Date: 11-10-21

WEBLEM 6

Introduction to Specialized Databases

Specialized Databases:

Specialized databases are a collection of focused information on one or more specific fields of study. This information or data is arranged or indexed so that the user can locate and retrieve it quickly and easily.

Features of specialized databases:

- Guaranteed Authoritative information
  - Specialized databases often have strict guidelines on the types of articles and journal sources that are accepted. By searching a database, the articles you find are more likely to be both accurate and reliable.
- They're Tailored to specific subjects and fields of study
  - The databases outlined in this module are geared towards specific subjects (i.e) medicine, nursing, etc.). When you use these for your research, the articles you find are more likely to be relevant towards your area of study.
- They Provide Full-text and diagrammatic access
  - When accessing these databases you get full text and diagrammatic representation of data available in simple and easy to chunks.

KEGG:

While the genome sequencing projects rapidly determine gene catalogs for an increasing number of organisms, functional annotation of individual genes is still largely incomplete. KEGG (Kyoto Encyclopedia of Genes and Genomes) is an effort to link genomic information with higher order functional information by computerizing current knowledge on cellular processes and by standardizing gene annotations.

Generally speaking, the biological function of the living cell is a result of many interacting molecules; it cannot be attributed to just a single gene or a single molecule. The functional assignment in KEGG is a process of linking a set of genes in the genome with a network of interacting molecules in the cell, such as a pathway or a complex, representing a higher order biological function.

OMIM:

Online Mendelian Inheritance in Man (OMIM), a continuation of Dr Victor A. McKusick's Mendelian Inheritance in Man (MIM) (1), is the primary repository of comprehensive, curated information on genes and genetic phenotypes and the relationships between them. MIM was published through 12 editions between 1966 and 1998, and OMIM has been online and searchable since 1987.

With the advent of new sequencing technologies, there is a rapid increase in the reports of presumed gene-phenotype relationships. OMIM.org was created to provide a user-friendly and easily searchable portal to a curated compilation of the literature to aid in clinical and molecular genetic research.

References:

1. Hamosh, A. (2004). Online Mendelian Inheritance in Man (OMIM), a knowledgebase of human genes and genetic disorders. *Nucleic Acids Research*, *33*(Database issue), D514–D517. https://doi.org/10.1093/nar/gki033

2. Kanehisa, M. (2000). KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Research*, *28*(1), 27–30. https://doi.org/10.1093/nar/28.1.27

Date: 11-10-21

WEBLEM 6a

(url: https://www.genome.jp/kegg/)

Aim:

To study the AKT Pathway using KEGG Database:

Introduction:

The KEGG database project was initiated in 1995 under the Japanese Human Genome Project, foreseeing the need for a reference resource that would enable understanding of the biological systems, such as the cell and the organism, from genome sequence data. Major efforts have been undertaken to represent the biological systems in terms of molecular networks (molecular wiring diagrams), especially in the form of KEGG pathway maps that are manually created by capturing knowledge from published literature. Continuous efforts have also been made to develop and improve the KO (KEGG Orthology) system for representation of gene/protein functional orthologs in molecular networks.

- **KEGG PATHWAY** is a collection of manually drawn pathway maps representing our knowledge of the molecular interaction, reaction and relation networks for:

- **KEGG BRITE** is a collection of hierarchical classification systems capturing functional hierarchies of various biological objects, especially those represented as KEGG objects. They are represented as BRITE hierarchy files, also called hierarchical text (htext) files, supplemented with BRITE table files using html tables.

- The **KEGG MODULE** database consists of KEGG modules identified by M numbers and KEGG reaction modules identified by RM numbers, which are manually defined functional units of gene sets and reaction sets, respectively. KEGG modules are further divided into pathway modules and signature modules as shown below.
    - Pathway modules – functional units of gene sets in metabolic pathways, including molecular complexes.
    - Signature modules – functional units of gene sets that characterize phenotypic features.
    - Reaction modules – functional units of successive reaction steps in metabolic pathways.

Protein kinase B (Akt), similar to many other protein kinases, is at the crossroads of cell death and survival, playing a pivotal role in multiple interconnected cell signaling mechanisms implicated in cell metabolism, growth and division, apoptosis suppression and angiogenesis. Akt protein kinase displays important metabolic effects, among which are glucose uptake in muscle and fat cells or the suppression of neuronal cell death.
Disruptions in the Akt-regulated pathways are associated with cancer, diabetes, cardiovascular and neurological diseases. The regulation of the Akt signaling pathway renders Akt a valuable therapeutic target. The discovery process of Akt inhibitors using various strategies has led to the identification of inhibitors with great selectivity, low side-effects and toxicity. The usefulness of Akt emerges beyond cancer therapy and extends to other major diseases, such as diabetes, heart diseases, or neurodegeneration.

Methodology:

- Open the homepage of KEGG.
- Enter the pathway in search bar.
- Interpret the result.

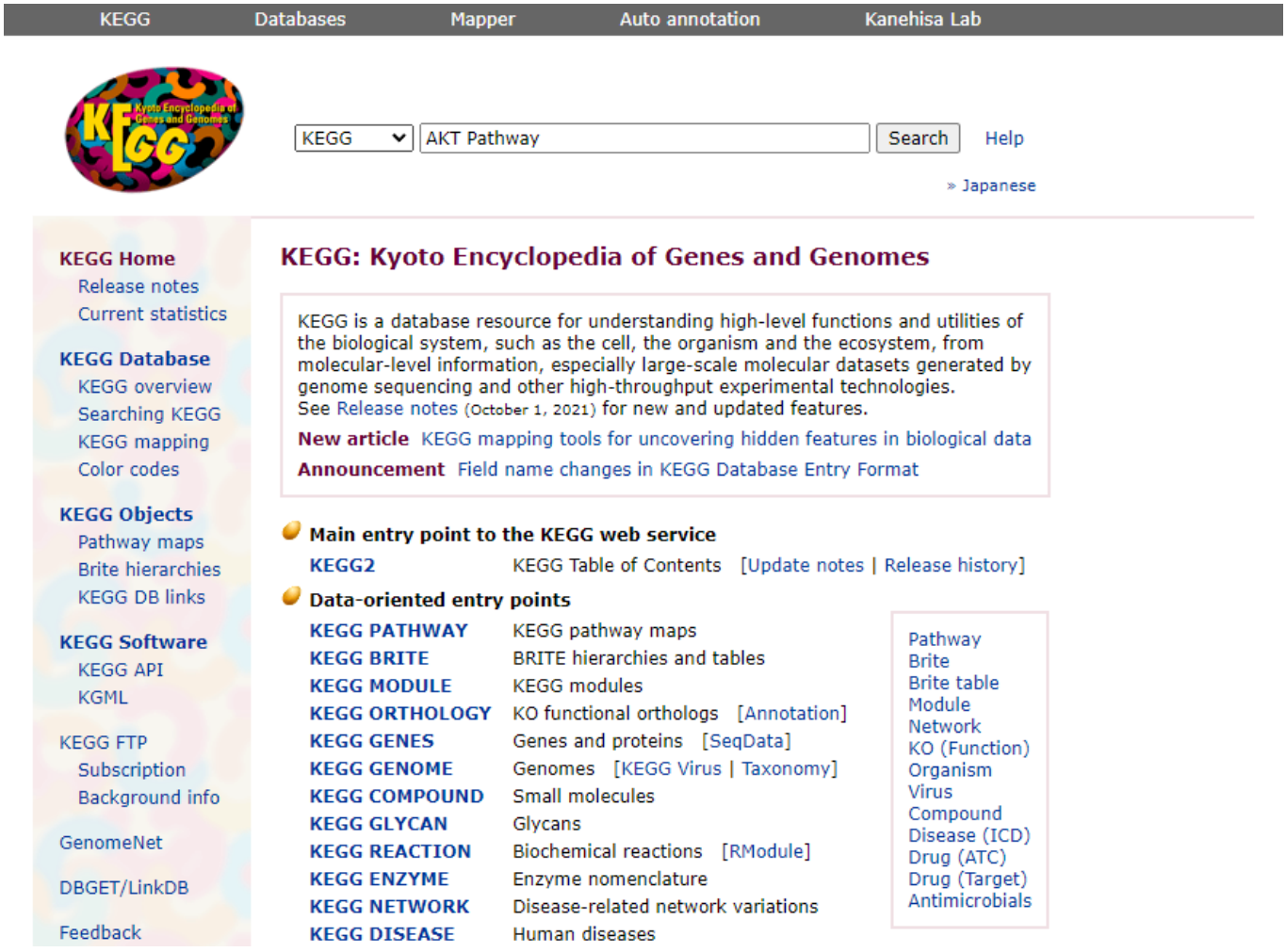


Fig1. Homepage of Kegg with query AKT Pathway

Search KEGG for AKT Pathway Go Clear

Database: KEGG - Search term: AKT Pathway

KEGG PATHWAY

map04151
PI3K-Akt signaling pathway

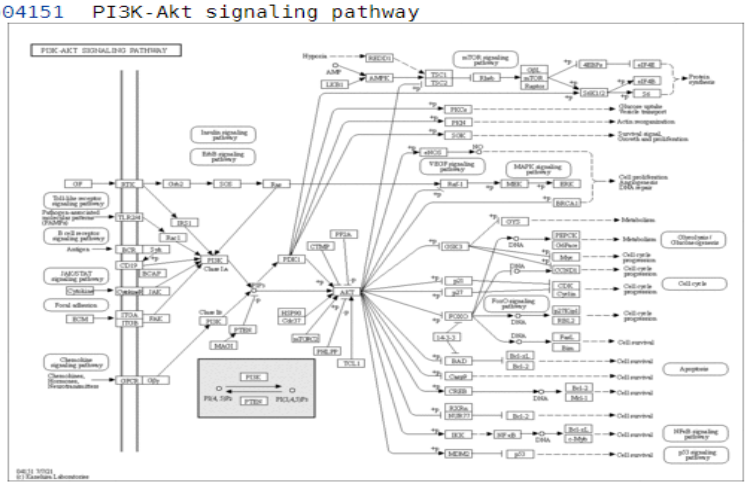
KEGG NETWORK

N00154
CXCR-GNB/G-PI3K-AKT signaling pathway
N00158
KSHV vGPCR to GNB/G-PI3K-AKT signaling pathway
N00220
PTEN-PIP3-AKT signaling pathway
N00353
HPV E6 to PTEN-PIP3-AKT signaling pathway
N00354
HPV E6 to PTEN-PIP3-AKT signaling pathway
• • • » display all

Fig2. Hit page of query AKT Pathway

PATHWAY: map04151

Help

Entry	map04151 Pathway
Name	PI3K-Akt signaling pathway
Description	The phosphatidylinositol 3' -kinase(PI3K)-Akt signaling pathway is activated by many types of cellular stimuli or toxic insults and regulates fundamental cellular functions such as transcription, translation, proliferation, growth, and survival. The binding of growth factors to their receptor tyrosine kinase (RTK) or G protein-coupled receptors (GPCR) stimulates class Ia and Ib PI3K isoforms, respectively. PI3K catalyzes the production of phosphatidylinositol-3,4,5-triphosphate (PIP3) at the cell membrane. PIP3 in turn serves as a second messenger that helps to activate Akt. Once active, Akt can control key cellular processes by phosphorylating substrates involved in apoptosis, protein synthesis, metabolism, and cell cycle.
Class	Environmental Information Processing; Signal transduction BRITE hierarchy
Pathway map	map04151 PI3K-Akt signaling pathway  Ortholog table

All links

Disease (1)
KEGG DISEASE (1)
Chemical substance (4)
KEGG COMPOUND (4)
Gene (594784)
KEGG ORTHOLOGY (263)
RefGene (594521)
Literature (19)
PubMed (19)
All databases (594808)

Download RDF

Fig3. Result page for Pathway: map04151

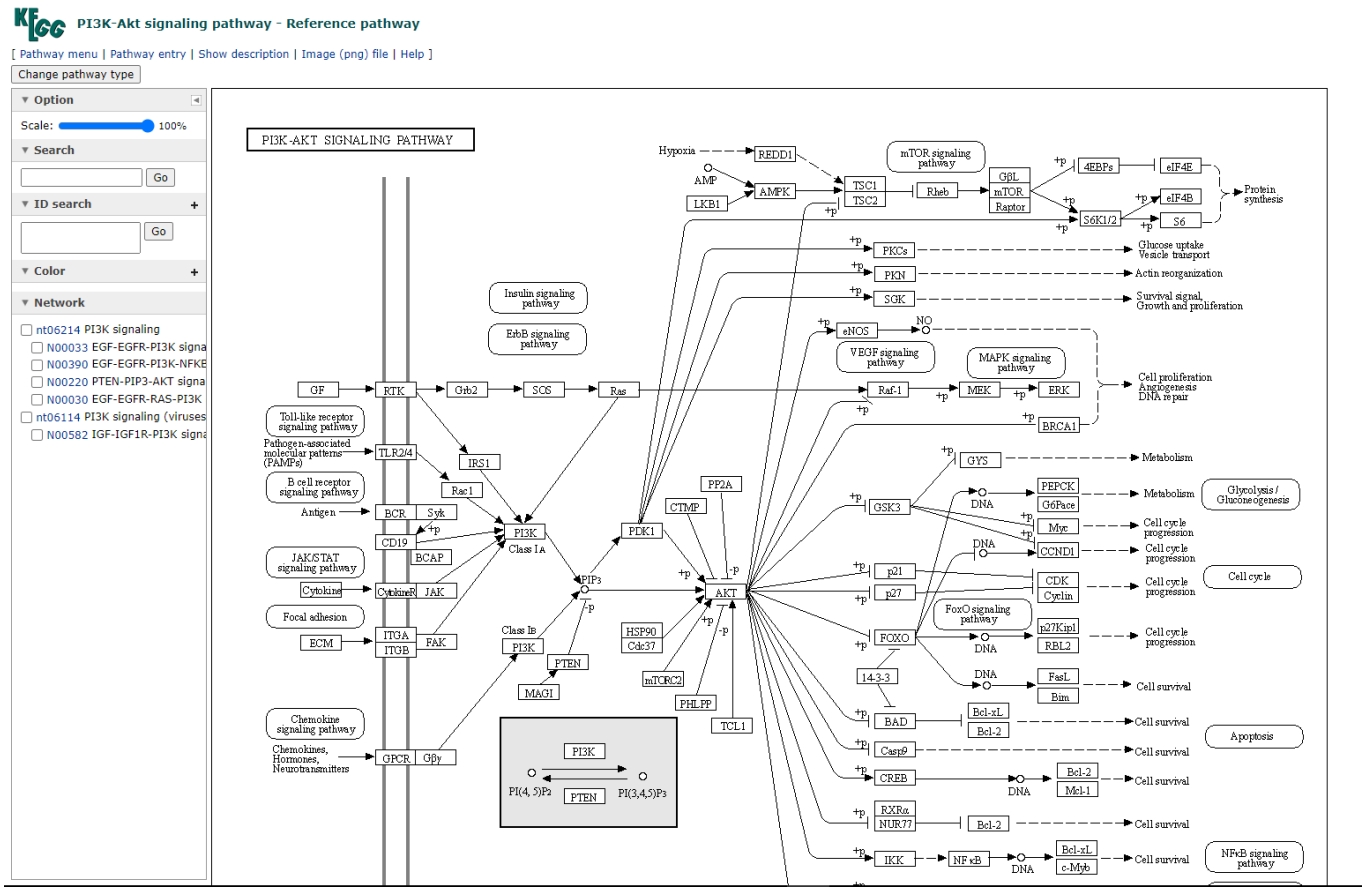


Fig4. AKT signalling pathway – Reference pathway.

KEGG

NETWORK: N00154

Help

Entry	N00154 Network
Name	CXCR-GNB/G-PI3K-AKT signaling pathway
Definition	CXCL8 -> CXCR2 -> GNB/G -> PI3Kgamma -> PIP3 -> AKT -> MTOR
Expanded	3576 -> 3579 -> (2782,2783,2784,59345,10681,54331,2785,2786,2787, 2788,94235,2790,2791,55970,51764,2792,2793) -> (5294,23533, 146850) -> C05981 -> (207,208,10000) -> 2475
Class	nt06224 CXCR signaling nt06124 Chemokine signaling (viruses) nt06150 Cytokine-cytokine receptor interaction (viruses) nt06167 Human cytomegalovirus (HCMV) nt06164 Kaposi sarcoma-associated herpesvirus (KSHV)
Type	Reference
Pathway	hsa04062 Chemokine signaling pathway
Gene	3576 CXCL8; C-X-C motif chemokine ligand 8 3579 CXCR2; C-X-C motif chemokine receptor 2 2782 GNB1; G protein subunit beta 1 2783 GNB2; G protein subunit beta 2 2784 GNB3; G protein subunit beta 3 59345 GNB4; G protein subunit beta 4 10681 GNB5; G protein subunit beta 5 54331 GNG2; G protein subunit gamma 2 2785 GNG3; G protein subunit gamma 3 2786 GNG4; G protein subunit gamma 4 2787 GNG5; G protein subunit gamma 5 2788 GNG7; G protein subunit gamma 7 94235 GNG8; G protein subunit gamma 8 2790 GNG10; G protein subunit gamma 10 2791 GNG11; G protein subunit gamma 11 55970 GNG12; G protein subunit gamma 12 51764 GNG13; G protein subunit gamma 13 2792 GNGT1; G protein subunit gamma transducin 1 2793 GNGT2; G protein subunit gamma transducin 2 5294 PIK3CG; phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma 23533 PIK3R5; phosphoinositide-3-kinase regulatory subunit 5 146850 PIK3R6; phosphoinositide-3-kinase regulatory subunit 6 207 AKT1; AKT serine/threonine kinase 1 208 AKT2; AKT serine/threonine kinase 2 10000 AKT3; AKT serine/threonine kinase 3 2475 MTOR; mechanistic target of rapamycin
Metabolite	C05981 Phosphatidylinositol-3,4,5-trisphosphate

All links

Pathway (1)
KEGG PATHWAY (1)
Chemical substance (1)
KEGG COMPOUND (1)
Gene (26)
KEGG GENES (26)
Literature (3)
PubMed (3)
All databases (31)

Download RDF

Fig5. KEGG network: N00154

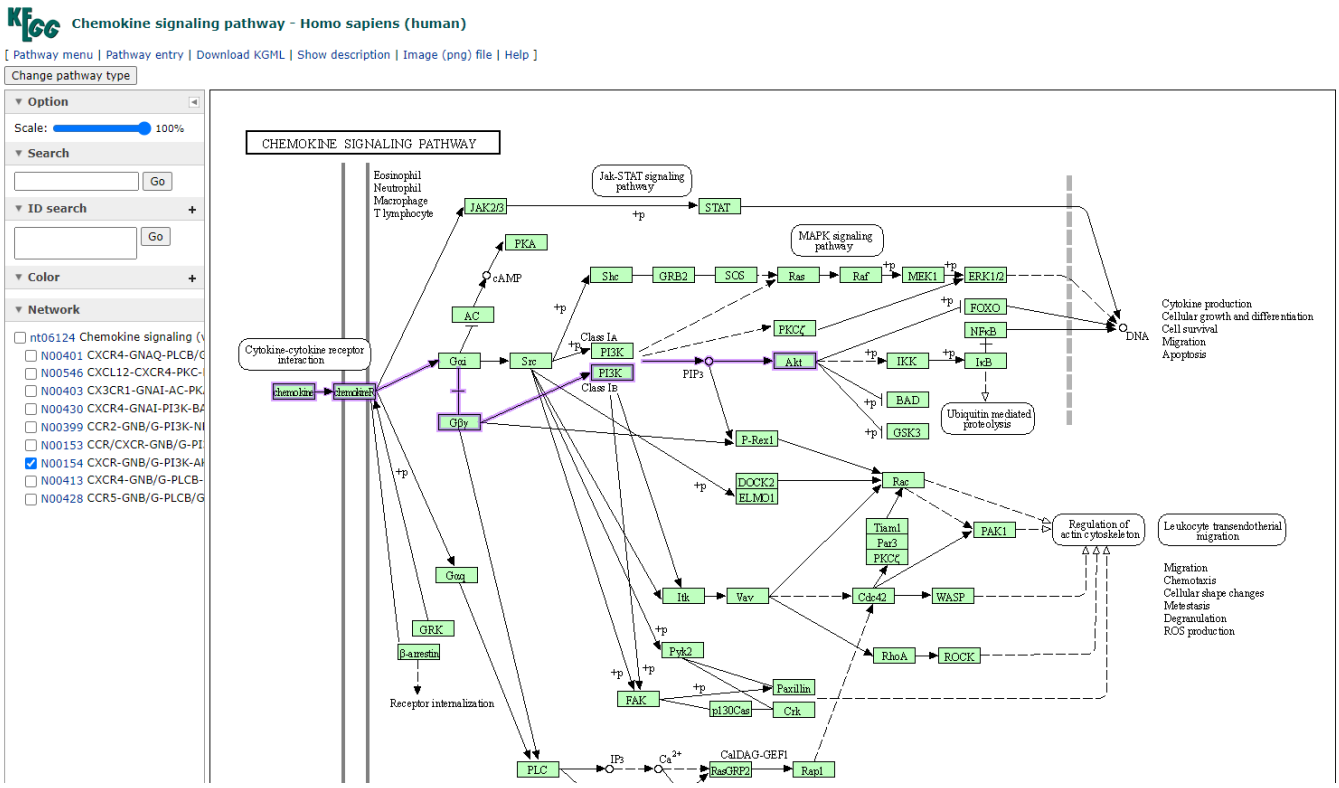


Fig6. KEGG chemokine signalling pathway homo sapiens

Results:

KEGG pathway is a great collection of manually drawn pathway maps representing our knowledge on the molecular interaction and reaction networks.

Conclusion:

KEGG is a great resource for the collection and cross checking of manually drawn pathways and information related to the same.

References:

1. The Akt Pathway in Oncology Therapy and Beyond (review) George Nitulescu-Maryna Van De Venter-Georgiana Nitulescu-Anca Ungurianu-Petras Juzenas-Qian Peng-Octavian Olaru-Daniela Grădinaru-Aristides Tsatsakis-Dimitris Tsoukalas-Demetrios Spandidos-Denisa Margina - https://www.spandidos-publications.com/10.3892/ijo.2018.4597
2. https://www.genome.jp/kegg/pathway.html
3. https://www.genome.jp/kegg/brite.html
4. https://www.genome.jp/kegg/module.html
5. https://www.genome.jp/entry/map04151
6. https://www.genome.jp/pathway/map04151
7. https://www.genome.jp/entry/N00154
8. https://www.genome.jp/pathway/hsa04062+N00154

Date: 11-10-21

WEBLEM 6b

(url: https://www.omim.org/)

Aim:

To study the disease Sickle Cell anemia using OMIM database.

Introduction:

Online Mendelian Inheritance in Man (OMIM), a continuation of Dr Victor A. McKusick's Mendelian Inheritance in Man (MIM) (1), is the primary repository of comprehensive, curated information on genes and genetic phenotypes and the relationships between them. MIM was published through 12 editions between 1966 and 1998, and OMIM has been online and searchable since 1987.
With the advent of new sequencing technologies, there is a rapid increase in the reports of presumed gene-phenotype relationships. OMIM.org was created to provide a user-friendly and easily searchable portal to a curated compilation of the literature to aid in clinical and molecular genetic research.

Advanced Search	:	In advanced search we can find history for our Entry.
Phenotype MIM Number	:	Main entry.
Genelocus MIM Number	:	Gene Information.

Symbols:

1. Phenotype Description , molecular basis known
2. Gene Discription
3. Phenotype & Gene Combine
4. No Symbol: Other , mainly phenotype with suspected mendelian basis.

Sickle cell anemia is one of a group of disorders known as sickle cell disease. Sickle cell anemia is an inherited red blood cell disorder in which there aren't enough healthy red blood cells to carry oxygen throughout your body. Normally, the flexible, round red blood cells move easily through blood vessels. In sickle cell anemia, the red blood cells are shaped like sickles or crescent moons. These rigid, sticky cells can get stuck in small blood vessels, which can slow or block blood flow and oxygen to parts of the body.

Methodology:

1. Open the homepage of OMIM.
2. Entry the query in search bar.
3. Open the Result page.
4. Interpret the Result.

Observation:

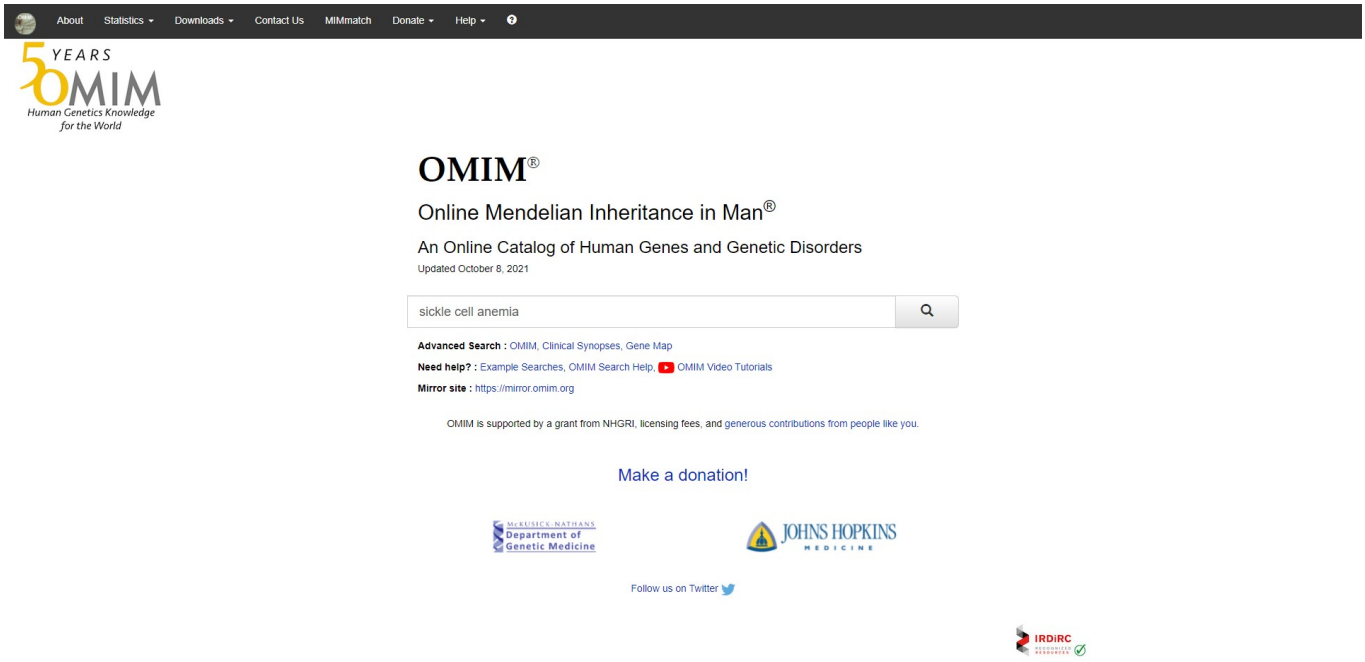


Fig1. Homepage of OMIM with query Sickle cell anemia

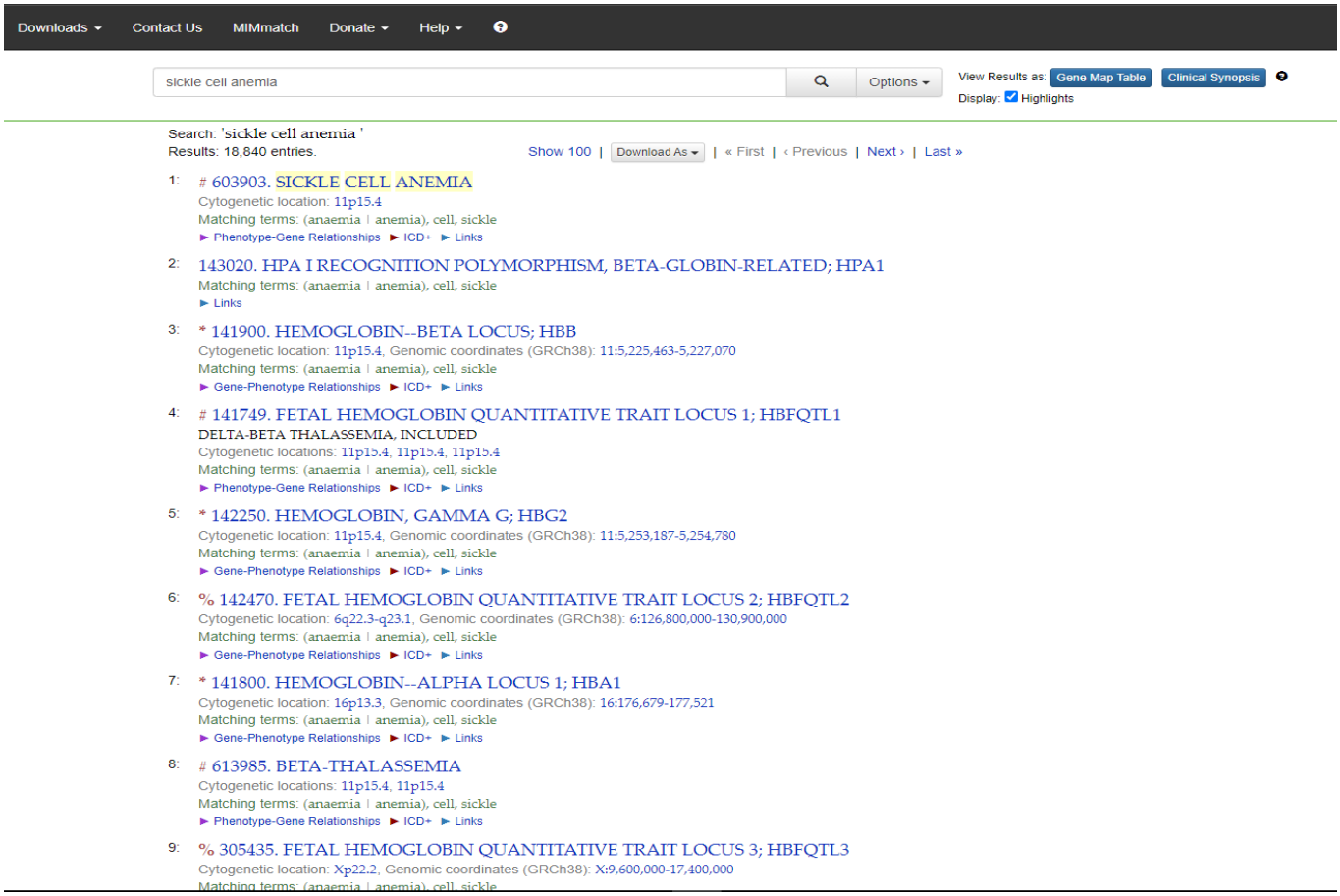


Fig2. Hit page for query Sickle cell anemia showing 18,840 entries

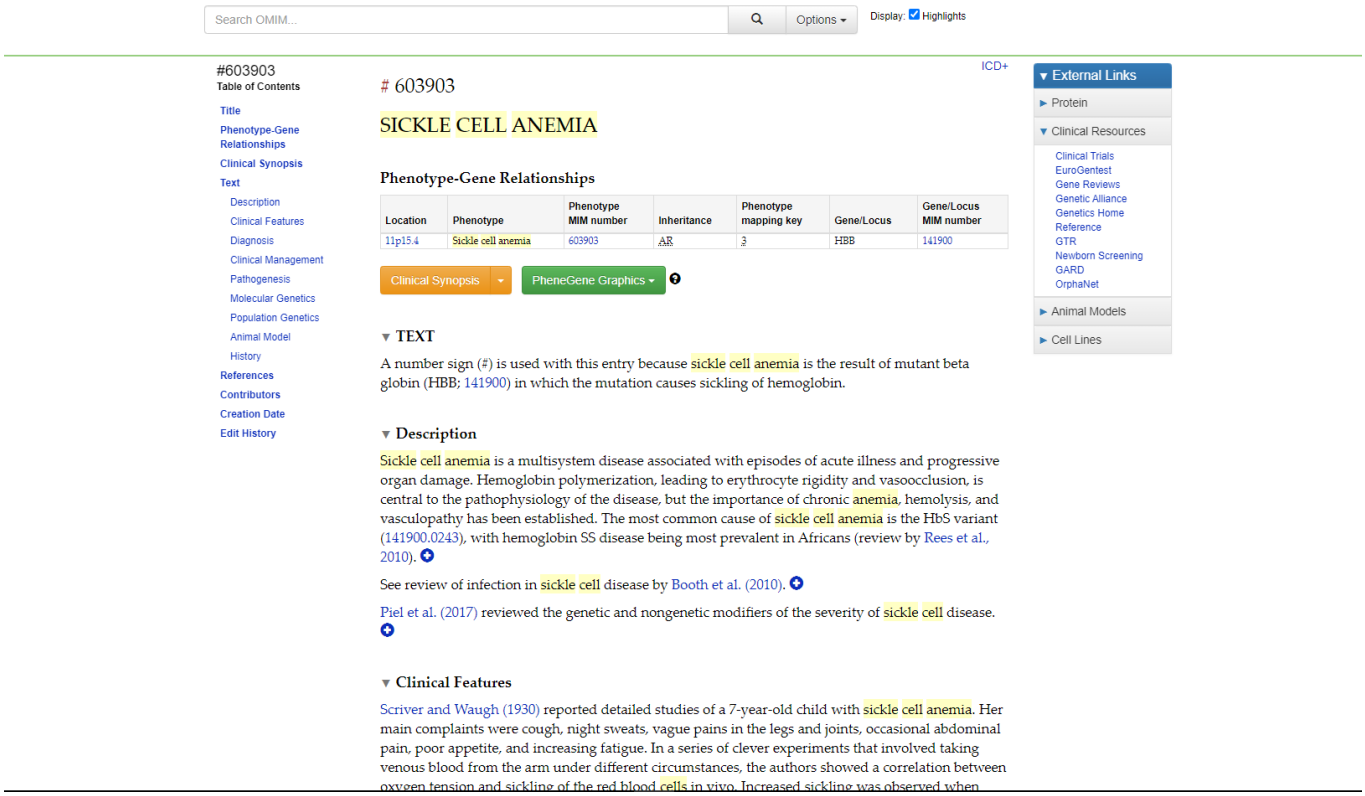


Fig3. Result page for Sickle cell anemia

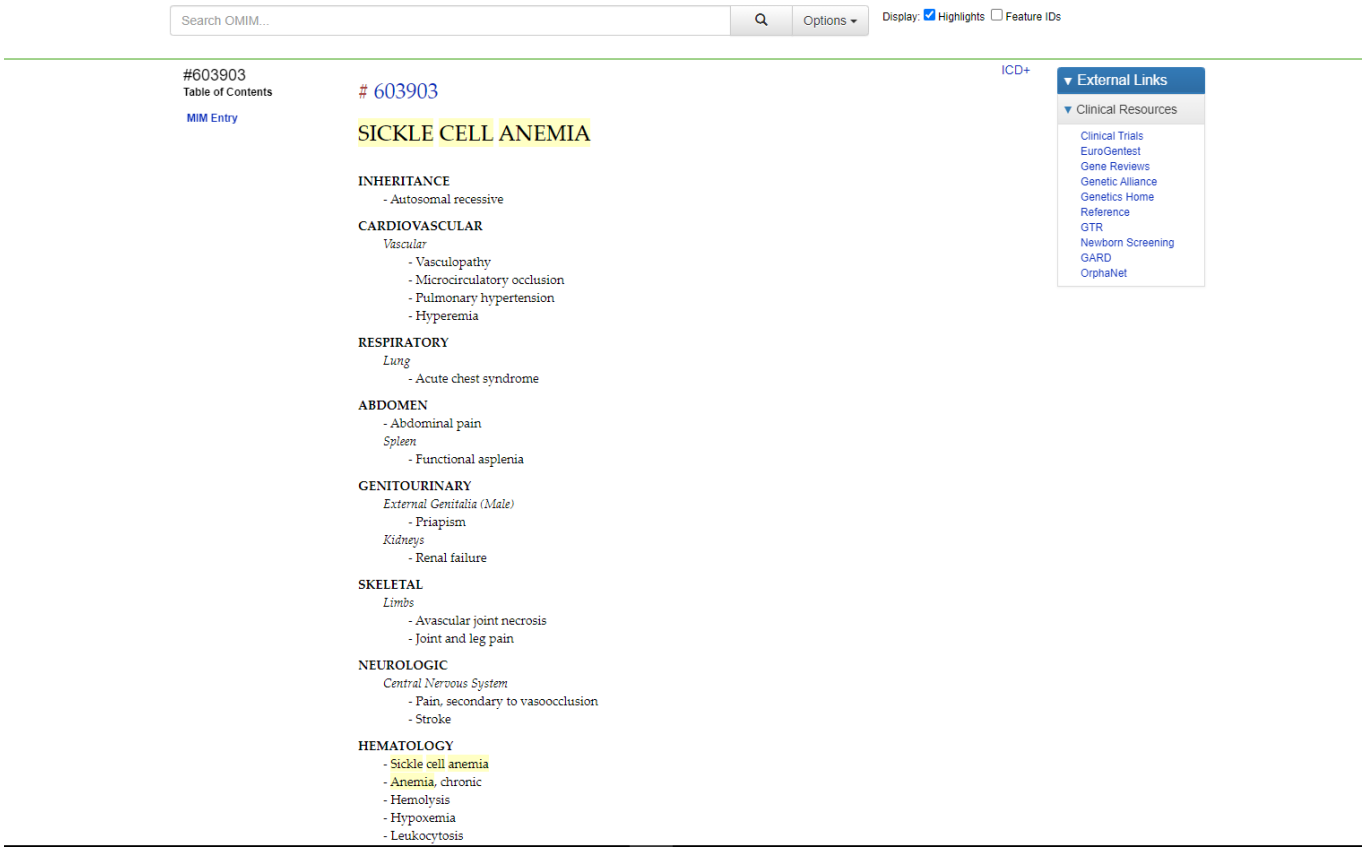


Fig4. Clinical synopsis for sickle cell anemia

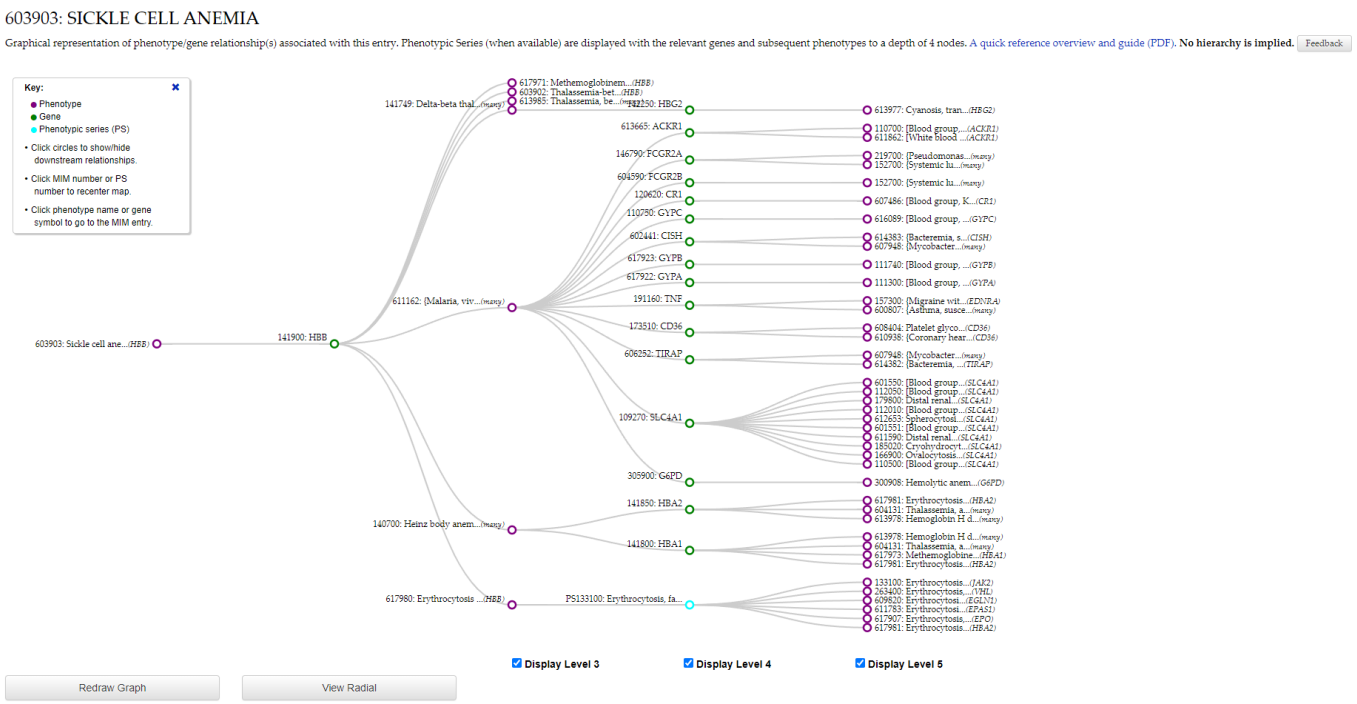


Fig5. Phenegene linear graphics

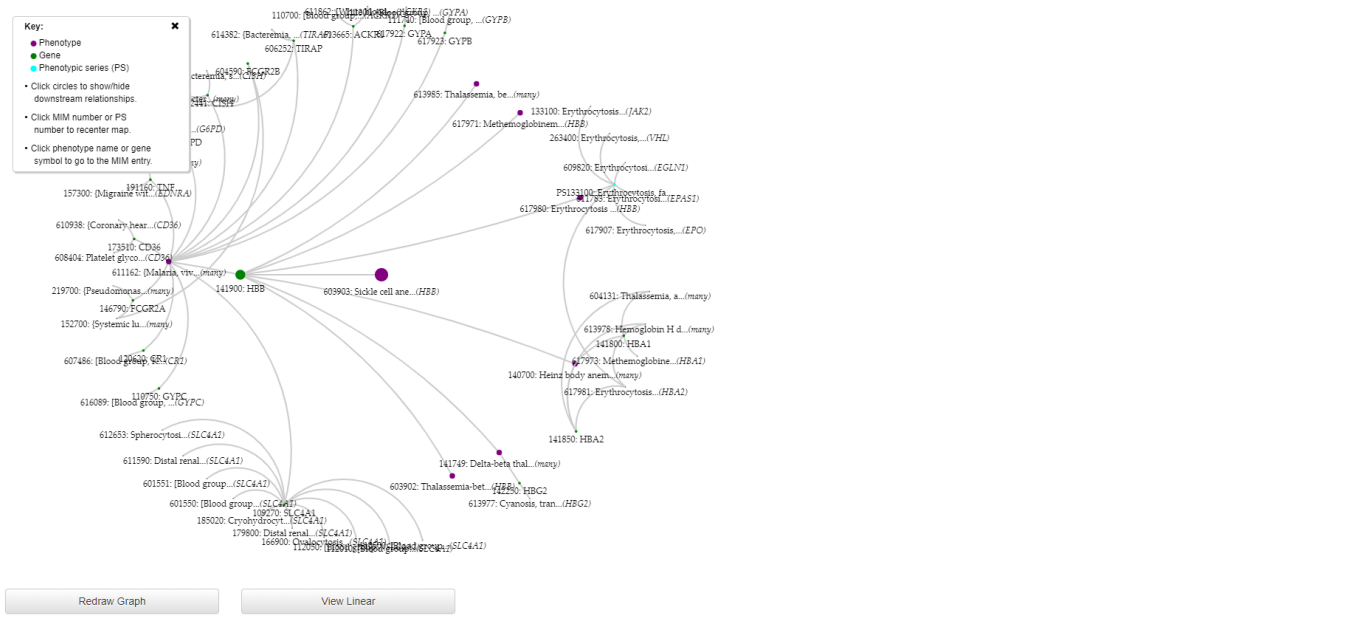


Fig6. Phenegene radial graphics

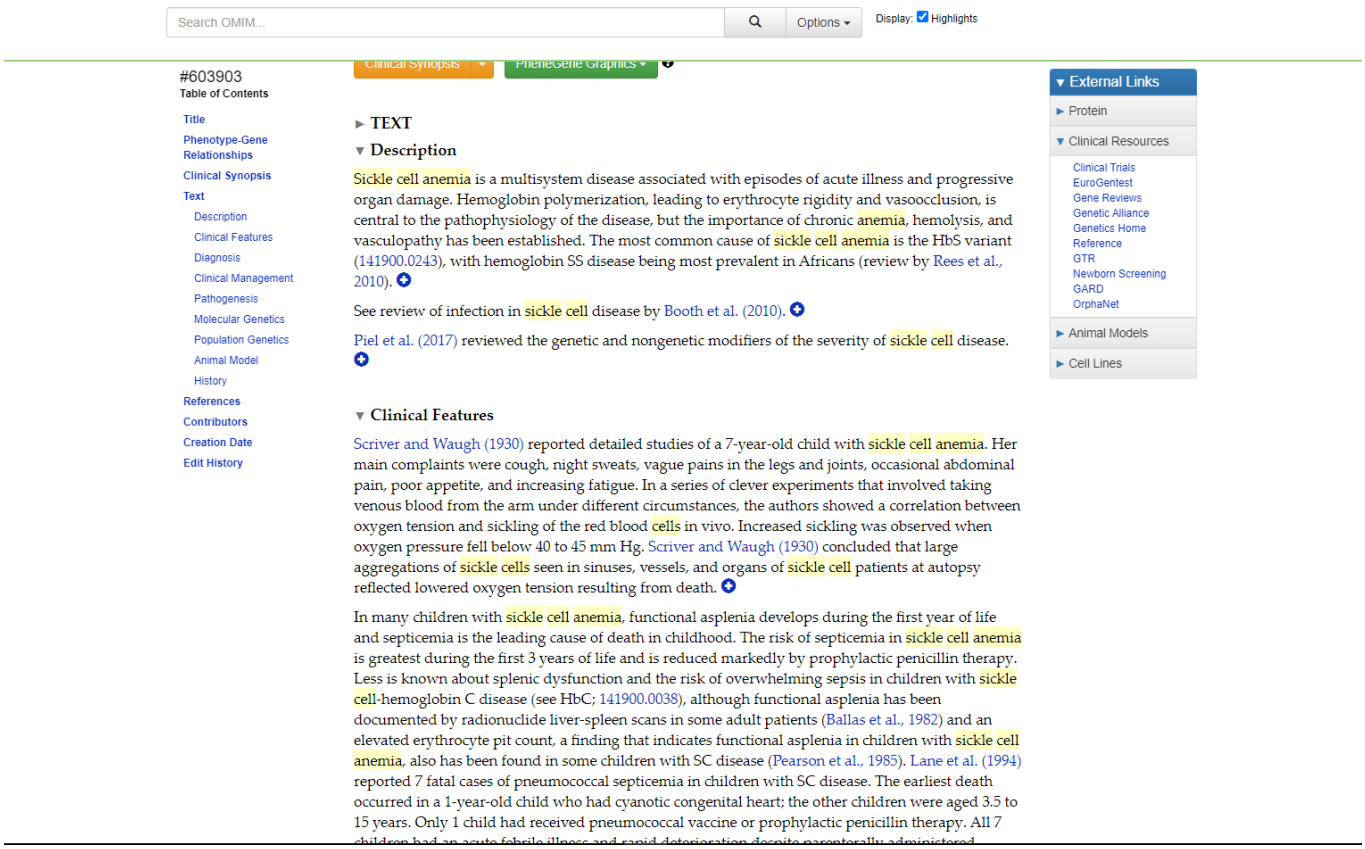


Fig7. Description for query sickle cell anemia

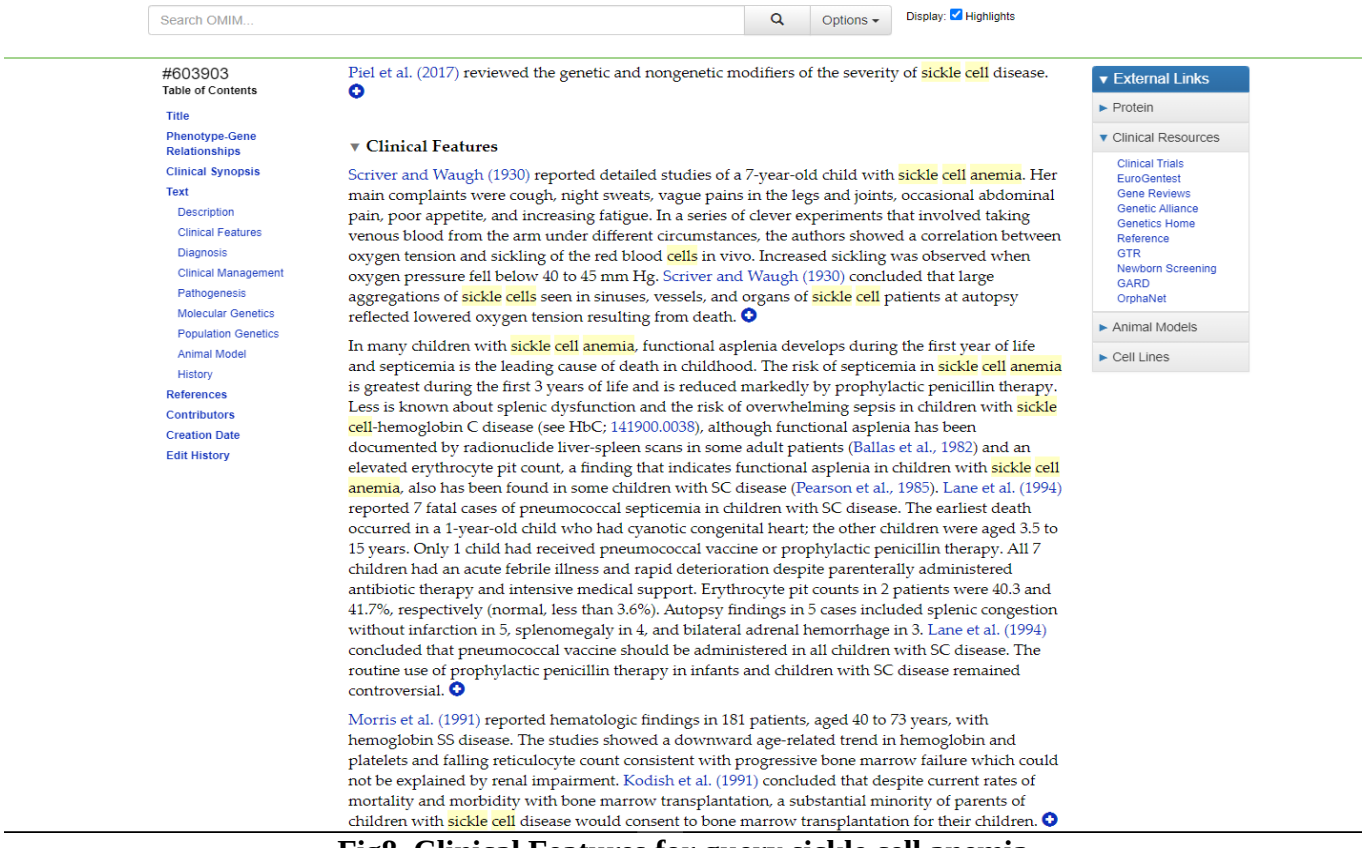


Fig8. Clinical Features for query sickle cell anemia

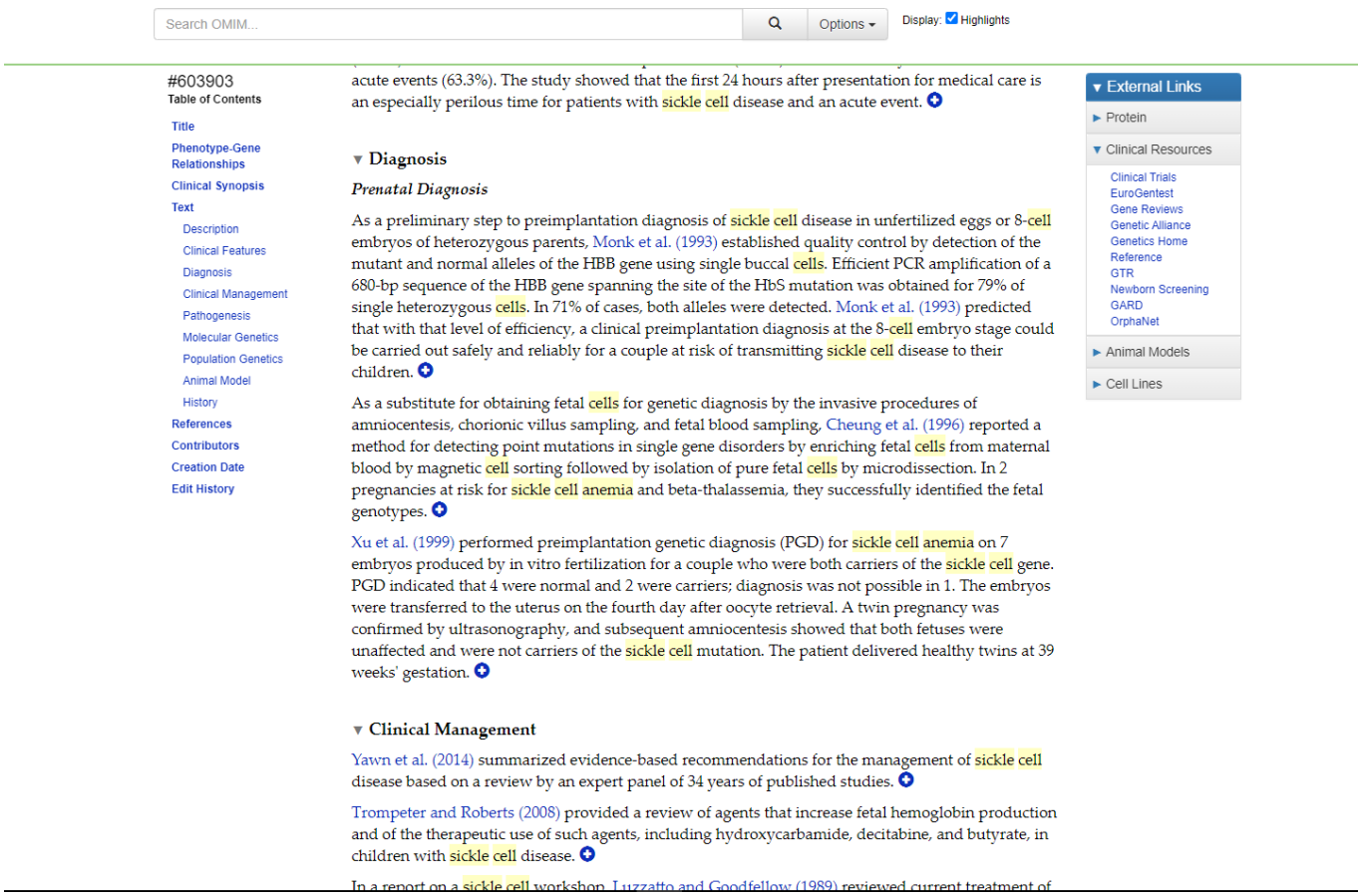


Fig9. Diagnosis for query sickle cell anemia

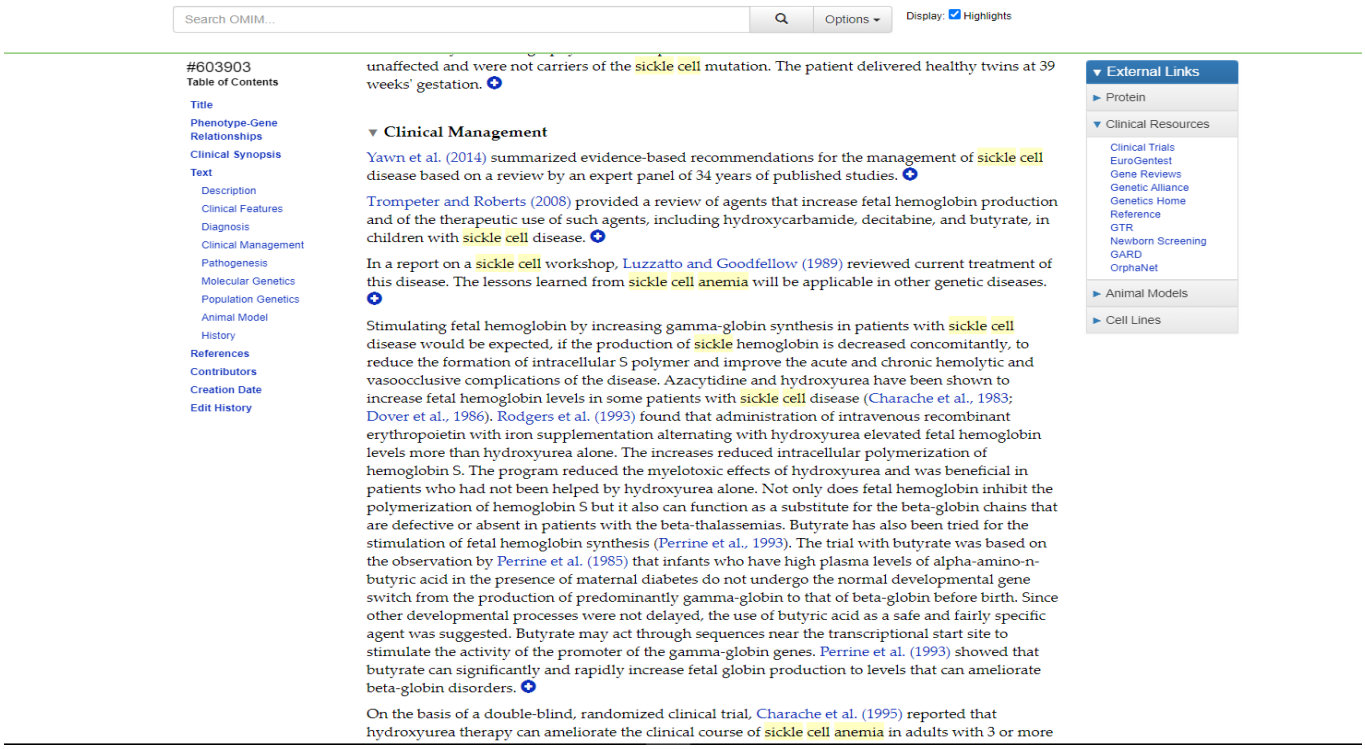


Fig10. Clinical Management for query sickle cell anemia

Results:

In OMIM database the query sickle cell anemia shows 18,841 entries. It gives information regarding Human Genes & Genetic Disorders

Conclusions:

OMIM is a very easy to use and accessible database of human genes and genetic disorders compiled to support human genetics research and education and the practice of clinical genetics.

References:

1. https://www.mayoclinic.org/diseases-conditions/sickle-cell-anemia/symptoms-causes/syc-20355876#:~:text=Sickle%20cell%20anemia%20is%20one,move%20easily%20through%20blood%20vessels.
2. https://www.omim.org/
3. https://www.omim.org/search?index=entry&sort=score+desc%2C+prefix_sort+desc&start=1&limit=10&search=Sickle+cell+anemia
4. https://www.omim.org/entry/603903?search=sickle%20cell%20anemia&highlight=%28anaemia%7Canemia%29%20cell%20sickle
5. https://www.omim.org/clinicalSynopsis/603903?highlight=(anaemia|anemia)%20cell%20sickle
6. https://www.omim.org/graph/linear/603903
7. https://www.omim.org/graph/radial/603903
8. https://www.omim.org/entry/603903?search=sickle%20cell%20anemia&highlight=%28anaemia%7Canemia%29%20cell%20sickle#description
9. https://www.omim.org/entry/603903?search=sickle%20cell%20anemia&highlight=%28anaemia%7Canemia%29%20cell%20sickle#diagnosis
10. https://www.omim.org/entry/603903?search=sickle%20cell%20anemia&highlight=%28anaemia%7Canemia%29%20cell%20sickle#clinicalFeatures
11. https://www.omim.org/entry/603903?search=sickle%20cell%20anemia&highlight=%28anaemia%7Canemia%29%20cell%20sickle#clinicalManagement