

Accordingly HOmo sapiens COmprehensive MOdel COllection (HOCOMOCO) v11, PMID: 29140464

Superclass

Basic domains

Zinc-coordinating DNA-binding domains

Helix-turn-helix domains

Other all-alpha-helical DNA-binding domains

alpha-Helices exposed by beta-structures

Immunoglobulin fold

beta-Hairpin exposed by an alpha/beta-scaffold

beta-Sheet binding to DNA

beta-Barrel DNA-binding domains

Yet undefined DNA-binding domains

## Class

Basic leucine zipper factors (bZIP)

Basic helix-loop-helix factors (bHLH)

Basic helix-span-helix factors (bHSH)

Nuclear receptors with C4 zinc fingers

Other C4 zinc finger-type factors

C2H2 zinc finger factors

DM-type intertwined zinc finger factors

CXXC zinc finger factors

C2HC zinc finger factors

C3H zinc finger factors

C2CH THAP-type zinc finger factors

Homeo domain factors

Paired box factors

Fork head / winged helix factors

Heat shock factors

Tryptophan cluster factors

TEA domain factors

ARID domain factors

High mobility group (HMG) domain

Heteromeric CCAAT-binding factors

MADS box factors

SAND domain factors

Rel homology region (RHR) factors

STAT domain factors

p53 domain factors

Runt domain factors

T-Box factors

NDT80 domain factors

Grainyhead domain factors

SMAD/NF-1 DNA-binding domain factors

GCM domain factors

TATA-binding proteins

A.T hook factors

Cold shock domain factors

Yet undefined DNA binding domains

Number in human genome

58

111

5

48

19

697

8

7

12

6

12

244

9

68

6

68

4

15

44

3

5

8

25

7

3

3

17

1

6

12



3

2

3

19

## Number in Supertargets

3

5

0

3

2

9

0

0

0

0

0

7

3

1

0

6

1

0

5

0

2

0

2

0

1

1

0

0

0

1

0

1

0

0

Supertargets/Genome, %

5.2%

4.5%

0.0%

6.3%

10.5%

1.3%

0.0%

0.0%

0.0%

0.0%

0.0%

2.9%

33.3%

1.5%

0.0%

8.8%

25.0%

0.0%

11.4%

0.0%

40.0%

0.0%

8.0%

0.0%

33.3%

33.3%

0.0%

0.0%

0.0%

8.3%

0.0%

50.0%

0.0%

0.0%