

## **DIPLOMARBEIT / DIPLOMA THESIS**

Titel der Diplomarbeit / Title of the Diploma Thesis

## "Development of a KNIME Workflow for the retrieval of molecules associated with solute carrier proteins linked to rare diseases"

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I

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#### ABSTRACT

SLCs, short for solute carrier, are a relatively unexplored group of transport proteins that control essential physiological functions. Despite being associated with several diseases, they represent a rather untapped source of new potential drug targets. Also, around 300 million people worldwide are suffering from rare diseases which are defined as diseases that affect only a small number of people. However, despite being so rare, rare diseases are numerous, and often include a lack of basic knowledge and treatment possibilities which makes them one of the key global health priorities. The aim of this work was to create a workflow on KNIME that shows the role of SLCs in rare diseases and the availability of possible modulators through the integration of data from, altogether, six databases, starting from a list of SLCs, provided by the RESO-LUTE project.

As the data include false-positive findings and often lack essential information, like the type of association between an SLC and a rare disease or a molecule, respectively, a second workflow was created. This workflow can be accessed through the KNIME WebPortal and can be used for filtering as well as for manual curation of associations. The collected data highly suggest that SLCs play an essential role in rare diseases. However, manual curation and research are needed to use the information further.

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#### ZUSAMMENFASSUNG

SLCs, kurz für Solute Carrier, sind eine relativ unerforschte Gruppe von Transportproteinen, die wesentliche physiologische Funktionen steuern. Obwohl sie mit mehreren Krankheiten verbunden sind, stellen sie eine eher unerschlossene Quelle für neue potenzielle Ziele für Arzneistoffe dar.

Darüber hinaus leiden weltweit rund 300 Millionen Menschen an seltenen Krankheiten, die als Krankheiten definiert werden, von denen nur eine geringe Anzahl von Menschen betroffen sind. Trotz ihrer Seltenheit sind seltene Krankheiten zahlreich und beinhalten häufig einen Mangel an Grundkenntnissen und Behandlungsmöglichkeiten, was sie zu einer der wichtigsten globalen Gesundheitsprioritäten macht.

Ziel dieser Arbeit war es, einen Workflow auf KNIME zu erstellen, der die Rolle von SLCs in seltenen Krankheiten und die Verfügbarkeit möglicher Modulatoren durch die Integration von Daten aus insgesamt sechs Datenbanken zeigt, ausgehend von einer Liste von SLCs, die vom RESOLUTE Projekt bereitgestellt wurde.

Da die Daten falsch positive Ergebnisse enthalten und häufig wesentliche Informationen, wie die Art der Assoziation zwischen einem SLC und einer seltenen Krankheit bzw. einem Molekül, fehlen, wurde ein zweiter Workflow erstellt. Auf diesen Workflow kann über das KNIME WebPortal zugegriffen werden und er kann sowohl zum Filtern als auch zum manuellen Kuratieren von Assoziationen verwendet werden.

Die gesammelten Daten legen nahe, dass SLCs bei seltenen Krankheiten eine wesentliche Rolle spielen. Manuelle Kuratierung und Recherche sind jedoch erforderlich, um die Informationen weiter zu nutzen.

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#### 1 INTRODUCTION

#### 1.1 Rare diseases

Rare diseases are diseases that affect only a small percentage of people. However, there is no single, worldwide accepted definition. In most countries, a rare disease is defined by a maximum total number of affected patients. An example would be the US definition defining a rare disease as a disease with less than 200.000 cases in the US. [17] In the EU, however, a rare disease is characterised by a prevalence of less than 5 in 10,000 (1 in 2,000) citizens. Genetic mutations cause a big part of rare diseases with a significant part starting at childhood. An example would be the 'Fragile X syndrome'. However, rare diseases also include rare infectious diseases, caused by bacteria or viruses, autoimmune diseases and cancers.[18] Despite being individually uncommon, rare diseases are numerous. Up to 8,000 unique diseases have been described and it is estimated that around 300 million people worldwide are affected by rare diseases.[18], [19] Some diseases are generally more well-known, like Cystic Fibrosis or Huntington's disease, others have a patient population below 100.

However, rare diseases are also sometimes referred to as 'orphan diseases', as they have been neglected by researchers as well as doctors for a long time. Under normal marketing conditions, developing medicine for rare diseases would not be profitable for pharmaceutical companies, as the process of discovering a molecule and reaching marketing authorisation takes a long time and is very expensive. Therefore, developing drugs for rare diseases would operate a financial deficit, as the expected sales would not even recover the money spent on development because of the small number of treatable patients. To support the research on so-called orphan drugs, countries introduced numerous incentives such as regulatory assistance or marketing exclusivity. The United States were the first ones with introducing the Orphan Drug Act in 1983 [20] while it took the European Union until 1999 to find a harmonised regulation, the Orphan Drug Regulation.[21], [22] Despite the increasing interest in research since, still only a small percentage of diseases is well-studied when it comes to basic knowledge and treatment possibilities. This makes rare diseases to one of the key global health priorities.[23]

#### 1.2 Solute Carriers

Transport of solutes, such as sugars, amino acids, nucleotides, neurotransmitters and ions across biological membranes, is an essential process for cellular homeostasis and is, apart from passive diffusion, controlled by transport proteins that serve as gatekeepers.[24]

These proteins can be divided according to passive and active mechanisms. Passive, also referred to as facilitated, transporters transport solutes in the direction of their electrochemical gradient while active transporters utilise energy-coupled mechanisms to move substances against their gradient. Furthermore, active transporters can be classified into primary and secondary-active ones. In primary-active transporters, the transport is directly coupled to the hydrolysis of the energy provider (e.g. ATP). However, in secondary-active transporters, the transport of one solute is directly dependent on the transport of a second, either as symporter, transferring a second solute in the same direction or as antiporter, transporting the second solute in the opposite direction. [24],[25]

Reflecting the high importance of transporters, it is, according to Hediger et al., 2013[1], estimated that around 10% of all human genes are related to transporters. Solute carrier proteins (SLCs) make the largest gene group of membrane transporters with more than 400 members. They constitute a heterogeneous group of transporters located mostly in the cell membrane, but also in intracellular organelles, like the mitochondrial SLC family 25, or vesicles as shown in Figure 1. SLCs are defined as either facilitated or second-ary-active transporters. In contrast, primary-active transporters, like the ABC-transport-ers, aquaporins and ion channels and pumps are not members of the SLC series.[1]



Figure 1: SLC transporters, based on Hediger et. al, 2013

Thus, the inclusion of a protein within the SLC series is based on function. This can lead to homology between different SLC families being very low to non-existent. However, members of a specific SLC family have at least 20-25% amino acid sequence identity to another member of the family.[1],[26]

The genes encoding the transporters are generally named after the HGNC (HUGO Gene Nomenclature Committee) system, starting with the root symbol 'SLC', followed by a number that specifies the family. The following letter defines the subfamily and is in most cases 'A', as most families are not further subdivided. The final number denotes the individual family member.[1], [25] However, there are some exceptions like the SLC family 21 that has its root symbol changed to SLCO.[27]

Also, some genes are referred to as 'putative SLCs' as they share an ancestral background with SLCs and are plausible facilitative or secondary active transporters but have not yet been classified into any of the existing SLC families and do not have a name according to the SLC root system.[28]

As solute carriers control essential biological functions, like nutrient uptake, waste removal and ion transport, genetic polymorphisms are associated with several diseases. According to Rives et al., 2017, human genetic data suggests that around 50% of SLCs are associated with human diseases compared to 20% of the broader genome, that illustrates their high importance in diseases.[29]

Some SLCs are already well studied and in use as drug targets. These drug targets include inhibitors of SGLT2, the renal sodium-glucose cotransporter 2, that is encoded by the gene SLC5A2. SGLT2 inhibitors are used in the treatment of diabetes type 2 as they lower blood sugar levels.[30] Another example would be the human monoamine transporters, mostly from SLC family 6, that are used as effective targets in the treatment of depression.[31]

Besides, SLCs can also cause rare diseases, especially monogenic (also referred to as Mendelian) diseases.[32] An example would be the association between Amish Lethal Microcephaly and SLC25A19.[33] Amish Lethal Microcephaly is a disease that has only been found in Amish families and leads to extreme microcephaly with an underdevel-oped brain and early death, which suggested a defect in 2-ketoglutarate metabolism. The gene SLC25A19 that encodes the mitochondrial deoxynucleotide carrier was found responsible for this disease. A method of treatment could include drugs that enhance the transporter's activity.[33]

Yet, the majority of SLCs have been getting only little research attention. More than 30% are even 'orphans' when it comes to the knowledge of their substrate specificity and function. It is assumable that many more than the SLCs are associated with diseases, especially rare diseases, and that they would represent a largely untapped source for drug targets.[32] Recently, however, the relevance of systematic research of SLCs for drug discovery is increasingly getting more attention. [32], [34] RESOLUTE (Research Empowerment on SOLUTE carriers) is a project with 13 partners from academia and industry with the goal of intensifying worldwide research on solute carriers within a 5-year research project. The project aims to provide tools and reagents as well as assays and data- and knowledgebases. [9] For this thesis, a file with a list of SLCs originating from the RESOLUTE project, formed the starting point.

#### 1.3 Aim of the thesis

The aim of this thesis is to collect data about the role of SLCs in rare diseases from databases through database integration. Also, possible modulators of these SLCs were aimed to be aggregated as they could form potential modulators of these diseases. This approach is based on the diploma thesis '*Development of a KNIME workflow for the retrieval of associations between orphan diseases and their possible drug repurposing candidates*' by Jana Gurinova, 2018.[2] In the cited thesis, Gurinova tried to retrieve possible connections between rare diseases and drugs through their shared association with targets to propose repositioning candidates for rare diseases.

For the present work, this approach was made more specific as it was limited to SLCs as targets only. Also, new databases were included: UniProt, ChEMBL and PubChem. Besides, this workflow is not aimed at proposing drugs as repositioning candidates, but more at giving an overall overview of the role of SLCs in rare diseases and the availability of possible modulators, which includes approved drugs as well as molecules showing activity.

## 2 METHODS

The used method for this thesis was the aggregation of data from databases through a workflow created on KNIME in the form of a triangulation. This approach was based on the diploma thesis '*Development of a KNIME workflow for the retrieval of associations between orphan diseases and their possible drug repurposing candidates*' (Gurinova, 2018)[2].





As the aggregated data needs manual curation, and this would, due to the amount of data, exceed the time constraints of a diploma thesis, a second workflow was created, that interested users can access through the KNIME WebPortal. This workflow offers the possibility to filter, curate and download the aggregated data.

The following chapter provides information about KNIME, the datasets and databases and the created workflows.

#### 2.1 KNIME

KNIME, which derives from 'Konstanz Information Miner', is a data-analytics, reporting and integration platform that was created by a group of software engineers under the lead of Michael Berthold at the University of Konstanz. They released their first tool, the first version of the KNIME Analytics Platform, in 2006.[35]

The next subsections are going to provide an overview about the two offered, complementary tools - the freely available KNIME Analytics Platform and the KNIME Server, a commercial product, both of which were in use for this work. Besides, the data format XML, API calls, as well as meta nodes and components, are going to be explained in more detail as they were especially crucial for the creation of the workflows.

#### 2.1.1 The KNIME Analytics Platform

The KNIME Analytics Platform is an open-source, freely available workflow management tool that provides a graphical user interface for interactive execution of a data pipeline that allows automated data analysis without extensive knowledge of programming.[35]

Workflows in the KNIME Analytics Platform are made of central, visualised units: socalled nodes. These hundreds of different available nodes can be combined by simple drag and drop and perform various tasks in processing the data. A simple workflow on KNIME starts with a node that reads in the data as the data is stored in an internal table-based format- the KNIME table. The KNIME table consists of a table with columns of a specific data type (e.g. integer, string, molecule) and an optional number of rows corresponding to the specification. Each node needs to be executed before handing the data to the following node. One of the most significant advantages of the KNIME Analytics platform is that the nodes store the data permanently. So, the workflow execution can be stopped and resumed at any time. The user can inspect intermediate results and also insert new nodes without losing previous results. [36]

Nodes on KNIME can be roughly divided into five categories:

- 1) Nodes, that read in the data, either directly from a file or via API call (see 2.1.5, p.10)
- 2) Nodes for data transformation, e.g. filters
- 3) Nodes for data analysis/mining
- 4) Nodes for visualisation that allow interactive exploration of the data
- 5) Nodes for data deployment

File Reader	Row Filter	Rule Engine	Scatter Plot	Excel Writer (XLS)
┣.►	→ <mark>→</mark>	→ 🖸 ►	→ ▦ ╄	×LS
1	2	3	4	5

Figure 3: KNIME Analytics Platform example workflow

Figure 3 shows a screenshot of an example workflow, using one node corresponding to each of the before mentioned categories. In addition to the nodes that are included in the core KNIME Analytics implementation, it is possible to download KNIME extensions or even implement self-programmed nodes.

Besides, KNIME provides several tutorials and example workflows that can be used to get easily familiar with KNIME.

The version of the KNIME Analytics Platform used for this work was version 4.1, which was the latest update at the time of the practical part of this work. In addition, the KNIME extension 'KNIME XML-processing' was downloaded.

#### 2.1.2 KNIME Metanodes and Components

Meta nodes look like a single node. However, they can contain several nodes. They can be used for making the workflow look 'tidied up' and make it easier for other people to understand the functionality of a workflow. [37]

Components, formerly called Wrapped Metanodes, however, are even more 'real KNIME nodes' as they bundle functionality and can have their own dialog and interactive view.[38]

In combination with widgets and view nodes, it is possible to create interactive web pages on the WebPortal, which is a feature part of the KNIME Server.

#### 2.1.3 The KNIME Server and WebPortal

The KNIME Server is a complementary, commercial product that offers the possibility to share workflows within a team. Workflows can be uploaded and stored on the server as well as downloaded to one's local KNIME Analytics Platform. Also, it is possible to schedule executions of workflows either for delayed or recurring jobs.[39] This function was used for the first workflow of this work, the workflow for data retrieval (see 2.3), which is scheduled to be run and update its data at the KNIME Server every

15 days.

On the other hand, workflows can be executed through the web browser using the interactive 'KNIME WebPortal'. The KNIME WebPortal is an extension to the KNIME Server and automatically turns KNIME workflows containing components with widgets or visualisation nodes into browser-based applications.[40]



## **Figure 4: Widgets on the KNIME Analytics Platform vs visualization via the WebPortal** The second workflow, the workflow for interested users, is primarily dedicated to being run at the KNIME WebPortal. Figure 4 shows the inside of an example Component on

the KNIME Analytics Platform versus the way it is being displayed through the WebPortal.

#### 2.1.4 Data format: XML

The majority of data used for the workflow for data retrieval was in XML format. XML stands for Extensive Markup Language. It is designed for the transport and storage of data and widely used in web development as it is both machine- and humanreadable.[41]

Usually, an XML file starts with a prologue that contains the XML version and the character encoding. The rest of the XML format structure can roughly be compared to a tree. Like in a tree, a single 'root' contains all the other data elements, and it is structured in a specific way. The terms 'parent', 'children' and 'siblings' are used to describe the relationships between the data elements. While parents are one level above children, siblings are at the same level.[42]

```
<?xml version="1.0" encoding="UTF-8"?>
</root>
</childl>A</childl>
</childl>C</subchildl>C</subchildl>
</childl>D</subchildl>
</childl>
</childl>
```

#### Figure 5: Example XML

Figure 5 shows an example XML file. A data element is always introduced and closed with a particular syntax, e.g. <child1> is used as an introduction while </child1> closes the element. All entries between the introduction and the closure define the value of the data element. In Figure 5, <child1> and <child2> are sibling elements, while <sub-child1> and <subchild2> are children elements with <child2> as a parent.

The syntax makes it possible to query an XML file for specific elements. This can be done with XPath, the XML Path Language. Instruction on how to create XPaths can be found at https://www.w3schools.com/xml/xpath\_intro.asp.

KNIME offers nodes to process XML files. XML files need to be imported into KNIME with the *XML reader* node. Afterwards, the XPath can be configured even easier as KNIME's *XPath* node proposes an XPath expression when clicking on the dedicated attribute.

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	Settings Namespace	Flow Variables Job Manage	r Selection Memory Po	icy		
	XML column: XML XM	L		~		
	Remove source o	olumn.				
	XPath summary					
	Column name	XPath query	Туре			
	subchild1 subchild2	/root/child2/subchild1 /root/child2/subchild2	String(SingleCell) String(SingleCell)			
	Selected XPath: /r	oot/child1				
		Add XPath Edit XPa	th Remove XPath			
	XML-Cell Preview	sion='1 0' encoding='	ITE-8'3			
	2 <root></root>	Sion- 1.0 encourng- t	511-0 17			
	3 < <mark>chil</mark> 4⊡ <chil< th=""><th>d1&gt;A d2&gt;</th><th></th><th></th><th></th><th></th></chil<>	d1>A d2>				
	5 <	<pre>subchild1&gt;C</pre>	1>			
	6 < 7 <th>subchild2&gt;Dld2&gt;</th> <th>2&gt;</th> <th></th> <th></th> <th></th>	subchild2>Dld2>	2>			
	8					
	9					
	<			>		
	OK	Apply	ancel			
	-					
Row I		ML			S subcr	nild1 S subchild2
	xm</th <th>l version='1.</th> <th>0' encoding</th> <th>='UTF-8'</th> <th>?&gt;</th> <th></th>	l version='1.	0' encoding	='UTF-8'	?>	
	<roo< th=""><th>t&gt;</th><th></th><th></th><th></th><th></th></roo<>	t>				
Row0		<childl>A<th>ildl&gt;</th><th></th><th>с</th><th>D</th></childl>	ildl>		с	D
		<child2></child2>				
		<subchild.< td=""><td>1&gt;C<td>ld1&gt;</td><th></th><th></th></td></subchild.<>	1>C <td>ld1&gt;</td> <th></th> <th></th>	ld1>		
		2 million and a 1 million	1 - D. Carlanda	1.405		

#### Figure 6: XPath in KNIME

Figure 6 shows the *XPath* node configuration as well as the results deriving from the Example XML file (see Figure 5).

The native data sets used for the workflow are, of course, much more complex. The used files and the extraction are described in more detail in section 2.3, p.26f.

#### 2.1.5 Web APIs

Some databases provide the possibility to download the data via Web API. Web API is short for Web Application Programming Interfaces and offers users the opportunity to get access to specific data from a database without downloading the whole one.

The API is usually a set of standard commands encoded into a URL syntax that is similar to the URL of the database. The databases having API access usually provide instruction on how their API URLs are built. Most of the times, the user can choose between different formats like JSON and XML. [14],[43],[44] For this work, API calls were used to retrieve data from three databases: UniProt, ChEMBL and PubChem. All of these API calls were performed via REST (representational state transfer) API, which refers to the type of software architectural style. KNIME offers specific nodes for performing REST API calls that can be found within the category 'REST Web Services'. Before accessing the web API, it is necessary to create the URL using, for example, a *String Manipulation* node. Afterwards, a *GET Request* node performs the retrieval of data from the dedicated resource.

Status	S Content type	IML body
200	application/xml;charset=UTF-8	<pre><?xml version='1.0' encoding='UTF-8'?> &lt;uniprot xmlns="http://uniprot.org/uniprot" xmlns:xsi="h&lt;/td&gt;</pre>
200	application/xml;charset=UTF-8	<pre><?xml version='l.0' encoding='UTF-8'?> &lt;uniprot xmlns="http://uniprot.org/uniprot" xmlns:xsi="h&lt;/td&gt;</pre>
200	application/xml;charset=UTF-8	<pre><?xml version='1.0' encoding='UTF-8'?> &lt;uniprot xmlns="http://uniprot.org/uniprot" xmlns:xsi="h&lt;/td&gt;</pre>

#### Figure 7: Result of an API call performed with a GET Request node

As shown in Figure 7, the *GET Request* node results in three columns: the 'status', the 'content type' and the 'body'. The 'status', referring to the HTTP status, shows the success of a query: A status starting with 2xx indicates a successful request while a status beginning with 4xx or 5xx flags failure. The 'content type' shows the type of data accessed through the API call, and the 'body' contains the accessed data. In the case of Figure 7, an *XPath* node could follow to further process the data.

The specific URLs and XPath queries used for this work are described in more detail in section 2.3, p.26ff.

#### 2.2 Sources of data

The data was generated via the integration of databases that include information about target-disease and target-molecule relationships starting from a list of SLCs. The work-flow for data-retrieval (see 2.3, p.26ff.) results into two tables that are saved on the KNIME Server and can be accessed through the second workflow (see 2.4, p.38ff.). The first one, *SLCs and rare diseases*, contains information about SLCs and their associated rare diseases. The second table, *SLCs and molecules*, includes information on related drugs and molecules.

The information about SLCs was derived from two sources: the file RESOLUTE\_SLCs that provided a list of all SLCs that were included into this work and the UniProt KB API that was used for the retrieval of additional information.

Orphanet and DisGeNET were the two databases used for the extraction of SLC-rare disease associations. DisGeNET provides an extensive set of gene-disease associations but does not include the option to filter for rare diseases. At the same time, Orphanet is dedicated to rare diseases and contains several disease identifiers that make it possible also to filter the results from DisGeNET.

Three databases were used to provide potential molecules for many of the SLC-rare disease associations and to provide interested users of the second workflow the choice between three different, widely used databases. DrugBank is fully curated, and roughly specialised to approved and experimental drugs. ChEMBL is also manually curated and specialised to bioactivity data with a significant part originating from medicinal papers. PubChem is an open database which means that everyone can upload their scientific data.

The following datasets, databases and their content are listed in the sequence of their occurrence in the workflow.

#### 2.2.1 RESOLUTE\_SLCs file

The file RESOLUTE\_SLCs was provided by the RESOLUTE project and was adapted for its integration into the workflow for data retrieval as only four attributes were kept: SLC name, family, EntrezGeneID and UniProtID..

It was last updated in June 2019 and contains a list of 446 SLCs from 65 SLC families, including 16 SLCs that can be classified as putative SLCs as they are not named according to the SLC nomenclature and are not organised into any of the existing SLC families (see section 1.2, p.3f.).

#### 2.2.2 UniProt KB.

The UniProt Knowledgebase is a database that contains annotated information about over 120 million proteins. It includes two types of entries: the curated SwissProt-Entries and the unreviewed TrEMBL entries that are annotated automatically. [45]



Figure 8: Example of a UniProt entry (screenshot from https://www.uniprot.org/uniprot/P43005, accessed 06/15/2020)

The provided information can either be accessed directly at the website at https://www.uniprot.org/ [10], downloaded as complete datasets in XML on the page 'Downloads' or accessed via several Web APIs.

For this workflow, the UniProt website REST API was used to retrieve additional information about solute carrier proteins. The relevant part for this work of the UniProt entry is shown in Figure 8 for SLC1A1.

#### 2.2.3 Orphanet

Orphanet was established to 'provide high-quality information on rare diseases and ensure equal access to knowledge for all stakeholders' which means that the database is adapted to the needs of patients and their families as well as of health care professionals and researchers. [46]

The curated information about rare diseases and orphan drugs provided can be accessed directly via the webpage (http://www.orpha.net) in nine languages.

An Orphanet entry for a rare disease contains information such as synonyms, several identifiers like Orphanet's specific terminology for rare diseases - the ORPHAnumber as well as cross-references to other databases (e.g. UMLS, MeSH, OMIM) and data about prevalence, age of onset and epidemiology.

#### SLC1A1 - solute carrier family 1 member 1



Figure 9: Example of an Orphanet entry (screenshot from https://www.orpha.net/consor/cgi-bin/Disease\_Genes.php?Ing=EN&data\_id=22150&Disease\_Disease\_Genes\_diseaseGroup=SLC1A1&Disease\_Disease\_Genes\_diseaseType=Gen&MISSING%20CONTENT=solute-carrier-family-1-member-1---SLC1A1&search=Disease\_Genes\_Simple&title=solute%20carrier%20family%201%20member%201%20-%20SLC1A1, accessed 06/15/2020)

Apart from searching for the name or identifiers of a rare disease, Orphanet can be directly queried for genes, leading to a list of rare diseases associated with them. Figure 9 shows the Orphanet entry for SLC1A1, presenting two associated rare diseases. Apart from the mentioned sections, Orphanet also offers information about orphan drugs, patient organisations, expert centres, ongoing clinical trials and more. All in all, Orphanet contains information about more than 9000 rare diseases. The high number of rare diseases on Orphanet is caused by the fact that it sometimes differentiates between manifestations of diseases that are elsewhere classified as a single disease.[46] The information provided on the website can also be downloaded from Orphadata at http://www.orphadata.org.[11] Orphadata is a platform powered by Orphanet on which it is possible to download thematically specialised data sets as XML files. It includes free datasets as well as on request data, for which a data transfer agreement needs to be signed.

For the present work, two of these files were downloaded and integrated into the workflow for data retrieval: *'Orphanet rare diseases with their associated genes'*, version 1.2.11/4.1.6 [2018/04/12] (orientdb version) [47] was used for retrieving associations between SLCs and rare diseases. The file *'Rare diseases and cross-referencing'*, version 1.2.11/4.1.6 [2018/04/12] (orientdb version) [48] was used for adding external identifiers to the emerging dataset due to two reasons: the first reason is the join with the dataset from DisGeNET, as DisGeNET uses the UMLS ID as the identifier for diseases. The second reason is to provide an extensive set of identifiers to users accessing the second workflow via the KNIME WebPortal, so that it would be easily possible to join the results with datasets from other databases.

#### 2.2.4 DisGeNET

DisGeNET [12] is a platform that offers one of the most extensive collections of genedisease and variant-disease associations. The latest release available at the time of the analysis part of this work (version 6.0) contains more than 600.000 gene-disease-associations.

The information about gene-disease-associations in the DisGeNET platform derives from sixteen different sources. These sources are classified into the categories 'curated', 'literature-derived', 'animal models' and 'inferred'.[49] Particular mention should be made of the "literature-derived" sources LHGDN and BeFree as the data is extracted by text mining. [50], [51] 60% of the gene-disease associations listed in DisGeNET derive from text mining and are not described in any of the curated sources.[49] Text mining can be a great advantage, as there is always an unmanageable amount of newly published literature which can only be efficiently accessed by automatic tools. [49] Because of this, DisGeNET contains many new possible associations, which can be especially interesting for rare diseases, as it significantly increases the number of retrieved genes associated with these diseases. [49] On the other hand, it also poses the threat of false-positive findings as further described in section 3.2,p.53f.

There are several ways to access the data provided on DisGeNET. It can be, for example, directly queried at https://www.disgenet.org/ where it is possible to search for specific diseases, genes or variants.

SLC1A1, solute can	rier family 1	member 1, 6505 Q		1 - 25 of 122 results >							er Downi	oad Share
N. diseases: 12; N. variants: 16 Source: ALL Results per page 25 ~												
Filter within current												
Disease \$	Туре \$	Disease Class \$	Semantic Type \$	N. genes <sub>d</sub> \$	N. SNPs <sub>d</sub> \$	Score <sub>gda</sub> 🗸	EL <sub>gda</sub> \$	El <sub>gda</sub> \$	N. PMIDs \$	N. SNPs <sub>gda</sub> \$	First Ref. \$	Last Ref. \$
✓ Dicarboxylicaminoaci 3	disease	Pathological Conditions,	Disease or Syndrome	2	2	0.910	limited	1.000	3	2	1992	2011
Low Tension Glaucoma	disease	Eye Diseases	Disease or Syndrome	103	56	0.530	None	1.000	5		2007	2018
<ul> <li>Schizophrenia</li> </ul>	disease	Mental Disorders	Mental or Behaviora	2872	2897	0.500	None	1.000	14	3	2001	2018
✓ Epilepsy	disease	Nervous System Diseases	Disease or Syndrome	1215	339	0.350	None	1.000	6		2002	2018
✓ Autism Spectrum Dis 3	disease	Mental Disorders	Mental or Behaviora	• 1071	331	0.320	None	1.000	3	1	2008	2019
✓ Seizures	phenotype	Pathological Conditions,	Sign or Symptom	2152	553	0.320	None	1.000	3	2	2002	2016
<ul> <li>Cortical Dysplasia</li> </ul>	disease	Congenital, Hereditary, a	Congenital Abnorm	<b>&gt;</b> 118	6	0.310	None	1.000	1		2002	2002
Epilepsy, Temporal Lo 3	disease	Nervous System Diseases	Disease or Syndrome	354	33	0.310	None	1.000	1		2002	2002
✓ Atonic Absence Seizu… 3	phenotype	Pathological Conditions,	Disease or Syndrome	102		0.300	None	1.000	1		2013	2013
Awakening Epilepsy	disease	Nervous System Diseases	Disease or Syndrome	83		0.300	None	1.000	1		2002	2002

# Figure 10: Example of gene-disease associations on DisGeNET for SLC1A1 (screenshot from https://www.disgenet.org/browser/1/1/0/6505/, accessed 06/15/2020)

Figure 10 shows an example part of the query of diseases associated with the gene SLC1A1. Apart from information about the condition like its full name, the type, the MeSH disease class, and the number of associated genes, it offers metrics that can be used for ranking and filtering the gene-disease associations.

An example would be DisGeNET's in-house developed metric system: the DisGeNET score. It is calculated based on the number and the type of sources (curated, animal model, inferred and literature-derived) supporting a gene-disease association. Further details on how it is calculated are provided at https://www.disgenet.org/dbinfo#score. Apart from the information shown in Figure 10, DisGeNET also includes details about the listed diseases such as the UMLS ID, the disease name and the associated MeSH disease class.

Besides the direct query on the website, DisGeNET offers different data sets for the download as tabulated files at http://www.disgenet.org/downloads. For this work, two of these files were implemented into the workflow. The link to the downloadable files is integrated inside the workflow for data retrieval to update the data automatically.

*'ALL gene-disease-pmid associations'* (https://www.disgenet.org/static/disgenet\_ap1/files/downloads/all\_gene\_disease\_pmid\_associations.tsv.gz) [52] was used for retrieving SLC-rare disease associations.

The second file was the '*BeFree gene-disease-pmid associations for Pubannotations*[53] dataset (https://www.disgenet.org/static/disgenet\_ap1/files/downloads/pubannotator.tsv.gz) that contains the sentence on MEDLINE causal for the association retrieved through BEFREE text mining. This file can make it easier to curate the associations later on.

As the links to the files are integrated into the workflow, the dataset is designated to be updated to its newest available version. The version used for the analysis part of this work is version 7.0, released on 05/04/2020.

#### 2.2.5 DrugBank

DrugBank is a wide-ranging, entirely curated web database that provides knowledge about drugs and drug-target-associations for drugs, that are already FDA-approved as well as experimental drugs and nutraceuticals. It was first released in 2006 and the latest big update at the time of the creation of the workflow, version 5.0, was published in 2018.[13], [54], [55]

Each drug entry on DrugBank contains more than 200 data fields, including information about the drug as well as about the associated drug targets. Compounds are annotated with detailed information about the chemical, pharmacological and pharmaceutical characteristics while the target information includes sequences, structures and pathways.

ORUGBANK			Browse ▼	COVID-19	Search 🔻	Downloads	Commercial Data 🔻	Help 🔻	About 🔻
Excitatory am	ino acid tra	ansporte	er 3						
DETAILS									
Name	Excitatory amino acid tra	nsporter 3							
Kind	protein								
Organism	Humans								
Protein	NAME Excitatory amino acid trans	UNIPROT ID	Details						
DRUG RELATIONS									
Drug Relations	Show 10 \$ entries							Search	
	DRUGBANK ID	NAME ↑↓	DRUG GROUP	↑↓	PHARMACOLOGI	CAL ACTION?	↑↓ ACTIONS	↑↓ DETAILS	5 ↑↓
	DB00128	Aspartic acid	approved, nutraceutic	al	unknown			De	etails
	DB00142	Glutamic acid	approved, nutraceutio	al	unknown			De	etails
	DB00230	Pregabalin	approved, investigation	onal	unknown		other	De	etails

Figure 11: Example of DrugBank entry for SLC1A1 (screenshot from https://www.drugbank.ca/bio\_entities/BE0001054, accessed 06/15/20)

Figure 11 shows the DrugBank entry for the target SLC1A1. Under 'DRUG RELA-TIONS', a list of drugs interacting with this protein is provided including their 'DRUG-BANK ID', Drugbank's unique accession number, their stage of approval and, when known, the pharmacological drug actions. For the present work, the data from DrugBank was downloaded as an XML file from the website containing the 'complete database'. It is necessary to create a free account (for non-commercial use) to get access to this dataset [56]. The version used for the work-flow and the analysis part of this work was version 5.1.2, released on 12/20/2018 [57].

#### 2.2.6 ChEMBL

ChEMBL is an extensive, manually curated database for bioactivity of drug-like molecules. The database contains bioactivity, molecule and target data from altogether 48 sources with a significant part of the data deriving from manual extraction of published medicinal chemistry literature. [58]–[61]

ChEMBL standardises the published activity values to make them better comparable, which means that they are, when possible, converted to a preferred standard type or unit (e.g. IC50\_mean, mean IC50 and IC50 are all standardised to the standard type IC50). In addition, the pChEMBL value has been added. This value makes several measures, like the molar IC50, EC50, Ki, Kd or Potency, better comparable as they are converted to a linear scale by taking their negative logarithmic values (e.g. the pChEMBL for an IC50 measurement of 1 nM has a value of 9). [58]

The ChEMBL database can be directly accessed using the website where it can be queried for entities such as compounds, targets, assays, documents and more.

Rec 20	ords per page:						Sho	w/Hide Columns							*		٩
S	howing 1-20 o	ut of 244 re	cords												< 1 2	345	>
	ChEMBL ID	≎ Name <	Synonyms	Туре ≑	Max Phase 🌩	Molecular Weight	Target	s ≜	Bioactivities 🗍	AlogP ᡇ	PSA ≑	НВА ≑	HBD ≑	#RO5 Violations <sup>\$</sup>	#Rotatable Bonds	Passes Ro3	QED Weighted
C		No Data		Small molecule	0	268.23	ľ	1 By Type:	1 By Std. Type:	0.25	143.76	5	3	0	6	N	0.49
		No Data		Small molecule	0	251.28	ľ	1 Ву Туре:	1 By Std. Type:	0.96	100.62	3	3	0	5	N	0.72
		No Data		Small molecule	0	237.25	Ľ	1 By Type:	1 By Std. Type:	0.65	100.62	3	3	0	5	N	0.70
		No Data	(S,Sr)-Beta-2 Naphthylmethylaspartate	Small molecule	0	273.29	Ľ	1 Ву Туре:	1 By Std. Type:	1.50	100.62	3	3	0	5	N	0.77

Figure 12: Example of compounds associated with SLC1A1 on ChEMBL (screenshot from https://www.ebi.ac.uk/chembl/g/#browse/compounds/filter/\_metadata.related\_tar-gets.all\_chembl\_ids%3ACHEMBL2721, accessed 06/15/20 )

Figure 12 shows the beginning of the list of 244 compounds associated with SLC1A1. It includes the 2D structure, its ChEMBL ID, the type, the stage of approval and chemical properties like the molecular weight, the AlogP or the number of rotatable bonds. Other possibilities to access ChEMBL are using the downloadable files, the semantic website or through the provided web services.

For this work, ChEMBL was accessed via ChEMBL web services. ChEMBL offers a RESTful API that can be accessed via the REST nodes in KNIME, which is further described at the chapter 'Workflows', starting from page 26ff. The default format is XML, but it can also be downloaded in JSON format [14]. As the API request is renewed, every time the workflow runs, it is designated to be updated automatically when a new version is released. The version used for the analysis part of this work, was ChEMBL 27, last updated on 05/18/2020.

#### 2.2.7 PubChem

PubChem is a database containing one of the most extensive sets of publicly available information about molecules and bioactivities. It is an open database, which means that everyone can upload their scientific data to PubChem [15], [16]. In May 2020, it contained more than 100 million unique structures and almost 270 million bioactivity data points from more than 700 sources [62]. The data on PubChem is organised into three interconnected databases: PubChem Bioassays, PubChem Substances and PubChem Compounds.

'SIDs' (Substance IDs) refer to the IDs given to a substance when uploaded by a contributor, which is why one structure can have several SIDs. In contrast, 'CIDs' (Compound IDs) denote to unique structures after a standardisation process that aggregates all of the substance records for the same molecule. PubChem's assay identifier is called 'AID' [16].

Apart from the direct query via the website, PubChem offers two ways to access its data programmatically - the PUG-REST and the PUG-SOAP. More information can be found at https://pubchemdocs.ncbi.nlm.nih.gov/programmatic-access.

Unfortunately, using the programmatic access would currently lead into many inconvenient, intermediate steps as it is, starting from targets (EntrezGeneIDs), only possible to search for AIDs. Receiving active CIDs associated with SLCs and their bioactivity data would result in five API calls with several intermediate steps. At the same time, it is possible to download CSV files with all tested compounds per target directly from the PubChem web interface. As these CSV files already contain all of the desired information, the data was automatically downloaded within the workflow. The data is updated to the newest version, every time the workflow runs on the server. The data used for the analysis part of this work has last been updated on 05/18/2020.

4.1 Tested Co	mpounds			0 Z
351 items View More	Rows & Details 🗾			👱 Download
			SORT BY 🔶 Activity	~
Structure	Activity	Activity Type	Activity Value, $\mu M$	Compound CID
	Active	IC50	8	4133412
- <mark>1</mark> 00	Active	IC50	6.5	12047100
-15-	Active	IC50	8.4	12047098

Figure 13: Example of compounds associated with SLC1A1 on PubChem (screenshot from https://pubchem.ncbi.nlm.nih.gov/gene/6505#section=Chemicals-and-Bioactivities, accessed 06/15/2020)

Figure 13 shows the beginning of the section that includes all tested compounds and that is downloaded per target for SLC1A1. It contains the structure, the activity type and value and the PubChem CID.

The PUG-REST API was additionally used for retrieving additional information: associated Molecule/Drug names and Canonical SMILES.

#### 2.2.8 Datasets and content of file 'SLCs and rare diseases'

The information extracted about SLCs and rare diseases can be roughly divided into three categories: attributes describing the genes/proteins, attributes describing the rare diseases and attributes describing the gene-disease associations.

The following tables, Table 1 -

Table 7, list the datasets together with the attributes used for the emerging table. The left column shows the name used in the emerging KNIME table while the right column offers a short description when necessary.

Table 1: attributes retrieved from the file RESOLUTE_SI
---

attributes describing the gene/protein	description of attributes
SLC name	HGNC gene symbol (see SLCs, p.3f.)
SLC family	
EntrezGene ID	identifier by NCBI
UniProt ID	identifier by UniProt KB

#### Table 2: attributes retrieved from the UniProt KB REST API

attributes describing the gene/protein	description of attributes
Protein name and aliases	protein name & aliases from UniProt KB
Gene aliases	gene aliases from UniProt KB

# Table 3: attributes retrieved from 'Orphanet rare diseases with their associated genes',version 1.2.11/4.1.6 [2018-04-12] (orientdb version)

attributes describing the gene/protein	description of attributes
UniProt ID	corresponding to SwissProt ID, used for
	joining with RESOLUTE_SLC
attributes describing the disease	description of attributes
OrphaNUMBER	Orphanet's specific terminology for rare
	diseases
disease name Orphanet	disease name
attributes describing the disease-gene	description of attributes
association	
PubMed ID	links to articles on PubMed as source of
	validation
DisorderGeneAssociation	e.g. 'disease-causing germline muta-
	tion(s) in', only available for few associa-
	tions

# Table 4: attributes retrieved from 'Rare diseases and cross-referencing', version1.2.11/4.1.6 [2018-04-12] (orientdb version)

attributes describing the disease	description of attributes
OrphaNUMBER	Orphanet's specific terminology for rare
	diseases
disease name Orphanet	disease name
synonyms	when available
ICD10	disease classification system
UMLS ID	external identifier, used for joining with
	DisGeNET
OMIM ID, MesH ID	external identifiers

#### Table 5: attributes retrieved from DisGeNET, 'ALL gene-disease-pmid associations', renewed every execution, analysis version: version 7.0 [2020-05-04]

attributes describing the gene	description of attributes
EntrezGene ID	corresponding to 'geneID', used for join-
	ing the results with RESOLUTE_SLCs
attributes describing the disease	description of attributes
UMLS ID	corresponding to 'diseaseID', used for
	joining the results with Orphanet
disease name DisGeNET	disease name
MeSH class code	disease classification system
attributes describing the disease-gene	description of attributes
association	
PubMed ID	links to articles on PubMed as source of
	validation
DisGeNET score,	metrics provided by DisGeNET,
DSI, DPI, EI.	see p.16
source	Sixteen different sources, see p. 15f.

Table 6: attributes retrieved from DisGeNET 'BeFree gene-disease-pmid associations', renewed every execution, analysis version: version 7.0 [2020-05-04]

attributes describing the disease-gene	description of attributes
association	
sentence	sentence on MEDLINE

#### Table 7: columns added within KNIME

MeSH class name	based on the MesH class code
Database	Orphanet/ DisGeNET as filtering option
Reliability of source	categories described at p. 15f., filtering option

#### 2.2.9 Datasets and content of file 'SLCs and molecules'

The information extracted about compounds can be, again, roughly divided into three categories: attributes describing the genes/proteins, attributes describing the compounds, and attributes describing the gene-compound associations. The following tables, **Fehler! Ungültiger Eigenverweis auf Textmarke.** - Table 12, list the datasets together with the attributes used for the emerging table.

Table 8: attributes retrieved from DrugBank, 'All drugs', version 5.1.2 [2018-12-20]

attributes describing the gene/protein	description of attributes
UniProt ID	used for joining with RESOLUTE_SLCs
attributes describing the compound	description of attributes
Molecule/Drug Name	name of drug
DrugBank ID	specific identifier from DrugBank
attributes describing the compound-	description of attributes
gene association	
Activity Comment	corresponding to 'action', e.g. inhibitor, in-
	ducer
PubMed IDs	links to articles on PubMed as source of
	validation
Table 9: attributes retrieved from ChEMBL via RESTful API, renewed every run, analysisversion: version 27, [2020-05-18].

attributes describing the gene/protein	description of attributes
UniProt ID	used for retrieving results via API
attributes describing the compound	description of attributes
ChEMBL ID	specific identifier from ChEMBL
Molecule/Drug name	Molecule name
Canonical SMILES	specification describing the structure,
	https://en.wikipedia.org/wiki/Simpli-
	fied_molecular-input_line-entry_system
attributes describing the compound-	description of attributes
gene association	
Activity name	e.g. $IC_{50}$ , $EC_{50}$ , inhibition
Activity value	activity value in nm or µm
pChEMBL value	standardised value, described at subsec-
	tion 'ChEMBL', p. 18ff.
Assay ID	ChEMBL identifier for assay
Assay description	description of assay
ChEMBL data validity comment	flags potential error, e.g. 'outside typical
	range'
ChEMBL potential duplicate flag	flags potential duplicate

Table 10: attributes retrieved from PubChem by download of .CSV files, renewed every
run, analysis: last updated 05/18/2020

attributes describing the gene/protein	description of attributes
EntrezGene ID	used for retrieving results via API
attributes describing the compound	description of attributes
PubChem CID	compound ID
PubChem SID	substance ID

attributes describing the compound-	description of attributes
gene association	
Activity Name	e.g. Km, EC50
Activity Value	activity value in µm
Assay ID	AID identifier
Assay Description	description of assay
PubMed IDs	links to articles on PubMed as source of
	validation

# Table 11: attributes retrieved from PubChem through API calls

attributes describing the compound	description of attributes			
Canonical SMILES	specification describing the structure			
Molecule/Drug Name	title			

# Table 12: Columns added within KNIME

Database	DrugBank, ChEMBL, PubChem as a filtering option
possible inducer/inhibitor	This column is added based on the type of action (DrugBank) or
	the assay description (ChEMBL, PubChem), further described at
	chapter 'Workflow for data retrieval', p.31ff.

## 2.3 Workflow for data retrieval

The first workflow is developed to be run on the KNIME Server. It is scheduled every fifteen days, mainly to update the data from DisGeNET, ChEMBL and PubChem.

The workflow consists of three major steps.



Figure 14: Overview of the workflow for the retrieval of SLC-rare disease-molecule associations Figure 14 shows an overview of the workflow, consisting of several Metanodes. Each of the Metanodes contains numerous nodes which make the workflow much more complex and are further described in the following subsections.

After the first and the second step, one tabulated file each is automatically saved directly on the KNIME Server. As the data needs to be curated, these files can be accessed, curated and downloaded through the second workflow at the WebPortal (see section 2.4, p.38ff.).

The file *RESOLUTE\_SLCs* forms the starting point of the workflow. As a first step, protein aliases are extracted from the UniProt KB by using the API to provide a more extensive set of parameters. Then, rare diseases associated with SLCs are retrieved from Orphanet and DisGeNET. As a third step, associated drugs and molecules are retrieved from DrugBank, ChEMBL and PubChem.

As the workflow consists, altogether, of more than 100 nodes, and some parts were adapted from workflows created by other members of the Pharmacoinformatics Research Group, not every node and its configuration is described in detail.

# 2.3.1 Extraction of additional information about SLCs

The starting point of the workflow is the file RESOLUTE\_SLCs. It was provided from the RESOLUTE project in June 2019 and is customised for its purpose in the workflow, as only the columns 'SLC name', 'SLC family', 'UniProt ID.' and 'Entrez Gene ID' were kept in the file used for this work.

After importing it with an *Excel Reader*, the URI for the UniProt REST API is generated with a *String Manipulation* node. The API is used to provide Protein and Gene Aliases for the curation of results in the second workflow, as shown in subsection 3.2,p.53ff.





The URL for the REST API call is generated in a *String Manipulation* node from the expression '*join("https://www.uniprot.org/uniprot/",*\$UniProt.ID\$,".xml")'.

The URL consists of a data set, here 'uniprot' and the entry's unique identifier, here '*\$UniProt.ID\$*'.

The expression '*\$UniProt.ID\$*' specifies that the value for each row is taken directly from the column *UniProt.ID* which means that the UniProt entry is downloaded for each UniProt ID listed in the SLC table. The syntax '*.xml*' specifies that the entries are downloaded in XML format. Other possible formats would be for example .txt, .rdf and .fasta. The *String Manipulation* node is followed by a *Parallel Chunk Start* node, that splits the API call rows into smaller chunks of the same size that are executed in parallel by the following *GET Request* node as this speeds up the process. The *Parallel Chunk End* node collects the results. The resulting XML files are further processed with an *XPath* node.



Figure 16: Example XML file as retrieved via UniProt API

Two XPath queries are used to retrieve the recommended and alternative names of the proteins (highlighted in yellow in Figure 16) as well as the names of their encoding genes (highlighted in light blue).

The XPath query for gene name aliases can easily be created in the configuration window of the XPath node by clicking on the required attribute. It only needs to be considered that the 'Multiple tag option' of the XPath query setting is set to 'Multiple Rows' as the default setting 'Single Cell' would result in a single row containing only the first entry. As the protein names are not used for further automatic processing, recommended as well as alternative protein names are combined in a single column named 'Protein Name'. The XPath expression used for this extraction is '//dns:fullname'. The double slash configures that not only attribute nodes from the root element, but all nodes in the documents that match the expression are selected.

A *GroupBy* node follows that groups the rows per 'UniProt ID'. 'Protein Name' and 'Gene Aliases' are aggregated and concatenated with commas in between. The new

information is then joined with the original table. Figure 17 shows a screenshot of the table before and after joining Gene and Protein names and aliases.

			Row ID		S	SLC	name	Ι	Entrez	[[	S	UniPro	t	S	SL(	C family	y	
		Ro	w0		SLC	1A1		650	5	P	430	005		SLC	1			
	Row1 SL			SLC	1A2	6506		P	430	004		SLC1						
		Ro	w2		SLC	1A3		650	7	P	430	003		SLC	1			
		Ro	w3		SLC	1A4		650	9	P	430	007		SLC	1			
		Ro	w4		SLC	1A5		651	.0	9	215	758		SLC	1			
S SLC name	Entrez	S UniProt	S SLC family	S Gene	name a	liases [	S Protein na	me										
SLC1A1	JLCIA1 6505 P43005 SLC1 SLCIA1; EAAC1; EAAC1; EAAT3 Excitatory amino acid transporter 3; Excitatory amino-acid carrier 1; Neuronal and epithelial glutamate transporter; Sodium-dependent glutamate/aspartate transporte								insporter; Sodium-dependent glutamate/aspartate transporter 3; Solu									
SLC1A2	6506	P43004	SLC1	SLC1A2; E	EAAT2; (	GLT1 E	xcitatory ami	no acid	transporter 2; G	lutamate	e/aspa	artate transp	orter II; S	Sodium	-depen	dent <mark>g</mark> lutama	ate/as	spartate transporter 2; Solute carrier family 1 member 2
SLC1A3	6507	P43003	SLC1	SLC1A3; E	EAAT1; (	GLAS E	Excitatory amino acid transporter 1; Sodium-dependent glutamate/aspartate transporter 1; Solute carrier family 1 member 3											
SLC1A4	6509	P43007	SLC1	SLC1A4; A	ASCT1; S	SATT N	leutral amino	eutral amino acid transporter A; Alanine/serine/cysteine/threonine transporter 1; SATT; Solute carrier family 1 member 4										
SI C1A5	6510	015758	SLC1	SLC1A5: A	ASCT2: I	M7V N	leutral amino	acid tra	ansporter B(0): Ba	aboon M	17 viru	s recentor: R	D114/sin	nian tvr	e Dire	trovirus recer	otor:	Sodium-dependent neutral amino acid transporter type 2: Solute carr

Figure 17: Table before and after joining Gene and Protein names

### 2.3.2 Extraction of rare diseases

The extraction of rare diseases was adapted from a workflow created by Jana

Gurinova[2].

It starts with reading in the file *ALL gene-disease-pmid associations*[52] from Dis-GeNET, which is automatically downloaded from the DisGeNET download page as a tab-separated file (.tsv) each time the workflow is executed. The *File Reader* node reads the data directly from the URL location.

	geneId	S geneSy	D DSI	D DPI	S diseaseId	S disease	S disease	S disease	S disease	D score	DEI	YearInitial	YearFinal	pmid	S source
Ī	1	A 1BG	0.857	0.172	C0019209	Hepatomegaly	phenotype	C06;C23	Finding	0.3	?	2017	2017	28108177	CTD_human
	1	A 1BG	0.857	0.172	C0013080	Down Syndr	disease	C10;C16	Disease or S	0.01	1	2011	2011	21360684	BEFREE
	1	A 1BG	0.857	0.172	C0036341	Schizophrenia	disease	F03	Mental or Be	0.3	?	2015	2015	25821032	CTD_human
	1	A 1BG	0.857	0.172	C0001418	Adenocarcin	group	C04	Neoplastic P	0.01	?	2008	2008	18706098	LHGDN
	1	A 1BG	0.857	0.172	C0002736	Amyotrophic	disease	C10;C18	Disease or S	0.01	1	2009	2009	18973555	BEFREE
	1	A 1BG	0.857	0.172	C0017636	Glioblastoma	disease	C04	Neoplastic P	0.01	1	2014	2014	24096582	BEFREE
	2	A2M	0.564	0.724	C0002395	Alzheimer's	disease	C10;F03	Disease or S	0.4	0.848	1998	2016	10505652	BEFREE
l	2	A2M	0.564	0.724	C0027627	Neoplasm M	phenotype	C04;C23	Neoplastic P	0.03	1	1996	2015	25056661	BEFREE
	2	A2M	0.564	0.724	C0002726	Amyloidosis	disease	C18	Disease or S	0.04	1	1999	2008	10899157	BEFREE
	2	A2M	0.564	0.724	C0007102	Malignant tu	disease	C04;C06	Neoplastic P	0.3	?	2004	2004	15059925	CTD_human
	2	A2M	0.564	0.724	C0239981	Hypoalbumin	disease	C15	Disease or S	0.01	1	1998	1998	9453001	BEFREE

Figure 18: Example part of DisGeNET's file "ALL gene-disease-pmid associations" as seen in the KNIME table

Figure 18 shows an example part of the file from DisGeNET, as seen in KNIME. The table contains 15 columns including gene & disease ID (Entrez Gene ID and UMLS), the disease name, the MeSH disease class, several metrics, PubMed IDs and sources. It is joined with the table from the first step to filter for SLCs as targets with the setting 'Inner Join', which means that only matching rows show up in the Output Table.

Next, the file '*BeFree gene-disease-pmid associations for Pubannotations*' is also read in with a *File Reader* node via URL. The sentence from MEDLINE causal for the association retrieved via BEFREE text mining is joined into the table as this makes it easier to curate the results manually later on (see section 3.2,p.53f.).

However, DisGeNET does not include the option to filter for rare diseases. For this reason, Orphanet is used as it is a database dedicated explicitly to rare diseases. The XML file *Orphanet: Rare diseases and cross-referencing* is read in with an *XML reader* node. Inside the *XML reader* node, it is possible to configure an XPath filter. The XPath filter '/JDBOR/DisorderList/Disorder' results in one row per rare disease. This file contains several external identifiers for rare diseases. The UMLS identifier is extracted to join the resulting table with the results from DisGeNET. Also, the identifiers OMIM and MeSH, the disease name, ORPHAnumber and synonyms are extracted to provide a comprehensive set of available identifiers. The extraction is achieved via an *XPath* node that follows the *XML reader* node on the workflow. The XPath queries are reused from the workflow of Jana Gurinova [2].

Some disease entries on Orphanet do not contain a known UMLS identifier. However, Orphanet offers its own dataset for target-disease-associations, *Orphanet rare diseases with their associated genes,* which is additionally used for retrieving SLC-rare diseaseassociations.

An *XPath* node extracts ORPHAnumber, disease name, the DisorderGeneAssociation (only provided for a few disease-target associations) as well as the UniProt ID and the GeneSymbol of the involved target and the PubMed ID as a source of validation. Also, some more adaptations to the dataset are made to provide a more extensive set of information.

The DisGeNET file contains the MeSH disease class codes. However, all disease class codes, separated with semicolons, are listed in one single cell, which would make it difficult to filter for specific MeSH disease classes via KNIME.





For this reason, the Cell Splitter node is integrated, which splits the cells of the column 'disease class' into parts after each semicolon. The output setting is set to 'list' which results in one column that contains collection cells. The Ungroup node leads to one row for each MeSH disease class code. The codes are then joined with a table that is manually created based on the MeSH tree view and additionally contains the MeSH disease class names.

Another parameter suitable for filtering at the second workflow would be the 'reliability of sources'. The Orphanet database as well as parts of DisGeNET is manually curated. However, some of the gene-disease-associations included in DisGeNET derive from sources that would need further curation. DisGeNET offers four categories for gene-disease associations according to the source, which are further described at subsection 2.2.4, p.15ff. As the source but not the category is included in the dataset, the categories are manually added with a *Rule Engine* node. Then, the results from both databases, Orphanet and DisGeNET, are concatenated and the resulting table is saved as a table file directly on the KNIME Server, as it can be accessed through the second workflow directly from the WebPortal (see subsection 2.4, p.38ff.)

#### 2.3.3 Extraction of drugs/ molecules

Drugs and molecules, associated with SLCs with retrieved rare disease associations, are extracted from three databases simultaneously. As a first step, the resulting table from step two is grouped by UniProt ID (for Drugbank and ChEMBL) and EntrezGene ID (for PubChem) respectively, to extract possible drugs and molecules per unique SLC.

## 2.3.3.1 Drugbank

The drug extraction from Drugbank was adapted from a workflow created by Jana Gurinova[2]. The XML file is read in with an *XML reader* node. As the file is really large, the execution needs to be done through the KNIME Server, as the memory of most laptops or computers would be overloaded. The XML file contains an extensive set of information. This is why it takes four *XPath* nodes to extract all the necessary information. The first *XPath* node, as shown in Figure 20, divides the large XML file into one drug XML entry per row. The used XPath query is '/dns:drugbank/dns:drug' and it is configured to create node cells, which means that the large XML file is split into smaller XML parts that can be further accessed through *XPath* nodes.

AL column: IML XML		
Remove source co	olumn.	
XPath summary		
Column name	XPath query	Туре
XMI	/dns:drugbank/dns:drug	Node(Multiple Rows)

Figure 20: Configuration of first XPath node for Drugbank

In the second *XPath* node, the drug name and the Drugbank identifier are extracted and the protein type is, again, extracted as node cell.

Remove source column.		· · · · · · · · · · · · · · · · · · ·
Column name	XPath query	Туре
Drug name	/dns:drug/dns:name	String(SingleCell)
protein type		Node(Multiple Rows)
Drugbank ID	/dns:drug/dns:drugban	String(SingleCell)
Selected XPath: Selected	d XML element is not a tag	nor an attribute.
A	dd XPath Edit XPath	h Remove XPath

#### Figure 21: Configuration of second XPath node for Drugbank

The XPath for the Drug name was reused from Gurinova[2]. The XPath for the protein type was changed as Drugbank lists proteins associated with the listed drugs in four categories: Target, Enzyme, Transporter and Carrier. A set of nodes was used to extract all of the included information as the information provided about proteins is located in different parts of the file based on the protein type.



Figure 22: Nodes for the retrieval of 'protein type' node via XPath

The first node is a *Table Creator* node, shown in Figure 23, that creates a table containing all of the four XPaths necessary for the extraction.

A *Table Row To Variable Loop* follows that turns each of the rows into variables because the following *XPath* node is configured to use the emerging variable 'type XPath' as XPath for the column 'protein type', extracted as node cell.

Table Crea	tor Settings Flow Variables Job Manager Sele	ection Memory Policy	
Input line:			
	S type Xpath	S Protein type	
Row0	/dns:drug/dns:targets/dns:target	Target	^
Row1	/dns:drug/dns:enzymes/dns:enzyme	Enzyme	
Row2	/dns:drug/dns:transporters/dns:transporter	Transporter	
Row3	/dns:drug/dns:carriers/dns:carrier	Carrier	

Figure 23: Table creator node for the retrieval of proteins associated with drugs on Drugbank

The *Variable to Table Column* node joins the 'protein type' column into the resulting table. After four iterations, the results are collected with a *Loop End* node.

Two more *XPath* nodes follow, with the first one extracting the type of action (only available for few associations) and references and extracting the information about the associated polypeptides as node cell starting from the node cell 'protein type'. The fourth *XPath* node extracts the protein's name and UniProt ID out of the node cell 'polypeptide'.

The extracted information is then joined with the list of UniProt IDs deriving from Step two only to keep only drugs associated with SLCs that are associated with rare diseases. In the next step, drug-protein associations listed as 'substrate' are excluded. Two *Rule Engine* nodes add the two columns 'possible inhibitor' and 'possible inducer' based on the type of action (e.g., The action type 'antagonist' would be listed as 'possible inhibitor' while the action type 'agonist' would result in 'possible inducer'). In the last step, columns are renamed and an additional column named 'Database' is inserted that contains the value 'Drugbank'.

## 2.3.3.2 ChEMBL

The extraction of drug-like compounds from ChEMBL was adapted from a Metanode created by Daniela Digles[63]. The sequence of nodes and the used APIs were reused from the mentioned Metanode. However, the format for data retrieval was changed from JSON to XML and the following nodes from *JSON Path* to *XPath* nodes to make the workflow more consistent.

This part of the workflow consists basically of two API calls.

The first API call starts with a *String Manipulation* node with the expression:

'join("https://www.ebi.ac.uk/chembl/api/data/target.xml?target\_components\_\_accession=",\$UniProt.ID\$)'. A *GET Request* node retrieves information about the targets for the provided UniProt IDs.

The following *XPath* node extracts the target's name, its ChEMBL ID and the target type, as shown in Figure 24.

Row ID	S 🔻 Uni	S pref_name	S target_chembl_id	S * target_type
Row332_1	Q9Y6R1	?	?	?
Row331_1	Q9Y6M7	Sodium bicarbonate cotransporter 3	CHEMBL3774290	SINGLE PROTEIN
Row330_1	Q9Y6M5	?	?	?
Row329_2	Q9Y6L6	Canalicular multispecific organic anion	CHEMBL3885536	PROTEIN FAMILY

#### Figure 24: Table after first ChEMBL API call

Since its update in 2014, ChEMBL distinguishes between different types of protein targets. The target type 'SINGLE PROTEIN' specifies that the compound is considered to interact specifically with the protein. However, the target type 'PROTEIN FAMILY' indicates, that either the compound interacts non-specifically with all members of a protein family or that the assay conditions make it impossible to identify the specific protein the compound is interacting with.[59]

Because of this, rows containing the target type 'PROTEIN FAMILY' as well as empty rows, which means that the specific UniProt ID is not associated with any targets listed on ChEMBL are excluded from the table.

The 'target\_chembl\_id' is necessary as it is part of the URI for the second API call that retrieves the bioactivity data. It starts with a *String Manipulation* node with the expression 'join("https://www.ebi.ac.uk/chembl/api/data/activity.xml?target\_chembl\_id=",\$target\_chembl\_id\$,"&limit=1000")'. The syntax 'limit=1000' specifies that the first 1000 bio-activities are returned. The default limit for an API call on ChEMBL would be 20. The limit can be increased, but 1000 is the maximum allowed value. The 'page\_meta' section of the resulting XML files provides information about the limit, offset and total count.

58000	¢.	<pre><pre><pre><pre><pre><pre><pre><pre></pre></pre></pre></pre></pre></pre></pre></pre>
58001		<li>limit&gt;1000</li>
58002		<pre><next>/chembl/api/data/activity.xml?target_chembl_id=CHEMBL1293277&amp;limit=1000&amp;offset=1000</next></pre>
58003	ф.	<offset></offset>
58004	-	
58005	ф.	<previous></previous>
58006	-	
58007		<total_count>18911</total_count>
58008	-	

Figure 25: Screenshot of the page\_meta section of the retrieved XML for NPC1

When a target is associated with more than 1000 bioactivities, like the NPC1 protein shown in Figure 25, the end part of the link to the next page is provided. The NPC1 protein is associated with 18911 bioactivity values, which means that, altogether, 19 API calls are needed to extract all of the data.



Because of this, a set of nodes is used, as shown in Figure 26.



Loop Start and a Recursive Loop End node.

Data passed to port 0 (the top port) of the *Recursive Loop End* node is collected while data passed to port 1 (the bottom port) of the *Recursive Loop End* is returned to the *Recursive Loop Start*. The end part of the link provided in the page\_meta section of the retrieved XML files is extracted with the *XPath* node that follows the API call. In addition, this *XPath* node extracts the bioactivity data as a node collection cell, which means that every row contains a list of XML files including information about the bioactivity only. After the extraction, a *Column Splitter* node splits the columns into two tables: The bioactivity data is passed to port 0 and therefore collected. The link is completed with a *StringManipulation* node and moved to port 1 and thus to the *Recursive Loop Start* node for the next iteration. After all of the data is retrieved, an *Ungroup* node leads to one row per bioactivity value and an *XPath* node extracts the desired information. The extracted data includes information about the bioassays, the molecules and the bioactivity data as well as the originating source.

ChEMBL contains data from altogether 48 sources, including parts of the database Pub-Chem. As PubChem is used as another source of SLC-molecule associations (see 2.3.3.3), the bioactivity values originating from this source are excluded in a first step. The extracted information about bioassays contains the assay ChEMBL ID, the assay description and the assay type. ChEMBL distinguishes between six types of assays including (A) for ADME data assays, (B) for Binding assays, (F) for Functional assay, (T) for Toxicity assays, (P) for Physicochemical assays and (U) for Unclassified. As only the results from binding assays are relevant for the aim of this work, the rest is filtered out. Only a few rows include an activity comment. However, as some of the bioactivity values contain the activity comment 'inactive' or 'not active', these rows are filtered out. The 'data validity comment' flags activity values that are, for example, outside a typical range for that specific activity type or seem to derive from a transcription error. Furthermore, potential duplicates are flagged in an additional column. These columns are integrated into the emerging table, to let users of the second workflow decide whether or not to keep these values in their results.

In the next step, substrates are excluded as all molecule-target associations containing the activity type 'Km' or 'Vmax' or the activity comment 'substrate' are filtered out. Two *Rule Engine* nodes add the columns 'possible inhibitor' and 'possible inducer' based on the activity comment and the assay description: Assay descriptions including the syntaxes 'inhibitor', 'inhibition' or 'antagonist' are listed as 'possible inhibitor'. In contrast, assay descriptions containing 'induction', 'inducer', 'activator' or 'modulator' are listed as 'possible inducer'.

In the last step, the columns are renamed and the additional column 'Database' is inserted with the value 'ChEMBL'.

# 2.3.3.3 PubChem

The extraction of compounds from PubChem was adapted from a workflow created by Anna Seiler[64].

It starts with a *String Manipulation* node creating the URL links for the download of tested compounds associated with SLCs (beforehand grouped by EntrezGene ID) using the expression 'join("https://pub-

chem.ncbi.nlm.nih.gov/sdq/sdqagent.cgi?infmt=json&outfmt=jsonp&query={%22down-load%22:%22\*%22,%22collection%22:%22bioactiv-

ity%22,%22where%22:{%22ands%22:[{%22geneid%22:%22", \$EntrezGene ID\$,"%22},{%22cid%22:%22notnull%22},{%22activity%22:%22Active%22}]},%22order%22:[%22relevancescore,desc%22],%22start%22:1,%22limit%22:1000000}")' As a very long list of 'inactive' compounds is listed for some of the SLCs and this would lead to a significant amount of unnecessary data as well as to a lag in time, the download is already specified to compounds listed as 'active'.



Figure 27: Nodes for the download of active CIDs associated with SLCs from PubChem A *Table Row To Variable Loop Start* node turns row after row into variables for each loop iteration, the *CSV Reader* node reads in the CSV files deriving from the provided URL and the *Loop End* node collects all of the data.

The result is a table containing compounds listed as 'active' towards SLCs, including information about the bioassay and the bioactivity values.

As PubChem contains data from ChEMBL, but ChEMBL is used as another source for retrieving SLC-molecule-association, data deriving from the source 'ChEMBL' is excluded in a first step.

Next, two API calls follow that retrieve additional information:

The first API call deriving from the *String Manipulation* node with the expression join("https://pubchem.ncbi.nlm.nih.gov/rest/pug/compound/cid/",string(\$cid\$),"/description/XML") retrieves all descriptions associated with the compound to extract the title which corresponds to the name of the molecule. The second API call retrieves Canonical SMILES describing the structure.

The additional columns 'possible inducer' and 'possible inhibitor' are then added based on the assay description similar to ChEMBL (see 2.3.3.2, p. 33f.). The results are joined with UniProt IDs for concatenating with the results from Drugbank and ChEMBL, and the additional column 'Database' with the value 'PubChem' is added.

The results from Drugbank, ChEMBL and PubChem are then concatenated and joined with SLC name, family and EntrezGene ID.

The resulting table is again saved as table file on the KNIME Server to be accessed through the second workflow.

## 2.4 Workflow for accessing data (end-user)

A second workflow was created for interested users to access, filter and curate the aggregated data at the KNIME WebPortal as the data needs manual curation, and this would, due to the amount of data, exceed the time constraints of a diploma thesis. This part of the work describes the workflow at the KNIME Analytics Platform, as shown in Figure 28. The workflow as seen by the user at the KNIME WebPortal is further described in section 3, p.53ff.



**Figure 28: Workflow for interested users as seen in the KNIME Analytics Platform** It starts with importing the file 'SLCs and rare diseases' directly from the KNIME Server, where it has been saved during the last scheduled execution of the data retrieval work-flow (see 2.3.2). Its content and originating databases are further described in section 2.2.8, p.20f.

The workflow is then made out of several components containing widgets or view nodes, offering interactive filtering options via the WebPortal.



#### Figure 29: Inside Component 'Filter disease classes/sources'

Figure 29 shows the inside of the first component. It consists of two *Interactive Value Filter Widget* nodes. The first node lets the user choose if results from all sources should be considered or only the ones from curated sources.

Show Label	Custom	Do you want to view all	associations or only r	esults from curated data sources	Open link for description of sour
General Options Filter Column	source		~		
Exclude		Manua	I Selection 🔿 Wildca	rd/Regex Selection	
Filter				<b>T</b> Filter	
	No value:	s in this list	> >>	Curated Data Textmining inferred Data Animal Model	
Enforce ex	dusion		< «	Enforce inclusion	

Figure 30: Dialog window for Interactive Filter Widget

As shown in Figure 30, it is possible to configure a label that is shown on the WebPor-

tal. Also, the column that is dedicated to being filtered needs to be selected.

The next component offers the user the possibility to choose between further filtering for specific SLCs or specific rare diseases.



Figure 31: Inside of Component 'SLCs or rare diseases'

As shown in Figure 31, this can be achieved with two associated nodes: The *Single Selection Widget* node allows the user to choose between the strings 'SLCs' or 'rare diseases'. The selected value is handed to the *Java IF* node through a variable called 'single-selection'.

🛕 Dialog - 0:1029:0:1024 -	Java IF (Table) (SLCs: 0)	—		×
File				
Expression Flow Variables Flow Variable List s <sup>•</sup> single-selection i <sup>•</sup> single-selection (index) s <sup>•</sup> knime.workspace	Job Manager Selection Memory Policy Method Body return \$\${Ssingle-selection}\$\$.equals("SLCs") ? 0 : 1;			
	<			>
	Compile on close			
	OK Apply Cancel	(	2	

#### Figure 32: Dialog window for Java IF node (screenshot)

Figure 32 shows the configuration window for the *Java IF* node, including the Method Body with the expression 'return \$\${Ssingle-selection}\$\$.equals("SLCs") ? 0 : 1;'. The *Java IF* node contains two output ports. When the user chooses 'SLCs' through the *Single Selection Widget* node, the data is handed to the first output port (port 0), making port 1 inactive. When the user chooses 'rare diseases', it leads to the reverse result. As this component leads to two branches with only one being active at a time, the data is then directed to either one of two nodes that are used for filtering either for SLCs or rare diseases dependent on the active port.



#### Figure 33: Inside of Component 'Bar Chart SLCs' (screenshot)

Figure 33 shows a screenshot of the inside of the component used for filtering for SLCs. It starts with a *GroupBy* node that groups the rows by unique SLCs (column: SLC name). At the same time, the number of associated rare diseases is aggregated through the aggregation method 'Unique Count'. This is due to the bulk of data that would lead to a confusing complexity inside the *Bar Chart* node.

After renaming the aggregation column into 'Number of associated rare diseases' and sorting the rows by descending numbers, the data is handed to two *JavaScript* nodes: a *Bar Chart* node and a *Table View* node.

As both of these nodes are placed in the same component, they allow interactive filtering via the WebPortal. The user can choose the dedicated SLCs or a single SLC via the *Bar Chart* node where the associations are visually displayed in the form of a Bar Chart graph with SLC names being the category column on the x-Axis and the number of associated diseases being shown on the y-Axis.

The selected values from the *Bar Chart* node are directly handed to the *Table View* node that includes an added column called 'Selected'. Once, SLCs are chosen via the *Bar Chart* node, the value of the corresponding row is set to 'true'.

The following *Row Filter* node filters for only selected values and the *Joiner* node joins the selected SLCs back with the full table of SLC-rare disease associations.

When the user chooses to filter for rare diseases, the component is constructed the same way, but with the 'disease name Orphanet' being displayed on the x-Axis of the

*Bar Chart* and the number of associated SLCs on the y-Axis. An *End IF* node collects the data either from the top or bottom input depending on the active branch. In the next step, the user can choose between manually curating the filtered data or continuing with downloading the file. This is, again, achieved with a *Java If* node in combination with a *Single Selection Widget* node as further explained at p.39.



Figure 34: Combination of nodes/metanodes for manual curation

When the user decides to curate the results manually, a set of nodes follow that is based on a workflow created by Riccardo Martini.

The first node is a *Chunk Loop Start* node that splits the table into one row at a time.

This node is followed by a metanode with the name 'Curation\_preparation', shown in Figure 35.



Figure 35: Inside of metanode 'curation\_preparation'

This metanode contains four *Column Filter* nodes that each include four to five columns, as shown in Figure 36 and filter out the rest to build a clearly-arranged structure for the curation step.

Exclude  Fitter  S EntrezGene ID  G Giease name Orphanet  G disease name DisGeNET  S Synonym  S OrphaNumber  S UNLS  S OMIM  MeSH  S DisorderGeneAssociation  S diseaseType	> >> <	r Indude Trifter S SLC name S Gene name aliases S Protein name S SLC family S UniProt.ID
Enforce exclusion		O Enforce indusion

Figure 36: Dialog window for Column Filter 1

The data of these four *Column Filter* nodes is handed to the component 'Curation\_step'. The content of each of these nodes is displayed through four *Table View* nodes.



Figure 37: Inside of component 'curation\_step'

Also, the component contains two *Single Selection* nodes and one *String Input* node, as shown in Figure 37. The *Single Selection* nodes offer the user the possibility to decide, whether the association is correct or not and to add the Mode of Action. In contrast, the

*String Input* node lets the user add a comment. These three answers are added to the table as three new columns, and the results for all selected SLC-rare disease associations are collected within the following *Loop End* node. A *Row Filter* node excludes rows with the manual annotation 'Wrong' as well as rows with the Mode of action 'Protein missing' or 'Biomarker'.

Either after the manual curation or after skipping the manual curation, the user gets the chance to download the results from the filtered SLC-rare disease table.



Figure 38: Combination of nodes/ components for downloading

Figure 38 shows the combination of nodes and components necessary for the download. The component *name\_file* contains a *String Configuration* node that gives the user the possibility to insert the name of the file. The *Create Temp Dir* node creates a temporary directory on which the file can be saved before it is downloaded. The *Java Edit Variable* node creates the output location for the *CSV Writer* node out of the chosen file name and the name of the created temporary directory. The *CSV Writer* node saves the file at the temporary directory and can then be downloaded inside the *downloadResults* component that contains a *File Download Widget* node.

Apart from the *File Download Widget* node, the *downloadResults* component contains a *Text Output Widget* node with the Text 'By clicking "next" you can continue downloading the molecules associated with the SLCs.'. This is because after downloading the SLCs-rare diseases results, the user can directly proceed with filtering and downloading the molecules.

The file 'SLCs and molecules' is imported directly from the KNIME Server and is then joined with the results from the *Java IF* node to only pass molecules associated with the selected SLC-rare disease associations. The file's content and its originating databases are mentioned in section 2.2.9, p.23f.

The last component gives the user a choice to include molecules from all three sources, PubChem, ChEMBL and Drugbank, or to choose one or two of them only, which is again achieved through an *Interactive Value Filter Widget*. This file can also be downloaded.

# 3 RESULTS

This part of the thesis shows the results from the workflow, separated into two sections. While section 3.1 sums up and visualises the results from the workflow for data retrieval, 3.2 shows an application example of the second workflow as seen by users accessing it from the KNIME WebPortal.

# 3.1 Results of the workflow for data retrieval

The results presented and described in this chapter are derived from datasets that have last been updated at 05/19/2020. The counts at different positions of the workflow for data retrieval are presented in Table 13. Two tables containing more detailed information about concrete rare diseases and SLCs are presented in the Appendix (starting from page 65).

The start of the workflow is the adapted version of the table *RESOLUTE\_SLCs*, last updated in June 2019. The file was provided by the RESOLUTE project and contains a list of 446 SLCs. The table is complemented with parameters received through the UniProt API.

The second step is the extraction of rare diseases. The information is retrieved from Orphanet and DisGeNET. The XML file 'Orphanet rare diseases and cross-references' acts as a starting point. It contains references for 9.614 diseases. As described in chapter 1.1, the number of rare diseases is usually estimated as up to 8.000. The high number of rare diseases on Orphanet is caused by the fact that it sometimes differentiates between manifestations of diseases that are elsewhere classified as a single disease.[46] 5.547 of these diseases are provided with an identifier in the Unified Medical Language System (UMLS) which is used to join the results with DisGeNET. The file '*ALL gene-disease-pmid associations*' from DisGeNET contains 3.241.576 diseasegene associations. However, the file is not specialised to rare diseases but includes all kinds of conditions. This is why it is joined with the results from 'Orphanet rare diseases and cross-references' which leads to 957.645 rows. When the results are joined with the list of SLCs from step one, the file introduces 4.295 rare disease-SLC associations with 1.021 unique rare diseases associated with 364 SLCs.

The file 'Orphanet rare diseases with their associated genes' was accessed as a second source that additionally introduces 3.766 unique diseases. This file contains 192 SLC- rare disease associations with 178 unique rare diseases associated with 130 SLCs.

After concatenating the results from these two sources, the second part of the workflow results into a file containing 4.377 SLC- rare disease associations with 1.097 unique rare diseases with 367 SLCs with the highest number of retrieved associated diseases (143) for SLC2A1. As a considerable part of the DisGeNET data derives from text mining, the results would require manual curation as there might be false-positive results included as well. When results originating from sources based on text mining are excluded, the workflow results in 916 associations between 458 unique rare diseases with 223 SLCs, also with the highest number of retrieved associated rare diseases per SLC when text mining is included.





The third part of the workflow is the extraction of associated molecules from three sources: PubChem, ChEMBL and Drugbank.

The XML file '*complete database*' from Drugbank was accessed as a source for the retrieval of SLC-molecule associations from Drugbank. It contains entries for 11.922 drugs and when joined with the results from step one and after filtering out substrates, 1.256 SLC-molecule associations with 583 unique molecules for 119 SLCs.

The extraction of molecules from ChEMBL was achieved through the use of several web APIs (see 2.2.6, p.18f.). The extraction of bioactivities leads to 21.822 SLC-molecule associations with 14.155 molecules associated with 85 SLCs.

The results from PubChem derive from a direct download of compounds associated with SLCs from the website. The download results, after the exclusion of results from ChEMBL, into the table contains 19.166 associations, including 18.375 molecules and 64 SLCs.

After concatenating the results from all three databases, 32.885 possible drugs and molecules could be retrieved for 147 out of the 367 SLCs associated with rare diseases, and accordingly when text mining is excluded, for 102 out of the 223 SLCs.



#### Figure 40: Bar Chart showing SLCs with number of associated molecules/drugs

As shown in Figure 40, few SLCs are associated with a high number of molecules, while the majority is associated with less than a hundred molecules. The highest number of molecules is associated with NPC1 (7626).

Figure 41 shows the number of molecules received from each database with the majority of molecules deriving from PubChem, another significant part deriving from

ChEMBL and, in relation, only a few molecules from DrugBank. This is due to results from high throughput screening assays, received from PubChem and ChEMBL, that lead to many compounds for a few solute carriers.

Although DrugBank includes the lowest number of unique molecules, it offers compounds for the broadest range of unique SLCs, as described at p. 47 and shown in Table 13.



Figure 41: Number of molecules received from each database

Figure 42 shows the last stage of the triangulation, the availability of molecules for rare diseases via the intermediate step of SLCs with 'Rare diabetes mellitus' being the rare disease with the highest number of possible, available molecules (28.640). Altogether, the workflow proposes potential molecules for 746 rare diseases. However, the associations would need manual curation as this result includes all molecules somehow active against the SLC and does not consider the role of the SLC in the specific rare disease. Furthermore, the workflow contains false-positive results as further described in chapter 4, p.58f.



Figure 42: Bar Chart showing rare diseases with number of associated molecules

Table 13: Counts at different	positions of the workflow
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	DATASET	ORIGIN	COUNT	SECTION	DESCRIPTION
А	RESOLUTE_SLCs	RESOLUTE project	446	2.3.1	Dataset with SLCs + identifiers
В	UniProt Aliases	UniProt API, starting from A	446	2.3.1	API adds Aliases for proteins and genes
С	Rare diseases and cross- references	Orphadata	9.614	2.3.2	Dataset with rare diseases + identifiers from Orphanet
D	UMLS identifiers	С	5.547	2.3.2	Rare diseases from C with valid UMLS identifier
E	All gene-disease-pmid as- sociations	DisGeNET	3.241.576	2.3.2	Dataset with all gene-disease-pmid associ- ations from DisGeNET
F	SLC-rare disease associa- tions from E	A+E	4.925	2.3.2	E filtered for SLCs as genes via UMLS ID and Entrez Gene ID
G	Rare diseases with their associated genes	Orphadata	3.766	2.3.2	Dataset with Rare disease-gene associa- tions from Orphanet
Н	SLC-rare disease associa- tions from G	A+G	192	2.3.2	G filtered for SLCs as genes via UniProt ID
I	Unique SLC-rare disease associations	F+H	4.377	2.3.2	SLC- rare disease associations from both sources
J	Unique rare diseases	based on I	1.097	2.3.2	number of unique rare diseases associ- ated with SLCs

	DATASET	ORIGIN	COUNT	SECTION	DESCRIPTION
Κ	Unique SLCs	based on I	367	2.3.2	number of unique SLCs associated with
					rare diseases
L	SLC-rare disease associa-	based on I	916	2.3.2	number of SLC-rare disease associations
	tions, text mining excluded				when text mining is excluded (DisGeNET)
М	full_database	Drugbank	11.922	2.3.3.1	Dataset with all drug entries from Drug-
					bank
Ν	unique SLC-molecule as-	K+M	1.817	2.3.3.1	SLC-molecule associations from Drugbank
	sociations Drugbank				
0	Unique SLCs Drugbank	based on N	119	2.3.3.1	number of unique SLCs associated with
					drugs on Drugbank
Ρ	SLC-molecule associa-	ChEMBL API, based	21.822	2.3.3.2	SLC-molecule associations retrieved
	tions ChEMBL	on K			through API calls, PubChem excluded
Q	Unique SLCs ChEMBL	based on P	85	2.3.3.2	number of unique SLCs associated with
					molecules on ChEMBL
R	SLC-molecule associa-	PubChem CIDs	19.166	2.3.3.3	SLC-molecule associations retrieved
	tions PubChem	download, based on			through download from PubChem,
		К			ChEMBL excluded
S	Unique SLCs PubChem	based on R	64	2.3.3.3	number of unique SLCs associated with
					molecules on PubChem
Т	Number of SLCs with	O+P+R	147	2.3.3	Number of SLCs associated with rare dis-
	retrieved molecules				eases that are associated with molecules

## 3.2 Workflow for accessing data as seen by users

When the workflow is opened at the KNIME WebPortal, it shows a starting window containing a short description and the names of the originating databases, as shown in Figure 43.

Workflow for interested users
This workflow was created for users interested in data about SLCs and rare diseases deriving from the workflow 'workflow_for_required_data_retrieval_SLCrarediseasesdrugs'. In a first step, the user is given the possibility to filter, manually curate and download data about SLCs and rare diseases. In a second step, the user can download the molecules associated with the chosen SLCs.
The data has been retrieved from the following databases:
SLCs and rare diseases: Orphanet, DisGeNET
SLCs and molecules: DrugBank, ChEMBL, PubChem
Mail notification on completion

```
Start 🕨
```

#### Figure 43: Starting window of 'Workflow for interested users' at the KNIME WebPortal

After clicking at 'Start', the user sees the first two filter possibilities. The first filter lets the user choose between curated data only or data from all sources, including text mining. Text mining offers great potential for retrieving new associations between rare diseases and SLCs. On the other hand, it also increases the risk of 'false positive' findings, which makes it necessary to curate the results manually afterwards. The page includes a link to the description of sources at the DisGeNET website.



Figure 44: First filtering options at WebPortal

The second filtering option lets the user choose between the inclusion or exclusion of MeSH disease classes, which may be especially interesting when there is a focus on specific diseases.

In the next step, as shown in Figure 45, the user can decide between further filtering for specific rare diseases or SLCs.

# Do you want to further filter for specific diseases or SLCs?



## Figure 45: Filtering option between SLCs or rare diseases

After choosing 'SLCs', the user is presented with a BarChart graph and a corresponding table, as shown in Figure 46.



	SLC name	SLC family	Number of associated rare diseases
	SLC5A7	SLC5	8
	SLC5A8	SLC5	19
	SLC6A1	SLC6	10
	SLC6A11	SLC6	2
	SLC6A12	SLC6	5
	SLC6A13	SLC6	1
	SLC6A14	SLC6	7
	SLC6A18	SLC6	1
	SLC6A19	SLC6	7
$\checkmark$	SLC6A2	SLC6	42

Figure 46: Bar Chart and corresponding table

The user can now decide between choosing all SLC-rare disease associations by crossing the box at the top or selecting a specific SLC or SLCs. The table can be sorted by SLC name, SLC family and the number of associated rare diseases. Besides, the user can choose specific SLCs directly from the Bar Chart.

### Do you want to curate your results manually or continue on downloading?

Curate

#### Figure 47: Curation or download

 $\sim$ 

After selecting SLCs or rare diseases, it is possible to curate the results manually. However, this step can also be skipped, and the results can be downloaded directly. Figure 48 shows an example screenshot of the curation step. The parameters describing SLCs, diseases and their associations are divided into four tables to arrange the page. The user can decide whether the association is correct or not and add the mode of action, which is especially essential for matching the results with possible drugs and molecules. Besides, it is possible to add a comment.

Figure 48 reveals the importance of the curation step, especially when text mining is included. DisGeNET's source BEFREE proposes an association between the rare disease 'Tarsal-carpal coalition syndrome' and SLC25A20. After taking a closer look at the sentence that supports this association, it is shown that the text mining failed in this case. The association was detected based on the abbreviation 'CAC' which can be an alias for the gene SLC25A20. However, in this case, 'CAC' marks a base sequence.

ode of Action Indefined Joss of Function Bain of Function Protein missing Biomarker	^ ~									
omment										
Gene name aliases	Protein na	me	SLC family	UniProt.ID	disease name Orphanet	disease name DisGeNET	Synonym	OrphaNumber		
SLC25A20; CAC; CACT	Mitochondri protein; Car	Mitochondrial carnitine/acylcarnitine carrier protein; Carnitine/acylcarnitine translocase;		Mitochondrial carnitine/acylcarnitine carrier SLi protein; Carnitine/acylcarnitine translocase;	SLC25	O43772	Tarsal-carpal coalition syndrome	TARSAL-CARPAL COALITION	?	1412
	Solute Carri	Showing 1 to 1 of 1 entries				Showing 1 to 1 of 1 entries				
DisorderGene	Association	sentence	P		DisGeNET score	Disease Source	Reliability of	source		
?		However, two of the mutations we	ere	8020137	0.01 BEFREE Textmining		Textmining			
		CGC>CAC base changes at co mutational hotspot for many tumo previously unreported in TCCs ex cases associated with inflammate	don 175, a or types but ccept in ory agents.			Showing 1 to 1 of 1 entries				

Figure 48: Curation example , Tarsal-carpal coalition syndrome'

Besides, BEFREE recognizes TCC as 'Tarsal-carpal coalition syndrome' as this abbreviation is also in use for this disease. However, when opening the entry on PubMed by using the available PubMedID, it is shown that the abbreviation TCC, in this case, stands for 'transitional cell carcinomas'.

Thus, the user can mark the association as 'wrong' which leads to the exclusion of the association from the table in the next step.

Besides, especially DisGeNET includes associations with a protein being altered in disease as a Biomarker, but not as the cause. These associations are also excluded in the next step as they do not pose a potential drug target.

However, some associations are also easily detected as correct and matched with a Mode of Action, as shown in Figure 50. 'Dicarboxylic aminoaciduria' is associated with SLC1A1 and the sentence suggests the Mode of Action 'loss of function'.

Is this correc	:t?									
Ocrrect (	⊖Wrong ⊖I	Maybe								
Mode of Acti	on									
Undefined Loss of Fun Gain of Fund Protein miss Biomarker	ction ction sing									
Comment										
SLC	Gene name			SLC		disease name Orphanet	disease name DisGeNET	Synon	ym	OrphaNumber
name	aliases	Prot	tein name	family	UniProt.ID	Dicarboxylic	Dicarboxylicaminoaciduria	Glutam	ate-	2195
SLC1A1	SLC1A1; EAAC1;	Exci Exci	tatory amino acid transporter 3; tatory amino-acid carrier 1;	SLC1	P43005	aminoaciduria		asparta defect	ate transport	
	EAAT3	neu tran: gluta Solu	ronai and epithelial glutamate sporter; Sodium-dependent amate/aspartate transporter 3; ite carrier family 1 member 1				Showing 1 to 1 of 1	1 entries		
			Showing 1 to 1 of 1 entries							
Disorder	GeneAssocia	tion	sentence	PubMe	dID	DisGeNET	Disease Source		Reliability o	fsource
?			Loss-of-function mutations in the glutamate transporter SLC1A1 cause human dicarboxylic aminoaciduria.	923379   92337   21123	2   21123949 92   1280334 949	0.91	MGD   CLINGEN   CTD_human ORPHANET   UNIPROT   BEFR CLINVAR	 REE	Animal Mode	l   Curated Data   inferred Data

#### Figure 50: Curation example 'Dicarboxylic aminoaciduria'

Besides, associations from SLC1A1 to rare forms of epilepsy, Huntington disease and Amyotrophic lateral sclerosis could be verified. However, it often takes a long time to detect the corresponding Mode of Action.

After the curation step, the table is extended with three columns, one containing the curation 'correct' or 'maybe', the second one holding the mode of action and the third one presenting the 'comment'. The user now gets the chance to download the filtered table file by entering the file's name and then clicking on 'Download' as shown in Figure 51.

SLCs_rarediseases		

Download

By clicking "next" you can continue on downloading the molecules associated with the SLCs.

#### Figure 51: Name file and download SLC\_rarediseases

In the last step, the user gets the possibility to download the file with associated drugs and molecules after choosing between results from all three databases, PubChem, ChEMBL and Drugbank, or results from only one or two of these sources as shown in Figure 52.

#### Do you want to download the results from all 3 databases or do you want to filter?





# 4 DISCUSSION

The aim of the thesis was to give an overview of the role of SLCs in rare diseases via database integration and to show the availability of possible modulators. The workflow created for that purpose was capable of collecting the data from different databases. However, the retrieved data would need manual curation, which would, due to the significant amount of data, exceed the time constraints of a diploma thesis. This is why a second workflow that can be accessed at the KNIME WebPortal was created that gives interested users the option to access, filter, curate and download the aggregated data. The workflow itself, however, is not capable of showing the exact numbers of SLCs in rare diseases as it includes false-positive results.

# 4.1 Limitations of the workflow

As mentioned before, the data aggregated within the first workflow needs manual curation, especially before joining the SLC-rare disease associations with the SLC-drug/molecule associations. This is due to several reasons.

The first reason is that the associations retrieved from databases are not always valid, but include false-positive results. This is mostly caused by data from sources based on text mining. However, text mining, on the other hand, offers excellent potential for re-trieving rather unexplored associations.

Another problem is that most SLC- rare disease associations, as well as most SLCdrug/molecule associations, do not include further information about the association. Because of this, the type of association (e.g. 'loss of function', 'gain of function' for rare diseases or 'inhibitor', 'inducer' for molecules/drugs) needs to be added manually in most cases.

While some wrong associations, as well as the types of association, are relatively easy to detect, as shown in section 3.2,p.53f., the curation of other associations takes a long time.

Besides, rare diseases are sometimes caused by the total deficiency of an SLC protein. In this case, a join with the retrieved SLC-molecule/drug associations would not bring a benefit as diseases caused by a missing protein are often treated with the specific protein itself instead of a drug that inhibits or activates the protein. Because of this, the workflow itself is not capable of being used for drug repurposing or the proposal of active molecules as drugs straight away. However, after the manual curation of data, the results could offer potential.

## 4.2 Possibilities for adaptation

The workflows offer the potential for adaptations and further developments at several positions.

## Possible adaptions for the workflow for data retrieval

The first workflow could be adapted especially at two positions of the workflow. The first position would be the DisGeNET dataset. At the moment, the workflow uses the native datasets, downloaded each time the workflow runs, directly from the Dis-GeNET website. In 2019, DisGeNET introduced an API that gives programmatic access to its data. With this API, it would be possible to reduce the amount of data, as data could be filtered in advance, and only data associated with SLCs could be downloaded. However, as this part of the workflow was already almost finished when the API was introduced, I did not remodel it due to time constraints.

The second position would be the download of bioassays from PubChem. PubChem also offers an API, and in the beginning, it has been tried to use the API instead of the direct download. However, using the API for that purpose would, at the moment, result in a high number of consecutive REST API calls. This is why the direct download per target was preferred. Because of the sometimes high amount of data for single targets, the download is limited to associations marked as 'active' and does not include mole-cules marked as 'unspecified' although they could also pose potential.

Besides, the workflow could also easily be adapted for retrieving data about other proteins as targets. The first file that now includes a list of SLCs can easily be switched with a list of other proteins containing EntrezGene ID and UniProt ID.

## Possible adaptions for the workflow for accessing data

The second workflow could be adapted by implementing more filtering options. A possibility would be to filter for 'probable' gene-disease associations by using the scores offered by DisGeNET. The DisGeNET GDA score, for example, is based on the number and types of sources and associations with a higher rank are more likely to be valid. However, also associations with a lower rank can be correct and offer a higher potential in being rather unexplored and are therefore especially interesting.
Another possibility would be adding more filtering options for the gene-molecule file. An opportunity would include filtering for the 'best' molecule when a long list of molecules is offered for an SLC-disease association. The filtering option could be based on the originating database, for example with the decision of preferencing drugs and experimental drugs from Drugbank and only proposing molecules from ChEMBL and PubChem respectively, when no associations could be retrieved from Drugbank. Another possibility would include ranking the molecules from ChEMBL and PubChem based on the activity values, e.g. proposing only the molecule with the lowest IC50. However, especially results from PubChem often do not contain bioactivity values, but the association is only marked as active.

In conclusion, the collected data suggest that SLCs do play an essential role in rare diseases and could offer great potential as possible drug targets. However, the data needs manual curation to be used to repurpose drugs or find active molecules as potential drug candidates.

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## 6 APPENDIX

## 6.1 Data tables

## 6.1.1 Rare diseases with number of associated molecules and SLCs

disease name Orphanet	OrphaNumber	Number of associated molecules	Number of associated SLCs
Rare diabetes mellitus	101952	28640	129
Rare neurodegenerative disease	182070	24079	41
Rare inborn errors of me- tabolism	68367	24062	44
Huntington disease	399	23982	32
Rare diabetes mellitus type 2	181376	23246	96
Neuroblastoma	635	22311	46
Rare parkinsonian disorder	68402	21960	15
Rare epilepsy	101998	20459	60
Hepatocellular carcinoma	88673	20005	106
Rare malignant breast tu- mor	180257	19883	143
Metachromatic leu- kodystrophy	512	17946	3
Rare tumor of liver and in- trahepatic biliary tract	306636	17921	29
Rare pulmonary disease	101944	17435	16
Rare movement disorder	102003	16909	15
Rare pervasive develop- mental disorder	168778	14491	12
Narcolepsy type 1	2073	14238	8
Bronchopulmonary dyspla- sia	70589	14191	8
Rare bacterial infectious disease	163582	12903	13
Amyloidosis	69	12854	14
Classic progressive supra- nuclear palsy syndrome	240071	12739	4
Progressive supranuclear palsy	683	12739	4
Rare inflammatory bowel disease	104012	12345	45
Cystic fibrosis	586	12317	27
Tuberous sclerosis complex	805	12288	7
Gastrointestinal stromal tu- mor	44890	11574	11
Rare sleep disorder	68354	11116	13
Rare carcinoma of pancreas	217074	10883	46
Angelman syndrome	72	10408	7

Frontotemporal dementia	282	10377	6
Alagille syndrome	52	10320	2
Testicular regression syn-	983	10320	4
drome			
Rare dystonia	68363	9644	10
Down syndrome	870	9615	10
Juvenile myoclonic epilepsy	307	9605	4
Rare carcinoma of stomach	423771	9186	44
Rare epithelial tumor of	63443	9163	42
stomach			
Rare anemia	108997	8995	23
Neurofibromatosis type 1	636	8951	2
Rare viral disease	163585	8506	19
Hodgkin lymphoma	98293	8435	11
Lymphoma	223735	8235	23
Multiple myeloma	29073	8215	30
Renal cell carcinoma	217071	8142	39
Nasopharyngeal carcinoma	150	8139	15
Clear cell renal carcinoma	319276	7935	48
Precursor B-cell acute lym-	99860	7848	10
phoblastic leukemia			
Burkitt lymphoma	543	7722	6
Tauopathy	98527	7641	4
Niemann-Pick disease type	646	7628	3
C			
Gaucher disease	355	7627	3
Alpha-1-antitrypsin defi-	60	7626	2
ciency			_
Brucellosis	1304	7626	3
Congenital muscular dys- trophy	97242	7626	1
Duchenne muscular dystro-	98896	7626	1
phy			
Ebola hemorrhagic fever	319218	7626	2
Gangliosidosis	309144	7626	1
Lissencephaly	48471	7626	2
Muscular dystrophy	98473	7626	1
Niemann-Pick disease type	77292	7626	1
A			
Niemann-Pick disease type	216986	7626	1
C, adult neurologic onset			
Niemann-Pick disease type	216981	7626	1
C, juvenile neurologic onset	0.4.007-5		
Niemann-Pick disease type	216978	7626	1
C, late infantile neurologic			
onset			

Niemann-Pick disease type C, severe early infantile	216975	7626	1
Niemann-Pick disease type C, severe perinatal form	216972	7626	1
Niemann-Pick disease type D	79289	7626	1
Sea-blue histiocytosis	158029	7626	1
Sphingolipidosis	79225	7626	1
Tangier disease	31150	7626	1
Viral hemorrhagic fever	341	7626	2
Rare disorder with ptosis	98578	7240	19
Rare vascular disease	68362	7100	7
Arthrogryposis syndrome	109007	7019	6
Hypertrophic cardiomyopa- thy	217569	6959	12
Prader-Willi syndrome	739	6852	6
Glial tumor	182067	6538	52
Extrapelvic endometriosis	137820	6109	17
Tuberculosis	3389	5972	24
Rare digestive tumor	98059	5939	7
Rare intestinal disease	117569	5872	6
Diffuse large B-cell lym-	544	5838	10
phoma			
Differentiated thyroid carci- noma	146	5802	14
Idiopathic pulmonary arte- rial hypertension	275766	5737	8
Pulmonary arterial hyper- tension	182090	5736	7
B-cell chronic lymphocytic leukemia	67038	5686	16
Cushing syndrome	553	5649	4
Cowden syndrome	201	5521	9
Systemic sclerosis	90291	5502	11
Fragile X syndrome	908	5477	6
Amyotrophic lateral sclero- sis	803	5434	25
Congenital myasthenic syn- drome	590	5434	3
Presynaptic congenital my- asthenic syndromes	98914	5434	3
Spinocerebellar ataxia type 3	98757	5428	5
Osteochondritis dissecans	2764	5386	2
Ovarian cancer	213500	5382	39
Behçet disease	117	5347	7

Rare choreic movement disorder	306715	5342	9
Parkinsonian-pyramidal syndrome	171695	5331	3
Rare congenital non-syn- dromic heart malformation	88991	5325	7
Synovial sarcoma	3273	5285	5
West syndrome	3451	5285	5
Kaposi sarcoma	33276	5276	6
Rare hemolytic anemia	98363	5275	6
Early-onset generalized limb-onset dystonia	256	5274	2
Spinocerebellar ataxia type 6	98758	5274	2
Autosomal monosomy	102020	5271	3
Best vitelliform macular dystrophy	1243	5270	1
Burning mouth syndrome	353253	5270	1
Chronic thromboembolic pulmonary hypertension	70591	5270	1
Familial dysautonomia	1764	5270	1
Harlequin ichthyosis	457	5270	1
High altitude pulmonary edema	330012	5270	1
Interstitial cystitis	37202	5270	2
Postpartum psychosis	443173	5270	1
Progressive pseudorheuma- toid arthropathy of child-	1159	5270	1
nood Drung helly syndrome	2070	5270	1
	2370	5270	1
disease	51657	5270	T
Superficial epidermolytic ichthyosis	455	5270	1
Sweet syndrome	3243	5270	2
Trigeminal neuralgia	221091	5270	1
Distal hereditary motor neuropathy type 7	139589	5214	1
Cerebrotendinous xantho- matosis	909	5171	5
Dopa-responsive dystonia	255	5107	2
Ear-patella-short stature syndrome	2554	5107	2
Elastosis perforans serpigi- nosa	79148	5107	2
Spinocerebellar ataxia type 2	98756	5107	3
Congenital diaphragmatic hernia	2140	5092	5

Mucolipidosis type II	576	5052	2
Autoimmune hemolytic	90033	5050	1
anemia, warm type			
Autoimmune lymphoprolif-	3261	5050	1
erative syndrome			
Autosomal recessive dopa-	101150	5050	1
responsive dystonia			
Desquamative interstitial	98852	5050	1
pneumonia	4766		
Dysequilibrium syndrome	1/66	5050	1
Ehlers-Danlos syndrome	98249	5050	2
Gaucher disease type 1	77259	5050	1
Idiopathic camptocormia	1320	5050	1
Infantile dystonia-parkin- sonism	238455	5050	1
Kufor-Rakeb syndrome	306674	5050	1
Monosomy 5p	281	5050	1
Neurodegeneration with	385	5050	2
brain iron accumulation			
Pantothenate kinase-asso-	157850	5050	1
ciated neurodegeneration			
Partial deletion of the short	261893	5050	1
arm of chromosome 5			
Shwachman-Diamond syn-	811	5050	1
drome	4000	5050	
I hanatophoric dysplasia	1860	5050	1
type 1 Bett sundrama	770	4560	F
Rett syndrome	778	4582	с С
Dravet syndrome	33069	4558	3
Insulhoma Development (second	97279	4471	9
Rare tumor of pancreas	180824	4459	12
Fleck corneal dystrophy	98970	4348	4
Isolated focal cortical dys-	65683	4323	3
piasia Companital humathalamia	2442	4245	2
Congenital hypothalamic	2113	4315	3
namartoma syndrome	672	4215	2
Pallister-Hall syndrome	0/2	4315	5
seizures of infancy	293181	4307	Z
Hereditary sensory and au- tonomic neuropathy type 2	970	4306	2
Dilated cardiomyopathy	217604	4148	9
Neuroendocrine neoplasm	877	4137	10
Rare cardiomyopathy	167848	4128	18
Small cell lung cancer	70573	4089	16
Multiple endocrine neo-	652	4051	4
Neuroendocrine tumor of pancreas	97253	4049	4

Dontin dycalacia	1652	2950	r
Dentin dyspiasia	1055	3833	2
Dentinogenesis imperiecta	49042	3859	2
Rare disease with dentino-	167762	3859	2
Senesis imperiecta	CF2	2825	
multiple endocrine neo-	053	3825	4
plasia type 2 Multiple opdocrine poo	247609	2025	л
plasia type 24	247058	3823	4
Retinoblastoma	790	3802	۵
Von Hinnel Lindau disease	902	2800	6
Canaliagliama	251040	2707	0 2
Vacculitic	231343	2708	۲ ۸
	32735	3708	4
central hervous system	251870	3682	3
primitive neuroectodermai			
Autoinflammatory syn-	03665	3681	1
drome	55005	5081	-
Choreoacanthocytosis	2388	3681	1
Hereditary poppolyposis	443909	3681	2
colon cancer	445909	3081	2
Lynch syndrome	144	3681	2
Neuroacanthocytosis	263440	3681	1
Osteogenesis imperfecta	666	3681	1
Postural orthostatic tachy	443236	2681	1
cardia syndrome due to	445250	3081	Т
NFT deficiency			
Pseudohypoaldosteronism	756	3681	1
type 1			-
Rare autonomic nervous	423662	3681	1
system disorder			
Rare diabetes mellitus type	181371	3669	45
1			
Glioblastoma	360	2982	59
Glycogen storage disease	2088	2940	4
due to GLUT2 deficiency			
Familial renal glucosuria	69076	2925	4
Glucose-galactose malab-	35710	2925	3
sorption			
Rare disorder with lens	98640	2294	18
opacification			
Rare hyperlipidemia	181422	2287	14
Rare dyslipidemia	101953	2177	13
Thyroid tumor	100087	2163	19
Astrocytoma	94	2156	13
Thyroid carcinoma	100088	2109	17
Acute myeloid leukemia	519	1917	47
Syndromic diarrhea	84064	1738	9
Glomerular disease	93548	1685	3

Rare pancreatic disease	101937	1645	5
Acromegaly	963	1586	2
Atypical glycine encephalo-	289863	1585	1
Congenital genu recurva-	295229	1585	1
tum Clysing anconholonathy	407	1505	c
Infantile glycine encenhalo-	289860	1585	2 1
nathy	289800	1992	T
Isolated trigonocephaly	3366	1585	1
Neonatal glycine encepha-	289857	1585	2
lopathy			
Bullous pemphigoid	703	1581	1
Recurrent acute pancreati-	64740	1581	1
tis			
Solar urticaria	97230	1581	1
Undifferentiated connec-	90002	1581	1
tive tissue syndrome	1201	4500	-
Atresia of small intestine	1201	1569	5
Cholera	1/3	1521	4
Bone sarcoma	223727	1350	28
Usteosarcoma	668	1350	28
Autosomal dominant optic atrophy	98672	1256	2
Listeriosis	533	1254	1
Congenital contractural	115	1176	9
Pare breast tumor	180250	112/	17
Matthew-Wood syndrome	2470	1121	47 10
Malignant enithelial tumor	2470	975	20
of ovary	556554	575	20
Angiosarcoma	263413	774	6
Primary biliary cholangitis	186	769	15
Squamous cell carcinoma of	99977	729	30
the esophagus			
Ataxia-telangiectasia	100	689	10
X-linked hypophosphatemia	89936	684	5
Medulloblastoma	616	675	9
Nephroblastoma	654	672	7
Hypoxanthine-guanine	206428	625	4
phosphoribosyltransferase deficiency			
Lesch-Nyhan syndrome	510	625	4
Rare cancer of cervix uteri	213761	610	26
Rare hypothyroidism	181396	577	21
Oligodendroglial tumor	46484	573	4
Oligodendroglioma	251627	573	4
Rare hyperthyroidism	181399	544	12

Chronic myeloid leukemia	521	525	13
Cholangiocarcinoma	70567	524	15
Isolated congenital micro-	199642	523	28
cephaly			
Congenital sodium diarrhea	103908	512	5
Myelodysplastic syndrome	52688	511	11
Aplasia cutis congenita	1114	504	3
Hereditary spastic paraple-	685	494	4
gia			
Immunoglobulin A vascu-	761	494	5
litis			
Carcinoma of esophagus	70482	486	27
Leiomyosarcoma	64720	480	3
Precursor T-cell acute lym-	99861	447	7
phoblastic leukemia			
Neonatal hypoxic and is-	137577	431	5
chemic brain injury			
Progressive familial intrahe-	172	426	3
patic cholestasis			
Hereditary renal hypourice-	94088	401	2
	445	207	
Hereditary breast and ovar-	145	397	1
Nonbrononbthicic	CEE	207	2
Nyelemeningesele	033	200	5 F
Nyelomeningocele	93909	390	2 1 C
	50251	388	10
Cushing disease	96253	384	4
Rolandic epilepsy	1945	369	3
Myocionic-astastic epilepsy	1942	368	2
Arrnythmogenic right ven-	247	305	T
	1250	265	1
Carrier complex	1559	200 265	1
	2041	505	Т
Kawasaki disease	2331	365	5
Loevs-Dietz syndrome	60030	365	2
Malignant tumor of penis	308043	365	1
Multiple endegrine nee	356043	265	1
plasia	270101	505	Т
Multiple polyglapdular tu-	100094	365	1
mor	100034	303	-
Sézary syndrome	3162	365	1
Familial multiple trichoepi-	867	357	5
thelioma			0
Alternating hemiplegia of	2131	355	2
childhood			·
Cytomegalic congenital ad-	95702	355	2
renal hypoplasia			
Malaria	673	355	8

	220480	240	11
Rare nereditary nemochro-	220489	349	11
Collecting duct carcinoma	247202	240	л
	247203	340	4
Juvenile Huntington disease	248111	335	T
Follicular lymphoma	545	333	8
X-linked adrenoleu-	43	325	8
kodystrophy	2222	224	~
Asbestos intoxication	2302	321	2
Adenocarcinoma of the	99976	318	9
esophagus		24.5	_
MODY	552	316	5
Encephalopathy due to	/12//	314	2
GLUI1 deficiency	201672	244	~
Necrotizing enterocolitis	391673	311	2
Fetal and neonatal alloim-	853	310	1
mune thrombocytopenia	171	240	
Primary scierosing cholangi-	1/1	310	4
us T coll non Hodgkin lym	171010	205	л
nhoma	1/1918	303	4
Papillary repaired cell carcia	310708	304	л
noma	515250	50-	-
Channelonathy	140503	303	2
Betinonathy of prematurity	90050	303	2
Congenital hilateral ab-	48	281	2
sence of vas deferens	+0	201	2
Soft tissue sarcoma	3394	281	6
Acerulonlasminemia	48818	279	1
Homochromatosis tuno 4	120401	275	1
Pernburia sutanea tarda	101220	279	1 2
	101350	279	2
Rare form of salmonellosis	795	279	1
Goriin syndrome	3//	278	2
Squamous cell carcinoma of	213767	270	4
the cervix uteri	00000	200	2
Amyotrophic lateral sciero-	90020	269	Z
sis-parkinsonism-dementia			
Contral diabotos insinidus	178020	267	2
	178023	207	~
Eosinophilic esophagitis	/324/	267	4
Microvillus inclusion dis-	2290	267	2
ease Drovimal ranal tubular aci	47150	267	2
	4/159	207	3
LUSIS	210	266	С
Lwing Salcuild	51 <i>5</i> 70402	200	с г
	19490	204	2
IVITH9-related disease	182050	204	2
Sepastian syndrome	807	204	2
Short bowel syndrome	104008	264	2

Proximal myotonic myopa- thy	606	257	6
Isolated spina bifida	823	256	7
Motor neuron disease	98503	256	4
Retinitis pigmentosa	791	255	12
Primary central nervous system lymphoma	46135	252	2
Familial adenomatous poly-	733	251	11
Acute erythroid leukemia	318	247	4
Adult-onset autosomal dominant leukodystrophy	99027	246	1
Birdshot chorioretinopathy	179	246	1
Rhabdomyosarcoma	780	238	7
Rare thyroid disease	101955	237	8
Disorder of lipid metabo- lism	309005	235	2
Central serous chorioreti- nopathy	443079	230	5
Paroxysmal dyskinesia	1431	229	2
Pituitary adenoma	99408	229	2
Rare adenocarcinoma of	213528	229	4
the breast			
Werner syndrome	902	229	3
Progressive autosomal re- cessive ataxia-deafness syn-	448251	228	1
drome	200	226	2
Hirschsprung disease	388	226	3
Chromophobe renal cell	319303	225	5
Non-Hodgkin lymphoma	547	225	8
Adenocarcinoma of the	10/075	223	1
small instestine	104075	227	-
Anaplastic oligodendrogli- oma	251630	224	1
Aromatase deficiency	91	224	1
Arterial tortuosity syn- drome	3342	224	3
Childhood absence epilepsy	64280	224	1
Classic homocystinuria	394	224	1
Coenzyme Q10 deficiency	35656	224	1
Congenital dyserythropoi- etic anemia type II	98873	224	2
Congenital myopathy	97245	224	2
Congenital myotonia	206973	224	1
Epilepsy with myoclonic ab- sences	86911	224	1
Epithelioid hemangioendo- thelioma	157791	224	1

Follicular dendritic cell sar- coma	86902	224	1
Ganglioneuroblastoma	251877	224	1
Ganglioneuroma	251992	224	1
Hemangioblastoma	252054	224	1
Hemolytic anemia due to	766	224	1
red cell pyruvate kinase de-			
ficiency			
Hereditary cryohydrocyto- sis with reduced stomatin	168577	224	1
Idiopathic hypereosino- philic syndrome	3260	224	1
Isolated megalencephaly	268920	224	7
Megalencephaly	2477	224	7
Microlissencephaly	1083	224	2
Myeloproliferative neo-	98274	224	2
plasm			_
Paroxysmal dystonic cho-	53583	224	1
reathetosis with episodic			
ataxia and spasticity			
Paroxysmal exertion-in-	98811	224	1
duced dyskinesia			
Paroxysmal kinesigenic dys-	98809	224	1
kinesia			
Paroxysmal non-kinesigenic	98810	224	2
dyskinesia			
Placental insufficiency	439167	224	1
Rapid-onset dystonia-par-	71517	224	1
kinsonism Deve extensioner average for	244266	224	2
Rare arteriovenous maitor-	211266	224	2
Mation Pare bereditary ataxia	192519	224	1
Pare lymphatic malfor	2415	224	1
mation	2415	224	Т
Bare venous malformation	211252	224	1
Simple vascular malfor-	2112.32	224	1
mation	211243	224	1
Thomsen and Becker dis-	614	224	1
ease			
Uveal melanoma	39044	224	3
X-linked dystonia-parkin-	53351	224	1
sonism			
Rare male infertility	98048	223	11
Fetal akinesia deformation	994	220	1
Lambert-Eaton myasthenic	43393	220	1
syndrome	-	-	_
Acute liver failure	90062	214	7
Dengue fever	99828	207	4

Sitosterolemia	2882	206	1
Oculocerebrorenal syn-	534	196	2
drome of Lowe			
Mohr-Tranebjaerg syn-	52368	192	2
drome			
Hereditary hyperekplexia	3197	178	1
Rotor syndrome	3111	178	2
Stiff person syndrome and	3198	178	2
related disorders			
Hepatoblastoma	449	167	8
Marfan syndrome	558	160	4
Rare primary hyperaldoste-	181415	159	3
ronism			
Rare peripheral neuropathy	98496	151	7
Acute lymphoblastic leuke-	513	147	12
mia			
Posterior urethral valve	93110	146	2
Autosomal dominant spas-	100991	145	1
tic paraplegia type 10			
Autosomal dominant spas-	171863	145	1
tic paraplegia type 42	00704	4.45	
Congenital arteriovenous	98731	145	1
Congonital cataract hearing	200212	1/5	1
loss-severe developmental	300313	145	T
delay syndrome			
Cryptococcosis	1546	145	9
Lennox-Gastaut syndrome	2382	144	1
Phenylketonuria	716	143	- 5
Classic phenylketonuria	79254	142	3
Hereditary diffuse gastric	26106	137	3
cancer	20100	157	5
Undetermined early-onset	442835	135	2
epileptic encephalopathy	112000	100	-
Fanconi anemia	84	132	5
Episodic ataxia type 6	209967	131	1
Eragile X-associated	93256	131	1
tremor/ataxia syndrome			-
Human prion disease	56970	131	2
Isolated cerebellar agenesis	1398	131	7
Spinocerebellar ataxia type	98755	131	1
1			_
Spinocerebellar ataxia type	94147	131	1
7			
Anaplastic astrocytoma	251589	130	3
Chromosomal anomaly	68335	130	7
Acute promyelocytic leuke- mia	520	126	4
Alexander disease	58	125	1

Lafora disease	501	125	2
Myotonic dystrophy	206647	125	2
Neuromyelitis optica	71211	125	2
Osteoglosphonic dysplasia	2645	125	3
Periventricular leukomala-	171676	125	1
cia			
Rasmussen subacute en- cephalitis	1929	125	1
Hermansky-Pudlak syn- drome	79430	119	4
Glycogen storage disease due to acid maltase defi- ciency	365	118	4
Cerebral cortical dysplasia	268950	116	4
Dejerine-Sottas syndrome	64748	116	5
Dicarboxylic aminoaciduria	2195	116	1
Glycogen storage disease	79201	116	3
Hot water reflex epilepsy	166412	116	1
Alpha-thalassemia	846	115	1
Hemoglobin H disease	93616	115	1
Rare parasitic disease	163588	115	2
Statin toxicity	413696	115	1
Familial tumoral calcinosis	53715	112	3
Autosomal dominant hypo- phosphatemic rickets	89937	110	4
Rare renal tubular disease	93603	109	3
Germ cell tumor	3399	101	2
Splenic marginal zone lym- phoma	86854	100	3
Lysinuric protein intoler- ance	470	98	7
Extranodal nasal NK/T cell lymphoma	86879	97	1
Histiocytic sarcoma	86896	97	1
Nodular lymphocyte pre- dominant Hodgkin lym- phoma	86893	97	1
Primary effusion lymphoma	48686	97	1
Primary mediastinal large B-cell lymphoma	98838	97	1
Spermatocytic seminoma	99865	97	1
T-cell/histiocyte rich large B cell lymphoma	300857	97	1
Hypocalcemic vitamin D-re- sistant rickets	93160	95	3
Hypophosphatemic rickets	437	95	3
Thymoma	99867	95	2
Perry syndrome	178509	94	2

No exected disk story molliture	224	02	h
Neonatal diabetes mellitus	224	92	2
Permanent neonatal diabe-	99885	92	2
tes mellitus			
Anaplastic thyroid carci-	142	91	4
noma			
Rare urinary tract tumor	98058	91	4
Berardinelli-Seip congenital	528	90	1
lipodystrophy			
Distomatosis	1685	90	1
Galactosemia	352	90	1
Hyperphenylalaninemia	238583	90	1
due to tetrahydrobiopterin			
deficiency			
Keratoderma hereditarium	494	90	2
mutilans			
Thymic carcinoma	99868	90	1
Carnitine-acylcarnitine	159	83	2
translocase deficiency			
Juvenile idiopathic arthritis	92	82	5
Mastocytosis	98292	81	2
Medullary thyroid carci-	1332	81	4
noma			
Familial medullary thyroid	99361	80	2
carcinoma			
Congenital isolated hyper-	657	79	2
insulinism			
Exercise-induced hyperin-	165991	79	1
sulinism			
Heparin-induced thrombo-	3325	79	1
cytopenia			
Ketoacidosis due to mono-	438075	79	1
carboxylate transporter-1			
deficiency			
Metabolic myopathy due to	171690	79	1
lactate transporter defect			
Oncogenic osteomalacia	352540	79	1
Systemic primary carnitine	158	77	2
deficiency			
Spinocerebellar ataxia type	98760	73	1
8			
Ichthyosis	79354	72	5
Sickle cell anemia	232	67	6
Chronic graft versus host	99921	65	2
disease			
Rare benign ovarian tumor	97293	65	2
Leptospirosis	509	63	2
Infant acute respiratory dis-	70587	58	3
tress syndrome	,,		5
a coo oynaronne			

Brain dopamine-serotonin vesicular transport disease	352649	57	1
Hypoparathyroidism-senso- rineural deafness-renal dis- ease syndrome	2237	57	1
Bartter syndrome	112	56	4
Classic Bartter syndrome	93605	56	ג
Familial hypocalciuric hy-	93372	56	2
nercalcemia type 1	55572	50	2
Testicular seminomatous	842	56	Δ
germ cell tumor	072	50	7
Autoimmune hepatitis	2137	54	4
Systemic-onset juvenile idi-	85414	54	5
opathic arthritis	0000	54	5
Endocardial fibroelastosis	2022	52	1
Mandibulofacial dysostosis	155899	52	1
Neutral lipid storage dis-	165	52	1
ease			
Neutral lipid storage dis-	98907	52	1
ease with ichthyosis			
Neutral lipid storage myo-	98908	52	1
pathy			
Primary hyperoxaluria	416	52	4
Primary hyperoxaluria type 1	93598	52	2
Propionic acidemia	35	52	1
Treacher-Collins syndrome	861	52	1
Embryonal carcinoma	180226	48	2
Extragonadal teratoma	883	48	3
Cleidocranial dysplasia	1452	47	2
Lymphedema-distichiasis syndrome	33001	47	1
Yolk sac tumor	876	47	1
Preeclampsia	275555	46	2
Cystinuria	214	45	7
Leishmaniasis	507	44	5
Hartnup disease	2116	43	2
Wilson disease	905	43	7
Early-onset nuclear cataract	98991	42	1
Gordon syndrome	376	42	2
IRIDA syndrome	209981	42	3
Microcytic anemia with	83642	42	1
liver iron overload			-
Pseudohypoaldosteronism	757	42	3
type 2			
Glycogen storage disease	79260	37	3
type 1c			
Cleft palate	2014	34	9

Congenital non-bullous ich- thyosiform erythroderma	79394	33	3
Familial calcium pyrophos-	1416	33	4
Ichthyosis-prematurity syn- drome	88621	33	1
Rare insulin-resistance syn- drome	181368	33	1
Restrictive dermopathy	1662	33	1
Severe combined immuno- deficiency	183660	33	2
Acute intermittent porphy- ria	79276	32	1
Alopecia	79364	32	8
Porphyria	738	32	1
Inherited retinal disorder	71862	30	4
Acute graft versus host dis- ease	99920	28	2
Arachnoid cyst	2356	28	1
Atrioventricular canal de- fect	98722	28	1
Cleft lip with or without	1991	28	5
cleft palate			
Cleft lip/palate	199306	28	1
Fetal alcohol syndrome	1915	28	1
Formiminoglutamic acidu-	51208	28	1
ria			
Gitelman syndrome	358	28	2
Hereditary folate malab-	90045	28	1
sorption			
Idiopathic hypercalciuria	2197	28	2
Isolated cleft lip	199302	28	5
Melioidosis	31202	28	2
Methotrexate toxicity or	413690	28	1
dose selection			
Nance-Horan syndrome	627	28	1
Neurodegenerative syn-	217382	28	1
drome due to cerebral fo-			
late transport deficiency			
Neurofibromatosis type 2	637	28	4
Omphalocele	660	28	1
Rare mycosis	163591	28	1
Vestibular schwannoma	252175	28	3
Citrin deficiency	247582	26	5
Citrullinemia type II	247585	26	5
Epithelioid trophoblastic tu-	254698	25	1
mor			
Placental site trophoblastic tumor	99928	25	1

Van der Woude syndrome	888	25	1
Hepatitis delta	402823	24	3
Rare renal tumor	93619	23	7
Gerstmann-Straussler-	356	22	1
Scheinker syndrome			
Glycogen storage disease	364	22	1
due to glucose-6-phospha-			
tase deficiency			
Glycogen storage disease	79258	22	1
due to glucose-6-phospha-			
tase deficiency type la			
Glycogen storage disease	79259	22	1
due to glucose-6-phospha-			
tase deficiency type lb		22	
Gorham-Stout disease	/3	22	1
Hepatocellular adenoma	54272	22	1
Severe congenital neutro-	42738	22	1
penia	457045	20	~
Hereditary hypophos-	157215	20	2
phatemic rickets with hy-			
percalciuria	631	20	^
non-acquired isolated	031	20	4
Bondrod syndromo	705	10	0
Allan Horndon Dudlov svn	705 E0	16	o n
drome	22	10	Z
Beta-thalassemia	848	16	5
Primary myelofibrosis	824	16	3
Rare biliary tract disease	101941	16	3
, Rare tumor of gallbladder	306633	16	3
and extrahepatic biliary		-	-
tract			
Autosomal recessive infan-	300547	15	1
tile hypercalcemia			
Carcinoma of gallbladder	56044	15	5
and extrahepatic biliary			
tract			
Dominant hypophos-	244305	15	1
phatemia with nephrolithi-			
asis or osteoporosis			
McCune-Albright syndrome	562	15	1
Peutz-Jeghers syndrome	2869	15	3
Primary Fanconi syndrome	3337	15	1
Rare bone development	139012	15	3
disorder			
Acute monoblastic leuke-	514	14	4
mia			
Antenatal Bartter syndrome	93604	14	1

Autosomal dominant pri- mary hypomagnesemia	34528	14	1
with hypocalciuria			
CHARGE syndrome	138	14	1
Chondrosarcoma	55880	14	7
Cysticercosis	1560	14	3
Dedifferentiated liposar- coma	99970	14	1
EAST syndrome	199343	14	1
Gardner syndrome	79665	14	1
Hemimegalencephaly	99802	14	1
Idiopathic intracranial hy- pertension	238624	14	1
Lateral meningocele syn- drome	2789	14	1
Limb-mammary syndrome	69085	14	1
Lymphangioleiomyomatosis	538	14	1
Nephrogenic diabetes insip- idus	223	14	2
Noonan syndrome with multiple lentigines	500	14	1
Rare hyperparathyroidism	181408	14	2
Relapsing fever	91547	14	2
Scleroderma	801	14	4
Subependymal giant cell as- trocytoma	251618	14	1
Timothy syndrome	65283	14	1
AL amyloidosis	85443	13	1
GNE myopathy	602	13	2
Mitochondrial disease	68380	13	8
Spastic tetraplegia-thin cor- pus callosum-progressive postnatal microcephaly syndrome	447997	13	1
Chronic enteropathy associ- ated with SLCO2A1 gene	468641	12	1
Cranio-osteoarthropathy	1525	12	1
Isolated congenital digital clubbing	217059	12	1
Pachydermoperiostosis	2796	12	1
Primary cutis verticis gyrata	671	12	1
Primary hypertrophic oste- oarthropathy	248095	12	1
Renal dysplasia	93108	12	2
Alveolar rhabdomyosar- coma	99756	11	1
Centronuclear myopathy	595	11	1

Early-onset autosomal dominant Alzheimer dis- ease	1020	11	3
Glycogen storage disease due to muscle glycogen phosphorylase deficiency	368	11	1
Glycogen storage disease type 1d	79261	11	1
Mitochondrial myopathy	206966	11	4
Simpson-Golabi-Behmel syndrome	373	11	2
Amelocerebrohypohidrotic syndrome	1946	10	1
Amelogenesis imperfecta	88661	10	5
Pyridoxine-dependent epi- lepsy	3006	10	1
Desmoplastic small round cell tumor	83469	9	1
Rare isolated myopia	98619	8	7
Panhypopituitarism	90695	7	2
Autoimmune polyendocri- nopathy	282196	6	5
Autosomal dominant pro- gressive external ophthal- moplegia	254892	6	1
Congenital cataract-hyper- trophic cardiomyopathy- mitochondrial myopathy syndrome	1369	6	1
Congenital hypothyroidism	442	6	4
Corneal dystrophy	34533	6	2
Facioscapulohumeral dys- trophy	269	6	2
Generalized resistance to thyroid hormone	3221	6	3
Kearns-Sayre syndrome	480	6	1
Leukodystrophy	68356	6	4
MELAS	550	6	1
MERRF	551	6	2
Mitochondrial DNA-related progressive external oph- thalmoplegia	663	6	1
Rare familial disorder with hypertrophic cardiomyopa- thy	99739	6	1
Achondroplasia	15	5	1
Acute myelomonocytic leu- kemia	517	5	1

Central congenital hypothy- roidism	226298	5	2
Chordoma	178	5	1
Diffuse astrocytoma	251595	5	1
Duplication/inversion	3306	5	1
15a11	3300	5	-
Helicoid peripapillary chori- oretinal degeneration	86813	5	2
Isolated follicle stimulating hormone deficiency	52901	5	1
Lipedema	77243	5	1
Neurofibromatosis type 3	93921	5	1
Partial deletion of the long arm of chromosome 6	262047	5	1
Pituitary deficiency	101957	5	1
Prolactinoma	2965	5	1
Rubinstein-Taybi syndrome	783	5	1
Sento-ontic dysnlasia spec-	3157	5	1
trum	5157	5	-
Somatotropic adenoma	96256	5	1
Tarsal-carpal coalition syn-	1412	5	4
drome	1712		-
ADan amyloidosis	97346	4	2
Benign familial infantile epi-	306	4	1
lepsy			
Benign familial neonatal ep-	1949	4	1
llepsy			
Benign familial neonatal-in-	140927	4	1
fantile seizures	1000		2
Bilateral striopallidodentate	1980	4	2
Carcinosis	157	٨	1
	137	4	T
Isolated cytochrome C oxi-	25/1005	Λ	1
dase deficiency	234303	7	1
Long chain 3-hydroxyacyl-	5	4	1
CoA dehydrogenase defi-	5		-
ciency			
Mitochondrial trifunctional	746	4	1
protein deficiency			
Multiple acyl-CoA dehydro-	26791	4	3
genase deficiency			
Peroxisome biogenesis dis-	79189	4	1
order			
Rare urticaria	79384	4	2
St. Louis encephalitis	83484	4	1
Very long chain acyl-CoA	26793	4	1
dehydrogenase deficiency			

Waldenström macroglobu- linemia	33226	4	2
Wiskott-Aldrich syndrome	906	4	1
, 22g11.2 deletion syndrome	567	3	3
Early-onset anterior polar	98988	3	4
cataract			
Hyperornithinemia-hyper-	415	3	3
ammonemia-homocitrulli-			
nuria syndrome			
Immune thrombocytopenic	3002	3	1
purpura			
MALT lymphoma	52417	3	3
Marginal zone lymphoma	300912	3	3
Monosomy X	99226	3	3
Photosensitive epilepsy	166409	3	1
Polycythemia vera	729	3	5
Potassium-aggravated myo-	612	3	2
tonia Rulmonary alvoolar micro	60025	2	1
lithiasis	60025	5	T
Shprintzen-Goldberg syn-	2462	3	2
drome			
Turner syndrome	881	3	3
Adrenomyeloneuropathy	139399	2	1
Autoimmune hemolytic anemia	98375	2	2
Autoimmune hemolytic	228312	2	1
anemia, cold type		2	~
Barth syndrome		2	2
Cold agglutinin disease	56425	2	1
Congenital hydrocephalus	2185	2	2
Conotruncal heart malfor- mations	2445	2	2
Cystinuria type B	93613	2	2
Ependymal tumor	301	2	1
Ependymoma	251636	2	1
Essential thrombocythemia	3318	2	3
Extragonadal germinoma	182127	2	1
Fish-eye disease	79292	2	1
Guanidinoacetate methyl-	382	2	1
, transferase deficiency			
Herpes simplex virus kerati-	137586	2	1
tis			
Idiopathic isolated micrope-	95707	2	5
nis			
Idiopathic pulmonary fibro-	2032	2	8
sis			
Iminoglycinuria	42062	2	4

Interatrial communication	1478	2	3
L-Arginine:glycine amidi-	35704	2	1
notransferase deficiency			
Leber congenital amaurosis	65	2	3
Leprosy	548	2	5
Non-functioning pituitary	91349	2	1
adenoma			
Penile agenesis	49	2	4
Piebaldism	2884	2	2
Rare coagulation disorder	98429	2	2
Rare hemorrhagic disorder	248308	2	2
Sideroblastic anemia	1047	2	2
Thiamine-responsive mega-	49827	2	1
loblastic anemia syndrome			
X-linked creatine trans-	52503	2	1
porter deficiency			
2p21 microdeletion syn-	163693	1	1
drome			
46,XX testicular disorder of	393	1	2
sex development			
Acquired purpura fulminans	49566	1	1
Adrenocortical carcinoma	1501	1	2
Aregenerative anemia	101096	1	2
Atypical hypotonia-cystinu-	238523	1	1
ria syndrome			
Autosomal recessive limb-	268	1	1
girdle muscular dystrophy			
type 2B			
Autosomal recessive spino-	95433	1	1
cerebellar ataxia-blindness-			
deatness syndrome	224222	4	2
Beta-thalassemia interme-	231222	1	2
ula Riotin thiaming responsive	65384	1	1
biotili-tiliariline-responsive	05204	T	T
Cardiomyonathy-hypoto-	91130	1	1
nia-lactic acidosis syndrome	51150	1	-
Charcot-Marie-Tooth dis-	166	1	3
ease/Hereditary motor and		-	•
sensory neuropathy			
Citrullinemia	187	1	2
Congenital thrombotic	93583	1	1
thrombocytopenic purpura			
Corpus callosum agenesis-	1496	1	1
neuronopathy syndrome			
Craniosynostosis	1531	1	7
Cutis laxa	209	1	2
Cystinuria type A	93612	1	1

Disseminated superficial ac- tinic porokeratosis	79152	1	1
Early infantile epileptic en- cephalopathy	1934	1	1
Early myoclonic encephalo- pathy	1935	1	1
Encephalitis	97275	1	2
Epileptic encephalopathy with global cerebral demye- lination	353217	1	1
Familial thyroid dyshor- monogenesis	95716	1	1
Giant cell tumor of bone	363976	1	1
Gray platelet syndrome	721	1	1
Gyrate atrophy of choroid and retina	414	1	1
Hereditary gingival fibroma- tosis	2024	1	2
Hyper-beta-alaninemia	309147	1	1
Hyperlysinemia	2203	1	1
Hypotonia-cystinuria syn- drome	163690	1	1
Infantile spasms-psychomo- tor retardation-progressive brain atrophy-basal ganglia disease syndrome	263410	1	1
Isolated brachycephaly	35099	1	2
Isolated craniosynostosis	139390	1	7
Isolated oxycenhaly	63440	1	, 2
Langer mesomelic dysplasia	2632	1	1
Leigh syndrome	506	1	1
Leigh syndrome with leu-	255241	1	1
Limb-girdle muscular dys- trophy	263	1	1
Léri-Weill dyschondrosteo- sis	240	1	1
Macroglossia	156207	1	2
Malignant peripheral nerve sheath tumor	3148	1	1
Marburg hemorrhagic fever	99826	1	1
Microsporidiosis	2552	1	1
Mucopolysaccharidosis type 4	582	1	2
Myasthenia gravis	589	1	2
Neonatal intrahepatic cho- lestasis due to citrin defi- ciency	247598	1	1
Noonan syndrome	648	1	1

Ornithine transcarbamylase deficiency	664	1	1
Overhydrated hereditary	3203	1	1
Porokeratosis	79358	1	1
Precocious puberty	95708	1	3
Pvruvate carboxvlase defi-	3008	1	1
ciency			
Rare disorder with hypertri- chosis	79365	1	4
Refractory anemia	98826	1	2
Rh deficiency syndrome	71275	1	1
Riboflavin transporter defi- ciency	97229	1	2
Roussy-Lévy syndrome	3115	1	2
Scrub typhus	83317	1	1
Spinocerebellar ataxia type 5	98766	1	1
Thiamine-responsive en- cephalopathy	199348	1	1
Thrombotic microangiopa- thy	93573	1	1
Thrombotic thrombocyto- penic purpura	54057	1	1
Uveitis	98715	1	1
X-linked centronuclear my-	596	1	1
opathy			
2-hydroxyglutaric aciduria	19	0	1
ALG2-CDG	79326	0	1
Achondrogenesis	932	0	1
Achondrogenesis type 1B	93298	0	4
Acquired idiopathic	75564	0	2
sideroblastic anemia			
Acrodermatitis enteropath- ica	37	0	2
Acute hepatic porphyria	95157	0	1
Acute megakaryoblastic leukemia	518	0	2
Adult T-cell leukemia/lym- phoma	86875	0	2
Adult neuronal ceroid lipofuscinosis	79262	0	2
Adult-onset autosomal re- cessive sideroblastic ane-	255132	0	1
IIIId African trypanosomiasis	2285	0	1
Agammaglohulinomia	183669	0	1 1
Aicardi-Goutiàres sundromo	51	0	1
Alcalui-Ooulieles syllui ollie	L L	0	т

Allergic bronchopulmonary aspergillosis	1164	0	1
Alpha-thalassemia-X-linked intellectual disability syn- drome	847	0	1
Alström syndrome	64	0	1
, American trypanosomiasis	3386	0	3
Amish lethal microcephaly	99742	0	1
Anaplastic large cell lym-	98841	0	1
phoma	500.12	0	-
Androgen insensitivity syn- drome	754	0	2
Angelman syndrome due to maternal 15q11q13 dele- tion	98794	0	1
Antisynthetase syndrome	81	0	1
Apparent mineralocorticoid excess	320	0	2
Atelosteogenesis type I	1190	0	1
Atelosteogenesis type II	56304	0	1
Athyreosis	95713	0	1
Audiogenic seizures	166415	0	1
Autism spectrum disorder-	370943	0	1
epilepsy-arthrogryposis syndrome			
Autoimmune pancreatitis	103919	0	1
Autosomal dominant Char-	64746	0	1
cot-Marie-Tooth disease type 2			
Autosomal dominant distal renal tubular acidosis	93608	0	1
Autosomal dominant non- syndromic sensorineural deafness type DFNA	90635	0	2
Autosomal dominant spas- tic paraplegia type 4	100985	0	2
Autosomal dominant spas- tic paraplegia type 6	100988	0	1
Autosomal erythropoietic protoporphyria	79278	0	1
Autosomal recessive distal renal tubular acidosis	402041	0	1
Autosomal recessive non- syndromic intellectual disa- bility	88616	0	2
Autosomal recessive non- syndromic sensorineural deafness type DFNB	90636	0	2

Autosomal recessive poly- cystic kidney disease	731	0	1
Autosomal recessive pri- mary microcephaly	2512	0	1
Autosomal recessive proxi- mal renal tubular acidosis	93607	0	1
Autosomal recessive sideroblastic anemia	260305	0	1
Autosomal recessive spastic paraplegia type 5A	100986	0	1
Autosomal recessive spon- dylocostal dysostosis	2311	0	1
Axenfeld-Rieger syndrome	782	0	1
Baraitser-Winter cerebro-	2995	0	1
frontofacial syndrome			
Beckwith-Wiedemann syn-	116	0	1
drome			
Beta-thalassemia major	231214	0	2
Bile acid CoA ligase defi-	276066	0	1
ciency and defective ami-			
dation	445000	•	
Bilirubin encephalopathy	415286	0	1
Blackfan-Diamond anemia	124	0	1
Bloom syndrome	125	0	2
Bowen syndrome	1271	0	1
Buerger disease	36258	0	2
CLN2 disease	228349	0	1
CLN3 disease	228346	0	1
CLN7 disease	228366	0	1
CLN8 disease	228354	0	1
Caffey disease	1310	0	1
Campomelic dysplasia	140	0	1
Camurati-Engelmann dis-	1328	0	1
ease	F07	0	1
Chandler syndrome	08070	0	1
Charlet Maria Teeth die		0	1
charcot-Marie-Tooth dis-	05755	0	Т
Charcot-Marie-Tooth dis-	101081	0	1
ease type 1A	101001	0	т
Charcot-Marie-Tooth dis-	101082	0	1
ease type 1B	101002	C C C C C C C C C C C C C C C C C C C	-
Chikungunya	324625	0	2
Christianson syndrome	85278	0	3
, Chronic bervllium disease	133	0	1
Chronic nonbacterial osteo-	324964	0	1
myelitis/Chronic recurrent multifocal osteomyelitis			-
Chédiak-Higashi syndrome	167	0	1

Cirrhosis-dystonia-polycy- themia-hypermanga- nesemia syndrome	309854	0	1
Classic Hodgkin lymphoma, mixed cellularity type	98844	0	1
Classic Hodgkin lymphoma, nodular sclerosis type	98843	0	1
Cleft velum	99772	0	1
Cockayne syndrome type 1	90321	0	2
Coloboma of iris	98944	0	1
Combined hyperlipidemia	79211	0	1
Congenital chloride diar-	53689	0	2
rhea			
Congenital disorder of gly- cosylation	137	0	9
Congenital hereditary en- dothelial dystrophy type I	98975	0	1
Congenital hereditary en- dothelial dystrophy type II	293603	0	1
Congenital mesoblastic nephroma	2665	0	1
Congenital neuronal ceroid lipofuscinosis	168486	0	3
Congenital radioulnar	3269	0	1
Congenital stationary night blindness	215	0	1
Congenital vertical talus	178382	0	1
Constitutional sideroblastic anemia	98362	0	1
Corneal dystrophy-percep- tive deafness syndrome	1490	0	1
Craniometaphyseal dyspla- sia	1522	0	1
Crigler-Najjar syndrome	205	0	1
Crigler-Najjar syndrome type 1	79234	0	1
Crimean-Congo hemor- rhagic fever	99827	0	1
Cutaneous neuroendocrine carcinoma	79140	0	1
Cyclic neutropenia	2686	0	1
Cystic echinococcosis	400	0	1
Cystic hygroma	79486	0	1
D,L-2-hydroxyglutaric acid- uria	356978	0	1
Darier disease	218	0	1
Dehydrated hereditary stomatocytosis	3202	0	1

Dentatorubral pallidolu- vsian atrophy	101	0	1
Dermatomyositis	221	0	2
Diastrophic dwarfism	628	0	9
Diphtheria	1679	0	5
Discoid lunus erythemato-	90281	0	5
	50201	0	J
Distal renal tubular acidosis	18	0	4
Distal renal tubular acidosis	93610	0	1
with anemia	55010	0	-
Dubin-Johnson syndrome	234	0	1
Dysosteosclerosis	1782	0	1
Dystonia-narkinsonism-by-	521406	0	1
nermanganesemia syn-	521400	0	-
drome			
EFC syndrome	1896	0	1
Ehlers-Danlos syndrome	157965	0	1
spondylocheirodysplastic	137,505	Ū	-
type			
Ehlers-Danlos syndrome.	286	0	1
vascular type			-
Embryonal rhabdomyosar-	99757	0	1
coma			
Endometrial stromal sar-	213711	0	1
coma			
Epidermodysplasia verruci-	302	0	4
formis			
Esophageal atresia	1199	0	1
Extramammary Paget dis-	2800	0	1
ease			
Familial Mediterranean fe-	342	0	1
ver			
Familial hyperaldosteron-	403	0	1
ism type I			
Familial isolated clinodac-	295014	0	2
tyly of fingers			
Familial multiple lipomato-	199276	0	1
sis		-	
Familial pancreatic carci-	1333	0	1
noma	1001	•	
Familial prostate cancer	1331	0	1
Femoral agenesis/hypo-	1987	U	1
plasia	2024	0	
Fibrochondrogenesis	2021	U	1
Fibrosarcoma	2030	0	4
Filariasis	2034	0	1
Foveal hypoplasia-optic	397618	0	1
nerve decussation defect-			

anterior segment dysgen-			
esis syndrome			
Fowler syndrome	221126	0	2
Free sialic acid storage dis- ease	834	0	1
Free sialic acid storage dis-	309324	0	1
ease, infantile form			
Friedreich ataxia	95	0	1
Fuchs endothelial corneal	98974	0	1
dystrophy			
GM2 gangliosidosis	309152	0	1
Germ cell tumor of testis	363504	0	3
Giant cell arteritis	397	0	2
Giant cell glioblastoma	251579	0	1
Gorlin-Chaudhry-Moss syn-	2095	0	1
drome			
Granulomatosis with pol-	900	0	1
yangiitis		_	
Growth and developmental	391348	0	1
delay-hypotonia-vision im-			
pairment-lactic acidosis			
Syndrome	70070	0	1
lin like growth factor type 1	13212	0	Т
deficiency			
Growth hormone insensitiv-	181393	0	1
ity syndrome			-
H syndrome	168569	0	1
HELLP syndrome	244242	0	1
Hemochromatosis type 2	79230	0	1
Hemoglobinopathy	68364	0	1
Hemophagocytic syndrome	158032	0	1
Hemophilia	448	0	1
Hemophilia A	98878	0	2
Hereditary breast cancer	227535	0	1
Hereditary clear cell renal	422526	0	1
cell carcinoma	122320	Ū	-
Hereditary cryohydrocyto-	398088	0	1
sis with normal stomatin			
Hereditary elliptocytosis	288	0	1
Hereditary motor and sen-	90120	0	1
sory neuropathy type 6			
Hereditary sensory and au-	140471	0	1
tonomic neuropathy			
Hereditary spherocytosis	822	0	4
Hereditary stomatocytosis	98365	0	1
Herpes simplex virus en-	1930	0	1
cephalitis		_	_
Hurler syndrome	93473	0	1

Hurler-Scheie syndrome	93476	0	1
Hydranencephaly	2177	0	1
Hydrops fetalis	1041	0	2
Hyperinsulinism due to	276556	0	1
Hyperostosis cranialis in-	443098	0	1
terna	20025	0	1
skip	/93/5	0	T
Hypersensitivity pneumon-	31740	0	1
itis	51/40	0	-
Hypocalcified amelogenesis	100032	0	1
Hypomaturation amelogen-	100033	0	1
esis imperfecta	100055	0	1
Hypopigmentation of the skin	79376	0	5
Idiopathic achalasia	930	0	1
Idiopathic bronchiectasis	60033	0	1
Idiopathic chronic eosino-	2902	0	1
philic pneumonia			
Incontinentia pigmenti	464	0	1
Infantile neuronal ceroid	79263	0	1
lipofuscinosis			
Interdigitating dendritic cell	86900	0	1
sarcoma	222224	•	
Intermediate severe Salla	309331	0	1
Uisease Interstitial lung disease	182095	0	л
Isolated Dandy-Walker mal-	217	0	7 2
formation	217	0	2
Isolated Pierre Robin syn-	718	0	1
drome			
Isolated agammaglobuline-	229717	0	2
mia			
Isolated aniridia	250923	0	2
Isolated biliary atresia	30391	0	1
Isolated focal cortical dys-	268973	0	1
plasia type la	127002	0	1
nlasia/anlasia	137902	0	T
Ito hypomelanosis	435	0	1
leune syndrome	474	0	1
luvenile cataract-microcor-	247794	0	1
nea-renal glucosuria syn-	217751	0	-
drome			
Juvenile neuronal ceroid	79264	0	2
lipofuscinosis			
Kennedy disease	481	0	1

LCAT deficiency  650  0  1    Lamellar ichthyosis  313  0  1    Langerhans cell histiocyto-  389  0  1    sis	Klatskin tumor	0	1
Lamellar ichthyosis  313  0  1    Langerhans cell histiocyto-  389  0  1    sis	LCAT deficiency	0	1
Langerhans cell histiocyto-  389  0  1    sis	Lamellar ichthyosis	0	1
sis Laron syndrome 633 0 1 Lassa fever 99824 0 1 Late infantile neuronal ce- 168491 0 2 roid lipofuscinosis Leber hereditary optic neu- 104 0 1 ropathy 0 104 0 1 ropathy 54260 0 1 paction Legg-Calvé-Perthes disease 2380 0 1 Lemierre syndrome 137839 0 1 Leukocyte adhesion defi- 2968 0 1	Langerhans cell histiocyto-	0	1
Laron syndrome  633  0  1    Lassa fever  99824  0  1    Late infantile neuronal ce-  168491  0  2    roid lipofuscinosis  1  1  2    Leber hereditary optic neu-  104  0  1    ropathy  54260  0  1    Legg-Calvé-Perthes disease  2380  0  1    Lemierre syndrome  137839  0  1    Leukocyte adhesion defi-  2968  0  1    Leukocyte adhesion defi-  99842  0  1	sis		
Lassa fever  99824  0  1    Late infantile neuronal ce- roid lipofuscinosis  168491  0  2    Leber hereditary optic neu- ropathy  104  0  1    Left ventricular noncom- paction  54260  0  1    Legg-Calvé-Perthes disease  2380  0  1    Lemierre syndrome  137839  0  1    Leukocyte adhesion defi- ciency  2968  0  1    Leukocyte adhesion defi-  99842  0  1	Laron syndrome	0	1
Late infantile neuronal ce- roid lipofuscinosis16849102Leber hereditary optic neu- ropathy10401ropathy5426001Left ventricular noncom- paction5426001Legg-Calvé-Perthes disease238001Lemierre syndrome13783901Leukocyte adhesion defi- ciency296801Leukocyte adhesion defi-9984201	Lassa fever	0	1
Leber hereditary optic neu- ropathy10401Left ventricular noncom- paction5426001Legg-Calvé-Perthes disease238001Lemierre syndrome13783901Leukocyte adhesion defi- ciency296801Leukocyte adhesion defi-9984201	Late infantile neuronal ce- roid lipofuscinosis	0	2
Left ventricular noncom- paction5426001Legg-Calvé-Perthes disease238001Lemierre syndrome13783901Leukocyte adhesion defi- ciency296801Leukocyte adhesion defi- 998429984201	Leber hereditary optic neu- ropathy	0	1
Legg-Calvé-Perthes disease238001Lemierre syndrome13783901Leukocyte adhesion defi- ciency296801Leukocyte adhesion defi- 998429984201	Left ventricular noncom- paction	0	1
Lemierre syndrome13783901Leukocyte adhesion defi-296801ciency1Leukocyte adhesion defi-9984201	Legg-Calvé-Perthes disease	0	1
Leukocyte adhesion defi- ciency296801Leukocyte adhesion defi- 998429984201	Lemierre syndrome	0	1
ciency Leukocyte adhesion defi- 99842 0 1	Leukocyte adhesion defi-	0	1
Leukocyte adhesion defi- 99842 0 1	ciency		
	Leukocyte adhesion defi-	0	1
ciency type I	ciency type I		
Leukocyte adhesion defi- 99843 0 1	Leukocyte adhesion defi-	0	1
ciency type II	ciency type II	0	
LOW phospholipid-associ- 69663 0 1	Low phospholipid-associ-	0	1
aled cholenthiasis		0	1
Lumphodoma 70282 0 1		0	1
Lymphonroliferative syn 222510 0	Lymphoproliforativo syn	0	1 2
drome	drome	0	5
Macrophage activation syn- 158061 0 1	Macrophage activation syn-	0	1
drome	drome		
Macular corneal dystrophy 98969 0 1	Macular corneal dystrophy	0	1
Malignant hyperthermia of 423 0 1	Malignant hyperthermia of	0	1
anesthesia	anesthesia	0	
Manganese poisoning 306682 0 4	Manganese poisoning	0	4
Marinesco-Sjögren syn- 559 0 1	Marinesco-Sjogren syn-	0	1
Maternal riboflavin defi- 411712 0 1	Maternal riboflavin defi-	0	1
ciency	ciency	Ū	-
Medium chain acyl-CoA de- 42 0 1	, Medium chain acyl-CoA de-	0	1
hydrogenase deficiency	hydrogenase deficiency		
Melkersson-Rosenthal syn- 2483 0 1	Melkersson-Rosenthal syn-	0	1
drome	drome		
Meningioma    2495    0    1	Meningioma	0	1
Meningococcal meningitis 33475 0 1	Meningococcal meningitis	0	1
Mesomelia-synostoses syn- 2496 0 1	Mesomelia-synostoses syn-	0	1
drome	drome	_	
IVIICIOTIA    83463    0    1		U	1
Miller-Dieker syndrome 531 0 1	Miller-Dieker syndrome	U	1
Mitochondrial DNA deple- 35698 0 1 tion syndrome	Mitochondrial DNA deple- tion syndrome	U	1
Mitochondrial pyruvate car- rier deficiency	447784	0	1
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, Moyamoya disease	2573	0	3
Mucolipidosis type IV	578	0	1
Mucopolysaccharidosis	579	0	1
type 1		-	
Mucopolysaccharidosis type 2	580	0	1
Multiple acyl-CoA dehydro- genase deficiency, mild type	394532	0	1
Multiple epiphyseal dyspla- sia	251	0	4
Multiple epiphyseal dyspla- sia type 4	93307	0	1
Multiple osteochondromas	321	0	2
Multiple symmetric lipoma- tosis	2398	0	1
Myofibrillar myopathy	593	0	2
Nail anomaly	79368	0	2
Nemaline myopathy	607	0	1
Neonatal severe cardiopul-	466784	0	1
monary failure due to mito- chondrial methylation de-			
fect			
Neuroendocrine cell hyper- plasia of infancy	217560	0	1
Neuromuscular disease	68381	0	1
Neuronal ceroid	216	0	3
lipotuscinosis	262.422	0	
Nevus of Ito	263432	0	1
Nijmegen breakage syn- drome	647	0	1
Non-syndromic male infer- tility due to sperm motility disorder	276234	0	1
Non-syndromic syndactyly	90025	0	1
Occipital horn syndrome	198	0	1
Ocular albinism	284804	0	4
Oculocutaneous albinism	55	0	4
Oculocutaneous albinism type 2	79432	0	2
Oculocutaneous albinism type 4	79435	0	1
Oculocutaneous albinism	370097	0	1
Ondine syndrome	661	0	1
Oral submucous fibrosis	357154	0	1

Osteopetrosis and related	2781	0	2
Osteopetrosis-hypogam-	178389	0	1
Overlapping connective tis-	251312	0	1
Papillary glioneuronal tu-	251962	0	1
Papillon-Lefèvre syndrome	678	0	1
Periodic paralysis	206976	0	1
Periventricular podular bet-	08807	0	1
erotonia	56652	0	Ŧ
Pitt-Bogers-Danks syn-	98788	0	1
drome	50,00	U C	-
Pneumocystosis	723	0	2
Polycythemia	98427	0	1
Polydactyly of a hinhalan-	93339	0	1
geal thumb	5555	0	Ŧ
Polymicrogyria	35981	0	2
Posterior column ataxia-	88628	0	1
retinitis nigmentosa syn-	00020	U C	-
drome			
Posterior polymorphous	98973	0	1
corneal dystrophy		-	
Prader-Willi syndrome due	98754	0	1
to maternal uniparental di-			
somy of chromosome 15			
Prader-Willi syndrome due	177901	0	1
to paternal deletion of			
15q11q13 type 1			
Prader-Willi syndrome due	177904	0	1
to paternal deletion of			
15q11q13 type 2			
Premature aging	79389	0	2
Primary cutaneous CD30+	541	0	1
T-cell lymphoproliferative			
disease			
Primary cutaneous T-cell	171901	0	1
lymphoma			
Primary cutaneous anaplas-	300865	0	1
tic large cell lymphoma	101007		
Primary immunodeficiency	101997	0	1
Primitive portal vein throm- bosis	854	0	1
Progeroid syndrome, Petty	2963	0	1
type			
Progressive bulbar paralysis of childhood	56965	0	1

Progressive essential tremor-speech impairment-	457212	0	1
facial dysmorphism-intel- lectual disability-abnormal behavior syndrome			
Progressive multifocal leu- koencephalopathy	217260	0	3
Progressive polyneuropathy with bilateral striatal necrosis	217396	0	1
Pseudoxanthoma elasticum	758	0	1
Psychomotor regression-oc- ulomotor apraxia-move- ment disorder-nephropathy syndrome	505242	0	1
Pulverulent cataract	98984	0	1
Pyle disease	3005	0	2
Pyruvate dehydrogenase E1-alpha deficiency	79243	0	1
Pyruvate dehydrogenase deficiency	765	0	1
RFT1-CDG	244310	0	2
Rabies	770	0	2
Rare acquired hemolytic	182047	0	1
anemia			
Rare benign breast tumor	180253	0	2
Rare deafness	68361	0	4
Rare disease with Pierre Robin syndrome	138044	0	1
Rare disorder with hy- pogonadotropic hy- pogonadism	181387	0	1
Rare genetic skin disease	68346	0	1
Rare hypoaldosteronism	181419	0	3
Rare nevus	294057	0	1
Rare refraction anomaly	98618	0	2
Rare soft tissue tumor	71209	0	1
Rare tumor of intestine	104011	0	1
Rare tumor of neuroepithe- lial tissue	251558	0	1
Rare tumor of salivary glands	276142	0	1
Rare uterine cancer	213564	0	1
Reactive arthritis	29207	0	1
Recombinant 8 syndrome	96167	0	1
Red cell aplasia	98421	0	1
Renal agenesis, unilateral	93100	0	1
Restrictive cardiomyopathy	217632	0	1
· · · · · · · · · · · · · · · · · · ·			

Rhabdoid tumor	69077	0	1
Rheumatic fever	3099	0	1
Rickettsial disease	102021	0	1
SIC35A1-CDG	238459	0	1
SLC35A2-CDG	356961	0	1
SLC39A8-CDG	468699	0	1
Salla disease	309334	0	1
Sanfilippo syndrome type A	79269	0	1
Sarcoidosis	797	0	3
Schistosomiasis	1247	0	2
Schneckenbecken dysplasia	3144	0	1
Sclerosing cholangitis	447771	0	2
Shigellosis	810	0	1
Short rib-polydactyly syn-	1505	0	1
drome			
Sialuria	3166	0	1
Situs inversus totalis	101063	0	1
Smith-Lemli-Opitz syn-	818	0	1
drome			
Southeast Asian ovalocyto-	98868	0	1
sis			
Spondyloepimetaphyseal	168451	0	1
dysplasia-abnormal denti-			
tion syndrome	95167	0	1
spondylometaphyseal dys-	85167	0	Т
syndrome			
Sporadic Creutzfeldt-Jakob	204	0	1
disease			-
Staphylococcal toxic-shock	99919	0	1
syndrome			
Stargardt disease	827	0	1
Stevens-Johnson syn-	95455	0	1
drome/toxic epidermal			
necrolysis spectrum			
Subcortical band heteroto-	99796	0	1
	00575	0	~
Syndromic telecanthus	98575	0	2
	314667	0	1
letralogy of Fallot	3303	0	2
Invroid hypoplasia	95720	0	1
Toxic epidermai necrolysis	537	0	1
I ransient myeloprolifera-	420611	0	1
uve synurome Trichinellosis	863	0	1
Tropical spactic paraparesis	280226	0	1 1
Typhoid	007/5	0	1 1
i ypilulu Vernal keratoconiunctivitic	55745 70476	0	1
vernal keratoconjunctivitis	/04/0	U	Т

Vogt-Koyanagi-Harada dis-	3437	0	1
Whooping cough	1/20	0	1
	1405	0	т
Williams-Campbell syn-	411501	0	1
drome			
Wolf-Hirschhorn syndrome	280	0	1
Wolman disease	75233	0	1
X-linked immunodeficiency	317476	0	1
with magnesium defect, Ep-			
stein-Barr virus infection			
and neoplasia			
X-linked myopathy with ex-	25980	0	1
cessive autophagy			
X-linked non-syndromic in-	777	0	1
tellectual disability			
X-linked recessive ocular al-	54	0	4
binism			

## 6.1.2 SLCs with number of associated diseases and disease classes

SLC	Uni-	Number of associated	associated MeSH disease classes
name	Prot.ID	rare diseases	
SLC2A1	P11166	143	C04, C06, C10, C23, C16, C17, C05, C14, C18, C20, C15,
			C12, C13, C08, C19, C07, C11, F01, F03, C01, C09
SLCO6A	Q86UG4	108	C06, C16, C17, C18, C04, C15, C20, C10, C08, C12, C13,
1			C23, C01, C05, C19, F03, C14, C07, C09, C11
SLC12A9	Q9BXP2	75	C04, C15, C20, C06, C10, C14, C16, C18, C23, C12, C13,
			C05, C08, C17, C07, C19, F03, C01, C11, C09
SLC12A3	P55017	65	C04, C12, C13, C16, C18, C19, C11, C06, C01, C09, C10,
			C23, F01, F03, C05, C07, C15, C20, C14, C17
SLC6A3	Q01959	60	C06, C14, C16, C18, C10, C15, C20, C04, C08, C11, C23,
			C12, C13, C05, C07, C09, C17, F03, C01, C19
SLC16A1	P53985	59	C04, C06, C15, C20, C01, C16, C18, C11, C23, C12, C13,
			C05, C19, C08, C17, C10, C14, C07, C09
SLC52A2	Q9HAB3	54	C16, C04, C19, C20, C10, C06, C12, C13, C18, C15, C07,
			C08, C05, C23, C01, C17, C14, C11, C09
SLC6A4	P31645	53	C06, C14, C16, C23, C07, C11, C17, C08, C04, C19, C10,
			C13, C18, F03, C12, C05
SLC6A8	P48029	52	C04, C15, C20, C06, C14, C16, C18, C12, C13, C08, C10,
			C23, C05, F01, F03, C19, C07, C09, C17, C11
SLC5A5	Q92911	51	C04, C18, C15, C10, C14, C16, C20, C05, C19, C06, C07,
			C08, C11, C09, C12, C13, C23, C17, C01
NPC1	015118	50	C06, C08, C16, C23, C18, C01, C04, C15, C20, C10, C11,
			C05, F03, C14, C07, C09, C19
SLC7A5	Q01650	48	C04, C06, C11, C10, C16, C18, C12, C13, C05, C19, C01,
			C09, C17, C23, C15, C20, C08, C14
XPR1	Q9UBH6	47	C04, C17, C23, C10, C18, C15, C05, C07, C11, C14, C16,
			C01, C12, C13, C06, C19, C08, C20
SLC17A5	Q9NRA2	45	C06, C20, C19, C16, C01, C11, C10, C18, C13, C04, C15,
			C23, C17, C08, F03, C14, C07, C25

SLC6A2	P23975	45	C08, C16, C04, C10, C06, C07, C19, C14, C18, F03, C05
			C17, C12, C13, C01, C11
OCA2	Q04671	42	C01, C18, C10, C16, C06, C20, C04, C15, C11, C17, C05
			C13, C19
MAGT1	Q9H0U3	41	C04, C15, C20, C10, C16, C06, C12, C13, C18, C01, C19
			F03, C08, C14, C07, C09, C23, C17, C11
SI C4A1	P02730	41	
010 1/11	102730		C17 C06 C01 C14
SI C 10A 1	P41440	20	
JLCIJAI	F41440	39	(220, 004, 013, 017, 023, 014, 010, 007, 003, 010, 011)
	042511	20	
SLC26A4	043511	38	
			08, 07, 09, 010, 023, 011, 001
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			C05, C11, C19, C17
SLC2A3	P11169	37	C04, C06, C20, C19, C13, C05, C07, C16, C10, F03, C17
			C15, C14, C12, C18, C01
SLC16A3	015427	35	C04, C06, C01, C15, C20, C12, C13, C16, C05, C10, C08
			C11, C14, C19, C17, C18
UCP2	P55851	35	C06, C10, C18, C04, C16, C15, F03, C19, C14, C17, C20
			C11
5102503	000325	34	
JLCZJAJ	000325	54	
SI C 2 A 4	D14672	24	
SLCZA4	P14672	54	
FLVCR1	Q9Y5Y0	33	C18, C10, C19, C20, C15, C16, C04, C12, C13, C06, F03
			C05, C17, C14, C11, C23, C01
SLC20A1	Q8WUM	33	C05, C16, C10, C19, C04, C20, C13, C17, C15, C18
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SLC26A3	P40879	33	C05, C16, C18, C12, C13, C19, C04, C17, C10, C23, C06
			C08, C01, C15, C20, C09, C14
SLC35A2	P78381	33	C04, C06, C15, C16, C10, C18, C05, C01, C17, F03, C20
			C11, C13, C19, C23, C14
SLC3A2	P08195	33	C04, C01, C15, C20, C06, C11, C12, C13, C05, C16, C10
			C09 C17 C23 C18 C14 C08
SIC16A4	01537/	22	
JICIUA4	010074	52	
	00/205	22	
SLC2/A5	Q912P5	32	017, 010, 010, 010, 011, 008, 023, 024, 026, 016, 014
			(17, (18, (10, (19
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			C15, C10, C18, C19
SLC18A2	Q05940	31	C04, C08, C16, C10, C05, C07, C09, C23, C17, C18, F03
			C06, C12, C13, C19, C11, C20, C14
SLC22A2	O15244	31	C04, C10, C14, C16, C18, C20, C15, C06, C12, C13, C01
			C07, C09, C19, C08
SLC22A3	075751	31	C11, C04, C12, C13, C05, C16, C06, C08, C17, C15, C09
			C10, C23, F01, F03, C07, C19, C18, C20
SLC25A2	043772	31	C15, C16, C01, C04, C20, C06, C18, C11, C17, C05, C10
0			C14 C13 C19
SICJENJ	P50//3	21	
JLUZUAZ		<u>эт</u>	-200, 010, 007, 007, 010, 010, 010, 010, 0

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- C18, C09, C06, C08

UCP1	P25874	31	C10, C18, C14, C04, C06, C12, C13, C16, C01, C15, C20, F03, C08, C11, C19, C17, C05, C23, F01
CLN3	Q13286	30	C10, C16, C18, C04, C06, C12, C13, C05, C19, C14, C20,
SLC52A1	Q9NWF	30	C19, C20, C04, C06, C05, C16, C08, C15, C13, C14, C11,
SLC5A2	4 P31639	30	C05, C10, C19, C04, C17, C20, C12, C13, C16, C18, C23,
SLC8A1	P32418	30	C06, C14, C11 C14, C16, C04, C19, C10, C15, C20, C17, C06, C08, C05,
SLC9A1	P19634	30	C12, C11, C13, C18 C04, C12, C13, C16, C18, C23, C06, C10, F03, C14, C19,
	D12225	20	C15, C20, C17, C01, C08 C11, C14, C04, C10, C16, C05, C18, C32, C10, C17, C12
SLC25A4	P12235	28	
SLCZAZ	P11108	28	C06, C16, C05, C18, C17, C12, C13, C10, C23, C04, C19, C20, C01
SLC2A10	095528	27	C05, C10, C14, C16, C17, C04, C23, C11, C08, C20, C18, C19
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SLC12A2	P55011	26	C06, C10, C18, C04, C16, C12, C13, C19, C08, C14, C25,
51 C 20 A 2	000700	26	C11, C05, C07, F03, C09 C17, C22, C07, C16, C05, C16, C18, C12, C10, C08, C10,
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LETM1	095202	25	C17, C09, C11, F01, F03, C12, C19 C11, C16, C04, C12, C13, C07, C05, C23, C06, C14, C10,
			C09, C19, C18
SLC22A5	076082	25	C07, C11, C14, C16, C17, C04, C15, C10, C18, C06, C05, C19, C20, C12, C23, C01
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	015750	24	C17, C06, F03, C23
SLC1A5	Q15758	24	C04, C10, C14, C16, C18, C20, C06, C12, C13, C08, C19, C01, C17
SLCO1B 1	Q9Y6L6	24	C04, C15, C16, C10, C18, C06, C20, C13, C19, C23, C17, C14, C01
SLC1A3	P43003	23	C10, C23, C18, C04, C16, C19, C15, C06, C01, F03, C05
SLC25A3	Q9NYZ2	23	C15, C20, C06, C10, C18, C16, C17, C04, C07, C14, C05,
/ SLC40A1	Q9NP59	23	C13, C19 C10, C18, C04, C16, C17, C08, C24, C13, C15, C20, F03,
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SLC9A6	Q92581	23	C01, C08, C20, C10, C16, C05, C11, C23, F01, F03, C06, C07, C09, C14, C04, C18, C13, C17
SLC12A6	Q9UHW	22	C15, C16, C10, C23, C05, C04, C17, C13, C11
SLC22A1	015245	21	C04, C15, C06, C05, C16, C13, C19, C23, C10, C18, C17,
SLC25A1	Q9HC21	21	C04, C05, C10, C16, C07, C19, C01, C06, C14, C17, C20,
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SFXN1	Q9H9B4	20	C06, C08, C16, C23, C04, C10, C15, C01, C13, C14, C20,
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SLCO2A 1	Q92959	20	C15, C16, C05, C04, C06, C10, F03, C23, C11, C12, C17
TUSC3	Q13454	20	C04, C06, C10, C16, C12, C13, C18, C05, C19, C23, C17, F03, C14
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SLC1A1	P43005	19	C10, C18, C04, C16, C12, C13, C23, F01, F03, C06, C05
SLC22A1 8	Q96BI1	19	C16, C04, C06, C15, C20, C17, C01, C13, C19, C12, C18
SLC25A2	Q9BQT8	19	C14, C16, C18, C07, C05, C04, C06, C01, C10, C15, C20,
1			C09, C17
SLC37A4	O43826	19	C01, C10, C16, C04, C18, C05, C06, C08, C14, C19, C20,
CL C 2 2 4 4	00110110	4.0	C15
SLC38A1	Q9H2H9	19	C04, C10, C14, C16, C18, C20, C05, C19, C13, C06, C15,
SICENS	020605	10	
SIC52A3		19	
	P13866	18	
JUJAI	F 13800	10	C20 C17
SLCO1B	Q9NPD5	18	C04, C15, C06, C20, C10, C16, F03, C01, C07, C09, C13,
3			C19, C23, C17, C18
MPC1	Q9Y5U8	17	C04, C12, C13, C16, C05, C10, C17, C06, C08, C14, C15,
			C20, C18, C19
SLC13A5	Q86YT5	17	C07, C10, C16, F03, C04, C06, C05, C13, C19, C09, C23,
			C11, C18, C17
SLC22A4	Q9H015	17	C04, C07, C11, C14, C16, C17, C15, C10, C13, C06, C08,
	OCONTE	47	C18, C19, C20, C05, C23, C01
SLC46A1	Q96N15	1/	C06, C08, C16, C18, C04, C13, C19, C01, C10, C15, C20
ANKH	Q9HCJ1	16	C16, C18, C20, C05, C13, C10, C11, C14, C17, C15, C19
SLC12A5	Q9H2X9	16	
SLC16A2	P36021	16	C10, C16, C23, C04, C19, C05, C18, C20, C11, C17, C13
SLC19A2	060779	16	004, 015, 011, 014, 016, 018, 019, 020, 017, 009, 010,
51 ( 27 \ 1	O6R1M0	16	
JLCZ/A4		10	C05
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SLC3A1	Q07837	16	C05, C10, C16, C12, C13, C04, C18, C23, F01, F03, C08,
			C14, C17, C19, C11

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SLC9A3	P48764
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SLC31A1	015431
SLC34A1	Q06495
SLC35A1	P78382
SLC7A7	Q9UM0 1
SLC12A1	Q13621
SLC14A2	Q15849
SLC20A2	Q08357
SLC25A3	Q96DW
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SLC26A5	P58743
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SLC35B2	Q8TB61
SLC6A9	P48067
SLC16A7	O60669
SLC25A1	Q9UBX3
0	
SLC7A4	O43246
NIPA1	Q7RTP0
SLC15A1	P46059
SLC22A1	Q86VW
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6	QJUAGS
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SLC30A8	Q8IWU4
SLC34A2	095436
SLC39A1	015043
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UCP3	P55916
LETMD1	Q6P1Q0
MFSD2A	Q8NA29
MFSD8	Q8NHS3
SLC18A3	Q16572
SLC23A2	Q9UGH
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	C09, C15, C23
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SLC17A3 000476

SLC17A9 Q9BYT1

SLC22A1 Q63ZE4

Q9Y289

Q8N8Q9

Q0D2K0

Q9P2U7

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