

Figure S1. Secondary structure context of the Dx[DN]xDG motifs, highlighting additional metal-binding residues (Table 1). The figure includes those motifs described in ref. [15], Rigden & Galperin (2004) The Dx₂DG motif for calcium binding: Multiple structural contexts and implications for evolution. *J Mol Biol* 343(4): 971-984. Residues binding to metal using side chains are in red (direct interaction with calcium) or purple (through-water interaction). Secondary structure as defined by STRIDE [74] is indicated as follows: α -helices, blue shading; β -strands, yellow shading; 3_{10} helices, green shading; turns, brackets.

New folds

2z2x

202 QAILGPDGVADKDG^{red}GI IAGD^{red}PDDAAEVISMSL 235

2zxq

591 LPQMAVAIA^{yellow}G^{red}DENED^{red}GAVNWQD^{red}GAIAYR^{blue}DI^{blue}MNNP 624

3c68

421 AYHDW^{blue}WLRNRD^{red}HNG^{red}GVPEY^{yellow}GAT^{red}RDKAHNT^{yellow}ESGE 454...544 YSL^{yellow}LQ^{red}ESVDQA 554

3km5

1169 GEAPAEW^{yellow}TTID^{red}ADG^{red}DGQGW^{yellow}LCLS^{yellow}SGQLD^{yellow}WLTAHG 1202..1216 ALNP^{yellow}D^{red}NYLISK 1226

Calcium blades

1jv2

274 AYFGF^{yellow}SVAAT^{red}DING^{red}DDYAD^{red}VFIGAP^{yellow}PLF^{yellow}MDR^{yellow}GSDG 307

2z8r

148 TYSANDASV^{yellow}GD^{red}VDG^{red}DGQYEL^{yellow}LKWDP^{yellow}SNSK^{yellow}DNSQ 181

3hx6

841 PNGLS^{yellow}SPRLAD^{red}NNSD^{red}GVAD^{red}YAYAGD^{yellow}LQGNL^{yellow}WRFD 874

2bwr

167 RLDRH^{yellow}LRFLAD^{red}VTGD^{red}GLLDV^{yellow}VGF^{yellow}GENQ^{yellow}VYIARNS 200

From Rigden & Galperin (2004)

1exr

10 AEFKEAFALF^{blue}DKD^{red}GDG^{yellow}TI^{yellow}TTKEL^{red}GTVMRS^{blue}L^{blue}GQNP 43

1gcg

124 AKHWQAN^{green}QGW^{green}DLNK^{red}DGKI^{yellow}QYVLLK^{yellow}GEPGHPDAEA 157...200 NANKI^{blue}EVVIAN 210

1kwh

161 YTVLKAFKEK^{blue}DPNG^{red}NGKA^{red}DEV^{green}PFIDRHP^{green}DEVFRL 184

1daq
1 ___MSTKLYGDVNDGKVNSTDAVALKRYVLRSG 21

1qut
227 MPSSYKQYAVDFSGDGHINLWDPVDAIGSVANYF 260

1acc
167 PELKQKSSVPDRDNDGIPDSLEVEGYTVDVKNKR 200

1lwj
3 GYQIYVRSFRDGNLDGVGDFRGLKNAVSYLKELG 36

1h71
39 QLTRSGASWHDLNNDGVINLTYTFLTAPPVGYAS 72...109 AARGDDGHQTF 119

1kap
436 AASKAGSLAIDFSGDAHADFAINLIGQATQADIV 469

lux6 binuclear
833 RIGDTCDNNQDIDEDGHQNNLDNCPYVPNANQAD 866

lux6 mononuclear
892 CRLVPNPDQKDSGDGRGDAKDDFDHDSVPDID 925

1vjj
291 RVITNFNSAHTDRNLSVDVYYDPMGNPLDKGSD 324