

1 Dehydrons as indicators of protein interactivity

If dehydrons provide mechanism for proteins to interact, then more interactive proteins should have more dehydrons, and vice versa.

We only expect a correlation since there are (presumably) other ways for proteins to interact.

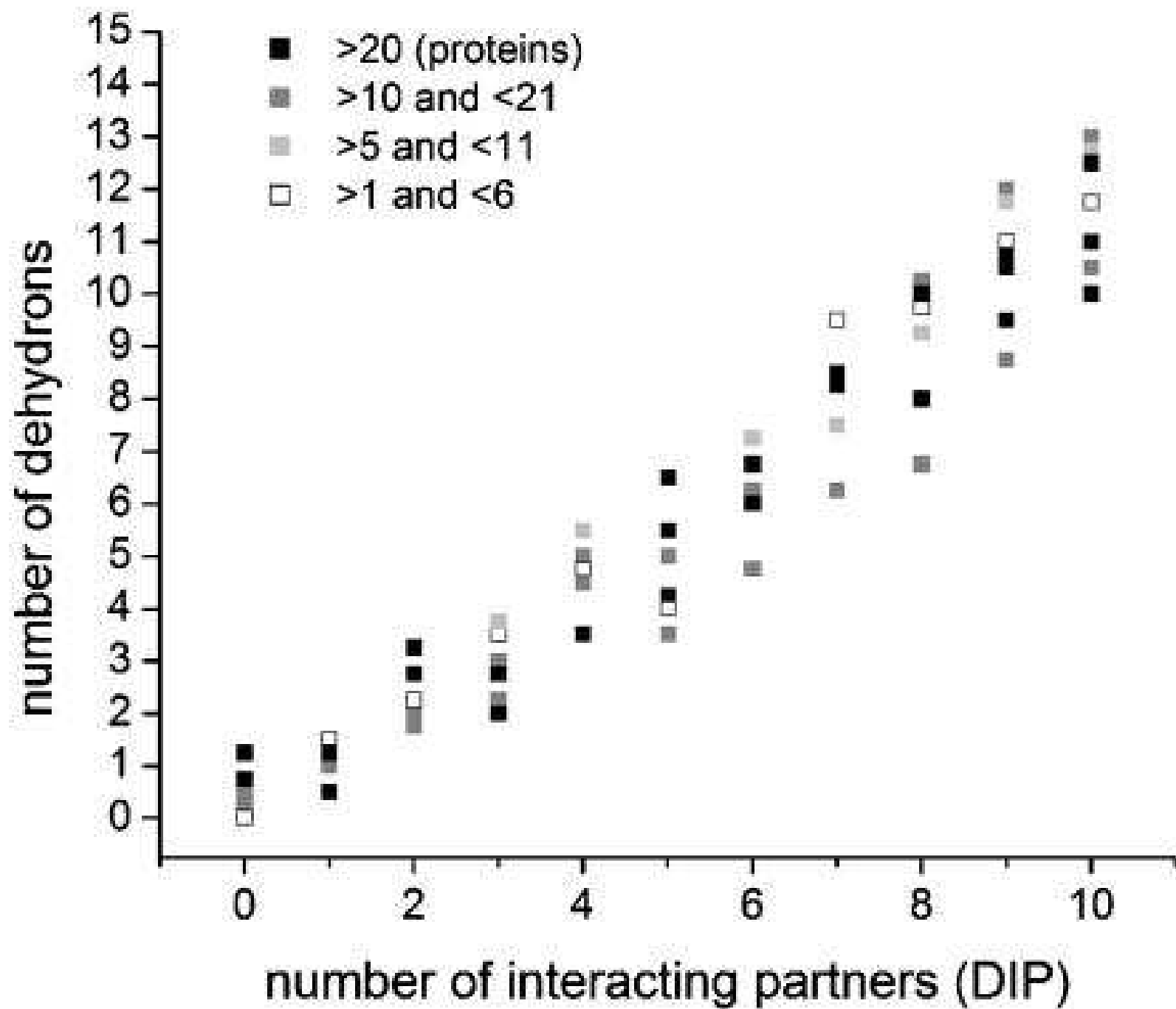
The DIP database collects information about protein interactions, based on individual protein domains: can measure interactivity of different regions of a given protein.

Result: Interactivity of proteins correlates strongly with number of dehydrons.

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The nonconserved wrapping of conserved protein folds reveals a trend toward increasing connectivity in proteomic networks.

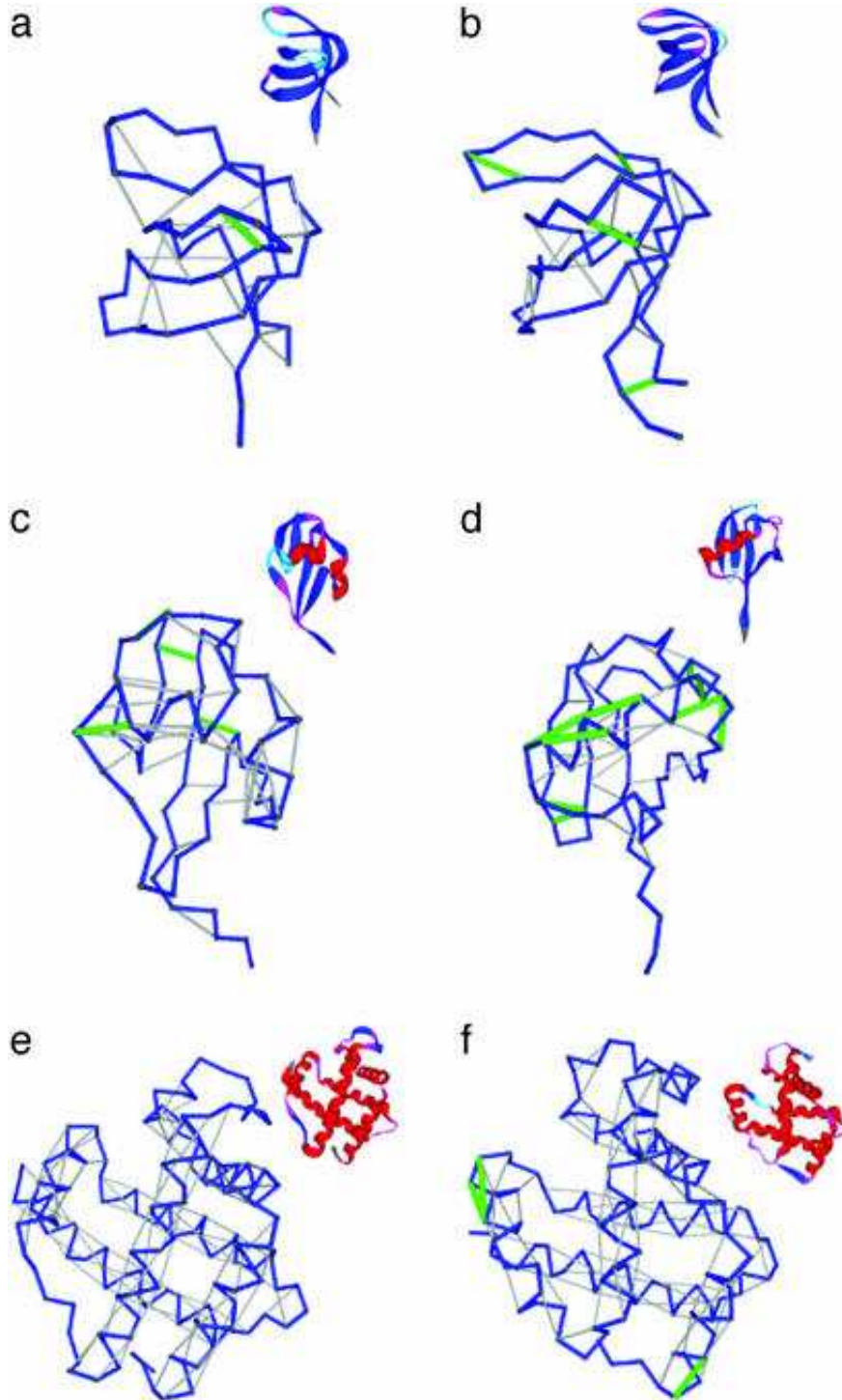
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1.1 Dehydron variation over different species

Species (common name)	peptides	H bonds	dehydrons
<i>Aplysia limacina</i> (mollusc)	146	106	0
<i>Chironomus thummi thummi</i> (insect)	136	101	3
<i>Thunnus albacares</i> (tuna)	146	110	8
<i>Caretta caretta</i> (sea turtle)	153	110	11
<i>Physeter catodon</i> (whale)	153	113	11
<i>Sus scrofa</i> (pig)	153	113	12
<i>Equus caballus</i> (horse)	152	112	14
<i>Elephas maximus</i> (Asian elephant)	153	115	15
<i>Phoca vitulina</i> (seal)	153	109	16
<i>H. sapiens</i> (human)	146	102	16

Number of dehydrons in Myoglobin of different species



Anecdotal evidence:
 the basic
 structure is similar, just the
 number of dehydrons increases.

SH3 domains are from
 nematode *C. elegans* (a)
H. sapiens (b);

ubiquitin is from
E. coli (c) and *H. sapiens* (d);

hemoglobin
 is from *Paramecium*
 (e). and *H. sapiens*-subunit (f).

1.2 Dehydrons as indicator of complexity?

Is this interactivity an indicator of complexity?

Is this complexity an indicator of evolution?

or is it just Intelligent Design?

The number of dehydrons is greater in more 'complex' species.

If this is evolution, then we imagine that protein interactivity became a dominant way to explore biological space, once genome complexity stabilized.