Механизмы регуляции транскрипции: описание в компьютерных базах данных

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Ген - протяженный участок ДНК, включает участки, соответствующие экзонам и интронам, старт транскрипции, сайт терминации транскрипции и регуляторные районы.

Экспрессия генов - последовательность реакций на пути от гена к белку. Включает:
- транскрипцию
- сплайсинг
- транспорт через поры ядерной мембраны
- трансляцию

Транскрипция - синтез РНК. Образуется незрелая РНК, содержащая участки, соответствующие экзонам и интронам

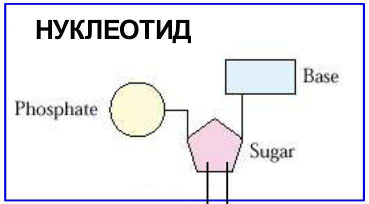
Сплайсинг процесс вырезания участков, соответствующих интронам, с образованиям зрелой матричной РНК Осуществляется в ядре.

Трансляция синтез белка в цитоплазме клетки при участии рибосом

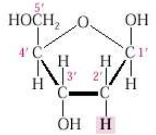
Регуляция экспрессии генов может осуществляться на всех этапах. Транскрипция - первый этап, на котором осуществляется выбор, будет ген экспрессироваться или нет.

Рассмотрим три вопроса

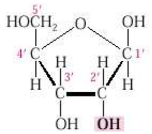
- как осуществляется транскрипция
- чем определяется старт транскрипции
- какие механизмы в клетке регулируют интенсивность транскпции



НУКЛЕОТИД СОДЕРЖИТ ДЕЗОКСИРИБОЗУ (в ДНК) либо РИБОЗУ (в РНК)



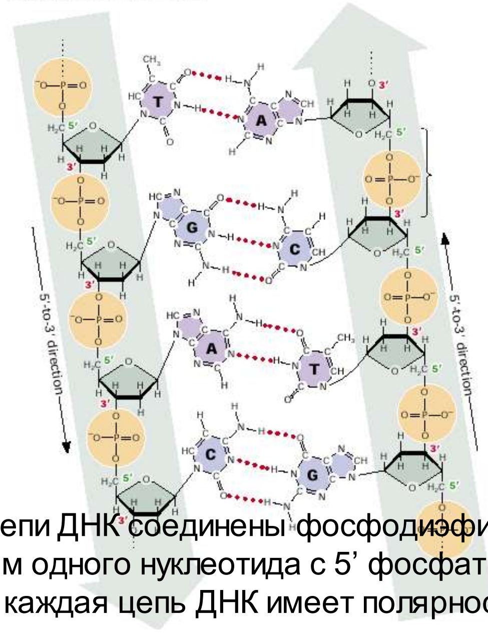
ДЕЗОКСИРИБОЗА

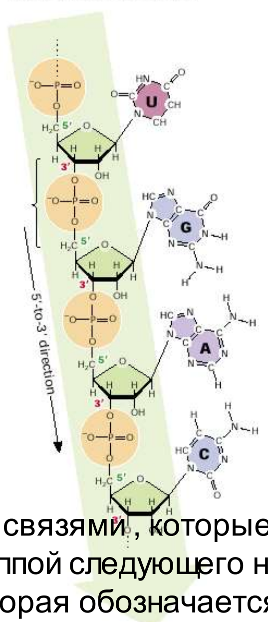


РИБОЗА

ДНК – состоит из двух комплиментарных и антипараллельных друг другу полинуклеотидных нитей

РНК – включает одну полинуклеотидную цепь

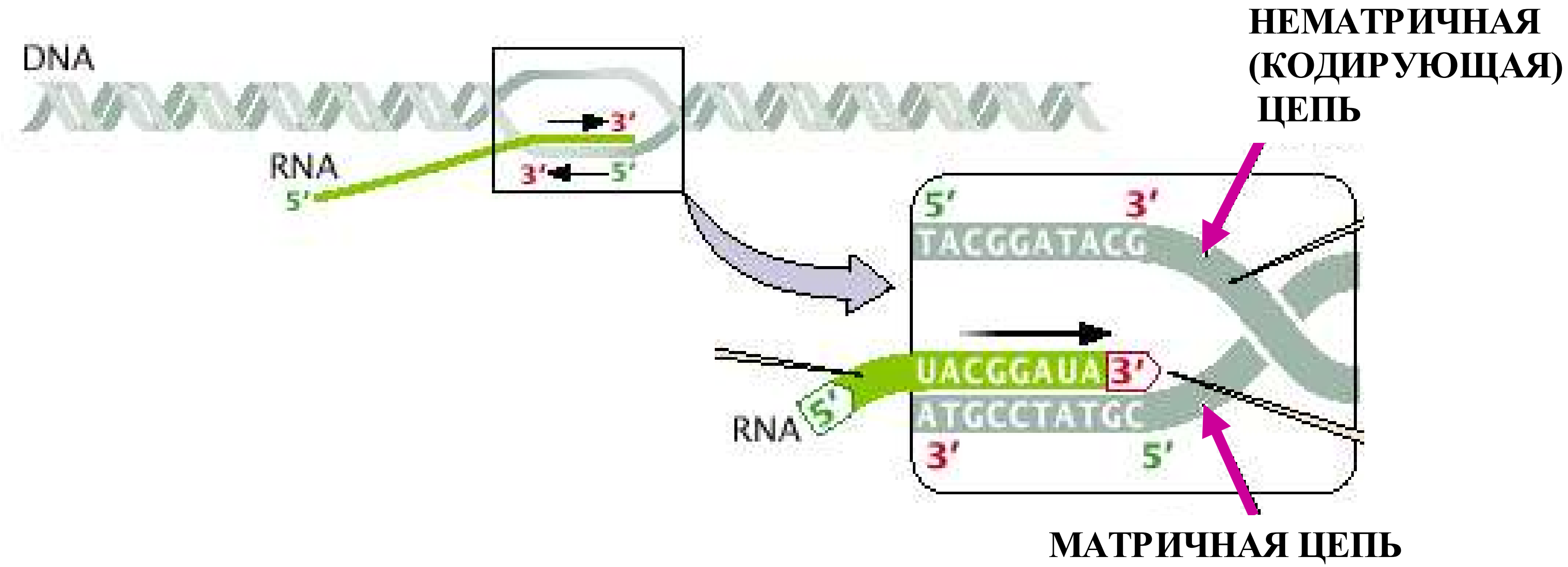




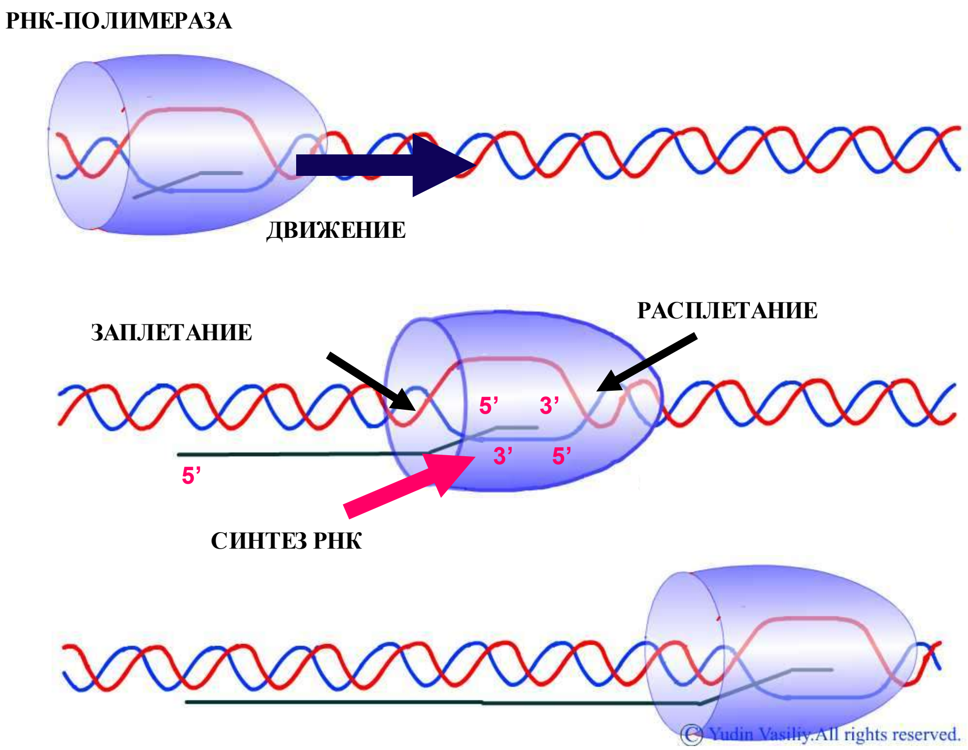
Нуклеотиды в цепи ДНК соединены фосфодиэфирными связями, которые соединяют 3’ углеродный атом одного нуклеотида с 5’ фосфатной группой следующего нуклеотида. Таким образом каждая цепь ДНК имеет полярность, которая обозначается как 5’ и 3’ конец

Genetics A Conceptual Approach Benjamin Pierce (Baylor U.), Ch.10, P.13

Транскрипция – синтез молекулы рнк, комплиментарной и антипараллельной одной из цепи днк (матричной цепи)



Genetics A Conceptual Approach Benjamin Pierce (Baylor U.), Ch.13, P.357

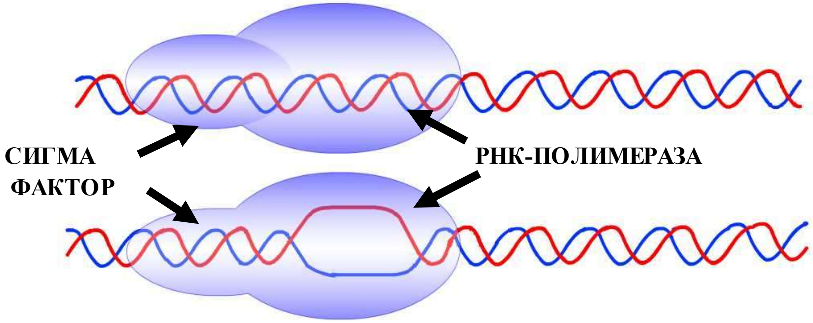


ТРАНСКРИПЦИЯ ОСУЩЕСТВЛЯЕТСЯ ПРИ УЧАСТИИ ФЕРМЕНТА – РНК ПОЛИМЕРАЗЫ.

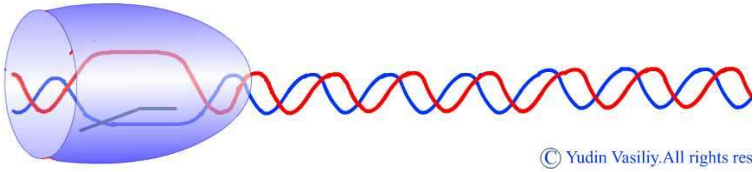
РНК-ПОЛИМЕРАЗА В ХОДЕ ТРАНСКРИПЦИИ ВЫПОЛНЯЕТ СЛЕДУЮЩИЕ ФУНКЦИИ :

- **РАСПЛЕТАНИЕ И ЗАПЛЕТАНИЕ ДНК**
- **СИНТЕЗ РНК**
- **ДВИЖЕНИЕ ВДОЛЬ ЦЕПИ ДНК**

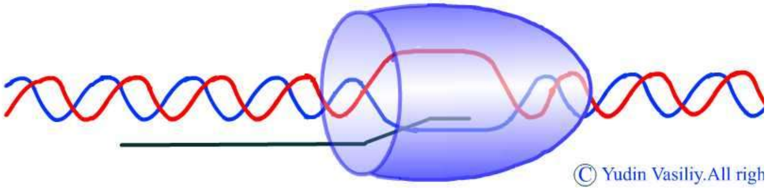
Четыре этапа транскрипции:



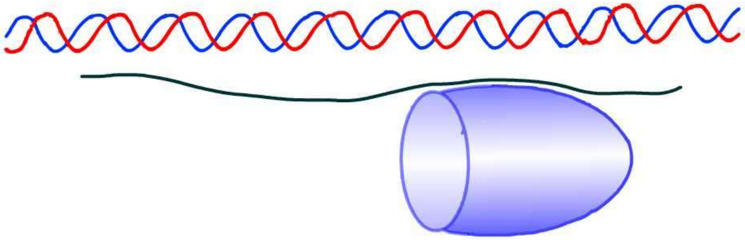
РАСПОЗНАВАНИЕ МАТРИЦЫ:
при участии сигма фактора (у E.coli) РНК полимераза связывается с ДНК и расплетает ДНК в точке инициации транскрипции



ИНИЦИАЦИЯ:
сигма фактор отсоединился и синтезирована цепь РНК
(2-9 пар оснований)



ЭЛОНГАЦИЯ:
движение РНК полимеразы вдоль ДНК, расплетание ДНК, синтез РНК, заплетание ДНК



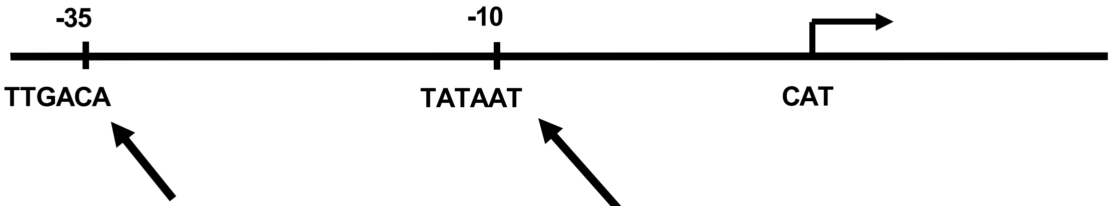
ТЕРМИНАЦИЯ: окончание транскрипции, распад комплекса ДНК-РНК-полимераза. Происходит после распознавания терминатора

ГЕНОМ E.coli - $4*10^{60}$ пар оснований
ПРОМОТОР ~60 пар оснований

КАК ОСУЩЕСТВЛЯЕТСЯ РАСПОЗНАВАНИЕ ТОЧКИ ИНИЦИАЦИИ ТРАНСКРИПЦИИ ???

У E.coli анализ последовательностей более 100 различных участков, прилегающих к старту транскрипции выявил сходное строение:
1) в районе старта транскрипции – пурины, часто «CAT»
2) в позиции «-10» гексамер TATAAT (последовательность «–10»)
3) в позиции «-35» гексамер TTGACA (последовательность «–35»)
4) расстояние между последовательностями «-35» и «-10» ~16-18 нуклеотидов

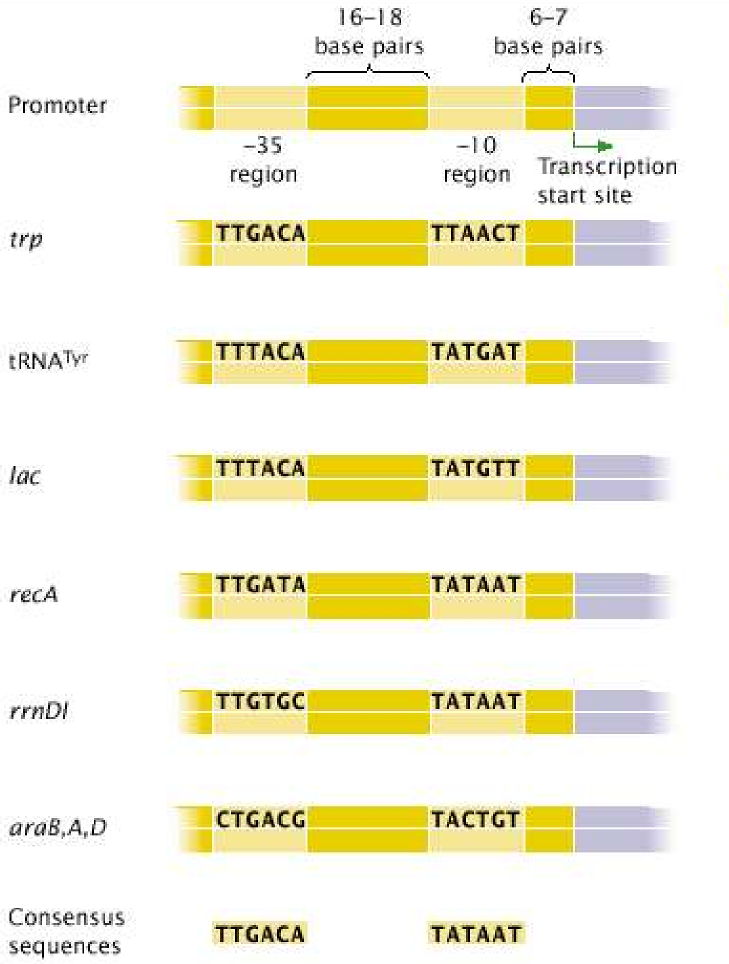
Изучение функции участка с помощью мутационного анализа



мутации замедляют скорость посадки комплекса сигма-фактор - полимераза на ДНК

мутации замедляют образование открытого комплекса

ПРОМОТОР – участок, прилегающий к старту транскрипции. Содержит регуляторные элементы, которые опознаются с белками, обеспечивающими инициацию транскрипции

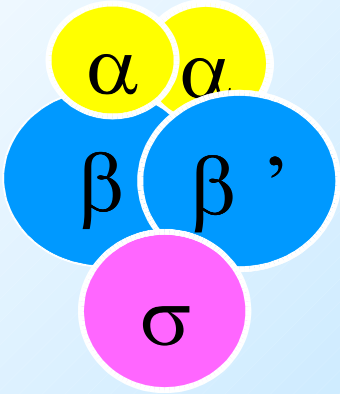


13.12 **In most prokaryotic promoters, the actual sequence is not TATAAT.** The sequences shown are

Genetics A Conceptual Approach Benjamin Pierce (Baylor U.), Ch.13, P.363

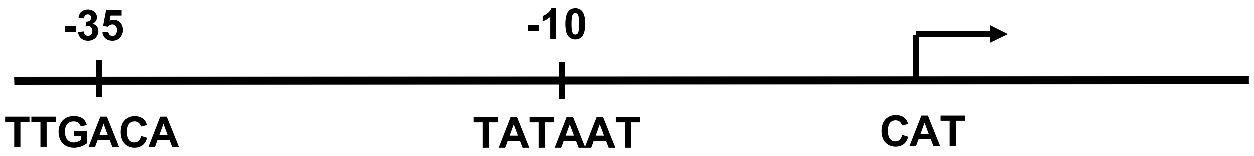
Субъединичный состав комплекса сигма фактор – РНК полимераза (E.coli)

субъединица	Мол. масса	Коли-чество	Локализация	Функция
альфа	40.000	2	РНК полимераза	Сборка фермента
бета	155.000	1	РНК полимераза	Связывание нуклеотидов
бета’	160.000	1	РНК полимераза	Связывание с матрицей
сигма	32-92.000	1	сигма фактор	Связывание с промотором



E.coli имеет несколько сигма факторов , специфичных для различных ситуаций, которые распознают промоторы разных групп генов

ситуация	Мол. Масса сигма фактора	«-35» последовательность	спейсер	«-10» последовательность
общая	70.000	TTGACA	16-18 п.о.	TATAAT
тепловой шок	32.000	CCCTTGAA	13-15 п.о.	CCCGATNT
отсутствие азота	54.000	CTGGNA	6 п.о.	TTGCA
хемотаксис	28.000	CTAAA	15 п.о.	GCCGATAA



Особенности транскрипции у эукариот.

1) У эукариот - три типа РНК полимераз и три группы генов

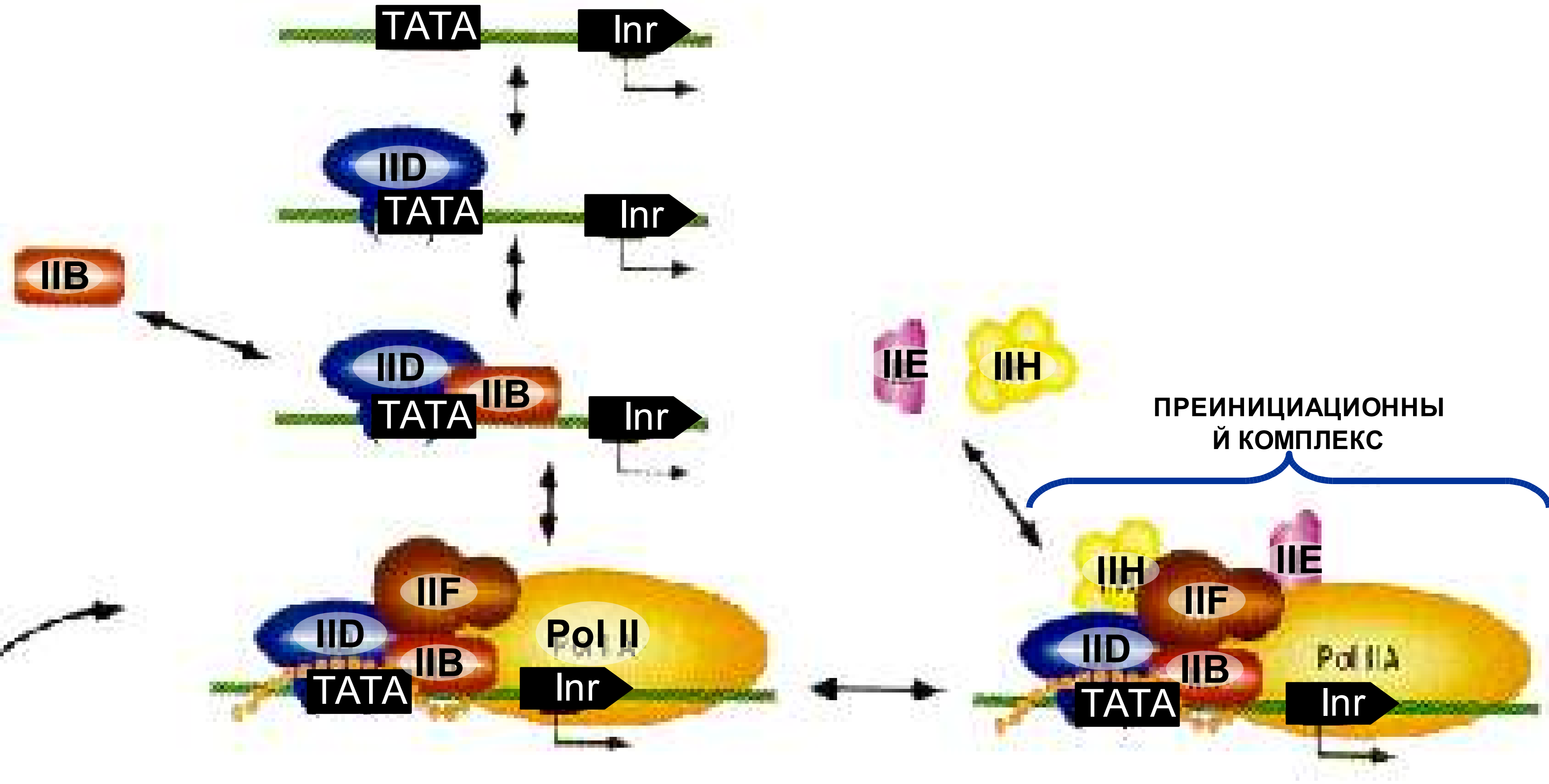
pol I транскрибируемые -рибосомные РНК
pol II транскрибируемые - матричные РНК
pol III транскрибируемые – транспортные РНК

2) Каждая полимераза имеет много субъединиц, например, pol II включает более 10 субъединиц

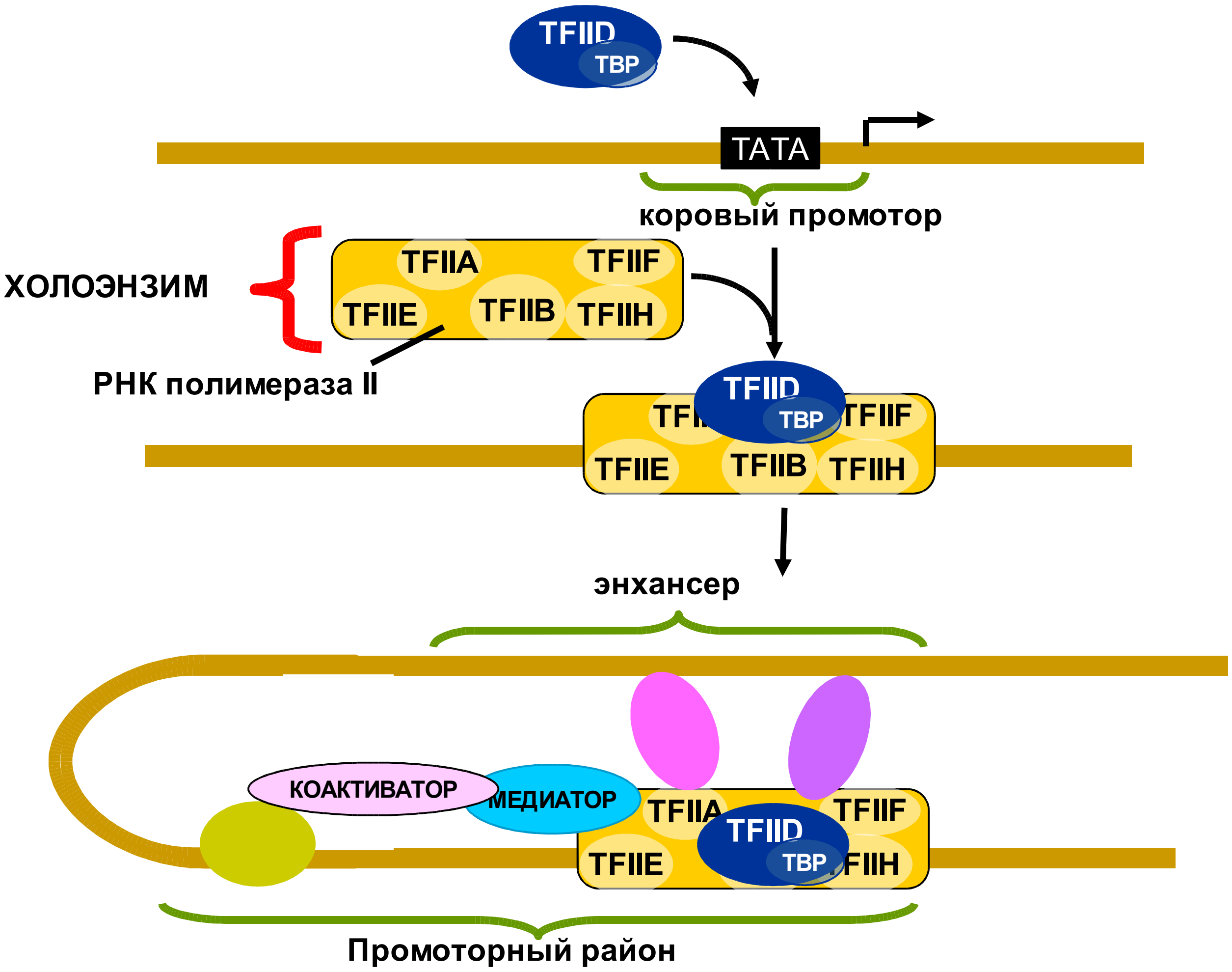
3) Для точной посадки полимеразы на участок, прилежащий к старту транскрипции нужны вспомогательные белки – базальные транскрипционные факторы

4) промоторы генов, транскрибируемых каждым типом полимераз имеют характерное строение

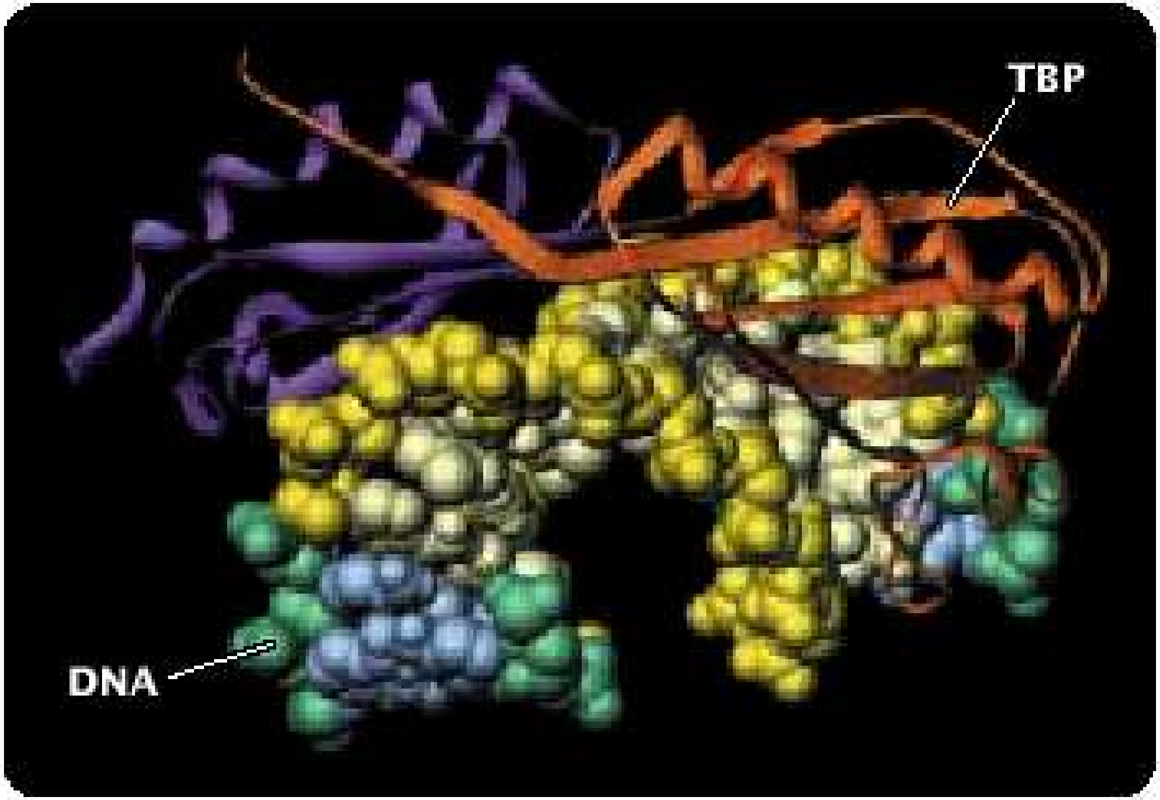
Схема пошаговой сборки преинициационного комплекса в районе старта транскрипции гена, транскрибируемого РНК полимеразой II



Инициация транскрипции при участии холоэнзима, включающего РНК полимеразу II

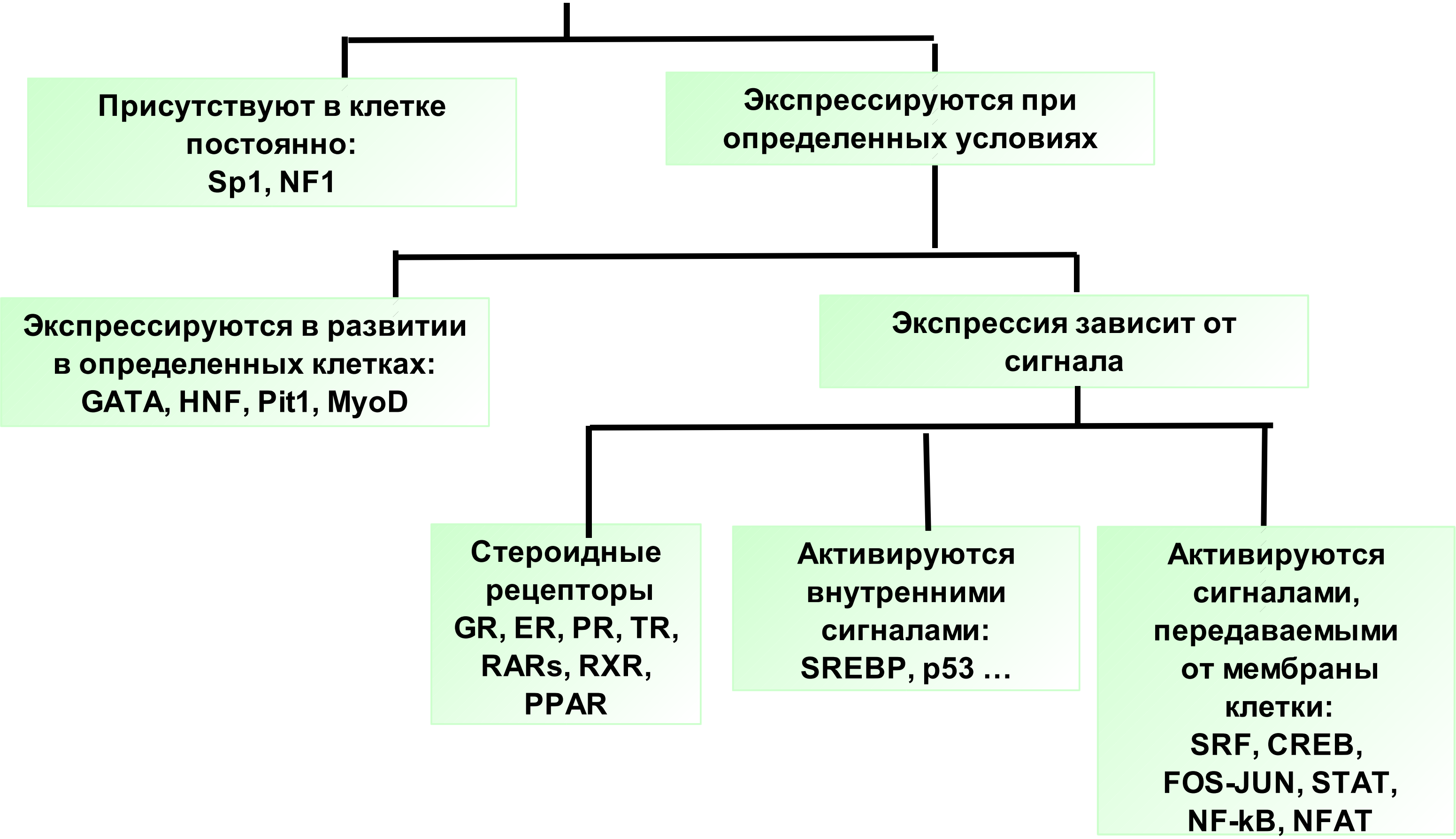


При взаимодействии с ТВР (ТАТА связывающий белок) ДНК изгибается



Genetics A Conceptual Approach Benjamin Pierce (Baylor U.), Ch.13, P.369

ФУНКЦИОНАЛЬНАЯ КЛАССИФИКАЦИЯ ТРАНСКРИПЦИОННЫХ ФАКТОРОВ:



Присутствуют в клетке постоянно:
Sp1, NF1

Экспрессируются при определенных условиях

Экспрессируются в развитии в определенных клетках:
GATA, HNF, Pit1, MyoD

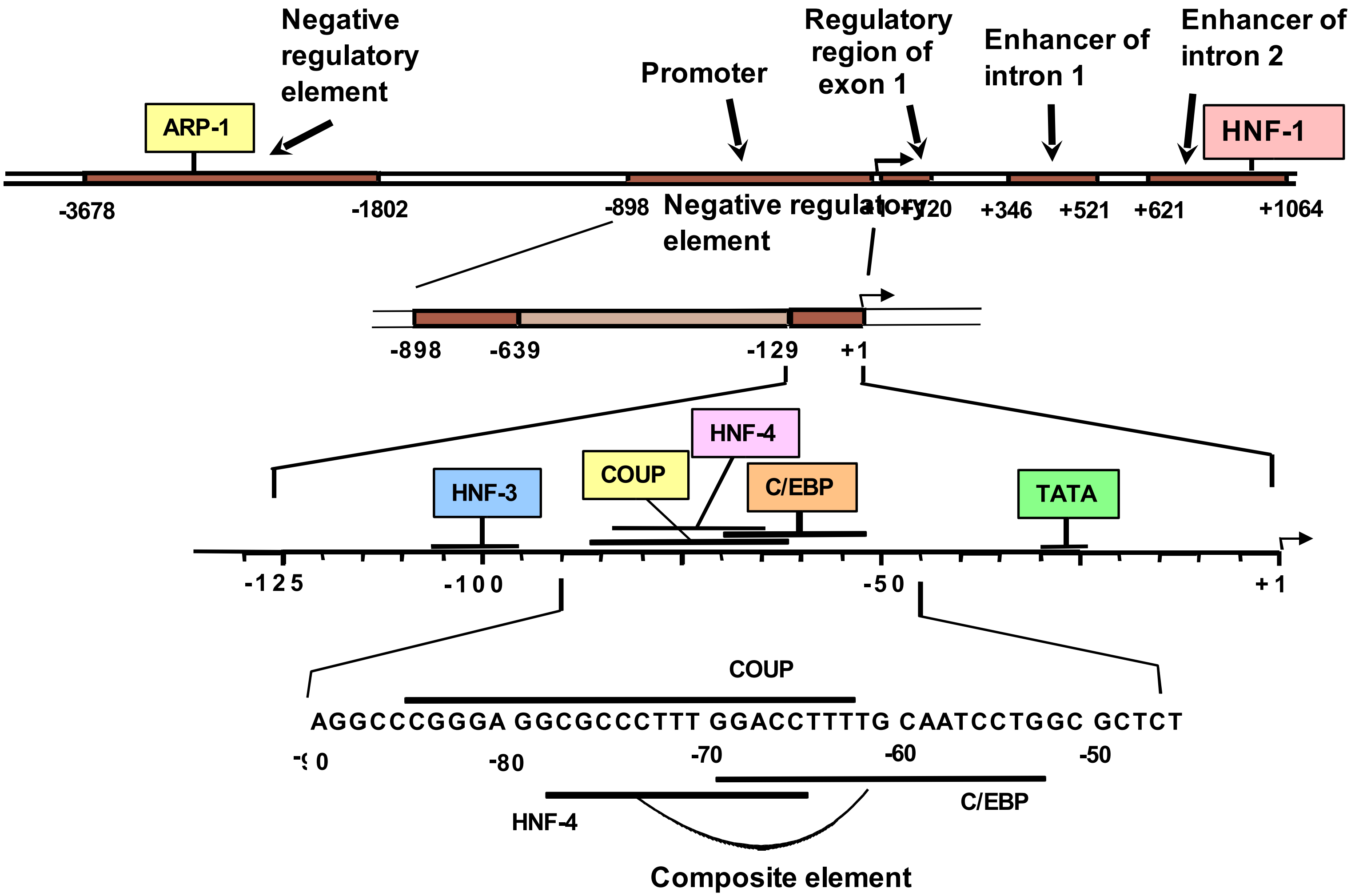
Экспрессия зависит от сигнала

Стероидные рецепторы
GR, ER, PR, TR, RARs, RXR, PPAR

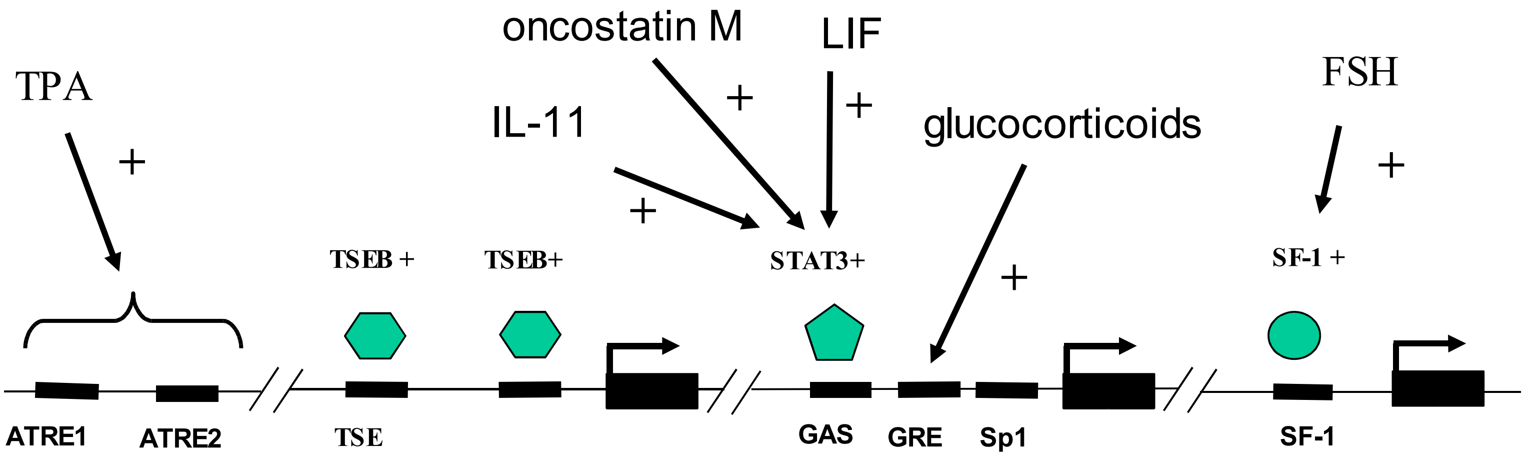
Активируются внутренними сигналами:
SREBP, p53 …

Активируются сигналами, передаваемыми от мембраны клетки:
SRF, CREB, FOS-JUN, STAT, NF-kB, NFAT

Регуляторные районы , контролирующие транскрипцию гена аполипопротеина в человека



Регуляторные районы, контролирующие экспрессию гена ароматазы человека



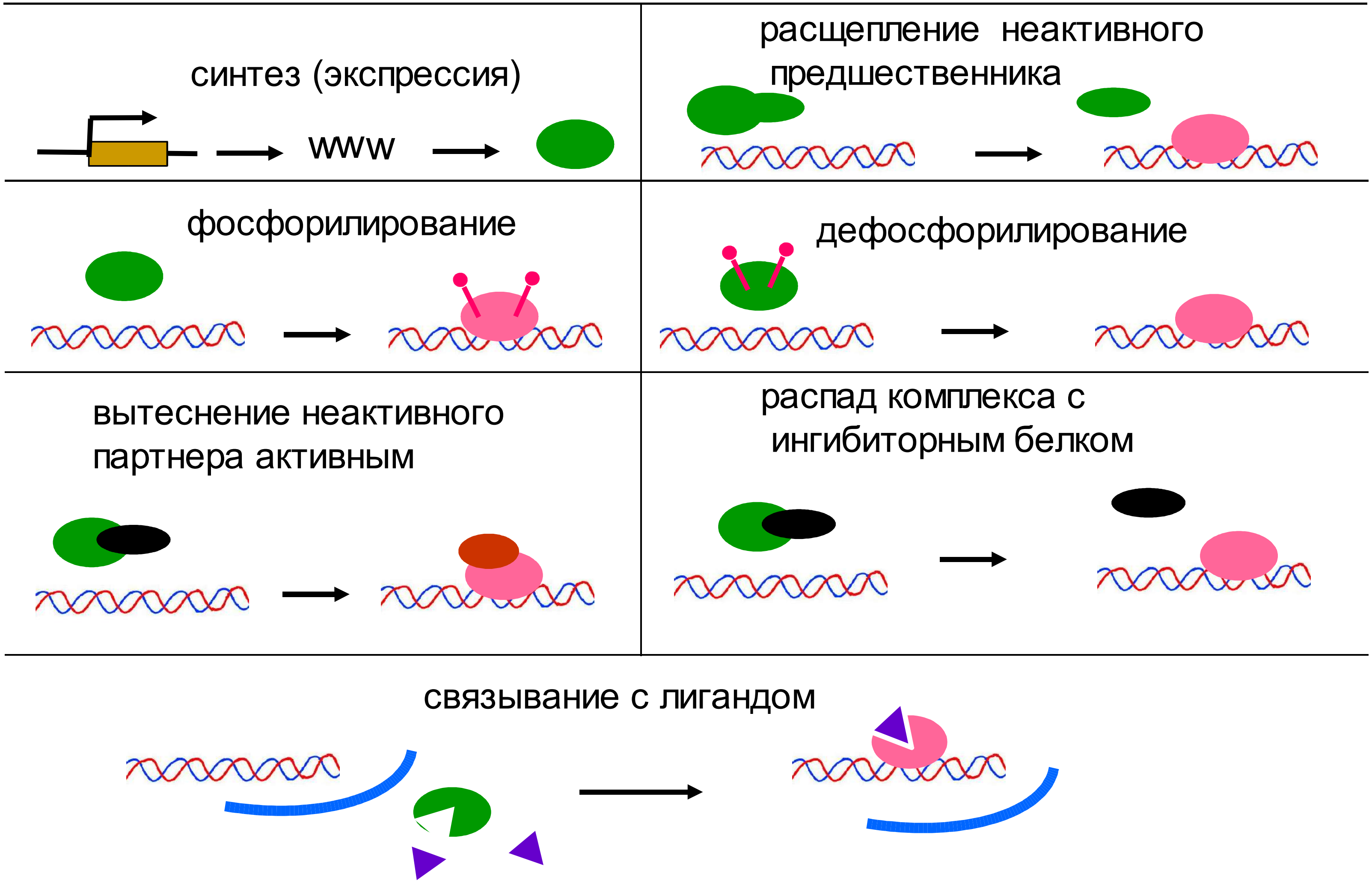
TPA responsive enhancer (P00436)
(choriocarcinoma cells)

promoter I.1 (P00437)
(fetus placenta
trophoblasts)

promoter I.4
(P00910)
(adipose stromal cells,
skin fibroblasts,
fetus liver hepatocytes,
adult hypothalamus
adult amygdala
adult hippocampus)

promoter II
(P00911)
(granulosa cells,
corpus luteum)

Пути регуляции активности транскрипционных факторов



синтез (экспрессия)

www

расщепление неактивного предшественника

фосфорилирование

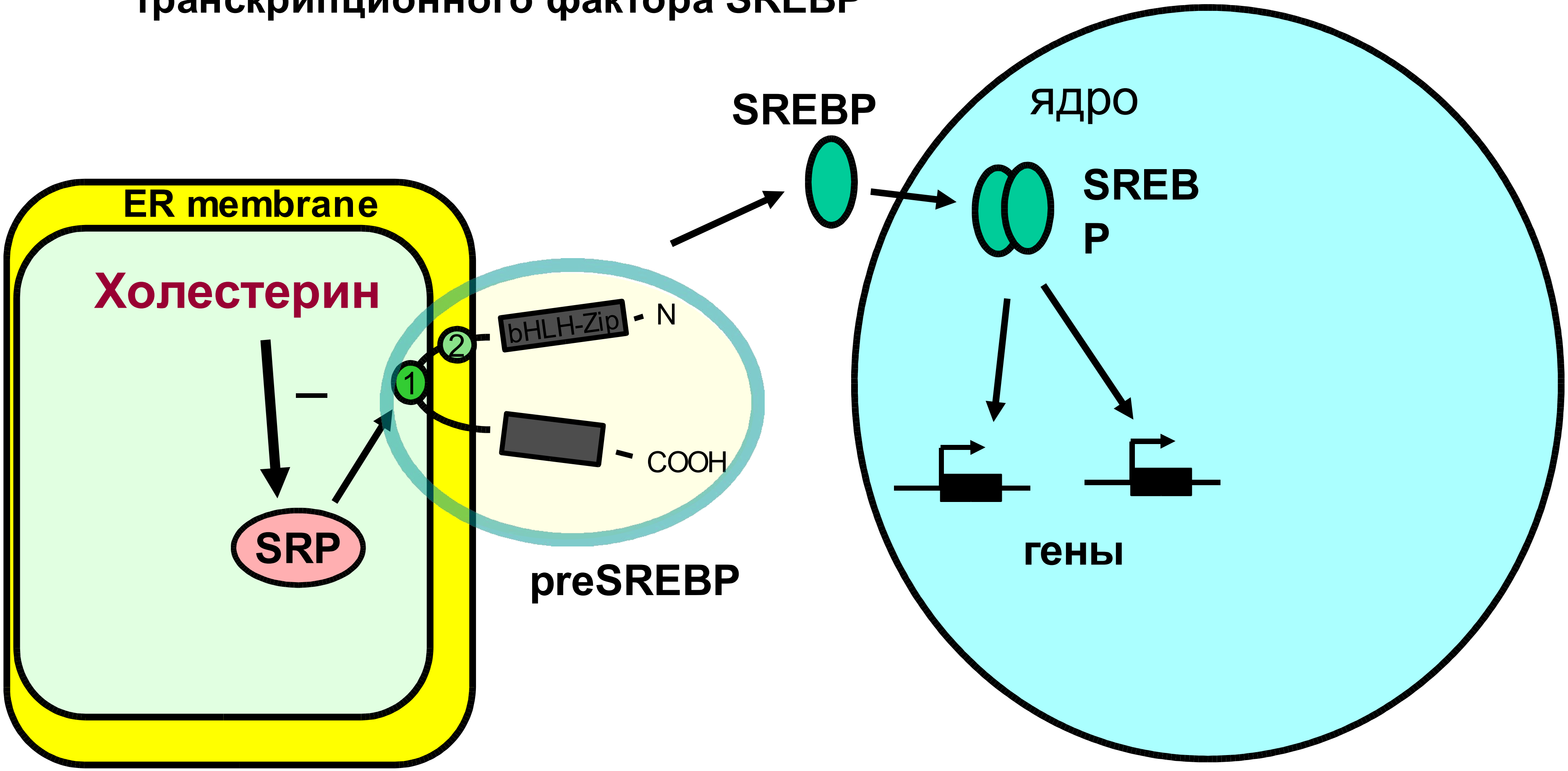
дефосфорилирование

вытеснение неактивного партнера активным

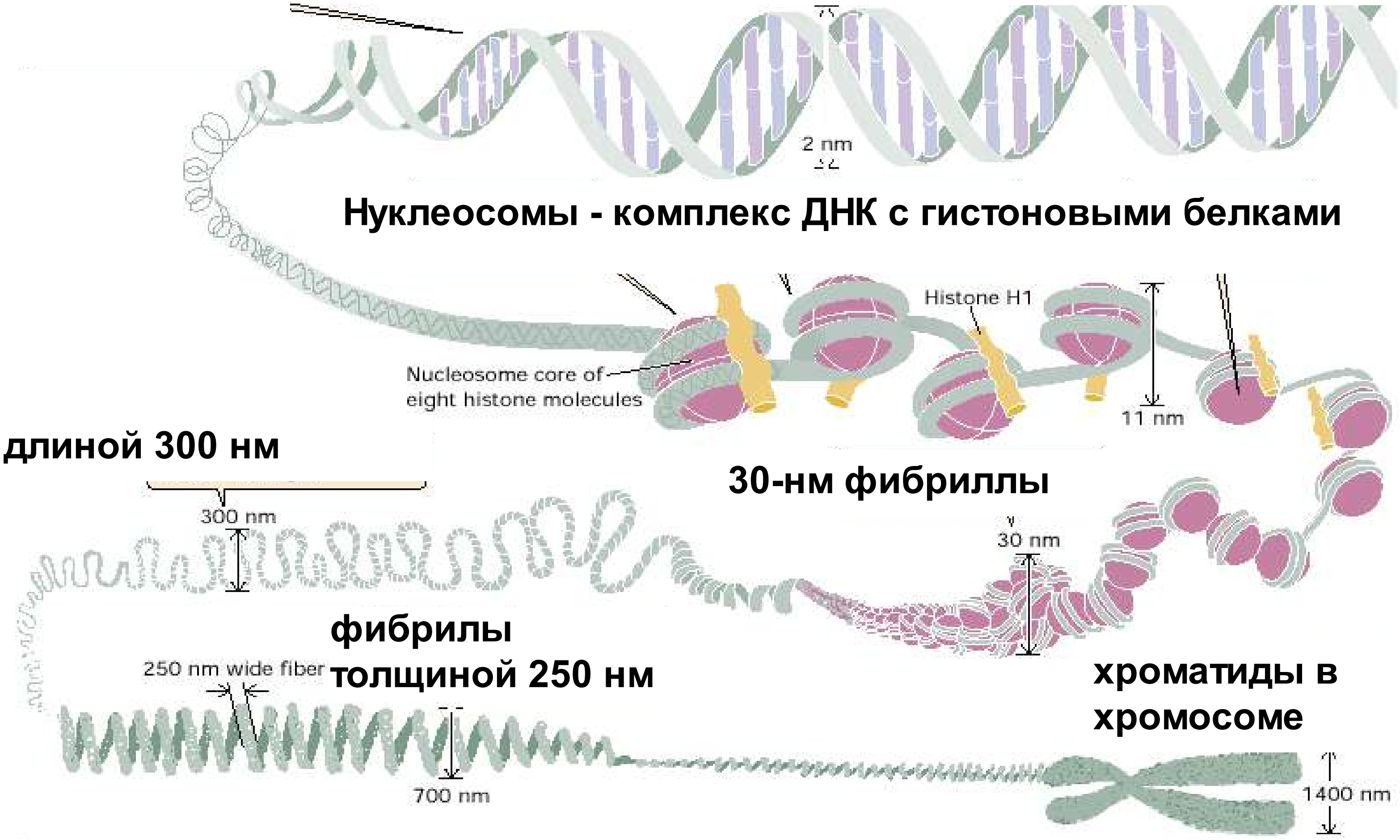
распад комплекса с ингибиторным белком

связывание с лигандом

<u>ПРИМЕР:</u> холестерин регулирует активность транскрипционного фактора SREBP



Уровни организации хроматина



ДНК (двойная спираль)

Нуклеосомы - комплекс ДНК с гистоновыми белками

петли длиной 300 нм

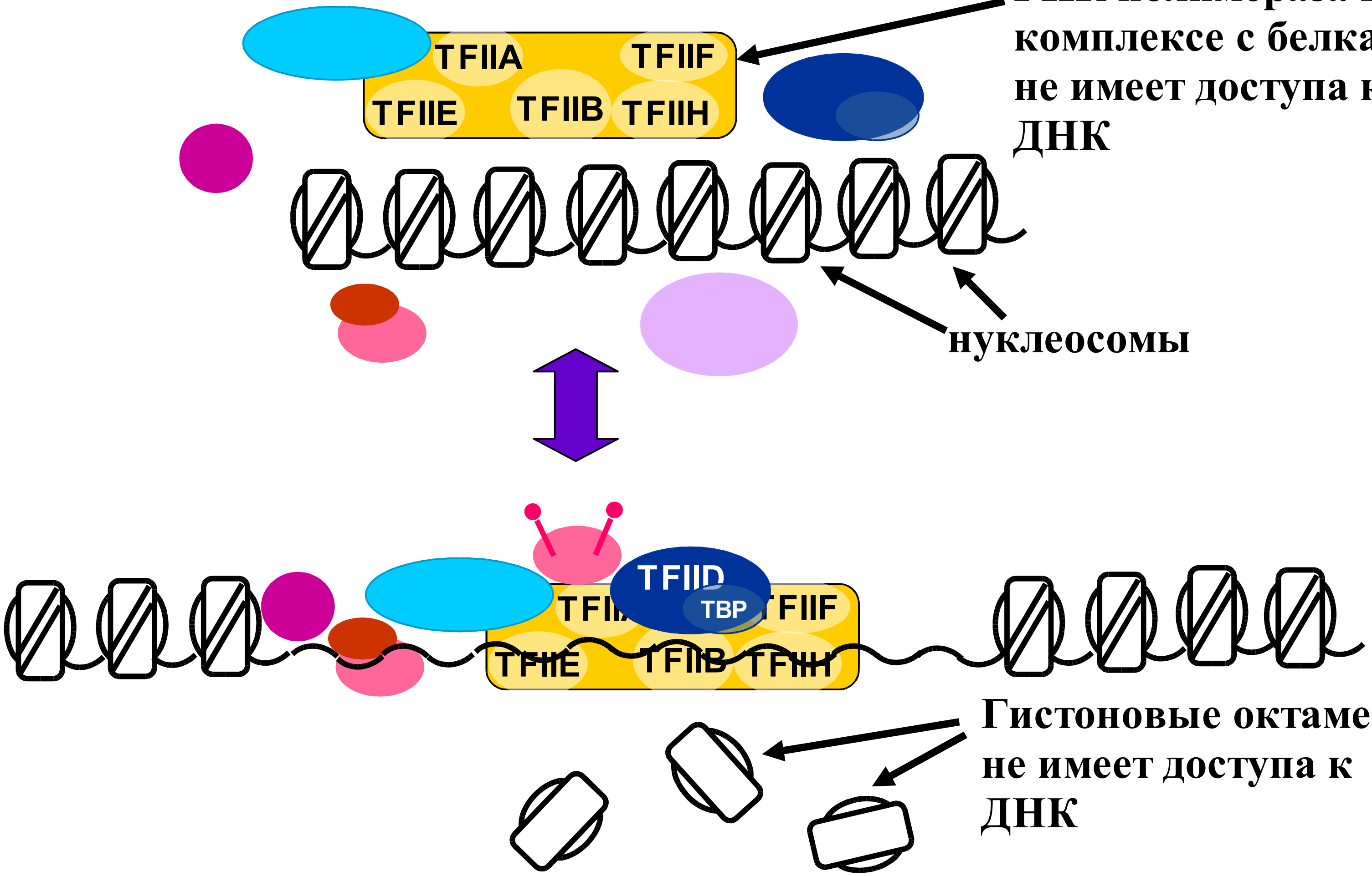
30-нм фибриллы

фибрилы толщиной 250 нм

хроматиды в хромосоме

Genetics A Conceptual Approach Benjamin Pierce (Baylor U.), Ch.11, P.7

Конкуренция между гистоновыми белками и транскрипционными факторами за доступ к ДНК



РНК полимераза в комплексе с белками не имеет доступа к ДНК

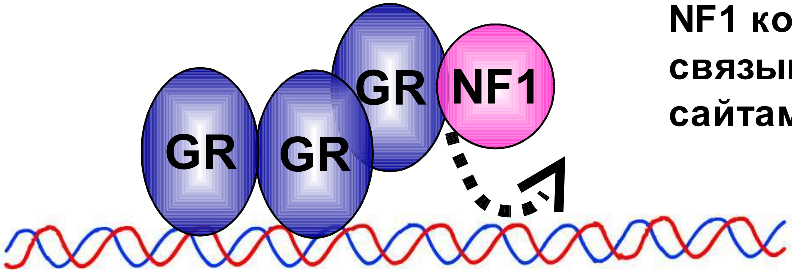
нуклеосомы

Гистоновые октамеры не имеет доступа к ДНК

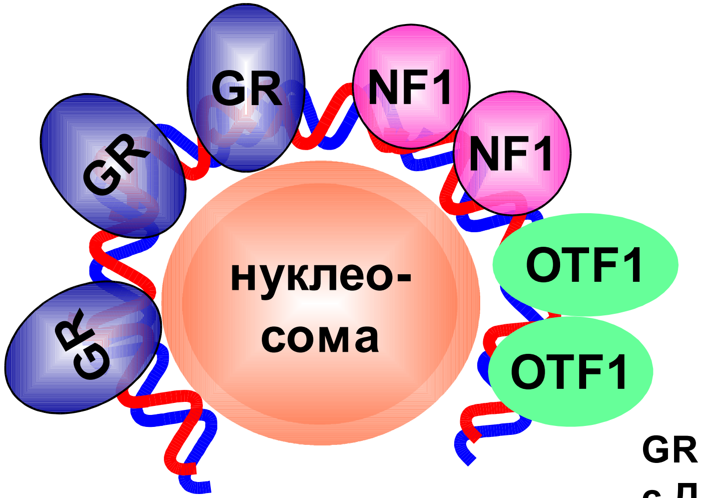
ТРАНСКРИПЦИОННЫЕ ФАКТОРЫ ДЕЛЯТСЯ НА ДВЕ ГРУППЫ ПО СПОСОБНОСТИ СВЯЗЫВАТЬСЯ С ДНК-САЙТАМИ В СОСТАВЕ НУКЛЕОСОМЫ:

- ОБЛАДАЮЩИЕ ТАКОЙ СПОСОБНОСТЬЮ
- НЕ СПОСОБНЫХ К ЭТОМУ

ПРИМЕР: промотор MMTV

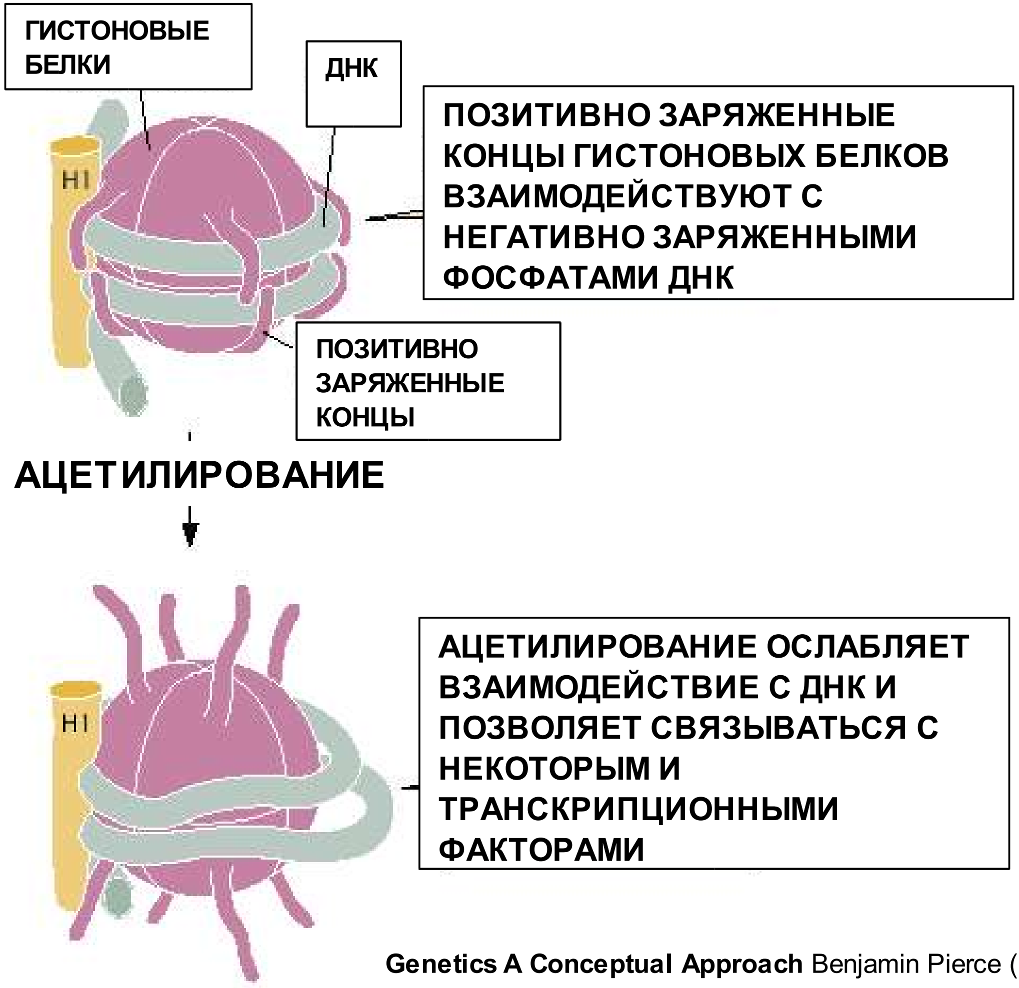


два транскрипционных фактора GR и NF1 конкурируют друг с другом за связывание с близко расположенными сайтами их связывания на ДНК



GR и NF1 одновременно связываются с ДНК, только когда она изогнута на поверхности нуклеосомы

Ацетилирование гистоновых белков дестабилизирует нуклеосомы



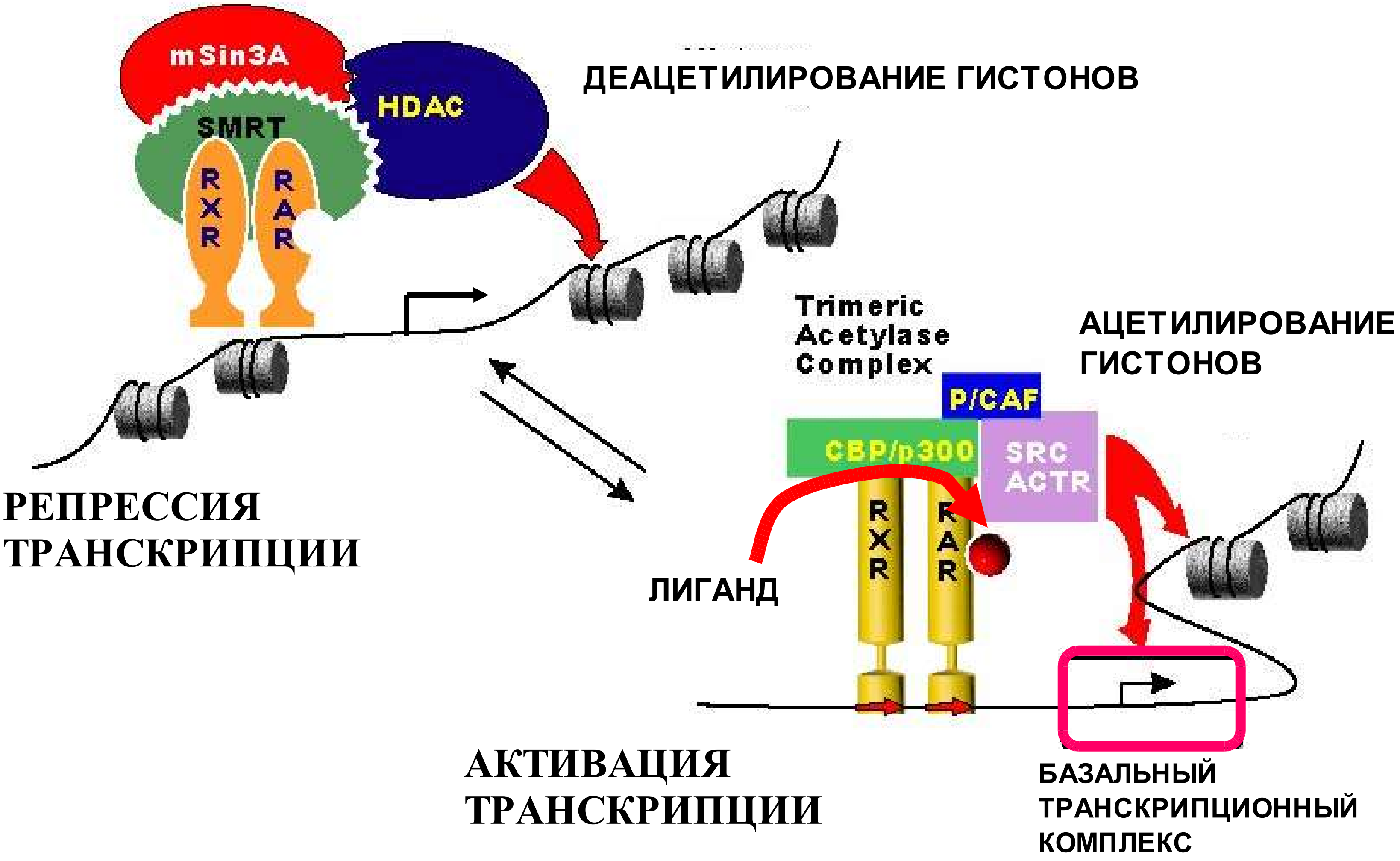
ПОЗИТИВНО ЗАРЯЖЕННЫЕ КОНЦЫ ГИСТОНОВЫХ БЕЛКОВ ВЗАИМОДЕЙСТВУЮТ С НЕГАТИВНО ЗАРЯЖЕННЫМИ ФОСФАТАМИ ДНК

АЦЕТИЛИРОВАНИЕ

АЦЕТИЛИРОВАНИЕ ОСЛАБЛЯЕТ ВЗАИМОДЕЙСТВИЕ С ДНК И ПОЗВОЛЯЕТ СВЯЗЫВАТЬСЯ С НЕКОТОРЫМ И ТРАНСКРИПЦИОННЫМИ ФАКТОРАМИ

Genetics A Conceptual Approach Benjamin Pierce (Baylor U.), Ch.16, P.456

Связывание рецептора с лигандом изменяет структуру хроматина



ДЕАЦЕТИЛИРОВАНИЕ ГИСТОНОВ

РЕПРЕССИЯ ТРАНСКРИПЦИИ

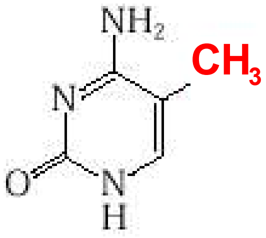
АЦЕТИЛИРОВАНИЕ ГИСТОНОВ

ЛИГАНД

АКТИВАЦИЯ ТРАНСКРИПЦИИ

БАЗАЛЬНЫЙ ТРАНСКРИПЦИОННЫЙ КОМПЛЕКС

В ЭУКАРИОТИЧЕСКИХ КЛЕТКАХ УРОВЕНЬ МЕТИЛИРОВАНИЯ ДНК ЧАСТО КОРРЕЛИРУЕТ С УРОВНЕМ ЭКСПРЕССИИ ГЕНА. МЕТИЛИРОВАННЫЕ УЧАСТКИ ДНК ТРАНСКРИБИРУЮТСЯ МЕНЕЕ АКТИВНО, ЧЕМ НЕМЕТИЛИРОВАННЫЕ УЧАСТКИ



метильная группа

5-метилцитозин

МЕТИЛИРОВАНИЕ ЦИТОЗИНА ПРИВОДИТ К ОБРАЗОВАНИЮ 5-МЕТИЛЦИТОЗИНА

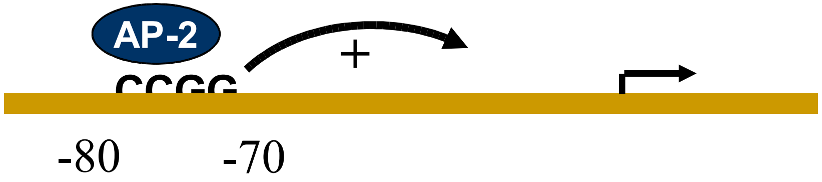
НАИБОЛЕЕ ЧАСТО МЕТИЛИРОВАНИЮ ПОДВЕРГАЮТСЯ ЦИТОЗИНОВЫЕ НУКЛЕОТИДЫ, СТОЯЩИЕ ПОСЛЕ ГУАНИНОВЫХ

…GC…

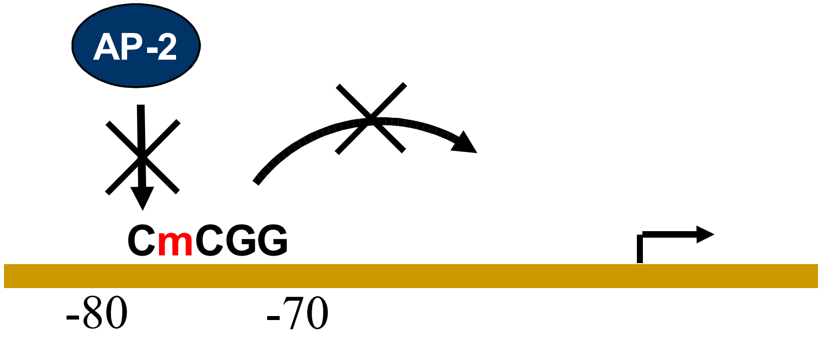
…CG…

Genetics A Conceptual Approach Benjamin Pierce (Baylor U.), Ch.10, P.18

ПРИМЕР: **ген проэнкефалина человека содержит сайт связывания транскрипционного фактора АР-2 районе -80/-70 от старта транскрипции.**



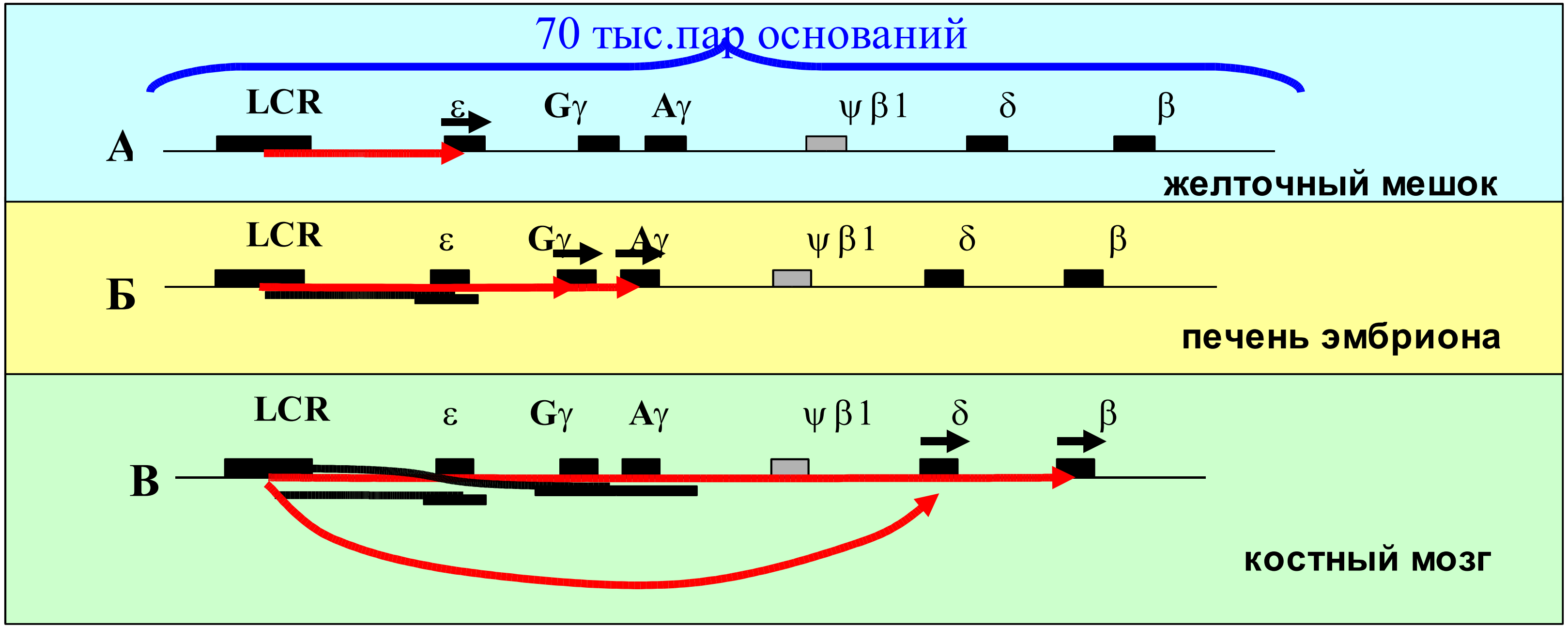
если сайт связывания АР-2 находится в деметилированном состоянии, АР-2 эффективно взаимодействует с этим сайтом, что приводит к активации транскрипции гена



метилирование нарушает связывание АР-2 с ДНК и транскрипция снижается

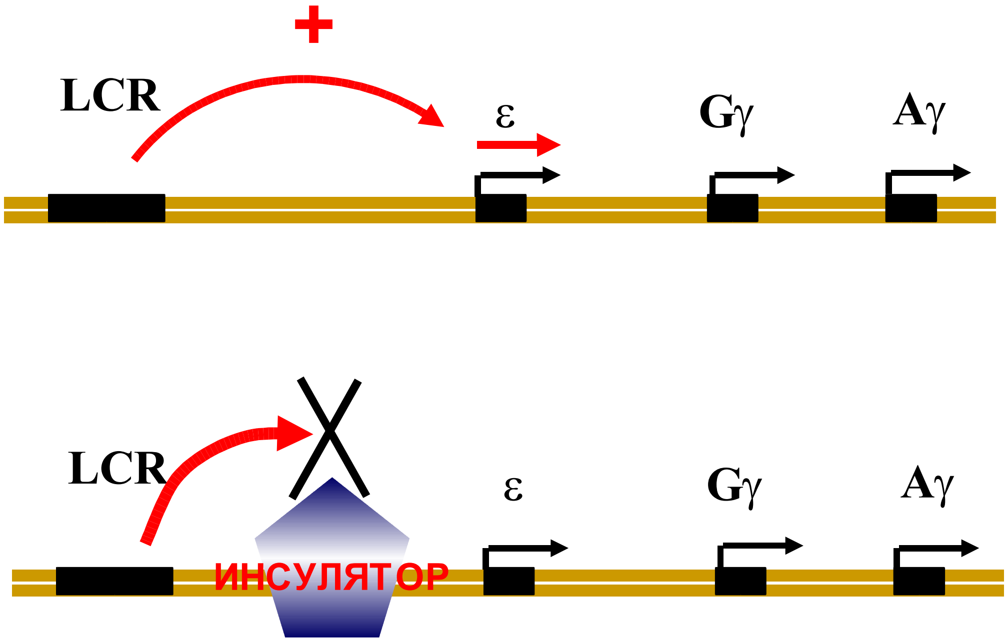
ЛОКУС-КОНТРОЛИРУЮЩИЙ РАЙОН (LCR) -УДАЛЕННЫЙ РЕГУЛЯТОРНЫЙ РАЙОН, ОБЕСПЕЧИВАЮЩИЙ ВКЛЮЧЕНИЕ И ВЫКЛЮЧЕНИЕ ГЕНОВ ЗА СЧЕТ ПОПЕРЕМННОГО ВЗАИМОДЕЙСТВИЯ С РЕГУЛЯТОРНЫМИ РАЙОНАМИ ГЕНОВ, НАХОДЯЩИХСЯ В КЛАСТЕРЕ

Пример: локус-контролирующий район кластера гемоглобиновых генов человека



ε, Gγ , Aγ, δ, β - гены гемоглобинов; ψβ1 - псевдоген

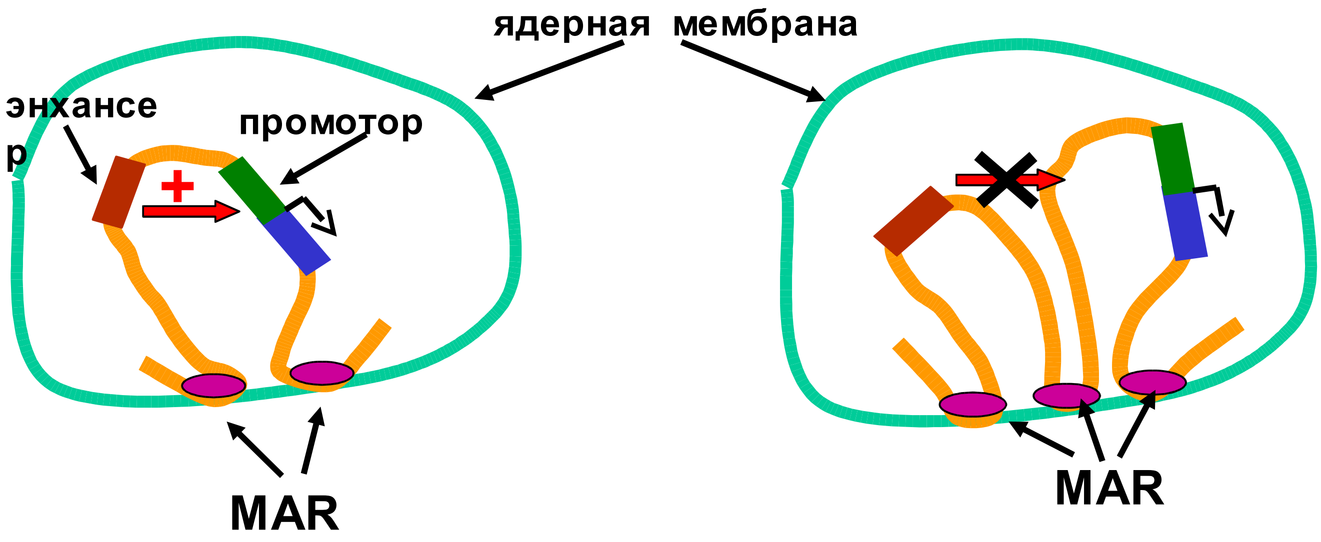
Инсулятор



ИНСУЛЯТОР – участок ДНК, который, будучи помещенным между двумя регуляторными элементами может препятствовать активирующему либо подавляющему действию одного элемента на другой
При включении инсулятора два регуляторных района оказываются в различных доменах, и не способны взаимодействовать

Роль инсулятора может выполнять участок прикрепления к ядерному матриксу (MAR). При включении такого инсулятора два регуляторных района оказываются в различных доменах, и не способны взаимодействовать

MARs =matrix attachment regions



энхансер активирует транскрипцию гена

энхансер не влияет на транскрипцию гена

БАЗЫ ДАННЫХ ПО РЕГУЛЯЦИИ ТРАНСКРИПЦИИ

TRANSCRIPTION REGULATORY REGIONS DATABASE (TRRD)

Институт цитологии и генетики Сибирского отделения Российской академии наук, Новосибирск-90, 630090

http://wwwmgs.bionet.nsc.ru/mgs/gnw/trrd/

Публикация по базам TRRD в Nucleic Acids Research

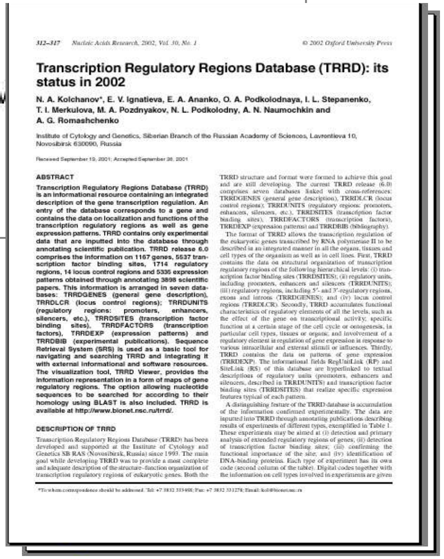
312–317 *Nucleic Acids Research, 2002, Vol. 30, No. 1* *© 2002 Oxford University Press*

Transcription Regulatory Regions Database (TRRD): its status in 2002

N. A. Kolchanov*, E. V. Ignatieva, E. A. Ananko, O. A. Podkolodnaya, I. L. Stepanenko, T. I. Merkulova, M. A. Pozdnyakov, N. L. Podkolodny, A. N. Naumochkin and A. G. Romashchenko

Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Lavrentiev
Novosibirsk 630090, Russia

Received September 19, 2001; Accepted September 26, 2001



312–317 *Nucleic Acids Research, 2002, Vol. 30, No. 1* *© 2002 Oxford University Press*

Transcription Regulatory Regions Database (TRRD): its status in 2002

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Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Lavrentieva 10,
Novosibirsk 630090, Russia

Received September 19, 2001; Accepted September 26, 2001

ABSTRACT

Transcription Regulatory Regions Database (TRRD) is an informational resource containing an integrated description of the gene transcription regulation. An entry of the database corresponds to a gene and contains the data on localization and functions of the transcription regulatory regions as well as gene expression patterns. TRRD contains only experimental data that are inputted into the database through annotating scientific publication. TRRD release 6.0 comprises the information on 1167 genes, 5537 transcription factor binding sites, 1714 regulatory regions, 14 locus control regions and 5335 expression patterns obtained through annotating 3898 scientific papers. This information is arranged in seven databases: TRRDGENES (general gene description), TRRDLCR (locus control regions); TRRDUNITS (regulatory regions: promoters, enhancers, silencers, etc.), TRRDSITES (transcription factor binding sites), TRRDFACTORS (transcription factors), TRRDEXP (expression patterns) and TRRDBIB (experimental publications). Sequence Retrieval System (SRS) is used as a basic tool for navigating and searching TRRD and integrating it with external informational and software resources. The visualization tool, TRRD Viewer, provides the information representation in a form of maps of gene regulatory regions. The option allowing nucleotide sequences to be searched for according to their homology using BLAST is also included. TRRD is available at http://www.bionet.nsc.ru/trrd/.

DESCRIPTION OF TRRD

Transcription Regulatory Regions Database (TRRD) has been developed and supported at the Institute of Cytology and Genetics SB RAS (Novosibirsk, Russia) since 1993. The main goal while developing TRRD was to provide a most complete and adequate description of the structure–function organization of transcription regulatory regions of eukaryotic genes. Both the TRRD structure and format were formed to achieve this goal and are still developing. The current TRRD release (6.0) comprises seven databases linked with cross-references: TRRDGENES (general gene description), TRRDLCR (locus control regions); TRRDUNITS (regulatory regions: promoters, enhancers, silencers, etc.), TRRDSITES (transcription factor binding sites), TRRDFACTORS (transcription factors), TRRDEXP (expression patterns) and TRRDBIB (bibliography).

The format of TRRD allows the transcription regulation of the eukaryotic genes transcribed by RNA polymerase II to be described in an integrated manner in all the organs, tissues and cell types of the organism as well as in cell lines. First, TRRD contains the data on structural organization of transcription regulatory regions of the following hierarchical levels: (i) transcription factor binding sites (TRRDSITES); (ii) regulatory units, including promoters, enhancers and silencers (TRRDUNITS); (iii) regulatory regions, including 5′- and 3′-regulatory regions, exons and introns (TRRDGENES); and (iv) locus control regions (TRRDLCR). Secondly, TRRD accumulates functional characteristics of regulatory elements of all the levels, such as the effect of the gene on transcriptional activity, specific function at a certain stage of the cell cycle or ontogenesis, in particular cell types, tissues or organs; and involvement of a regulatory element in regulation of gene expression in response to various intracellular and external stimuli or influences. Thirdly, TRRD contains the data on patterns of gene expression (TRRDEXP). The informational fields RegUnitLink (RP) and SiteLink (RS) of this database are hyperlinked to textual descriptions of regulatory units (promoters, enhancers and silencers, described in TRRDUNITS) and transcription factor binding sites (TRRDSITES) that realize specific expression features typical of each pattern.

A distinguishing feature of the TRRD database is accumulation of the information confirmed experimentally. The data are inputted into TRRD through annotating publications describing results of experiments of different types, exemplified in Table 1. These experiments may be aimed at (i) detection and primary analysis of extended regulatory regions of genes; (ii) detection of transcription factor binding sites; (iii) confirming the functional importance of the site; and (iv) identification of DNA-binding proteins. Each type of experiment has its own code (second column of the table). Digital codes together with the information on cell types involved in experiments are given

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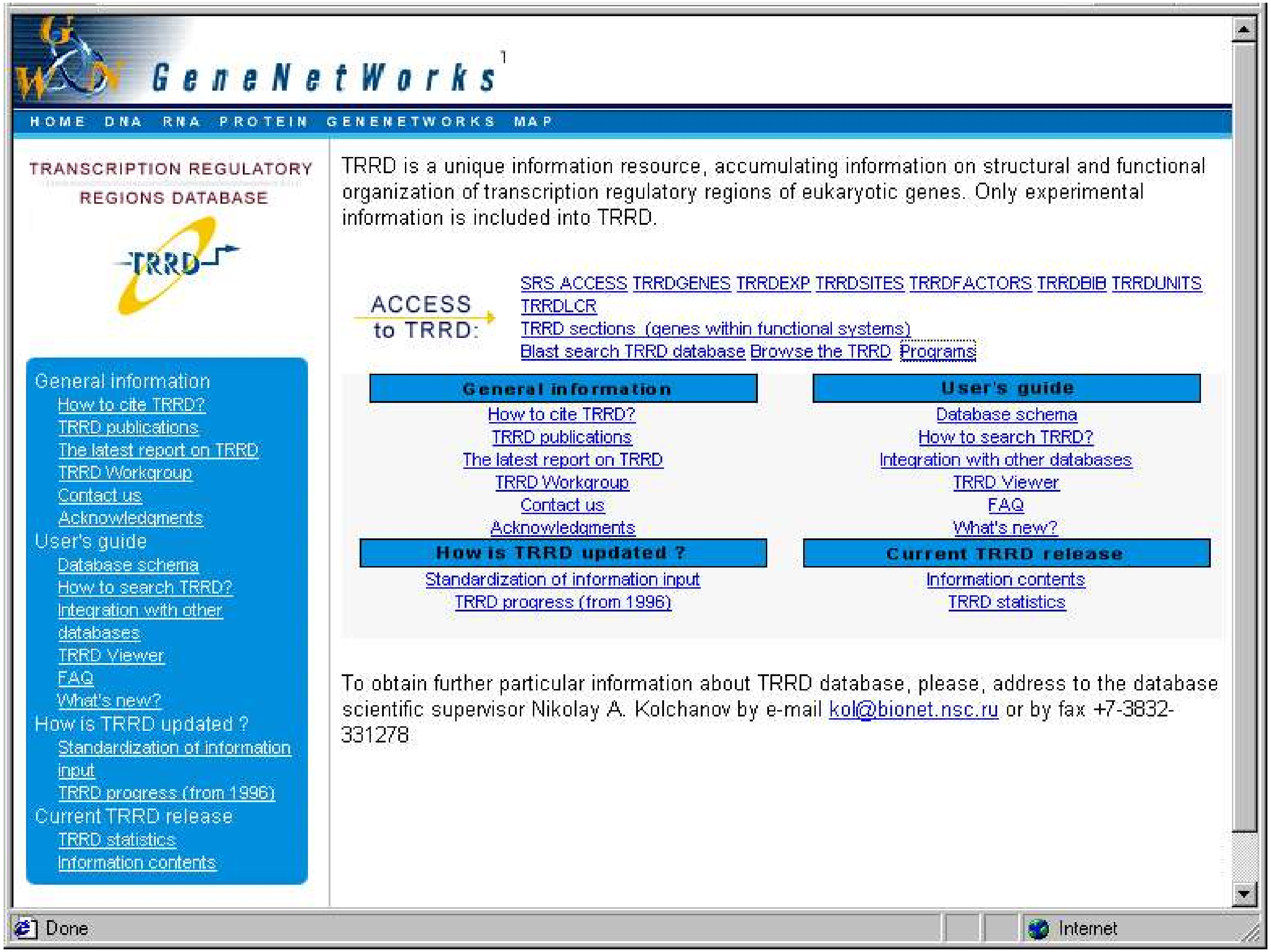
*To whom correspondence should be addressed. Tel: +7 3832 333468; Fax: +7 3832 331278; Email: kol@bionet.nsc.ru

Главная страница для входа в TRRD через интернет http://www.bionet.nsc.ru/trrd/



TRANSCRIPTION REGULATORY REGIONS DATABASE

TRRD

General information
- How to cite TRRD?
- TRRD publications
- The latest report on TRRD
- TRRD Workgroup
- Contact us
- Acknowledgments

User's guide
- Database schema
- How to search TRRD?
- Integration with other databases
- TRRD Viewer
- FAQ
- What's new?

How is TRRD updated ?
- Standardization of information input
- TRRD progress (from 1996)

Current TRRD release
- TRRD statistics
- Information contents

TRRD is a unique information resource, accumulating information on structural and functional organization of transcription regulatory regions of eukaryotic genes. Only experimental information is included into TRRD.

ACCESS to TRRD:
SRS ACCESS TRRDGENES TRRDEXP TRRDSITES TRRDFACTORS TRRDBIB TRRDUNITS TRRDLCR
TRRD sections (genes within functional systems)
Blast search TRRD database Browse the TRRD Programs

General information
How to cite TRRD?
TRRD publications
The latest report on TRRD
TRRD Workgroup
Contact us
Acknowledgments

User's guide
Database schema
How to search TRRD?
Integration with other databases
TRRD Viewer
FAQ
What's new?

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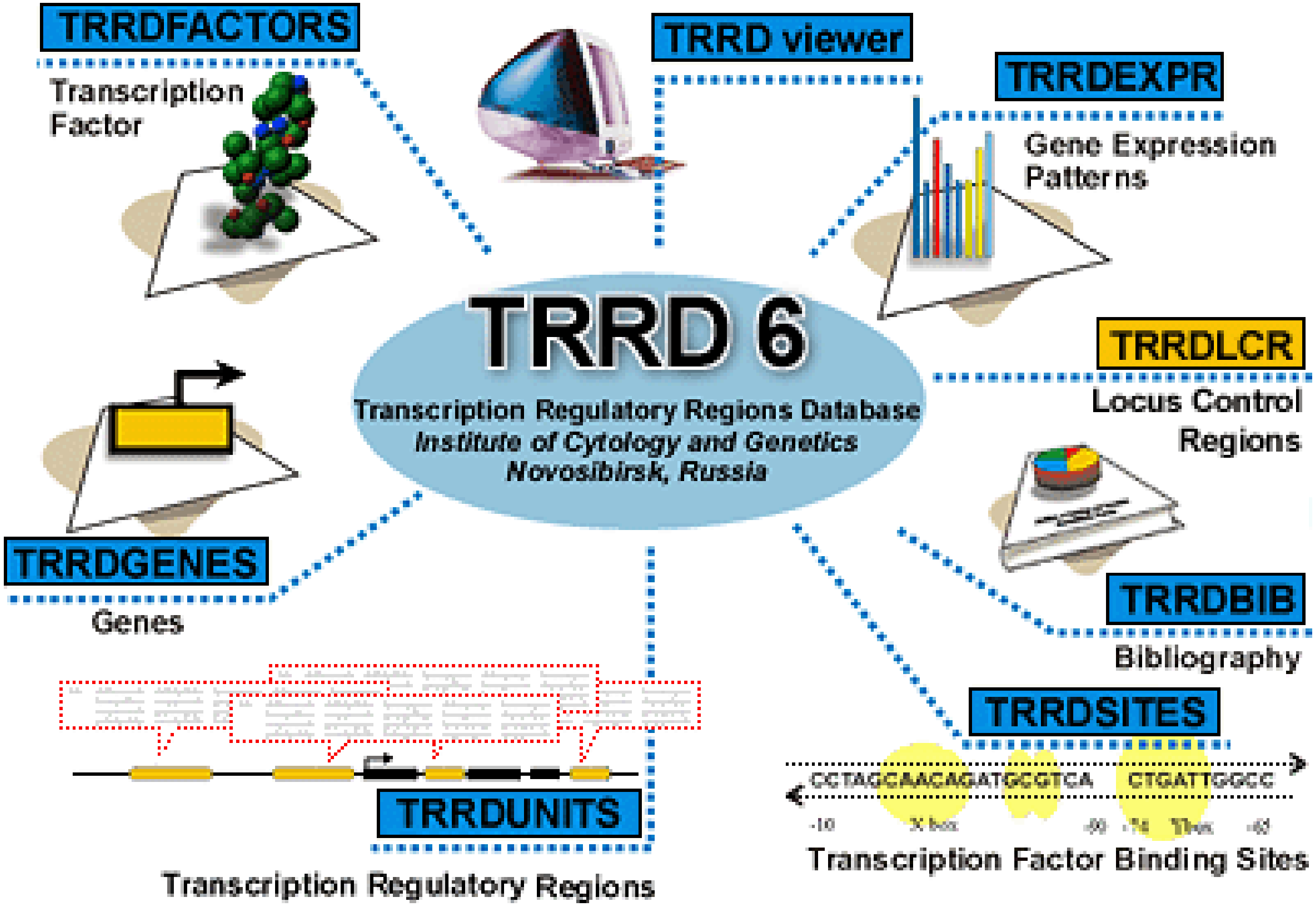
Standardization of information input
TRRD progress (from 1996)

Current TRRD release
Information contents
TRRD statistics

To obtain further particular information about TRRD database, please, address to the database scientific supervisor Nikolay A. Kolchanov by e-mail kol@bionet.nsc.ru or by fax +7-3832-331278

Вход В базы TRRD 6.0

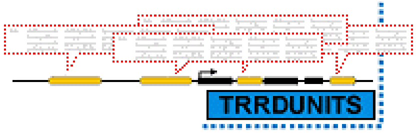


TRRD Включает данные о:

1) СТРУКТУРНО-ФУНКЦИОНАЛЬНОЙ ОРГАНИЗАЦИИ ТРАНСКРИПЦИОННЫХ РЕГУЛЯТОРНЫХ РАЙОНОВ. СТРУКТУРНЫЕ И ФУНКЦИОНАЛЬНЫЕ ХАРАКТЕРИСТИКИ:

САЙТОВ СВЯЗЫВАНИЯ ТРАНСКРИПЦИОННЫХ ФАКТОРОВ

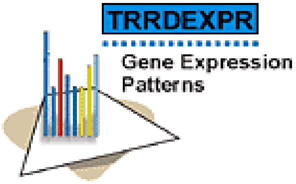
РЕГУЛЯТОРНЫХ РАЙОНОВ (ПРОМОТОРОВ, ЭНХАНСЕРОВ, САЙЛЕНСЕРОВ)



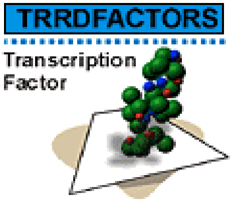
ЛОКУС-КОНТРОЛИРУЮЩИХ РАЙОНОВ

TRRDLCR

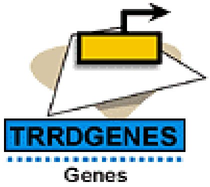
2) ДАННЫЕ О ПАТТЕРНАХ ЭКСПРЕССИИ ГЕНОВ



3) ДАННЫЕ О ТРАНСКРИПЦИОННЫХ ФАКТОРАХ

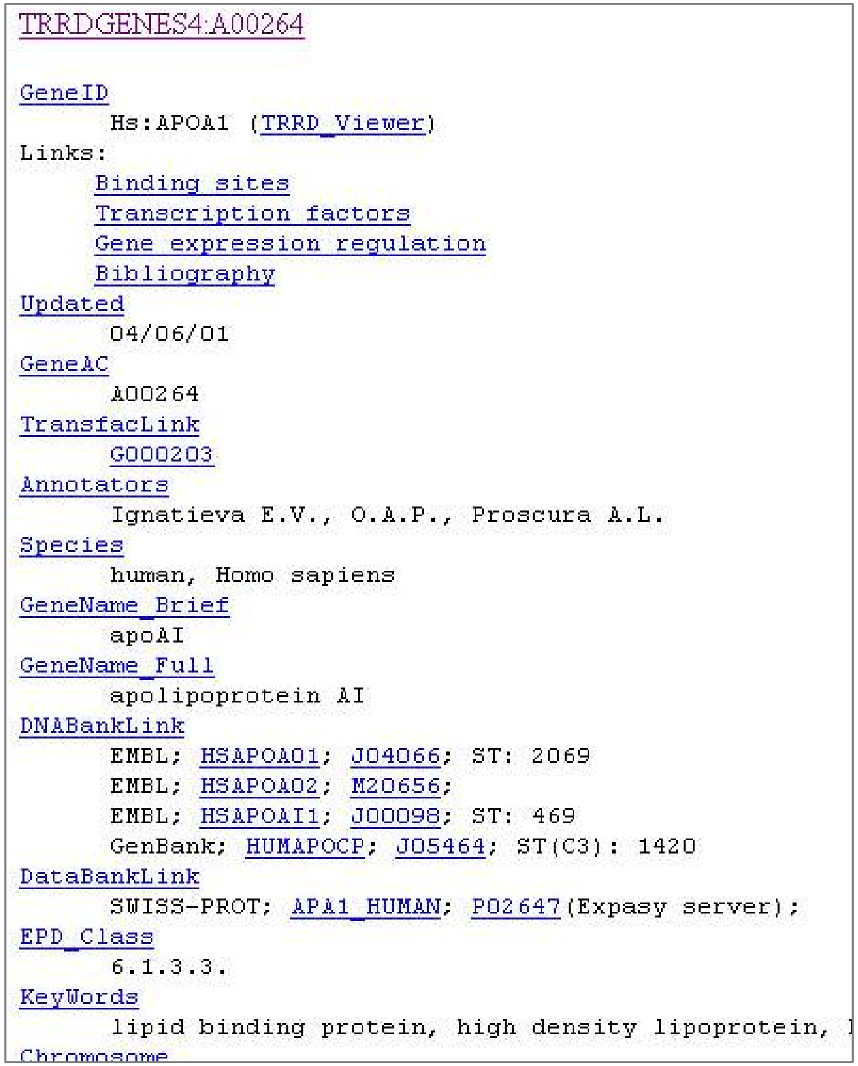


4) ОБЩУЮ ИНФОРМАЦИЮ О ГЕНАХ ВМЕСТЕ С ПЕРЕЧИСЛЕНИЕМ РЕГУЛЯТОРНЫХ ЭЛЕМЕНТОВ ВСЕХ УРОВНЕЙ



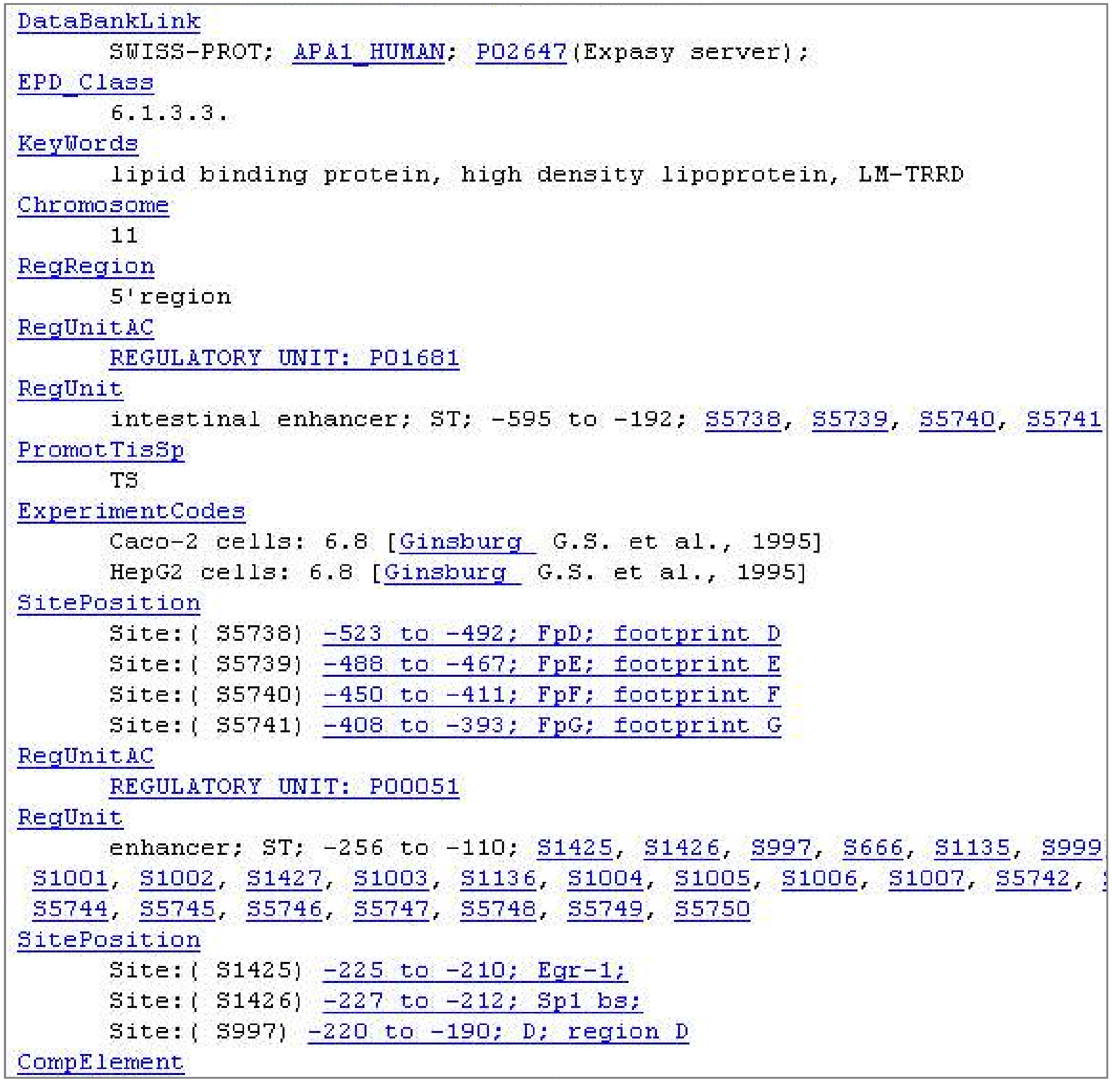
ОБЩЕЕ ОПИСАНИЕ ГЕНА

ID Hs:AAP
DT 09/02/00
AC A00596
CR Ignatieva E.V., Stepanenko I.L.
OS human, Homo sapiens
SN AAP
NG Alzheimer's disease amyloid A4 precursor protein
SY amyloid beta protein precursor gene
SY amyloid precursor protein gene
SY APP
BI EMBL;HSPADP;X12751; ST:3700
DR GDB; 119692; APP
DR SWISS-PROT; A4_HUMAN; P05067
KW heat shock-induced, TATA-less promoter, pathogenesis-related protein, multiple transcription initiation sites
CH 21
RG 5'region
AP REGULATORY UNIT: P01087
PR regulatory region; ST; -2260 to -1800; S3936, S3937
AP REGULATORY UNIT: P00760
PR promoter; ST;-160 to -1; S2907, S3931, S3932, S3933, S3934, S3935
//



TRRDGENES4:A00264

```
GeneID
       Hs:APOA1 (TRRD_Viewer)
Links:
      Binding sites
      Transcription factors
      Gene expression regulation
      Bibliography
Updated
       04/06/01
GeneAC
       A00264
TransfacLink
       G000203
Annotators
       Ignatieva E.V., O.A.P., Proscura A.L.
Species
       human, Homo sapiens
GeneName_Brief
       apoAI
GeneName_Full
       apolipoprotein AI
DNABankLink
       EMBL; HSAPOA01; J04066; ST: 2069
       EMBL; HSAPOA02; M20656;
       EMBL; HSAPOAI1; J00098; ST: 469
       GenBank; HUMAPOCP; J05464; ST(C3): 1420
DataBankLink
       SWISS-PROT; APA1_HUMAN; P02647(Expasy server);
EPD_Class
       6.1.3.3.
KeyWords
       lipid binding protein, high density lipoprotein,
Chromosome
```



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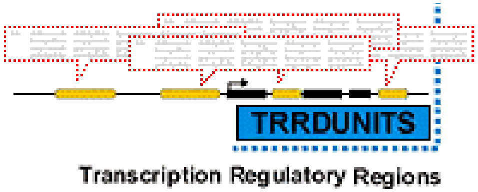
DataBankLink
       SWISS-PROT; APA1_HUMAN; P02647(Expasy server);
EPD_Class
       6.1.3.3.
KeyWords
       lipid binding protein, high density lipoprotein, LM-TRRD
Chromosome
       11
RegRegion
       5'region
RegUnitAC
       REGULATORY UNIT: P01681
RegUnit
       intestinal enhancer; ST; -595 to -192; S5738, S5739, S5740, S5741
PromotTisSp
       TS
ExperimentCodes
       Caco-2 cells: 6.8 [Ginsburg  G.S. et al., 1995]
       HepG2 cells: 6.8 [Ginsburg  G.S. et al., 1995]
SitePosition
       Site:( S5738) -523 to -492; FpD; footprint D
       Site:( S5739) -488 to -467; FpE; footprint E
       Site:( S5740) -450 to -411; FpF; footprint F
       Site:( S5741) -408 to -393; FpG; footprint G
RegUnitAC
       REGULATORY UNIT: P00051
RegUnit
       enhancer; ST; -256 to -110; S1425, S1426, S997, S666, S1135, S999
 S1001, S1002, S1427, S1003, S1136, S1004, S1005, S1006, S1007, S5742,
 S5744, S5745, S5746, S5747, S5748, S5749, S5750
SitePosition
       Site:( S1425) -225 to -210; Egr-1;
       Site:( S1426) -227 to -212; Sp1 bs;
       Site:( S997) -220 to -190; D; region D
CompElement
```

```
CompElement
        WH$C4_002; C00123; -213 to -147; S666, S1136
        [Harnish  D.C. et al., 1994]
SitePosition
        Site:( S5742) -220 to -190; D; region D
        Site:( S666) -220 to -188; HNF-4; HNF-4 binding site
        Site:( S1135) -220 to -192; PPRE; peroxisome proliferator-respons
        Site:( S999) -212 to -191; NF-BA1; NF-BA1 binding site
        Site:( S1000) -214 to -192; RARE; retinoic acid-responsive elemen
        Site:( S5743) -214 to -192; T3R/RXR bs; T3R/RXR alpha binding sit
        Site:( S1001) -214 to -192; ARP-1; ARP-1 binding site
        Site:( S1002) -210 to -189; S (1); site (1)
        Site:( S1427) -193 to -178; Egr-1 bs;
        Site:( S5744) -180 to -147 ; FpB; Footprint B
        Site:( S1003) -175 to -155; C (1); region C (1)
        Site:( S5745) -175 to -148; NFY bs;
        Site:( S1136) -174 to -151; HNF-3 beta; HNF-3 beta binding site
        Site:( S1004) -168 to -148; C (2) (B); region C (2)
        Site:( S1005) -174 to -144; S (2); site S (2)
        Site:( S5746) -149 to -130; ARE; antioxidant response element
        Site:( S5747) -142 to -118; FpC; Footprint C
        Site:( S1006) -134 to -119; C; site C
        Site:( S5748) -134 to -119; T3R/RXR bs; T3R beta / RXR alpha bind
        Site:( S5749) -134 to -119; ARP1 bs; ARP 1 binding site
        Site:( S5750) -134 to -119; HNF-4 bs; HNF-4 binding site
        Site:( S1007) -133 to -110; S (3); site (3)
RegUnitAC
        REGULATORY UNIT: P00052
RegUnit
        promoter; ST; -128 to +17; S1008, S1137, S1010, S1011, S5751
PromotTisSp
        0
SitePosition
        Site:( S1008) -128 to -77; F (1); footprint (1)
        Site:( S1137) -93 to -63; bs;
```

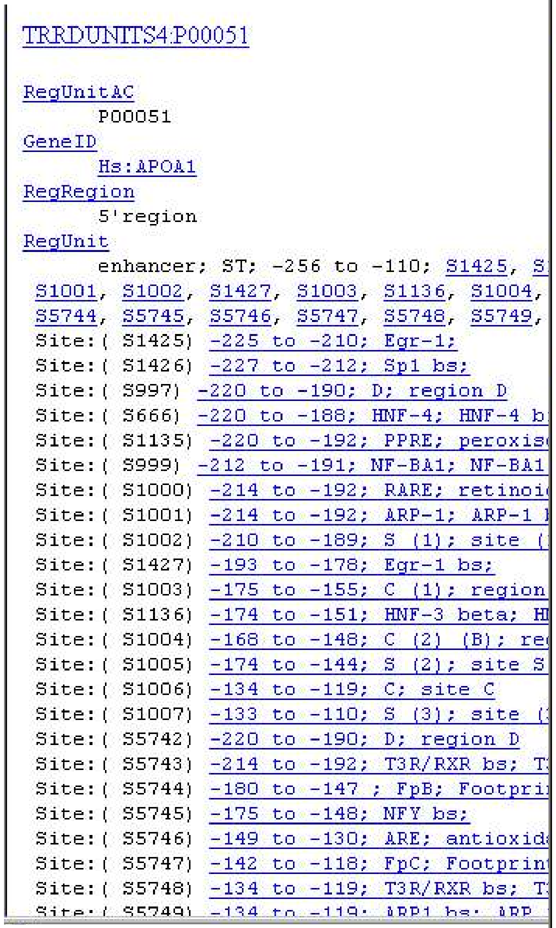
```
RegUnit
        promoter; ST; -128 to +17; S1008, S1137, S1010, S1011, S5751
PromotTisSp
        0
SitePosition
        Site:( S1008) -128 to -77; F (1); footprint (1)
        Site:( S1137) -93 to -63; bs;
        Site:( S5751) -77 to -45; DRE; drug responsive element
        Site:( S1010) -35 to -20; TATA box;
        Site:( S1011) -22 to +17; F (2); footprint (2)
RegRegion
        3'region
RegUnitAC
        REGULATORY UNIT: P00689
RegUnit
        small intestinal enhancer; ST(C3); 520 to 780; S1009, S998
ExperimentCodes
        human CaCo-2 cells: 6.1.1 [Bisaha  J.G. et al., 1995]
Comments
        The small intestinal enhancer is positioned 9 kilobases 3' to the
        between nucleotides -780 to -520 of the convergently transcribed
        gene [Bisaha  J.G. et al., 1995].
SitePosition
        Site:( S1009) 680 to 700; FII; footprint II
        Site:( S998) 725 to 745; HNF-4 bs; HNF-4 binding site
Alignment
        Rat and rabbit apo A-1 promoter regions are greater than 80%
        similar to the human apo A-1 promoter sequence between -240
        and -20. [Reisher  S.R. et al., 1993]
StartPoints
        ST; ~9000; ST(C3)
Comments
        rAIC1 and rAIC3 have overlapping binding sites on the apo A-I -16
        -148 region [Papazafiri  P. et al., 1991]
        The protein bound to site (3) is also bound to site (1)
```

TRRDUNITS

ОПИСАНИЕ ТРАНСКРИПЦИОННЫХ РЕГУЛЯТОРНЫХ ЕДИНИЦ (ПРОМОТОРОВ, ЭНХАНСЕРОВ, САЙЛЕНСЕРОВ)



RegUnitAC	P00562
GeneID	Rn:D2
RegRegion	5'region
RegUnit	Promoter; ST; -150 to +1; S79, S80
DNA_BankLink	EMBL; RND2RPR; X77137; 704 to 855
LeftTrunc	0
RightTrunc	0
SeqLength	152
Sequence	cccaggcccc acagtgcaga gatagttctg gggccctggg tgggtggggc ctctgtacaa ggggcggggt tcccgggcgc ctcgtggcca gggtgacccc gccccctcct cctgcgcagc gctctgattc cgcggagctg tccagcctca gt
PromotTisSp	0
PromotInd	1
ExperimentCodes	6.1.1, 6.8 [Minowa T. et al., 1992]



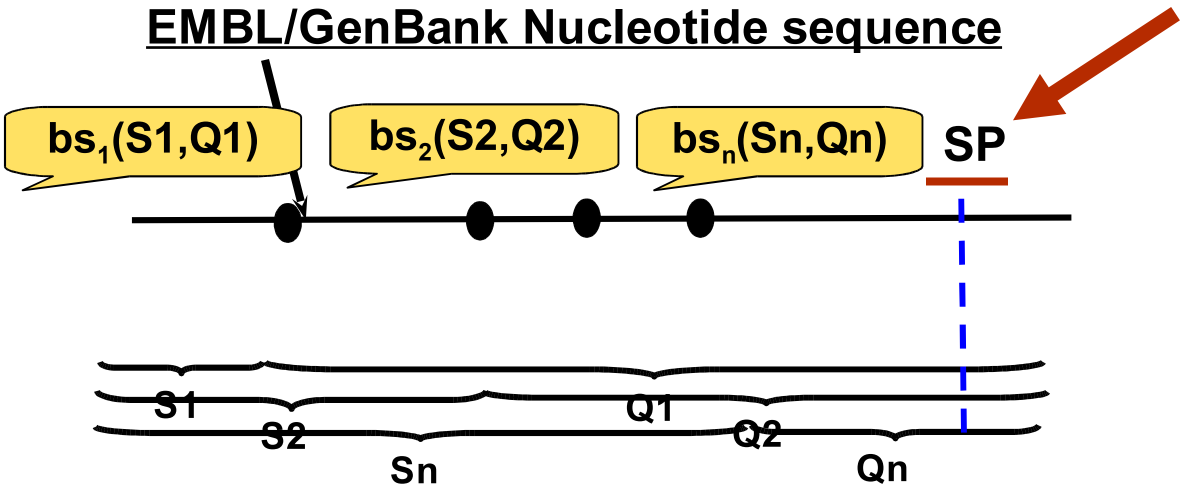
```
TRRDUNITS4:P00051

RegUnitAC
       P00051
GeneID
       Hs:APOA1
RegRegion
       5'region
RegUnit
       enhancer; ST; -256 to -110; S1425, S
 S1001, S1002, S1427, S1003, S1136, S1004,
 S5744, S5745, S5746, S5747, S5748, S5749,
 Site:( S1425) -225 to -210; Egr-1;
 Site:( S1426) -227 to -212; Sp1 bs;
 Site:( S997) -220 to -190; D; region D
 Site:( S666) -220 to -188; HNF-4; HNF-4 b
 Site:( S1135) -220 to -192; PPRE; peroxis
 Site:( S999) -212 to -191; NF-BA1; NF-BA1
 Site:( S1000) -214 to -192; RARE; retinoi
 Site:( S1001) -214 to -192; ARP-1; ARP-1
 Site:( S1002) -210 to -189; S (1); site (
 Site:( S1427) -193 to -178; Egr-1 bs;
 Site:( S1003) -175 to -155; C (1); region
 Site:( S1136) -174 to -151; HNF-3 beta; H
 Site:( S1004) -168 to -148; C (2) (B); re
 Site:( S1005) -174 to -144; S (2); site S
 Site:( S1006) -134 to -119; C; site C
 Site:( S1007) -133 to -110; S (3); site (
 Site:( S5742) -220 to -190; D; region D
 Site:( S5743) -214 to -192; T3R/RXR bs; T
 Site:( S5744) -180 to -147 ; FpB; Footpri
 Site:( S5745) -175 to -148; NFY bs;
 Site:( S5746) -149 to -130; ARE; antioxid
 Site:( S5747) -142 to -118; FpC; Footprin
 Site:( S5748) -134 to -119; T3R/RXR bs; T
 Site:( S5749) -134 to -119; ARP1 bs; ARP
```

```
 Site:( S5750) -134 to -119; HNF-4 bs; HNF-4 binding site
DNA_BankLink
       EMBL; HSAPOA01; J04066; 1813 to 1959
LeftTrunc
       0
RightTrunc
       0
SeqLength
       147
Sequence
       ccacccggga gacctgcaag cctgcagcac tcccctcccg cccccactga
       acccttgacc cctgccctgc agcccccgca gcttgctgtt tgcccactct
       atttgcccag ccccagggac agagctgatc cttgaactct taagttc
DNA_BankLink
       EMBL; HSAPOA01; J04066; 1813 to 1959
LeftTrunc
       0
RightTrunc
       0
SeqLength
       147
Sequence
       ccacccggga gacctgcaag cctgcagcac tcccctcccg cccccactga
       acccttgacc cctgccctgc agcccccgca gcttgctgtt tgcccactct
       atttgcccag ccccagggac agagctgatc cttgaactct taagttc
DNA_BankLink
       EMBL; HSAPOAI1; J00098; 215 to 361
LeftTrunc
       0
RightTrunc
       0
SeqLength
       147
Sequence
       cccgggagac ctgcaagcct gcagcactcc cctcccgccc ccactgaacc
       cttgacccct gccctgcacg ccccgcagct tgctgtttgc ccactcctat
       ttgcccagtc ccagggacag agctgatcct tgaactctta agttcca
```

Экстракция последовательностей днк регуляторных единиц, описанных в TRRD из входов баз EMBL/GENBANK

<u>ЭТАП 1:</u> определение позиции точки отсчета в карточке из EMBL/GenBank



EMBL/GenBank Nucleotide sequence

<u>ЭТАП 2:</u> локализация и экстракция нуклеотидной последовательности регуляторной единицы

<u>EMBL/GenBank</u> :

SQ

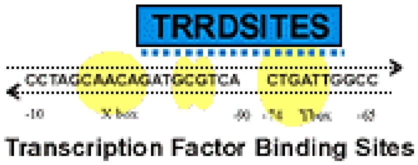
```
aagcttatcgatgataagcggtca
aacatgagaattcgcgataggggat
cacctcgatccagccttatctagg
cccctccccctgtcaaacacccctt
gtcctttgttaccagaacaggcca
cctttgcacctgctgttccctcct
ccaagggggtgggggttatccttc
cagagagttcctgcctacttcagg
aaatagctaaaccctctcccatgg
cctgtttcagtcggccgcagtggg
ggtacatatttgaccctcactcag
gagactggaaatcaga
```

<u>TRRDUNITS</u> :

“Sequence”

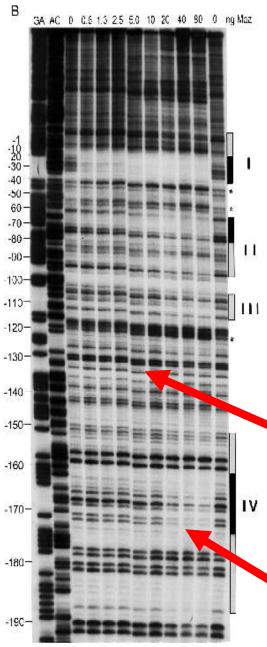
```
ggtcaaacatgagaattcgc
gatagggatcacctcgatcc
agccttatctaggcccctcc
ccctgtcaaacacccttgtc
ctttgttaccagaacaggcc
acctttgcacctgctgttcc
ctcctccaagggggtggggg
ttatc
```

TRRDSITES

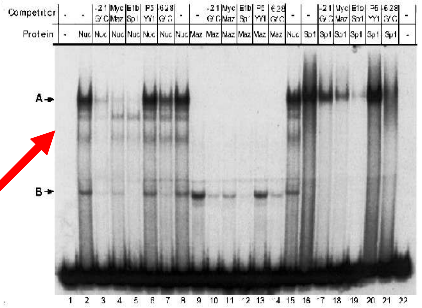


ОПИСАНИЕ САЙТА СВЯЗЫВАНИЯ ТРАНСКРИПЦИОННОГО ФАКТОРА

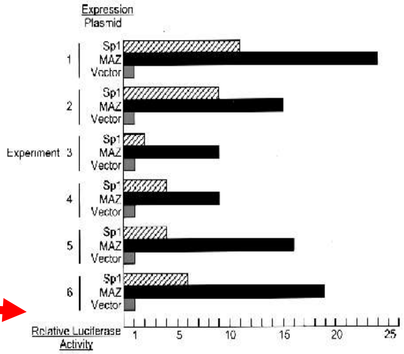
AN S1160
ID Gene: Hs:APOB
AP REGULATORY UNIT: P00670
NM HNF-4 bs; HNF-4 binding site
NY AF-1 binding site
NY BA1 binding site
NS R01612
TF HNF-4; hepatic nuclear factor 4
AT increase
SQ cccgggaggCGCCCTTTGGACCTtttg
PQ -88 to -62
PF -82 to -62
BF EMBL: M15053 : 68
AG 1.1.5, 3.5 [Metzger S. et al., 1993]
AG rat liver cells: 3.6 [Metzger S. et al., 1993]
AG human HepG2 cells: 6.2 [Metzger S. et al., 1993]
AG HeLa cells: 6.2, 6.6 [Metzger S. et al., 1993]
AG 1.1.5, 3.3, 3.5, 4.2 [Ladias J.A. et al., 1992]
//



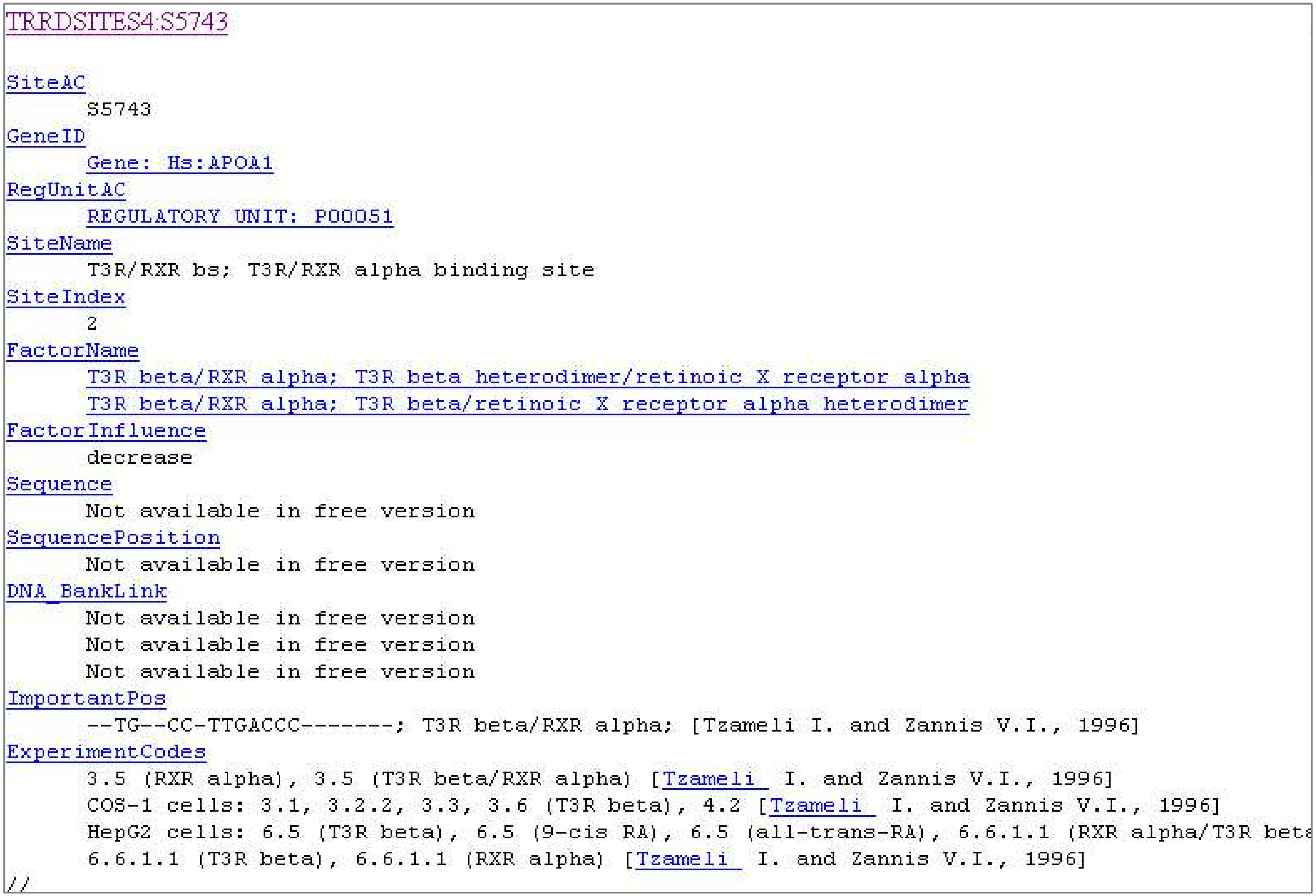
DNASE I FOOTPRINTING



GEL-MOBILITY SHIFT ASSAY



TRANSIENT EXPRESSION ANALYSIS



```
TRRDSITES4:S5743

SiteAC
       S5743
GeneID
       Gene: Hs:APOA1
RegUnitAC
       REGULATORY UNIT: P00051
SiteName
       T3R/RXR bs; T3R/RXR alpha binding site
SiteIndex
       2
FactorName
       T3R beta/RXR alpha; T3R beta heterodimer/retinoic X receptor alpha
       T3R beta/RXR alpha; T3R beta/retinoic X receptor alpha heterodimer
FactorInfluence
       decrease
Sequence
       Not available in free version
SequencePosition
       Not available in free version
DNA_BankLink
       Not available in free version
       Not available in free version
       Not available in free version
ImportantPos
       --TG--CC-TTGACCC-------; T3R beta/RXR alpha; [Tzameli I. and Zannis V.I., 1996]
ExperimentCodes
       3.5 (RXR alpha), 3.5 (T3R beta/RXR alpha) [Tzameli  I. and Zannis V.I., 1996]
       COS-1 cells: 3.1, 3.2.2, 3.3, 3.6 (T3R beta), 4.2 [Tzameli  I. and Zannis V.I., 1996]
       HepG2 cells: 6.5 (T3R beta), 6.5 (9-cis RA), 6.5 (all-trans-RA), 6.6.1.1 (RXR alpha/T3R bet
       6.6.1.1 (T3R beta), 6.6.1.1 (RXR alpha) [Tzameli  I. and Zannis V.I., 1996]
//
```

THE TABLE TRRDSITES: THREE NEW FIELDS

TRRDSITES4:S5743

SiteAC

S5743

GeneID

Gene: Hs:APOA1

RegUnitAC

REGULATORY UNIT: P00051

SiteName

T3R/RXR bs; T3R/RXR alpha binding site

SiteIndex

2

FactorName

T3R beta/RXR alpha;

FactorInfluence

decrease

Sequence

ACTGAACCCTTGACCCCTGCCCT

SequencePosition

-214 to -192

DNA_BankLink

J04066:1858, M20656:2264, J00098:257

ImportantPos

--TG--CC-TTGACCC--------; T3R beta/RXR alpha; [Tzameli I. and Zannis V.I., 1996]

SeqContradiction

ACTGAACCCTTGACCCCTGCAAA

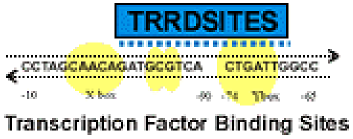
PosContradiction

-218 to -196

ExperimentCodes

3.5 (RXR alpha), 3.5 (T3R beta/RXR alpha) [Tzameli I. and Zannis V.I., 1996]

COS-1 cells: 3.1, 3.2.2, 3.3, 3.6 (T3R beta), 4.2 [Tzameli I. and Zannis V.I., 1996]



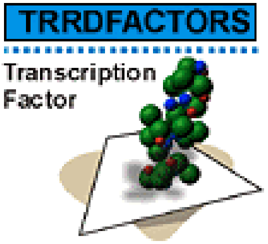
1. ВАЖНЫЕ ПОЗИЦИИ

- METHYLATION INTERFERENCE ASSAY
- ELECTROPHORETIC MOBILITY SHIFT ASSAY PERFORMED WITH WILD TYPE AND MUTANT PROBES OR COMPETITORS
- EFFECT OF MUTATIONS IN BINDING SITES ON GENE PROMOTER ACTIVITY IN THE TRANSIENT TRANSFECTION ASSAY

2. Противоречия по последовательности

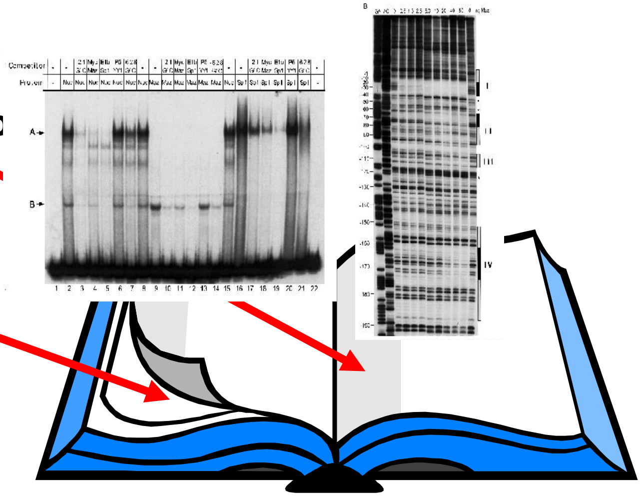
3. Противоречия по позициям

TRRDFACTORS



ОПИСАНИЕ ТРАНСКРИПЦИОННОГО ФАКТОРА

ID Hs:APOA1
AN Site: S1135
TF PPARgamma/RXRalpha; PPARgamma and retinoic X receptor alpha heterodimer
FS PPARgamma; peroxisome proliferator-activated receptor gamma
TS human
TO in vitro synthesized
TR [Vu-Dac N. et al., 1994]
FS RXRalpha; retinoic X recep
TS mouse
NF TRANSFAC link: T01331
TO in vitro synthesized
TR [Vu-Dac N. et al., 1994]
//



☐ TRRDFACTORS4:F5743.1

```
Identifier
      F5743.1
GeneID
      Hs:APOA1
SiteAC
      Site: S5743
FactorName
      T3R beta/RXR alpha; T3R beta heterodimer/retinoic X receptor alpha
FactorSubunitName
      T3R beta;
FactorSource
      recombinant
Cells
      COS-1
Reference
      [Tzameli  I. and Zannis V.I., 1996]
FactorSubunitName
      RXR alpha; retinoic X receptor alpha
FactorSource
      recombinant
Cells
      COS-1
Reference
      [Tzameli  I. and Zannis V.I., 1996]
//
```

☐ TRRDFACTORS4:F5743.2

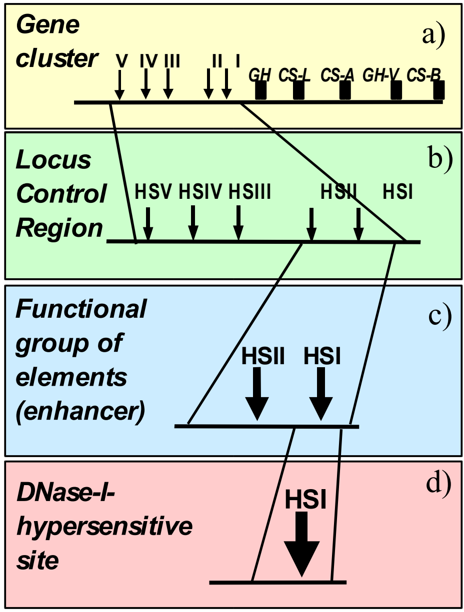
```
Identifier
      F5743.2
GeneID
      Hs:APOA1
```

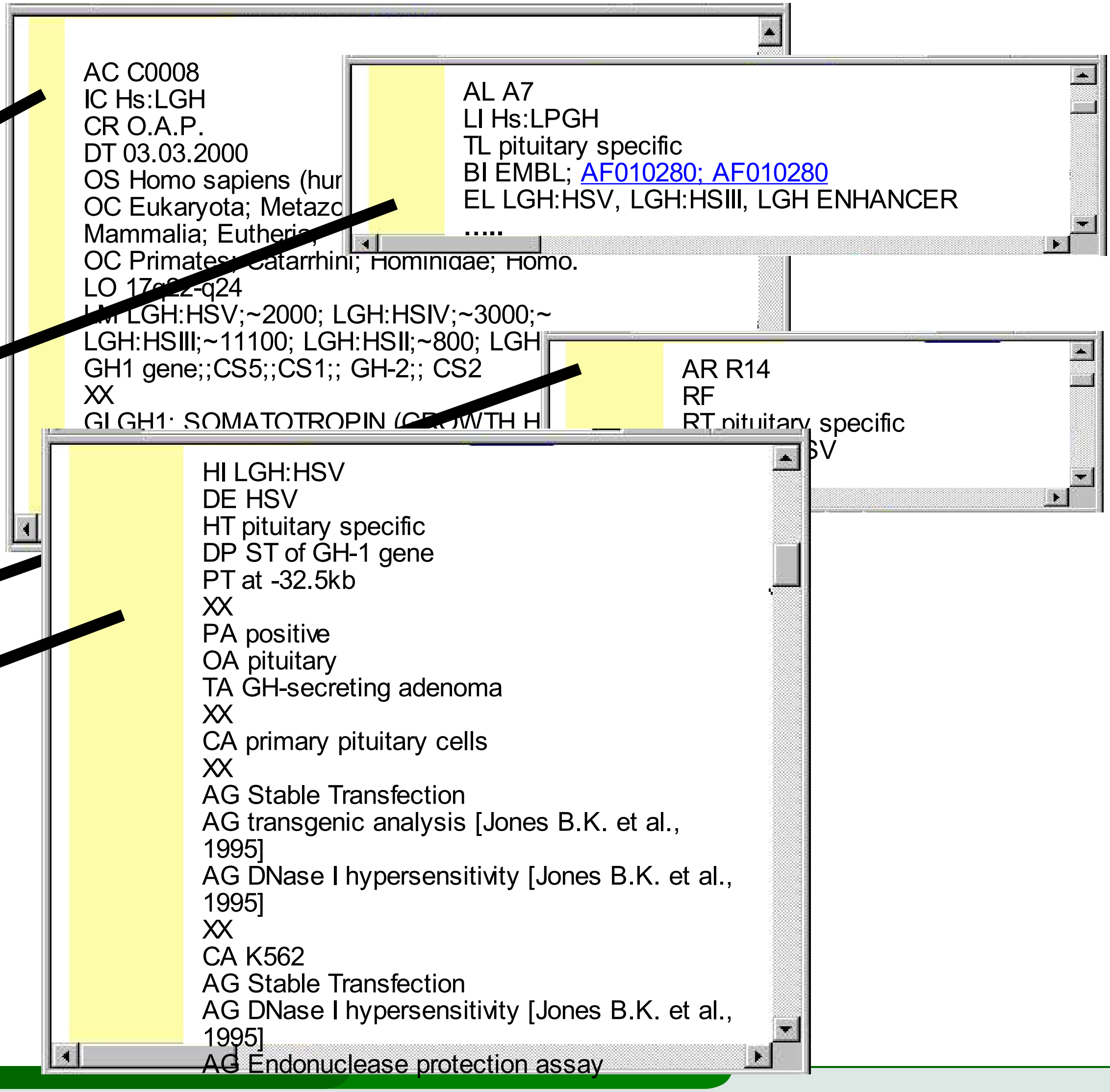
TRRDLCR

ОПИСАНИЕ ЛОКУС-КОНТРОЛИРУЮЩЕГО РАЙОНА

```
AC C0002
IC Hs:ADA
CR O.A.P.
DT 15.02.2000
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
OC Primates; Catarrhini; Hominidae; Homo.
LO 20
LM ST; ;Exon1;;LADA:HSSII;; LADA:HSSIII;; LADA:EFS;; LADA:Exon2
XX
GI ADA; adenosine deaminase
DR TRRD;; A00862
DR SWISS-PROT; ADA_HUMAN; P00813(Expasy server)
XX
AL L1
LI Hs:LADA
TL thymus-specific
EL LADA:HSSII; LADA:HSSIII; LADA:EFS
BI EMBL; HSADAG; M13792
.......
//
```

TRRDLCR: Иерархическое описание





```
AC C0008
IC Hs:LGH
CR O.A.P.
DT 03.03.2000
OS Homo sapiens (hur
OC Eukaryota; Metazo
Mammalia; Eutheria;
OC Primates; Catarrhini; Hominidae; Homo.
LO 17q22-q24
LM LGH:HSV;~2000; LGH:HSIV;~3000;~
LGH:HSIII;~11100; LGH:HSII;~800; LGH
GH1 gene;;CS5;;CS1;; GH-2;; CS2
XX
GI GH1: SOMATOTROPIN (GROWTH H
```

```
AL A7
LI Hs:LPGH
TL pituitary specific
BI EMBL; AF010280; AF010280
EL LGH:HSV, LGH:HSIII, LGH ENHANCER
.....
```

```
AR R14
RF
RT pituitary specific
SV
```

```
HI LGH:HSV
DE HSV
HT pituitary specific
DP ST of GH-1 gene
PT at -32.5kb
XX
PA positive
OA pituitary
TA GH-secreting adenoma
XX
CA primary pituitary cells
XX
AG Stable Transfection
AG transgenic analysis [Jones B.K. et al.,
1995]
AG DNase I hypersensitivity [Jones B.K. et al.,
1995]
XX
CA K562
AG Stable Transfection
AG DNase I hypersensitivity [Jones B.K. et al.,
1995]
AG Endonuclease protection assay
```

*TCR*α/δ (мышь)

L0009

HS1 - энхансер

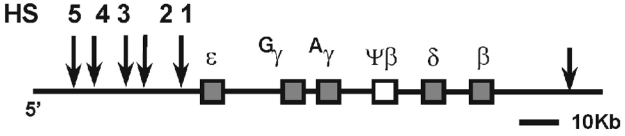
HS1, HS1` район определяющий распространенность в тканях

HS2 - HS6 район открывающий хроматин

Цифрами обозначены экзоны гена *Dad1*

Кластер β глобиновых генов (человек)

L0014

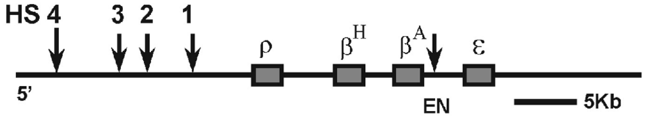


HS5 - инсулятор

HS4 - HS1 - энхансер

Кластер β глобиновых генов (цыпленок)

L0005



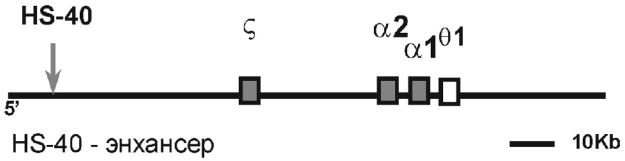
HS4 - инсулятор

HS3, HS2 - энхансер

EN - межгенный энхансер

Кластер а -глобиновых генов (человек)

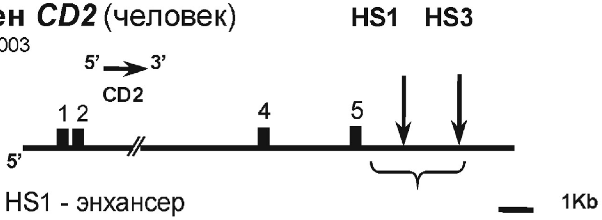
L0006



HS-40 - энхансер

Ген *CD2* (человек)

L0003



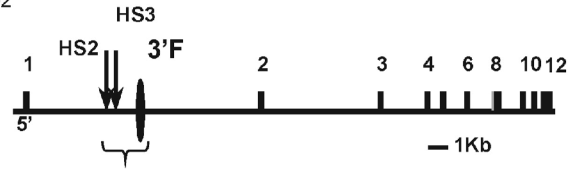
HS1 - энхансер

HS3 - инсулятор

Цифрами обозначены экзоны гена *CD2*

Ген *ADA* (человек)

L0002



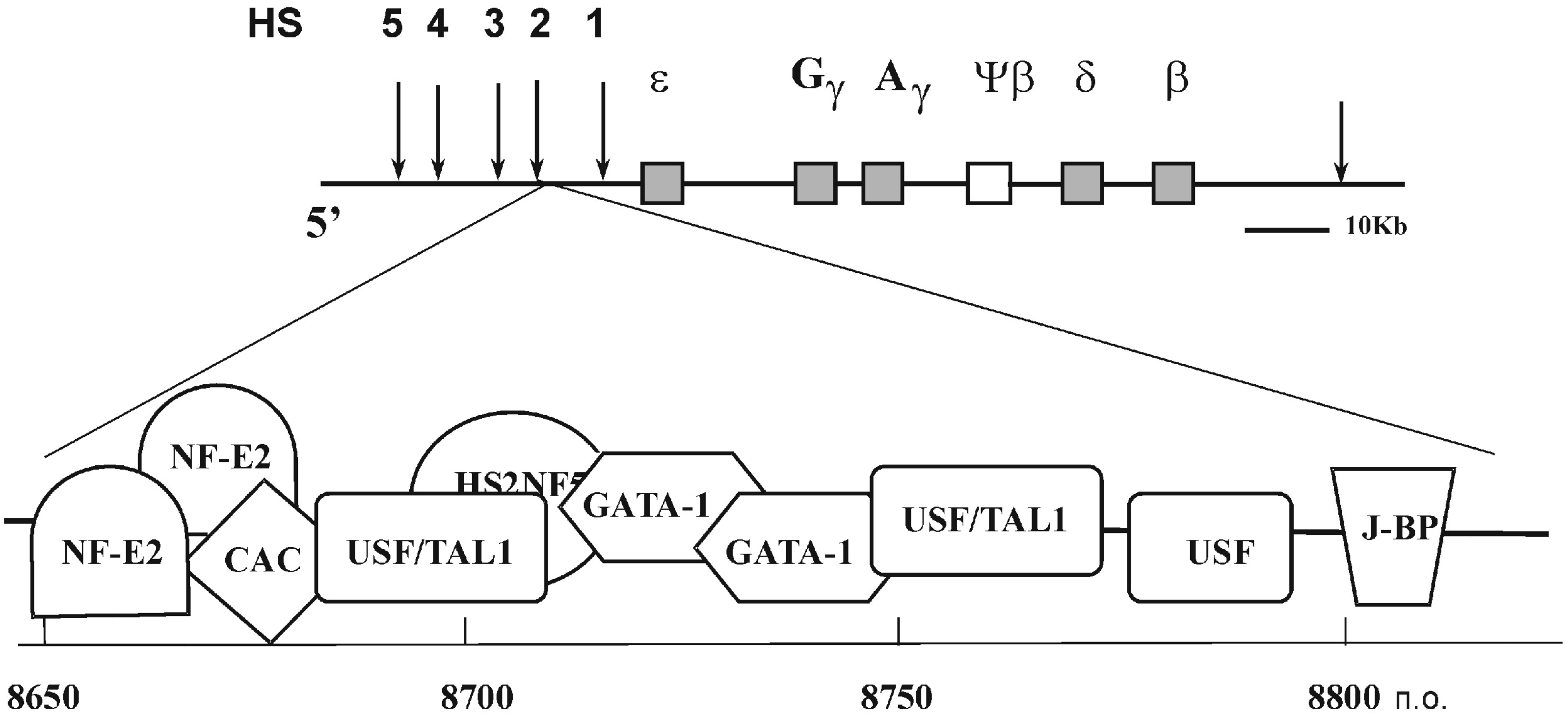
HS2 - 5'вспомогательный элемент

HS3 - энхансер;

3'F - 3'вспомогательный элемент

Цифрами обозначены экзоны гена *ADA*

LCR глобинового локуса человека

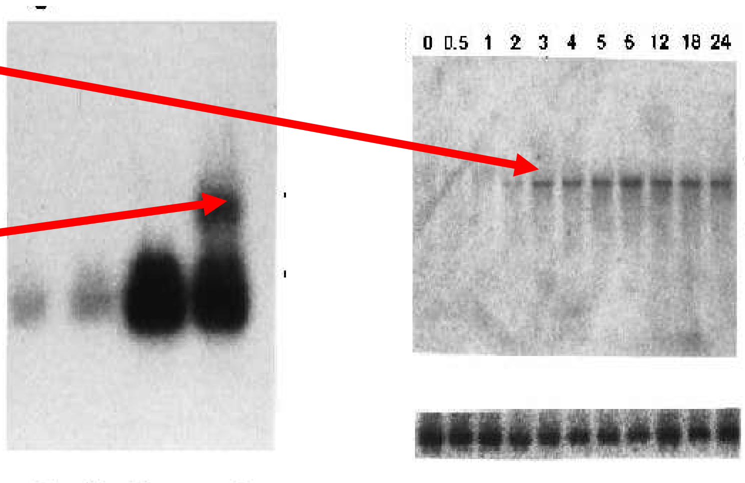


ОСОБЕННОСТИ ЭКСПРЕССИИ ГЕНОВ

TRRDEXPR
Gene Expression Patterns

RE A00596.002
ID Hs:AAP
RT mRNA
RN lymphoblastoid cells
RL present
RI heat shock
FF induction
RH 3 h
RR [Abe K. et al., 1991]

RE A00596.001
ID Hs:AAP
RT mRNA
RN astrocytes
RL present
RR [Amara F.M., et al., 1999]



RNA BLOT ANALYSIS

TRRDBIB

NN 2027
ID [Hs:AAP]
AU Trejo J., Massamiri T., Deng T., Dewji N.N., Bayney R.M., Brown J.H.
TI A direct role for protein kinase C and the transcription factor Jun/AP-1
TI in the regulation of the Alzheimer's beta-amyloid precursor protein gene.
SO J.Biol.Chem.
VL 269
IS 34
YR 1994
PG 21682-21690
ML MEDLINE:[94342362], [See Related Articles]
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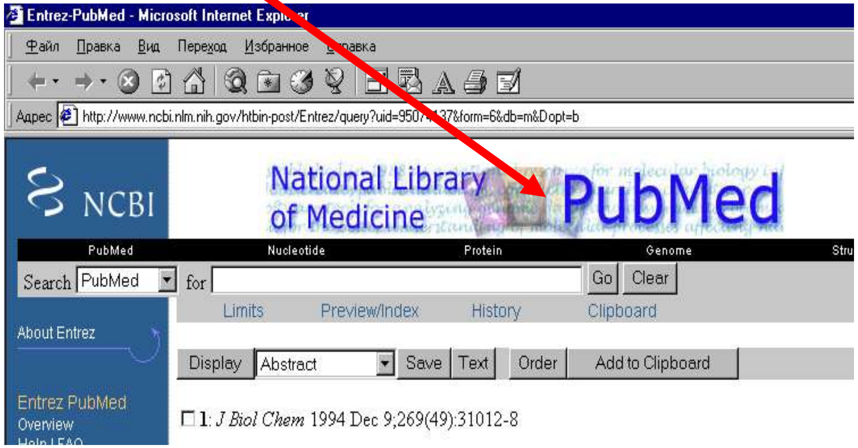
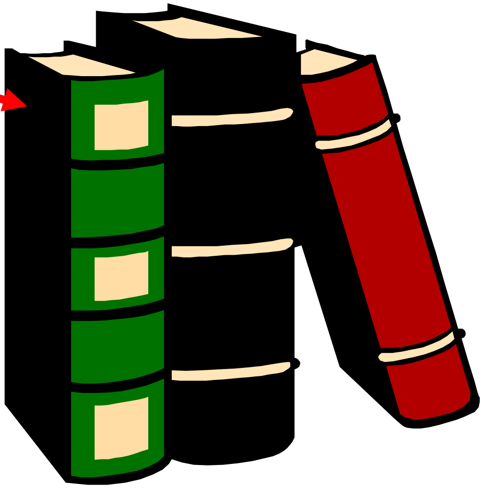
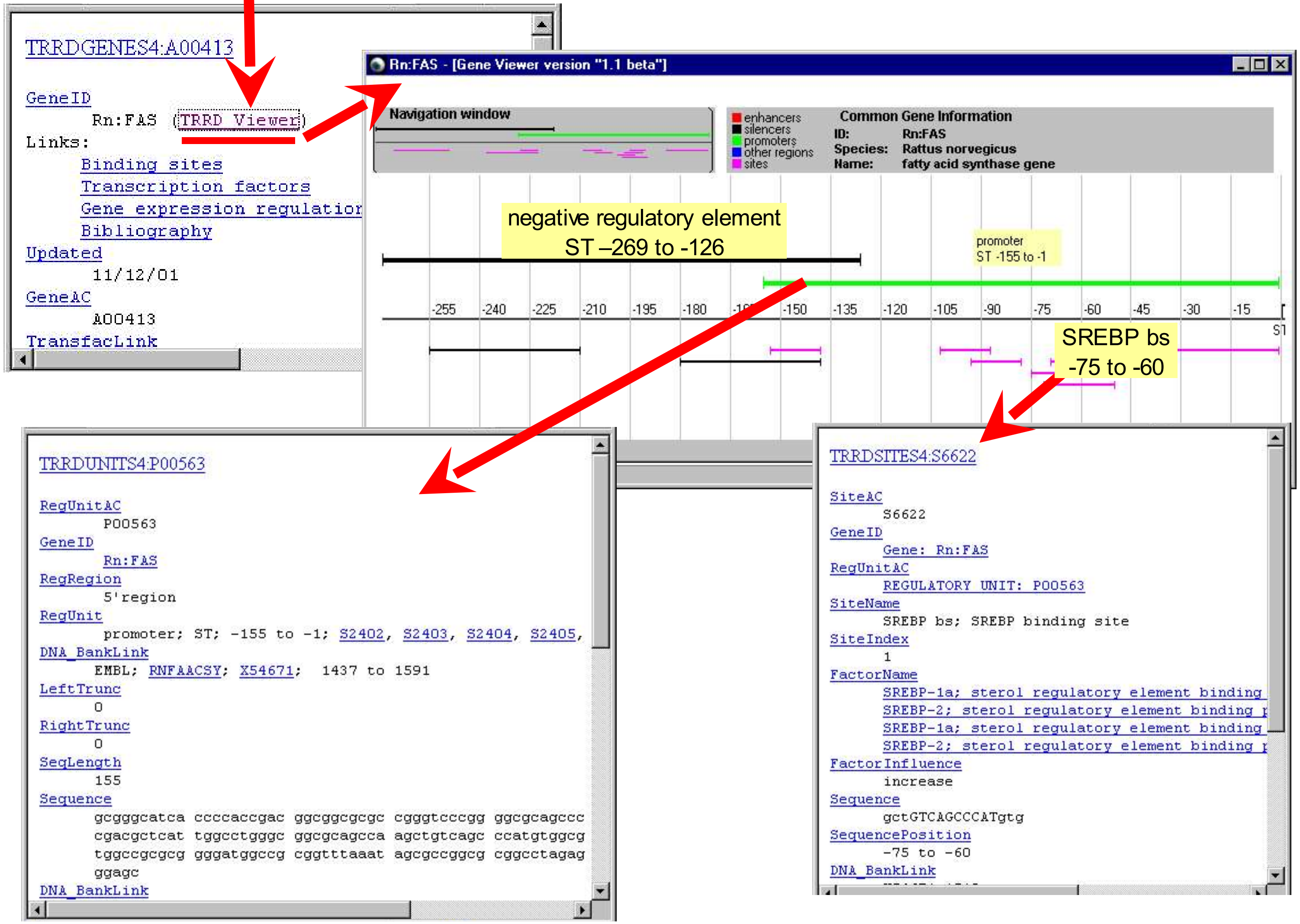


http://www.ncbi.nlm.nih.gov/htbin-post/Entrez/query?uid=9507[illegible]37&form=6&db=m&Dopt=b

☐ 1: *J Biol Chem* 1994 Dec 9;269(49):31012-8



Визуализация информации в виде карт регуляторных районов генов



[TRRDGENES4:A00413](#)

GeneID
Rn:FAS (TRRD Viewer)
Links:
Binding sites
Transcription factors
Gene expression regulatior
Bibliography
Updated
11/12/01
GeneAC
A00413
TransfacLink

Rn:FAS - [Gene Viewer version "1.1 beta"]

Common Gene Information
ID: Rn:FAS
Species: Rattus norvegicus
Name: fatty acid synthase gene

negative regulatory element
ST –269 to -126

promoter
ST -155 to -1

SREBP bs
-75 to -60

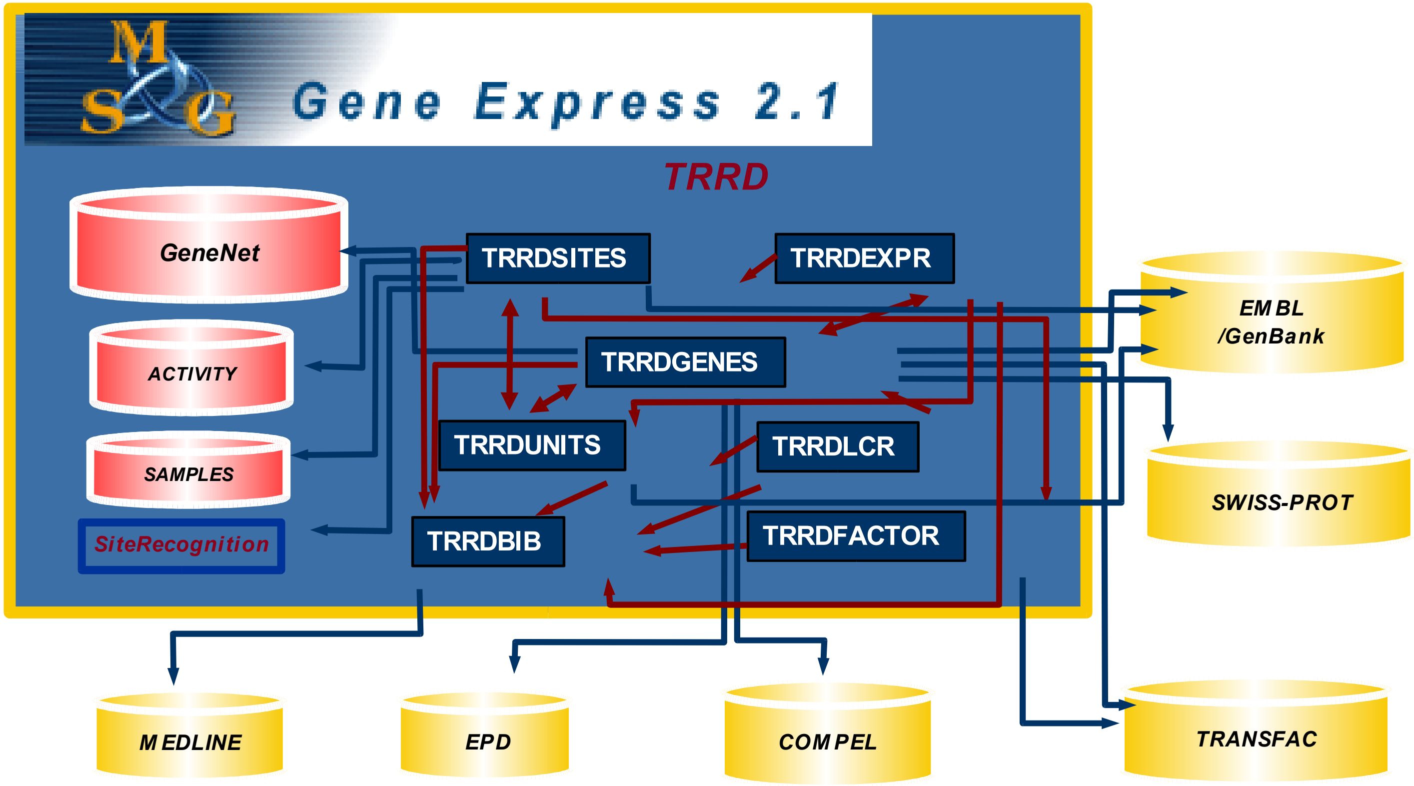
[TRRDUNITS4:P00563](#)

RegUnitAC
P00563
GeneID
Rn:FAS
RegRegion
5'region
RegUnit
promoter; ST; -155 to -1; S2402, S2403, S2404, S2405,
DNA_BankLink
EMBL; RNFAACSY; X54671; 1437 to 1591
LeftTrunc
0
RightTrunc
0
SeqLength
155
Sequence
gcgggcatca ccccaccgac ggcggcgcgc cggtcccgg ggcgcagccc
cgacgctcat tggcctgggc ggcgcagcca agctgtcagc ccatgtggcg
tggccgcgcg gggatggccg cggtttaaat agcgccggcg cggcctagag
ggagc
DNA_BankLink

[TRRDSITES4:S6622](#)

SiteAC
S6622
GeneID
Gene: Rn:FAS
RegUnitAC
REGULATORY UNIT: P00563
SiteName
SREBP bs; SREBP binding site
SiteIndex
1
FactorName
SREBP-1a; sterol regulatory element binding
SREBP-2; sterol regulatory element binding p
SREBP-1a; sterol regulatory element binding
SREBP-2; sterol regulatory element binding p
FactorInfluence
increase
Sequence
gctGTCAGCCCATgtg
SequencePosition
-75 to -60
DNA_BankLink

TRRD – один из информационных модулей системы GENEEXPRESS-2



Гиперссылки на базы данных и программные модули системы GENEEXPRESS из БАЗЫ TRRDSITES

```
AN S161
ID Gene: Hs:PAI1
AP REGULATORY UNIT:
NM USF bs;
WW http://wwwmgs.bionet.nsc.ru/Programs/acts2/AFF_USF.htm
DR ACTIVITY ; A00DF026;
DR SAMPLES; USF;
TF USF; upstream sequence fac
AT increase
SQ gaca tcacgtggct
PQ -574 to -559
PF -57  to -559
BF EMBL: X13323 : 236
AG 1.1.1, 1.1.2, 3.1, 3.3, 6.1, 6.2, 6.3 [Riccio A. et al.,
199 ]
//
```

TRRDGENE

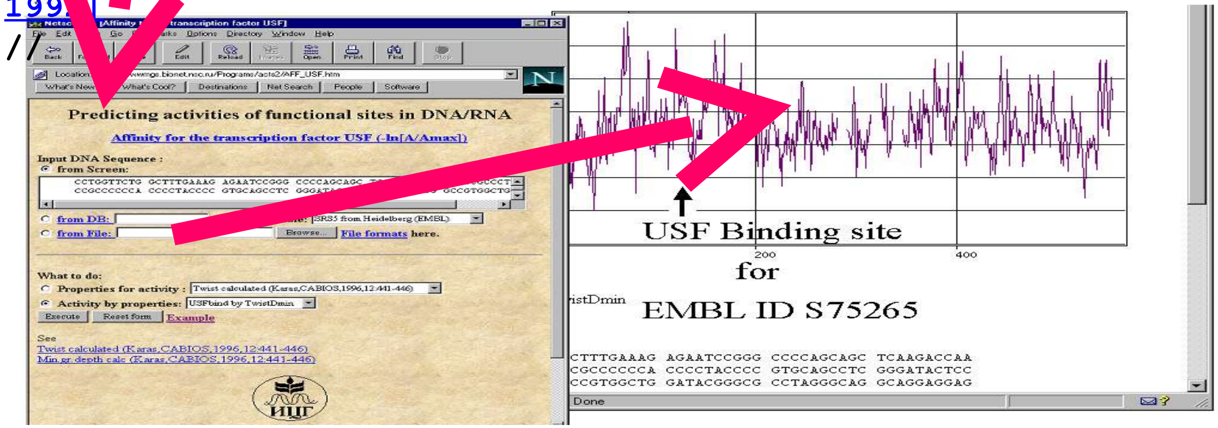
ACTIVITY

SAMPLES

TRRDFACTORS

EMBL

TRRDBIB



Predicting activities of functional sites in DNA/RNA

Affinity for the transcription factor USF (-ln[A/Amax])

Input DNA Sequence :

● from Screen:

CCTGGTTCTG GCTTTGAAAG AGAATCCGGG CCCCAGCAGC

CCGCCCCCCA CCCCTACCCC GTGCAGCCTC GGGAT GCCGTGGCTG

○ from DB: SRS5 from Heidelberg (EMBL)

○ from File: File formats here.

What to do:

○ Properties for activity : Twist calculated (Karas,CABIOS,1996,12:441-446)

● Activity by properties: USFbind by TwistDmin

Example

See

Twist calculated (Karas,CABIOS,1996,12:441-446)

Min.gr. depth calc (Karas,CABIOS,1996,12:441-446)

USF Binding site

for

EMBL ID S75265

istDmin

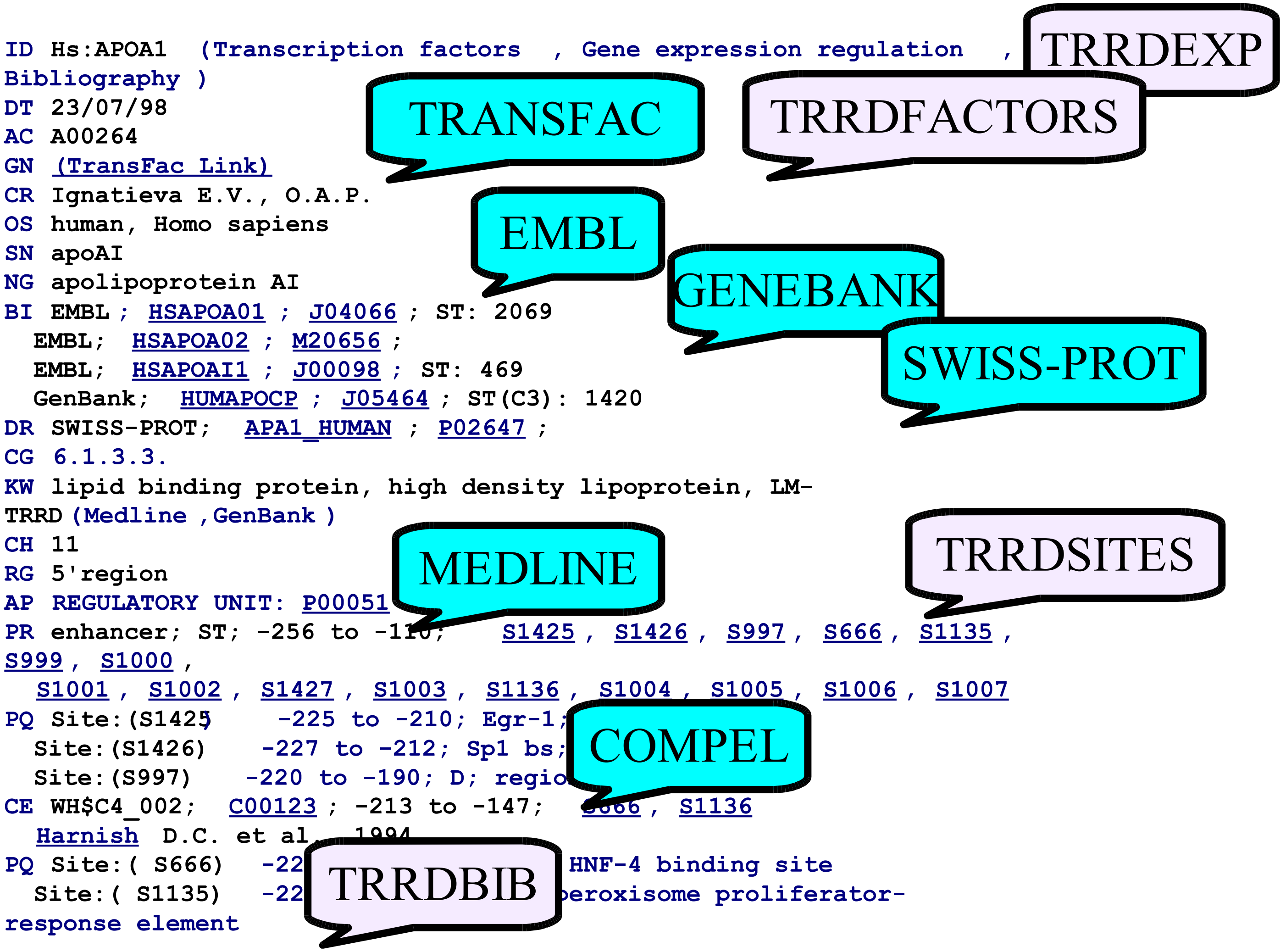
CTTTGAAAG AGAATCCGGG CCCCAGCAGC TCAAGACCAA

CGCCCCCCA CCCCTACCCC GTGCAGCCTC GGGATACTCC

CCGTGGCTG GATACGGGCG CCTAGGGCAG GCAGGAGGAG

© ИЦиГ СО РАН

Гиперссылки на базы данных из базы TRRDGENES



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ID Hs:APOA1  (Transcription factors  , Gene expression regulation  ,
Bibliography )
DT 23/07/98
AC A00264
GN  (TransFac Link)
CR Ignatieva E.V., O.A.P.
OS human, Homo sapiens
SN apoAI
NG apolipoprotein AI
BI EMBL ; HSAPOA01 ; J04066 ; ST: 2069
  EMBL; HSAPOA02 ; M20656 ;
  EMBL; HSAPOAI1 ; J00098 ; ST: 469
  GenBank; HUMAPOCP ; J05464 ; ST(C3): 1420
DR SWISS-PROT;  APA1_HUMAN ; P02647 ;
CG 6.1.3.3.
KW lipid binding protein, high density lipoprotein, LM-
TRRD (Medline ,GenBank )
CH 11
RG 5'region
AP REGULATORY UNIT: P00051
PR enhancer; ST; -256 to -110;    S1425 , S1426 , S997 , S666 , S1135 ,
S999 , S1000 ,
  S1001 , S1002 , S1427 , S1003 , S1136 , S1004 , S1005 , S1006 , S1007
PQ Site:(S1425)    -225 to -210; Egr-1;
  Site:(S1426)    -227 to -212; Sp1 bs;
  Site:(S997)    -220 to -190; D; regio
CE WH$C4_002;  C00123 ; -213 to -147;   666 , S1136
  Harnish  D.C. et al.  1994
PQ Site:( S666)   -22                    HNF-4 binding site
  Site:( S1135)   -22                    eroxisome proliferator-
response element
```
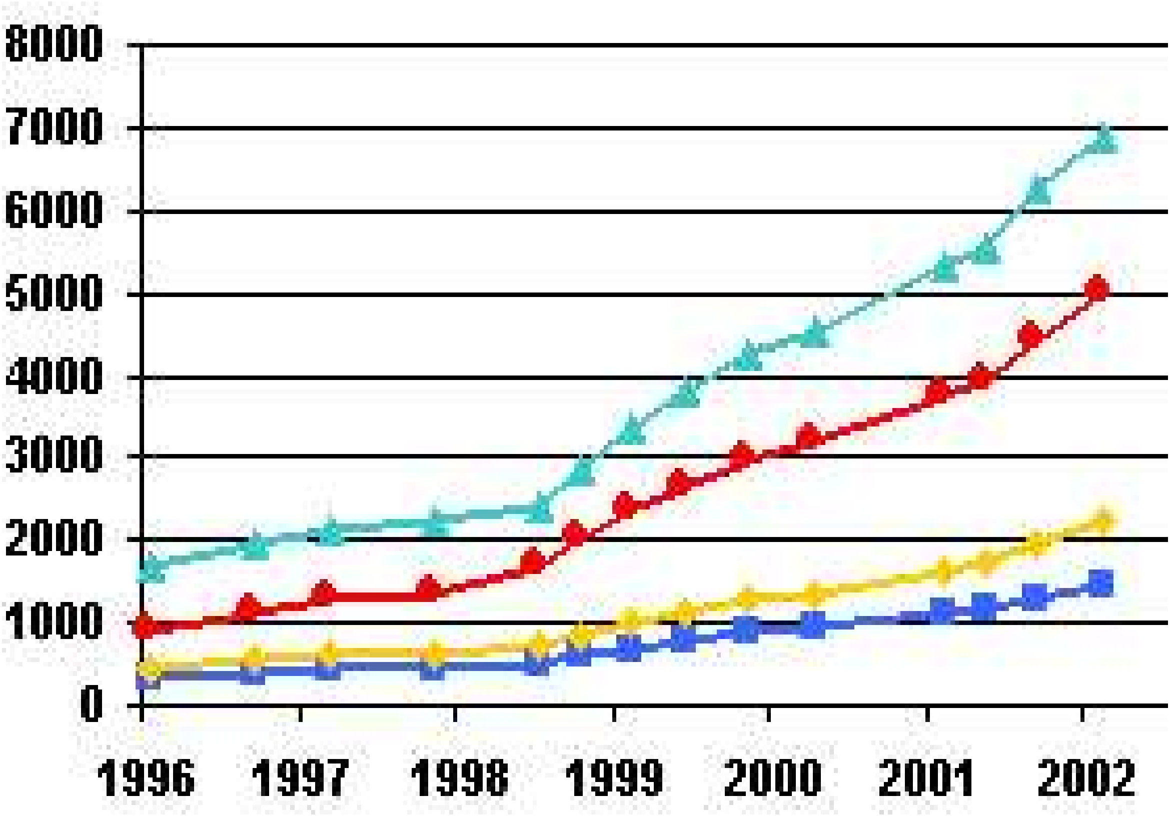

Динамика пополнения TRRD



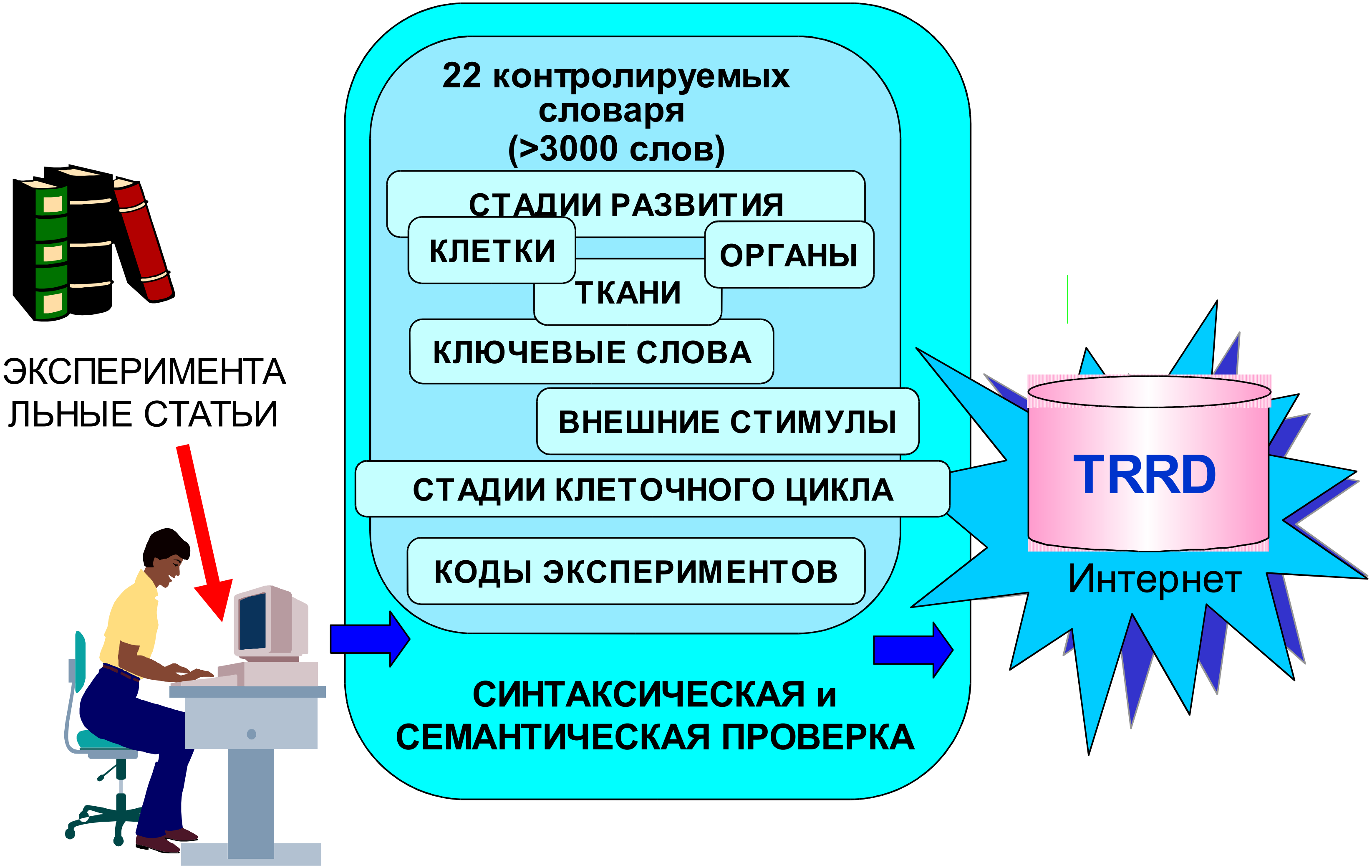
6867 САЙТОВ СВЯЗЫВАНИЯ ТРАНСКРИПЦИОННЫХ ФАКТОРОВ

4955 НАУЧНЫХ ПУБЛИКАЦИЙ

2242 РЕГУЛЯТОРНЫХРАЙОНОВ

1460 ГЕНОВ

Процесс ввода данных в TRRD



ЭКСПЕРИМЕНТАЛЬНЫЕ СТАТЬИ

22 контролируемых словаря (>3000 слов)

СТАДИИ РАЗВИТИЯ

КЛЕТКИ

ОРГАНЫ

ТКАНИ

КЛЮЧЕВЫЕ СЛОВА

ВНЕШНИЕ СТИМУЛЫ

СТАДИИ КЛЕТОЧНОГО ЦИКЛА

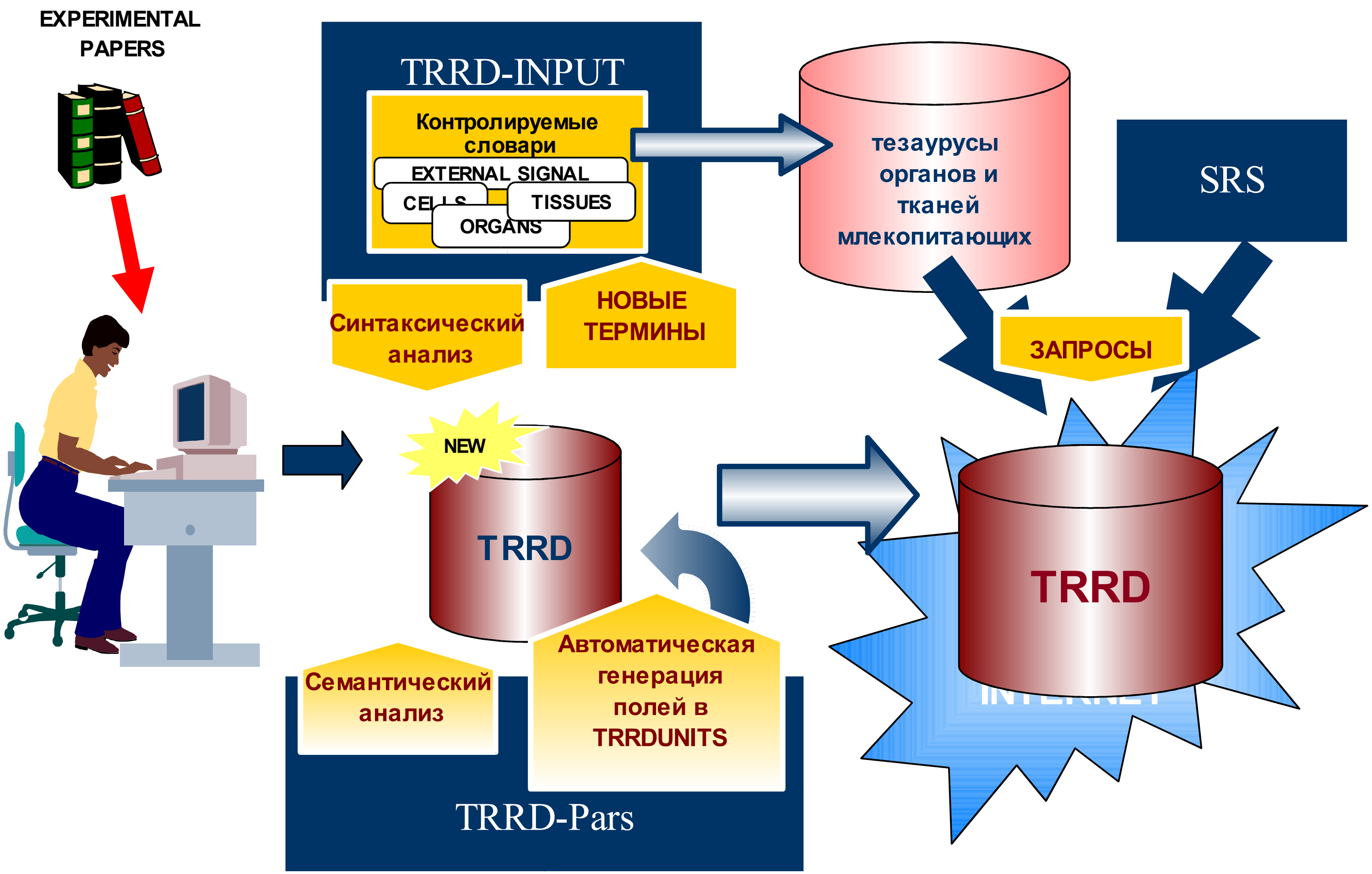
КОДЫ ЭКСПЕРИМЕНТОВ

СИНТАКСИЧЕСКАЯ и СЕМАНТИЧЕСКАЯ ПРОВЕРКА

TRRD

Интернет

ВВОД и ПРОЦЕССИНГ ДАННЫХ



EXPERIMENTAL PAPERS

TRRD-INPUT

Контролируемые словари

EXTERNAL SIGNAL

CELLS

TISSUES

ORGANS

тезаурусы органов и тканей млекопитающих

SRS

Синтаксический анализ

НОВЫЕ ТЕРМИНЫ

ЗАПРОСЫ

NEW

TRRD

TRRD

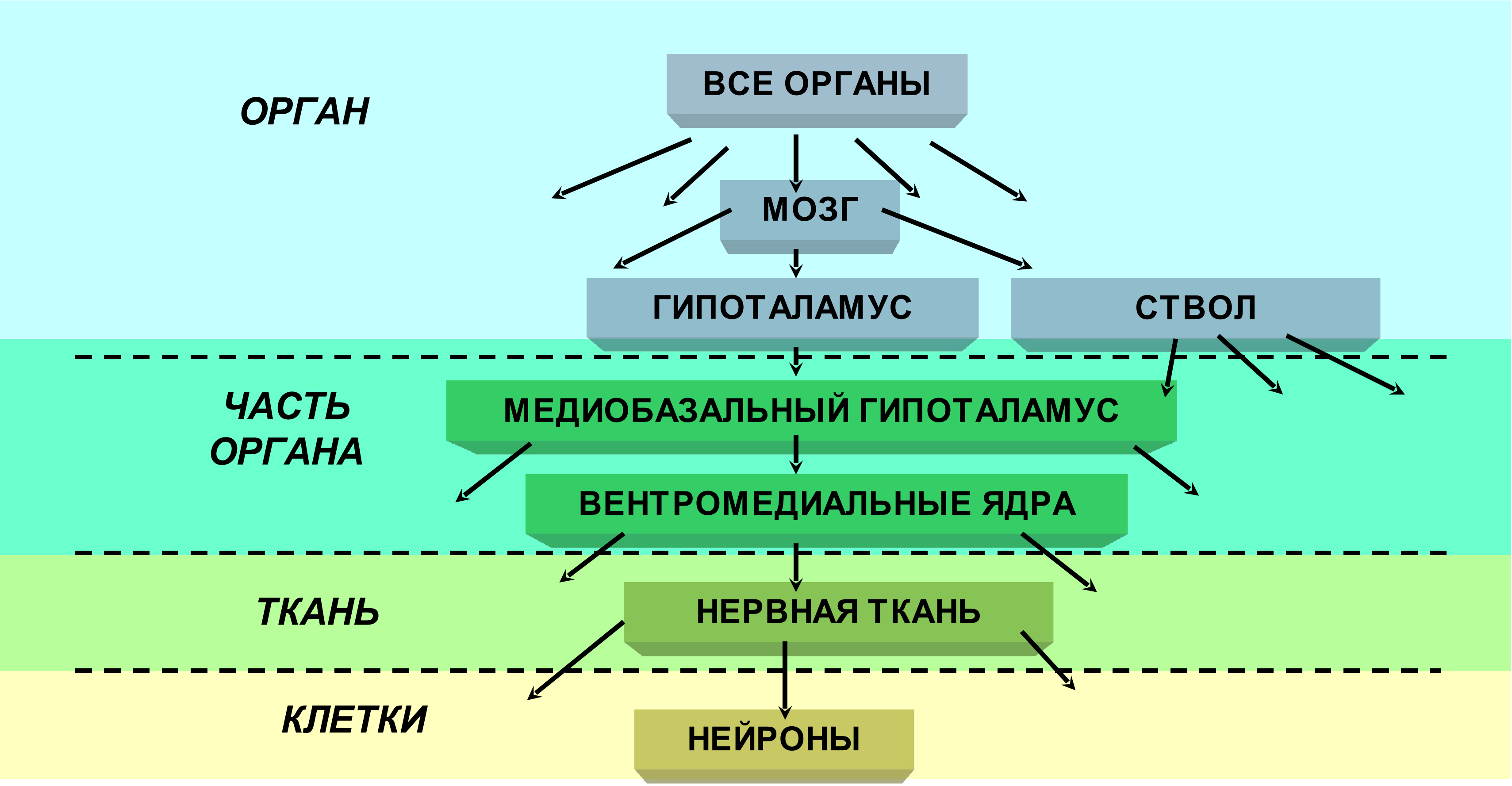
INTERNET

Семантический анализ

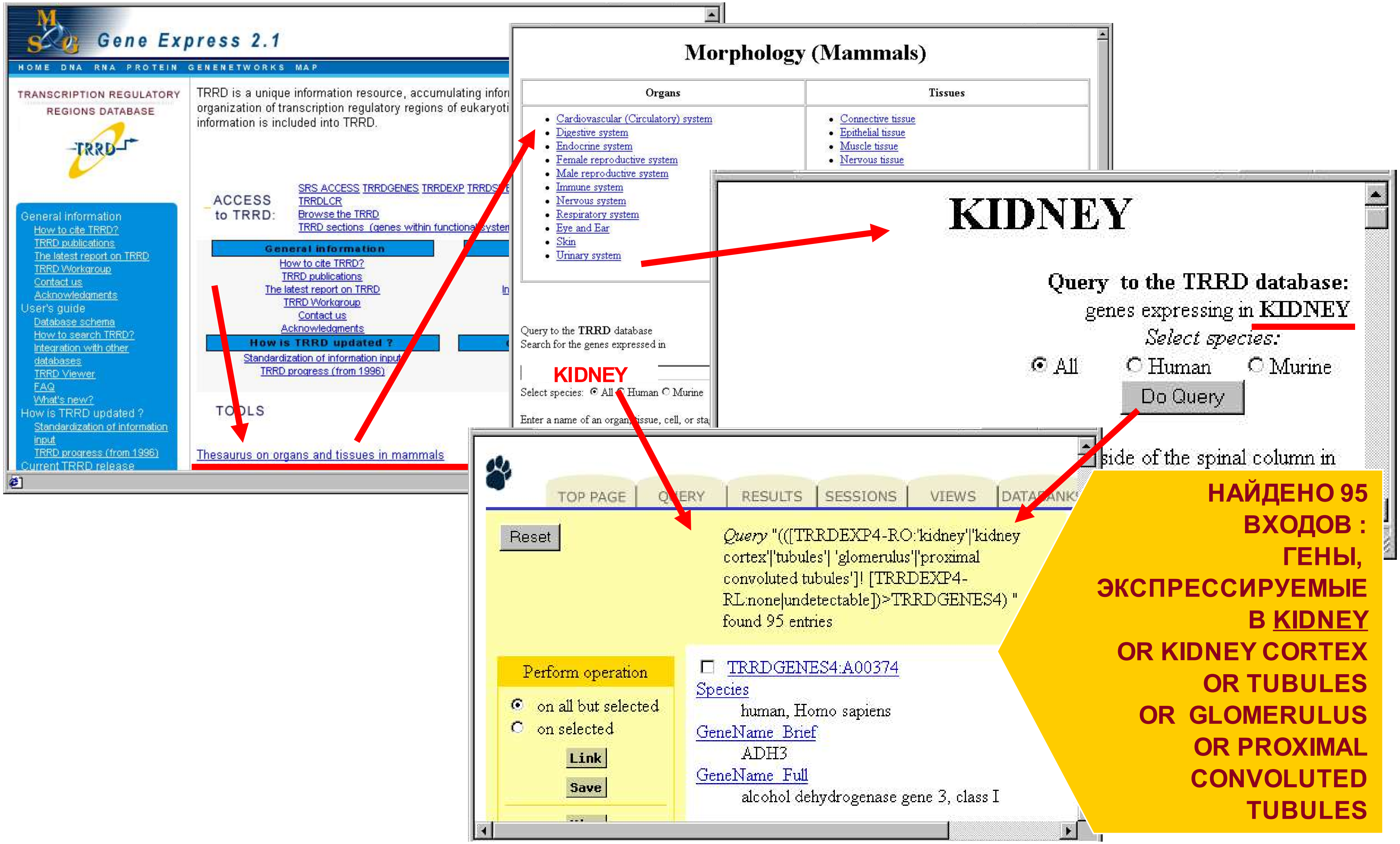
Автоматическая генерация полей в TRRDUNITS

TRRD-Pars

Иерархическая организация контролируемых словарей морфологических терминов в TRRD



Поиск данных вTRRD: запрос на основе тезауросов органов и тканей млекопитающих



TRRD is a unique information resource, accumulating infor
organization of transcription regulatory regions of eukaryoti
information is included into TRRD.

ACCESS to TRRD:

SRS ACCESS TRRDGENES TRRDEXP TRRDS
TRRDLCR
Browse the TRRD
TRRD sections (genes within functional systen

General information
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- The latest report on TRRD
- TRRD Workgroup
- Contact us
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- Database schema
- How to search TRRD?
- Integration with other databases
- TRRD Viewer
- FAQ
- What's new?

How is TRRD updated ?
- Standardization of information input
- TRRD progress (from 1996)

Current TRRD release

TOOLS

Thesaurus on organs and tissues in mammals

Morphology (Mammals)

Organs	Tissues
Cardiovascular (Circulatory) system Digestive system Endocrine system Female reproductive system Male reproductive system Immune system Nervous system Respiratory system Eye and Ear Skin Urinary system	Connective tissue Epithelial tissue Muscle tissue Nervous tissue

Query to the **TRRD** database
Search for the genes expressed in

KIDNEY

Select species: ● All ○ Human ○ Murine

Enter a name of an organ, tissue, cell, or sta

KIDNEY

Query to the TRRD database:
genes expressing in KIDNEY
Select species:
● All ○ Human ○ Murine
Do Query

side of the spinal column in

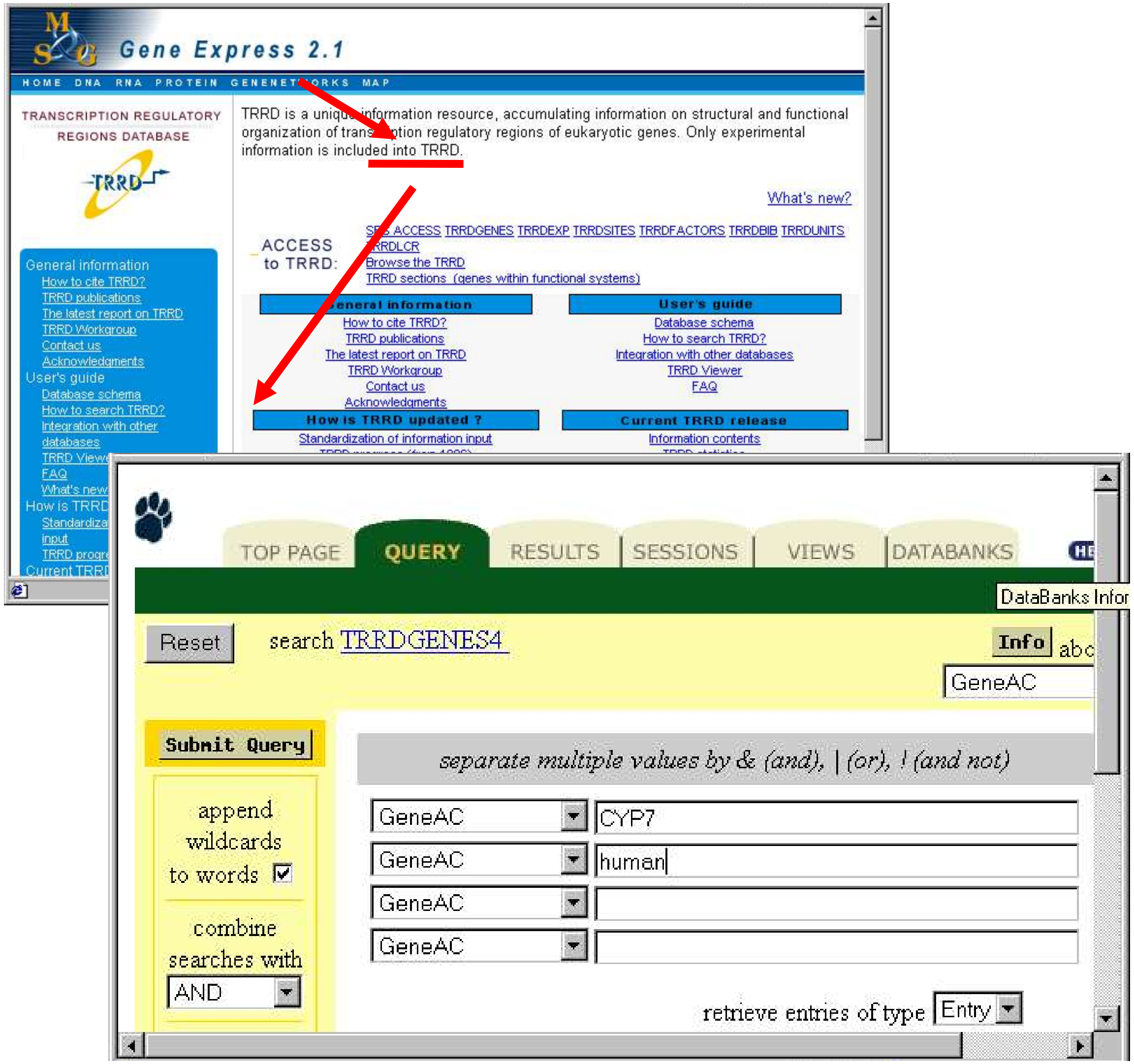
Query "(([TRRDEXP4-RO:'kidney'|'kidney cortex'|'tubules'| 'glomerulus'|'proximal convoluted tubules']! [TRRDEXP4-RL:none|undetectable])>TRRDGENES4) " found 95 entries

Perform operation
● on all but selected
○ on selected
Link
Save

☐ TRRDGENES4:A00374
Species
human, Homo sapiens
GeneName_Brief
ADH3
GeneName_Full
alcohol dehydrogenase gene 3, class I

НАЙДЕНО 95 ВХОДОВ : ГЕНЫ, ЭКСПРЕССИРУЕМЫЕ В KIDNEY OR KIDNEY CORTEX OR TUBULES OR GLOMERULUS OR PROXIMAL CONVOLUTED TUBULES

Поиск данных в TRRD: SRS



TRRD is a unique information resource, accumulating information on structural and functional organization of transcription regulatory regions of eukaryotic genes. Only experimental information is included into TRRD.

search TRRDGENES4

abc GeneAC

separate multiple values by & (and), | (or), ! (and not)

GeneAC CYP7

GeneAC human

GeneAC

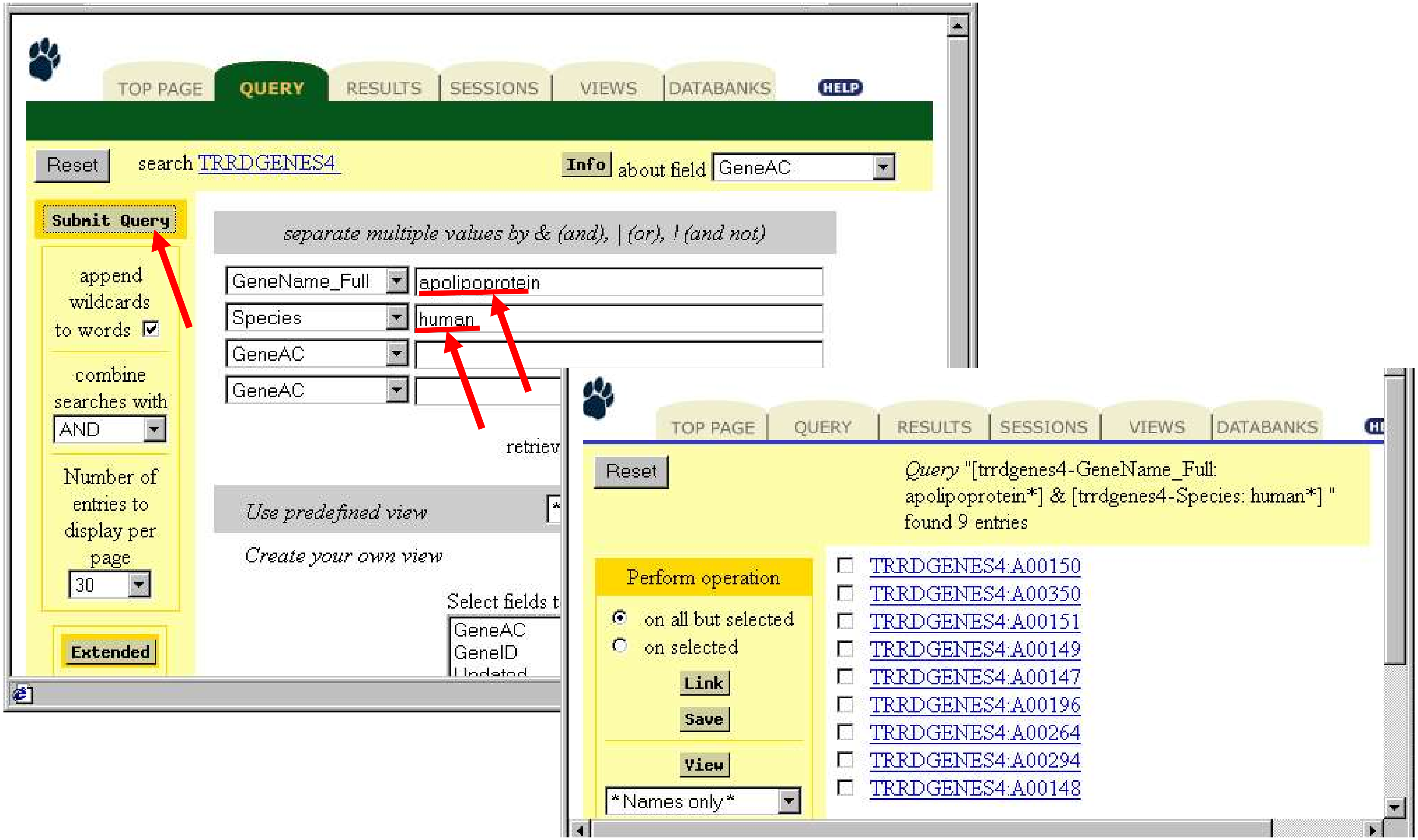
GeneAC

combine searches with AND

retrieve entries of type Entry

DATABASE	КОЛИЧЕСТВО ПОЛЕЙ, ПРОИНДЕКСИРОВАННЫХ для РЕЛИЗА 6.01
TRRDGENES	24
TRRDUNITS	11
TRRDEXP	17
TRRDSITES	16
TRRDFACTORS	14
TRRDLCR	40
TRRDBIB	9
TOTAL NUMBER	131

Главное окно для поиска в TRRDGENES через поисковую систему SRS (Sequence Retrieval System)



search TRRDGENES4

about field GeneAC

separate multiple values by & (and), | (or), ! (and not)

GeneName_Full: apolipoprotein

Species: human

GeneAC:

GeneAC:

append wildcards to words ☑

combine searches with AND

Number of entries to display per page 30

Use predefined view

Create your own view

Select fields t

GeneAC
GeneID
Updated

Query "[trrdgenes4-GeneName_Full: apolipoprotein*] & [trrdgenes4-Species: human*] " found 9 entries

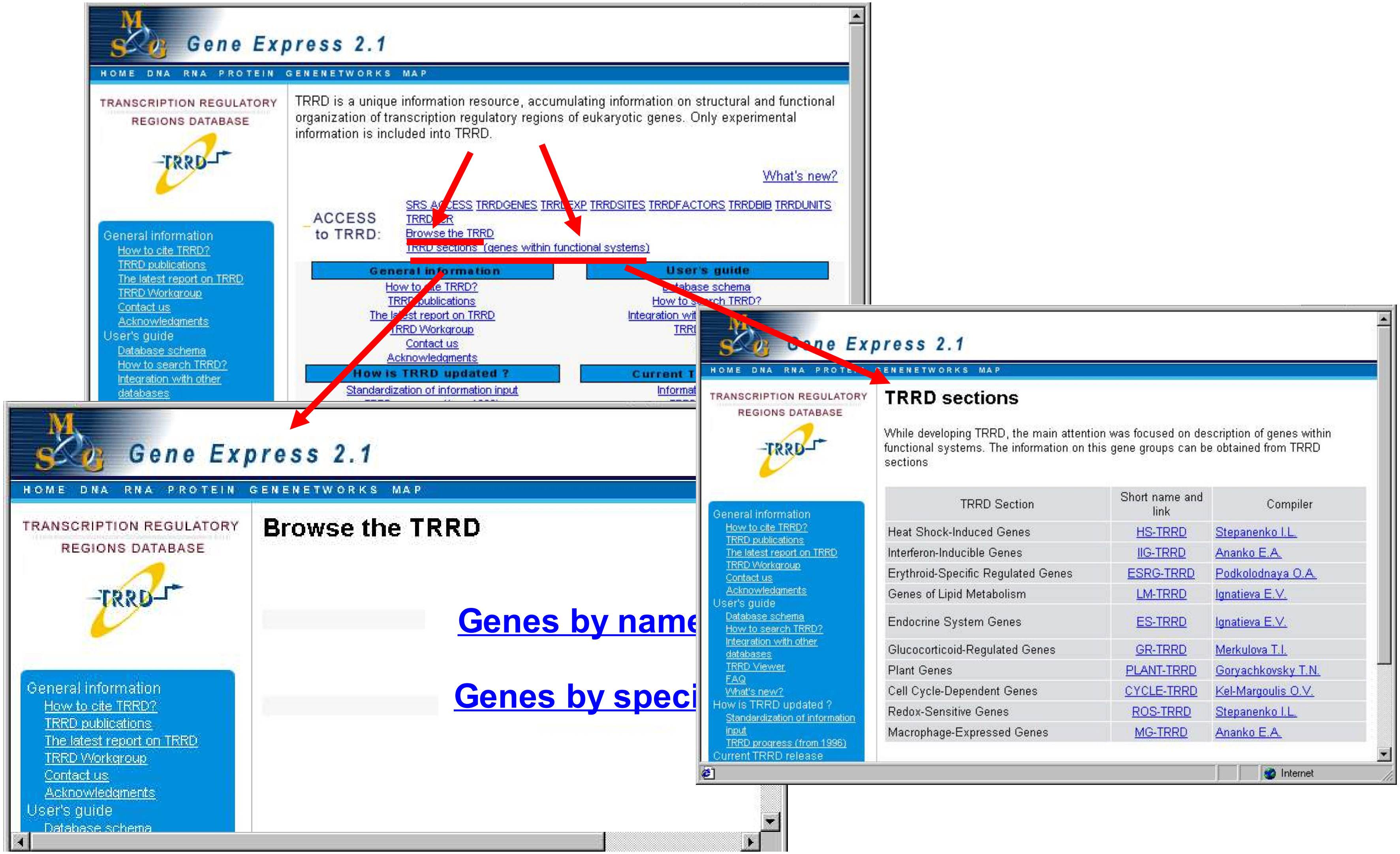
Perform operation

● on all but selected
○ on selected

Names only

☐ TRRDGENES4:A00150
☐ TRRDGENES4:A00350
☐ TRRDGENES4:A00151
☐ TRRDGENES4:A00149
☐ TRRDGENES4:A00147
☐ TRRDGENES4:A00196
☐ TRRDGENES4:A00264
☐ TRRDGENES4:A00294
☐ TRRDGENES4:A00148

Поиск данных в TRRD: браузеры и тематические секции



Gene Express 2.1

HOME DNA RNA PROTEIN GENENETWORKS MAP

TRANSCRIPTION REGULATORY REGIONS DATABASE

TRRD is a unique information resource, accumulating information on structural and functional organization of transcription regulatory regions of eukaryotic genes. Only experimental information is included into TRRD.

What's new?

ACCESS to TRRD:
SRS ACCESS TRRDGENES TRRDEXP TRRDSITES TRRDFACTORS TRRDBIB TRRDUNITS
TRRD[illegible]ER
Browse the TRRD
TRRD sections (genes within functional systems)

General information	User's guide
How to cite TRRD? TRRD publications The latest report on TRRD TRRD Workgroup Contact us Acknowledgments	Database schema How to search TRRD? Integration wit TRRI

How is TRRD updated ?	Current T
Standardization of information input	Informat

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Gene Express 2.1

HOME DNA RNA PROTEIN GENENETWORKS MAP

TRANSCRIPTION REGULATORY REGIONS DATABASE

Browse the TRRD

Genes by name

Genes by speci

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- Database schema

Gene Express 2.1

HOME DNA RNA PROTE GENENETWORKS MAP

TRANSCRIPTION REGULATORY REGIONS DATABASE

TRRD sections

While developing TRRD, the main attention was focused on description of genes within functional systems. The information on this gene groups can be obtained from TRRD sections

TRRD Section	Short name and link	Compiler
Heat Shock-Induced Genes	HS-TRRD	Stepanenko I.L.
Interferon-Inducible Genes	IIG-TRRD	Ananko E.A.
Erythroid-Specific Regulated Genes	ESRG-TRRD	Podkolodnaya O.A.
Genes of Lipid Metabolism	LM-TRRD	Ignatieva E.V.
Endocrine System Genes	ES-TRRD	Ignatieva E.V.
Glucocorticoid-Regulated Genes	GR-TRRD	Merkulova T.I.
Plant Genes	PLANT-TRRD	Goryachkovsky T.N.
Cell Cycle-Dependent Genes	CYCLE-TRRD	Kel-Margoulis O.V.
Redox-Sensitive Genes	ROS-TRRD	Stepanenko I.L.
Macrophage-Expressed Genes	MG-TRRD	Ananko E.A.

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Current TRRD release

Тематические секции TRRD

В базе TRRD, развиваются тематические секции, объединяющие гены по функциональным особенностям:

Heat Shock-Induced Genes

Cell Cycle Genes

Glucocorticoid Controlled Genes

Erythroid-Specific Regulated Genes

Redox-Sensitive Genes

Genes Expressed in Endocrine Pancreas

Macrophage-Expressed Genes

NEW Apoptosis Genes

NEW Genes, controlling blood coagulation and fibrinolysis

(BCF-TRRD)
Khlebodarova T.M., Podkolodnaya O.A.

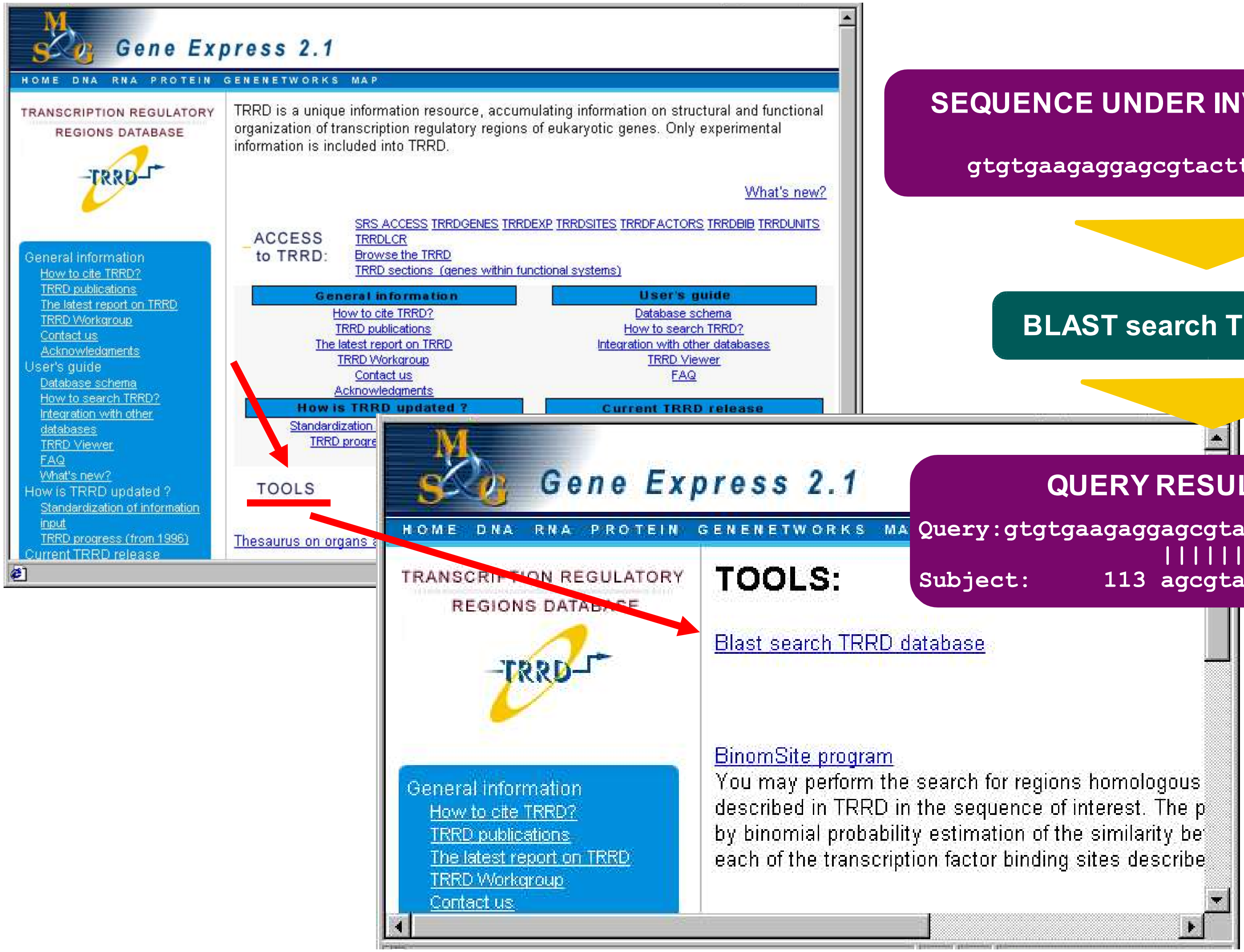
Plant Genes

Endocrine System Genes

Genes of Lipid Metabolism

Interferon-Inducible Genes
(IIG-TRRD)
Ananko E.A.

Поиск данных в TRRD: BLAST



TRANSCRIPTION REGULATORY REGIONS DATABASE

TRRD is a unique information resource, accumulating information on structural and functional organization of transcription regulatory regions of eukaryotic genes. Only experimental information is included into TRRD.

What's new?

ACCESS to TRRD: SRS ACCESS TRRDGENES TRRDEXP TRRDSITES TRRDFACTORS TRRDBIB TRRDUNITS TRRDLCR
Browse the TRRD
TRRD sections (genes within functional systems)

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Thesaurus on organs a

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TRANSCRIPTION REGULATORY REGIONS DATABASE

TOOLS:

Blast search TRRD database

BinomSite program
You may perform the search for regions homologous described in TRRD in the sequence of interest. The p by binomial probability estimation of the similarity be each of the transcription factor binding sites describe

General information
- How to cite TRRD?
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- The latest report on TRRD
- TRRD Workgroup
- Contact us

SEQUENCE UNDER INVESTIGATION:

gtgtgaagaggagcgtacttttgtgtgtgaac

BLAST search TRRDUNITS

QUERY RESULTS:

```
Query:gtgtgaagaggagcgtacttttgtgtgtga
                  |||||||||||
Subject:      113 agcgtactttt 103
```

© ИЦиГ СО РАН

TRRD – информационная основа для создания выборок

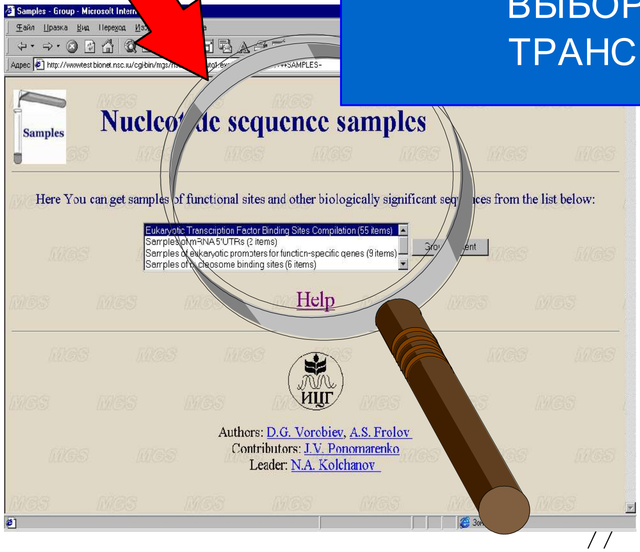
```
ID   es_250_1; DNA
AC   es_250_1
CC   DE   adrenodoxin gene
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DR   EMBL; M23665; HSADRDO01; ; join(133..382)
```

ВЫБОРКИ ЭУКАРИОТИЧЕСКИХ ПРОМОТОРОВ

```
SQ   ctttcaaaat atttgtttc tgcacggcaa cttcagccgc taaaaaagca
     tccagcttac aacggaacct ggagggttgg taaaggcccc ctgcgctggc
```

ВЫБОРКИ САЙТОВ СВЯЗЫВАНИЯ
ТРАНСКРИПЦИОННЫХ ФАКТОРОВ

```
ggcgc
acct
gcccc
```



Nucleotide sequence samples

Here You can get samples of functional sites and other biologically significant sequences from the list below:

- Eukaryotic Transcription Factor Binding Sites Compilation (55 items)
- Samples of mRNA 5'UTRs (2 items)
- Samples of eukaryotic promoters for function-specific genes (9 items)
- Samples of nucleosome binding sites (6 items)

Help

Authors: D.G. Vorobiev, A.S. Frolov
Contributors: J.V. Ponomarenko
Leader: N.A. Kolchanov

```
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
EMBL; M23665; HSADRDO01; ; join(133..382)
ST (EMBL/GENBANK) 333
TRRDGENES; A00860; Hs:ADX; 4.2;
{0,0} [1;250]; EXP
ctttcaaaat atttgtttc tgcacggcaa cttcagccgc taaaaaagca
tccagcttac aacggaacct ggagggttgg taaaggcccc ctgcgctggc
cccgccccat gggaccgggc ggcgtgggcg tgagaggcgg ggcggggcgc
gctctgcttg ccaatgtctt tataggtcac ccggaaggca cgcggaacct
cggcgcggtg cttccagcag ggtctctccg ccactccagc cccgcgcccc
//
```

Состав рабочей группы базы TRRD

Scientific Supervisor

- Nikolay A. Kolchanov, Prof., Dr.Sci., Head of the Laboratory Theoretical Genetics

Scientific Consultants

- Aida G. Romashenko, Ph.D., Head of the Laboratory of Animal Molecular Genetics

- Irina M. Korostishevskaya, Ph.D.

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- Ignatieva Elena V. , Ph.D.
- Podkolodnaya Olga A., Ph.D.
- Merkulova Tatyana I. , Ph.D.
- Stepanenko Irina L. , Ph.D.

TRRD Software Developers

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- Naumochkin Andrey N.
- Pozdnyakov Mikhail A.

WEB Resources

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- Grigorovich Dmitry A.

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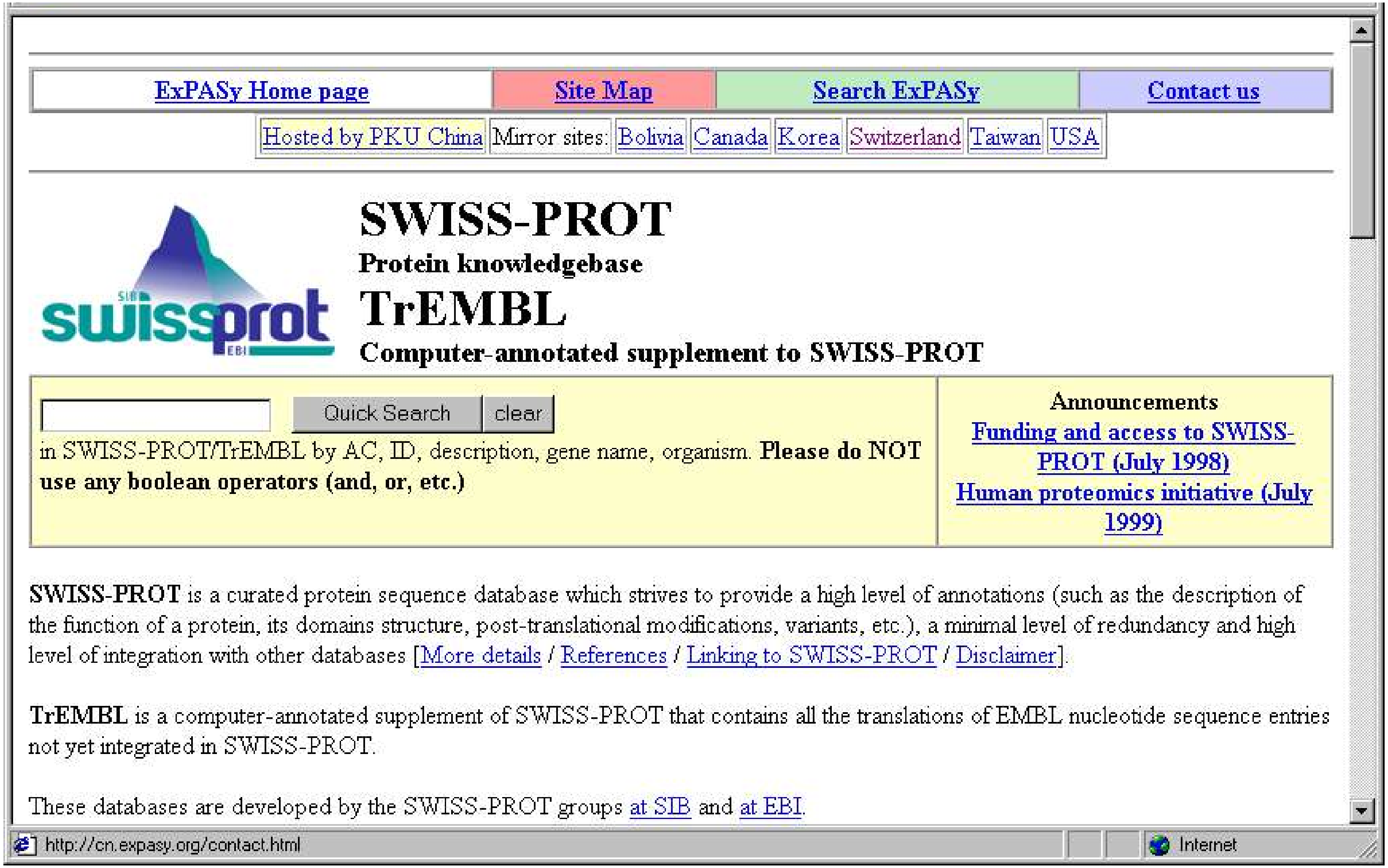
- Busigina Tatyana N.
- Goryachkovsky Tatyana N.
- Fedorova Svetlana A.
- Ibragimova Salmaz S., Ph.D
- Merkulov Vasily M. , Ph.D.
- Smirnova Olga G., Ph.D.
- Suslov Valentin V.
- Khlebodarova Tamara M., Dr.Sci.
- Turnaev I.I.
- Mischenko Elena L., Ph.D
- Furman Dagmara P., Dr.Sci.
- Proskura Anna L.

Bibliographic support

- Lokhova Irina V.
- Katokhina Ludmila V.

SWISS-PROT – база данных о белках

http://cn.expasy.org/sprot/



SWISS-PROT

Protein knowledgebase

TrEMBL

Computer-annotated supplement to SWISS-PROT

in SWISS-PROT/TrEMBL by AC, ID, description, gene name, organism. **Please do NOT use any boolean operators (and, or, etc.)**

Announcements

Funding and access to SWISS-PROT (July 1998)

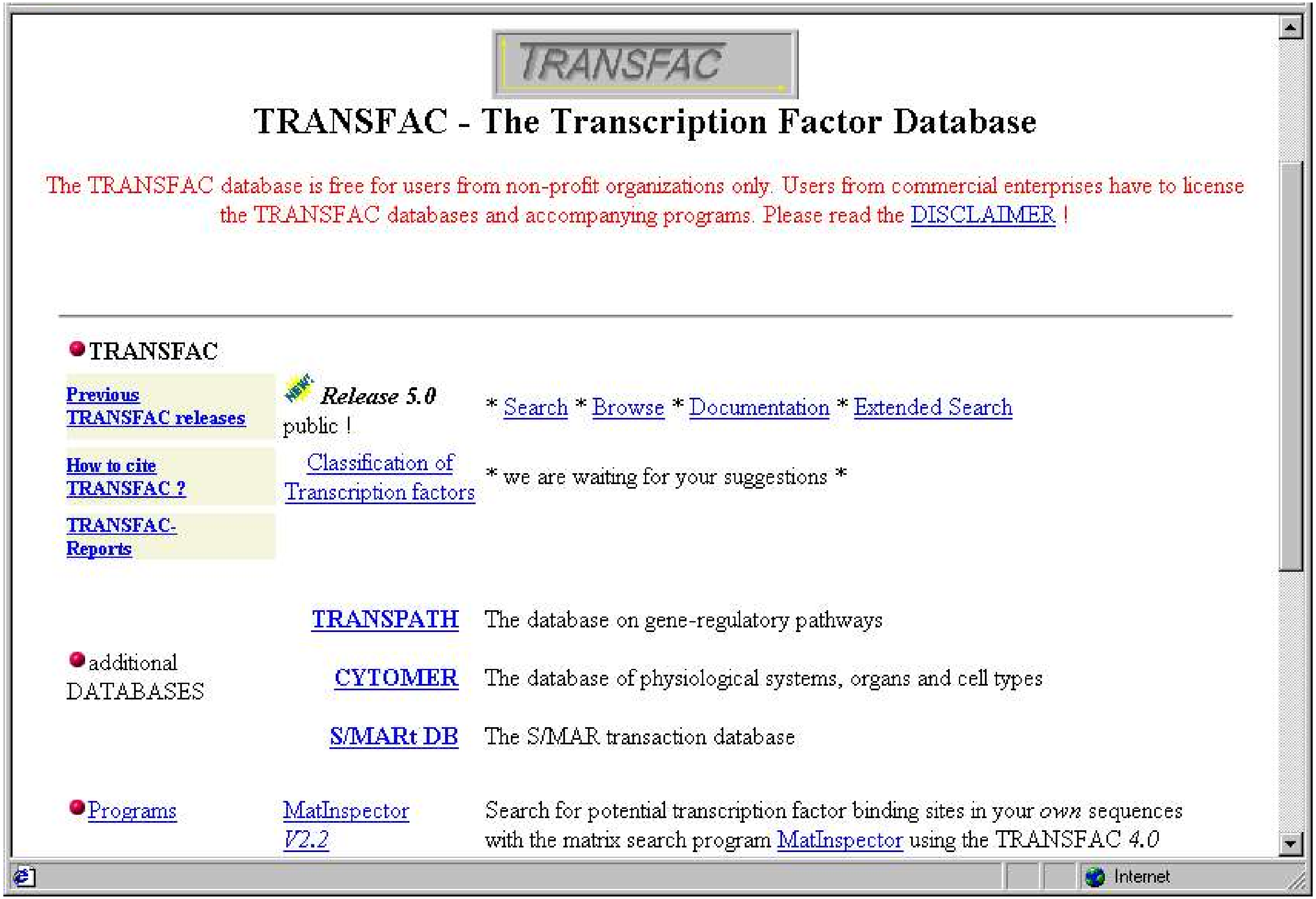
Human proteomics initiative (July 1999)

SWISS-PROT is a curated protein sequence database which strives to provide a high level of annotations (such as the description of the function of a protein, its domains structure, post-translational modifications, variants, etc.), a minimal level of redundancy and high level of integration with other databases [More details / References / Linking to SWISS-PROT / Disclaimer].

TrEMBL is a computer-annotated supplement of SWISS-PROT that contains all the translations of EMBL nucleotide sequence entries not yet integrated in SWISS-PROT.

These databases are developed by the SWISS-PROT groups at SIB and at EBI.

Информация о транскрипционных факторах http://transfac.gbf.de/TRANSFAC/index.html



TRANSFAC - The Transcription Factor Database

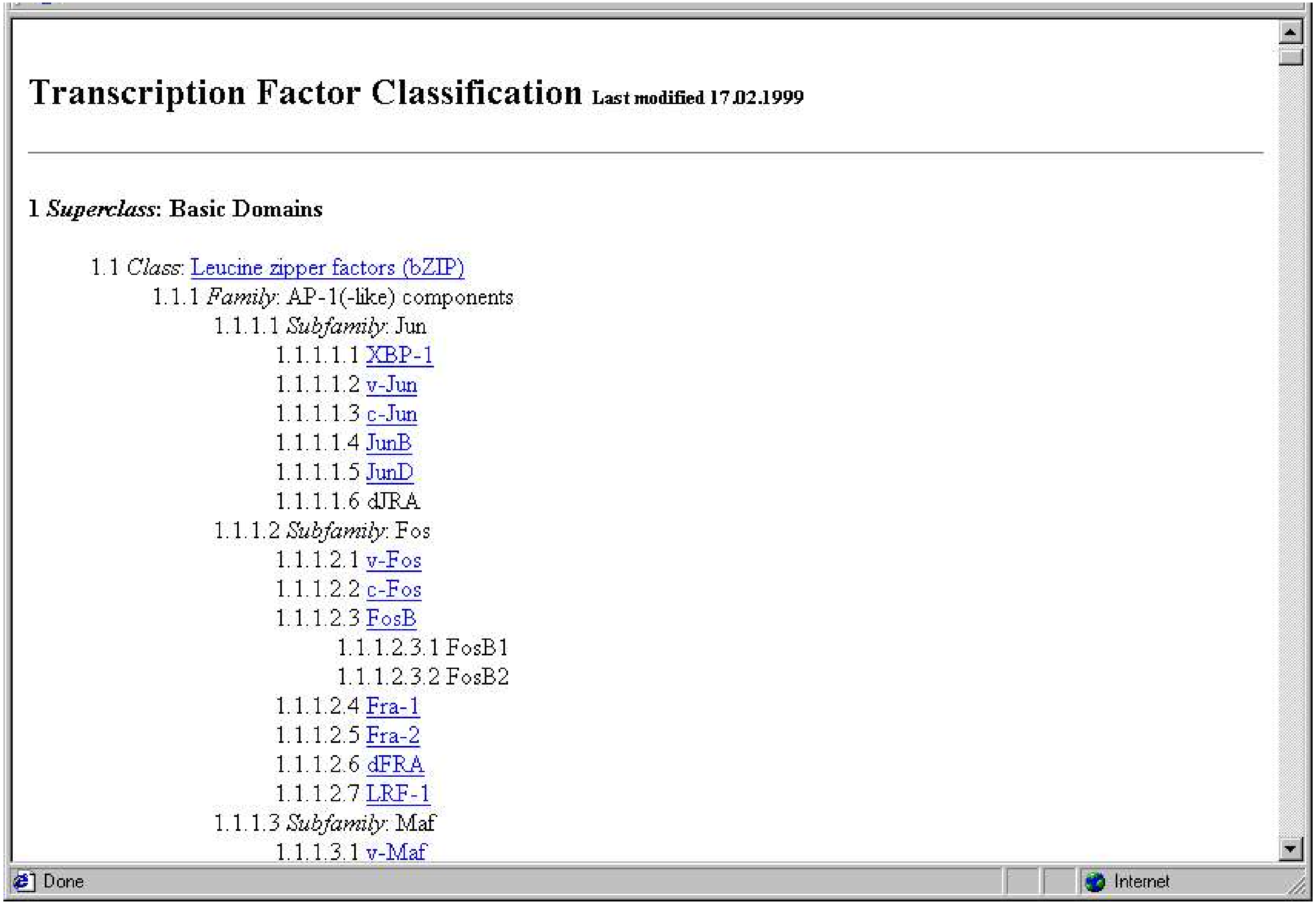
The TRANSFAC database is free for users from non-profit organizations only. Users from commercial enterprises have to license the TRANSFAC databases and accompanying programs. Please read the DISCLAIMER !

● **TRANSFAC**

Previous TRANSFAC releases	NEW! ***Release 5.0*** public !	* Search * Browse * Documentation * Extended Search
How to cite TRANSFAC ?	Classification of Transcription factors	* we are waiting for your suggestions *
TRANSFAC-Reports		

● additional DATABASES	**TRANSPATH**	The database on gene-regulatory pathways
	CYTOMER	The database of physiological systems, organs and cell types
	S/MARt DB	The S/MAR transaction database
● Programs	MatInspector *V2.2*	Search for potential transcription factor binding sites in your *own* sequences with the matrix search program MatInspector using the TRANSFAC *4.0*

http://transfac.gbf.de/TRANSFAC/cl/cl.html

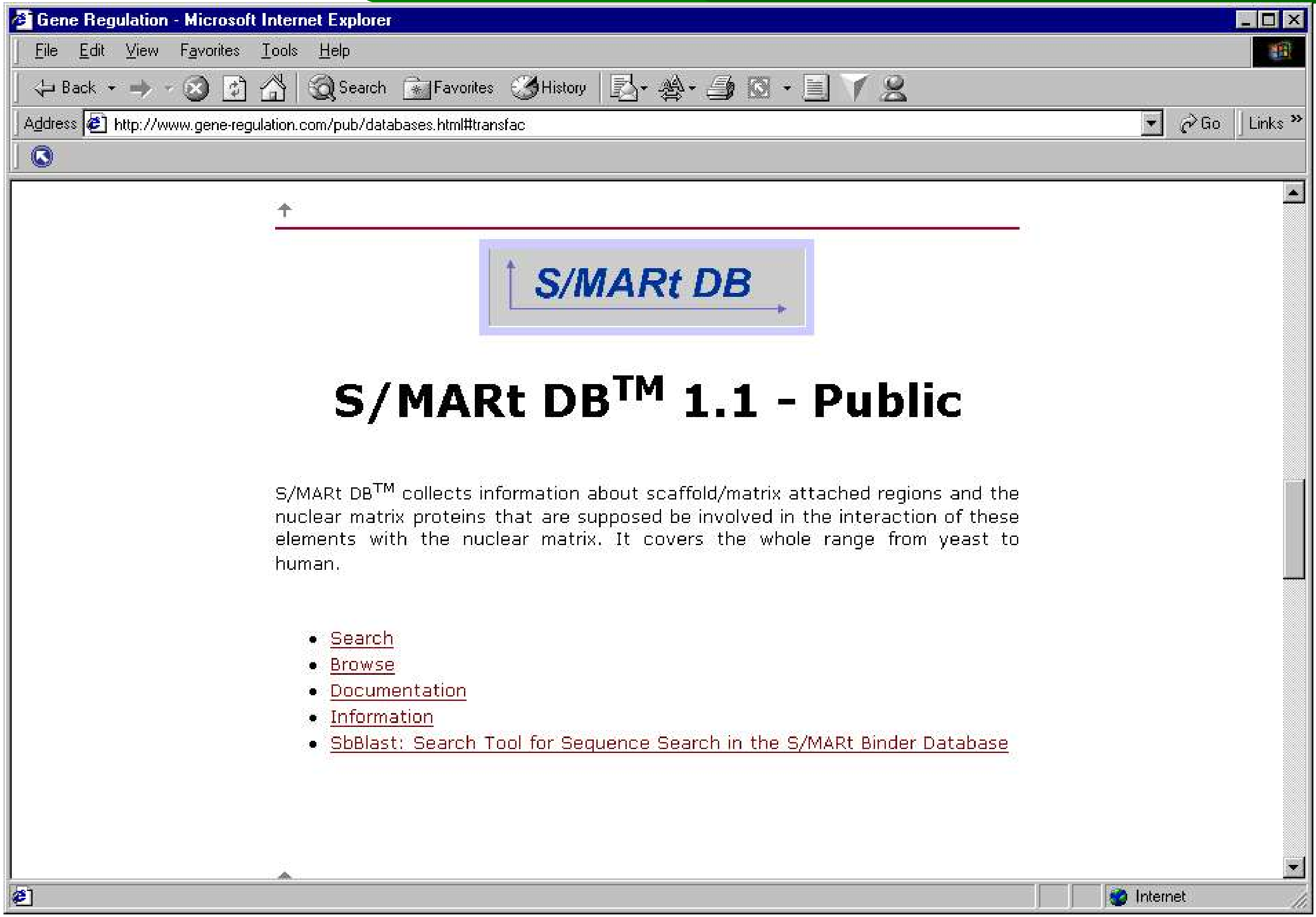


Transcription Factor Classification Last modified 17.02.1999

1 *Superclass*: Basic Domains

1.1 *Class*: Leucine zipper factors (bZIP)
1.1.1 *Family*: AP-1(-like) components
1.1.1.1 *Subfamily*: Jun
1.1.1.1.1 XBP-1
1.1.1.1.2 v-Jun
1.1.1.1.3 c-Jun
1.1.1.1.4 JunB
1.1.1.1.5 JunD
1.1.1.1.6 dJRA
1.1.1.2 *Subfamily*: Fos
1.1.1.2.1 v-Fos
1.1.1.2.2 c-Fos
1.1.1.2.3 FosB
1.1.1.2.3.1 FosB1
1.1.1.2.3.2 FosB2
1.1.1.2.4 Fra-1
1.1.1.2.5 Fra-2
1.1.1.2.6 dFRA
1.1.1.2.7 LRF-1
1.1.1.3 *Subfamily*: Maf
1.1.1.3.1 v-Maf

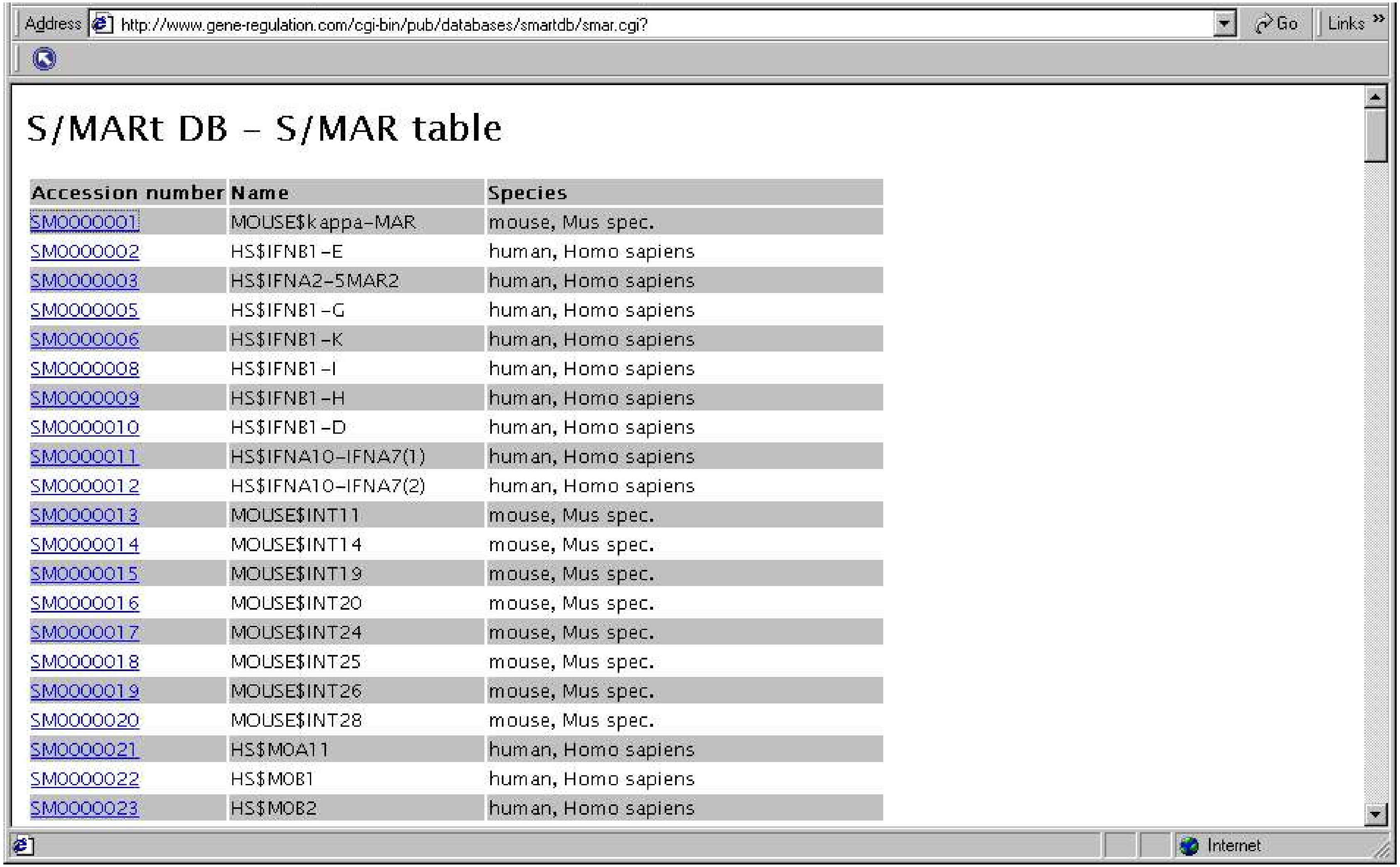
http://www.gene-regulation.com/pub/databases/smartdb/toc.html



S/MARt DB™ 1.1 - Public

S/MARt DB™ collects information about scaffold/matrix attached regions and the nuclear matrix proteins that are supposed be involved in the interaction of these elements with the nuclear matrix. It covers the whole range from yeast to human.

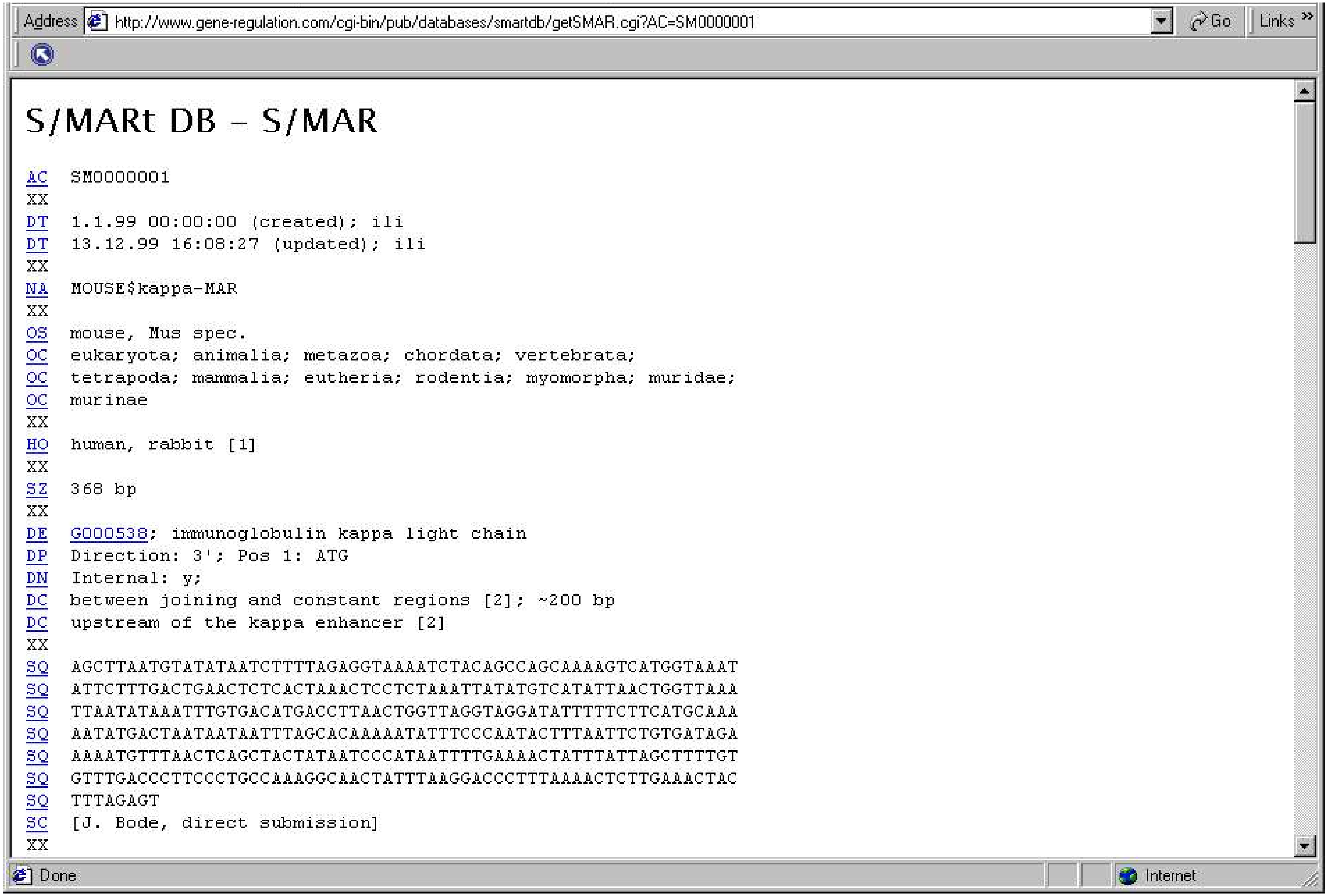
- Search
- Browse
- Documentation
- Information
- SbBlast: Search Tool for Sequence Search in the S/MARt Binder Database



Address http://www.gene-regulation.com/cgi-bin/pub/databases/smartdb/smar.cgi?

S/MARt DB – S/MAR table

Accession number	Name	Species
SM0000001	MOUSE$kappa-MAR	mouse, Mus spec.
SM0000002	HS$IFNB1-E	human, Homo sapiens
SM0000003	HS$IFNA2-5MAR2	human, Homo sapiens
SM0000005	HS$IFNB1-G	human, Homo sapiens
SM0000006	HS$IFNB1-K	human, Homo sapiens
SM0000008	HS$IFNB1-I	human, Homo sapiens
SM0000009	HS$IFNB1-H	human, Homo sapiens
SM0000010	HS$IFNB1-D	human, Homo sapiens
SM0000011	HS$IFNA10-IFNA7(1)	human, Homo sapiens
SM0000012	HS$IFNA10-IFNA7(2)	human, Homo sapiens
SM0000013	MOUSE$INT11	mouse, Mus spec.
SM0000014	MOUSE$INT14	mouse, Mus spec.
SM0000015	MOUSE$INT19	mouse, Mus spec.
SM0000016	MOUSE$INT20	mouse, Mus spec.
SM0000017	MOUSE$INT24	mouse, Mus spec.
SM0000018	MOUSE$INT25	mouse, Mus spec.
SM0000019	MOUSE$INT26	mouse, Mus spec.
SM0000020	MOUSE$INT28	mouse, Mus spec.
SM0000021	HS$MOA11	human, Homo sapiens
SM0000022	HS$MOB1	human, Homo sapiens
SM0000023	HS$MOB2	human, Homo sapiens



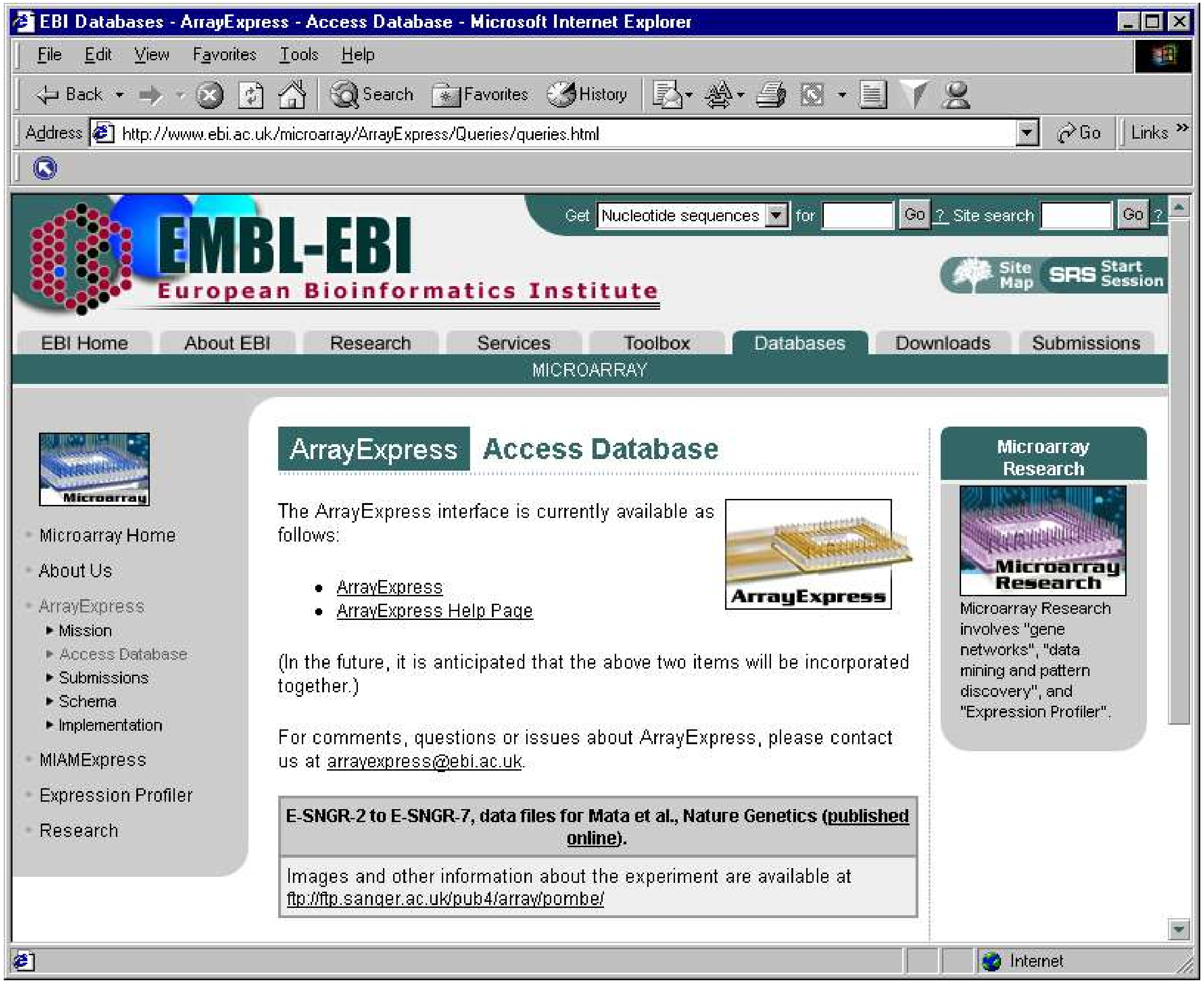
http://www.gene-regulation.com/cgi-bin/pub/databases/smartdb/getSMAR.cgi?AC=SM0000001

S/MARt DB - S/MAR

```
AC   SM0000001
XX
DT   1.1.99 00:00:00 (created); ili
DT   13.12.99 16:08:27 (updated); ili
XX
NA   MOUSE$kappa-MAR
XX
OS   mouse, Mus spec.
OC   eukaryota; animalia; metazoa; chordata; vertebrata;
OC   tetrapoda; mammalia; eutheria; rodentia; myomorpha; muridae;
OC   murinae
XX
HO   human, rabbit [1]
XX
SZ   368 bp
XX
DE   G000538; immunoglobulin kappa light chain
DP   Direction: 3'; Pos 1: ATG
DN   Internal: y;
DC   between joining and constant regions [2]; ~200 bp
DC   upstream of the kappa enhancer [2]
XX
SQ   AGCTTAATGTATATAATCTTTTAGAGGTAAAATCTACAGCCAGCAAAAGTCATGGTAAAT
SQ   ATTCTTTGACTGAACTCTCACTAAACTCCTCTAAATTATATGTCATATTAACTGGTTAAA
SQ   TTAATATAAATTTGTGACATGACCTTAACTGGTTAGGTAGGATATTTTTCTTCATGCAAA
SQ   AATATGACTAATAATAATTTAGCACAAAAATATTTCCCAATACTTTAATTCTGTGATAGA
SQ   AAAATGTTTAACTCAGCTACTATAATCCCATAATTTTGAAAACTATTTATTAGCTTTTGT
SQ   GTTTGACCCTTCCCTGCCAAAGGCAACTATTTAAGGACCCTTTAAAACTCTTGAAACTAC
SQ   TTTAGAGT
SC   [J. Bode, direct submission]
XX
```

БАЗЫ ДАННЫХ, СОДЕРЖАЩИЕ ИНФОРМАЦИЮ О ПАТТЕРНАХ ЭКСПРЕССИИ

http://www.ebi.ac.uk/microarray/ArrayExpress/Queries/queries.html



ArrayExpress Access Database

The ArrayExpress interface is currently available as follows:

- ArrayExpress
- ArrayExpress Help Page

(In the future, it is anticipated that the above two items will be incorporated together.)

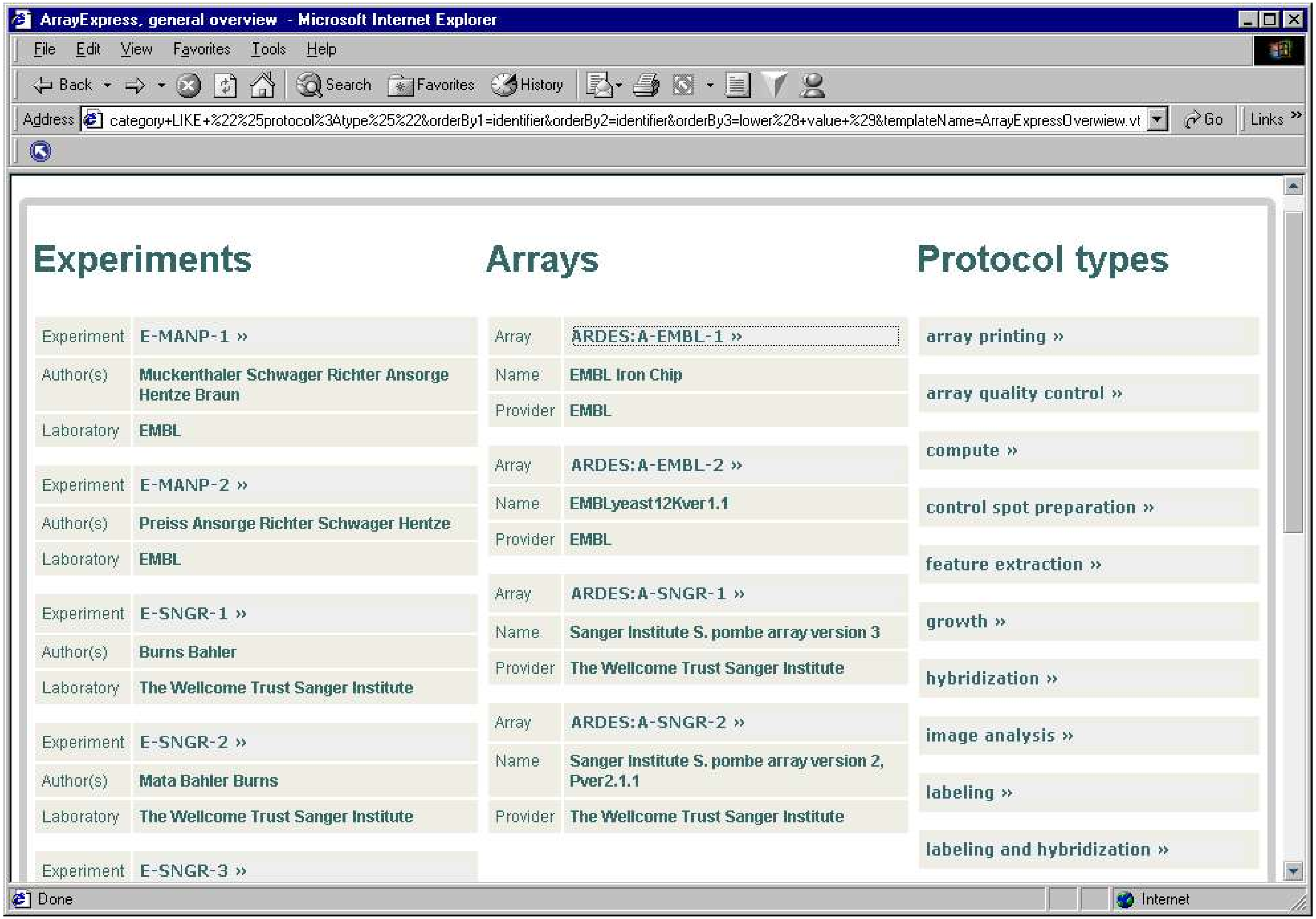
For comments, questions or issues about ArrayExpress, please contact us at arrayexpress@ebi.ac.uk.

E-SNGR-2 to E-SNGR-7, data files for Mata et al., Nature Genetics (published online).

Images and other information about the experiment are available at ftp://ftp.sanger.ac.uk/pub4/array/pombe/

Microarray Research

Microarray Research involves "gene networks", "data mining and pattern discovery", and "Expression Profiler".



Address: category+LIKE+%22%25protocol%3Atype%25%22&orderBy1=identifier&orderBy2=identifier&orderBy3=lower%28+value+%29&templateName=ArrayExpressOverview.vt

Experiments

Experiment	E-MANP-1 »
Author(s)	Muckenthaler Schwager Richter Ansorge Hentze Braun
Laboratory	EMBL
Experiment	E-MANP-2 »
Author(s)	Preiss Ansorge Richter Schwager Hentze
Laboratory	EMBL
Experiment	E-SNGR-1 »
Author(s)	Burns Bahler
Laboratory	The Wellcome Trust Sanger Institute
Experiment	E-SNGR-2 »
Author(s)	Mata Bahler Burns
Laboratory	The Wellcome Trust Sanger Institute
Experiment	E-SNGR-3 »

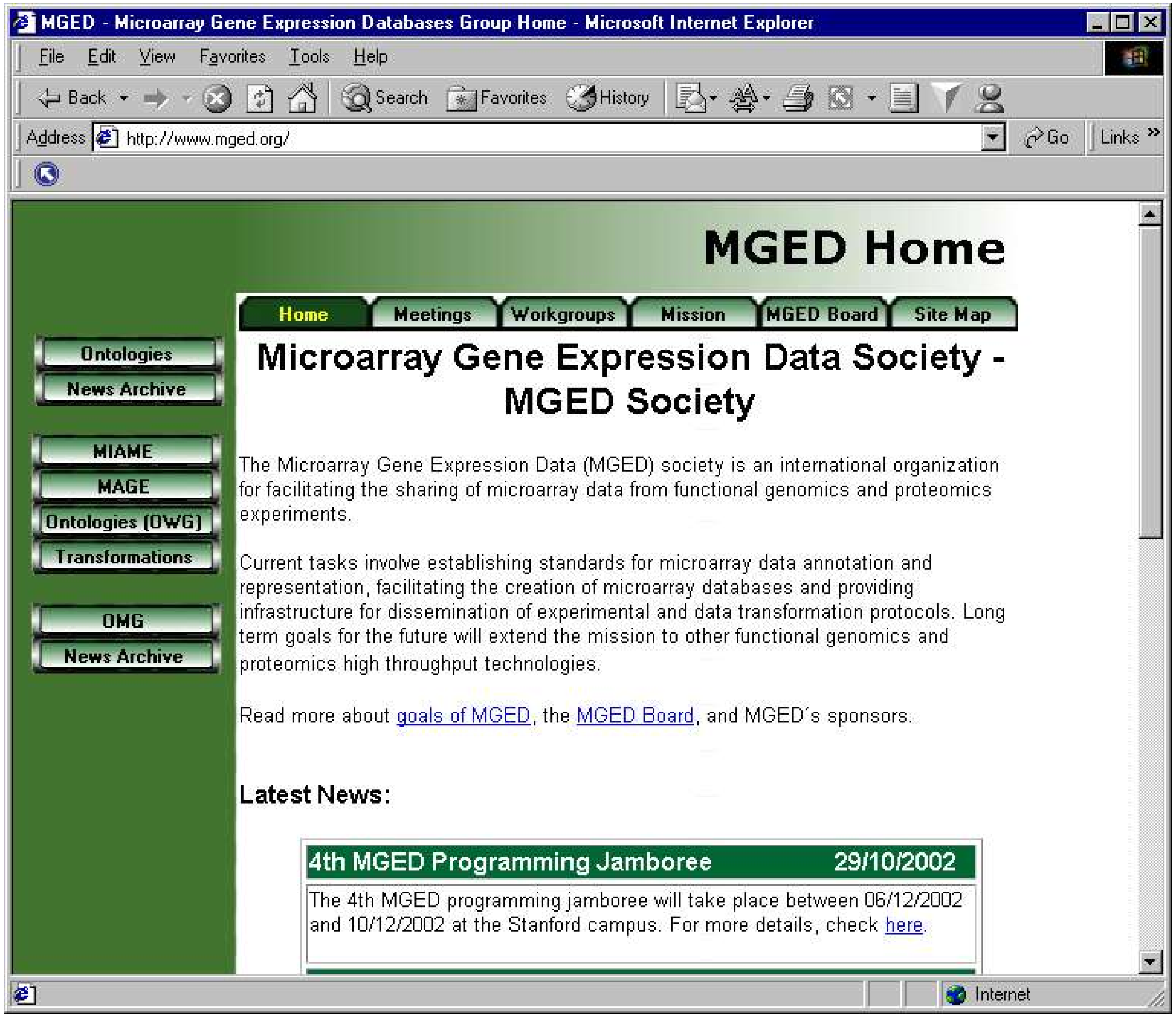
Arrays

Array	ARDES:A-EMBL-1 »
Name	EMBL Iron Chip
Provider	EMBL
Array	ARDES:A-EMBL-2 »
Name	EMBLyeast12Kver1.1
Provider	EMBL
Array	ARDES:A-SNGR-1 »
Name	Sanger Institute S. pombe array version 3
Provider	The Wellcome Trust Sanger Institute
Array	ARDES:A-SNGR-2 »
Name	Sanger Institute S. pombe array version 2, Pver2.1.1
Provider	The Wellcome Trust Sanger Institute

Protocol types

- array printing »
- array quality control »
- compute »
- control spot preparation »
- feature extraction »
- growth »
- hybridization »
- image analysis »
- labeling »
- labeling and hybridization »

http://www.mged.org/



MGED Home

Microarray Gene Expression Data Society - MGED Society

The Microarray Gene Expression Data (MGED) society is an international organization for facilitating the sharing of microarray data from functional genomics and proteomics experiments.

Current tasks involve establishing standards for microarray data annotation and representation, facilitating the creation of microarray databases and providing infrastructure for dissemination of experimental and data transformation protocols. Long term goals for the future will extend the mission to other functional genomics and proteomics high throughput technologies.

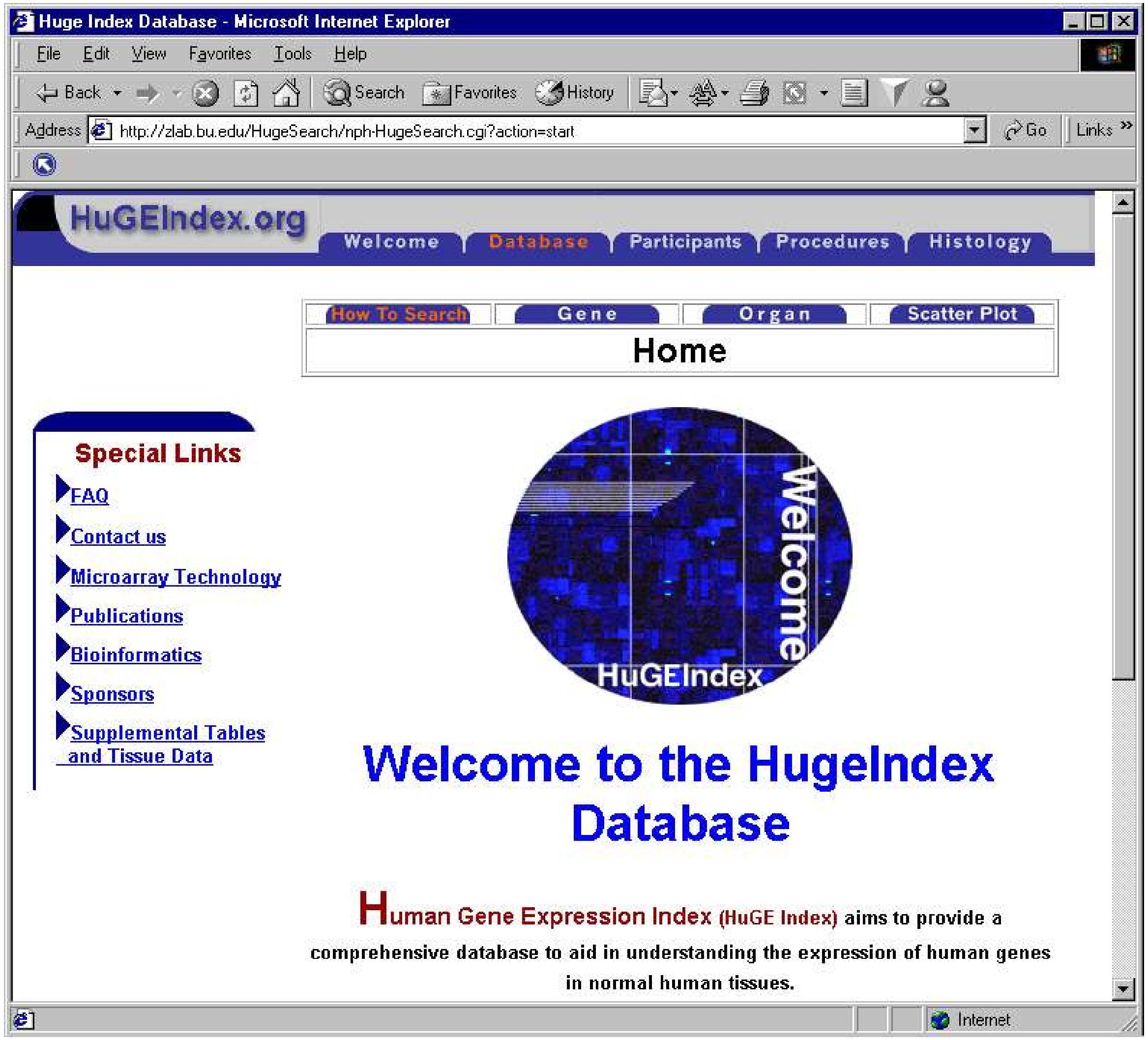
Read more about goals of MGED, the MGED Board, and MGED´s sponsors.

Latest News:

4th MGED Programming Jamboree 29/10/2002

The 4th MGED programming jamboree will take place between 06/12/2002 and 10/12/2002 at the Stanford campus. For more details, check here.

http://zlab.bu.edu/HugeSearch/nph-HugeSearch.cgi?action=start



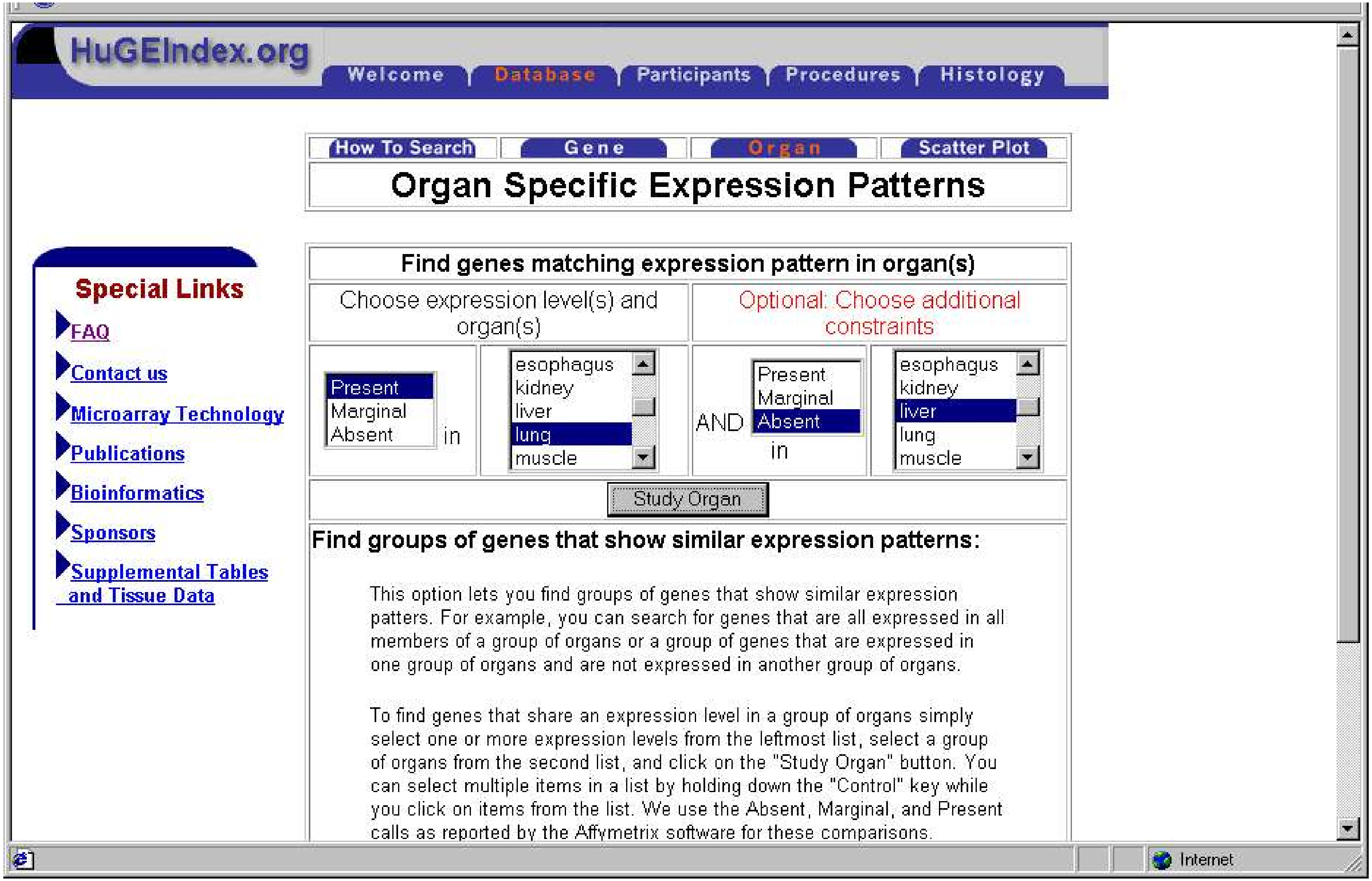
Special Links

- FAQ
- Contact us
- Microarray Technology
- Publications
- Bioinformatics
- Sponsors
- Supplemental Tables and Tissue Data

Welcome to the HugeIndex Database

Human Gene Expression Index (HuGE Index) aims to provide a comprehensive database to aid in understanding the expression of human genes in normal human tissues.

Поиск генов, экспрессирующихся в легких, но не экспрессирующихся в печени



Organ Specific Expression Patterns

Find genes matching expression pattern in organ(s)

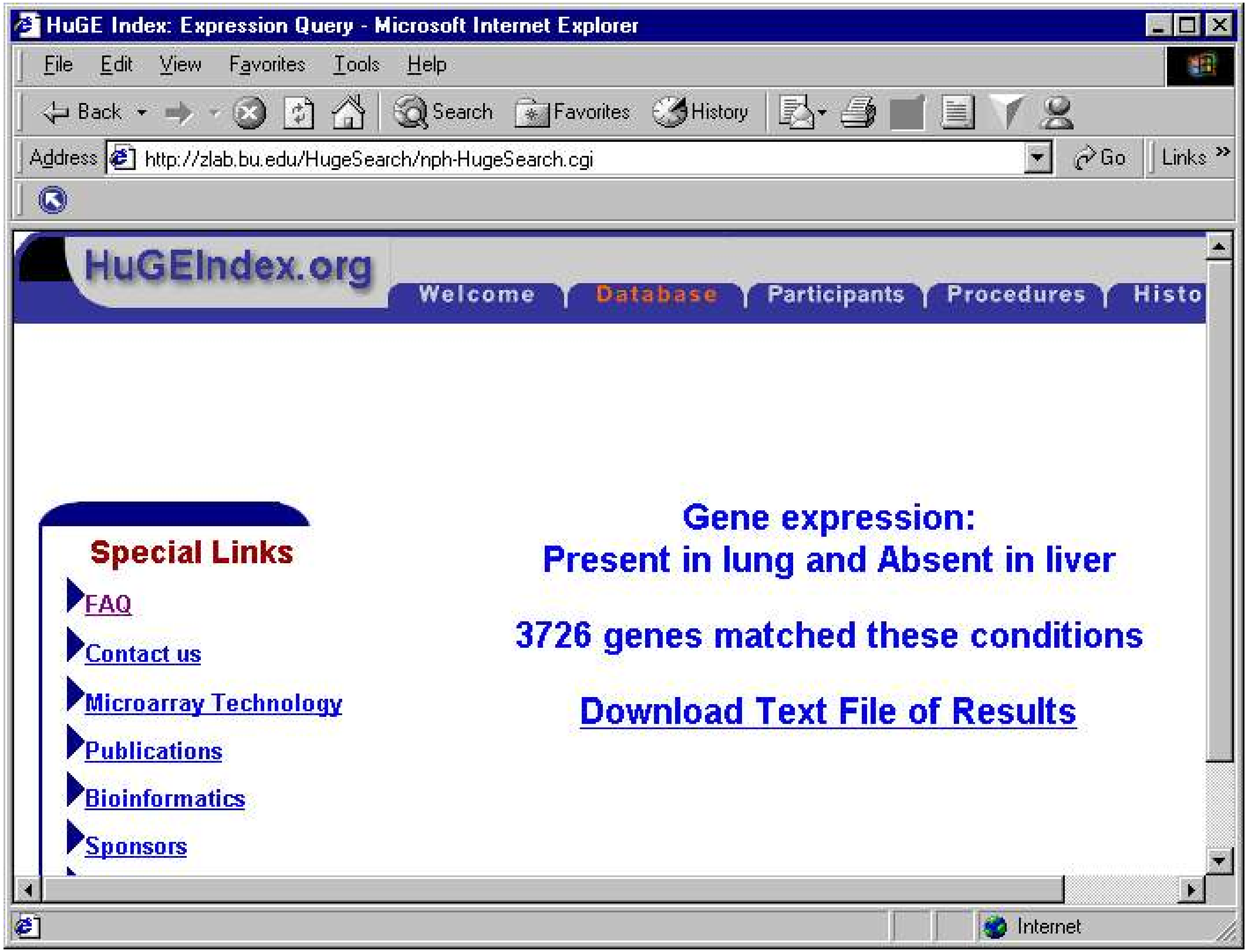
Choose expression level(s) and organ(s)		Optional: Choose additional constraints	
Present (selected) Marginal Absent — in	esophagus kidney liver lung (selected) muscle	AND Present Marginal Absent (selected) — in	esophagus kidney liver (selected) lung muscle

Find groups of genes that show similar expression patterns:

This option lets you find groups of genes that show similar expression patters. For example, you can search for genes that are all expressed in all members of a group of organs or a group of genes that are expressed in one group of organs and are not expressed in another group of organs.

To find genes that share an expression level in a group of organs simply select one or more expression levels from the leftmost list, select a group of organs from the second list, and click on the "Study Organ" button. You can select multiple items in a list by holding down the "Control" key while you click on items from the list. We use the Absent, Marginal, and Present calls as reported by the Affymetrix software for these comparisons.

Результат поиска – 3726 генов



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Gene expression:
Present in lung and Absent in liver

3726 genes matched these conditions

Download Text File of Results