Rosetta Scoring Function (Rosetta Energy Function)

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Rosetta Workshop

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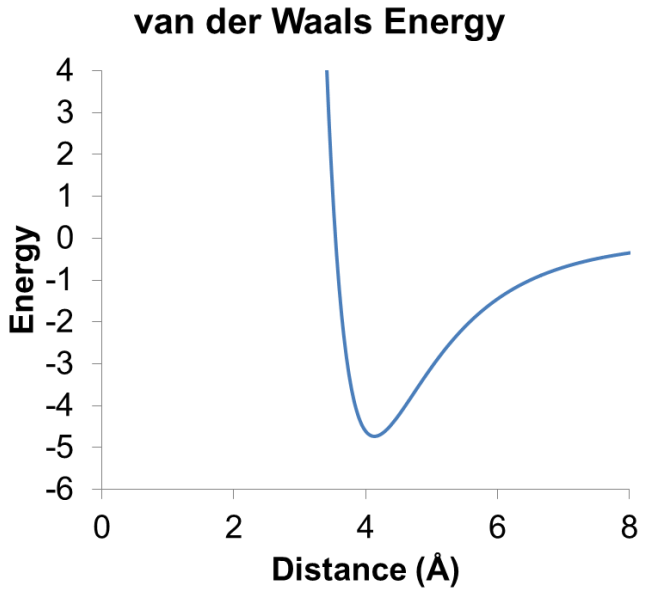
Rosetta Combines Physics-Based and Knowledge-Based Potentials to Build the Energy Function

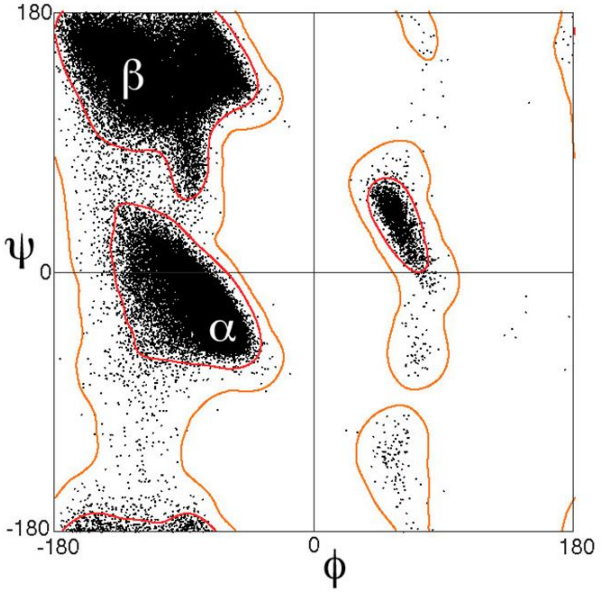
Lennard-Jones Potential

$$\sum_{i<j}\left[\frac{A_{ij}}{r_{ij}^{12}}-\frac{B_{ij}}{r_{ij}^{6}}\right]$$



Ramachandran Plot

Statistical mining of
Protein Databank (PDB)



The Score Function is a Weighted Linear Combination of Individual Score Terms

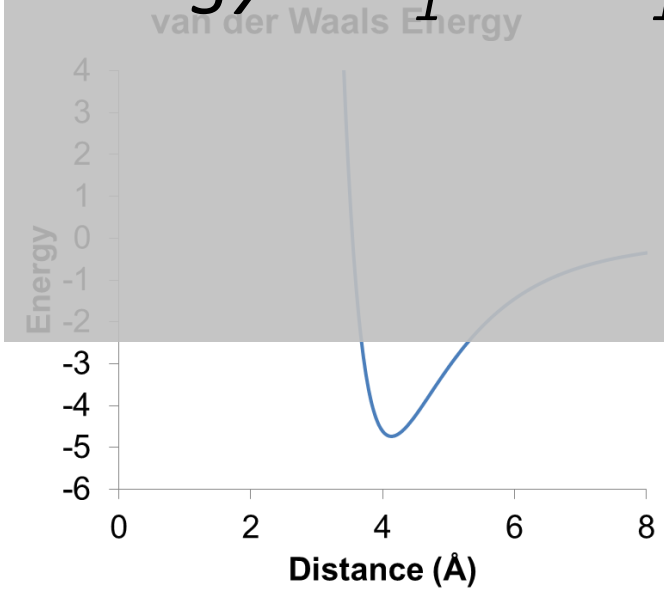
Lennard-Jones Potential

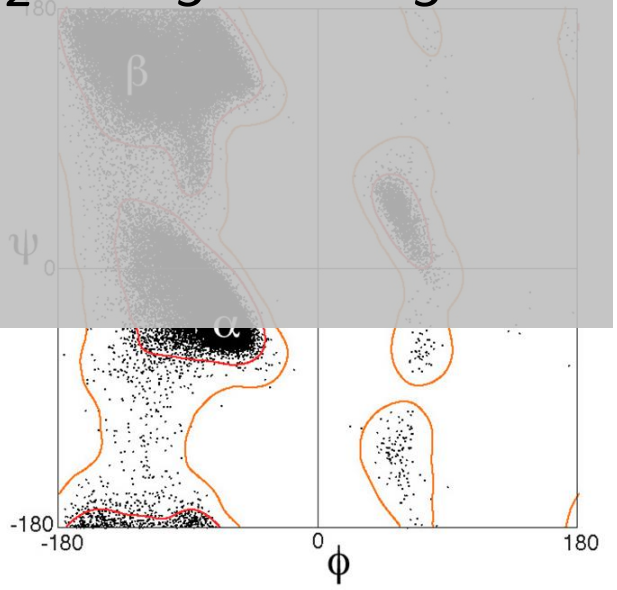
$$\sum_{i<j}\left[\frac{A_{ij}}{r_{ij}^{12}}-\frac{B_{ij}}{r_{ij}^{6}}\right]$$

Ramachandran Plot

Statistical mining of Protein Databank (PDB)

$$Energy = w_1*term_1 + w_2*term_2 + w_3*term_3 + \ldots$$





Rosetta is a Residue-Centric Scoring Function

One Body	Two Body	Whole Struct
		

Rosetta is a Residue-Centric Scoring Function

One Body	Two Body	Whole Struct
Backbone terms • rama • p_aa_pp • omega Sidechain terms • fa_dun • yhh_planarity Reference energies • ref	Lennard-Jones • fa_atr • fa_rep Solvation Energy • fa_sol Hydrogen bonding • Hbond_lr_bb • Hbond_sr_bb • Hbond_bb_sc • Hbond_sc Electrostatics • fa_elec Sidechain-sidechain • fa_pair Disulfides Constraints	Radius of Gyration • rg Contact Order • co 2^{o} Structure Alignment • hs_pair • ss_pair • Sheet

Rosetta Scoring Function Classes

1. **Low resolution:**

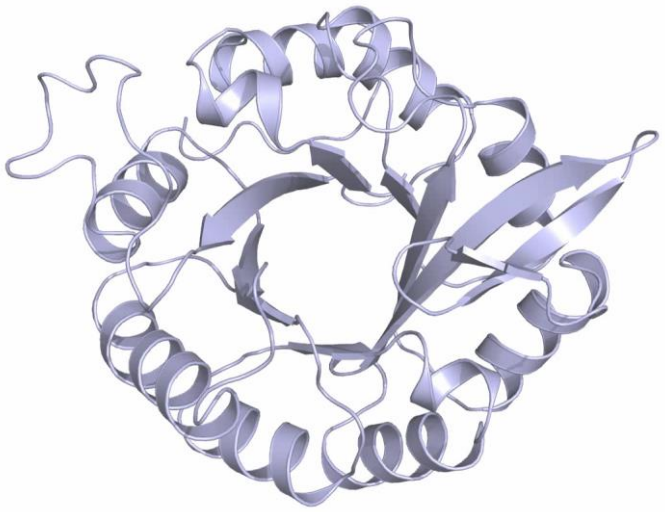
   Reduced atom representation (centroid)
   Simple energy function
   Aggressively search conformational space

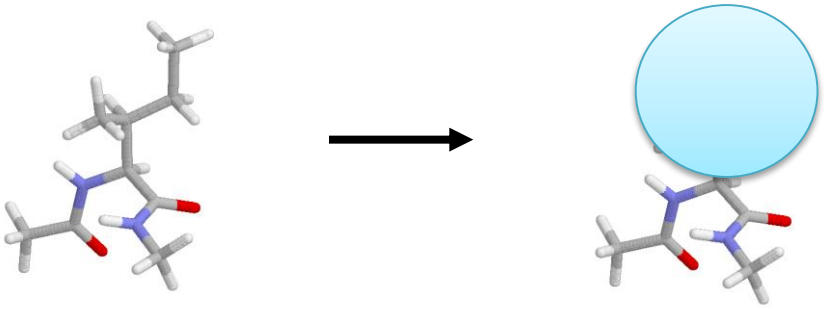
2. **High resolution:**

   Full atom (FA)
   More sophisticated energy function
   “Local” search of conformational (and sequence) space

Slide by: Glenn Butterfoss
–Rosetta Design Group

Low Resolution
Atom Representation: Centroid

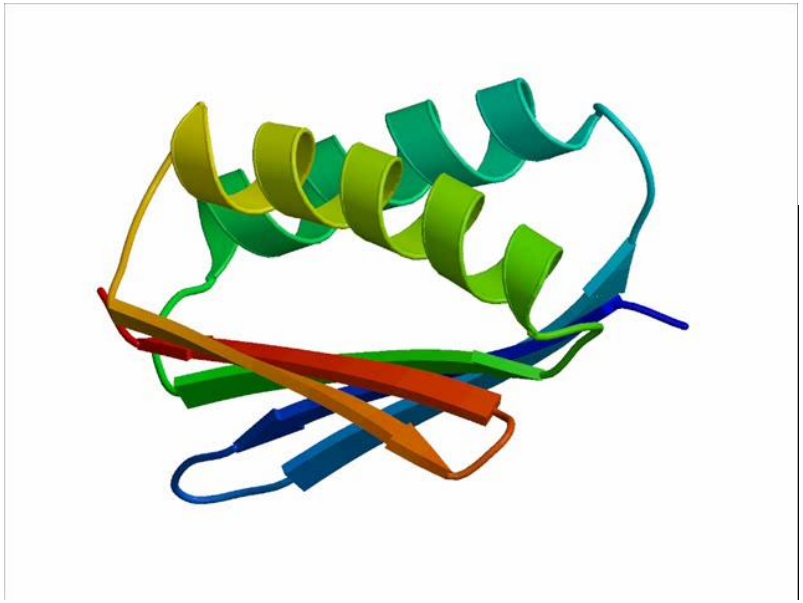


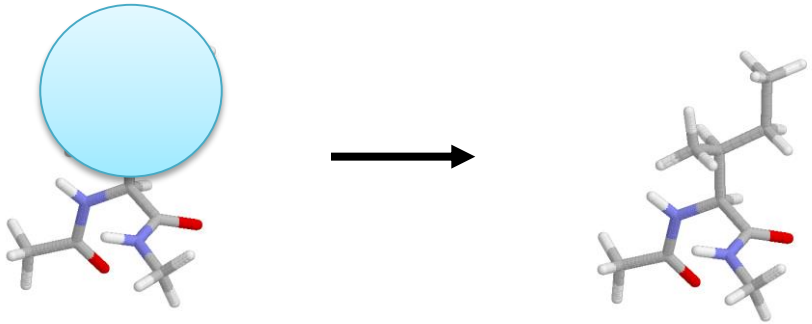


- Backbone full atom
- Side-chain represented as a “super atom” at the center of mass of the full atom sidechain
- Sample large conformational space

`database/chemical/residue_type_sets/centroid`

High Resolution
Atom Representation: Full-atom

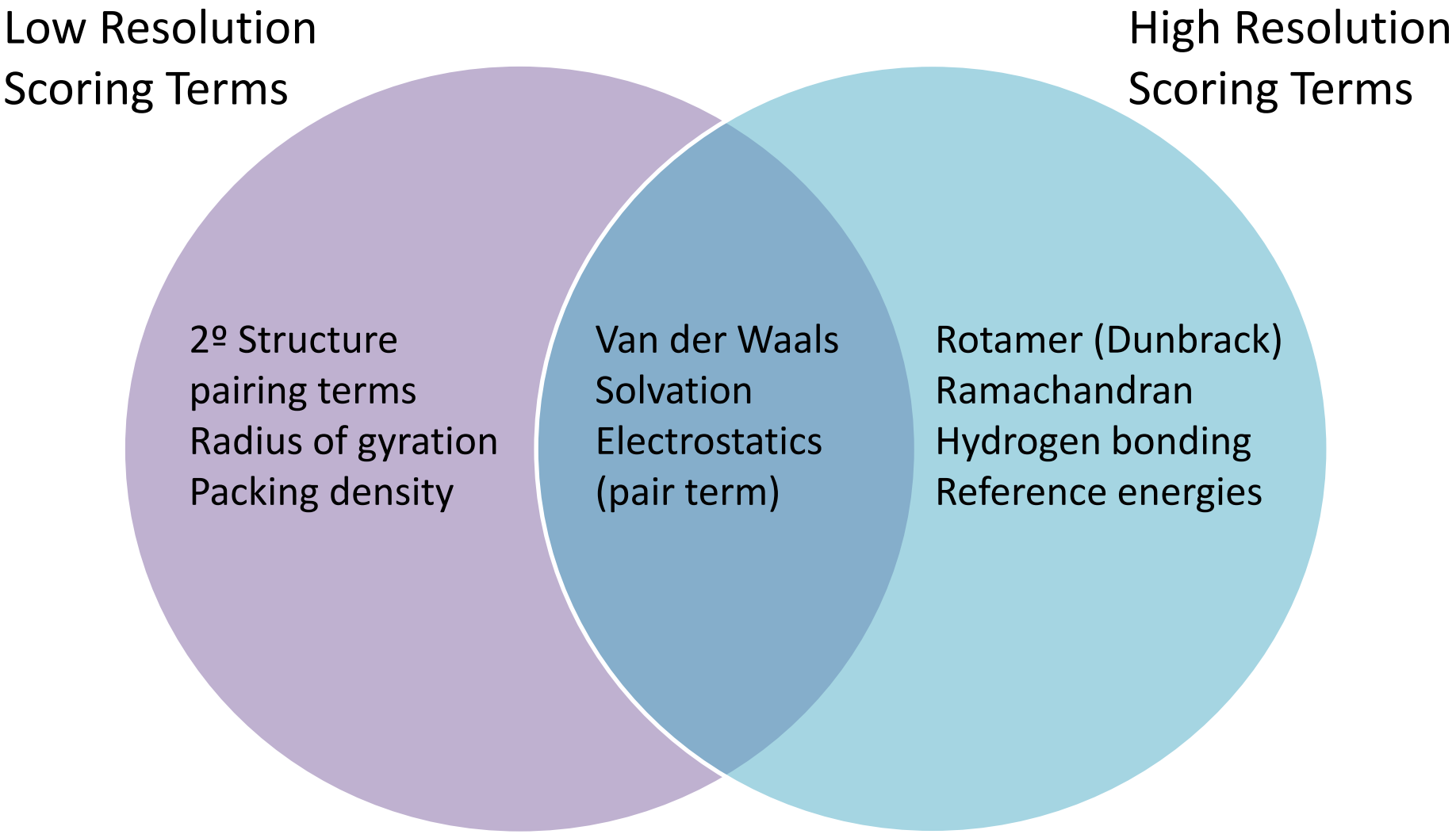




- All atoms represented
- Side-chain represented as rotamers

`database/chemical/residue_type_sets/fa_standard`

Common Score Types



Breakdown of Score Terms by Class

Table 2. Standard Rosetta Score Function Terms

score term	definition
low-resolution scoring terms	
env	hydrophobicity term for each amino acid
vdw	steric repulsion between two residues
pair	probability of two residues interacting
rg	radius of gyration
cbeta	solvation term based on a number of surrounding residues
hs_pair, ss_pair, and sheet	secondary structure terms
high-resolution scoring terms (talaris2014)	
fa_atr, fa_rep, and fa_intra_rep	decomposed 6−12 Lennard-Jones potential
fa_sol	EEF1 solvation term
pro_close	proline ring closure energy
omega	omega backbone dihedral potential
dslf_fa13	updated disulfide geometry potential
rama	potential of ϕ and ψ angles for each amino acid
p_aa_pp	probability of an amino acid given a set of ϕ and ψ angles
fa_dun	rotamer likelihood
hbond_sr_bb, hbond_lr_bb, hbond_bb_sc, and hbond_sc	combined covalent−electrostatic hydrogen bond potentials for α-helices, β-sheets, side-chain backbone, and side-chain−side-chain interactions, respectively
yhh_planarity	tyrosine hydroxyl out-of-plane penalty
fa_elec	Coulombic electrostatic potential between two residues with a distance-dependent dielectric (deprecates fa_pair)

Reference Energy

- `ref`
- Unique “cost” for *designing* in each residue type
- Free energy of given aa in unfolded state
- New meaning
  - Optimized for aa composition recovery

talaris2014 is the Default Score Function

```
METHOD_WEIGHTS ref 0.773742 0.443793 -1.63002 -1.96094 0.61937 0.173326
0.388298 1.0806 -0.358574 0.761128 0.249477 -1.19118 -0.250485 -1.51717 -0.32436
0.165383 0.20134 0.979644 1.23413 0.162496
fa_atr 1
fa_rep 0.55
fa_sol 0.9375
fa_intra_rep 0.005
fa_elec 0.875
pro_close 1.25
hbond_sr_bb 1.17
hbond_lr_bb 1.17
hbond_bb_sc 1.17
hbond_sc 1.1
dslf_fa13 1.25
rama 0.25
omega 0.625
fa_dun 0.7
p_aa_pp 0.4
yhh_planarity 0.625
ref 1
```

Score Function =
List of score terms and corresponding weight

Constraints (actually “restraints”)

- Supplements energy function with additional information
  - Commonly from experimental information
- Various types:

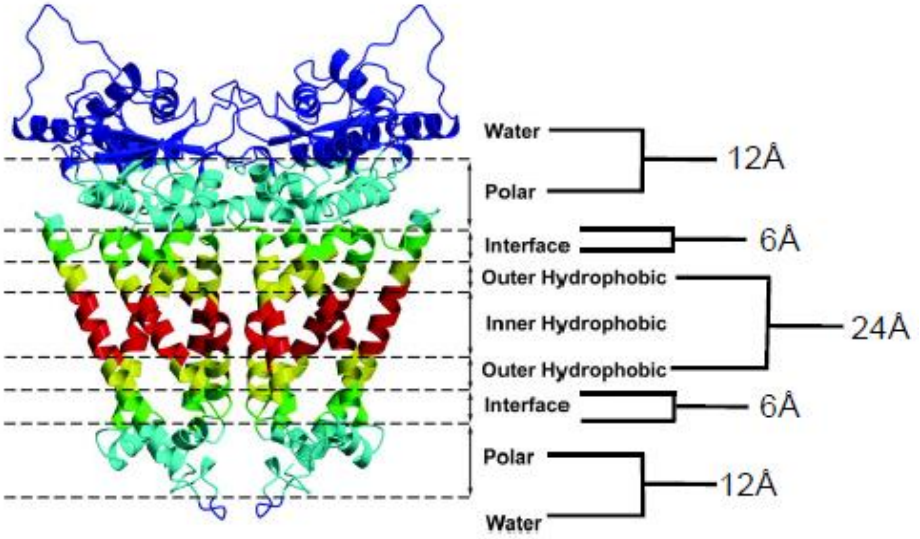
  atom_pair_constraint, dihedral_constraint, angle_constraint, coordinate_constraint, residue_type_constraint …
- Interface with Rosetta using constraint files

Other terms

Membrane terms:

fa_mbsolv

fa_mbenv

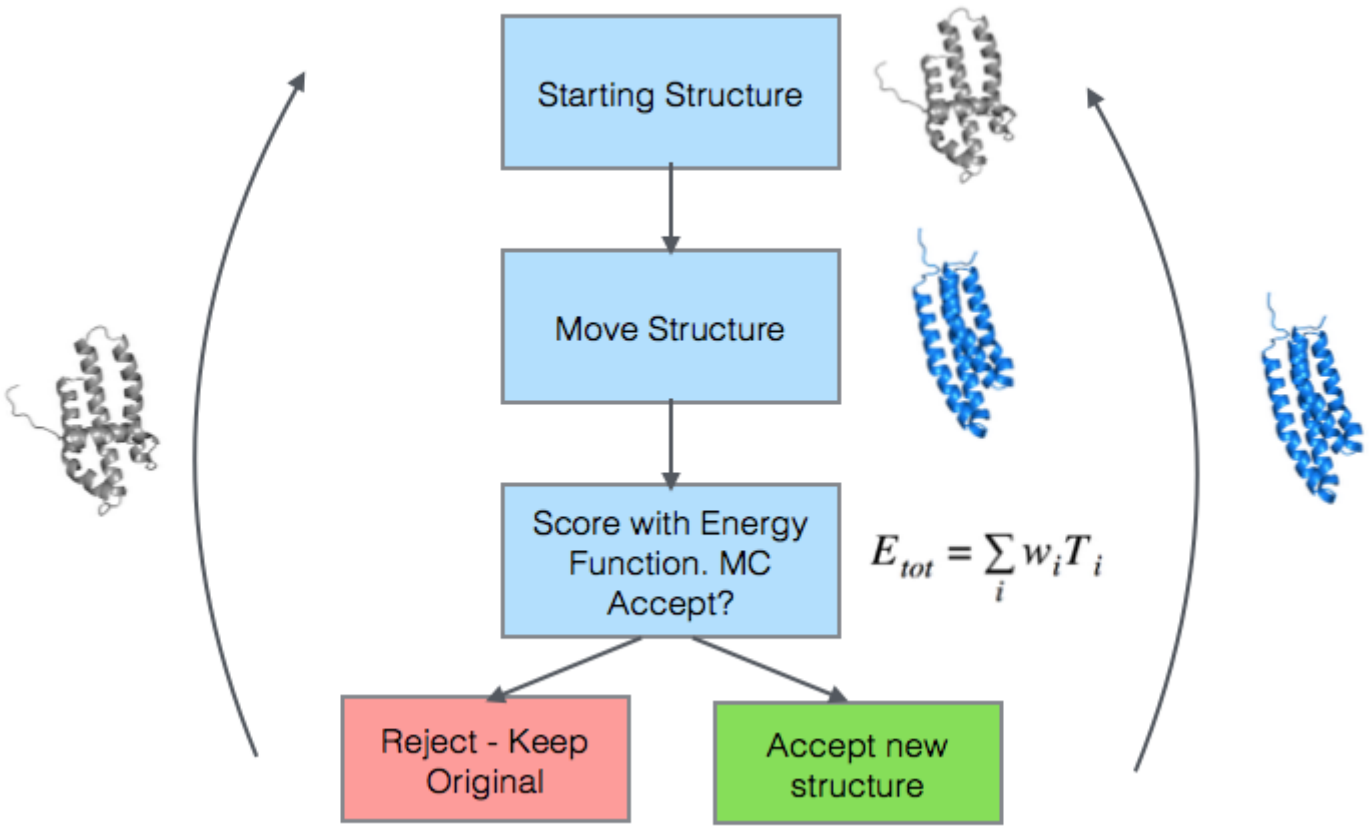


Yarov-Yarovoy, Schonbrun, and Baker 2006

Over 100+ score terms

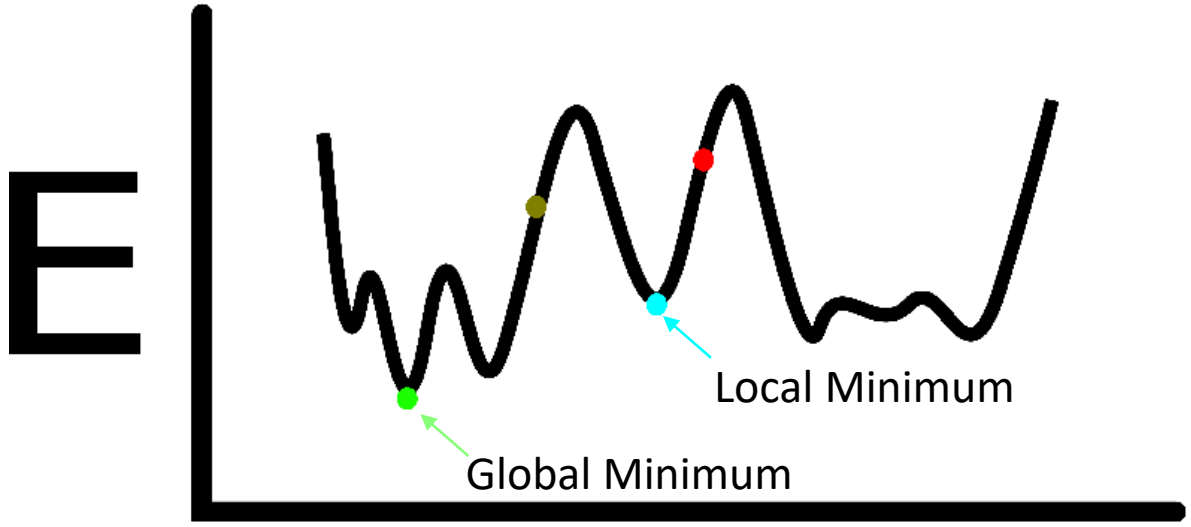
- Most are turned off (weight is set to 0)
- To turn on score term, set weight to non-zero value

Score is Central to Monte Carlo Selection



Score is Central to Monte Carlo Selection

- Criteria for accepting structures (Metropolis Criterion):
- If Enew < Eold : Accept new structure
- If Enew > Eold :
  - Pick a random number p(0, 1)
  - if $e^{[-(E_{new}-E_{old})/kBT]} > p$, accept new structure



Output Score Table

Found in output score table and at the end of every output pdb

```
# All scores below are weighted scores, not raw scores.
#BEGIN_POSE_ENERGIES_TABLE design_3UKM.pdb
label fa_atr fa_rep fa_intra_rep fa_mbenv fa_mbsolv pro_close fa_pair
hbond_sr_bb hbond_lr_bb hbond_bb_sc hbond_sc dslf_ss_dst dslf_cs_ang
dslf_ss_dih dslf_ca_dih rama omega fa_dun p_aa_pp ref Menv_smooth total
weights 0.8 0.44 0.004 0.3 0.35 1 0.49 1.17 1.17 2.34 2.2 0.5 2 5 5 0.2
0.5 0.56 0.32 1 0.5 NA
pose -2065.11 325.373 4.42479 124.101 312.059 0.66056 -18.5298 -257.704
-8.99415 -52.1492 -79.8909 -1.76827 8.00442 0.30851 3.12137 -15.362
46.2914 253.303 -32.8605 -42.76 -193.732 -1691.22
LEU_p:NtermProteinFull_1 -4.60762 0.57643 0.01812 4.16856 0.56856 0 0 0
0 0 0 0 0 0 0 0 0.02487 1.03873 0 -0.2 -1.74471 -0.15705
```

Score terms

Output Score Table

```
# All scores below are weighted scores, not raw scores.
#BEGIN_POSE_ENERGIES_TABLE design_3UKM.pdb
label fa_atr fa_rep fa_intra_rep fa_mbenv fa_mbsolv pro_close fa_pair
hbond_sr_bb hbond_lr_bb hbond_bb_sc hbond_sc dslf_ss_dst dslf_cs_ang
dslf_ss_dih dslf_ca_dih rama omega fa_dun p_aa_pp ref Menv_smooth total
weights 0.8 0.44 0.004 0.3 0.35 1 0.49 1.17 1.17 2.34 2.2 0.5 2 5 5 0.2
0.5 0.56 0.32 1 0.5 NA
pose -2065.11 325.373 4.42479 124.101 312.059 0.66056 -18.5298 -257.704
-8.99415 -52.1492 -79.8909 -1.76827 8.00442 0.30851 3.12137 -15.362
46.2914 253.303 -32.8605 -42.76 -193.732 -1691.22
LEU_p:NtermProteinFull_1 -4.60762 0.57643 0.01812 4.16856 0.56856 0 0 0
0 0 0 0 0 0 0 0 0.02487 1.03873 0 -0.2 -1.74471 -0.15705
```

Weights

Output Score Table

```
# All scores below are weighted scores, not raw scores.
#BEGIN_POSE_ENERGIES_TABLE design_3UKM.pdb
label fa_atr fa_rep fa_intra_rep fa_mbenv fa_mbsolv pro_close fa_pair
hbond_sr_bb hbond_lr_bb hbond_bb_sc hbond_sc dslf_ss_dst dslf_cs_ang
dslf_ss_dih dslf_ca_dih rama omega fa_dun p_aa_pp ref Menv_smooth total
weights 0.8 0.44 0.004 0.3 0.35 1 0.49 1.17 1.17 2.34 2.2 0.5 2 5 5 0.2
0.5 0.56 0.32 1 0.5 NA
pose -2065.11 325.373 4.42479 124.101 312.059 0.66056 -18.5298 -257.704
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LEU_p:NtermProteinFull_1 -4.60762 0.57643 0.01812 4.16856 0.56856 0 0 0
0 0 0 0 0 0 0 0 0.02487 1.03873 0 -0.2 -1.74471 -0.15705
```

Total energies for score terms

Total energy for protein

Output Score Table

```
# All scores below are weighted scores, not raw scores.
#BEGIN_POSE_ENERGIES_TABLE design_3UKM.pdb
label fa_atr fa_rep fa_intra_rep fa_mbenv fa_mbsolv pro_close fa_pair
hbond_sr_bb hbond_lr_bb hbond_bb_sc hbond_sc dslf_ss_dst dslf_cs_ang
dslf_ss_dih dslf_ca_dih rama omega fa_dun p_aa_pp ref Menv_smooth total
weights 0.8 0.44 0.004 0.3 0.35 1 0.49 1.17 1.17 2.34 2.2 0.5 2 5 5 0.2
0.5 0.56 0.32 1 0.5 NA
pose -2065.11 325.373 4.42479 124.101 312.059 0.66056 -18.5298 -257.704
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LEU_p:NtermProteinFull_1 -4.60762 0.57643 0.01812 4.16856 0.56856 0 0 0
0 0 0 0 0 0 0 0 0.02487 1.03873 0 -0.2 -1.74471 -0.15705
```

Individual residue energies for score terms

Modifying Scorefunctions in Rosetta

Command line flags

-score:weights <filename>

-score:set_weight <scoreterm$_1$> <weight$_1$> <scoreterm$_2$> <weight$_2$>

-score:patch <patchfile>

Patchfile example

```
fa_atr = 0.423
fa_rep = 0.100
```

Modifying Scorefunctions in Rosetta

```
<ROSETTASCRIPTS>
    <SCOREFXNS>
        <ligand_soft_rep weights=ligand_soft_rep>
            <Reweight scoretype=fa_elec weight=0.42/>
        </ligand_soft_rep>
        <hard_rep weights=ligandprime>
        </hard_rep>
    </SCOREFXNS>
    <OUTPUT scorefxn=hard_rep />
</ROSETTASCRIPTS>
```

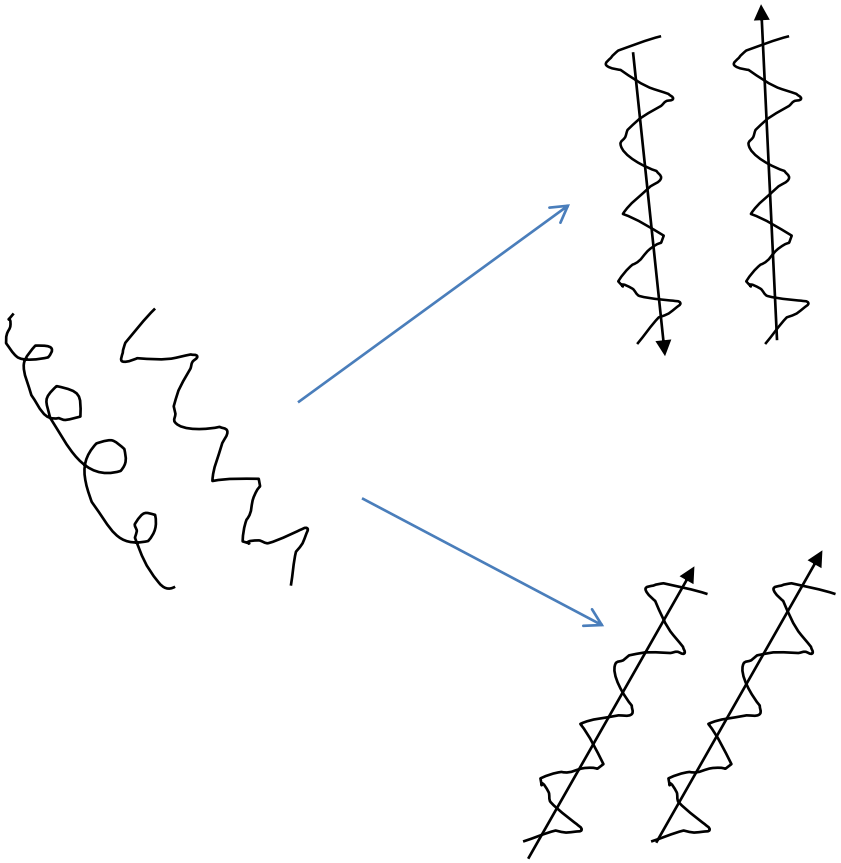
XML script options

- Weights filename or path to file
- Reweight specific terms as needed (as in patch file)
- Must include top-level output tag to ensure proper scoring in output files

Resources

- https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/score-types
- https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/scoring-explained

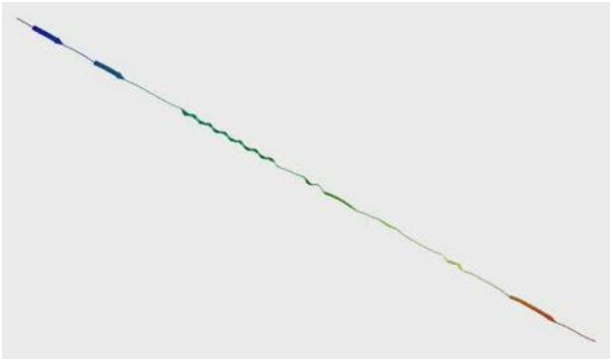
2º Structure pairing terms

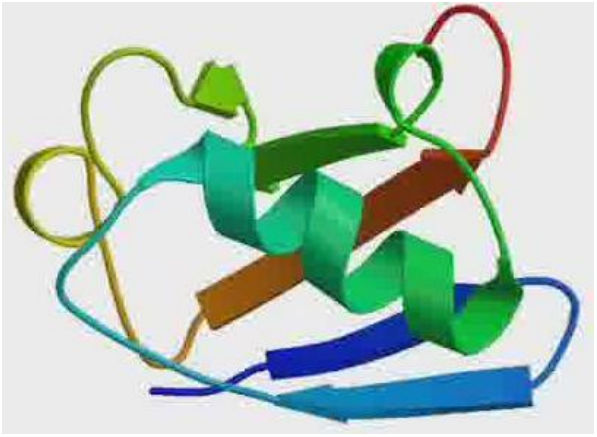


- `hs_pair / ss_pair / sheet`
- Aligns secondary structures to form helix/strand secondary structures
- Represent protein as vectors of 2 residue “strands”
- Scores selected to discriminate “near native structures for “non native”

Image by: Glenn Butterfoss
–Rosetta Design Group

Radius of Gyration / Packing Density

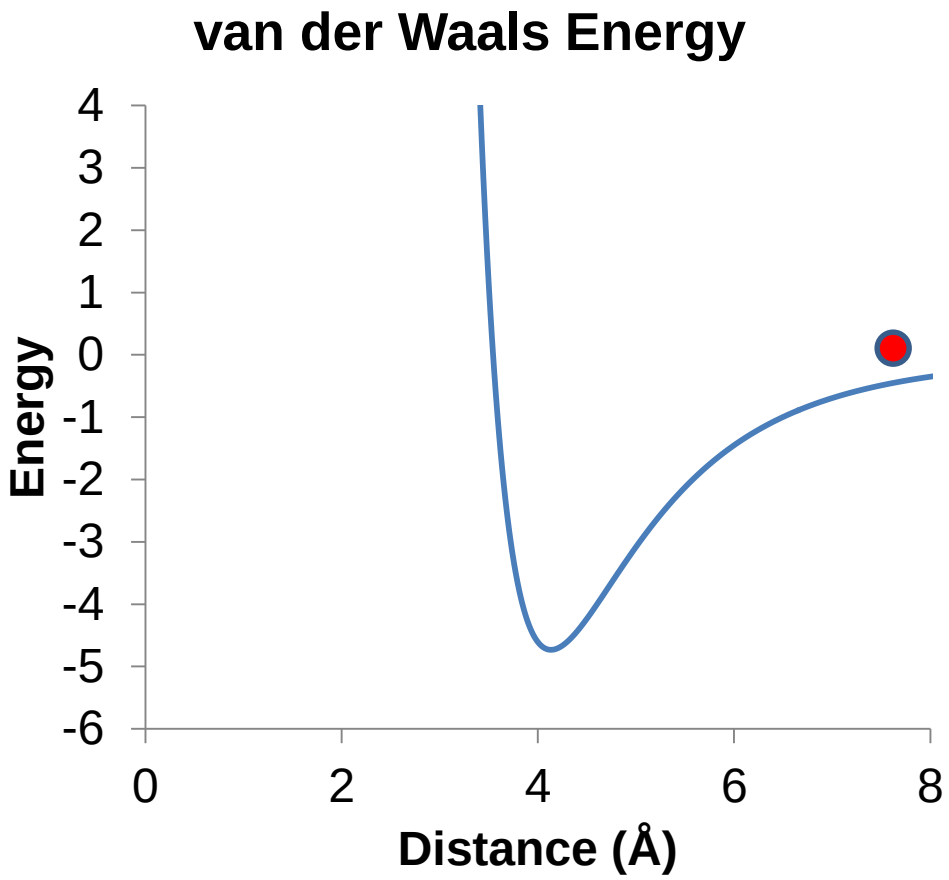




- rg / cenpack
- Promotes a compact fold
- Used early in the folding algorithm for filtering

Van der Waals

- `fa_atr / fa_rep / fa_intra_rep`
- 12-6 Lennard-Jones potential



Solvation

- `fa_sol`
- Based on Lazaridis Karplus term
- Implicit consideration of water
- Both penalty and bonus

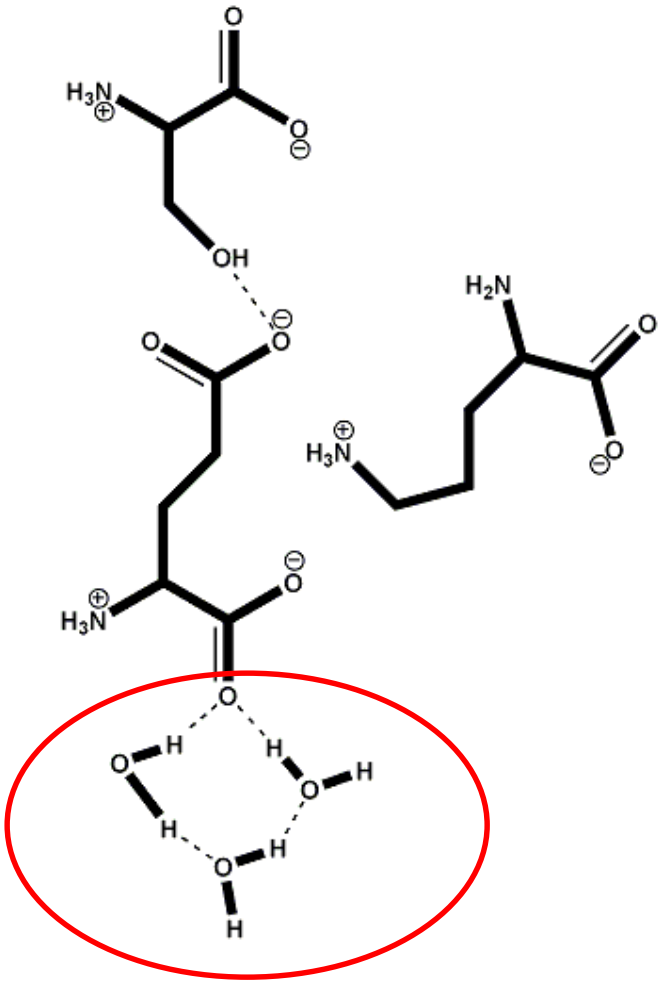
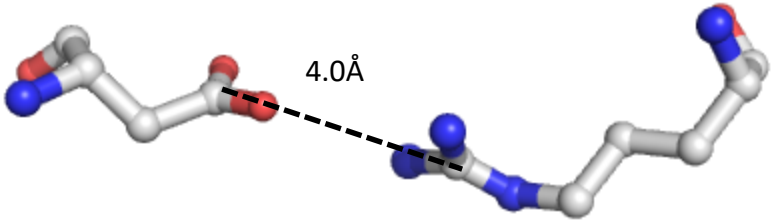


Image by:
Kristian Kaufmann

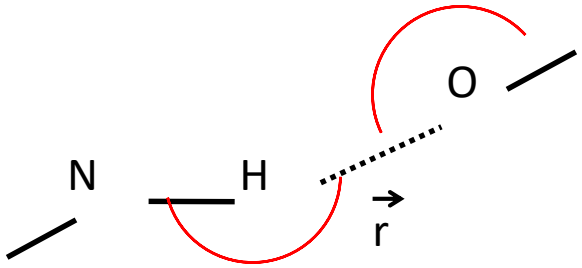
Electrostatics



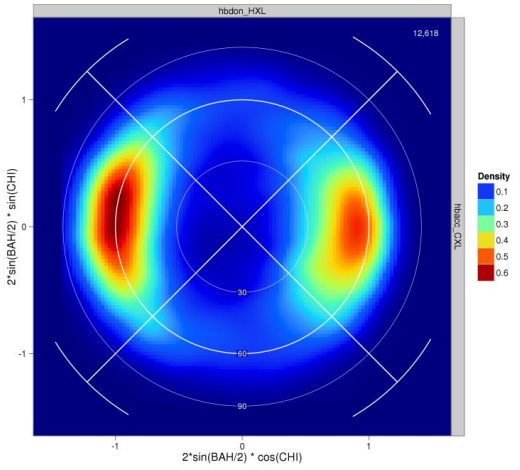
- `fa_elec`
- coulombic electrostatic potential with a distance-dependant dielectric
- Improved decoy discrimination
- Previously fa_pair – statistics based pair term

Hydrogen Bond Terms

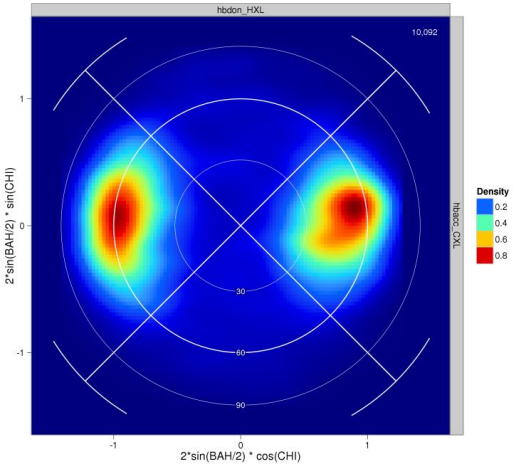
- hbond_lr_bb: long-range backbone
- hbond_sr_bb: short-range backbone
- hbond_bb_sc: backbone-sidechain
- hbond_sc: sidechain-sidechain
- Geometry dependent



Crystal Structure



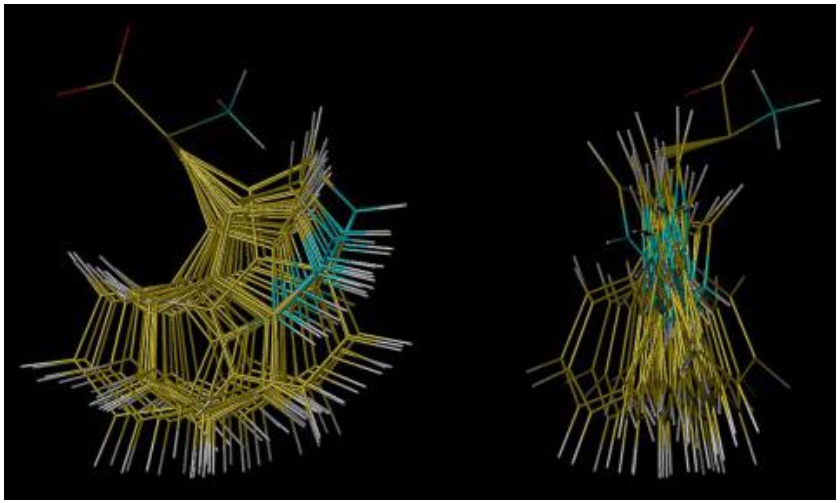
talaris2013



yhh_planarity: fixes geometry of hydrogen to lay within plane of Tyrosine ring

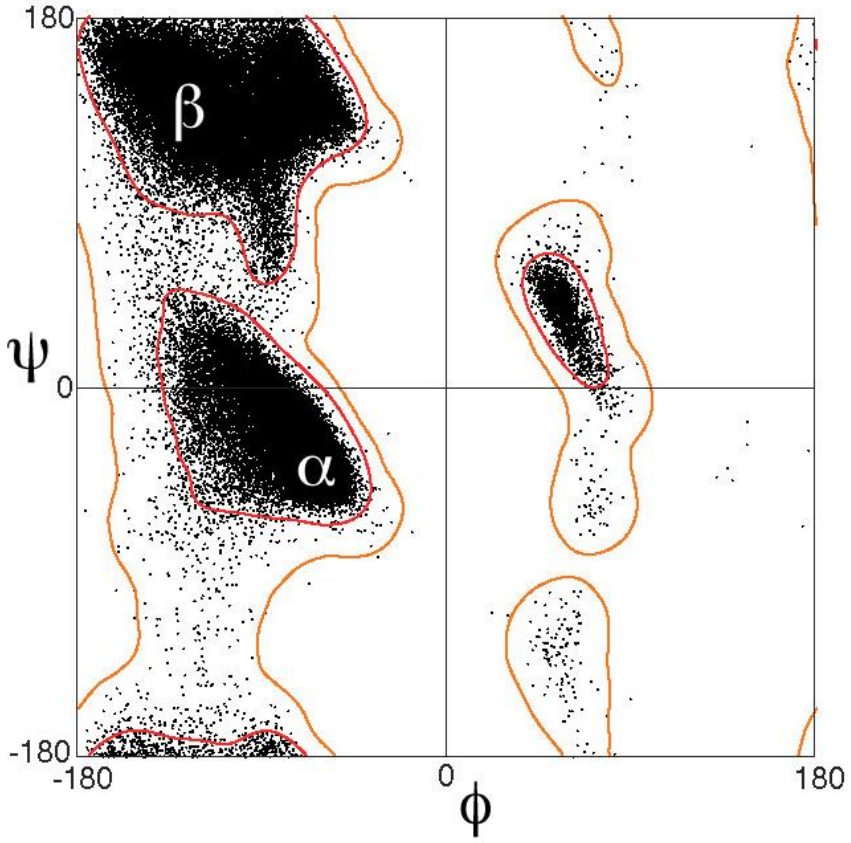
Dunbrack Rotamer Energy

- fa_dun
- Internal energy of a given rotamer
- Based on statistics of conformations of sidechains in the PDB
  - Compiled by Roland Dunbrack for the widely-used Dunbrack rotamer library.



Ramachandran and Phi Psi angles

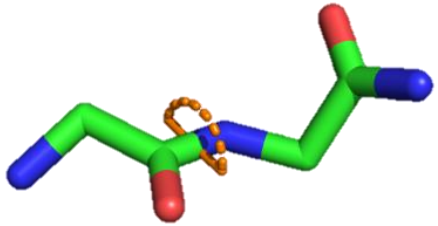
- `rama-` ramachandran preference
- `p_aa_pp-` probability of amino acid for phi, psi

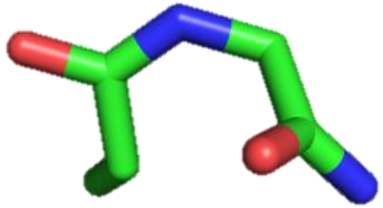


Lovell SC et al. (2003) *Proteins* **50** (3): 437–450.

Bonding penalties

- omega – omega angle penalty





- pro_close – proline ring closure

- dslf_fa13 – disulfide closure
  - Statistics based. (distance, angles, dihedrals)