PIPSA

tutorial

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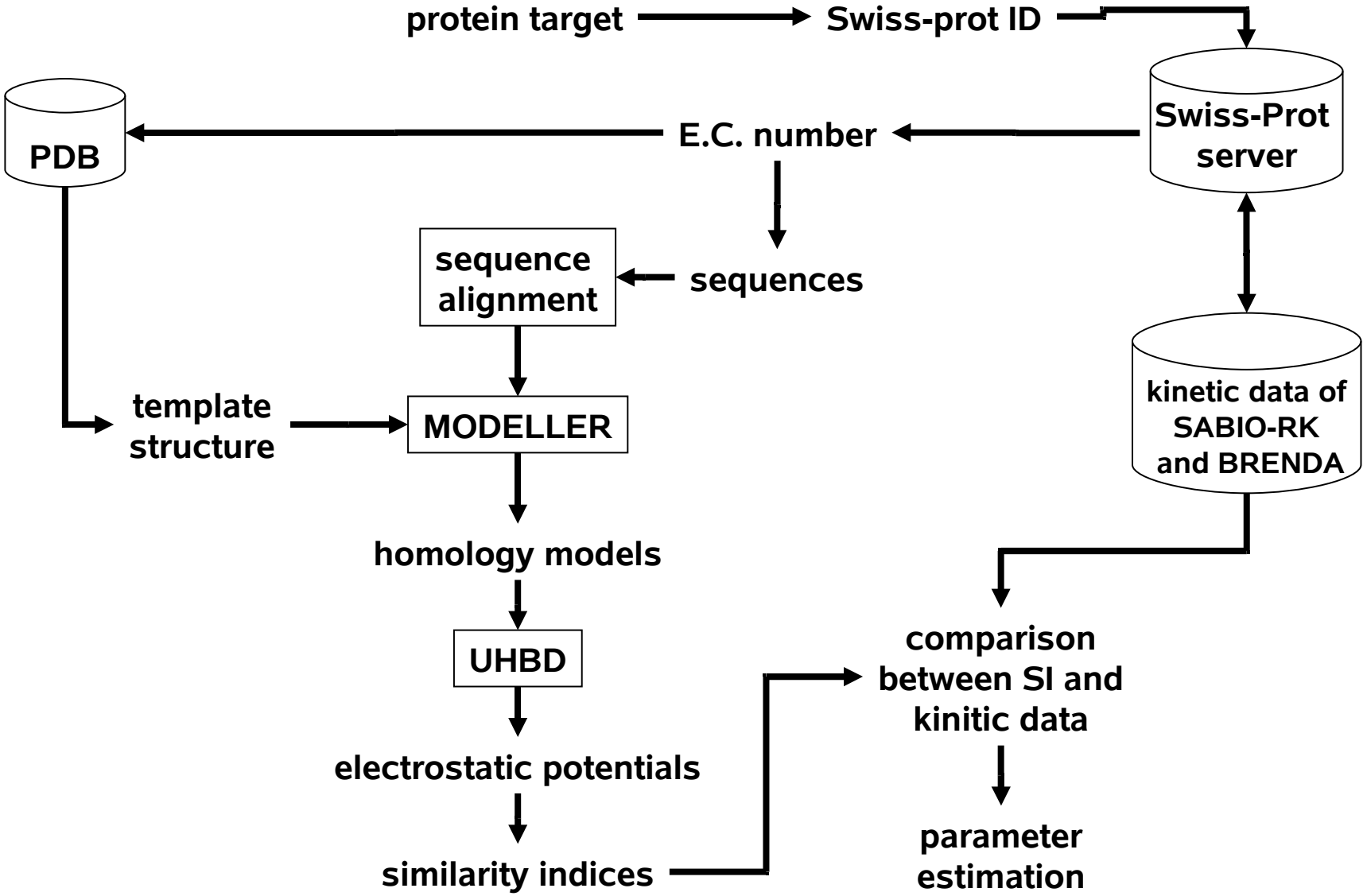
webPIPSA: workflow with homology modeling



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Similarity-Based Estimate of Kinetic Constants

measurement **@ condition 1**

measurement **@ condition 2**

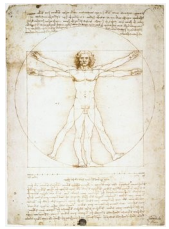
kinetic constant 1

kinetic constant 2

Yeast@35°C

Cow@5°C

??



??

kinetic constant 3

Human@37°C

metabolic network simulations @ **condition 3**

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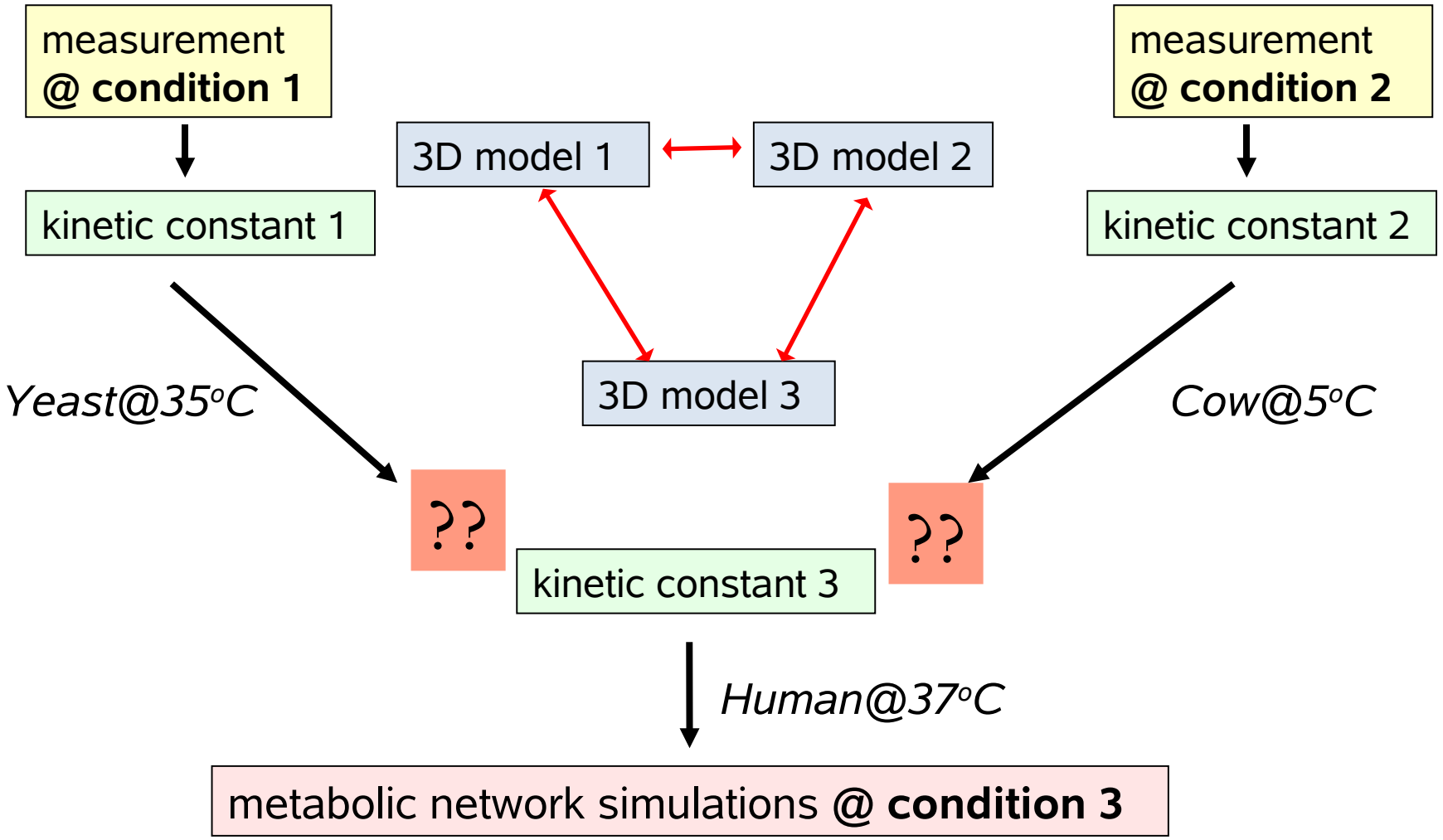
Similarity-Based Estimate of Kinetic Constants



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webPIPSA

glucokinase (hexokinase)

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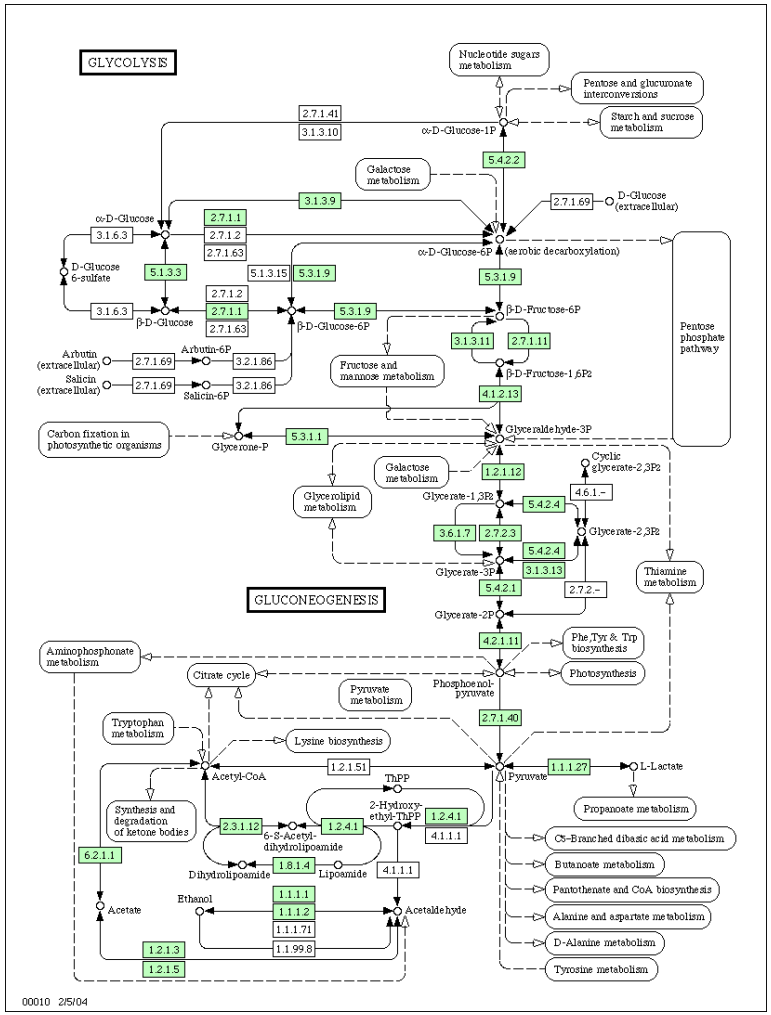
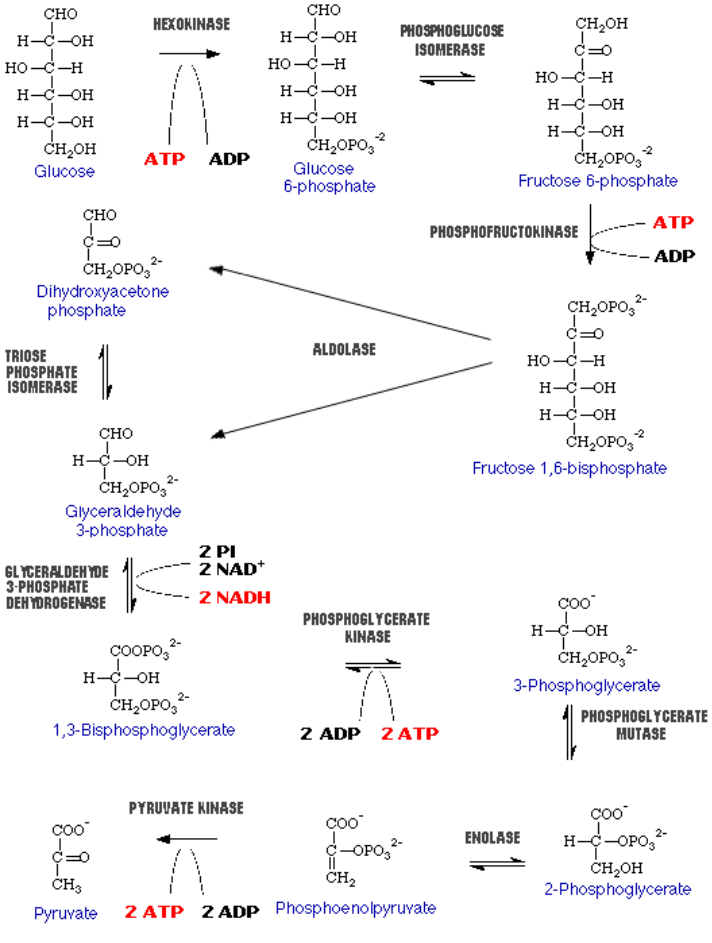
glycolyse





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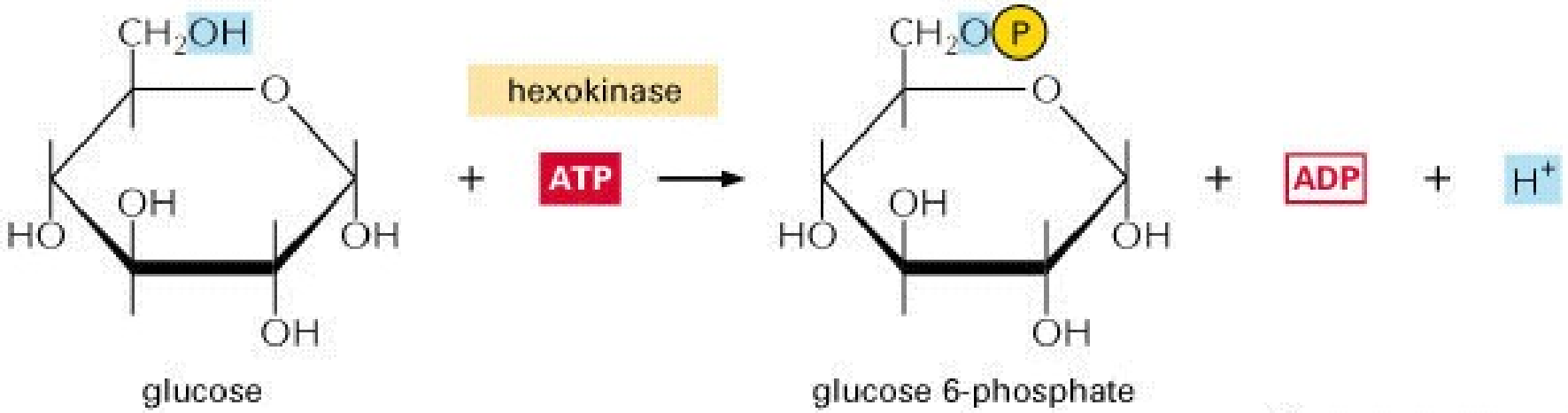
glucokinase (hexokinase)



1. Identify Chemical Reaction of Interest

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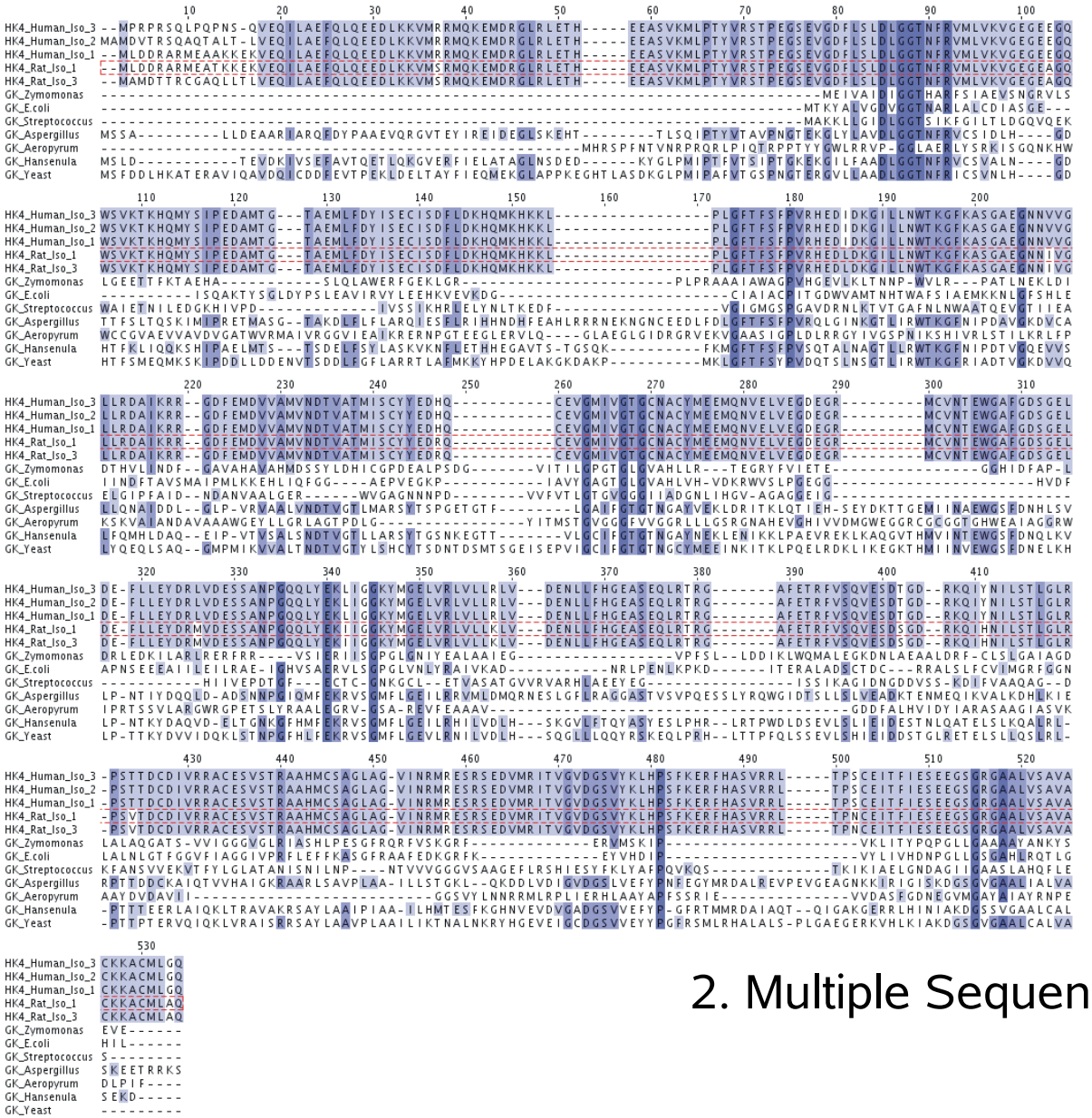
glucokinase (hexokinase)



2. Multiple Sequence Alignment

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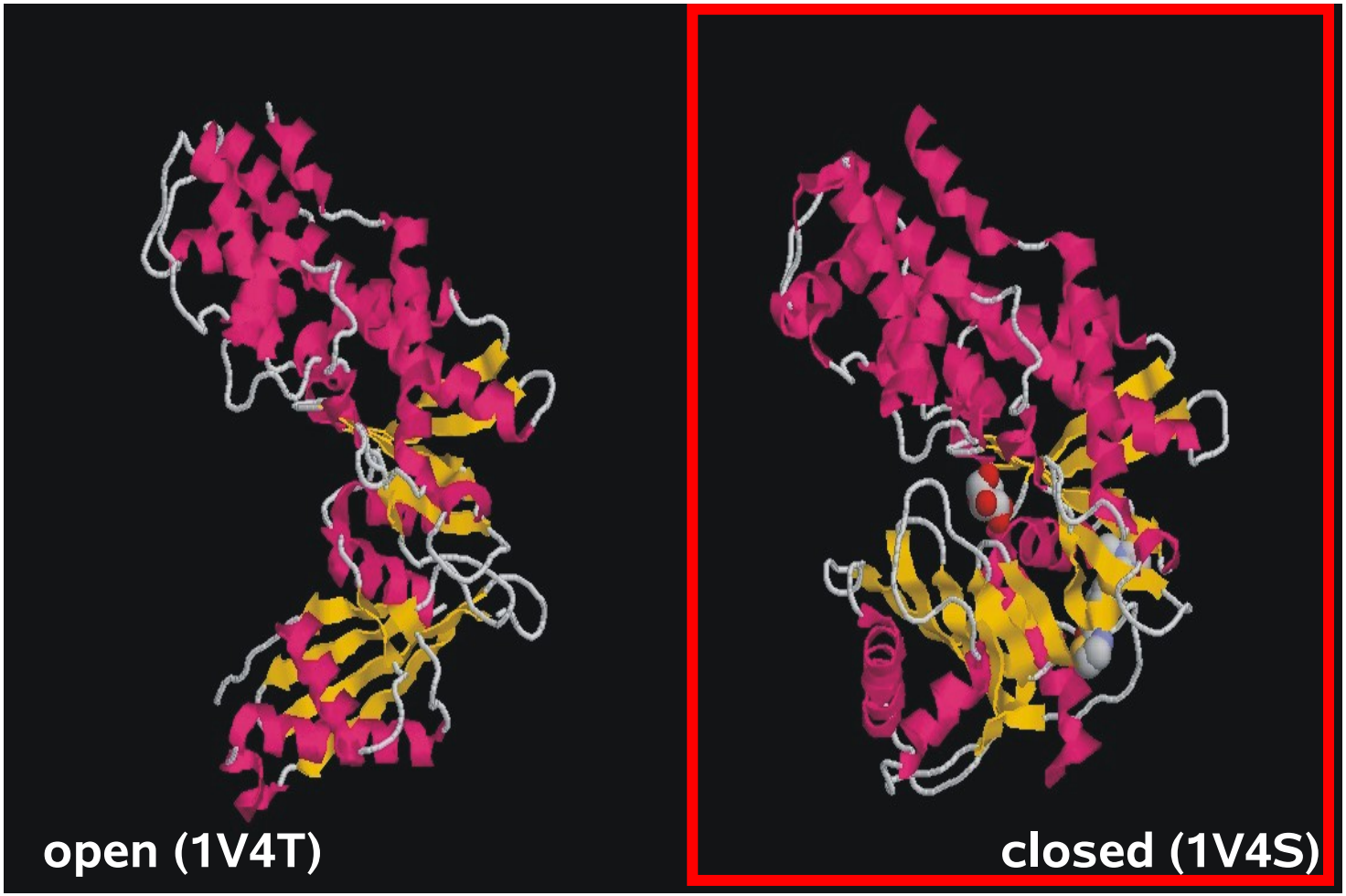
glucokinase (hexokinase)



3. choice of appropriate template

two human glucokinase isoforms
(open and closed form)

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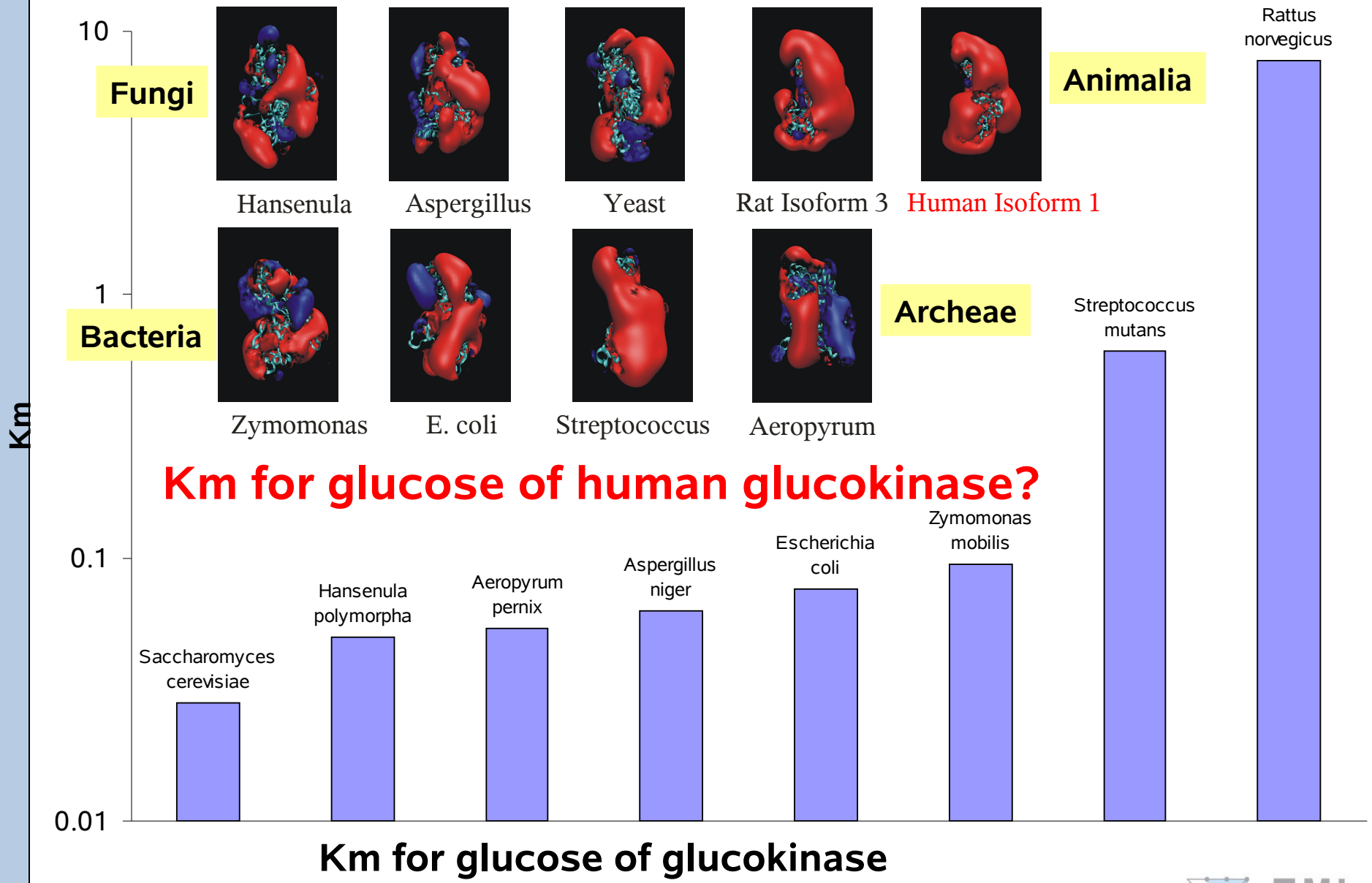
glucokinase (hexokinase)



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webPIPSA

http://sycamore.eml.org

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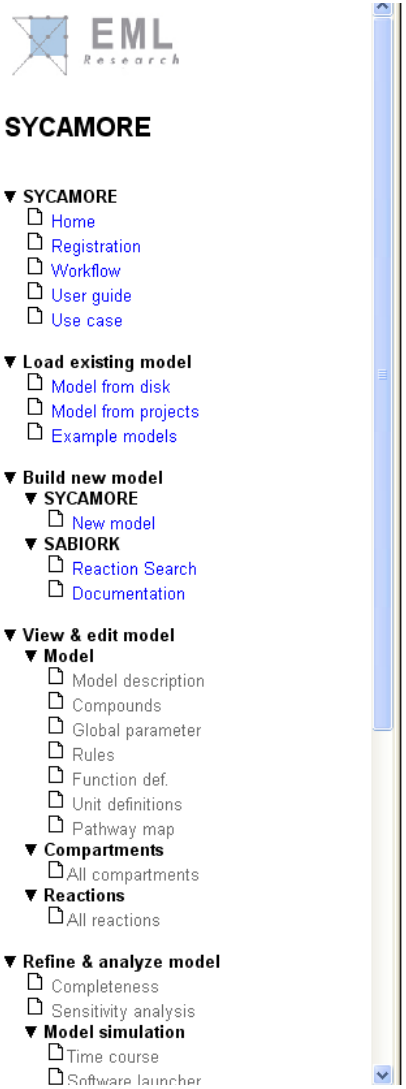

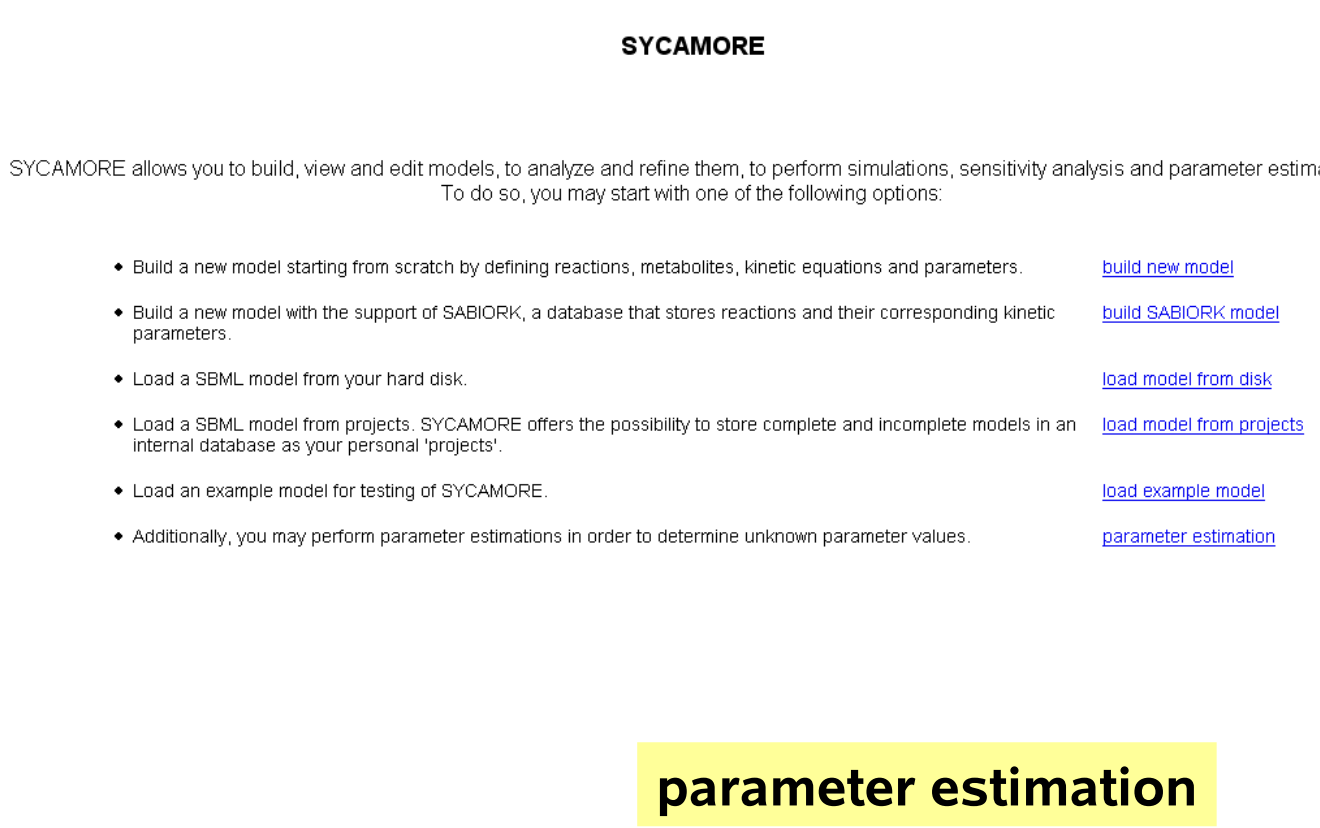

parameter estimation

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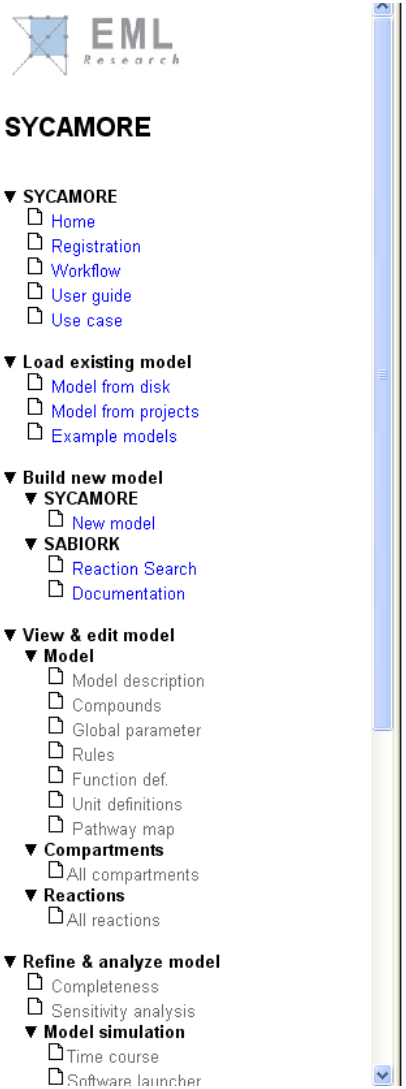

Registration

We request registration because parameter estimations may take between a couple of minutes and - in case of very complex calculations - several days. In addition, because CPU capacity is restricted, all requests are queued, thus it might be that it takes some time even for simple estimations. In any case, you will be notified by email on the result of the estimation(s), therefore an email adress is required. Without email registration, parameter calculations will not be performed.

In order to access (load, view, edit, save) your personal models, you must register. In case that you are not registered yet, choose 'new registration'.

Additionally, the workflow for parameter calculations makes use of the program MODELLER, which requires an End-User Software License Agreement. You also need a MODELLER-key for using the program within the parameter estimation workflow.

REGISTERED USERS

Name: (user name) (password)

enter

I can't remember user name / password

new registration

register:

- **user name**
- **YOUR email address**
- **password**

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qPIPSA Parameter Retrieval and Estimation Module

What this module does?

1. Retrieval of relevant parameters and associated information from BRENDA and SABIO-RK, as well as protein sequences from Swiss-Prot and protein structures from PDB, MODBASE and SWISSMODEL
2. Parameter estimation using available protein structure information. Currently the PIPSA method is used to do this. PIPSA analysis can be used to aid the estimation of kinetic parameters from a similarity analysis of the electrostatic potentials of the enzyme for which the parameter is needed and the enzymes for which parameters are already known.
   NOTE:
   This is an initial beta release. All results generated by this server for PIPSA analysis should be considered preliminary at this stage![1]

For more information on the use of this module click here.

Retrieval of parameters and related information

This is based on insertion of a unique protein identifier. Currently a Swiss-Prot accession code must be given. The workflow depends on an EC annotation in the description line of your Swiss-Prot entry. This EC link is used to search in BRENDA and SABIO-RK entries.

Please enter :	
	Swiss-Prot accession code (eg. P35557 or P35520) [?]
	a valid email address [?]
	Start search

In case of unknown or only vaguely known protein functionality ProFAT may assist in detecting protein function and structural homology.

http://cluster-1.mpi-cbg.de/profat/profat.html

ProFAT is a tool for the functional annotation of proteins via the detection of weak homologies. Sequence homology is detected with NCBI's PSI-BLAST system. Structural homology is detected with UCL's Threader software. These results are then combined by the use of GenBank annotation and basic text mining.

ProFAT requires the user to submit a keyword list along with the protein sequence. Several pre-made keyword lists are available, however, the system is used optimally with a user defined keyword list consisting of suspected or experimentally determined information.

Bradshaw C. R., Surendranath V., and Habermann B. BMC Bioinformatics 2006, 7:466

[1]: Limitations currently are:

- Only single chain protein modelleing
- Neglect of protein flexibility

•Swiss-Prot accession code
•YOUR email address

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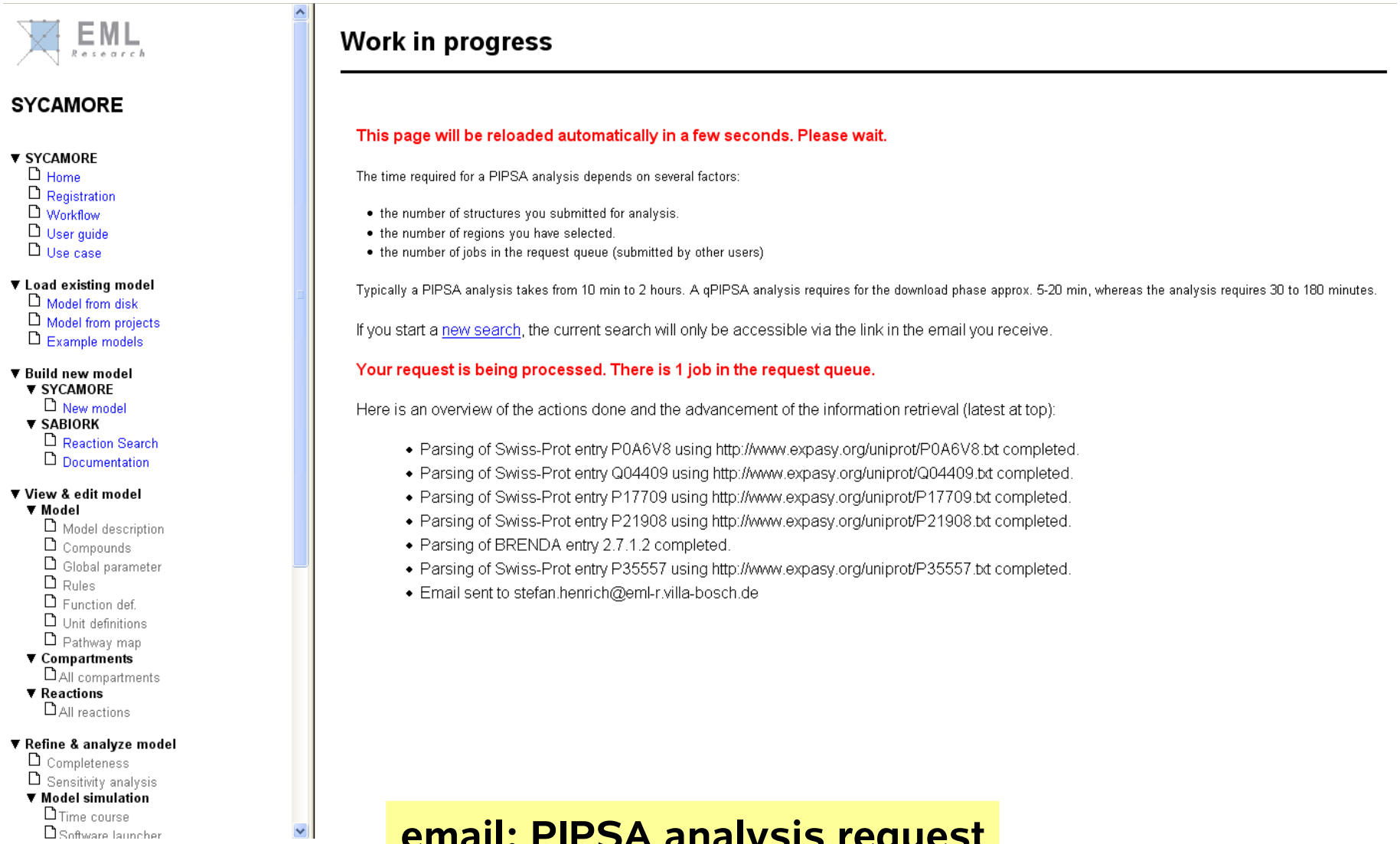
webPIPSA: hexokinase IV or D (P35557)



email: PIPSA analysis request

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webPIPSA: hexokinase IV or D (P35557)

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Parameter Retrieval and estimation

Parameter retrieval: available information

After successful retrieval of kinetic data and structural models, do one of the following:

1. If no information was found, or the information is not suitable, start a new search with a new Swiss-Prot accession code. For this click here .
2. Select a parameter from below and copy/paste it into your SBML model.
3. Assign a parameter based on an average of several retrieved values below and use it in your SBML model.
4. If there is structural information available, select a structural template and do a PIPSA to aid parameter assignment based on calculated electrostatical potentials of the retrieved proteins. The PIPSA analysis can be launched from this page [?].

   To start a workflow for PIPSA, do the following:

   1. In the section **Protein Structural Information** choose a template protein structure that you consider most suitable for protein structural modeling of your enzyme of interest (Click on arrow first). This is going to be used as a structural template in the subsequent homology modeling.
   2. In the section **Region selection** below the structural information, you can make selections for Swiss-Prot features of your protein (eg. active site, binding region etc, click on arrow first). Additional PIPSA runs will then be performed to restrict the comparison to these regions
   3. In the section **Kinetic data** select Swiss-Prot sequences with relevant kinetic data (by default all sequences are selected).

Please find additional information about the Parameter Retrieval and Estimation on our help page.

On this page, you'll find all the information gathered concerning the Swiss-Prot entry specified. This concerns both structural and kinetic data. There may be a lot of data, so use the triangles to display or hide information.

Here is the information found using the Swiss-Prot accession P35557.
This entry is for the organism *Homo sapiens*.

Calculate electrostatically similar proteins (please first check selected models and sequence below)

At registration you have provided the following
key for MODELLER [?] Please correct if needed.

required MODELLER key

- (•) Use modeller version 8v2
- ( ) Use modeller version 9v1 (including loop refinement)
- ( ) Use modeller version 9v1 (including loop refinement using DOPE score, takes longer)

email: Download for analysis of P35557 is complete

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webPIPSA: hexokinase IV or D (P35557)

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▶ Structural information

▶Region selection

▼ Kinetic data

Kinetic data is retrieved from the SABIO-RK and Brenda databases and concerns information associated with the Swiss-Prot entry given.

▼Information retrieved from Brenda

The results specific to the query Swiss-Prot entry organism are presented first.

Information retrieved using EC 2.7.1.2

Literature links refer to BRENDA. In case where no PubMed entry is linked in BRENDA, you will get the details of the reference paper.

☑ **1. Data specific to Swiss-Prot entry *P21908*, sequence derived from organism *Zymomonas mobilis***

▼	*Km information*				
Km value [mM]	**Km value [mM] Maximum**	**Substrate**	**Organism**	**Comment**	**References**
0.5	-	6-N-(carboxyethyl)ATP	Zymomonas mobilis	-	641063 PubMed
0.55	-	6-N-(carboxymethyl)ATP	Zymomonas mobilis	-	641063 PubMed
0.38	-	6-N-(succinyl)ATP	Zymomonas mobilis	-	641063 PubMed
1.25	-	6-N-[N-(6-aminohexhyl)carbamoyl]ATP	Zymomonas mobilis	-	641063 PubMed
0.5	-	ATP	Zymomonas mobilis	-	641063 PubMed
0.8	-	ATP	Zymomonas mobilis	-	641056 PubMed
0.22	-	D-Glucose	Zymomonas mobilis	-	641056 PubMed

☑ **1. Data specific to Swiss-Prot entry *P17709,Q04409*, sequence derived from organism *Saccharomyces cerevisiae***

▼	*Km information*				
Km value [mM]	**Km value [mM] Maximum**	**Substrate**	**Organism**	**Comment**	**References**
0.05	-	ATP	Saccharomyces cerevisiae	-	641066 PubMed
0.028	-	D-Glucose	Saccharomyces cerevisiae	-	641066 PubMed

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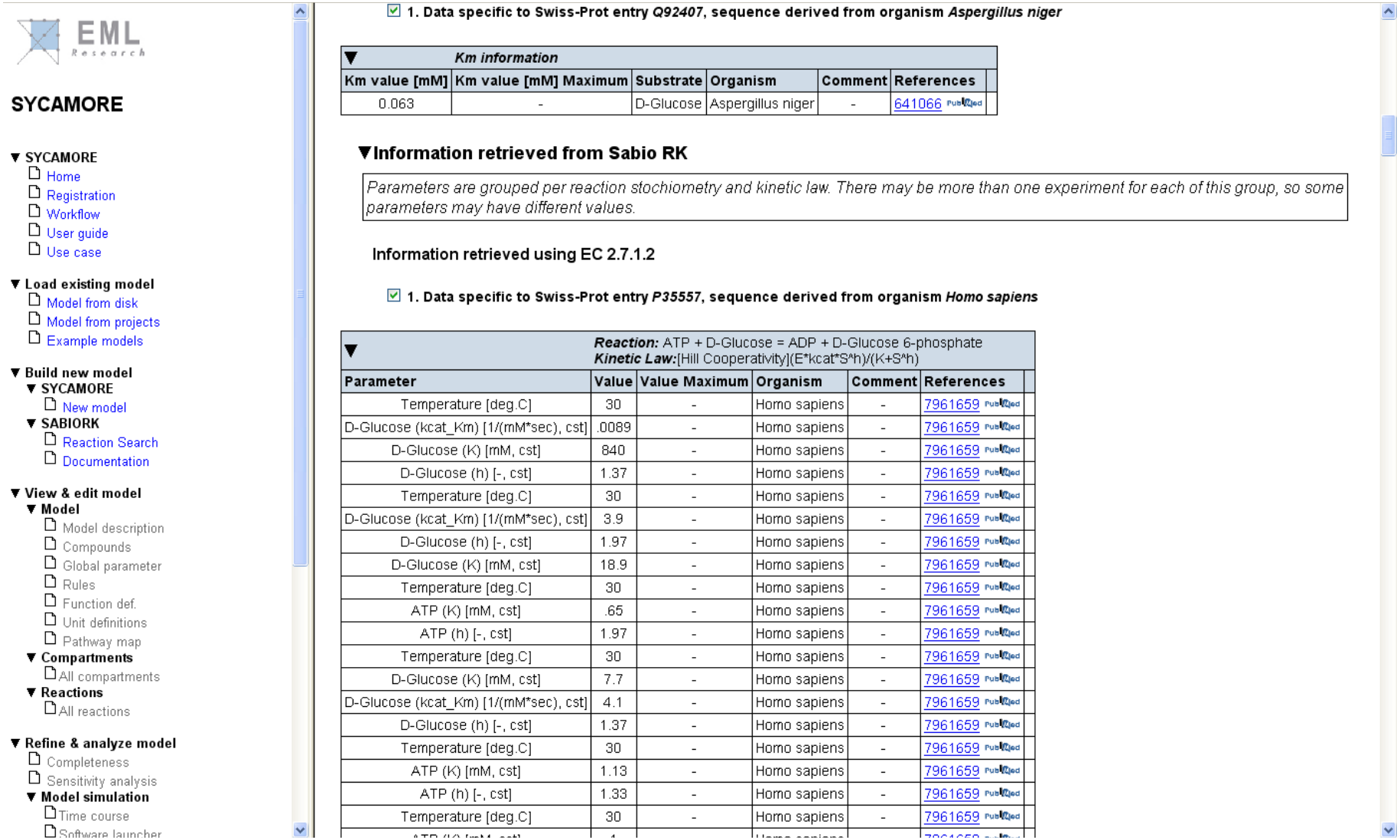
webPIPSA: hexokinase IV or D (P35557)



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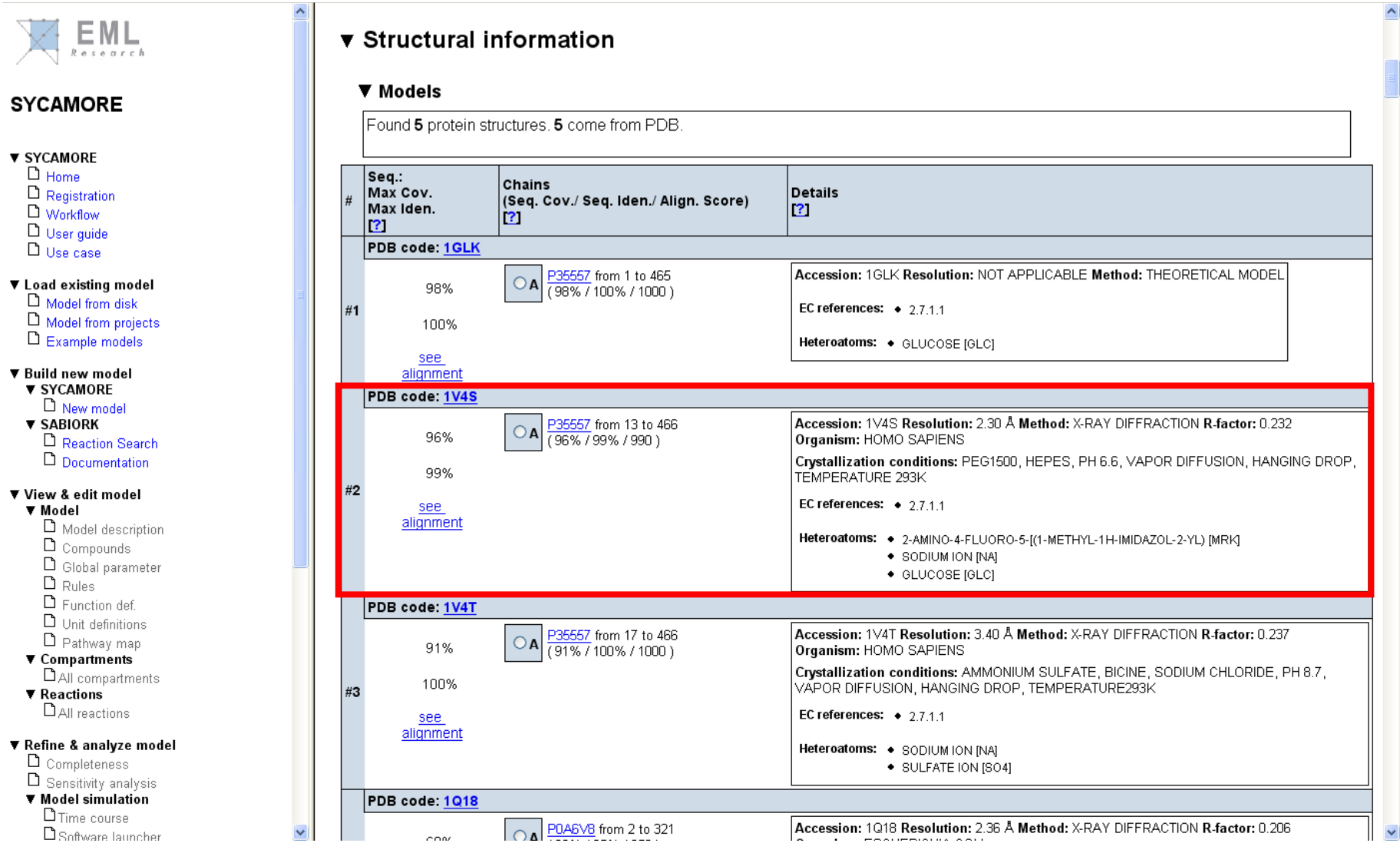

1V4S: *Homo spiens, closed form*

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webPIPSA: hexokinase IV or D (P35557)

```
T-COFFEE, Version_4.70(Mon Nov 6 18:05:42 2006)
Cedric Notredame
CPU TIME:0 sec.
SCORE=100
*
 BAD  AVG  GOOD
*
1V4S        : 100
P35557      : 100

1V4S      ----------TLVEQILAEFQLQEEDLKKVMRRMQKEMDRGLRLETHEEAS
P35557    MLDDRARMEAAKKEKVEQILAEFQLQEEDLKKVMRRMQKEMDRGLRLETHEEAS

cons                ****************************************

1V4S      VKMLPTYVRSTPEGSEVGDFLSLDLGGTNFRVMLVKVGEGEEGQWSVKTKHQMY
P35557    VKMLPTYVRSTPEGSEVGDFLSLDLGGTNFRVMLVKVGEGEEGQWSVKTKHQMY

cons      ************************************************************

1V4S      SIPEDAMTGTAEMLFDYISECISDFLDKHQMKHKKLPLGFTFSFPVRHEDIDKG
P35557    SIPEDAMTGTAEMLFDYISECISDFLDKHQMKHKKLPLGFTFSFPVRHEDIDKG

cons      ************************************************************

1V4S      ILLNWTKGFKASGAEGNNVVGLLRDAIKRRGDFEMDVVAMVNDTVATMISCYYE
P35557    ILLNWTKGFKASGAEGNNVVGLLRDAIKRRGDFEMDVVAMVNDTVATMISCYYE

cons      ************************************************************

1V4S      DHQCEVGMIVGTGCNACYMEEMQNVELVEGDEGRMCVNTEWGAFGDSGELDEFL
```

sequence alignment between SwissProt sequence P35557 and crystal structure 1V4S

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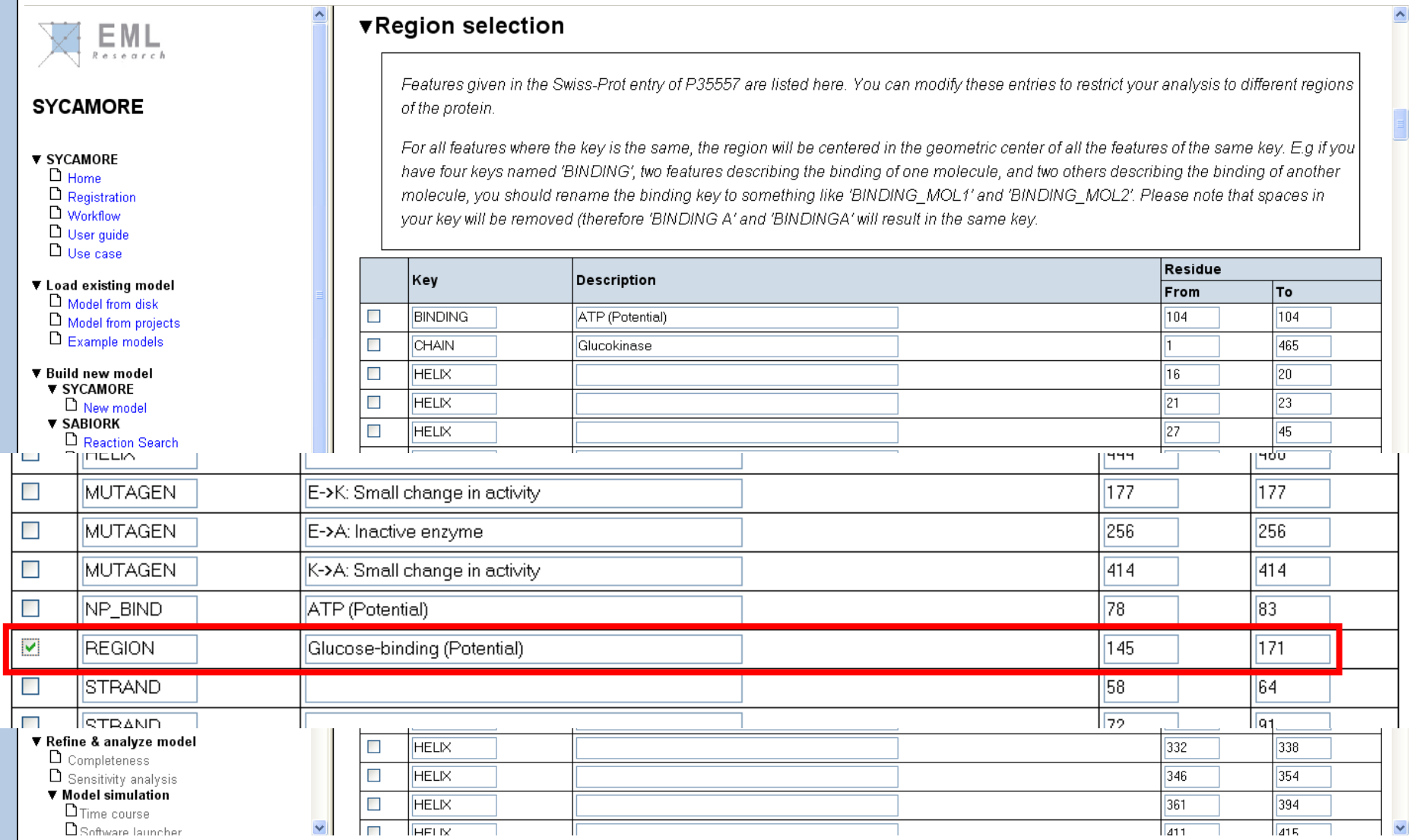

region selection

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select/deselect kinetic data

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▼Information retrieved from Brenda

The results specific to the query Swiss-Prot entry organism are presented first.

Information retrieved using EC 2.7.1.2

Literature links refer to BRENDA. In case where no PubMed entry is linked in BRENDA, you will get the details of the reference paper.

☑ **1. Data specific to Swiss-Prot entry *P21908*, sequence derived from organism *Zymomonas mobilis***

▼ *Km information*					
Km value [mM]	**Km value [mM] Maximum**	**Substrate**	**Organism**	**Comment**	**References**
0.5	-	6-N-(carboxyethyl)ATP	Zymomonas mobilis	-	641063
0.55	-	6-N-(carboxymethyl)ATP	Zymomonas mobilis	-	641063
0.38	-	6-N-(succinyl)ATP	Zymomonas mobilis	-	641063
1.25	-	6-N-[N-(6-aminohexhyl)carbamoyl]ATP	Zymomonas mobilis	-	641063
0.5	-	ATP	Zymomonas mobilis	-	641063
0.8	-	ATP	Zymomonas mobilis	-	641056
0.22	-	D-Glucose	Zymomonas mobilis	-	641056

☑ **1. Data specific to Swiss-Prot entry *P17709,Q04409*, sequence derived from organism *Saccharomyces cerevisiae***

▼ *Km information*					
Km value [mM]	**Km value [mM] Maximum**	**Substrate**	**Organism**	**Comment**	**References**
0.05	-	ATP	Saccharomyces cerevisiae	-	641066
0.028	-	D-Glucose	Saccharomyces cerevisiae	-	641066

☑ **1. Data specific to Swiss-Prot entry *P0A6V8,Q1R8X8*, sequence derived from organism *Escherichia coli***

▼ *Km information*					
Km value [mM]	**Km value [mM] Maximum**	**Substrate**	**Organism**	**Comment**	**References**
0.5	-	ATP	Escherichia coli	-	641064
0.15	-	D-Glucose	Escherichia coli	-	641064

☑ **1. Data specific to Swiss-Prot entry *Q92407*, sequence derived from organism *Aspergillus niger***

▼ *Km information*

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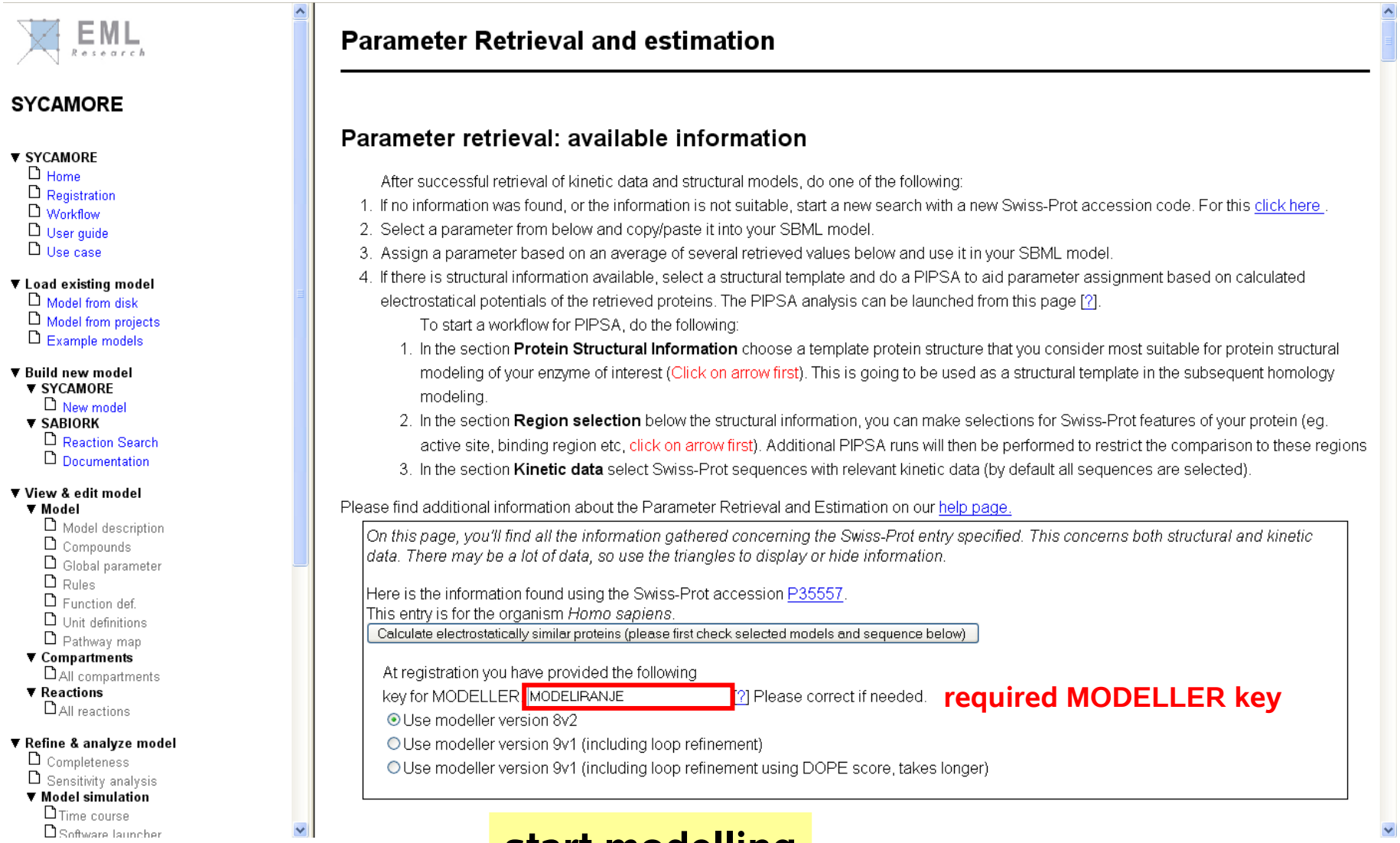

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Work in progress

This page will be reloaded automatically in a few seconds. Please wait.

The time required for a PIPSA analysis depends on several factors:

- the number of structures you submitted for analysis.
- the number of regions you have selected.
- the number of jobs in the request queue (submitted by other users)

Typically a PIPSA analysis takes from 10 min to 2 hours. A qPIPSA analysis requires for the download phase approx. 5-20 min, whereas the analysis requires 30 to 180 minutes.

If you start a new search, the current search will only be accessible via the link in the email you receive.

Your request is being processed. There is 1 job in the request queue.

Here is an overview of the actions done and the advancement of the information retrieval (latest at top):

- Download of entries from databases complete.
- Parsing of pdb entry 1V4T completed.
- Parsing of pdb entry 1V4S completed.
- Parsing of pdb entry 1SZ2 completed.
- Parsing of pdb entry 1Q18 completed.
- Parsing of pdb entry 1GLK completed.
- Parsing of Swiss-Prot entry Q9CE25 using http://www.expasy.org/uniprot/Q9CE25.txt completed.
- Parsing of Swiss-Prot entry Q9YA47 using http://www.expasy.org/uniprot/Q9YA47.txt completed.
- Parsing of Swiss-Prot entry P17712 using http://www.expasy.org/uniprot/P17712.txt completed.
- Retrieval of SABIO-RK entry 2.7.1.2 completed.
- Parsing of Swiss-Prot entry Q92407 using http://www.expasy.org/uniprot/Q92407.txt completed.
- Parsing of Swiss-Prot entry Q1R8X8 using http://www.expasy.org/uniprot/Q1R8X8.txt completed.
- Parsing of Swiss-Prot entry P0A6V8 using http://www.expasy.org/uniprot/P0A6V8.txt completed.
- Parsing of Swiss-Prot entry Q04409 using http://www.expasy.org/uniprot/Q04409.txt completed.
- Parsing of Swiss-Prot entry P17709 using http://www.expasy.org/uniprot/P17709.txt completed.
- Parsing of Swiss-Prot entry P21908 using http://www.expasy.org/uniprot/P21908.txt completed.

email: Parameter analysis for P35557 is complete

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webPIPSA: hexokinase IV or D (P35557)

qPIPSA workflow for P35557 (Glucokinase (EC 2.7.1.2) (Hexokinase type IV) (HK IV) (Hexokinase-4) (HK4) (Hexokinase-D).) completed

start new search
show workflow tasks

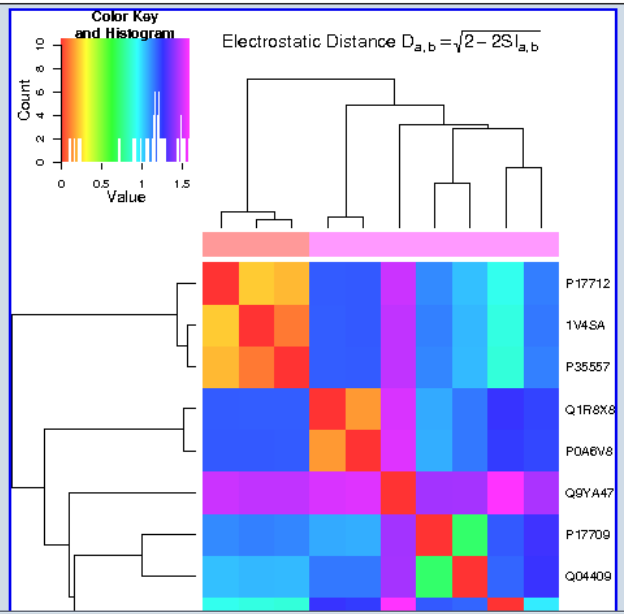
The result of qPIPSA is a tree-like diagram (dendrogram, which we call an epogram) which puts the electrostatic potential of the query sequence into relation with other enzymes for which kinetic data are available. Additional information about the interpretion of the output can be found in the STAPAC help.

Please click on the tabs to get results based on regions of the protein (in case you have selected regions for analysis before). In case you print this document, all graphs will be shown.

Whole Protein | REGION | Structure view

The following graph shows the comparison based on the electrostatic potential around the whole protein:

Distances range from 0.10954 to 1.59185 (maximum range is from 0 to 2)



results

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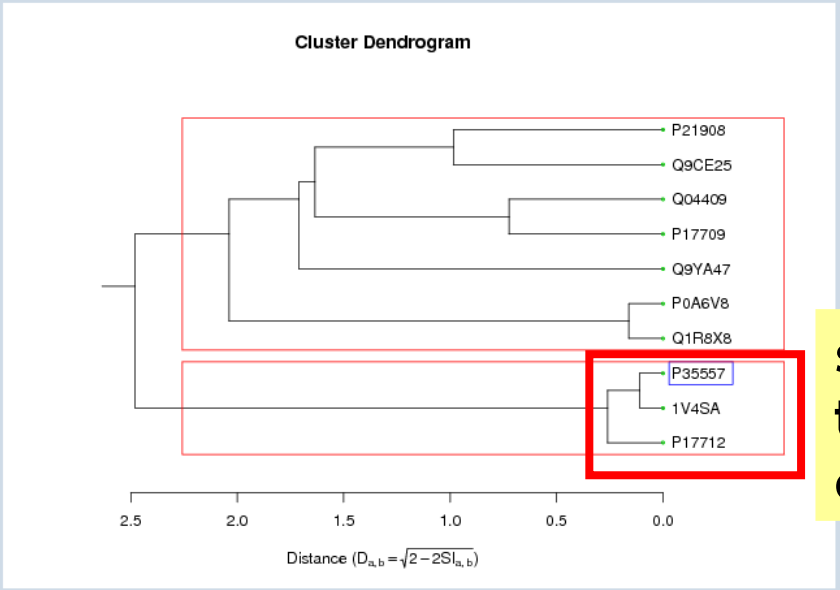
webPIPSA: hexokinase IV or D (P35557)

close



search model
template structure
closest model

Do a cluster analysis of the dendrogram with 2 clusters, show HODGKIN no epogram: start

The proteins sorted according to the similarity of electrostatic potentials to the input sequence are:

No.	Protein	Description	Organism	Kinetic parameter
1	P35557	Glucokinase (EC 2.7.1.2) (Hexokinase type IV) (HK IV) (Hexokinase-4) (HK4) (Hexokinase-D).	Homo sapiens	click here
2	P17712	Glucokinase (EC 2.7.1.2) (Hexokinase type IV) (HK IV) (Hexokinase-4) (HK4) (Hexokinase-D).	Rattus norvegicus	click here
3	Q9CE25	Glucose kinase (EC 2.7.1.2).	Lactococcus lactis subsp	click here
4	P21908	Glucokinase (EC 2.7.1.2) (Glucose kinase).	Zymomonas mobilis	click here
5	Q9YA47	ATP-dependent glucokinase (EC 2.7.1.2).	Aeropyrum pernix	click here
6	Q04409	Glucokinase EMI2 (EC 2.7.1.2) (Glucose kinase) (GLK) (Early meiotic induction protein 2).	Saccharomyces cerevisiae	click here
7	P17709	Glucokinase GLK1 (EC 2.7.1.2) (Glucose kinase) (GLK).	Saccharomyces cerevisiae	click here
8	P0A6V8	Glucokinase (EC 2.7.1.2) (Glucose kinase).	Escherichia coli	click here
9	Q1R8X8	Glucokinase (EC 2.7.1.2) (Glucose kinase).	Escherichia coli	click here

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webPIPSA: hexokinase IV or D (P35557)

Kinetic parameters for P17712

▼Information retrieved from Brenda

The results specific to the query Swiss-Prot entry organism are presented first.

Information retrieved using EC 2.7.1.2

Literature links refer to BRENDA. In case where no PubMed entry is linked in BRENDA, you will get the details of the reference paper.

▼Information retrieved from Sabio RK

Parameters are grouped per reaction stochiometry and kinetic law. There may be more than one experiment for each of this group, so some parameters may have different values.

Information retrieved using EC 2.7.1.2

1. Data specific to Swiss-Prot entry *P17712*, sequence derived from organism *Rattus norvegicus*

▼ ***Reaction:*** D-Glucose + ATP = D-Glucose 6-phosphate + ADP
Kinetic Law:[unknown]unknown

Parameter	Value	Value Maximum	Organism	Comment	References
D-Glucose (Km) [mM, cst]	7.61	-	Rattus norvegicus	-	6296127
ATP (Km) [mM, cst]	.55	-	Rattus norvegicus	-	999645
Temperature [deg.C]	30	-	Rattus norvegicus	-	999645
pH [-]	8	-	Rattus norvegicus	-	999645
D-Glucose (Km) [mM, cst]	3	5	Rat	-	1854332
pH [-]	7.4	-	Rat	-	1854332
pH [-]	7.45	-	Rattus norvegicus	-	8804424
ATP (Km) [mM, cst]	.2	-	Rat	-	1854332
pH [-]	7.4	-	Rat	-	1854332
pH [-]	7.45	-	Rattus norvegicus	-	8804424
ATP (Km) [mM, cst]	.2	-	Rat	-	1854332
pH [-]	7.4	-	Rat	-	1854332
pH [-]	7.45	-	Rattus norvegicus	-	8804424
D-Glucose (Km) [mM, cst]	8	10	Rat	-	1854332
pH [-]	7.4	-	Rat	-	1854332

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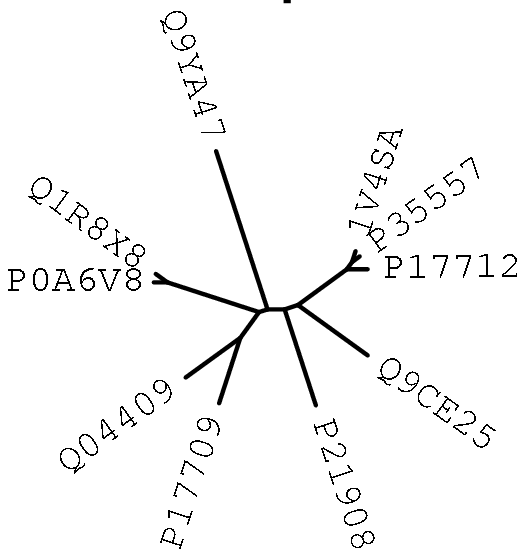
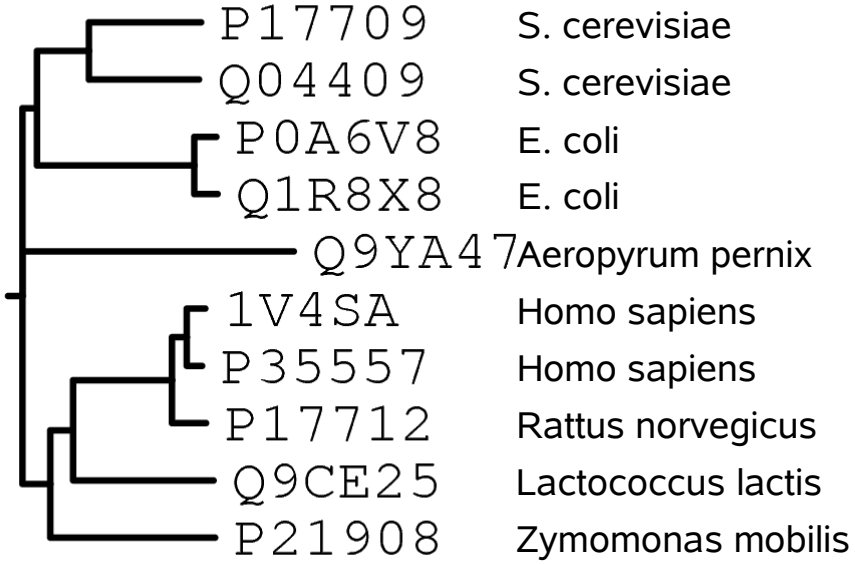
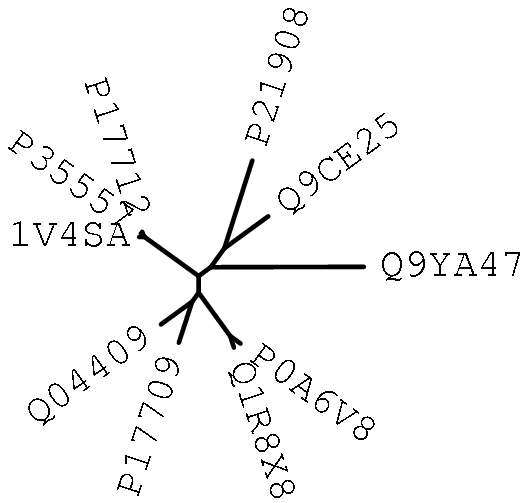
webPIPSA: hexokinase IV or D (P35557)

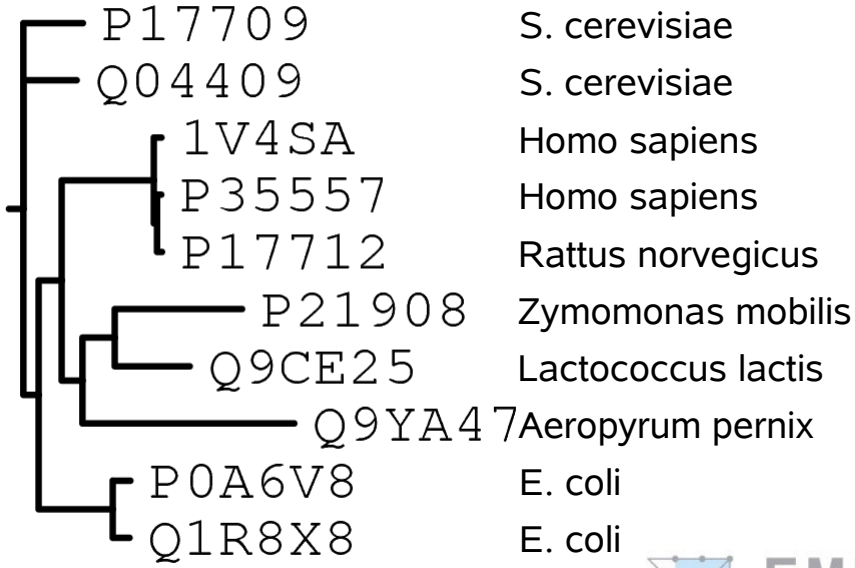
whole protein





glucose binding region





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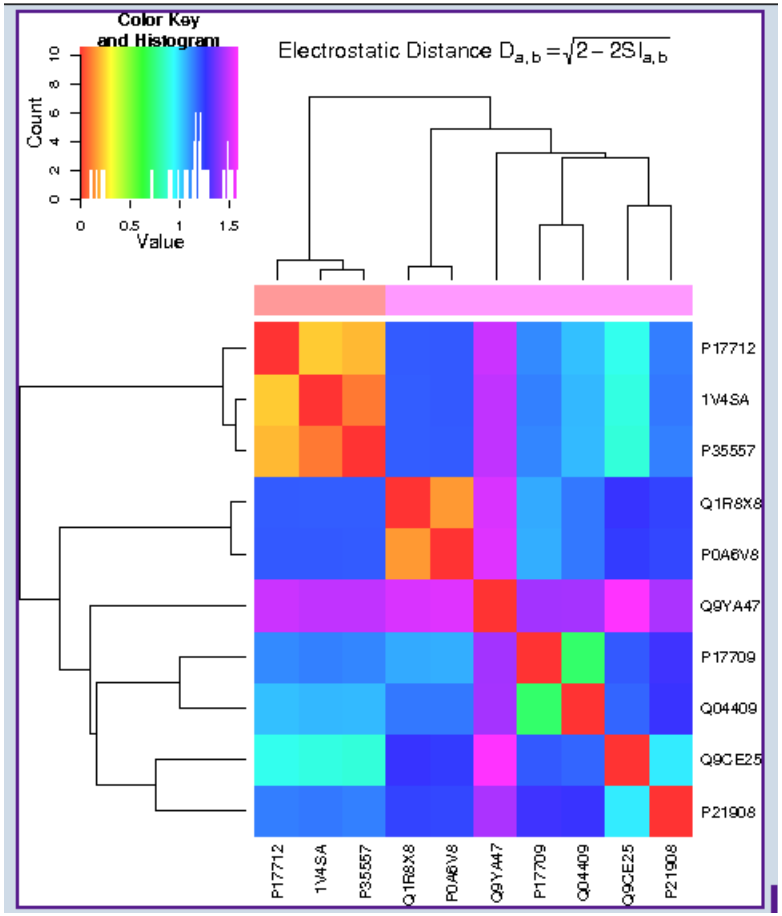
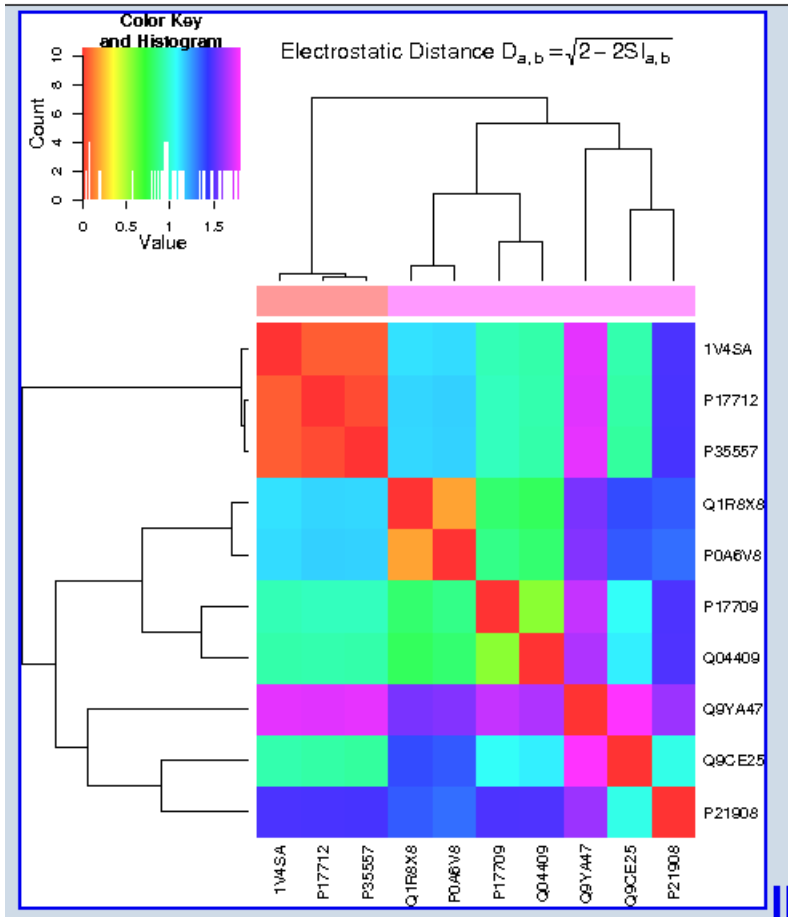
webPIPSA: hexokinase IV or D (P35557)

whole protein



glucose binding region



distances range from (maximum range is from 0 to 2)

0.11 to 1.59 0.04 to 1.81

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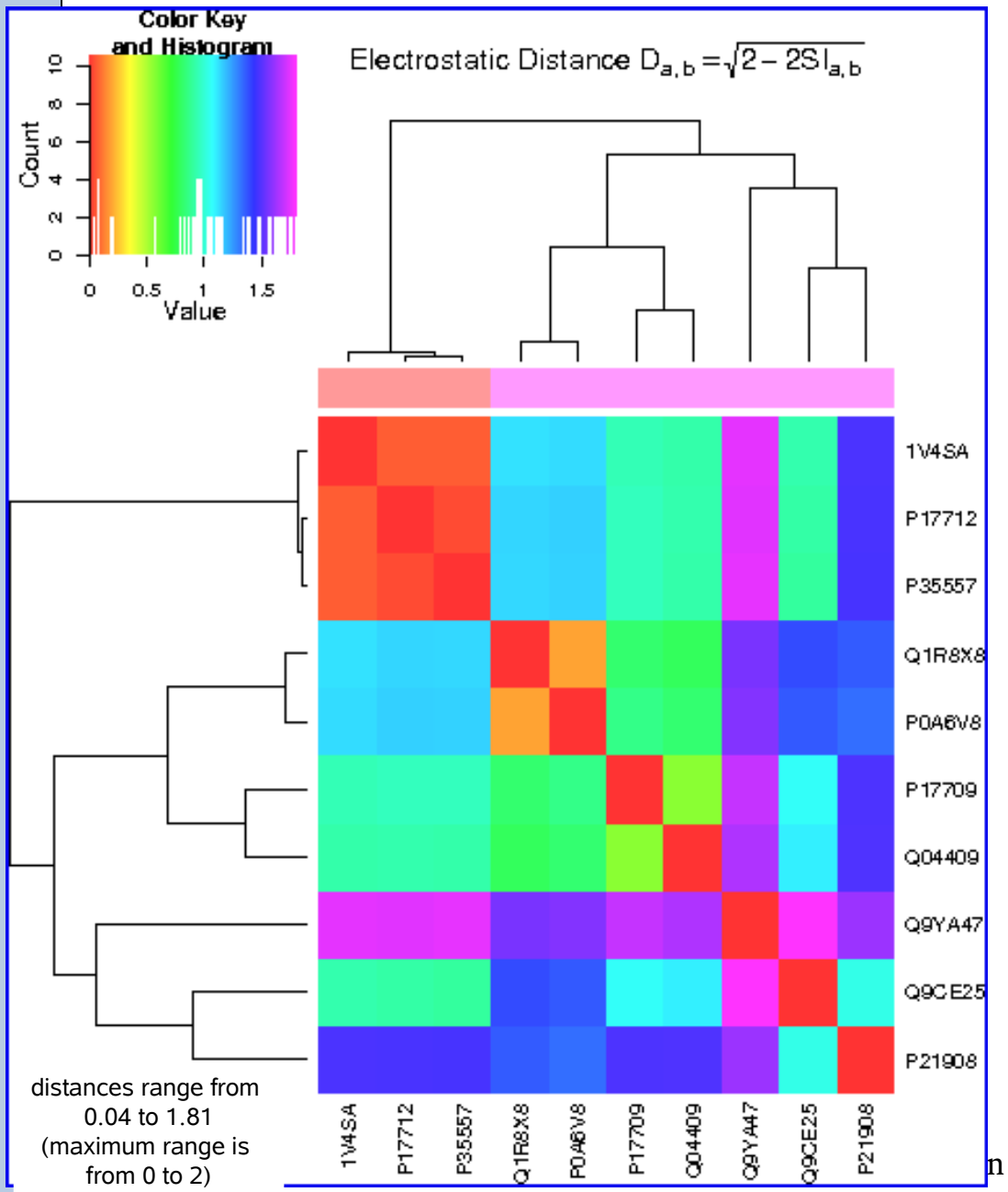
webPIPSA: hexokinase IV or D (P35557)



hexokinase IV

glucose binding region

- Homo sapiens (template)
- Rattus norvegicus
- Homo sapiens
- Escherichia coli
- Escherichia coli
- Saccharomyces cerevisiae
- Saccharomyces cerevisiae
- Aeropyrum pernix
- Lactococcus lactis subsp
- Zymomonas mobilis

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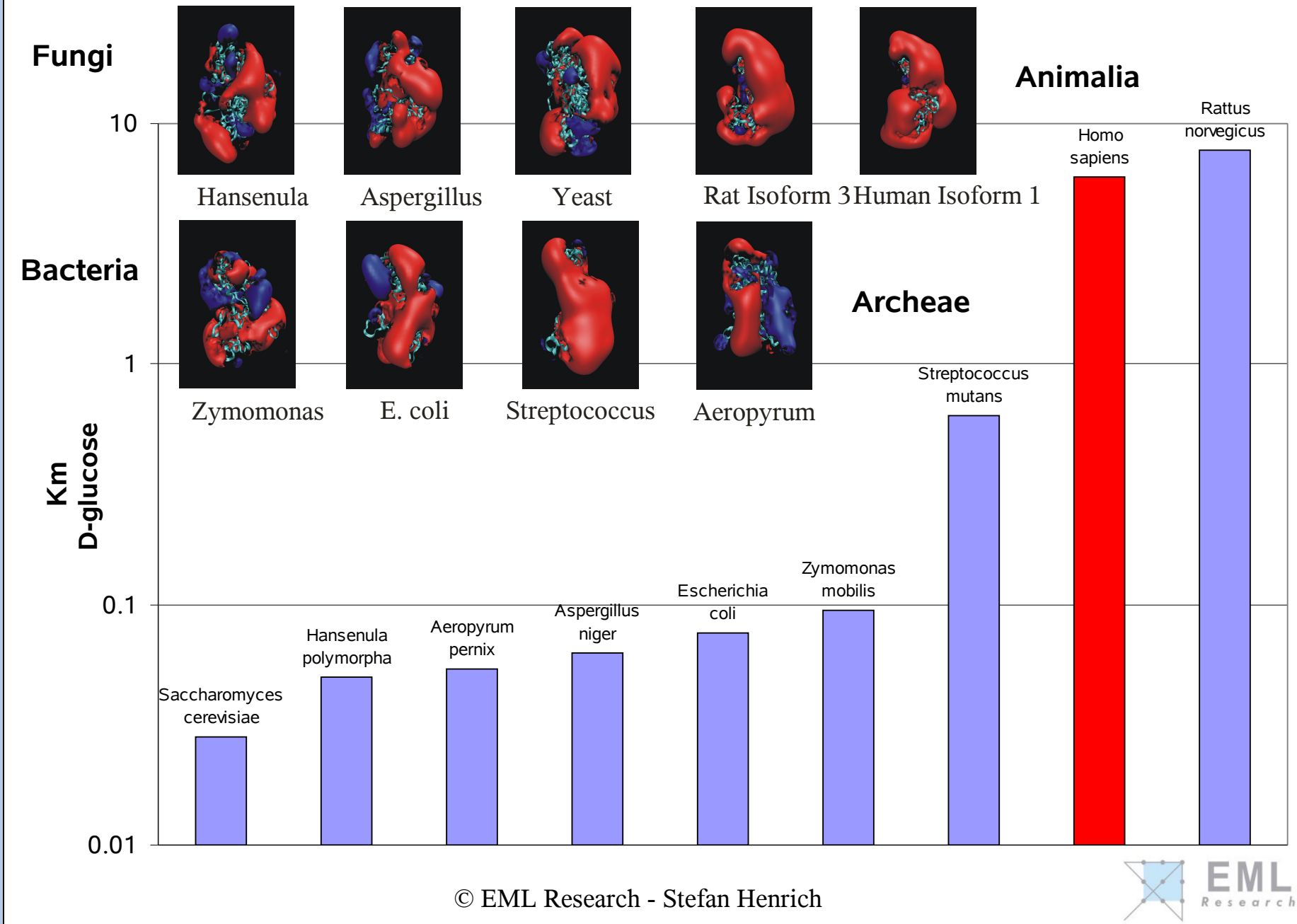
glucokinase (hexokinase)



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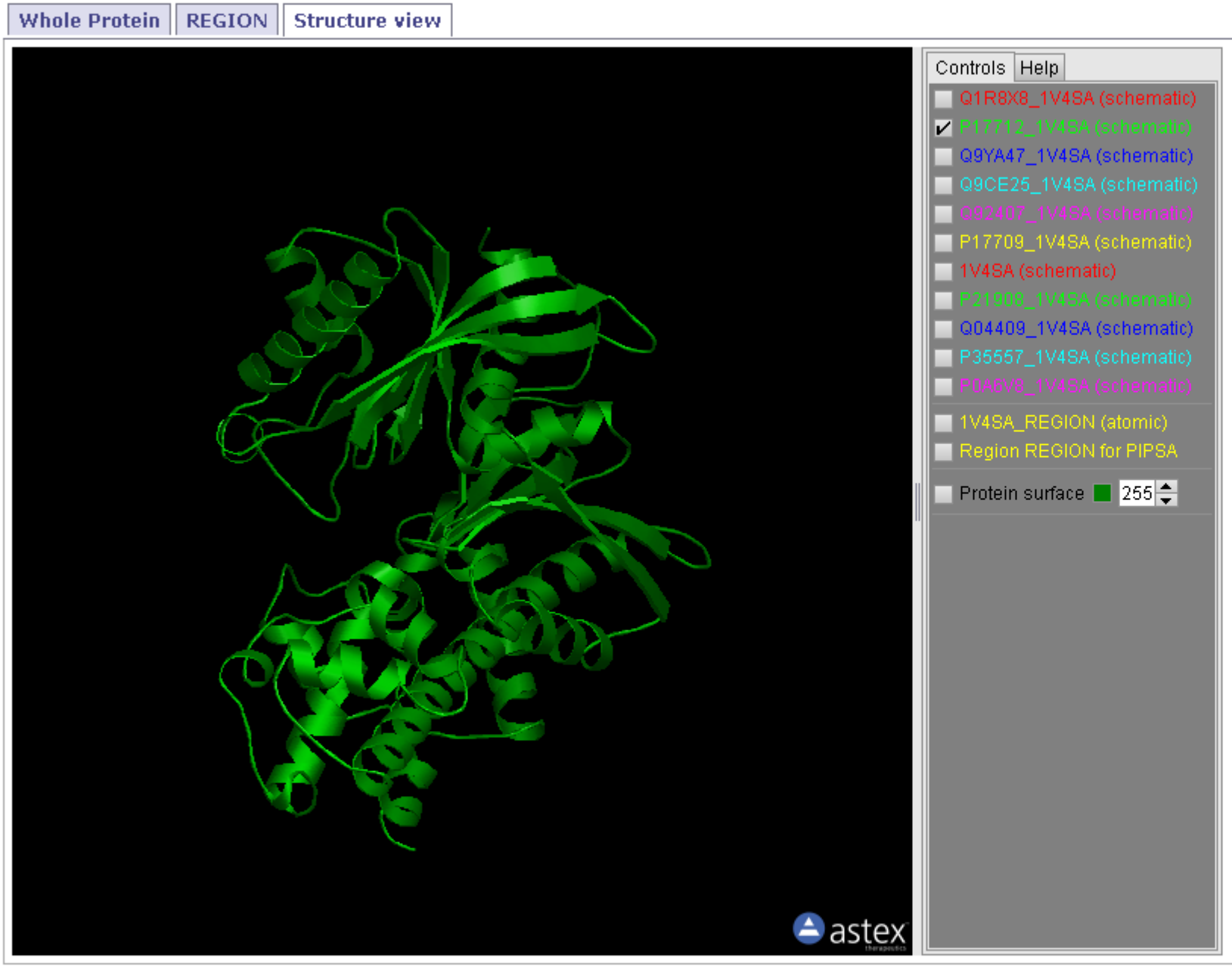
webPIPSA: hexokinase IV or D (P35557)



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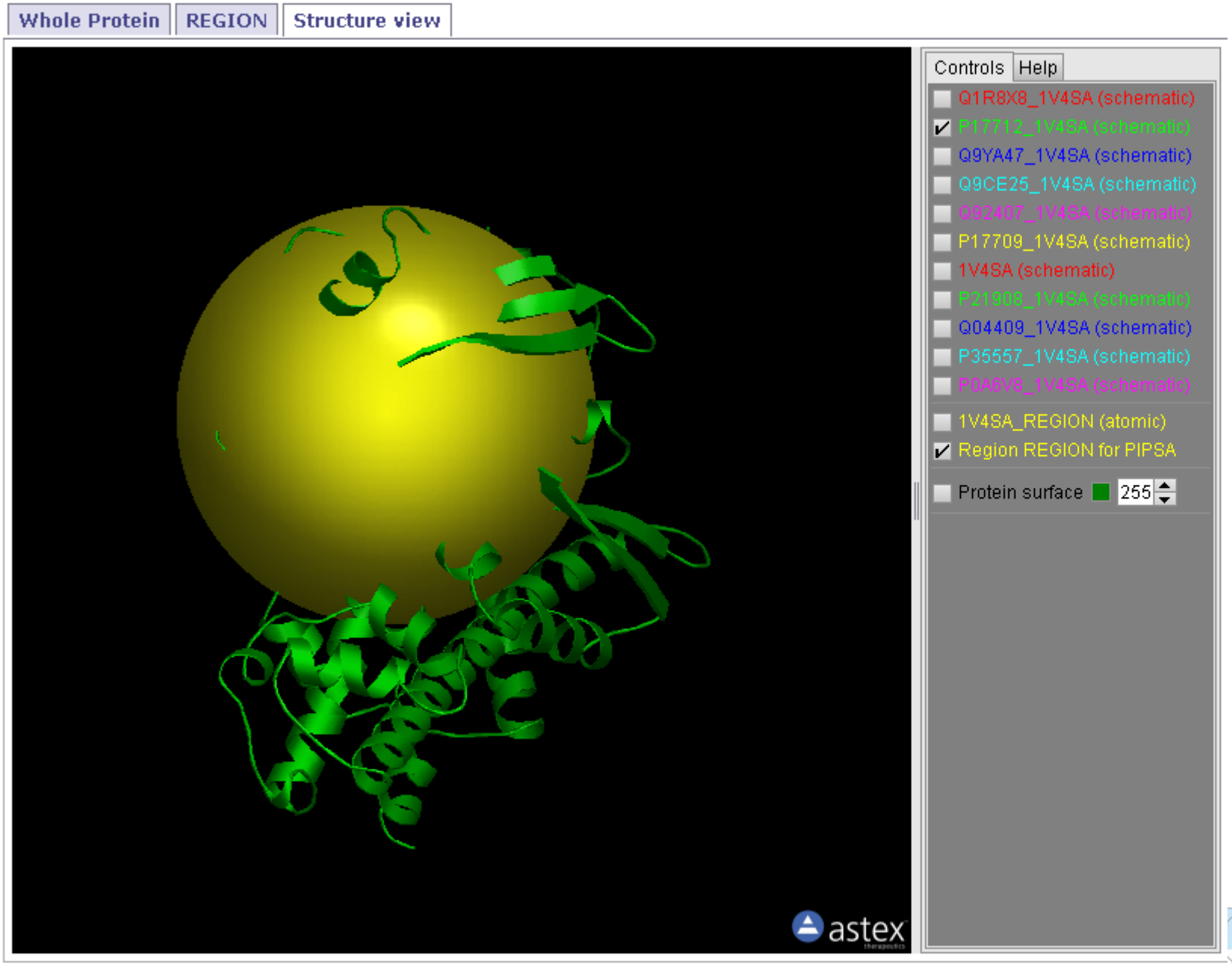
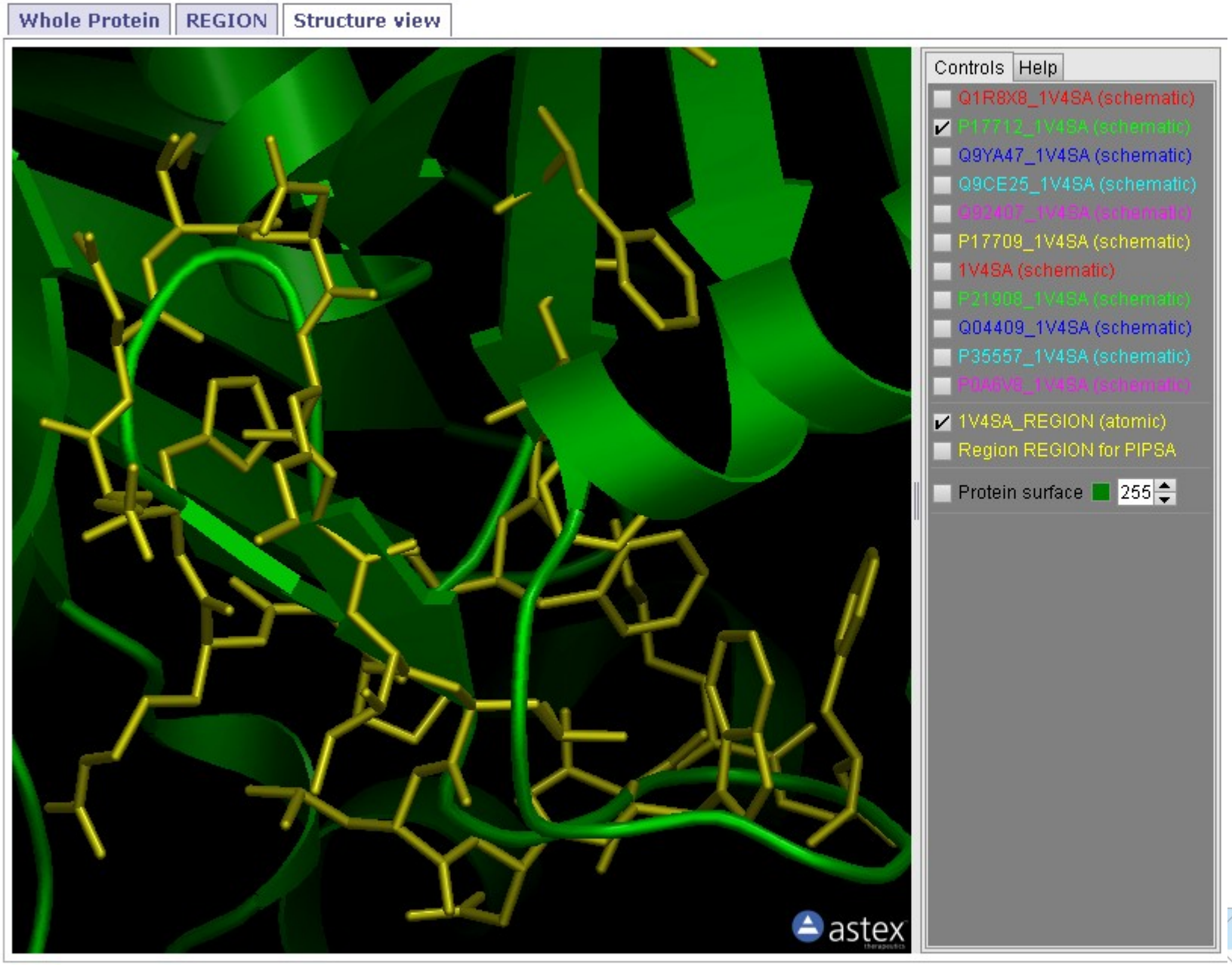


webPIPSA: hexokinase IV or D (P35557)



Example cases of PIPSA

DHFR

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DHFR

- compare Dihydrofolate Reductase (DHFR) of different species
- starting with humand DHFR sequence (P00374)
- choose template structure:
  Homo sapiens (1u72)
- define DHF and NADPH binding region
- run modelling
- check models
- estimate parameters

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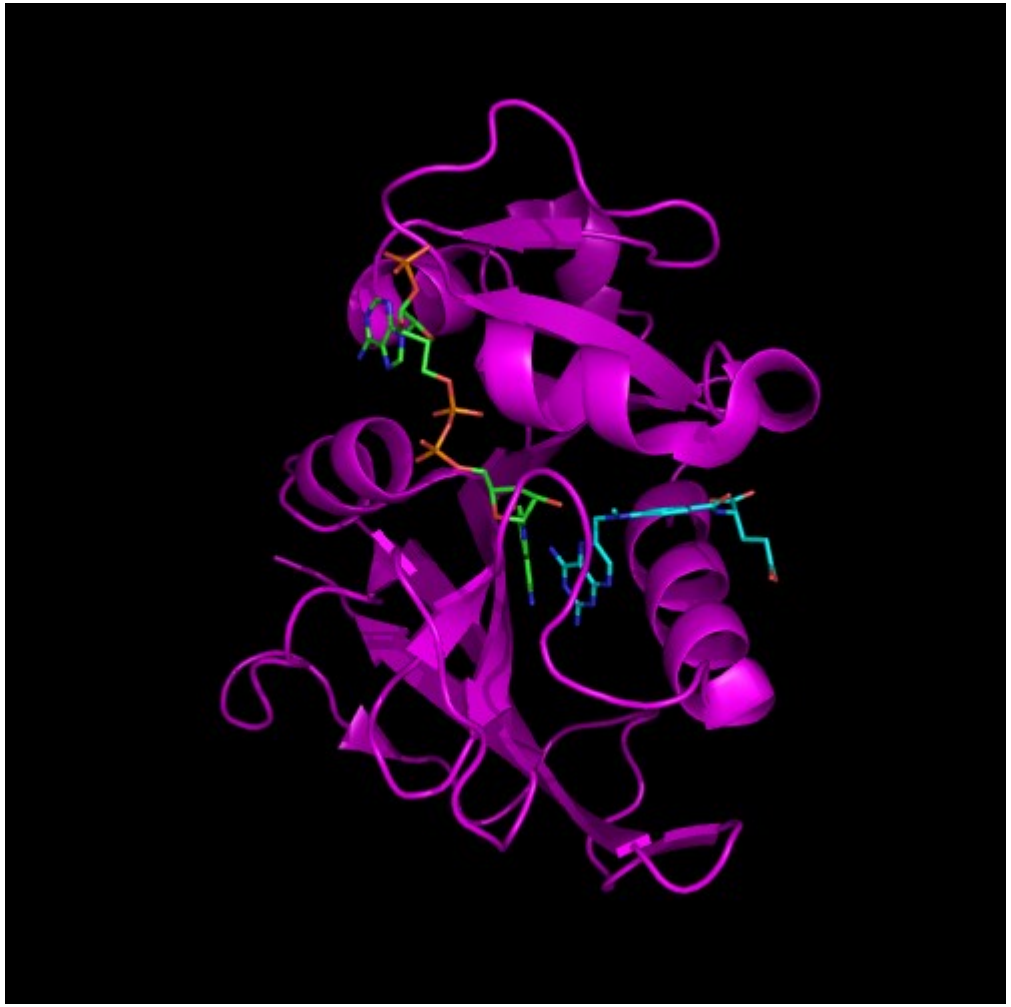
human DHFR (1u72)

crystal structures of DHFR
pink: human (1u72)

green: cofactor NADPH

blue: inhibitor MTX



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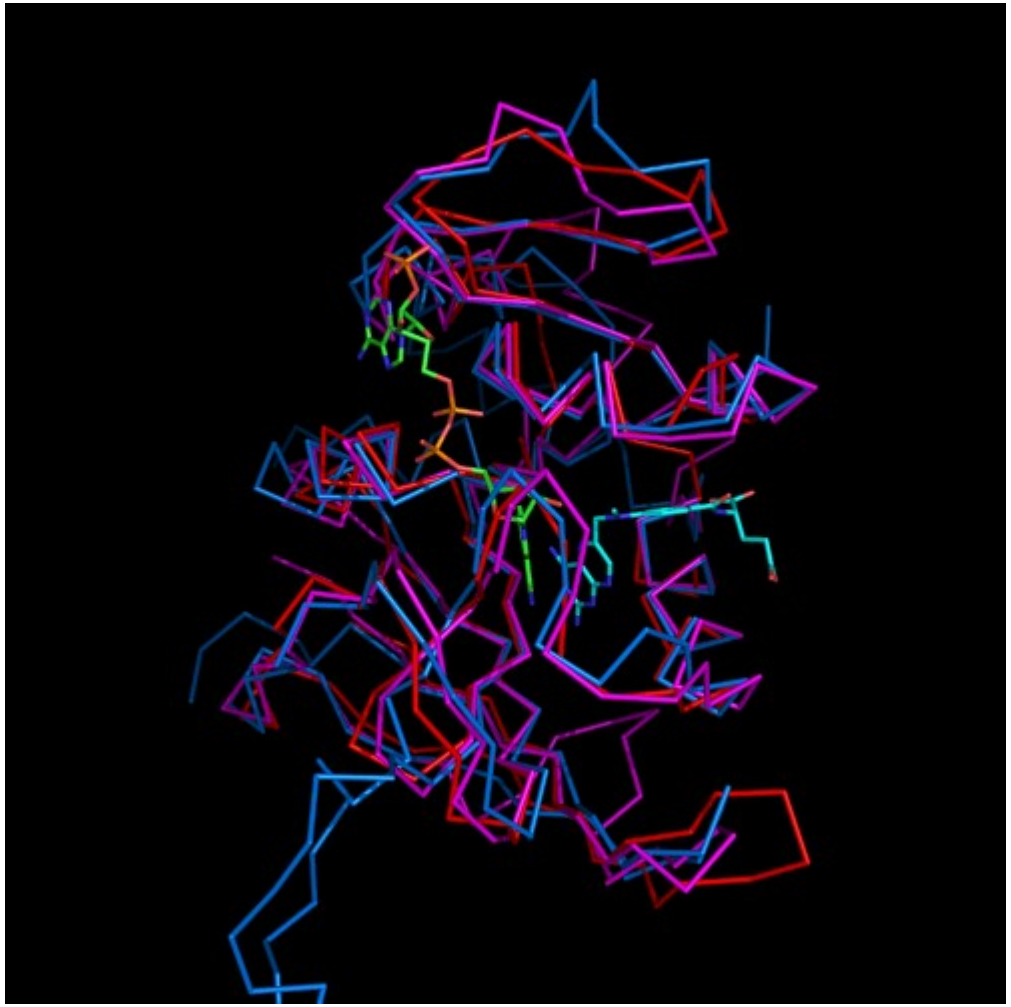
superposition of crystal structures

crystal structures of DHFR
pink: human (1u72)
blue: Plasmodium falciparum (1j31)
red: E. coli (1rh3)

green: cofactor NADPH

blue: inhibitor MTX



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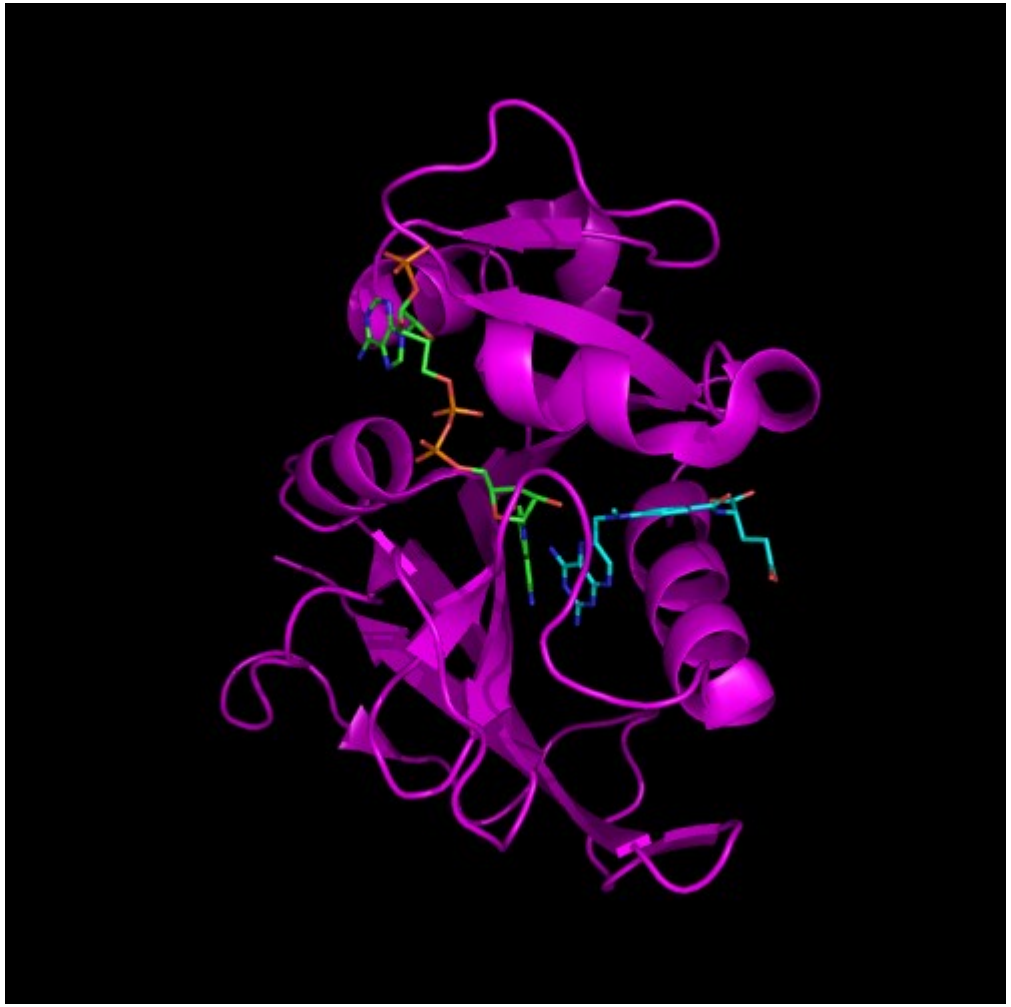
human DHFR (1u72)

crystal structures of DHFR
pink: human (1u72)

green: cofactor NADPH

blue: inhibitor MTX



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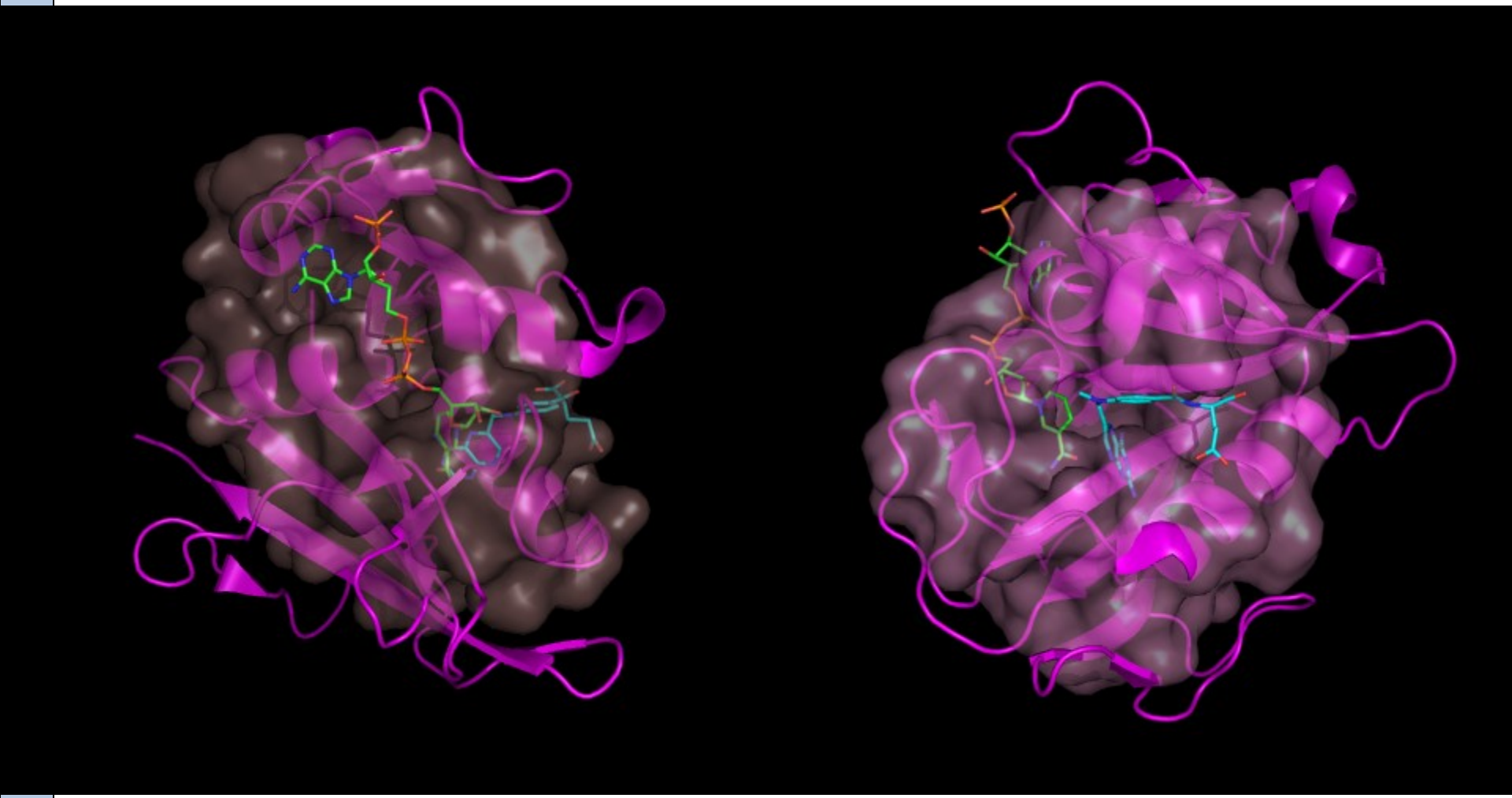
human DHFR (1u72)



focus on cofactor binding region

focus on substrate binding region

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DHFR: region selection

▼Region selection

Features given in the Swiss-Prot entry of P00374 are listed here. You can modify these entries to restrict your analysis to different regions of the protein.

For all features where the key is the same, the region will be centered in the geometric center of all the features of the same key. E.g if you have four keys named 'BINDING', two features describing the binding of one molecule, and two others describing the binding of another molecule, you should rename the binding key to something like 'BINDING_MOL1' and 'BINDING_MOL2'. Please note that spaces in your key will be removed (therefore 'BINDING A' and 'BINDINGA' will result in the same key.

	Key	Description	Residue	
			From	To
☑	DHF	Dihydrofolate binding region	23	23
☑	DHF	Dihydrofolate binding region	35	35
☑	DHF	Dihydrofolate binding region	57	57
☑	DHF	Dihydrofolate binding region	61	62
☑	DHF	Dihydrofolate binding region	68	68
☑	DHF		116	116
☑	DHF		136	137
☑	NADPH		9	9
☑	NADPH		23	23
☑	NADPH		56	56
☑	NADPH		76	76
☑	NADPH		94	94
☑	NADPH		115	115
☑	NADPH		119	119
☑	NADPH		121	121
☐	STRAND		146	148

DHF:

23, 35, 57, 61-62, 68, 116, 136-137

NADPH:

9, 23, 56, 76, 94, 115, 119, 121

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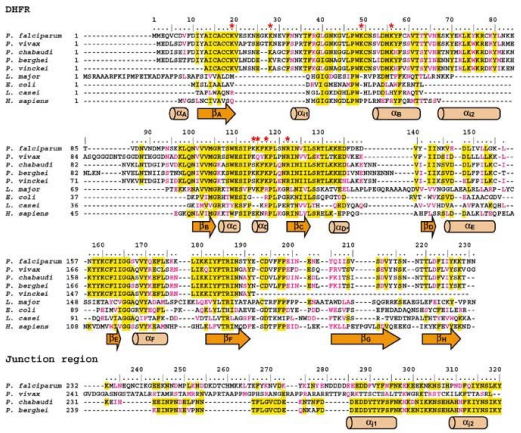
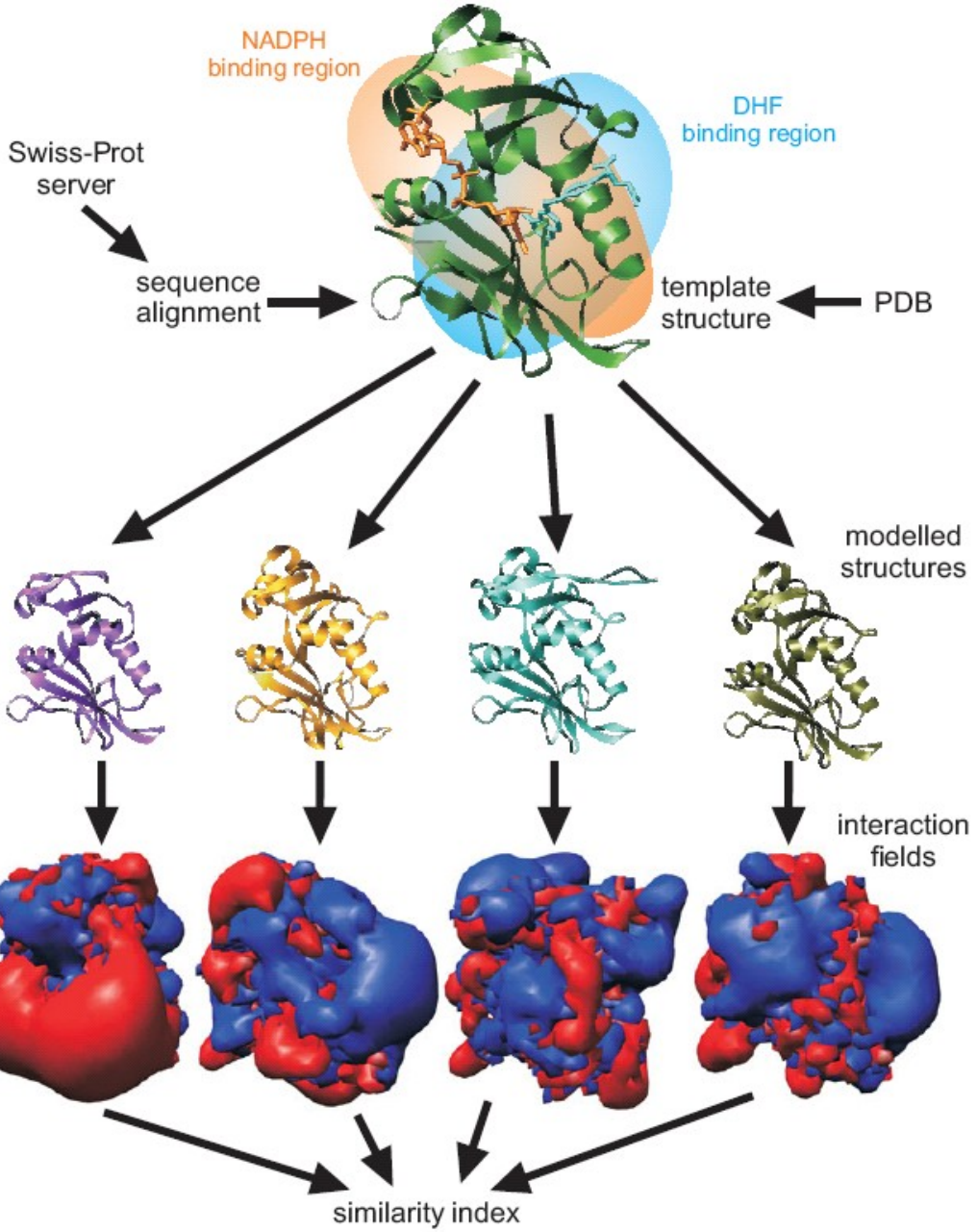
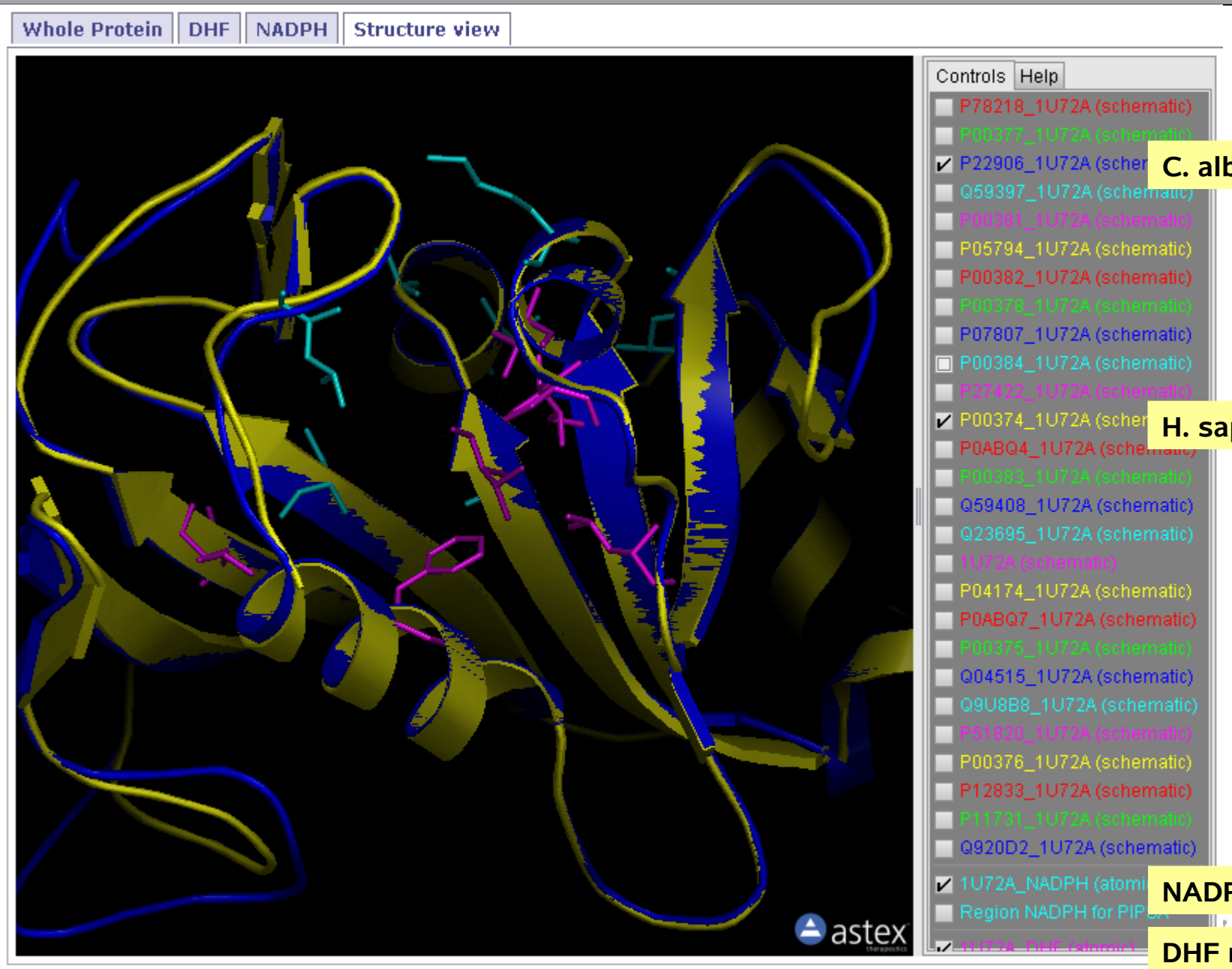
DHFR: Homology Modeling





e.g. dihydrofolate reductases (DHFR) from 20 species

Henrich et al., ChemMedChem, 2008


Whole Protein
DHF
NADPH
Structure view
Controls
Help
P78218_1U72A (schematic)
P00377_1U72A (schematic)
P22906_1U72A (scher
Q59397_1U72A (schematic)
P00381_1U72A (schematic)
P05794_1U72A (schematic)
P00382_1U72A (schematic)
P00378_1U72A (schematic)
P07807_1U72A (schematic)
P00384_1U72A (schematic)
P27422_1U72A (schematic)
P00374_1U72A (scher
P0ABQ4_1U72A (schematic)
P00383_1U72A (schematic)
Q59408_1U72A (schematic)
Q23695_1U72A (schematic)
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P04174_1U72A (schematic)
P0ABQ7_1U72A (schematic)
P00375_1U72A (schematic)
Q04515_1U72A (schematic)
Q9U8B8_1U72A (schematic)
P51820_1U72A (schematic)
P00376_1U72A (schematic)
P12833_1U72A (schematic)
P11731_1U72A (schematic)
Q920D2_1U72A (schematic)
1U72A_NADPH (atomi
Region NADPH for PIP
astex
C. albicans
H. sapiens
NADPH region
DHF region


Whole Protein
DHF
NADPH
Structure view
Controls
Help
P78218_1U72A (schematic)
P00377_1U72A (schematic)
P22906_1U72A (schematic)
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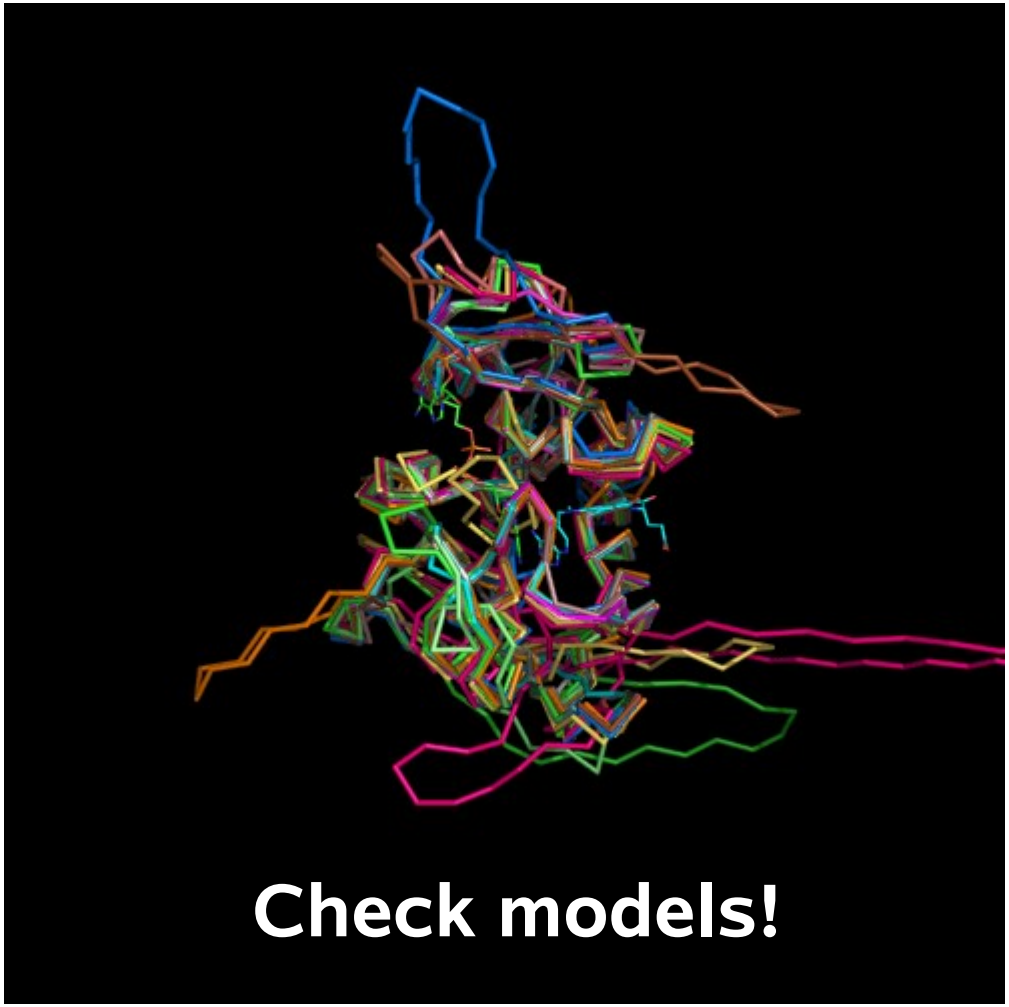
P00376_1U72A (schematic)
P12833_1U72A (schematic)
P11731_1U72A (schematic)
Q920D2_1U72A (schematic)
1U72A_NADPH (atomic)
Region NADPH for PIPSA
astex
E. coli
H. sapiens
NADPH region
DHF region

superposition of all modelled structures



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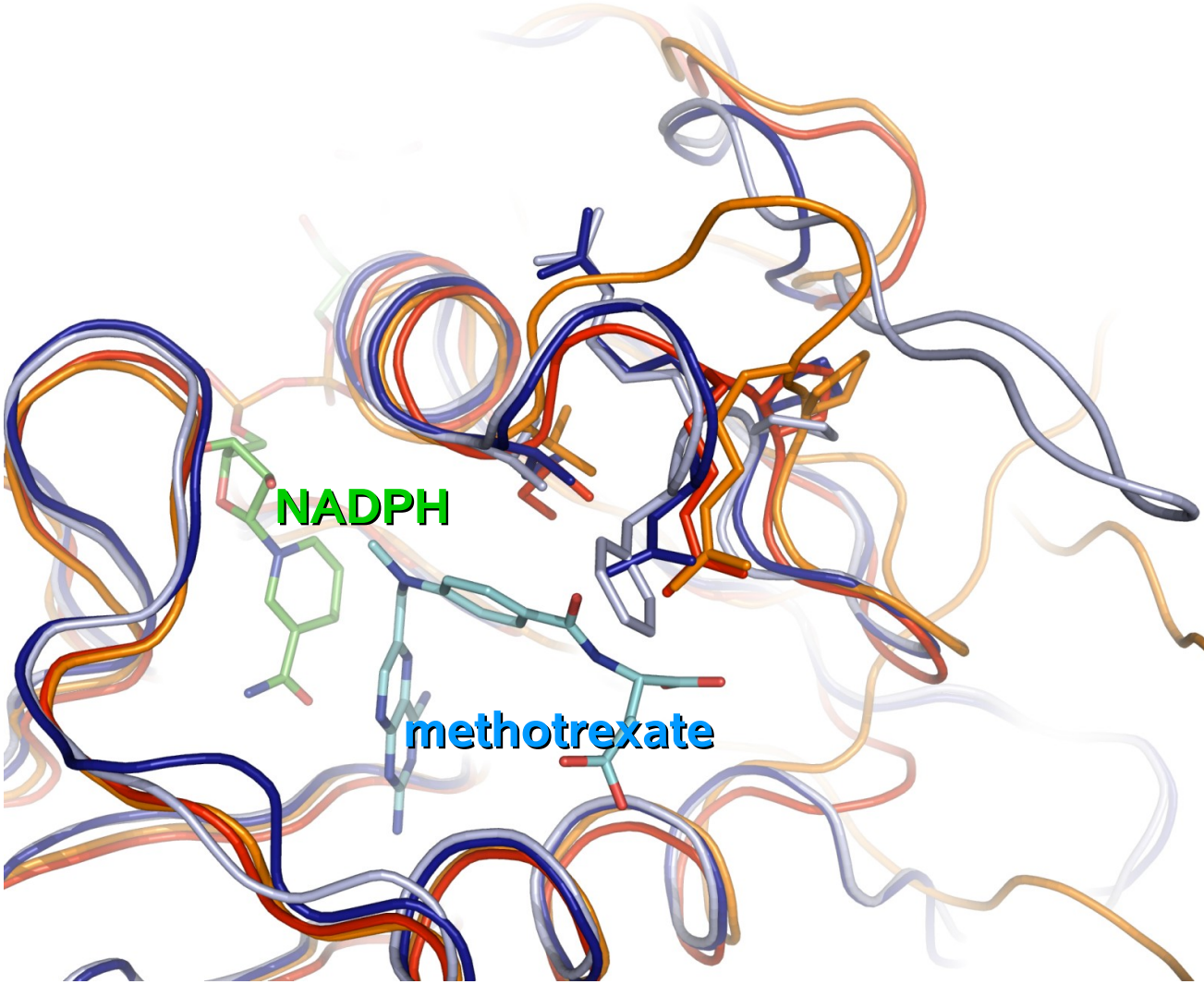
Structural modeling issues



crystal structure DHFR of
human (1u72)
E. coli (1rh3)

Modelled DHFR of *Leishmania major* (P07382)
human (1u72)-based
E. coli (1rh3)-based

Henrich et al., ChemMedChem, 2008

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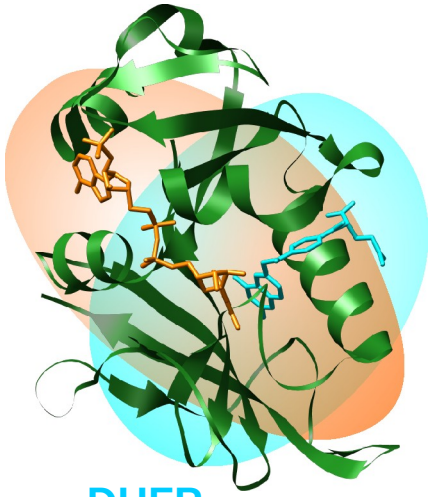
webPIPSA: clustering

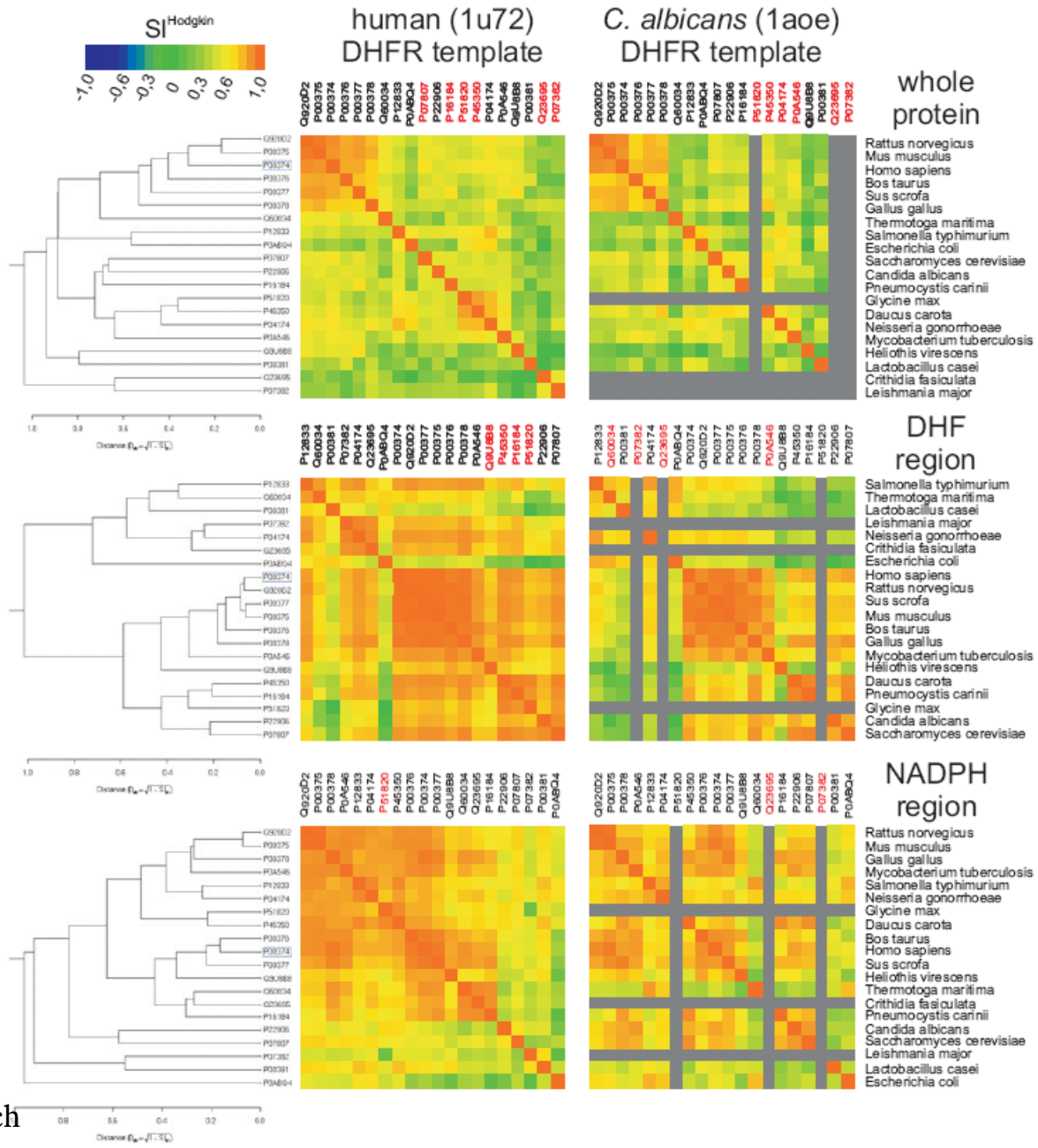
dihydrofolate reductases (DHFR) from 20 species

NADPH binding region



DHFR binding region

Henrich et al., ChemMedChem, 2008



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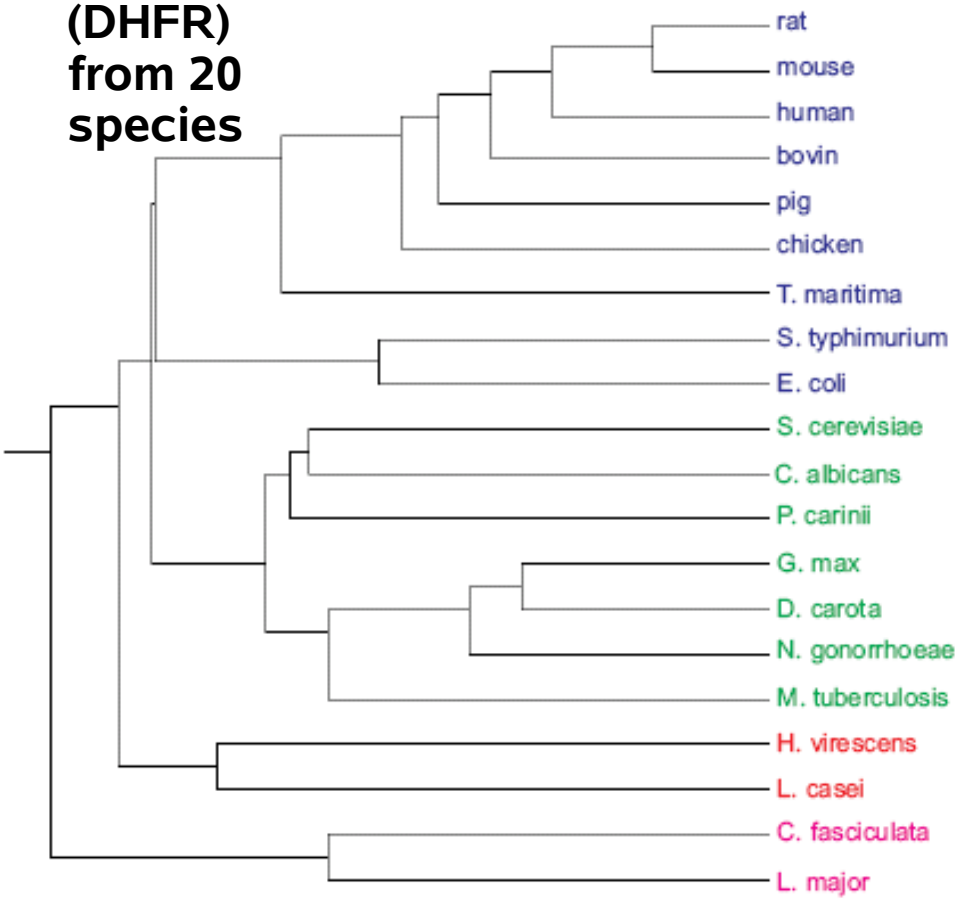
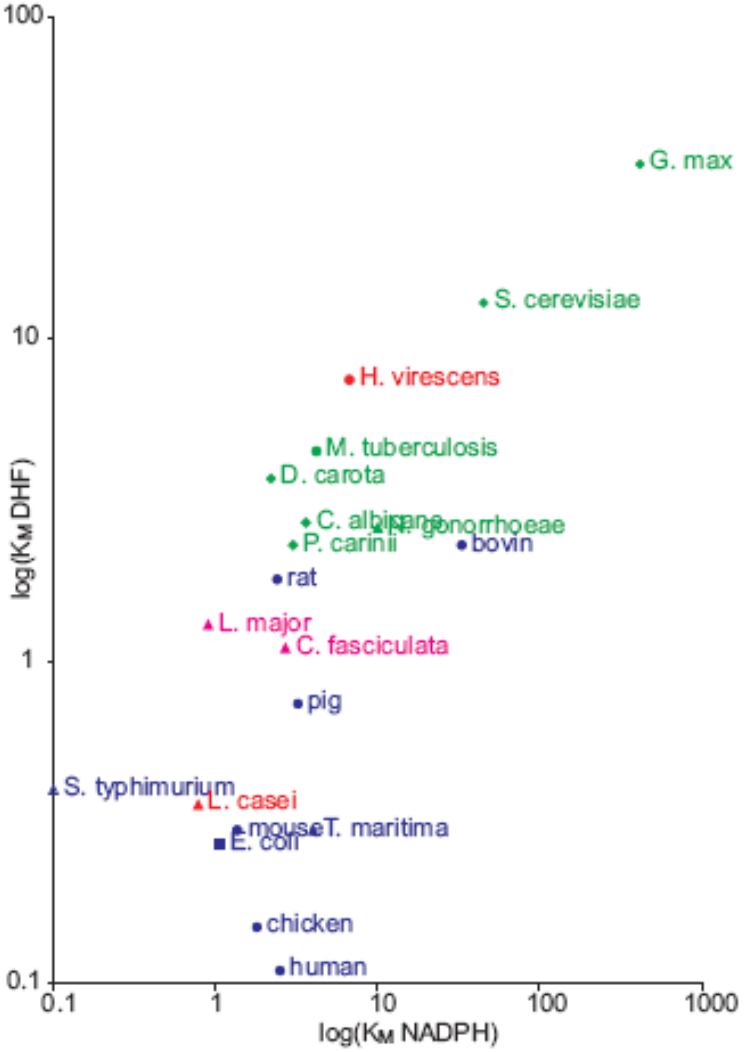
webPIPSA: clustering and relation to K_m values

dihydrofolate reductases (DHFR) from 20 species



whole protein



Henrich et al., ChemMedChem, 2008

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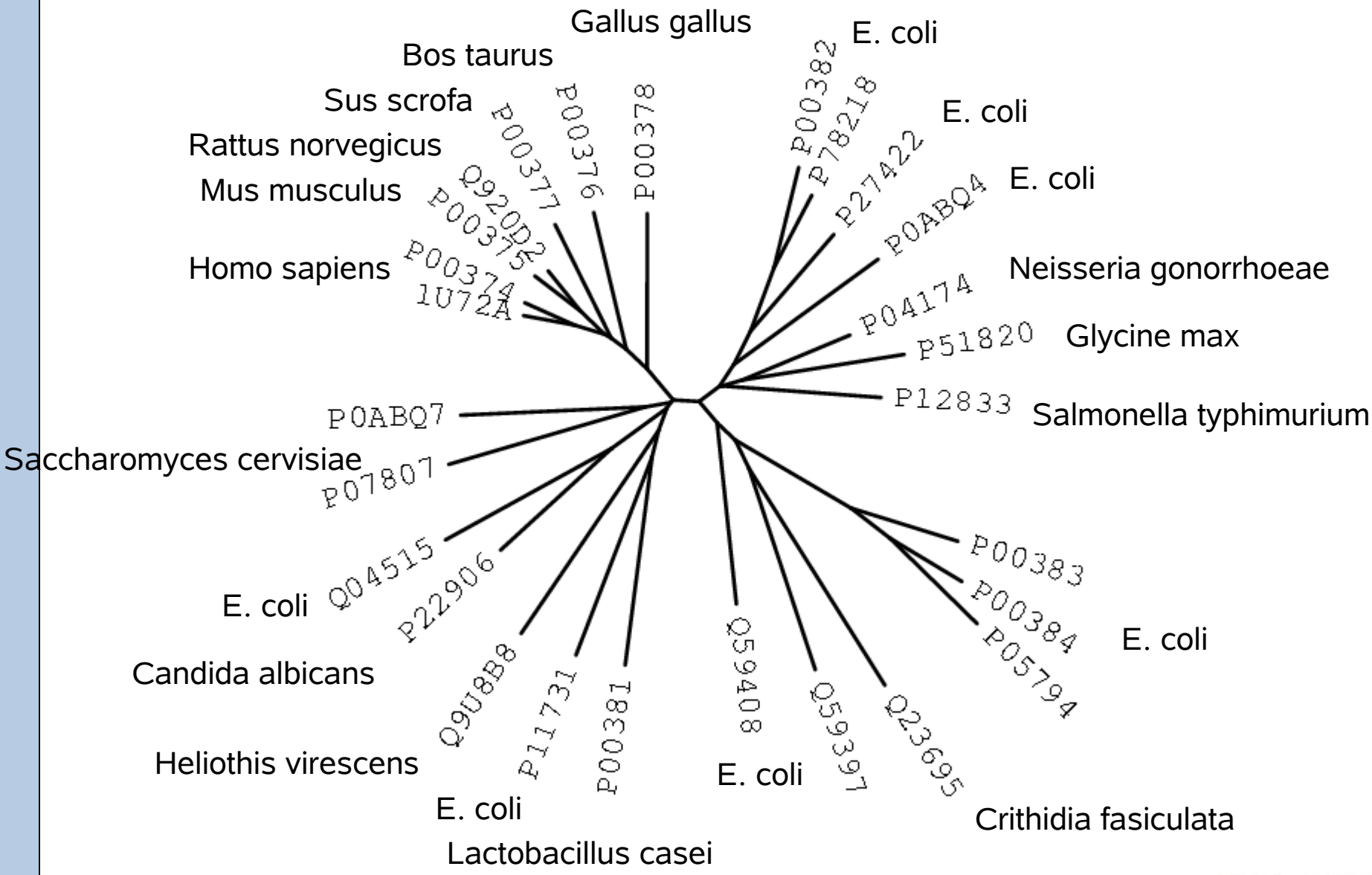

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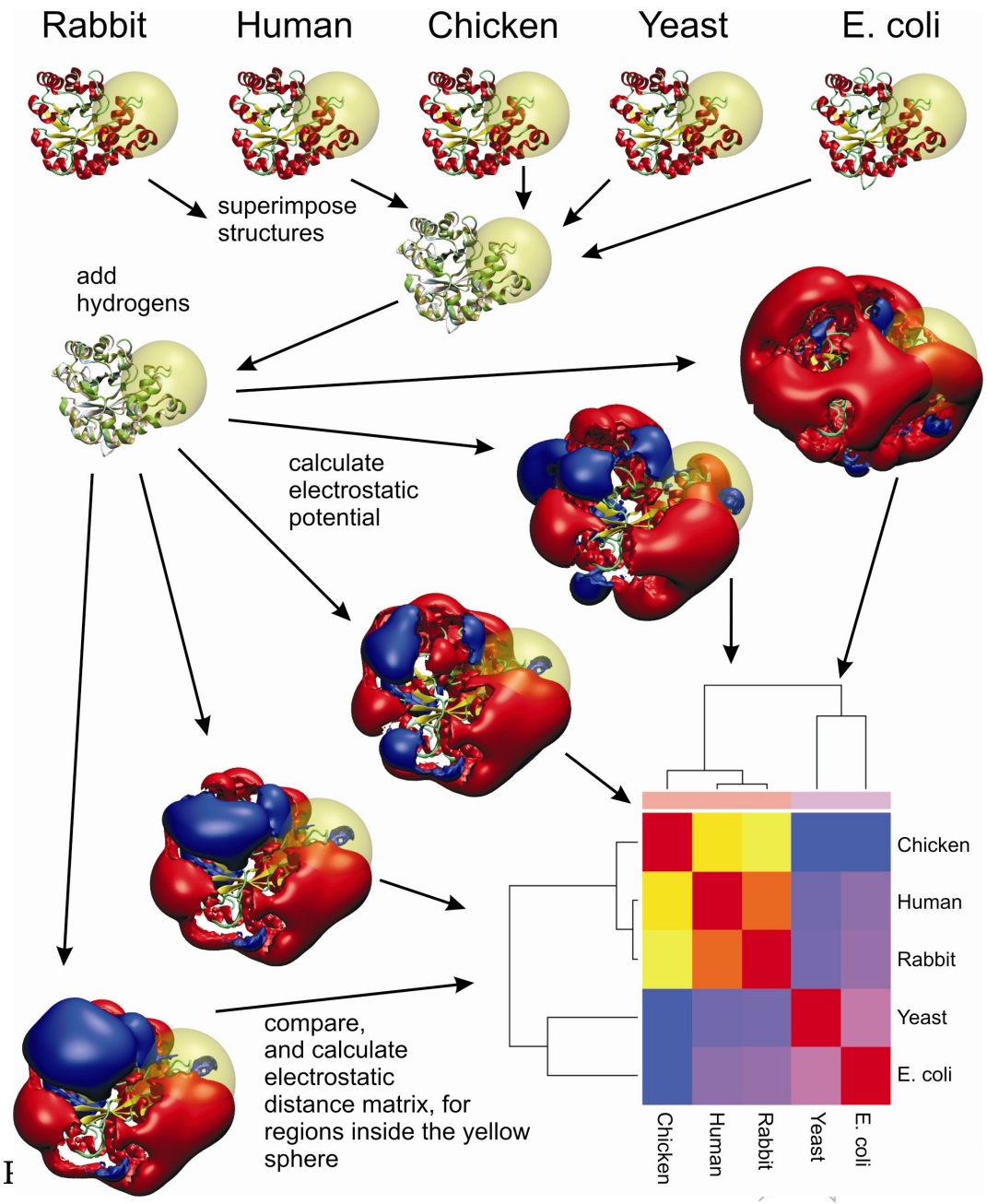
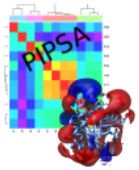
webPIPSA: pipsa.eml.org

triosephosphate isomerase

Richter et al.,
Nucleic Acids Research, 2008



© EML I



webPIPSA

Protein Interaction Property Similarity Analysis

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Demonstration

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Introduction

This PIPSA service is provided for the comparison of the electrostatic interaction properties of proteins. It permits the classification of proteins according to their interaction properties. PIPSA may assist in function assignment, the estimation of binding properties and enzyme kinetic parameters. See References for details.

Method

To perform PIPSA on this webserver, you need to upload a set of related protein structures in PDB format. After calculation of the protein electrostatic potentials, the server will calculate similarity indices for all pairs of proteins based on the electrostatic similarity. These indices will be computed for complete protein 'skins' or for a user defined region. The similarity indices are then converted to electrostatic 'distances'. The electrostatic potential distance matrix is displayed in color coded form (heat map) and as a tree (epogram).

Start a PIPSA analysis (input PDB format coordinate files).

Start a PIPSA analysis (input SWISSPROT entries with EC annotation)*.

* This type of analysis involves a protein structural modelling step utilizing Modeller. Therefore this part is subject to the Modeller license conditions. Please obtain a Modeller license to use this service.

http://pipsa.eml.org

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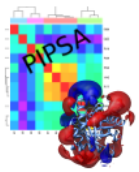

webPIPSA

Protein Interaction Property Similarity Analysis

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PIPSA analysis with input of protein structures in PDB format.

Enter the file names of the coordinates of the proteins to be analyzed. The pdb files can be selected either from your local disk (left panel) or by entering pdb identifiers (e.g. 1hti 1dkw 1b9b 1ci1 1i45 1tim, right panel). The selected pdb files/entries will be shown in a list and can be removed if necessary.

Input protein structures

Select local PDB files*	Specify PDB IDs from the RCSB.
Browse... Upload	Import Zurücksetzen
*Files names will be cut after 23 characters	

Please upload at least two, better more PDB files before proceeding!

http://pipsa.eml.org

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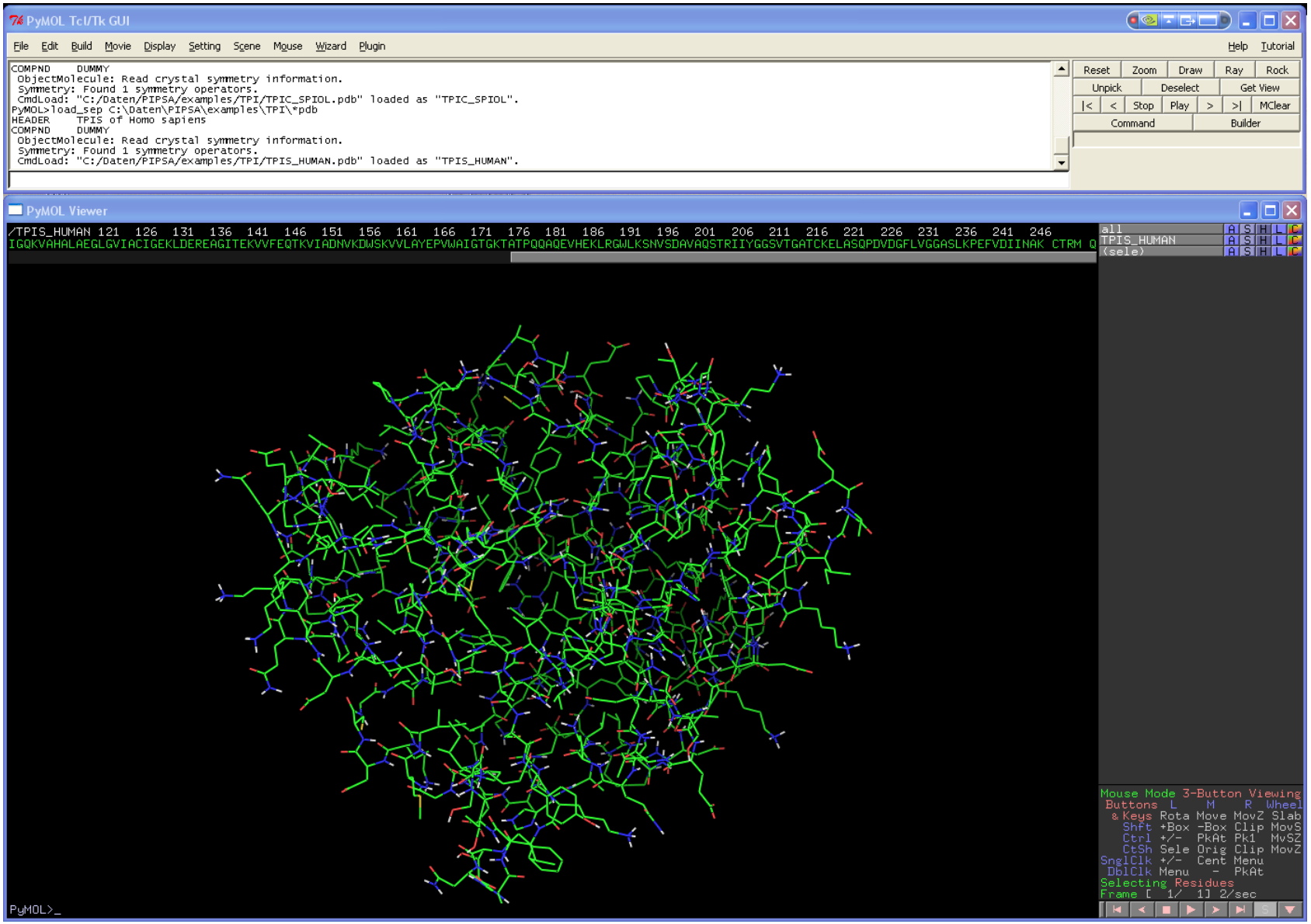
PyMol



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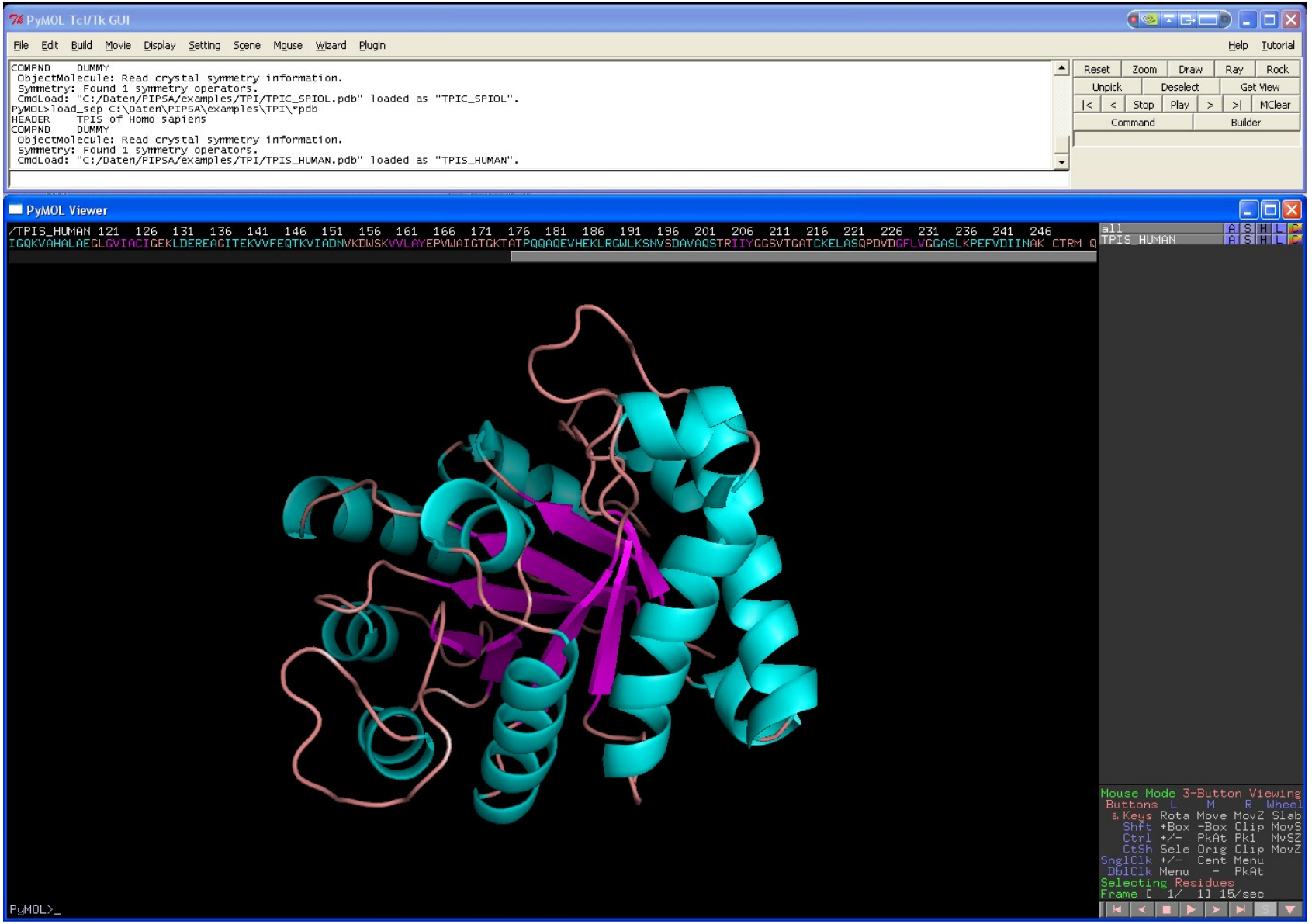

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