

ZZ domain of dystrophin and utrophin: topology and mapping of a beta-dystroglycan interaction site.

Karim Hnia, Dora Zouiten, Sonia Cantel, Delphine Chazalette, Gérald Hugon, Jean-Alain Fehrentz, Ahmed Masmoudi, Ann Diment, Janice Bramham, Dominique Mornet, et al.

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6ECPIIGF ¹⁹YRSLKHF ³¹YDICQSC 4KECPIIG ¹⁸RYRSLKH ²⁹NYDICQS ²CKECPII ¹⁷FRYRSLK ²⁷FNYDICQ ¹ICKECPI ¹⁶GFRYRSL ²⁵HFNYDIC NICKECP 14IGFRYRS 23KHFNYDI CNICKEC ¹²IIGFRYR ²²LKHFNYD ³⁵ICQSCFF KCNICKE ¹⁰PIIGFRY ²¹SLKHFNY AKCNICK ⁸CPIIGFR ²⁰RSLKHFN ³³DICQSCF Dys 3311...AKCNICKECPIIGFRYRSLKHFNYDICQSCFF...3342 1111111111:11111111111:11111 Utr 3068...AKCNICKECPIVGFRYRSLKHFNYDVCQSCFF...3099 ²⁴KHFNYDV 5KECPI**V**G ²⁶HFNYDVC 7ECPI**V**GF ²⁸FNYDVCQ ⁹CPI**V**GFR ³⁰NYDVCQS ¹¹PIVGFRY ³²YDVCQSC ¹³IVGFRYR ³⁴DVCQSCF

¹⁵VGFRYRS

³⁶VCQSCFF









Α.

1. MVWLPVLHRVAAAETAKHQA 2. VWLPVLHRVAAAETAKHQAK 3. WLPVLHRVAAAETAKHQAKC 4. LPVLHRVAAAETAKHQAKCN 5. PVLHRVAAAETAKHQAKCNI 6. VLHRVAAAETAKHQAKCNIC 7. LHRVAAAETAKHQAKCNICK 8. HRVAAAETAKHQAKCNICKE 9. RVAAAETAKHQAKCNICKEC 10. VAAAETAKHQAKCNICKECP 11. AAAETAKHQAKCNICKECPI 12. AAETAKHQAKCNICKECPIV 13. AETAKHQAKCNICKECPIVG 14. ETAKHQAKCNICKECPIVGF 15. TAKHQAKCNICKECPIVGFR 16. AKHQAKCNICKECPIVGFRY **17. KHQAKCNICKECPIVGFRYR 18. HQAKCNICKECPIVGFRYRS** 19. QAKCNICKECPIVGFRYRSL 20. AKCNICKECPIVGFRYRSLK 21. KCNICKECPIVGFRYRSLKH 22. CNICKECPIVGFRYRSLKHF 23. NICKECPIVGFRYRSLKHFN 24. ICKECPIVGFRYRSLKHFNY 25. CKECPIVGFRYRSLKHFNYD



KECPIVGFRYRSLKHFNYDV 26. ECPIVGERYRSI KHENYDVC 27. CPIVGFRYRSLKHFNYDVCQ 28. PIVGFRYRSLKHFNYDVCQS 29. IVGFRYRSLKHFNYDVCQSC 30. VGFRYRSLKHFNYDVCQSCF 31. GFRYRSLKHFNYDVCQSCFF 32. FRYRSLKHFNYDVCQSCFFS 33. RYRSLKHFNYDVCQSCFFSG 34. YRSLKHFNYDVCQSCFFSGR 35. RSLKHFNYDVCQSCFFSGRT 36. SLKHFNYDVCQSCFFSGRTA 37. LKHFNYDVCQSCFFSGRTAK 38. KHENYDVCQSCFFSGRTAKG 39. HENYDVCQSCFFSGRTAKGH 40. **FNYDVCQSCFFSGRTAKGHK 41.** NYDVCQSCFFSGRTAKGHKL 42. YDVCQSCFFSGRTAKGHKLH 43. DVCQSCFFSGRTAKGHKLHY 44. VCQSCFFSGRTAKGHKLHYP 45. CQSCFFSGRTAKGHKLHYPM 46.

- 47.
- 48.
- 49.
- 50.









Rabbit

Rabbit

Rabbit



Rabbit skeletal muscle



С

D

mdx mouse skeletal muscle

Figure 5CD Hnia et al





Figure 7 Hnia et al

| A | |
|----------------------|---|
| UTRO_HUMAN/3064-3109 | AKHQAK <mark>C</mark> NICKECPIVGFRYRSLKHFNYDVCQSCFFSGRTAKGHKL |
| DMD_HUMAN/3307-3354 | AKHQAKCNICKECPIIGFRYRSLKHFNYDICQSCFFSGRVAKGHKL |
| DTNB_HUMAN/237-282 | VFHPVECSYCRCESHMGFRYRCQQCHNYQLCQNCFHRGHAGGPHSN |
| CBP_human/1701-1744 | DRFVYTCNECKHHVETRMHCTVCEDYDLCINCYNTKSHAHKM |
| MIB_DROME/173-218 | KHEGTMCDTCRQQPIFGIRMKCAECINVDLCSICYHGDKHHLRHRF |
| REF2P_DROME/121-165 | IHDAVECDGCGLAPLIGFRYKCVQCSNYDLCQKCELA-HKHPEHLM |
| YOY6_CAEEL/8-52 | THEGVSCDGCAFTAFAGNRYKCLRCSDYDLCFSCFTT-KNYGDQQT |
| CBP1_CAEEL/1493-1532 | KGMEYTCNKCSSPAVNHCQSCDDFDLCDGCKPTTQHPHEM |
| ADA2_YEAST/1-46 | MSNKFHCDVCSADCTNRVRVSCAICPEYDLCVPCFSQGSYTGKH |
| RSC8_YEAST/254-298 | IHKVYICHTCGN-ESINVRYHNLRARDINLCSRCFQEGHFGANF |
| SMCL_ARATH/304-350 | PAVEYHCNSCSAD-CSRKRYHCPKQADFDLCTECPNSGKFSSDM |
| PRT1_ARATH/2005-255 | VHFGAGCDSCGVYPIIGDRYRCKDCKEEIGYDLCKDCYE-TPSKVPGRF |
| SMART Consensus/60% | spppspCssC.pbsGhRa+ChbC. DaDLCpsCbspbphpH. |
| | |
| В | |
| UTRO_HUMAN/3064-3109 | AKHQAKCNICKECPIVGFEYESLKHFNYDVCQSCFFSGRTAKGHKL |
| DYS/UTR In binding | 1 1 1 1 2 2 2 2 2 |
| CBP_human/1701_1744 | DREVVTCNECKHHVETRNHCTVCRDVDLCINCVNTKSHAHKM |
| CDD In hinding | |
| car an binding | |

| СВР | Zn | binding | 1 | 1 | 2 | 2 | |
|-----|----|---------|---|---|---|---|--|
| | | | | | | | |