

A

## Search for unique ZFP-binding sites in the DNA sequence

1. Enter/Paste the DNA Sequence here without any space:

```
>(gi|349631:88-202, 581-734, 943-1127, 1336-1475, 2239-2401, 2934-3030, 3283-3352, 3708-3893) Homo sapiens interleukin-2 receptor gamma subunit (IL2RG) gene, complete cds
ATGTTGAAGCCATCATTACCATTACATCCCTCTTATTCTGCAGCTGCCCTGCTGGGAGT
GGGGCTGA
ACACGACAATTCTGACGCCAATGGGAATGAAGACACCACAGCTGATTCTTCTGACCACT
```

2. Or, upload a sequence file in raw format directly from your local disk:

B

### Result of Zif-BASE search using sequence data

Length of Sequence is 1316

Total number of motif found: 1

[Input sequence showing specified zinc finger motif binding sequences](#)

[Detailed list of position and the specified zinc finger motif](#)

#### Input sequence showing specified zinc finger motif binding sequences

```
>(gi|349631:88-202, 581-734, 943-1127, 1336-1475, 2239-2401, 2934-3030, 3283-3352, 3708-3893) Homo sapiens interleukin-2 receptor gamma subunit (IL2RG) gene, complete cds
ATGTTGAAGCCATCATTACCATTACATCCCTCTTATTCTGCAGCTGCCCTGCTGGGAGTGGGGCTGA
ACACGACAATTCTGACGCCAATGGGAATGAAGACACCACAGCTGATTCTTCTGACCACTATGCCCACT
GACTCCCTCAAGTGTTCACCTCTGCCCTCCCAAGAGTTCAGTGTTTTGTGTTCAATGTCAGTACATG
AATTGCACTTGGAAACAGCAGCTCTGAGCCCCAGCCTACCAACCTCACTCTGCATTATTGGTACAAGAACT
CGAATAATGATAAAGTCCAGAAAGTGCAGCACTATCTATTCTCTGAAGAAATCACTTCTGGCTGTCAAGT
GCAAAAAAAGGAGATCCACCTCTACCAAAACATTTGTGTTTCAGCTCCAGGACCCACGGGAACCCAGGAGA
CAGGCCACACAGATGCTAAAATGCAGAACTCTGGTATCCCTGGGCTCCAGAGAACCTAACACTTCACA
AACTGAGTGAATCCAGCTAGAACTGAACCTGGAAACAAGATTCTGAACCACTGTTTGGAGCACTTGGT
GCACTACCGGATGACTGGGACCCAGCTGGACTGAACAACTCACTGGATTATAGACATAAGTTCTCCTTG
CCTAGTGTGATGGCAGAAACGCTACACGTTTCGTGTTTCGGAGCCGCTTTAACCCACTCTGTGGAAGTG
CTCAGCATTTGGAGTGAATGGAGCCACCCCAATCCACTGGGGGAGCAATCTTCAAAAGAGAAATCCTTTCT
GTTTGCATTGGAGCCGTGGTTATCTCTGTTGGCTCCATGGGATTGATTATCAGCCCTTCTCTGTGTAT
TTCTGGCTGGAACGAGATGCCCGGAATCCCAACCTGAAGAACCTAGAGGATCTTGTACTGAATACC
ACGGGAACCTTTTCGCCCTGGAGTGGTGTCTAAGGGACTGGCTGAGAGTCTGCAGCCACAGCTACAGTGA
ACGACTCTGCTCTGCTGAGATTCCCCCAAAGGAGGGGCCCTTGGGAGGGGCTGGGGCTCCCA
TGCAACCGCATAGCCCCCTACTGGGCCCCCCCATGTTACACCCCTAAAGCCTGAAACCTGA
```

[Detailed list of position and the specified zinc finger motif](#)

| S.No | Position  | Sequence  | Protein name |
|------|-----------|-----------|--------------|
| 1    | 1226-1235 | GGGGAGGGG | GNG-GA3      |

C

#### General Information

|                                                                                                             |                                                                                                      |       |                       |                      |
|-------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------|-------|-----------------------|----------------------|
| Protein name                                                                                                | GNG-GA3                                                                                              |       | Organism              | Engineered Construct |
| Class                                                                                                       | C2H2 (ZF)                                                                                            |       | Molecular Weight *    | 11.34 kDa            |
| Framework                                                                                                   | Sp1                                                                                                  |       | Iso-Electric Point *  | 10.94                |
| Length of Protein                                                                                           | 95 aa                                                                                                |       | Dissociation Constant | NA                   |
| Protein Sequence                                                                                            | MDPGRKKQKHICHIQGGCKVYGRSDHLARHLRWHTG<br>ERFPMTWSYCGKRFTRSDNLRHHRHTGKFKFA<br>CPECPRKPRMSDHLRRIKTHQNKU |       |                       |                      |
| Key amino acid residues at positions -1, +1, +2, +3, +4, +5 and +6 relative to the start of the alpha-helix | Finger 1                                                                                             | 22-28 | RSDDLAR               |                      |
|                                                                                                             | Finger 2                                                                                             | 52-58 | RSNLLAR               |                      |
|                                                                                                             | Finger 3                                                                                             | 80-86 | RSDDLAR               |                      |
| Binding Sequence                                                                                            | GGGGAGGGG                                                                                            |       |                       |                      |

\* Determined theoretically

#### Reference

Lin, Q., Xia, Z., Zhong, X. and Case, C.C.(2002) Validated zinc finger protein designs for all 16 GNN DNA triplet targets. J Biol Chem, 277, 3850-3856. [ [Pubmed](#) ]