#### 3D protein shape density representation in Hex



# Surface representation



5 9 Q C

# Protein shape complementarity



	Graham J.L. Kemp
Penalty Factor:	Q=11
Score:	$S_{AB} = \int (\sigma_A  au_B +  au_A \sigma_B - Q  au_A  au_B) \mathrm{d}V$
Unfavourable:	$\int \tau_A(\underline{r}_A) \tau_B(\underline{r}_B) \mathrm{d}V$
Favourable:	$\int (\sigma_{A}(\underline{r}_{A})\tau_{B}(\underline{r}_{B}) + \tau_{A}(\underline{r}_{A})\sigma_{B}(\underline{r}_{B}))\mathrm{d}V$

# Atomic group in proteins

Classifcation proposed by Tsai et al. (J. Mol. Biol., 1999, 290:253-266), based on:

- ▶ heavy-atom types,
- the number of covalently attached hydrogen atoms, and
- ► the number of all covalently attached atoms.

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#### Surface Triplet Propensities

Mehio, W., Kemp, G.J.L., Taylor P. and Walkinshaw, M.D. (2010) Identification of Protein Binding Surfaces using Surface Triplet Propensities. **Bioinformatics** 



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Graham J.L. Kemp

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# Surface Triplet Propensities



#### Surface Triplet Propensities



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### Surface Triplet Propensities



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