 190 mg caffeine reduced the mean migalastat $AUC_{0-\infty}$ by 55% and C_{max} by 60%. The rate of absorption (t_{max}) of migalastat was not affected by administration of caffeine in comparison to water, nor was any effect observed when migalastat was taken with natural (sucrose) or artificial (aspartame or acesulfame K) sweeteners.

Distribution

In healthy volunteers, the volume of distribution (V_z/F) of migalastat following ascending single oral doses (25 to 675 mg migalastat HCl) ranged from 77 to 133 L, indicating that it is well distributed into tissues and greater than total body water (42 L). There was no detectable plasma protein binding following administration of [^{14}C]-migalastat hydrochloride in the concentration range between 1 and 100 μM.

Biotransformation

Based upon *in vivo* data, migalastat is a substrate for UGT, being a minor elimination pathway. Migalastat is not a substrate for P-glycoprotein (P-gP) *in vitro*, and it is considered unlikely that migalastat would be subject to drug-drug interactions with cytochrome P450s. A pharmacokinetic trial in healthy male volunteers with 150 mg [^{14}C]-migalastat hydrochloride revealed that 99% of the radiolabelled dose recovered in plasma was comprised of unchanged migalastat (77%) and 3 dehydrogenated O-glucuronide-conjugated metabolites, M1 to M3 (13%). Approximately 9% of the total radioactivity was unassigned.

Elimination

A pharmacokinetic trial in healthy male volunteers with 150 mg [^{14}C]-migalastat hydrochloride revealed that approximately 77% of the radiolabelled dose was recovered in urine; 55% of the dose was excreted as unchanged migalastat, 4% as M1 to M3, and 5% was from unassigned components, for a total of 64%. The remaining 5% represents metabolites below quantifiable concentrations. Approximately 20% of the total radiolabelled dose was excreted in faeces, with unchanged migalastat being the only measured component.

Following ascending single oral doses (25 to 675 mg migalastat hydrochloride), no trends were found for clearance, CL/F. At the 150-mg dose, CL/F was approximately 11 to 14 L/hr. Following administration of the same doses, the mean elimination half-life ($t_{1/2}$) ranged from approximately 3 to 5 hours.

Special populations

Renal impairment

Galafold has not been studied in patients with Fabry disease who have a GFR less than 30 mL/min/1.73 m^2. In a single-dose study with Galafold in non-Fabry subjects with varying degrees of renal insufficiency, exposures were increased by 4.3-fold in subjects with severe renal impairment (GFR <30 mL/min/1.73 m^2).

Hepatic impairment

No studies have been carried out in subjects with impaired hepatic function. From the metabolism and excretion pathways, it is not expected that a decreased hepatic function may affect the pharmacokinetics of migalastat.

Elderly (>65 years)

Clinical studies of Galafold included small number of patients aged 65 and over. The effect of age was evaluated in a population pharmacokinetic analysis on plasma migalastat clearance in the ERT-naïve study population. The difference in clearance between Fabry patients ≥65 years and those <65 years was 20%, which was not considered clinically significant.

Paediatric population

The pharmacokinetics of migalastat were characterised in 20 adolescent subjects (12 to <18 years and weighing ≥45 kg) with Fabry disease who received the same dosage regimen as adults (123 mg migalastat capsule every other day) in an open-label Phase 3b trial (AT1001-020).

Assessment of bioequivalence of exposure was simulated in adolescent subjects (12 to <18 years and weighing ≥45 kg) and receiving migalastat 123 mg once every other day compared to adults receiving the same dosing regimen. Model derived AUC_{tau} in adolescent subjects (12 to <18 years) were similar to adult exposures.

No dosage adjustment is required for adolescents 12 to <18 years of age and weighing ≥45 kg.

Gender

The pharmacokinetic characteristics of migalastat were not significantly different between females and males in either healthy volunteers or in patients with Fabry disease.

5.3 PRECLINICAL SAFETY DATA

Genotoxicity

Migalastat hydrochloride was not genotoxic in a bacterial mutation assay, a forward mutation test and a rat micronucleus test.

Carcinogenicity

In a rat 104-week carcinogenicity study, there was an increased incidence of pancreatic islet cell adenomas in males at a dose level 19-fold higher than the exposure (AUC) at the clinically efficacious dose. This is a common spontaneous tumour in *ad libitum*-fed male rats. In the absence of similar findings in females, no findings in the genotoxicity studies or in the carcinogenicity study with Tg.rasH2 mice (at 27 times the AUC exposure expected clinically), and no pre-neoplastic pancreatic findings in the rodents or monkeys, this observation in male rats is not considered related to treatment and its relevance to humans is unknown.

6 PHARMACEUTICAL PARTICULARS

6.1 LIST OF EXCIPIENTS

Galafold hard capsules contain the following inactive ingredients: pregelatinised maize starch and magnesium stearate. The capsule shells are made of gelatin and contain the following colouring agents: titanium dioxide (E171) and indigo carmine (E132). The capsules are marked with printing ink (2328), containing shellac (E904), iron oxide black (E172), and potassium hydroxide.

6.2 INCOMPATIBILITIES

Incompatibilities were either not assessed or not identified as part of the registration of this medicine.

6.3 SHELF LIFE

4 years

6.4 SPECIAL PRECAUTIONS FOR STORAGE

Store in the original package in order to protect from moisture. Store below 30ºC.

6.5 NATURE AND CONTENTS OF CONTAINER

PVC/PCTFE/PVC/Al blister.

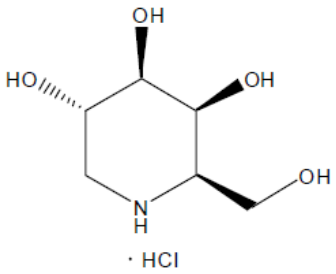
Pack size of 14 capsules.

6.6 SPECIAL PRECAUTIONS FOR DISPOSAL

Any unused medicine or waste material should be disposed of in accordance with local requirements.

6.7 PHYSICOCHEMICAL PROPERTIES

Chemical structure



Australian Approved Name (AAN): Migalastat hydrochloride

Molecular formula: $C_6H_{13}NO_4.HCl$
Molecular weight: 199.63 (hydrochloride salt)
163.17 (free base)
Chemical name: (+)-(2R, 3S, 4R, 5S)-2-(hydroxymethyl)-piperidine-3,4,5-triol, hydrochloride

Migalastat hydrochloride is a white to pale brown powder, freely soluble between pH 1.2 and pH 7.5 in aqueous media. The pKa is 7.47 ± 0.01.

CAS number

75172-81-5

7 MEDICINE SCHEDULE (POISONS STANDARD)

Prescription only medicine

8 SPONSOR

Pharmacy Retailing NZ Ltd t/a Healthcare Logistics

58 Richard Pearse Drive Airport Oaks Auckland

9 DATE OF FIRST APPROVAL

5 Oct 2023

10 DATE OF REVISION

21 Mar 2025

Summary table of changes

Section changed	Summary of new information
4.8	Updated data under post-marketing experience to include Angioedema