

Supplementary Material

A strong ^{13}C chemical shift signature provides the coordination mode of histidines in zinc-binding proteins

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Supplementary Table 1

Complete chemical shift database used in this study ordered by BMRB entry codes and by histidine coordination modes.

^a Histidine residue number as reported in the BMRB entry. See also the note regarding histidine numbering in C₂H₂ zinc-fingers at the end of the table.

^b Topology of the zinc-site in which this histidine is involved. If several histidines are coordinating the same zinc ion, the corresponding histidine is underlined in the motif.

BMRB entry	Protein name	Residue range	Histidine residue number ^a	Zinc site ^b	Cδ2 (ppm)	Cε1 (ppm)	Cε1 - Cδ2 (ppm)	coordination mode
4928	WSTF-PHD	1-51	26	CCHC	120.50	140.50	20.00	Nδ1
5668	m ³ A DNA glycosylase I	1-187	175	CH <u>H</u> C	123.85	137.76	13.91	Nδ1
6238	CBP-ZZ	1-52	42	CCH <u>H</u>	118.00	138.40	20.40	Nδ1
6374	AIRE-PHD	1-66	31	CCHC	116.04	136.00	19.96	Nδ1
6658	FLIX3	1-182	144	CCCH	120.02	138.55	18.54	Nδ1
6682	hZNF593	1-116	75	CCH <u>H</u>	120.20	141.70	21.50	Nδ1
7174	Hdm2-RING	429-491	457	CCH <u>H</u>	118.67	140.85	22.18	Nδ1
7210	ING4-PHD	1-63	37	CCHC	118.95	137.69	18.75	Nδ1
7297	RPA1320	1-102	63	CCH <u>H</u>	117.30	139.90	22.60	Nδ1
7297	RPA1320	1-102	7	CCHD	118.70	138.17	19.47	Nδ1
10013	Kiaa1045-RING	1-89	40	CCHC	119.01	139.05	20.04	Nδ1
10098	hC1-PKC-delta	1-84	28	HCCC	120.45	139.78	19.33	Nδ1
10098	hC1-PKC-delta	1-84	67	CCHC	119.46	138.45	19.00	Nδ1
10108	At1g60420	1-89	72	CCHC	119.68	139.10	19.42	Nδ1
10108	At1g60420	1-89	38	H <u>H</u> CC	120.06	137.69	17.62	Nδ1
10247	NEDD9-LIM	1-82	39	CCHC	119.43	138.43	19.00	Nδ1
10247	NEDD9-LIM	1-82	71	CCCH	118.36	139.39	21.03	Nδ1
11036	KAP1-PHD	624-812	648	CCHC	118.27	138.59	20.33	Nδ1
11061	APOBEC2	1-192	60	HCC	116.41	140.27	23.87	Nδ1
11093	ITK-BTK	1-64	16	HCCC	118.95	138.38	19.43	Nδ1
11151	C1-PKC-delta	1-83	18	HCCC	121.34	140.25	18.91	Nδ1
11151	C1-PKC-delta	1-83	56	CCHC	119.32	138.62	19.29	Nδ1
11157	BMX-BTK	1-50	16	HCCC	122.59	142.25	19.66	Nδ1
11161	Tmp30-RING	1-85	39	CHCC	118.78	138.16	19.39	Nδ1
11162	ZNF126-RING	1-78	38	CHCC	118.60	138.35	19.75	Nδ1
11162	ZNF126-RING	1-78	41	CCHC	118.10	138.73	20.64	Nδ1
11163	Tmp5-RING	1-85	39	CHCC	118.55	138.33	19.78	Nδ1
11164	TNF3-RING	1-66	35	CHCC	119.14	138.49	19.35	Nδ1
15059	MLP-LIM	1-194	31	CCCH	119.40	138.35	18.95	Nδ1
15059	MLP-LIM	1-194	141	CCCH	118.12	139.02	20.90	Nδ1
15112	C2-SOD	20-173	92	H <u>H</u> HD	116.72	136.50	19.79	Nδ1
15112	C2-SOD	20-173	101	H <u>H</u> HD	119.47	139.77	20.30	Nδ1
15112	C2-SOD	20-173	109	H <u>H</u> HD	117.12	138.47	21.34	Nδ1
15208	Churchill	2-107	71	H <u>H</u> CC	118.57	139.75	21.18	Nδ1
15796	E2-c-Cbl	355-437	398	CHCC	116.19	135.37	19.18	Nδ1
15948	E3-Arkadia-RING	1-69	40	CCHC	118.50	138.00	19.50	Nδ1
15948	E3-Arkadia-RING	1-69	37	CHCC	118.86	138.00	19.14	Nδ1
17112	C1B-PKC-delta	214-295	231	HCCC	120.82	139.30	18.48	Nδ1
17112	C1B-PKC-delta	214-295	269	CCHC	119.50	139.64	20.14	Nδ1
17113	C1A-PKC-delta	149-228	159	HCCC	121.27	140.14	18.88	Nδ1
17113	C1A-PKC-delta	149-228	197	CCHC	119.12	139.03	19.91	Nδ1
17157	PARP-1-ZNF1	1-108	53	CCHC	118.69	139.20	20.52	Nδ1
17158	PARP-1-ZNF2	103-214	159	CCHC	119.65	138.59	18.94	Nδ1

BMRB entry	Protein name	Residue range	Histidine residue number ^a	Zinc site ^b	Cδ2 (ppm)	Cε1 (ppm)	Cε1 - Cδ2 (ppm)	coordination mode
5668	m ³ A DNA glycosylase I	1-187	17	CHHC	126.23	138.32	12.09	Nε2
5987	CBP TAZ1-Zn1	1-100	23	HCCC	128.71	139.64	10.94	Nε2
5987	CBP TAZ1-Zn2	1-100	54	HCCC	128.82	139.20	10.39	Nε2
5987	CBP TAZ1-Zn3	1-100	78	HCCC	127.34	139.69	12.36	Nε2
6005	TIS11d-TZF-Zn1	1-70	28	CCCH	123.91	137.46	13.55	Nε2
6005	TIS11d-TZF-Zn2	1-70	66	CCCH	122.79	138.33	15.54	Nε2
6238	CBP-ZZ	1-52	40	CCHH	126.00	140.20	14.20	Nε2
6275	MTF-1-ZNF1	1-177	28	CCHH	127.20	139.40	12.20	Nε2
6275	MTF-1-ZNF2	1-177	58	CCHH	128.20	140.10	11.90	Nε2
6275	MTF-1-ZNF3	1-177	88	CCHH	128.20	140.00	11.80	Nε2
6275	MTF-1-ZNF4	1-177	117	CCHH	127.20	139.70	12.50	Nε2
6275	MTF-1-ZNF6	1-177	177	CCHH	126.30	139.40	13.10	Nε2
6682	hZNF593	1-116	69	CCHH	128.10	140.00	11.90	Nε2
7174	Hdm2-RING	429-491	452	CCHH	128.21	139.02	10.81	Nε2
7194	TFIIIA-zf46-ZNF1	1-87	22	CCHH	127.77	139.44	11.67	Nε2
7194	TFIIIA-zf46-ZNF1	1-87	26	CCHH	127.28	139.45	12.17	Nε2
7194	TFIIIA-zf46-ZNF2	1-87	52	CCHH	127.58	140.15	12.57	Nε2
7194	TFIIIA-zf46-ZNF2	1-87	56	CCHH	127.38	139.35	11.97	Nε2
7194	TFIIIA-zf46-ZNF3	1-87	80	CCHH	126.09	139.57	13.48	Nε2
7194	TFIIIA-zf46-ZNF3	1-87	85	CCHH	127.08	139.47	12.38	Nε2
10038	hZNF295-Zn1	1-107	35	CCHC	128.79	139.06	10.28	Nε2
10038	hZNF295-Zn2	1-107	61	CCHC	128.38	139.41	11.03	Nε2
10038	hZNF295-Zn3	1-107	88	CCHH	127.13	139.65	12.52	Nε2
10038	hZNF295-Zn3	1-107	93	CCHH	127.30	139.54	12.25	Nε2
10057	IscU	1-130	101	CDCH	129.54	139.80	10.26	Nε2
10108	At1g60420	1-89	35	HHCC	126.61	141.49	14.88	Nε2
10148	Osr2-ZNF1	1-106	36	CCHH	128.24	139.56	11.32	Nε2
10148	Osr2-ZNF1	1-106	40	CCHH	128.48	140.08	11.60	Nε2
10148	Osr2-ZNF2	1-106	64	CCHH	127.02	139.55	12.53	Nε2
10148	Osr2-ZNF2	1-106	68	CCHH	127.99	140.46	12.47	Nε2
10148	Osr2-ZNF3	1-106	92	CCHH	127.30	139.17	11.88	Nε2
10148	Osr2-ZNF3	1-106	96	CCHH	127.26	139.86	12.61	Nε2
10151	hZNF268	887-919	31	CCHH	127.26	139.43	12.17	Nε2
10151	hZNF268	887-919	35	CCHH	127.05	139.70	12.65	Nε2
10152	hZNF268	495-525	31	CCHH	127.39	139.31	11.92	Nε2
10152	hZNF268	495-525	35	CCHH	126.99	139.79	12.79	Nε2
10153	hZNF484	519-551	31	CCHH	127.26	140.02	12.77	Nε2
10153	hZNF484	519-551	35	CCHH	127.95	139.85	11.90	Nε2
10154	hZNF473	557-589	31	CCHH	127.61	139.37	11.76	Nε2
10154	hZNF473	557-589	35	CCHH	127.86	140.20	12.34	Nε2
10155	hZNF484	603-635	31	CCHH	126.98	139.84	12.86	Nε2
10155	hZNF484	603-635	35	CCHH	127.85	140.40	12.55	Nε2
10156	hZNF484	715-747	31	CCHH	127.41	139.62	12.20	Nε2
10156	hZNF484	715-747	35	CCHH	127.88	140.10	12.22	Nε2
10157	B-cell lymphoma 6 protein	626-654	30	CCHH	127.34	139.43	12.09	Nε2
10157	B-cell lymphoma 6 protein	626-654	34	CCHH	128.03	140.30	12.27	Nε2
10158	hZNF473	370-400	31	CCHH	127.44	139.35	11.91	Nε2
10158	hZNF473	370-400	35	CCHH	127.09	139.77	12.68	Nε2
10166	hZNF268	637-667	29	CCHH	127.17	139.92	12.75	Nε2
10166	hZNF268	637-667	33	CCHH	127.50	139.86	12.36	Nε2

BMRB entry	Protein name	Residue range	Histidine residue number ^a	Zinc site ^b	Cδ2 (ppm)	Cε1 (ppm)	Cε1 - Cδ2 (ppm)	coordination mode
10167	hZNF28-homolog	584-616	31	CCHH	127.27	139.60	12.33	Nε2
10167	hZNF28-homolog	584-616	35	CCHH	127.60	140.06	12.46	Nε2
10168	hZNF28-homolog	440-472	31	CCHH	127.22	139.81	12.58	Nε2
10168	hZNF28-homolog	440-472	35	CCHH	127.01	140.18	13.17	Nε2
10169	hZNF224	171-203	31	CCHH	127.09	139.75	12.66	Nε2
10169	hZNF224	171-203	35	CCHH	127.51	139.98	12.47	Nε2
10170	hZNF28-homolog	415-447	31	CCHH	127.12	139.54	12.42	Nε2
10170	hZNF28-homolog	415-447	35	CCHH	127.61	139.72	12.11	Nε2
10171	hZNF224	311-343	31	CCHH	127.22	139.57	12.36	Nε2
10171	hZNF224	311-343	35	CCHH	127.91	140.19	12.29	Nε2
10172	hZNF224	395-427	31	CCHH	128.55	139.12	10.57	Nε2
10172	hZNF224	395-427	35	CCHH	127.42	139.95	12.52	Nε2
10173	hZNF347	592-624	31	CCHH	127.22	139.68	12.45	Nε2
10173	hZNF347	592-624	35	CCHH	127.70	140.02	12.32	Nε2
10174	hZNF347	340-372	31	CCHH	127.32	139.66	12.35	Nε2
10174	hZNF347	340-372	35	CCHH	127.70	140.06	12.35	Nε2
10175	hZNF28-homolog	556-588	31	CCHH	127.03	139.77	12.73	Nε2
10175	hZNF28-homolog	556-588	35	CCHH	127.53	140.29	12.76	Nε2
10176	hZNF28-homolog	596-728	31	CCHH	128.28	139.09	10.80	Nε2
10176	hZNF28-homolog	596-728	35	CCHH	127.78	140.11	12.33	Nε2
10177	hZNF484	687-719	31	CCHH	127.25	139.49	12.24	Nε2
10177	hZNF484	687-719	35	CCHH	127.63	140.12	12.49	Nε2
10178	hZNF473	204-236	31	CCHH	127.17	139.10	11.93	Nε2
10178	hZNF473	204-236	35	CCHH	126.95	139.57	12.62	Nε2
10179	hZNF28-homolog	724-756	31	CCHH	127.59	139.47	11.89	Nε2
10179	hZNF28-homolog	724-756	35	CCHH	127.04	139.87	12.83	Nε2
10180	hZNF224	339-371	31	CCHH	127.34	139.55	12.21	Nε2
10180	hZNF224	339-371	35	CCHH	127.55	139.97	12.42	Nε2
10181	hZNF224	367-399	31	CCHH	127.20	139.82	12.62	Nε2
10181	hZNF224	367-399	35	CCHH	127.51	139.97	12.46	Nε2
10182	hZNF473	725-757	31	CCHH	127.35	139.68	12.33	Nε2
10182	hZNF473	725-757	35	CCHH	128.36	140.25	11.89	Nε2
10183	hZNF484	379-411	31	CCHH	127.26	139.53	12.27	Nε2
10183	hZNF484	379-411	35	CCHH	127.73	140.10	12.37	Nε2
10184	hZNF484	463-495	31	CCHH	127.32	139.57	12.25	Nε2
10184	hZNF484	463-495	35	CCHH	127.64	140.13	12.49	Nε2
10185	hZNF268	607-639	31	CCHH	127.39	139.44	12.05	Nε2
10185	hZNF268	607-639	35	CCHH	126.96	139.87	12.91	Nε2
10186	hZNF95-homolog	369-401	31	CCHH	126.07	139.64	13.57	Nε2
10186	hZNF95-homolog	369-401	35	CCHH	127.51	139.96	12.46	Nε2
10187	hZNF224	479-511	31	CCHH	127.27	139.84	12.57	Nε2
10187	hZNF224	479-511	35	CCHH	127.57	139.97	12.40	Nε2
10188	hZNF347	564-596	31	CCHH	127.30	139.63	12.32	Nε2
10188	hZNF347	564-596	35	CCHH	127.80	140.07	12.27	Nε2
10189	hZNF95-homolog	341-373	31	CCHH	126.52	139.77	13.25	Nε2
10189	hZNF95-homolog	341-373	35	CCHH	128.45	140.00	11.55	Nε2
10190	hZNF95-homolog	425-457	31	CCHH	127.29	138.98	11.69	Nε2
10190	hZNF95-homolog	425-457	35	CCHH	127.06	139.77	12.71	Nε2
10191	hZNF268	719-751	31	CCHH	127.16	139.64	12.48	Nε2
10191	hZNF268	719-751	35	CCHH	127.65	139.99	12.34	Nε2
10192	hZNF224	283-315	31	CCHH	126.95	139.47	12.52	Nε2
10192	hZNF224	283-315	35	CCHH	127.80	140.14	12.34	Nε2

BMRB entry	Protein name	Residue range	Histidine residue number ^a	Zinc site ^b	Cδ2 (ppm)	Cε1 (ppm)	Cε1 - Cδ2 (ppm)	coordination mode
10196	hZNF95-homolog	768-800	31	CCHH	127.27	139.46	12.19	Nε2
10196	hZNF95-homolog	768-800	35	CCHH	127.66	140.00	12.34	Nε2
10197	hZNF224	199-231	31	CCHH	127.13	139.91	12.78	Nε2
10197	hZNF224	199-231	35	CCHH	127.61	140.37	12.76	Nε2
10198	hZNF224	423-455	31	CCHH	126.50	139.41	12.91	Nε2
10198	hZNF224	423-455	35	CCHH	127.64	139.92	12.28	Nε2
10199	hZNF347	312-344	31	CCHH	127.10	139.67	12.57	Nε2
10199	hZNF347	312-344	35	CCHH	127.61	140.00	12.39	Nε2
10200	hZNF473	342-372	31	CCHH	126.96	139.80	12.84	Nε2
10200	hZNF473	342-372	35	CCHH	126.96	140.13	13.17	Nε2
10201	hZNF473	641-673	31	CCHH	127.15	139.57	12.42	Nε2
10201	hZNF473	641-673	35	CCHH	127.62	140.03	12.42	Nε2
10202	hZNF484	491-523	31	CCHH	127.26	139.53	12.27	Nε2
10202	hZNF484	491-523	35	CCHH	127.59	140.42	12.83	Nε2
10203	hZNF484	547-579	31	CCHH	127.22	139.54	12.31	Nε2
10203	hZNF484	547-579	35	CCHH	127.57	140.08	12.52	Nε2
10204	hZNF28-homolog	612-644	31	CCHH	127.19	139.68	12.49	Nε2
10204	hZNF28-homolog	612-644	35	CCHH	127.69	139.99	12.30	Nε2
10205	hZNF28-homolog	668-700	31	CCHH	127.25	139.76	12.51	Nε2
10205	hZNF28-homolog	668-700	35	CCHH	127.44	139.97	12.52	Nε2
10206	hZNF28-homolog	780-812	31	CCHH	127.14	139.72	12.59	Nε2
10206	hZNF28-homolog	780-812	35	CCHH	127.37	138.97	11.61	Nε2
10207	hZNF347	368-400	31	CCHH	127.17	139.61	12.44	Nε2
10207	hZNF347	368-400	35	CCHH	127.10	139.71	12.62	Nε2
10208	hZNF473	315-345	31	CCHH	127.22	139.57	12.35	Nε2
10208	hZNF473	315-345	35	CCHH	127.63	139.93	12.30	Nε2
10209	hZNF473	809-841	31	CCHH	127.16	139.78	12.63	Nε2
10209	hZNF473	809-841	35	CCHH	127.58	140.21	12.64	Nε2
10210	hZNF28-homolog	528-560	31	CCHH	126.81	139.60	12.79	Nε2
10210	hZNF28-homolog	528-560	35	CCHH	127.66	140.26	12.61	Nε2
10216	hZNF268	411-441	31	CCHH	127.37	139.12	11.75	Nε2
10216	hZNF268	411-441	35	CCHH	127.08	139.76	12.67	Nε2
10217	hZNF268	693-723	29	CCHH	127.83	139.36	11.53	Nε2
10217	hZNF268	693-723	33	CCHH	127.26	139.85	12.59	Nε2
10218	hZNF268	355-385	31	CCHH	127.31	139.45	12.14	Nε2
10218	hZNF268	355-385	35	CCHH	126.92	139.82	12.90	Nε2
10219	hZNF268	441-469	29	CCHH	127.22	139.49	12.27	Nε2
10219	hZNF268	441-469	33	CCHH	128.23	139.84	11.61	Nε2
10220	hZNF95-homolog	397-429	31	CCHH	127.38	139.71	12.33	Nε2
10220	hZNF95-homolog	397-429	35	CCHH	127.61	140.32	12.72	Nε2
10221	hZNF224	255-287	31	CCHH	127.15	139.56	12.41	Nε2
10221	hZNF224	255-287	35	CCHH	127.59	139.82	12.23	Nε2
10222	hZNF268	775-807	31	CCHH	127.81	139.34	11.54	Nε2
10222	hZNF268	775-807	35	CCHH	127.14	139.84	12.69	Nε2
10223	hZNF347	760-792	31	CCHH	127.24	139.66	12.42	Nε2
10223	hZNF347	760-792	35	CCHH	127.74	140.02	12.28	Nε2
10224	hZNF268	859-889	31	CCHH	127.25	139.75	12.50	Nε2
10224	hZNF268	859-889	35	CCHH	127.13	139.95	12.82	Nε2
10225	hZNF268	301-331	29	CCHH	127.11	139.32	12.21	Nε2
10225	hZNF268	301-331	33	CCHH	127.58	140.00	12.42	Nε2

BMRB entry	Protein name	Residue range	Histidine residue number ^a	Zinc site ^b	Cδ2 (ppm)	Cε1 (ppm)	Cε1 - Cδ2 (ppm)	coordination mode
10226	hZNF268	273-303	29	CCHH	127.71	139.55	11.84	Nε2
10226	hZNF268	273-303	33	CCHH	127.20	139.89	12.69	Nε2
10227	hZNF268	551-583	31	CCHH	127.16	139.80	12.63	Nε2
10227	hZNF268	551-583	35	CCHH	126.89	139.79	12.90	Nε2
10228	hZNF95-homolog	628-660	31	CCHH	127.36	139.48	12.12	Nε2
10228	hZNF95-homolog	628-660	35	CCHH	127.24	139.79	12.55	Nε2
10229	hZNF268	385-413	29	CCHH	127.35	139.42	12.08	Nε2
10229	hZNF268	385-413	33	CCHH	127.95	140.11	12.16	Nε2
10230	hZNF224	563-595	31	CCHH	127.25	139.87	12.62	Nε2
10230	hZNF224	563-595	35	CCHH	127.57	139.87	12.30	Nε2
10231	B-cell lymphoma 6 protein	598-626	30	CCHH	127.19	139.63	12.43	Nε2
10231	B-cell lymphoma 6 protein	598-626	34	CCHH	127.82	140.37	12.55	Nε2
10232	hZNF95-homolog	796-828	31	CCHH	126.97	140.36	13.40	Nε2
10232	hZNF95-homolog	796-828	35	CCHH	126.93	139.84	12.91	Nε2
10233	hZNF347	284-316	31	CCHH	127.22	139.64	12.42	Nε2
10233	hZNF347	284-316	35	CCHH	127.61	140.06	12.45	Nε2
10234	hZNF347	648-680	31	CCHH	127.23	139.85	12.63	Nε2
10234	hZNF347	648-680	35	CCHH	127.70	139.99	12.29	Nε2
10243	hZNF24	1-72	33	CCHH	127.17	139.61	12.44	Nε2
10243	hZNF24	1-72	37	CCHH	127.53	139.91	12.37	Nε2
10243	hZNF24	1-72	65	CCHH	127.51	139.71	12.20	Nε2
10244	hZNF462	1-88	44	CCHH	127.14	139.64	12.49	Nε2
10244	hZNF462	1-88	48	CCHH	127.47	140.39	12.92	Nε2
10246	CTCF-ZNF1	1-86	34	CCHH	127.88	138.84	10.96	Nε2
10246	CTCF-ZNF1	1-86	39	CCHH	128.91	139.17	10.26	Nε2
10246	CTCF-ZNF2	1-86	66	CCHC	128.62	139.32	10.71	Nε2
10257	BED-protein 2	1-76	54	CCHH	126.75	140.40	13.65	Nε2
10257	BED-protein 2	1-76	59	CCHH	127.47	139.81	12.34	Nε2
10303	hZNF28-homolog	752-784	31	CCHH	127.16	139.63	12.47	Nε2
10303	hZNF28-homolog	752-784	35	CCHH	127.77	140.44	12.67	Nε2
10304	hZNF95-homolog	544-576	31	CCHH	127.17	139.68	12.52	Nε2
10304	hZNF95-homolog	544-576	35	CCHH	127.64	139.99	12.35	Nε2
10305	hZNF347	536-568	31	CCHH	127.05	139.74	12.69	Nε2
10305	hZNF347	536-568	35	CCHH	127.69	140.03	12.34	Nε2
10306	B-cell lymphoma 6 protein	518-541	29	CCHH	127.41	140.58	13.17	Nε2
10306	B-cell lymphoma 6 protein	518-541	34	CCHH	127.77	139.63	11.86	Nε2
10307	hZNF473	426-458	31	CCHH	127.15	139.65	12.50	Nε2
10307	hZNF473	426-458	35	CCHH	127.57	140.07	12.51	Nε2
10308	hZNF473	484-512	29	CCHH	126.95	139.90	12.94	Nε2
10308	hZNF473	484-512	33	CCHH	127.27	139.87	12.60	Nε2
10309	hZNF484	771-803	31	CCHH	127.30	139.66	12.36	Nε2
10309	hZNF484	771-803	35	CCHH	127.66	140.03	12.37	Nε2
10310	hZNF347	396-428	31	CCHH	127.27	139.42	12.16	Nε2
10310	hZNF347	396-428	35	CCHH	127.65	139.79	12.14	Nε2
11130	hZNF512	1-96	81	CCHH	125.87	137.18	11.30	Nε2
11130	hZNF512	1-96	86	CCHH	125.65	137.51	11.86	Nε2
11165	hZNF268	329-359	29	CCHH	127.10	139.58	12.48	Nε2
11165	hZNF268	329-359	33	CCHH	127.58	140.12	12.55	Nε2

BMRB entry	Protein name	Residue range	Histidine residue number ^a	Zinc site ^b	Cδ2 (ppm)	Cε1 (ppm)	Cε1 - Cδ2 (ppm)	coordination mode
11166	hZNF268	581-609	29	CCHH	127.40	139.71	12.31	Nε2
11166	hZNF268	581-609	33	CCHH	127.62	139.75	12.13	Nε2
11167	hZNF347	508-540	31	CCHH	127.66	139.94	12.27	Nε2
11167	hZNF347	508-540	35	CCHH	127.34	139.59	12.24	Nε2
11168	hZNF347	732-764	31	CCHH	127.77	139.99	12.23	Nε2
11168	hZNF347	732-764	35	CCHH	127.30	139.58	12.29	Nε2
11169	hZNF484	435-467	31	CCHH	128.26	140.01	11.75	Nε2
11169	hZNF484	435-467	35	CCHH	127.30	139.62	12.32	Nε2
11170	hZNF484	631-663	31	CCHH	127.75	140.05	12.30	Nε2
11170	hZNF484	631-663	35	CCHH	127.28	139.73	12.45	Nε2
11171	hZNF484	659-691	31	CCHH	127.36	139.73	12.37	Nε2
11171	hZNF484	659-691	35	CCHH	132.37	139.43	7.06	Nε2
15002	CtBP-THAP	1-91	62	CCCH	126.99	140.20	13.21	Nε2
15074	Parkin-IBR	1-80	69	CCCH	127.94	139.20	11.26	Nε2
15160	Polymerase-eta-UBZ domain	1-39	27	CCHH	127.50	140.06	12.56	Nε2
15160	Polymerase-eta-UBZ domain	1-39	31	CCHH	126.99	143.10	16.11	Nε2
15161	ETO-MYND	658-707	695	CCCH	129.79	138.66	8.87	Nε2
15208	Churchill	2-107	66	CCCH	129.66	143.02	13.37	Nε2
15208	Churchill	2-107	59	HCC	126.96	140.05	13.10	Nε2
16596	hAPLF-PBZ	363-451	392	CCHH	126.31	138.08	11.77	Nε2
16596	hAPLF-PBZ	363-451	398	CCHH	127.47	139.92	12.45	Nε2
16596	hAPLF-PBZ	363-451	434	CCHH	127.64	137.44	9.79	Nε2
16596	hAPLF-PBZ	363-451	440	CCHH	127.66	139.94	12.27	Nε2

Note regarding histidine numbering in C₂H₂ zinc-fingers:

A large number of entries of histidine coordinating zinc via Nε2 come from C₂H₂ zinc fingers solved by the RIKEN Structural Genomics Initiative. Proteins containing the classical C₂H₂ zinc-finger domain are amongst the most abundant in eukaryotic genomes, and RIKEN chose to determine structures of a large number of those C₂H₂ zinc-fingers. The procedure used for residue numbering in these proteins was such that many entries have identical histidine sequence positions (31 and 35). As this could be misinterpreted as duplicated entries in our database, we wanted to make clear here that each of these entries come from truly unique protein domains.