MEME
Multiple Em for Motif Elicitation

Программа **MEME**

Множественное локальное выравнивание

http://meme.nbcr.net/meme4_3_0/cgi-bin/meme.cgi

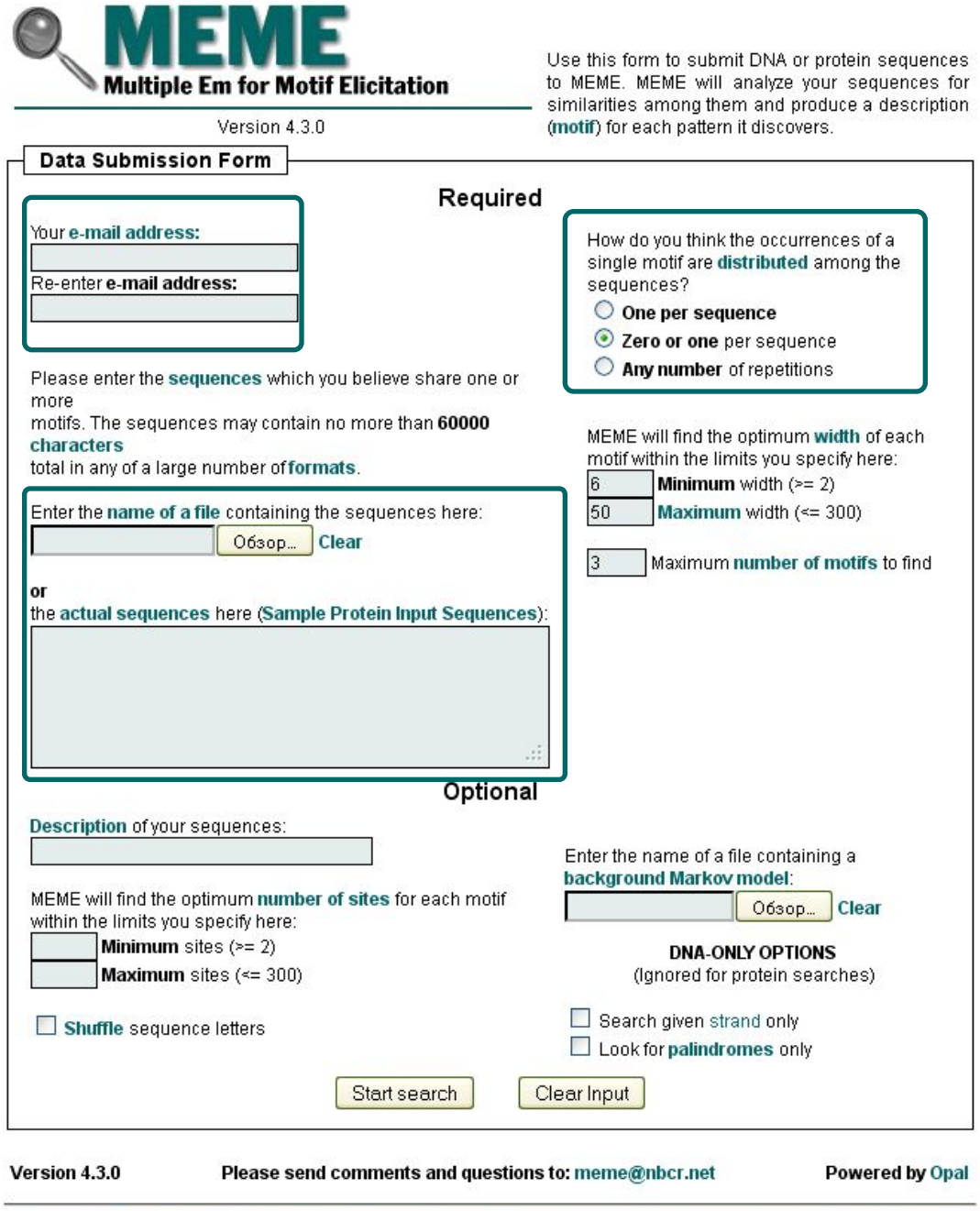
MEME
Multiple Em for Motif Elicitation

- Локальное выравнивание довольно часто имеет больший биологический смысл, чем глобальное

- MEME – наиболее популярная программа множественного локального выравнивания

- MEME находит **блоки**, т.е.участки локальных выравниваний <u>без</u> гэпов

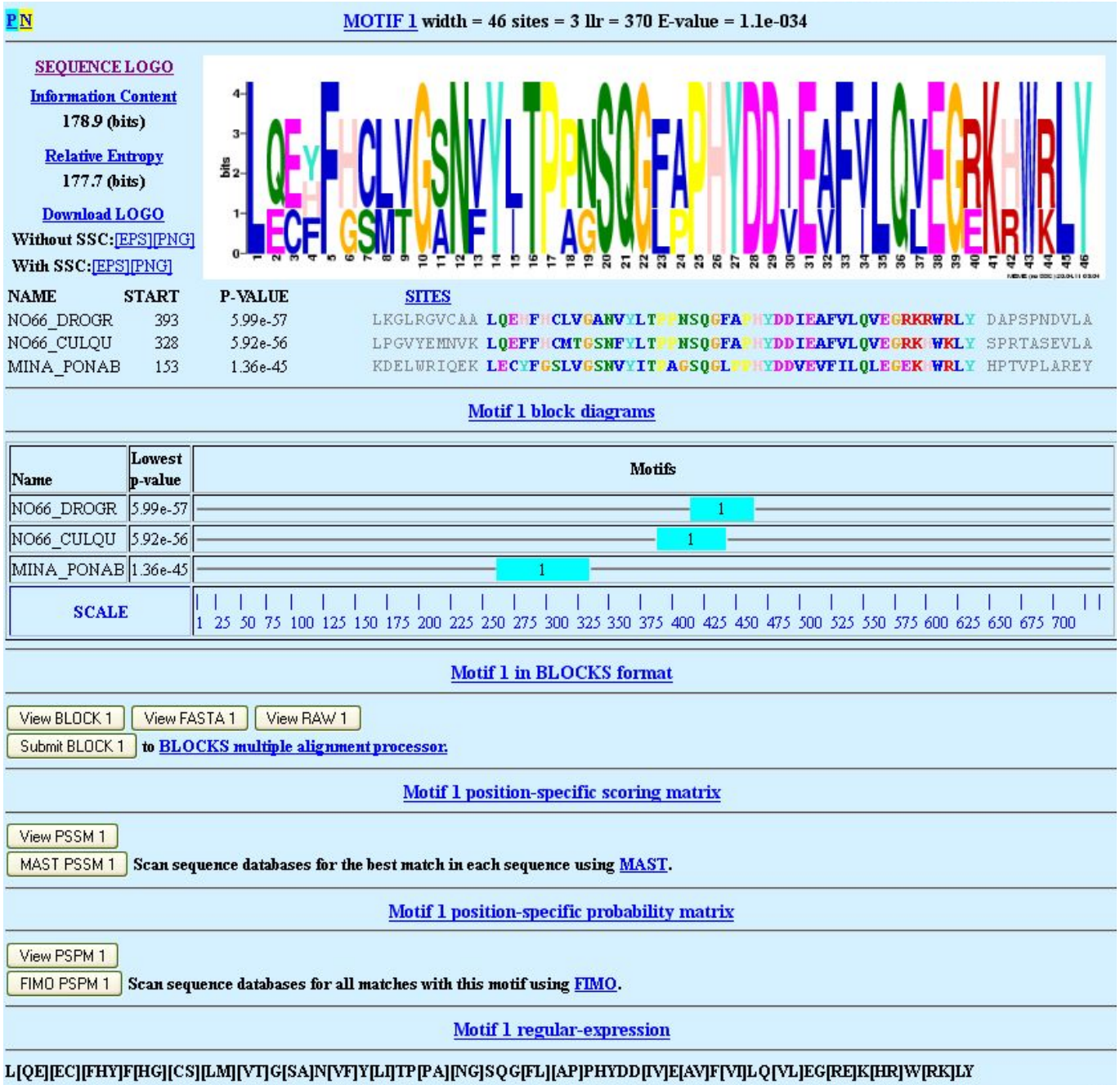
Онлайн форма **MEME**



Следует заполнить:

1. Email
2. Загрузить файл с последовательностями в FASTA-формате (или paste в текстовое поле)
3. Указать, сколько раз найденный блок может встречаться в заданном выравнивании
   - Один
   - От нуля до одного
   - Любое число раз

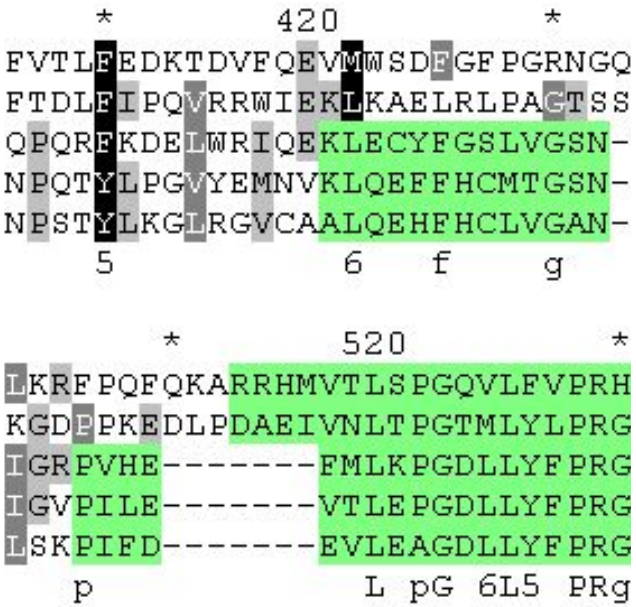
Основные результаты MEME



Для каждого **блока**

- SEQUENCE LOGO
- log likelihood ratio(LLR)
- E-value
- p-value
- PSSM (position-specific scoring matrix
- PSPM (position-specific probability matrix)

MEME vs Muscle



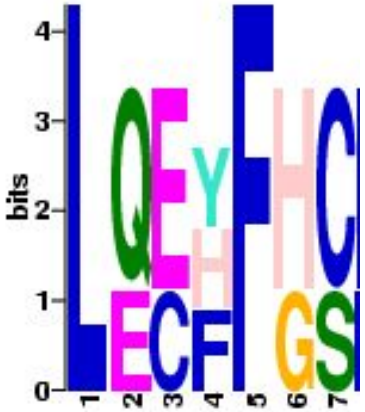
- Блоки MEME не обязательно во всех последовательностях
- Блоки MEME могут не совпадать с выравниванием Muscle

View PSSM 1

MAST PSSM 1

PSSM
(position-specific scoring matrix)

	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
1	-276	-201	-435	-395	-91	-381	-330	21	-364	**312**	48	-358	-384	-288	-298	-360	-253	-99	-249	-239
2	-191	-252	-142	**60**	-350	-286	-44	-249	-171	-257	-124	-154	-295	**389**	-145	-231	-209	-284	-286	-318
3	-270	**164**	-161	**344**	-395	-321	-319	-291	-303	-399	-312	-251	-427	-236	-310	-316	-294	-330	-427	-371
4	-182	-128	-264	-276	**264**	-269	**242**	-125	-266	-169	-108	-182	-310	-204	-205	-205	-210	-181	-3	**360**
5	-319	-179	-422	-448	**454**	-397	-348	-145	-444	-144	-149	-379	-413	-426	-416	-333	-363	-237	-153	-21
6	-186	-190	-135	-207	-188	**169**	**420**	-246	-197	-279	-183	-23	-297	-61	-126	-165	-172	-264	-221	-58
7	-202	**597**	-438	-455	-389	-317	-418	-291	-458	-409	-304	-358	-449	-417	-399	**-76**	-239	-339	-460	-431

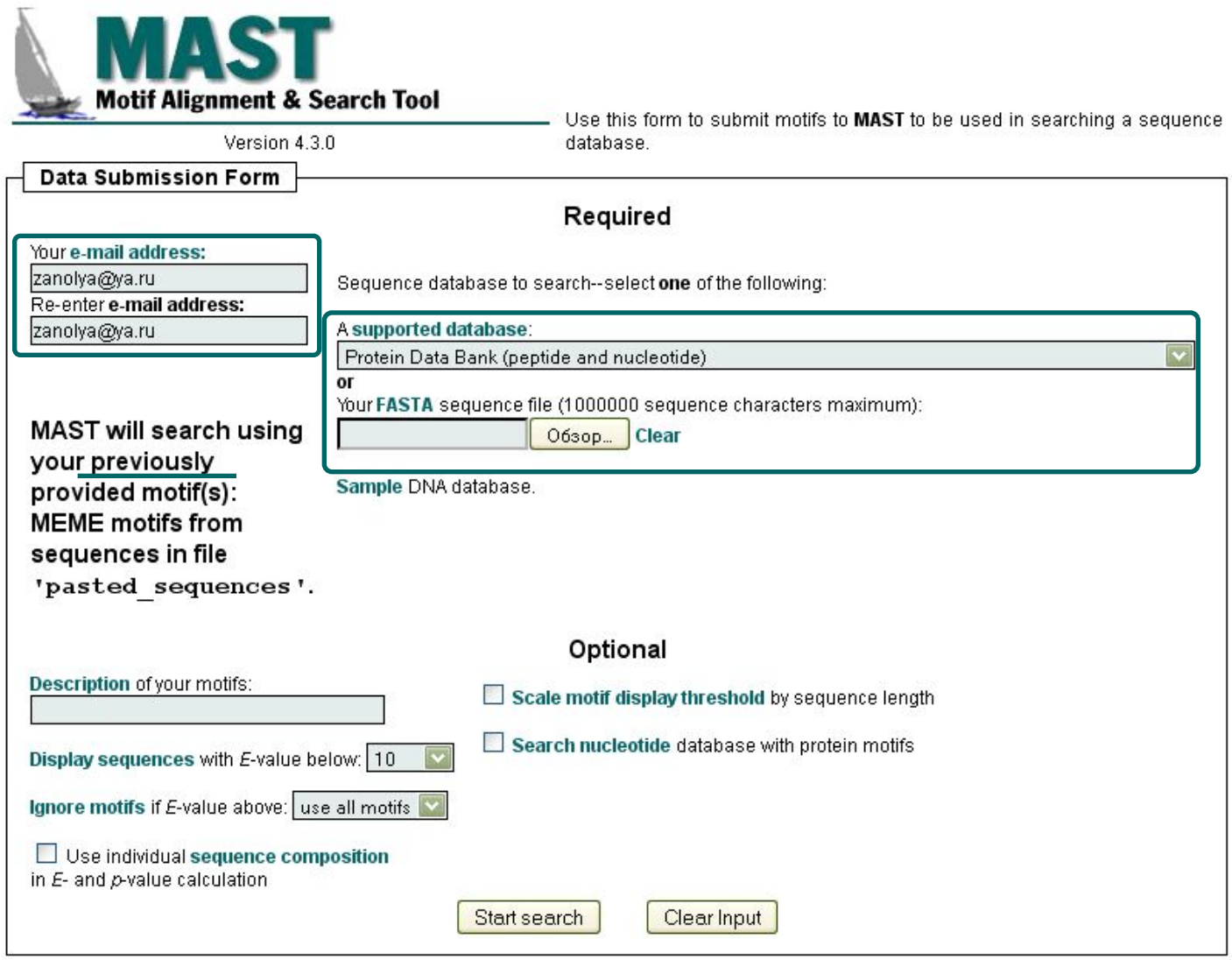


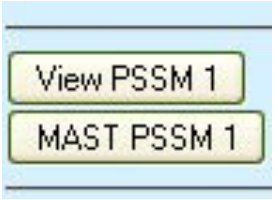
LQEHFHC

LQEFFHC

LECYFGS

1234567





- Motif file name: **MEME motifs from sequences in file pasted_sequences.**
- Number of motifs: **1**
- Total motif columns: **46**
- Motif alphabet: **PROTEIN**
- Database to search: **Protein Data Bank (peptide and nucleotide) (pdb.aa)**
- Displaying sequences with ***E*-value < 10**
- Motif display threshold: **motif *p*-value < 0.0001**

Основные результаты MAST

SECTION III: ANNOTATED SEQUENCES

- The positions and p-values of the non-overlapping motif occurrences are shown above the actual sequence for each of the high-scoring sequences from Section I.
- A motif occurrence is defined as a position in the sequence whose match to the motif has POSITION p-value less than 0.0001 as defined in Section II.
- For each sequence, the first line specifies the name of the sequence.
- The second (and possibly more) lines give a description of the sequence.
- Following the description line(s) is a line giving the length, combined p-value, and E-value of the sequence as defined in Section I.
- The next line reproduces the motif diagram from Section II.
- The entire sequence is printed on the following lines.
- Motif occurrences are indicated directly above their positions in the sequence on lines showing
  - the motif number of the occurrence,
  - the position p-value of the occurrence,
  - the best possible match to the motif, and
  - columns whose match to the motif has a positive score (indicated by a plus sign).

ESD ?gi|62738146|pdb|1VRB|A
Chain A, Crystal Structure Of Putative Asparaginyl Hydroxylase (2636534) From Bacillus Subtilis At 2.60 A Resolution

- pdb|1VRB|B Chain B, Crystal Structure Of Putative Asparaginyl Hydroxylase (2636534) From Bacillus Subtilis At 2.60 A Resolution
- pdb|1VRB|C Chain C, Crystal Structure Of Putative Asparaginyl Hydroxylase (2636534) From Bacillus Subtilis At 2.60 A Resolution
- pdb|1VRB|D Chain D, Crystal Structure Of Putative Asparaginyl Hydroxylase (2636534) From Bacillus Subtilis At 2.60 A Resolution

LENGTH = 342 COMBINED P-VALUE = 1.77e-05 E-VALUE = 0.78
DIAGRAM: 131-[1]-165

```
                                                        [1]
                                                        6.0e-08
                                                        LQEYFHCLVGSNVYLTPPN
                                                                   +     +
76   XVVGDAVIEESEGITDRFLVSPAEALEWYEKGAALEFDFTDLFIPQVRRWIEKLKAELRLPAGTSSKAIVYAAKN

     SQGFAPHYDDIEAFVLQVEGRKHWRLY
       ++  +++     + ++ +++ +++
151  GGGFKAHFDAYTNLIFQIQGEKTWKLAKNENVSNPXQHYDLSEAPYYPDDLQSYWKGDPPKEDLPDAEIVNLTPG
```