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AIFM3_HUMAN/70-165      -AAVCHVKDLENGQMREVELG--WGKVLVVKDNGEFHALGHKCPHYGAPLVKGVLS-RGRVRCCPWHGACFNIS-TGDLEDFPGLDSLHKFQVKIEKEKVYV-----
AIFM3_MOUSE/70-165     -ATVCHVKDLENGQMREVELG--WGKVLVVKDNGEFHALGHKCPHYGAPLVKGVLS-RGRVRCCPWHGACFNIS-TGDLEDFPGLDSLHKFQVKIEKEKVYV-----
AIF1_SCHPO/56-154      -LEFDPSSVSKNGTKTEAKVVGTEFGVLLVRARNTYFATAGKCSHYGAPLAKGVVTSDGHIVCPWHGACFNAA-TGDVEDTPAIAALRTFPVTEEGDGSSLW-----
BEDB_PSEPU/4-99        -TYILRQSDLPPG-EMQRYEGGSEP-VMVCNVDGEFFAVQDTCTHGDWALSEG-YLDGDVVECTLHFGKFCVR-TGKVKALPACKPIKVYPIKIEGDEVHV-----
BNZC_PSEPU/4-99        -TYILRQSDLPPG-EMQRYEGGSEP-VMVCNVDGEFFAVQDTCTHGDWALSDG-YLDGDVVECTLHFGKFCVR-TGKVKALPACKPIKVYPIKIEGDEVHV-----
BPHA3_RHOJR/4-99       -TKICSSGDLAPG-EMLRFEEGPEP-ILVCNVGGEFFATQDTCSHADWALSEG-YLEDDVVECTLHWAKFCVR-TGKAKALPACVPLRTFVVKLEGDDVLV-----
BPHA3_PSES1/4-100      -TKACSVDEVPPG-EALQVSHDAQK-VAIFNVGGEFFATQDQCTHGEWSLSEGGYLDGDVVECSLHMGKFCVR-TGKVKSPPPCEPLKVYPIRIEGRDVLV-----
ANDAB_BURCE/9-105     -WHPLGAIDFETED-EPAARVAGQKP-IAVFRIGDELFAMHDLCSHGHARLSEG-YVEDGCVECPLHQGLIDIR-TGAPKCAPITEPVRVIPIRIVDQQVEV-----
CAO_ARATH/221-321     -WYPVAFTADLKHDT-MVPIECFEQPWVIFRGEDGKPGCVRNTCAHRACPLDLG-TVNEGRIQCPYHGWEYSTD--GECKKMPSTKLLK-VKIKSLPCLEQEGMIWI-----
CAO_CHLRE/305-406     -WYPAEFSARLPKDT-LVPFELFGEPWVMFRDEKGPSCIRDECAHRGCPLSLG-KVVEGQVMCPYHGWEFNGD--GACTKMPSTPFCRNVGVAALPCAEKDGFIWV-----
BNZA_PSEP1/54-163     -WLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLNQCRHRGMRICRADAGNAKAFTCSYHGWAYDTA--GNLVNVPYEAESFACLNKKEWSPLKARVETYKGLIFA-----
BNZA_PSEPU/54-163     -WLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLNQCRHRGMRICRADAGNAKAFTCSYHGWAYDTA--GNLVNVPYEAESFACLNKKEWSPLKARVETYKGLIFA-----
BEDC1_PSEPU/65-163    -----KPGDYFTTYMGEDPVVVVRQKDASIAVFLNQCRHRGMRICRADAGNAKAFTCSYHGWAYDTA--GNLVNVPYEAESFACLNKKEWSPLKARVETYKGLIFA-----
BPHA1_PSES1/59-141    -WLLLGHEAHIPKTGDYLTTYMGEDPVIMVVRQKDSIKVFLNQCRHRGMRICRADAGNAKAFTCTYHGWAYDIA--GNLVNVPYEK-----
BPHA_PARXL/58-140     -WLLLGHESHVPETGDFLATYMGEDPVVVVRQKDSIKVFLNQCRHRGMRICRADAGNAKAFTCSYHGWAYDIA--GKLVNVPFEK-----
BENA_ACIAD/54-134    -VYLAHESQIPNNNDYTYTYIGRQPILIARNRNGELNAMINACSIRGAQLCRHKRGNKTYTCPFHGWTFNNS--GKLLKVKDP-----
AIOB_ALCFA/62-158    --NEPVSFTYPDTSSPCVAVKLGSPVGGVGNNDIVAYSVLCTHMGCPTSYD--KSSKTFKCPCHFEFDAEKAGQMICGQATENLPRVLLRYDEASDAL-----
AIOB_HERAR/60-156    --DAPVSNYDPDASSPCVAIKMQPTPGGVGNNDIVAHSILCTHMGCPVSYD--ASAKTFKCPCHFSVFPDPNHGQMVCGQATENLPQIQLSYNAANDTF-----

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Rieske [2Fe-2S] 鉄硫黄ドメイン  
のプロファイル

C-x-H-x(15-17)-C-x-x-H  
鉄結合部位のモチーフ

図3.13 Rieske型鉄硫黄クラスター結合部位のドメインとモチーフの例