

SUPPLEMENTARY INFORMATION

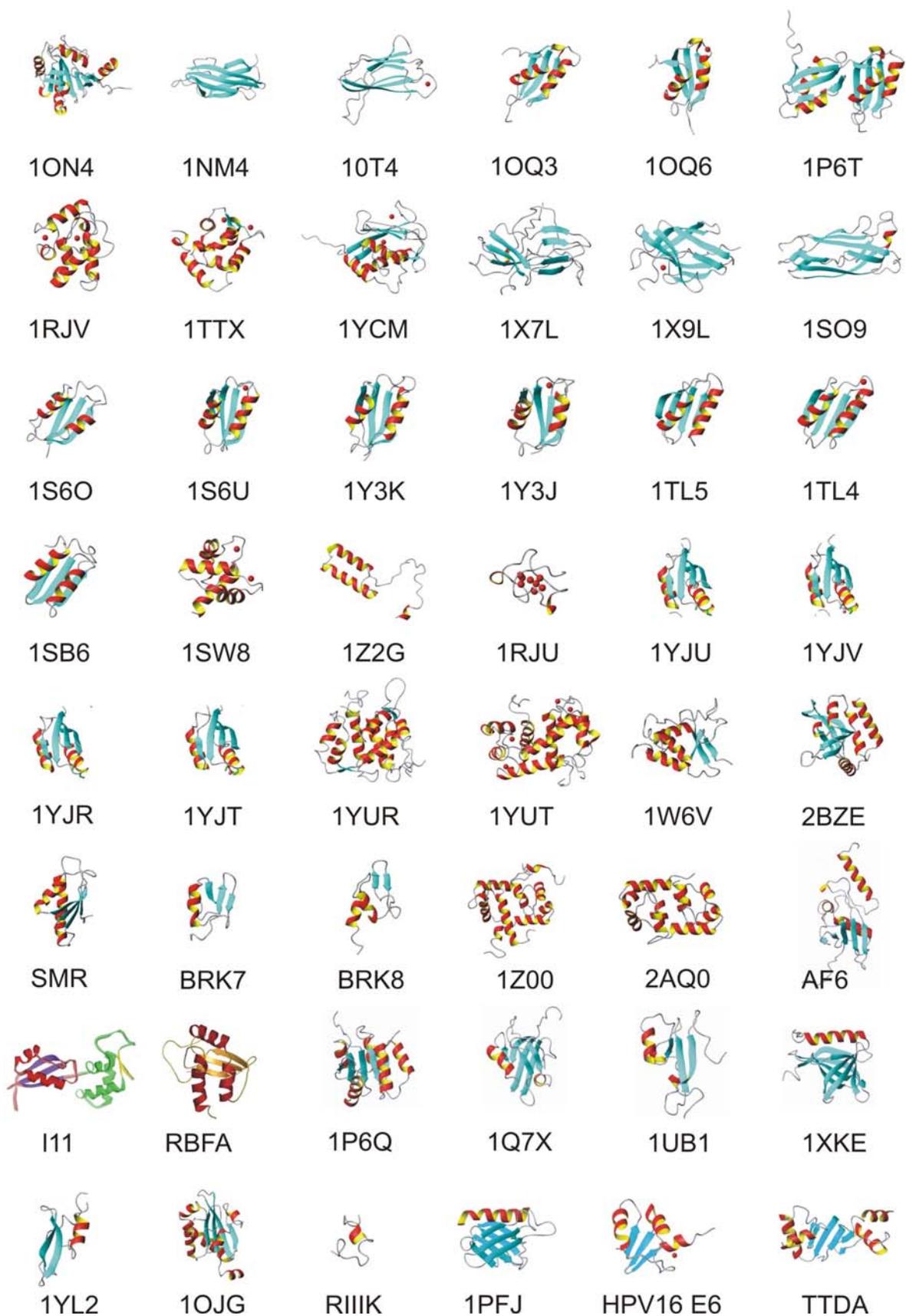


Figure 1 Structures solved in the NMR mode of SPINE

Protein structures by the NMR node of SPINE

Protein Name	Accession number (Swiss-Prot)	Protein domain (Pfam)	Protein Size (kD)	pI	Species	M	PDB entry	Ref
Sco1	P54178	SCO1/SenC	19.1	4.7	Bs	N	1ON4	Balatri <i>et al.</i> , 2003
CopC (Cu(I))	P12376	CopC	11.2	8.3	Ps	N	1NM4	Arnesano <i>et al.</i> , 2003c
CopC (Cu(II))	P12376	CopC	11.2	8.3	Ps	N	1OT4	Arnesano <i>et al.</i> , 2003b
S46VCopAa (apo)	O32220	HMA	8.3	5.3	Bs	N	1OQ3	Banci <i>et al.</i> , 2003a
S46VCopAa (Cu(I))	O32220	HMA	8.4	5.3	Bs	N	1OQ6	Banci <i>et al.</i> , 2003a
S46VCopAab	O32220	HMA	16.6	5.1	Bs	N	1P6T	Banci <i>et al.</i> , 2003b
Parvalbumin	P20472	EFhand	12.1	5.0	Hs	N	1RJV	Baig <i>et al.</i> , 2004
Oncomodulin	P32930	EFhand	12.0	4.2	Hs	N	1TTX	Babini <i>et al.</i> , 2004a
MMP12	P39900	Peptidase_M10	17.4	6.1	Hs	N	1YCM	Bertini <i>et al.</i> , 2005a
DR1885 (apo)	Q9RT80	DUF461	16.3	10.3	Dr	N	1X7L	Banci <i>et al.</i> , 2005d
DR1885 (Cu(I))	Q9RT80	DUF461	16.3	10.3	Dr	N	1X9L	Banci <i>et al.</i> , 2005d
Cox11-like protein	Q92RG6	CtaG_Cox11	18.0	4.9	Sm	N	1SO9	Banci <i>et al.</i> , 2004b
Menkes protein ATP7A (apo)	Q04656	HMA_2	8.4	8.7	Hs	N	1S6O	Banci <i>et al.</i> , 2004c
Menkes protein ATP7A (Cu(I))	Q04656	HMA_2	8.4	8.7	Hs	N	1S6U	Banci <i>et al.</i> , 2004c
Menkes protein ATP7A (apo)	Q04656	HMA_5	8.5	6.4	Hs	N	1Y3K	Banci <i>et al.</i> , 2005c
Menkes protein ATP7A (Cu(I))	Q04656	HMA_5	8.5	6.4	Hs	N	1Y3J	Banci <i>et al.</i> , 2005c
Hah1 (apo)	O00244	HMA	7.5	6.7	Hs	N	1TL5	Anastassopoulou <i>et al.</i> , 2004
Hah1 (Cu(I))	O00244	HMA	7.5	6.7	Hs	N	1TL4	Anastassopoulou <i>et al.</i> , 2004
Atx1	P73213	HMA	7.0	4.6	Ss	N	1SB6	Banci <i>et al.</i> , 2004a
Calmodulin	P62158	EFhand	8.7	4.2	Hs	N	1SW8	Bertini <i>et al.</i> , 2004a
Cox17	Q12287	Cox17	7.6	4.9	Sc	N	1Z2G	Arnesano <i>et al.</i> , 2005a
Copper Thionein	P07215	WAP	4.0	5.5	Sc	N	1RJU	Calderone <i>et al.</i> , 2005
Menkes protein ATP7A (apo)	Q04656	HMA_6	8.3	6.9	Hs	N	1YJU	Banci <i>et al.</i> , 2005b
Menkes protein ATP7A (Cu(I))	Q04656	HMA_6	8.3	6.9	Hs	N	1YJV	Banci <i>et al.</i> , 2005b
Menkes protein ATP7A (apo) (A69P)	Q04656	HMA_6	8.3	6.9	Hs	N	1YJR	Banci <i>et al.</i> , 2005b
Menkes protein ATP7A (Cu(I)) (A69P)	Q04656	HMA_6	8.3	6.9	Hs	N	1YJT	Banci <i>et al.</i> , 2005b
S100A13 (apo)	Q99584	S_100	10.8	5.9	Hs	N	1YUR	Arnesano <i>et al.</i> , 2005b
S100A13 (Ca(II))	Q99584	S_100	10.8	5.9	Hs	N	1YUT	Arnesano <i>et al.</i> , 2005b
UBP15	Q9Y4E8	DUSP	13.9	4.7	Hs	N	1W6V	De Jong <i>et al.</i>
RTF1	Q92541	PLUS3	15.2	9.4	Hs	N	2BZE	
N4BP2	Q86UW6	SMR	12.9	9.3	Hs	N		

CHD7	Q9P2D1	BRK	8.4	9.2	Hs	N	2CKC	
CHD8	Q9HCK8	BRK	8.7	4.8	Hs	N	2CKA	
ERCC1/ERCC4	P079921/ Q92889	HhH	8.0/ 9.1	5.2/ 7.0	Hs	N	1Z00	Tripsianes <i>et al</i>
ERCC4	Q92889	HhH	9.1	7.0	Hs	N	2AQ0	
Ribosomal protein L11	P29395	L11	15.1	9.7	Tm	N		
Ribosome binding factor A	Q9WZV9	RBFA	14.2	9.3	Tm	N		
CheY2	Q52884	Response-reg	13.7	9.5	Sm	N	1P6Q	Riepl <i>et al.</i> 2004
PTP-BAS	Q12923	PDZ2B	11.3	7.1	Hs	N	1Q7X	Kachel <i>et al.</i> 2003
ARBP	O42403	MBD	14.8	10.6	Gg	N	1UB1	Heitmann <i>et al.</i> 2003
Ran-BP2	P49792	Ran_BP1	15.1	8.6	Hs	N	1XKE	Geyer <i>et al.</i> 2005
AF6 (rnAfadin)	O35889	RA	16.4	6.1	Rn	N		
Conkunitzin-S1		KU	6.9	9.1	Cs	N	1YL2	Bayrhuber <i>et al.</i> , 2005
Sensor protein Dcus	P39272		15.1	8.0	Ec	N	1OJG	Pappalardo <i>et al.</i> , 2003
TFIIH p62 subunit	P32780	PH/PTB	12	10.0	Hs	NX	1PFJ	Gervais <i>et al.</i> 2004
HPV16 E6	P03126	Zinc Finger	9	9.6	Pv	NX		
TFIIH p8- subunit	Q6ZYL4	REX1	8	4.8	Hs	NX		
TFIIH p44 subunit	Q13888	C4C4 RING	8	4.9	Hs	NX	1Z60	Kellenberger <i>et al.</i> 2005
ZHX1	Q9UKY1	HD	8.9	9.5	Hs	NX		
BOFC	O05391		16.1	5.3	Bs	NX	2BWZ	Patterson <i>et al</i>
YisI	Q81SJ3		6.4	9.8	Ba	NX	2BZB	Au <i>et al.</i> , 2006
Spo0E	Q81XQ9		6.8	9.8	Ba	NX	2C0S	Au <i>et al.</i> , 2006
CsrA	P33911	CsrA	8.2	6.1	Ba	NX	1t30	Ilin <i>et al.</i> , 2005
Kalioxin 1	P24662	Toxin_2	4.2	9.3	Am	NS	1XSW	Lange <i>et al.</i> , 2005
CutA1	P36654	CutA1	11.7	4.9	Ec	XN	1NAQ	Arnesano <i>et al.</i> , 2003a
CutA1	Q6MGD0	CutA1	11.8	4.9	Rn	XN	1OSC	Arnesano <i>et al.</i> , 2003a
SOD-like protein	O31851	Sod_Cu	16.7	5.3	Bs	XN	1S4I	Banci <i>et al.</i> , 2005a
NcoA-1/ STAT6	P70366/ P42226	PASB/ LxxLL	12.0/ 1.6	8.9/ 4.4	Mm/ Hs	XN	1OJ5	Razeto <i>et al.</i> , 2004
Tomosyn	P32851	SNARE	6.2	6.1	Rn	XN	1URQ	Pobbati <i>et al.</i> , 2004
CylR2	Q8VL32	HTH	7.7	9.1	Ef	XN	1UTX	Rumpel <i>et al.</i> , 2004
GFA	Q51669	DUF636	21.1	6.1	Pd	XN	1X6M	Neculai <i>et al.</i> , 2005
GFA /gluthation	Q51669	DUF636	21.1	6.1	Pd	XN	1XA8	Neculai <i>et al.</i> , 2005
Atx1/Ccc2a	P38636/ P38995	HMA HMA	7.9/ 7.9	8.6/ 4.4	Sc	ND	1UV1	Arnesano <i>et al.</i> , 2004
AF6(rnAfadin)/ Rap1A	O35889/ P10113	RA/ RAS	16.4/ 20.9	6.1/ 6.4	Rn	ND		
M-Conotoxin RIIK/Tsha1	P69769		2.7	8.7	Cr	ND		Verdier <i>et al.</i> , 2005
CylR2 / B-DNA	Q8VL32	HTH	29.6	9.1	Ef	ND		Rumpel <i>et al.</i> , 2004

Table legends:

¹N: NMR structure, NX: NMR structure in collaboration with an X-ray group, NS: solid state NMR structure XN: X-ray structure in collaboration with an NMR group, ND: NMR structure of a complex modeled by docking

²Protein domain classification according to Pfam, if blank: no domain classification available.

³*Bacillus subtilis*: Bs, *Pseudomonas syringae*: Ps, *Escherichia coli*: Ec, *Homo sapiens*: Hs, *Rattus norvegicus*: Rn, *Deinococcus radiodurans*: Dr, *Sinorhizobium meliloti*: Sm, *Saccharomyces cerevisiae*: Sc, *Synechocystis sp. pcc 6803*: S, *Bacillus anthracis*: Ba, *Staphylococcus scarnosus*: Ss, *Staphylococcus aureus*: Sa, *Gallus gallus*: Gg, *Enterococcus faecalis*: Ef, *Conus radiatus*: Cr,

Thermotoga maritime: Tm, Papilloma virus: Pv., *Conus striatus*: Cs, *Androctonus mauretanicus*: Am, *Mus musculus*: Mm, *Paracoccus denitrificans*: Pd.

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