Supplement to "Ranking predicted protein structures with support vector regression"

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Feature	Description
T32S3	pairwise atomic potential
bk_tot-rep	full atom score without backbone H-bonds or repulsion
bup	buried unsatisfied polar groups
cb	C beta atom density solvation
co	contact order
env	residue burial preference
fa_atr	full atom attractive potential
fa_prob	full atom torsion angle preference
gsolt	surface area solvation
hb_lrbb	long range backbone hydrogen bonds
hb_sc	side chain hydrogen bonds
hb_srbb	short range backbone hydrogen bonds
hs	helix/sheet packing score
mGDT	median GDT_TS
mMS	median MaxSub
mTM	median TM
mrmsd	median RMSD
num_residues	number of residues
pair	residue-based pairwise potential
rama	phi/psi torsion angle preference
rg	radius of gyration
sasa	solvent accessible surface area
sasapack	packing quality score
sheet	beta strand arrangement score
vdw	van der waals repulsion

Table 1: **The features included in the training.**

Feature	Description	Weight
T32S3	pairwise atomic potential	3.695
num_residues	number of residues	3.026
env	residue burial preference	2.931
fa_prob	torsion angle preference	2.799
hb_lrbb	long range backbone hydrogen bonds	2.567
sasapack	packing quality score	2.208
sasa	solvent accessible surface area	2.097
pair	residue-based pairwise potential	1.952
hb_srbb	short range backbone hydrogen bonds	0.510
co	contact order	0.396
sheet	beta strand arrangement score	0.211
hb_sc	side chain hydrogen bonds	0.106

Table 2: **The weights of the features in the SVR score without consensus-based features.**