

hHDC

1 10 20 30 40 50

<i>hHDC</i>	PDBID	CHAIN	SEQUENCE
1JS6_A	PDBID	CHAIN	MEP EYERERGRMVDYICQYVLSVTRER . RVTTPDVQPGYLRAQLP...ESAPEDP
2OKJ_A	PDBID	CHAIN	TDFSNFLFARDLLPAKNGE EQT VQFLLEVDIILLN YVRKTFDRST KVLDFPHH PQLLEGM EGFNLSHDP

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60 70 80 90 100 110 120

<i>hHDC</i>	PDBID	CHAIN	SEQUENCE
1JS6_A	PDBID	CHAIN	DSWDS TFGDI ER IIMP GVVHWQS PHMHAYYPALTSWPS LLGDM LADAINCLG FTWASSPACTEL EBMNVMD
2OKJ_A	PDBID	CHAIN	DTFED TLQDV EK IIMP GVT HWHS PYFFAYFP TASSYPAMLADM LCGAIGCIG FSWAASPACTEL EBTVMMD
2OKJ_A	PDBID	CHAIN	ESL EQ TLVDC RD TL KY GVR TGH . PRFFNQLSTGLDII GLA GEWLTS TANTNM FTY EIAPV FV LMEQITL K

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130 140 150 160 170 180 190

<i>hHDC</i>	PDBID	CHAIN	SEQUENCE
1JS6_A	PDBID	CHAIN	WLAKM TLGLPEHFLHHHPSSQ GGCVLQSTV SESTLIALLAARKNKILEM KTS EPDADESC LNA RL VAYASD
2OKJ_A	PDBID	CHAIN	WLGKMLQLPEAPLAGEAG . EGGGVIQGSA SEATLVALLAARTKVVRRLQAA SPGLTQGA VLE KL VAYASD
2OKJ_A	PDBID	CHAIN	KMR E TLV G WSSKD G DGI F S PGG AIS NMY SIMAAR YKYFP E V KTK G MA AV P KL V L F T S E

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200 210 220 230 240 250

<i>hHDC</i>	PDBID	CHAIN	SEQUENCE
1JS6_A	PDBID	CHAIN	QAHSSVEKAGLIS . . LVKMKFLPVDNFSLRG EALQKAI EEDKQRGLVVFVVCATLGTGVC AFDCLLS E
2OKJ_A	PDBID	CHAIN	QAHSSVERAGLIG . . GVKLKAIPSDGKFAMRRASALQEALERDKAAGLIPFFV VVATLGTTSCCSFDNLL E
2OKJ_A	PDBID	CHAIN	QSHY SIKKAGAA LGFGTDNVIL ICKNERG KIIIPADF EAKILEAKQKGYVBFYV NATA GTTVYGA FDFPIQE

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260 270 280 290 300 310 320

<i>hHDC</i>	PDBID	CHAIN	SEQUENCE
1JS6_A	PDBID	CHAIN	LGP TCA REGLWLWHIDAA YACTAF LCP EFRGFLKGEHYADSF TFPNPSKWMVHFDC TGFVVKDKYKIQ QTF
2OKJ_A	PDBID	CHAIN	VGP TCH EED IWLHV DAA YAGSAFI CPEFRHRLN GVEFADSFNF NPHKWL VNFDCS AMWVKRR TDLTGAFN
2OKJ_A	PDBID	CHAIN	IAD TCEKYNLWLHV DAA WEGGLMSRKH RHKLN GHERANS V T W NPHKMMGV L LQCS A I L VKEKGLIQ GCN

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hHDC	PDBID	CHAIN	SEQUENCE
1JS6_A	PDBID	CHAIN	SVNPI YLRHAN . . SGVATDFMHWQIPLSRFRFSVRLWVFI R SFGVKNLQAHV RHGTEMAKYFESLVRNDP
2OKJ_A	PDBID	CHAIN	KLDPV YLKHSHQSGSLITD YRHWQLPLGRFRFRSLKMFVFRMYGVKGLQAYIRKHVQLSHEFEAFVQLQDP
2OKJ_A	PDBID	CHAIN	QMCAC YL FQPDKQYD VSYD TGD KAI QCGRHVD I L F K F W L M W K A K G T V G F E N Q I N K K L E L A E Y L Y A K I L K N R E

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Supplementary Figure S1. Deduced amino acid sequence alignment of hHDC (UniProt ID: P19113, PDB ID: 4E1O), pig DDC (UniProt ID: P80041, PDB ID: 1JS6), and human GAD67 (UniProt ID: Q99259, PDB ID: 2OKJ) using ClustalW. The conserved regions are highlighted in red. The secondary structures of hHDC are indicated above the sequence.