

Energy Landscapes for Soft Matter

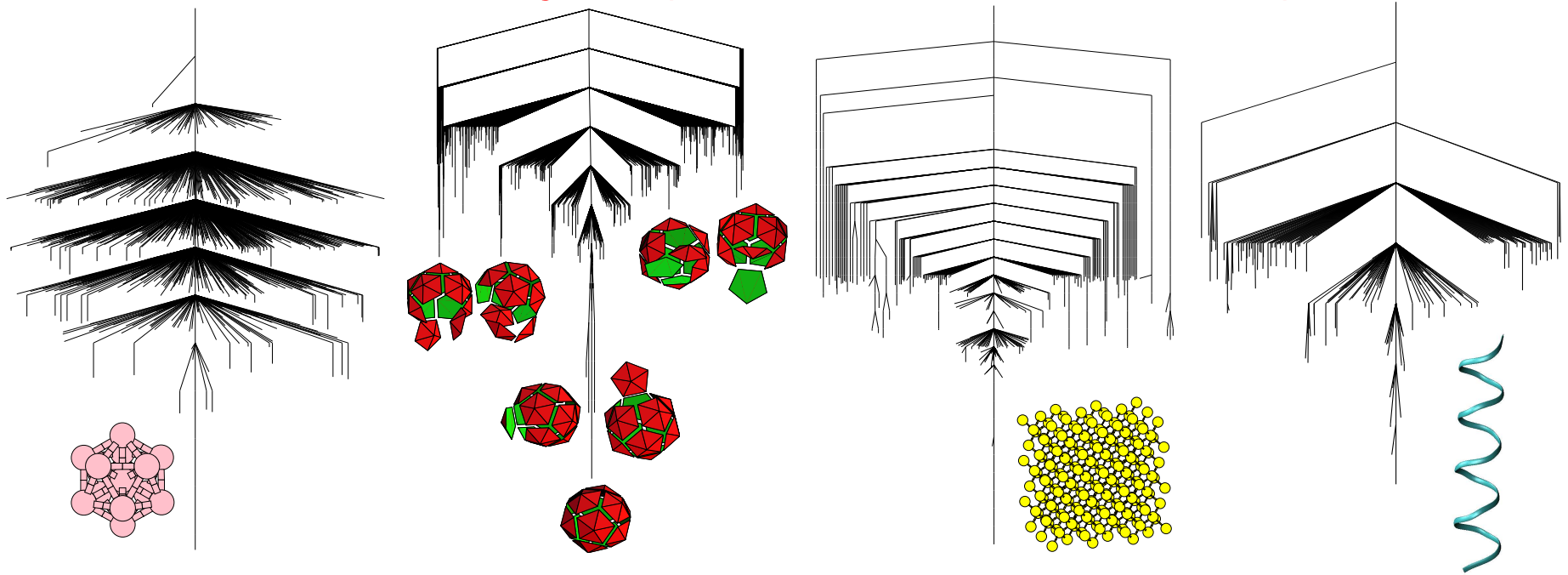
Objective: to use **stationary points** (minima and transition states) of the PES as a conceptual/computational framework (*J. Phys. Chem. B*, **110**, 20765, 2006):

- **Basin-hopping** for global optimisation (*J. Phys. Chem. A*, **101**, 5111 1997)
- **Superposition** approach for thermodynamics (*J. Chem. Phys.*, **124**, 044102, 2006)
- **Discrete path sampling** for global kinetics (*Mol. Phys.*, **100**, 3285, 2002)

For m weakly coupled subsystems of $N/m = n$ atoms each the number of local minima satisfies $f_{\min}(mn) = f_{\min}(n)^m$, so that $f_{\min}(N) = e^{\alpha N}$. For transition states we expect $f_{\text{ts}}(mn) = m f_{\min}(n)^{m-1} f_{\text{ts}}(n)$ so that $f_{\text{ts}}(N) = N e^{\alpha N} = N f_{\min}(N)$. Two important consequences:

- Appropriate **sampling** schemes are required for **larger** systems,
- Low-dimensional **projections** of the landscape can only represent the **connectivity** faithfully for a **few** anharmonic degrees of freedom.

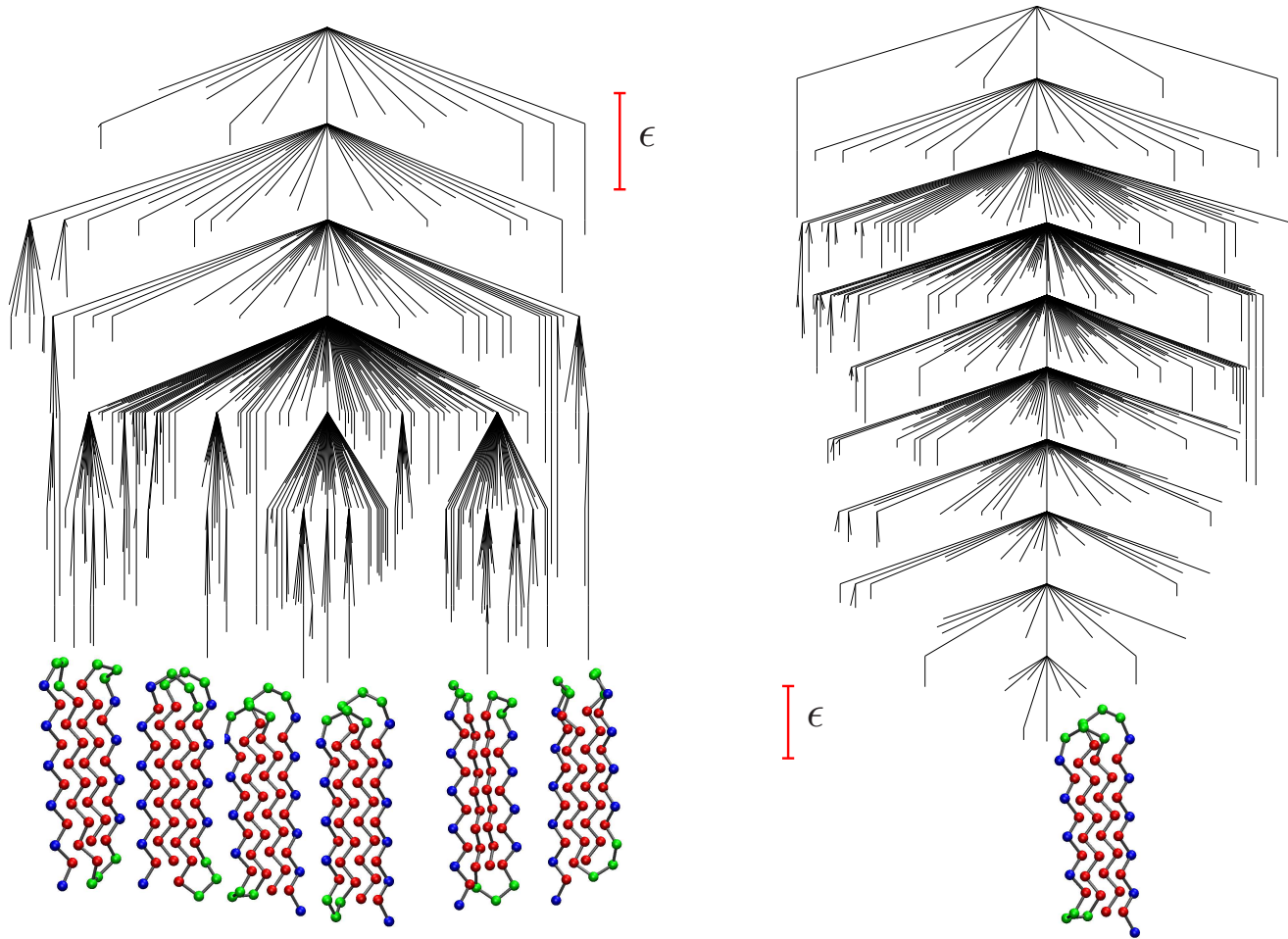
Disconnectivity Graphs of 'Funnelled' Landscapes



The nonrandom searches that result in **magic number** clusters, **crystallisation**, **self-assembly**, and **protein folding** are associated with a 'palm tree' organisation of the potential energy landscape (*Phil. Trans. Roy. Soc. A*, **363**, 357, 2005).

This 'funnelling' pattern has been verified for various **structure-seeking** systems, including the **LJ₁₃** cluster, **icosahedral shells** composed of pentagonal and hexagonal pyramids, crystalline (Stillinger-Weber) **silicon**, and the polyalanine **ala₁₆**. **Large** systems can exhibit relatively **simple** phenomenology.

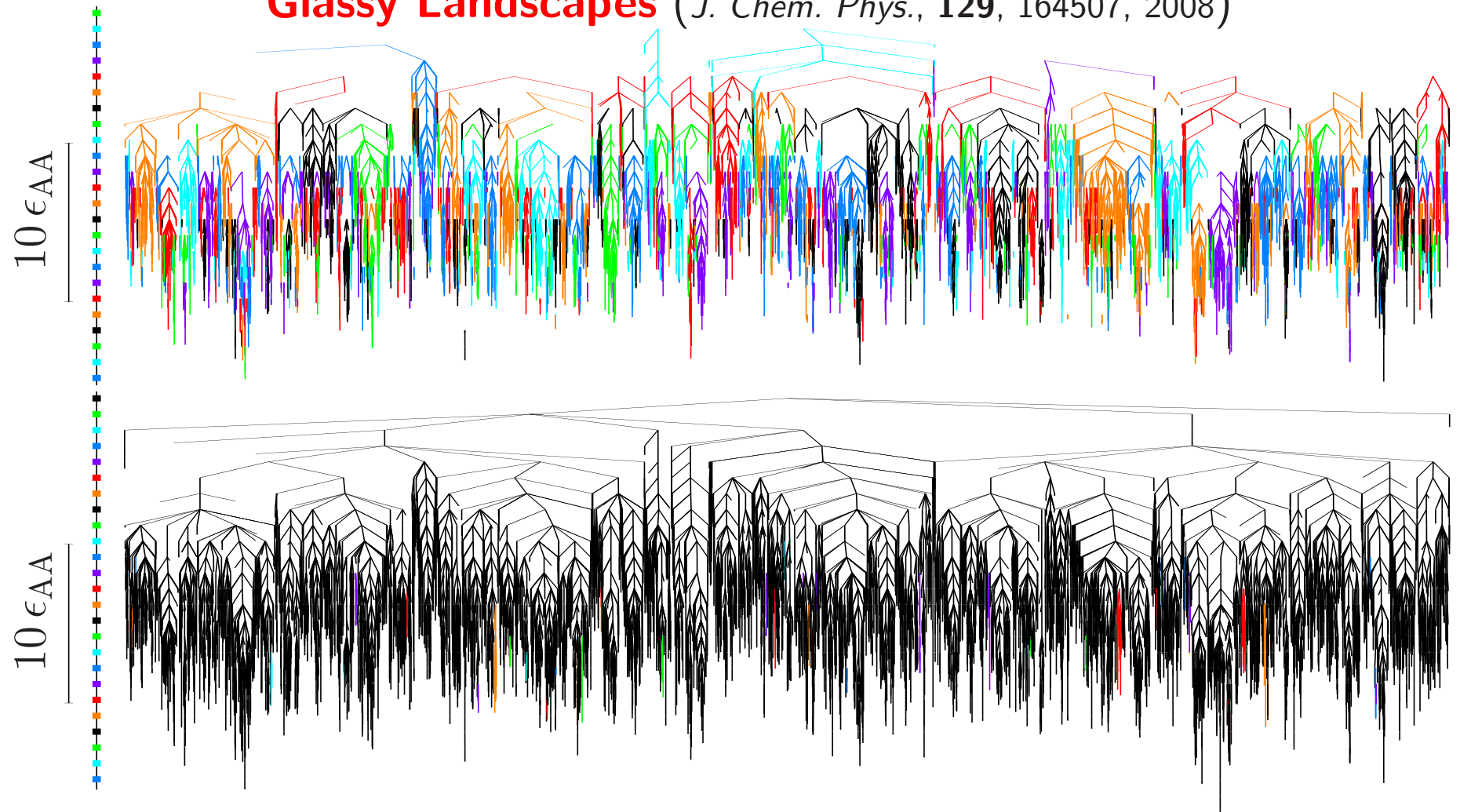
Frustrated or Funnelled? A Model Protein



For $B_9N_3(LB)_4N_3B_9N_3(LB)_5L$ low-lying minima are separated by high barriers, where the beads are B =hydrophobic, L =hydrophilic, and N =neutral.

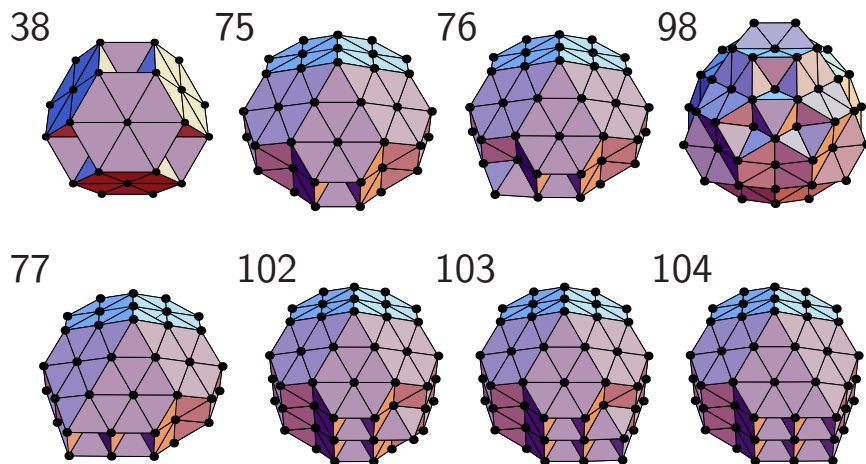
This 'frustration' affects the observed heat capacity and results in distinct relaxation time scales, which are eliminated in the corresponding $G\bar{o}$ model.

Glassy Landscapes (*J. Chem. Phys.*, **129**, 164507, 2008)

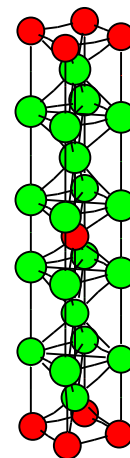


Disconnectivity graphs for **BLJ₆₀** including only transition states for **noncage-breaking** (top) and **cage-breaking** (bottom) paths. Changes in colour indicate **disjoint** sets of minima. Cage-breaking transitions, defined by **two** nearest-neighbour changes, define a higher order **metabasin** structure.

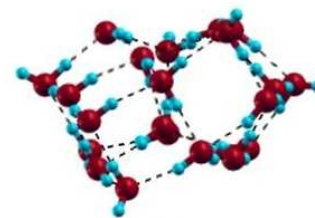
Basin-Hopping Global Optimisation (*J. Phys. Chem. A*, **101**, 5111, 1997)



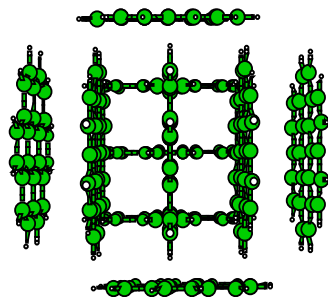
Non-icosahedral Lennard-Jones Clusters



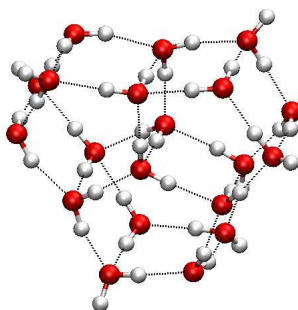
Binary LJ unit cell



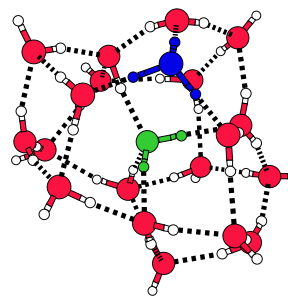
$C_{60}(H_2O)_{20}$



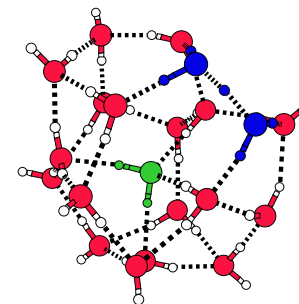
coronene₁₀



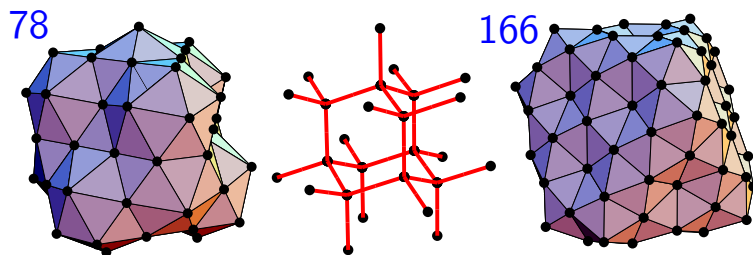
$(H_2O)_{20}$



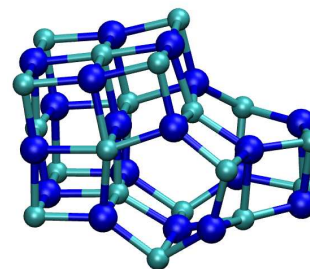
$H_3O^+(H_2O)_{20}$ Eigen



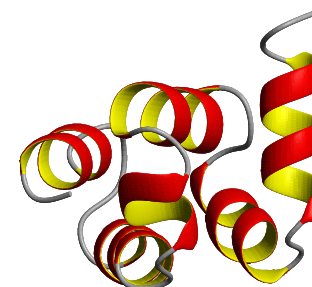
$H_3O^+(H_2O)_{20}$ Zundel



polytetrahedral clusters

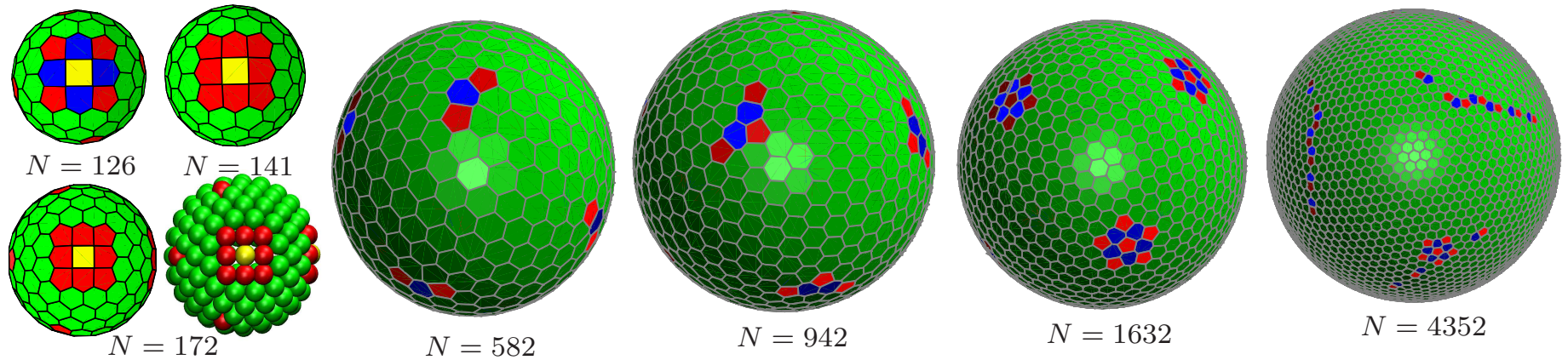


$(NaCl)_{18}Na^+$



HYPA/FBP11

The Thomson Problem (*Phys. Rev. B*, **74**, 212101, 2006; **79**, 224115, 2009)



Long-ranged potential: $V = \sum_{i < j} 1/|\mathbf{r}_i - \mathbf{r}_j|$ with $|\mathbf{r}_i| = 1$. Twelve five-coordinate particles (**disclinations**) enable a spherical system to obey Euler's rule for the **disclination charge**.

Pentagon patches, extended dislocations (**scars**), **twinned** defects, **rosettes**, and embryonic **grain boundaries** occur in larger systems.

Structures provide models for **spherically constrained** systems: multielectron bubbles in superfluid helium, cell surface layers, 'colloidosomes', colloidal silica microspheres, superconducting films, lipid rafts deposited on vesicles.

Angle-Axis Coordinates for Rigid Bodies (*PCCP*, 11, 1970, 2009)

Rodrigues' formula for the rotation matrix **R** corresponding to a rotation of magnitude $\theta = (p_1^2 + p_2^2 + p_3^2)^{1/2}$ around the axis defined by **p** is

$$\mathbf{R} = \mathbf{I} + (1 - \cos \theta) \tilde{\mathbf{p}} \tilde{\mathbf{p}} + \sin \theta \tilde{\mathbf{p}},$$

where **I** is the identity matrix, and $\tilde{\mathbf{p}}$ is the skew-symmetric matrix

$$\tilde{\mathbf{p}} = \frac{1}{\theta} \begin{pmatrix} 0 & -p_3 & p_2 \\ p_3 & 0 & -p_1 \\ -p_2 & p_1 & 0 \end{pmatrix}.$$

The product of $\tilde{\mathbf{p}}$ and any vector **v** returns the cross product: $\tilde{\mathbf{p}} \mathbf{v} = \hat{\mathbf{p}} \times \mathbf{v}$.

All terms involving rigid-body angle-axis coordinates can be obtained by the action of the rotation matrix and its derivatives, whose forms are programmed in system-independent subroutines.

The angle-axis representation is free of singularities and constraints.

1st derivatives: $\mathbf{R}_k \equiv \frac{\partial \mathbf{R}}{\partial p_k} = \frac{p_k \sin \theta}{\theta} \tilde{\mathbf{p}}^2 + (1 - \cos \theta)(\tilde{\mathbf{p}}_k \tilde{\mathbf{p}} + \tilde{\mathbf{p}} \tilde{\mathbf{p}}_k) + \frac{p_k \cos \theta}{\theta} \tilde{\mathbf{p}} + \sin \theta \tilde{\mathbf{p}}_k$, with $\tilde{\mathbf{p}}_1 = \frac{1}{\theta^3} \begin{pmatrix} 0 & p_1 p_3 & -p_1 p_2 \\ -p_1 p_3 & 0 & p_1^2 - \theta^2 \\ p_1 p_2 & \theta^2 - p_1^2 & 0 \end{pmatrix}$

2nd derivatives : $\mathbf{R}_{kk} \equiv \frac{\partial^2 \mathbf{R}}{\partial p_k^2} = \frac{2p_k \sin \theta}{\theta} (\tilde{\mathbf{p}}_k \tilde{\mathbf{p}} + \tilde{\mathbf{p}} \tilde{\mathbf{p}}_k) + \left(\frac{p_k^2 \cos \theta}{\theta^2} - \frac{p_k^2 \sin \theta}{\theta^3} + \frac{\sin \theta}{\theta} \right) \tilde{\mathbf{p}}^2$
 $+ (1 - \cos \theta)(2\tilde{\mathbf{p}}_k^2 + \tilde{\mathbf{p}}_{kk} \tilde{\mathbf{p}} + \tilde{\mathbf{p}} \tilde{\mathbf{p}}_{kk}) + \left(-\frac{p_k^2 \sin \theta}{\theta^2} - \frac{p_k^2 \cos \theta}{\theta^3} + \frac{\cos \theta}{\theta} \right) \tilde{\mathbf{p}} + \frac{2p_k \cos \theta}{\theta} \tilde{\mathbf{p}}_k + \sin \theta \tilde{\mathbf{p}}_{kk},$

and $\mathbf{R}_{kl} \equiv \frac{\partial^2 \mathbf{R}}{\partial p_k \partial p_l} = \frac{p_k \sin \theta}{\theta} (\tilde{\mathbf{p}}_l \tilde{\mathbf{p}} + \tilde{\mathbf{p}} \tilde{\mathbf{p}}_l) + \left(\frac{p_k p_l \cos \theta}{\theta^2} - \frac{p_k p_l \sin \theta}{\theta^3} \right) \tilde{\mathbf{p}}^2 + \frac{p_l \sin \theta}{\theta} (\tilde{\mathbf{p}}_k \tilde{\mathbf{p}} + \tilde{\mathbf{p}} \tilde{\mathbf{p}}_k)$
 $+ (1 - \cos \theta)(\tilde{\mathbf{p}}_{kl} \tilde{\mathbf{p}} + \tilde{\mathbf{p}}_k \tilde{\mathbf{p}}_l + \tilde{\mathbf{p}}_l \tilde{\mathbf{p}}_k + \tilde{\mathbf{p}} \tilde{\mathbf{p}}_{kl}) - \left(\frac{p_k p_l \sin \theta}{\theta^2} + \frac{p_k p_l \cos \theta}{\theta^3} \right) \tilde{\mathbf{p}} + \frac{p_k \cos \theta}{\theta} \tilde{\mathbf{p}}_l + \frac{p_l \cos \theta}{\theta} \tilde{\mathbf{p}}_k + \sin \theta \tilde{\mathbf{p}}_{kl}.$

Denote positions in the **body-fixed** frame by superscript 0. For rigid bodies **I** and **J** with sites **i** and **j** defining site-site **isotropic** potentials U_{ij}^{IJ} the **potential energy** is

$$U = \sum_I \sum_{J < I} \sum_{i \in I} \sum_{j \in J} f_{ij}(r_{ij}), \quad \text{where} \quad r_{ij} = |\mathbf{r}_{ij}| = |\mathbf{r}_i - \mathbf{r}_j| \quad \text{and} \quad f_{ij} \equiv U_{ij}^{IJ} \quad \text{so that}$$

$$\frac{\partial U}{\partial \zeta} = \sum_{J \neq I} \sum_{i \in I} \sum_{j \in J} f'_{ij}(r_{ij}) \frac{\partial r_{ij}}{\partial \zeta}, \quad \text{where} \quad f'_{ij} = \frac{df_{ij}(r_{ij})}{dr_{ij}}, \quad \frac{\partial r_{ij}}{\partial \mathbf{r}^I} = \hat{\mathbf{r}}_{ij}, \quad \frac{\partial r_{ij}}{\partial p_k^I} = \hat{\mathbf{r}}_{ij} \cdot \frac{\partial \mathbf{r}_{ij}}{\partial p_k^I} = \hat{\mathbf{r}}_{ij} \cdot (\mathbf{R}_k^I \mathbf{r}_i^0), \quad \mathbf{r}_{ij} = \mathbf{r}^I + \mathbf{R}^I \mathbf{r}_i^0 - \mathbf{r}^J - \mathbf{R}^J \mathbf{r}_j^0.$$

$$\frac{\partial^2 U_{ij}^{IJ}}{\partial r_k^I \partial r_l^J} = f_2(r_{ij}) r_{ij,k} r_{ij,l} \epsilon_{IJ} + f_1(r_{ij}) \delta_{kl} \epsilon_{IJ},$$

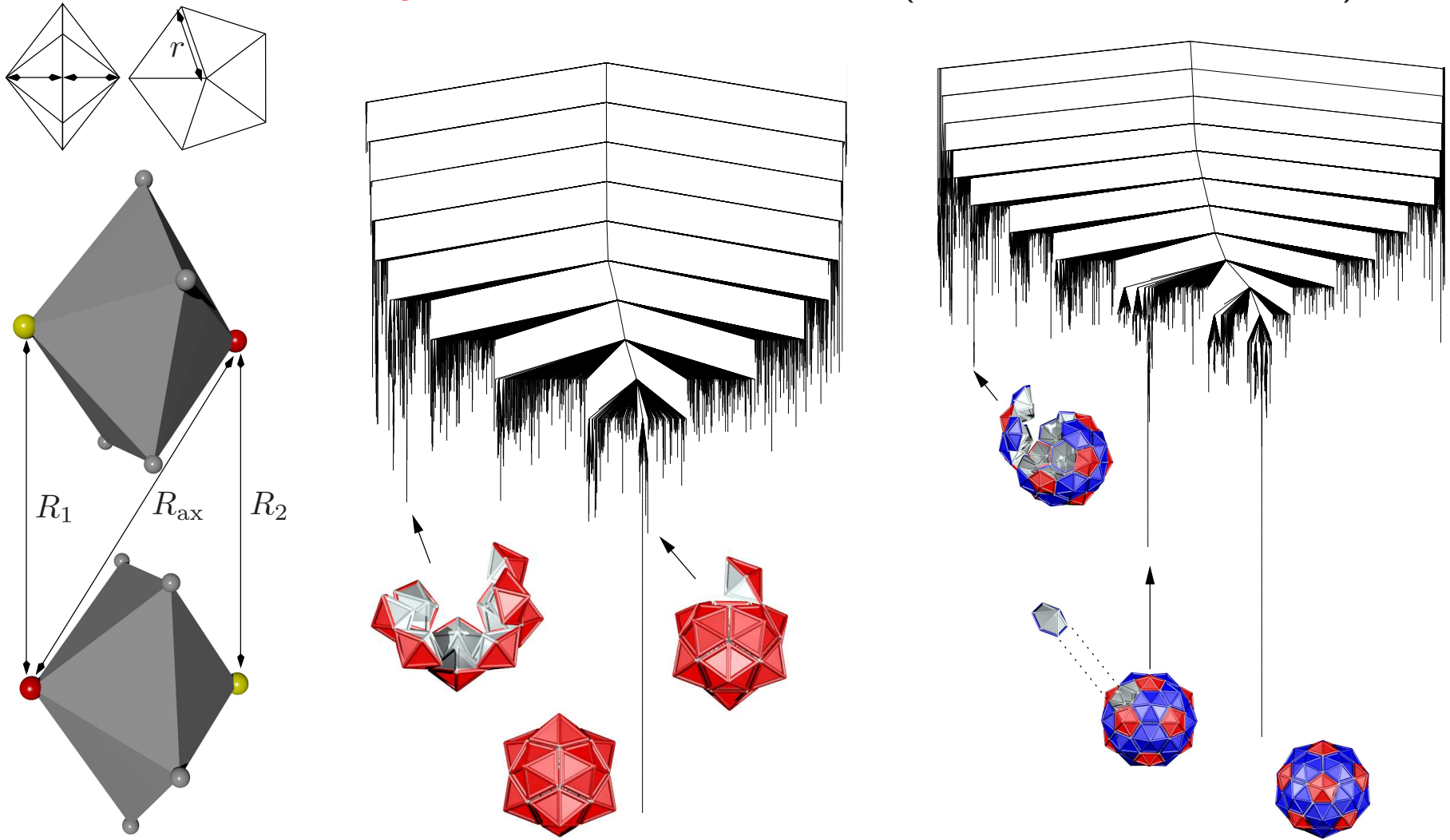
$$\frac{\partial^2 U_{ij}^{IJ}}{\partial p_k^I \partial p_l^J} = f_2(r_{ij}) (\mathbf{r}_{ij} \cdot \mathbf{R}_k^I \mathbf{r}_i^0) (\mathbf{r}_{ij} \cdot \mathbf{R}_l^J \mathbf{r}_j^0) \delta_{IJ} - f_2(r_{ij}) (\mathbf{r}_{ij} \cdot \mathbf{R}_k^I \mathbf{r}_i^0) (\mathbf{r}_{ij} \cdot \mathbf{R}_l^J \mathbf{r}_j^0) (1 - \delta_{IJ}) + f_1(r_{ij}) (\mathbf{R}_k^I \mathbf{r}_i^0) \cdot (\mathbf{R}_l^J \mathbf{r}_j^0) \delta_{IJ}$$

$$- f_1(r_{ij}) (\mathbf{R}_k^I \mathbf{r}_i^0) \cdot (\mathbf{R}_l^J \mathbf{r}_j^0) (1 - \delta_{IJ}) + f_1(r_{ij}) (\mathbf{r}_{ij} \cdot \mathbf{R}_{kl}^I \mathbf{r}_i^0) \delta_{IJ},$$

$$\frac{\partial^2 U_{ij}^{IJ}}{\partial r_k^I \partial p_l^J} = f_2(r_{ij}) (\mathbf{r}_{ij} \cdot \mathbf{R}_l^J \mathbf{r}_j^0) r_{ij,k} \delta_{IJ} - f_2(r_{ij}) (\mathbf{r}_{ij} \cdot \mathbf{R}_l^J \mathbf{r}_j^0) r_{ij,k} (1 - \delta_{IJ}) + f_1(r_{ij}) [\mathbf{R}_k^I \mathbf{r}_i^0]_l \delta_{IJ} - f_1(r_{ij}) [\mathbf{R}_l^J \mathbf{r}_j^0]_l (1 - \delta_{IJ}).$$

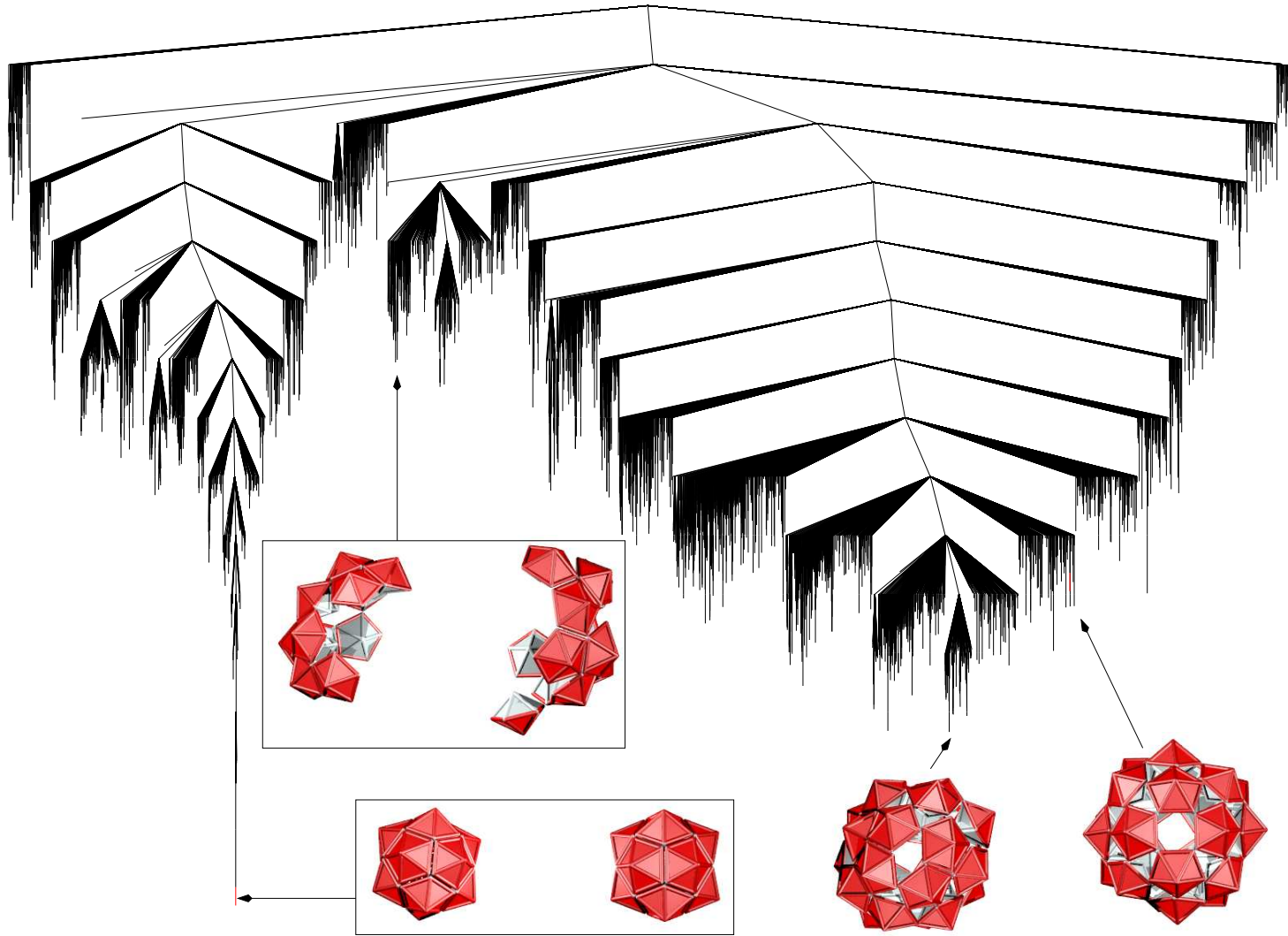
where $f_1(r_{ij}) = f'_{ij}(r_{ij})/r_{ij}$, $f_2(r_{ij}) = f''_{ij}(r_{ij})/r_{ij}$, $\epsilon_{IJ} = 1$ for $I = J$ and $\epsilon_{IJ} = -1$ for $I \neq J$, and δ_{IJ} is the Kronecker delta.

Self-Assembly of Icosahedral Shells (*PCCP*, **11**, 2098-2104, 2009)



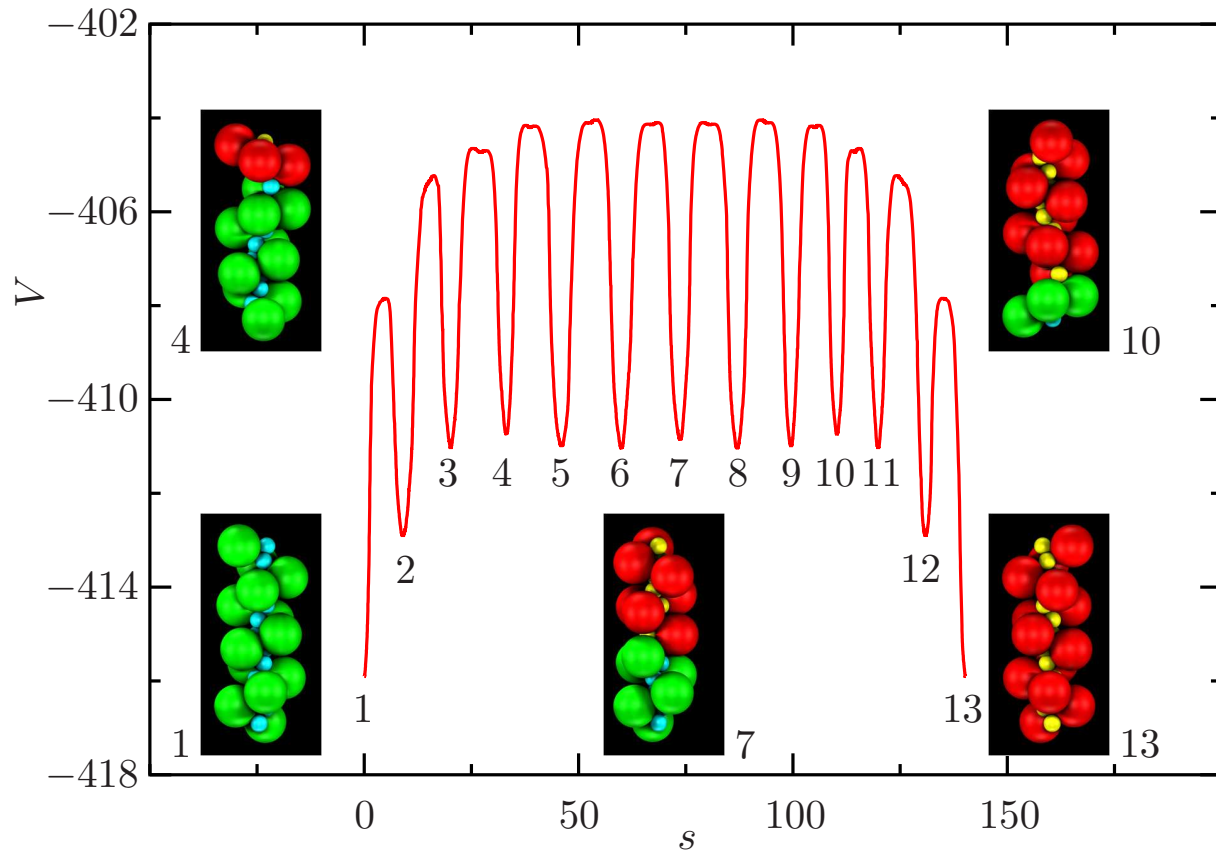
Palm tree disconnectivity graphs with I_h global minima are found for $T = 1$ and $T = 3$ shells constructed from **pentagonal** and **hexagonal** pyramids. **Landscapes** of this form are associated with good **structure-seekers**.

24 Pentagonal Pyramids



For the same parameters two $T = 1$ icosahedra are similar in energy to a single shell based on a snub cube. *Polyoma virus* capsid protein VP₁ forms a left-handed snub cube from alkaline solution in the absence of the genome.

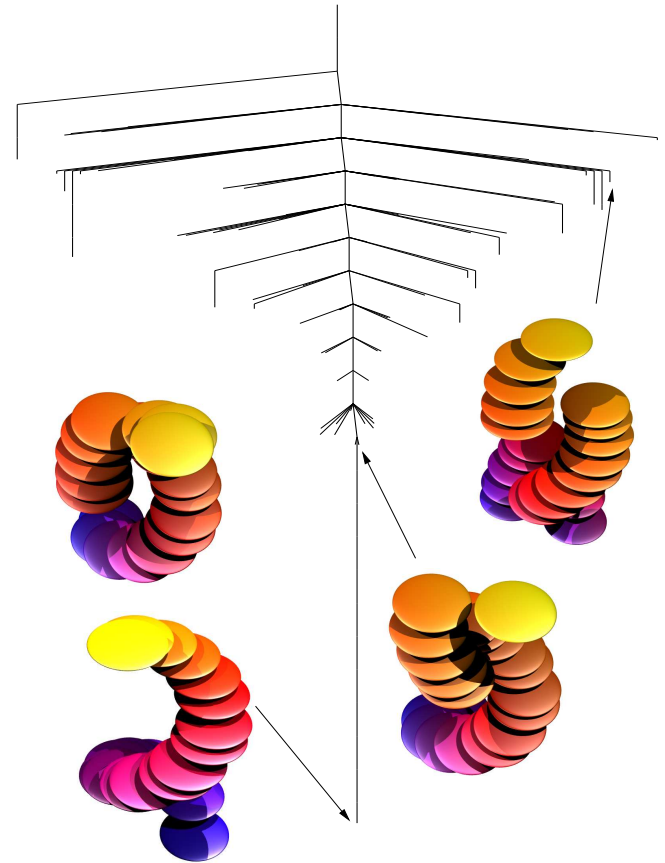
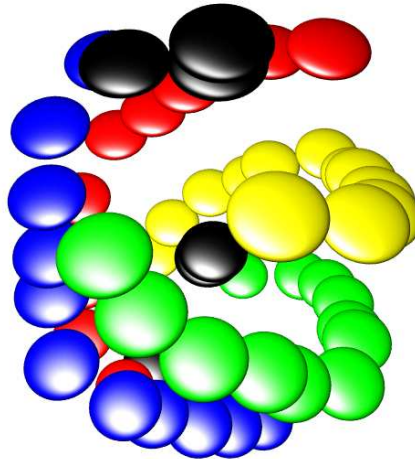
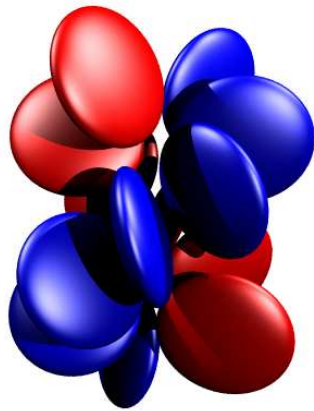
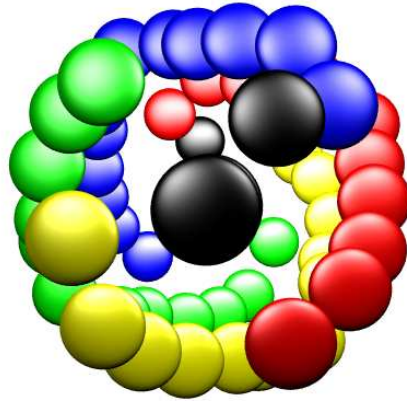
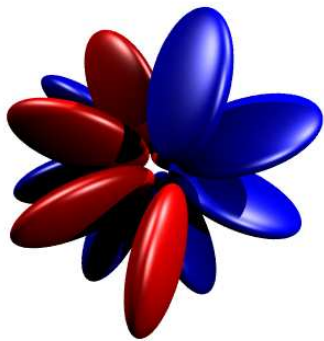
A Molecular Machine



Coupled **linear** and **rotary** motion has been characterised for a helix composed of 13 asymmetric **dipolar dumbbells** in the presence of an **electric field**.

The helix changes **handedness** as the boundary between segments propagates along the strand via successive steps that switch the dumbbells.

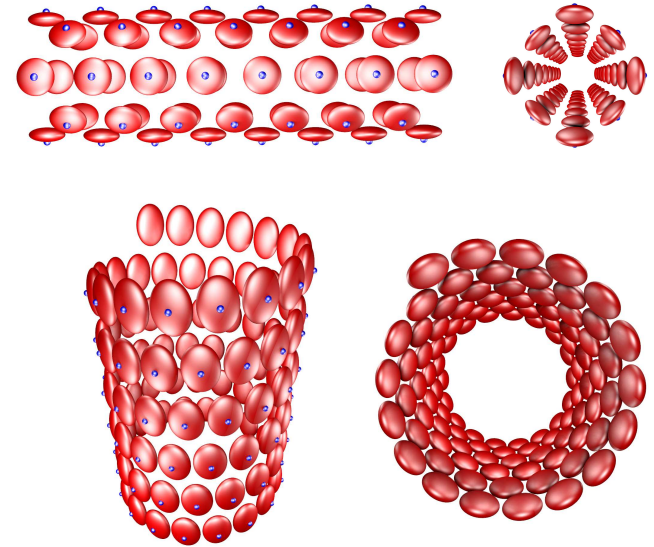
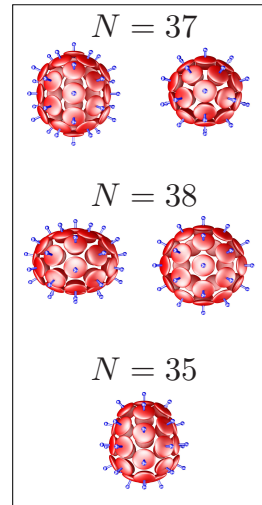
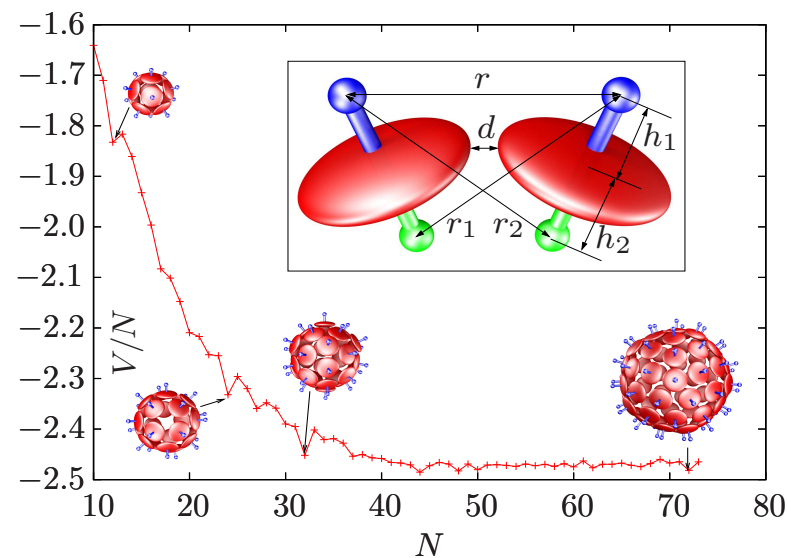
Clusters of Ellipsoids (*Phys. Rev. Lett.*, **99**, 086106, 2007)



Clusters of **discoids** bound by the **Paramonov-Yaliraki** potential exhibit **helical** global minima when the dimer has a shifted stacked configuration.

The corresponding energy landscapes generally have **single funnel** topologies for both single and **multiple** strand helices.

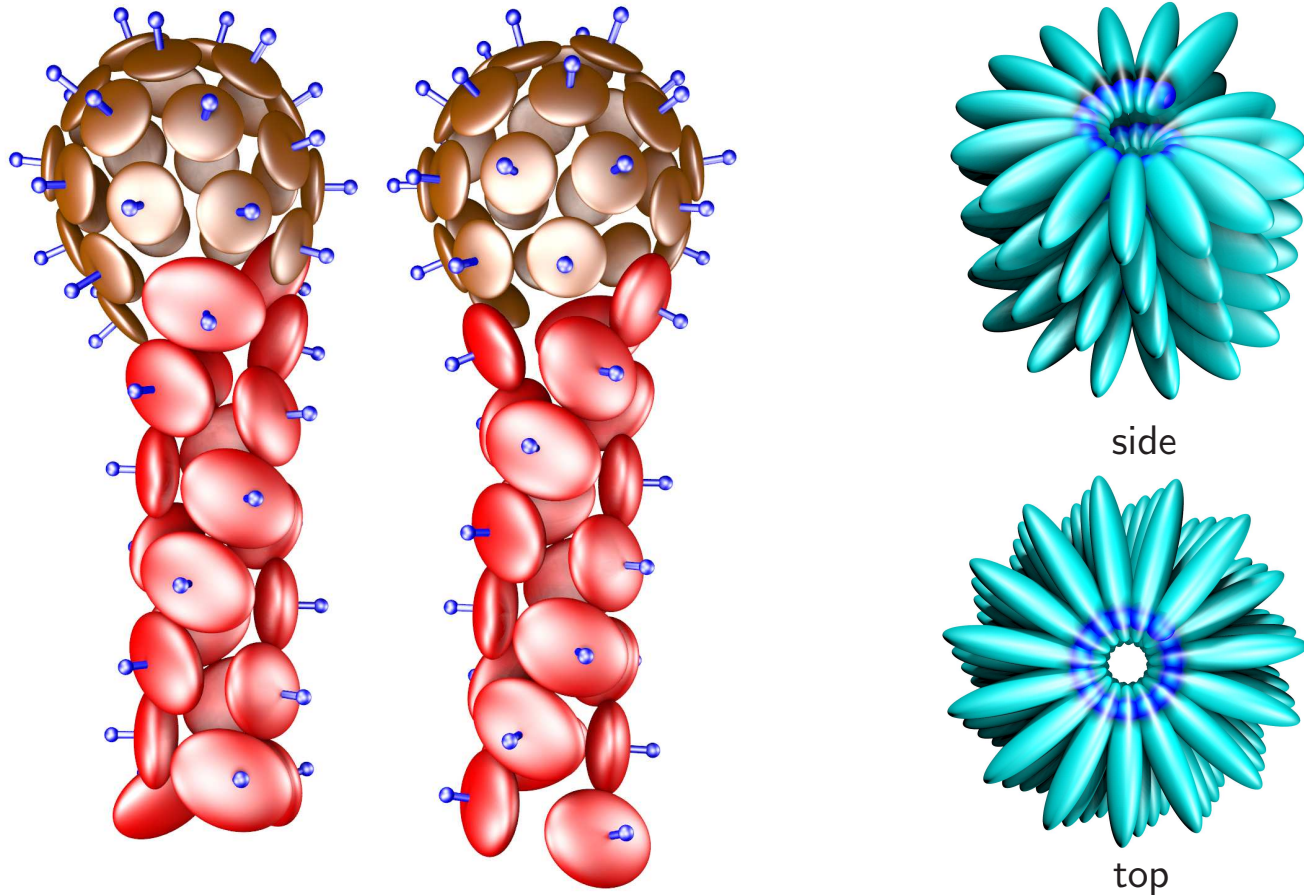
Emergent Behaviour from Simple Building Blocks



Adding two repulsive **axial** Lennard-Jones sites to the **ellipsoidal** core produces remarkably versatile building blocks. **Oblate** ellipsoids favour **shells**, while stronger repulsion for the longer semiaxis produces **tubes** and **spirals**.

Global minima for the **oblate** ellipsoids include **icosahedra** for $N = 12, 32$ and 72 ($T = 1, 3$ and 7), the **snub cube** observed for polyoma virus capsids at $N = 24$, and **conical**, **biaxial**, **prolate**, and **oblate** shells at other sizes.

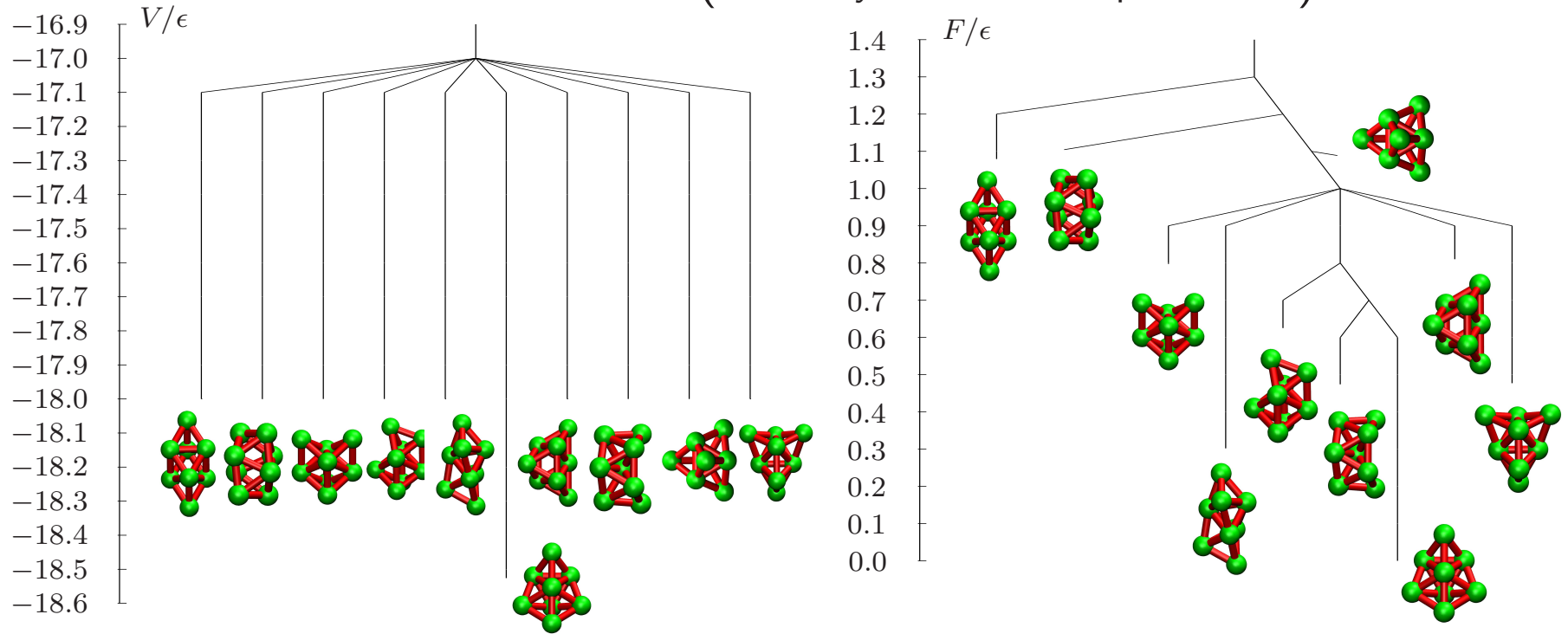
Modelling Mesoscopic Structures (ACS Nano, 4, 219, 2010)



Mixing building blocks that favour shells and tubes produces structures with distinct head and tail regions (left): the Frankenphage.

Particles with a Lennard-Jones site buried in the ellipsoid assemble into a spiral structure (right) with parameters similar to tobacco mosaic virus.

Colloidal Clusters (*ChemPhysChem*, **11**, in press, 2010)



The structures of **colloidal** clusters formed from polystyrene microspheres by **depletion interactions** have recently been resolved using **optical microscopy**.

For these **short-ranged** interactions the isomer populations are quantitatively reproduced by the partition functions $Z_\alpha = e^{-\beta V_\alpha} / o_\alpha (\beta h \bar{\nu}_\alpha)^{3N-6} = e^{-F_\alpha / k_B T}$, calculated for a **Morse** potential with range parameter $\rho = 30$. The order of the point group, o_α , plays a key role, as shown for 8-particle clusters, above.

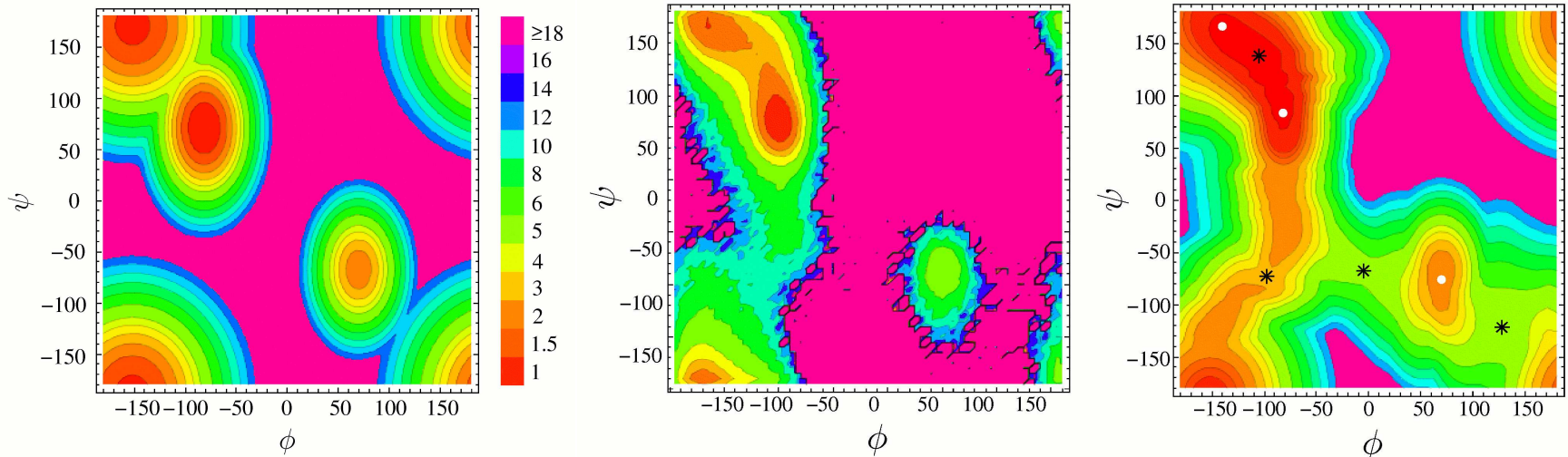
A Modified Superposition Approach (*Chem. Phys. Lett.*, **466**, 105, 2008)

Here the partition function is broken down into contributions from local **minima** and **pathways** as a function of order parameter a , with terms like

$$Z_i(a, T) = \left(\frac{kT}{h\bar{\nu}_i} \right)^{3N-6} \frac{\exp(-V_i/kT)}{\sqrt{2\pi kT A_i}} \exp \left[-\frac{(a - a_i)^2}{2kT A_i} \right],$$

where A_i is a weighted sum of order parameter derivatives.

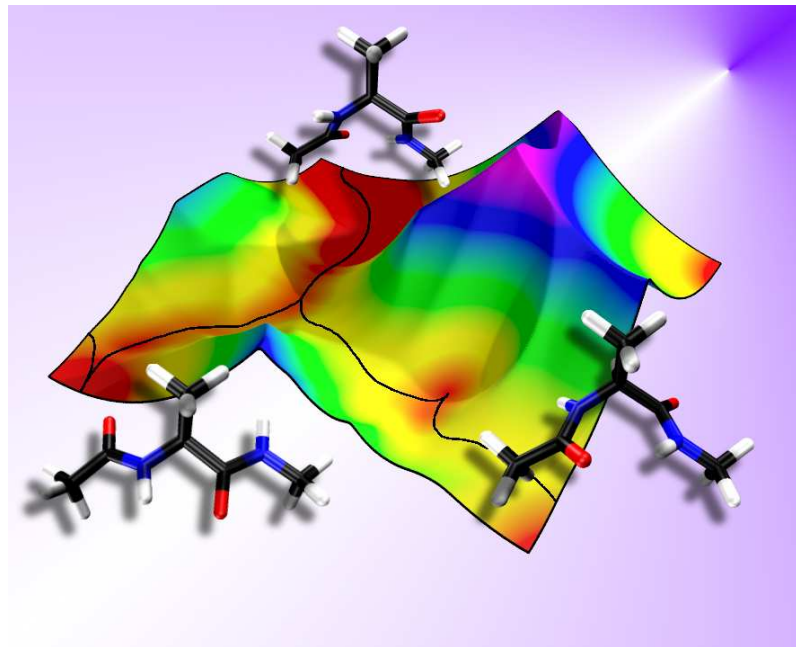
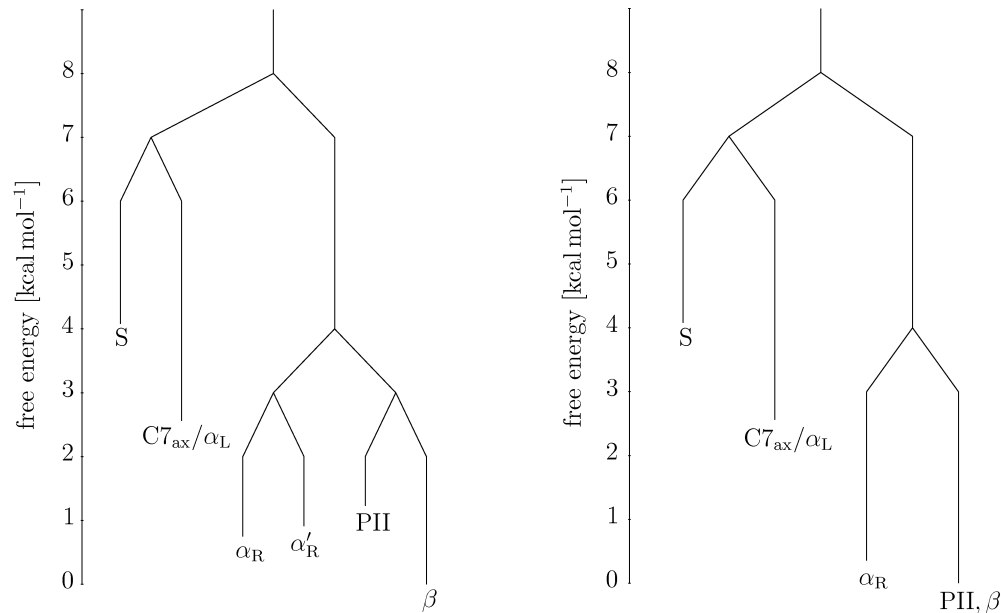
Free energy surfaces for **alanine dipeptide** (CHARMM22/vacuum) from **superposition**, **replica exchange**, and **reaction path Hamiltonian** superposition:



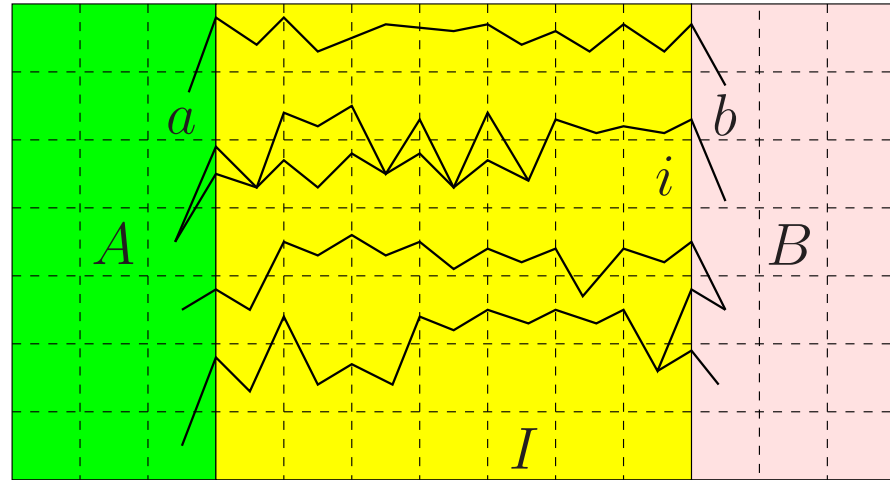
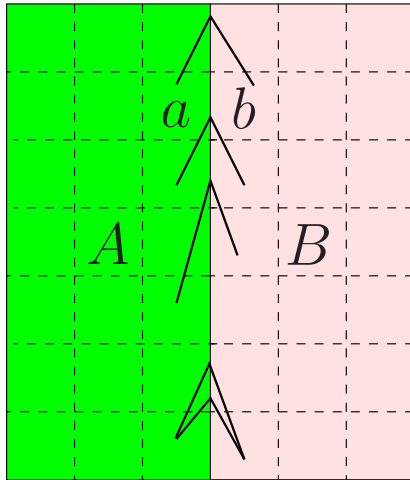
The ‘**filling in**’ problem for barrier regions in **low-dimensional** projections due to **overlapping** distributions can be avoided using **disconnectivity graphs**.

The effect of **regrouping** for a barrier threshold of 3 kcal/mol is shown below for AMBER(ff03)/GB^{OCB} (left) and compared with the CHARMM22/vacuum surface (right). Free energy of **group** J : $F_J(T) = -kT \ln \sum_{j \in J} Z_j(T)$ with

$$F_{LJ}^\dagger(T) = -kT \ln \sum_{l \leftarrow j} Z_{lj}^\dagger(T), \quad \text{and} \quad k_{LJ}(T) = \frac{kT}{h} e^{-[F_{LJ}^\dagger(T) - F_J(T)]/kT}.$$



Discrete Path Sampling (Mol. Phys., 100, 3285, 2002).



no intervening minima

$$\frac{p_a(t)}{p_{a'}(t)} = \frac{p_a^{\text{eq}}}{p_{a'}^{\text{eq}}} \quad \dot{p}_i(t) = 0 \quad \frac{p_b(t)}{p_{b'}(t)} = \frac{p_b^{\text{eq}}}{p_{b'}^{\text{eq}}}$$

Phenomenological $A \leftrightarrow B$ rate constants can be formulated as sums over **discrete paths**, defined as sequences of local minima and the transition states that link them, weighted by equilibrium occupation probabilities, p_b^{eq} :

$$k_{AB}^{\text{SS}} = \frac{1}{p_B^{\text{eq}}} \sum_{a \leftarrow b} P_{ai_1} P_{i_1 i_2} \cdots P_{i_{n-1} i_n} P_{i_n b} \tau_b^{-1} p_b^{\text{eq}} = \frac{1}{p_B^{\text{eq}}} \sum_{b \in B} \frac{C_b^A p_b^{\text{eq}}}{\tau_b},$$

where $P_{\alpha\beta}$ is a **branching probability** and C_b^A is the **committor** probability that the system will visit an A minimum **before** it returns to the B region.

Discrete path sampling is a framework for growing databases of stationary points that are relevant to global **kinetics** (*Int. Rev. Phys. Chem.*, **25**, 237, 2006).

A **hierarchy** of expressions can be obtained for the rate constants:

$$k_{AB}^{\text{SS}} = \frac{1}{p_B^{\text{eq}}} \sum_{b \in B} \frac{C_b^A p_b^{\text{eq}}}{\tau_b}, \quad k_{AB}^{\text{NSS}} = \frac{1}{p_B^{\text{eq}}} \sum_{b \in B} \frac{C_b^A p_b^{\text{eq}}}{t_b}, \quad k_{AB} = \frac{1}{p_B^{\text{eq}}} \sum_{b \in B} \frac{p_b^{\text{eq}}}{\mathcal{T}_{Ab}}.$$

τ_b , t_b and \mathcal{T}_{Ab} are the mean **waiting times** for a transition from b to an adjacent minimum, to any member of $A \cup B$, and to the A set, with $\tau_b \leq t_b \leq \mathcal{T}_{Ab}$.

k_{AB} is formally **exact** within a **Markov** assumption for transitions between the states, which can be **regrouped**. Additional approximations come from **incomplete sampling**, and the **densities of states** and **transition state theory** used to describe the **local** thermodynamics and kinetics.

Calculating k_{AB} using **diagonalisation**, successive overrelaxation (**SOR**), or kinetic Monte Carlo (**KMC**) can become **unfeasible** for large databases.

Kinetic Analysis by Graph Transformation (*JCP*, 124, 234110, 2006)

The **graph transformation** procedure is **non-stochastic** and **non-iterative**. Minima, x , are progressively **removed**, while the branching probabilities and waiting times in adjacent minima, $\beta \in \Gamma$, are **renormalised**:

$$P'_{\gamma\beta} = P_{\gamma\beta} + P_{\gamma x}P_{x\beta} \sum_{m=0}^{\infty} P_{xx}^m = P_{\gamma\beta} + \frac{P_{\gamma x}P_{x\beta}}{1 - P_{xx}}, \quad \tau'_{\beta} = \tau_{\beta} + \frac{P_{x\beta}\tau_x}{1 - P_{xx}}.$$

Each transformation **conserves** the **MFPT** from every reactant state to the set of product states with an execution time **independent** of temperature:

kT/K	$\Delta F_{\text{barrier}}$	N_{min}	N_{ts}	NGT/s	SOR/s	KMC/s
298	5.0	272	287	8	13	85,138
298	4.5	2,344	2,462	8	217,830	
1007	-	40,000	58,410	35	281	1,020,540
1690	-	40,000	58,410	39	122,242	

Finding Stationary Points

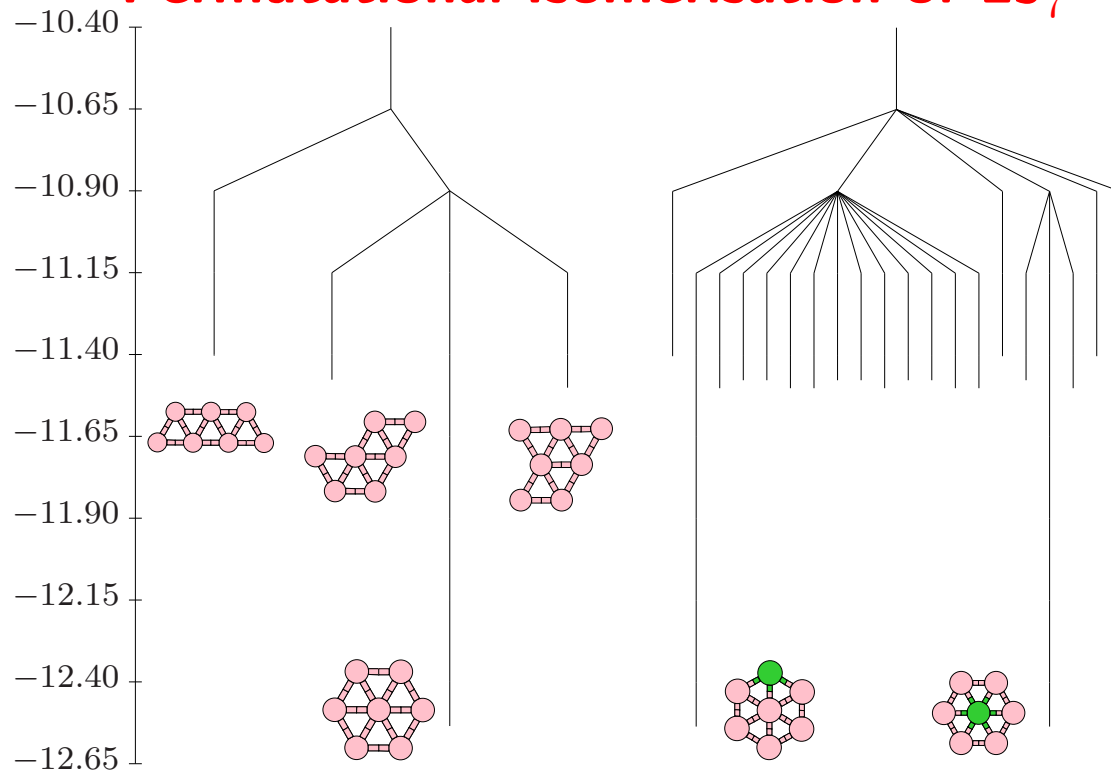
Minimisation: Nocedal's algorithm, **LBFGS**, with line searches removed.

Transition states: single-ended searches use **hybrid eigenvector-following** (*Phys. Rev. B*, **59**, 3969, 1999; *Chem. Phys. Lett.*, **341**, 185, 2001), double-ended searches use the **doubly-nudged elastic band** approach (*J. Chem. Phys.*, **120**, 2082, 2004).

These methods can be combined with **electronic structure** calculations.

- **Hydrocarbon dissociation** on Pt{110} (1×2) (*J. Chem. Phys.*, **126**, 044710, 2007). For ethane, **low** barriers (0.3 to 0.4 eV) are found for initial formation of ethene and ethylidene, **medium** barriers (0.7 to 1.1 eV) are found for dehydrogenation of C₂H₄, and **higher** barriers for further dehydrogenation.
- **Ammonia synthesis** and dissociation on Fe{211}: the **Haber-Bosch** process. We predict that atomic nitrogen can be **hydrogenated** above around 340 K, with **ammonia** being evolved at temperatures above 570-670 K.

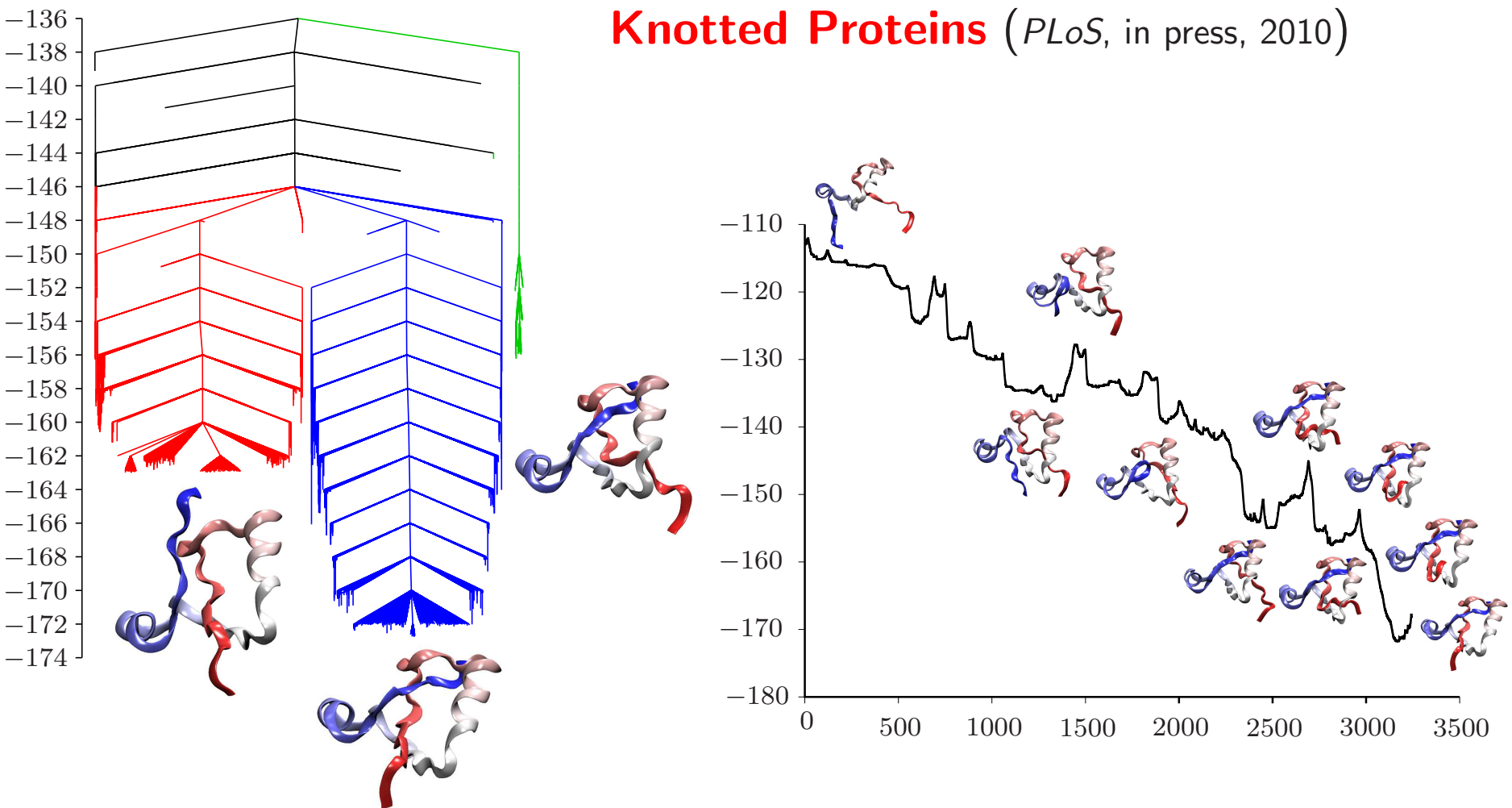
Permutational Isomerisation of $\text{LJ}_7^{2\text{D}}$



Disconnectivity graphs for $\text{LJ}_7^{2\text{D}}$. Left: permutation-inversion isomers of the four local minima are collected **together**. Right: one of the atoms is **tagged**, lowering the permutational degeneracy.

The fastest ten paths contribute about **74%** of the total rate constant at $kT/\epsilon = 0.05$. Various combinations of **diamond-square-diamond** rearrangements make significant contributions.

Knotted Proteins (*PLoS*, in press, 2010)

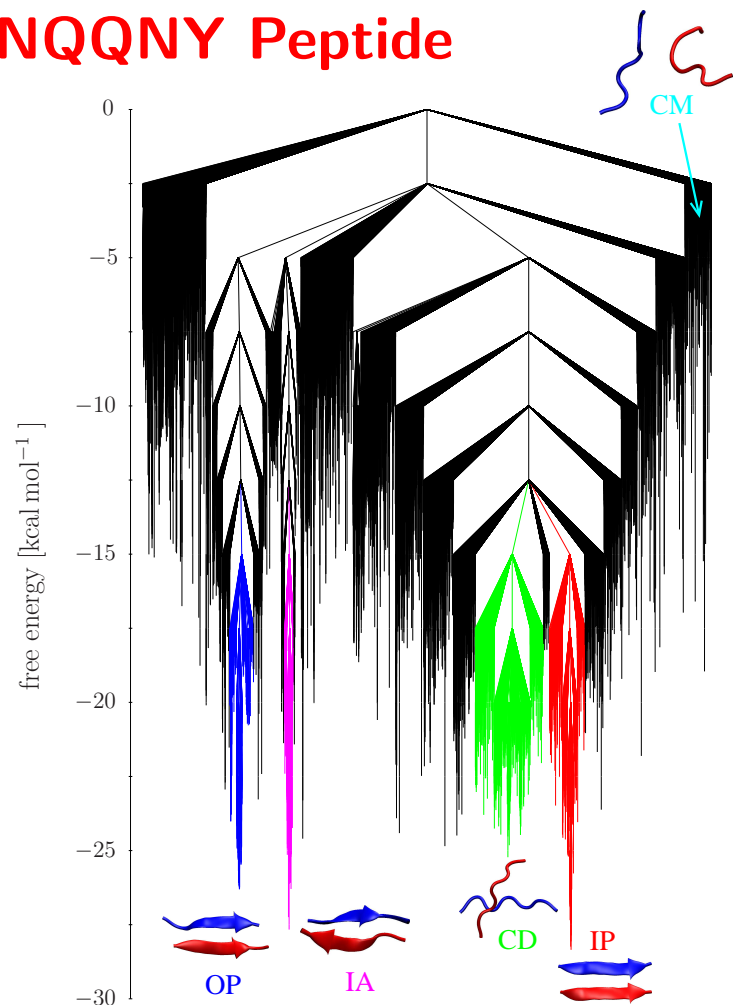
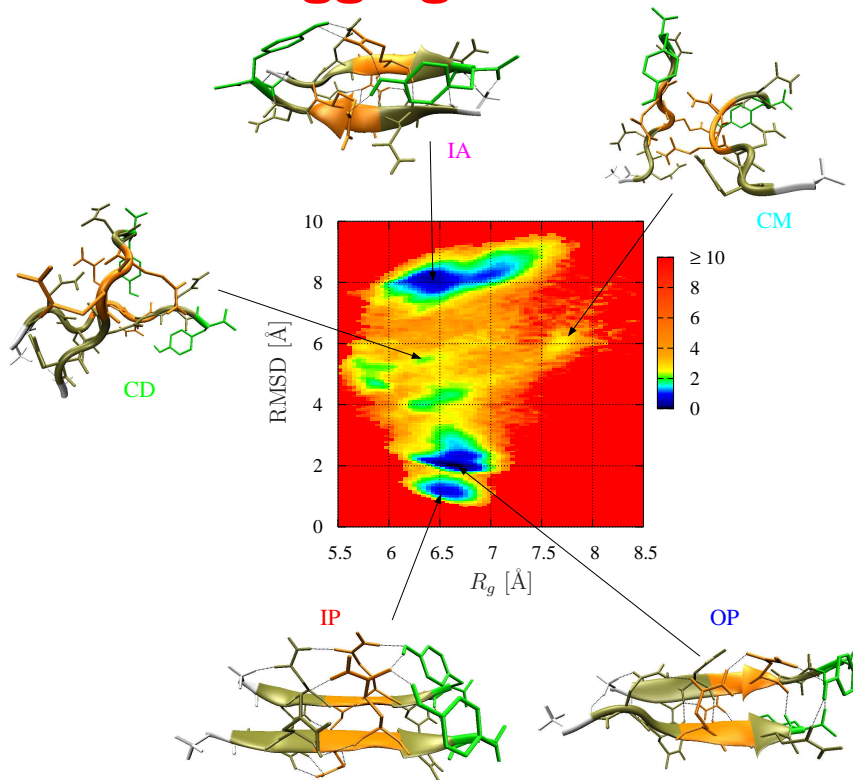


The tRNA methyltransferase protein 1UAM contains a deep **trefoil knot**.

The folding pathway has two **slipknot**-type steps for a truncated (residues 78–135) **Gō model** representation using an **associated memory Hamiltonian**.

The estimated rate constant is between 0.04 and 0.4 s^{-1} .

Aggregation of the GNNQQNY Peptide

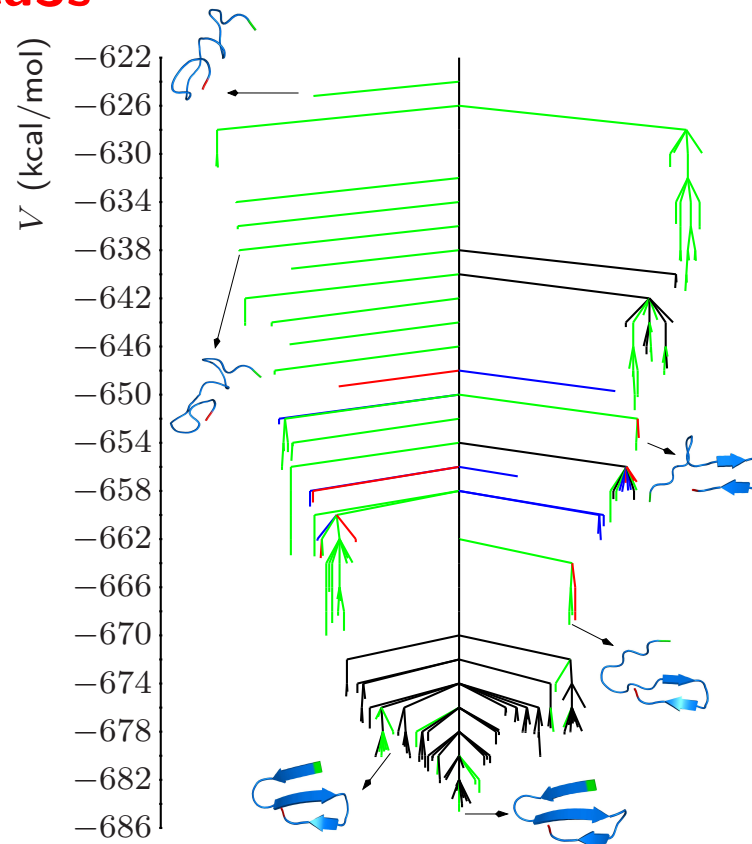
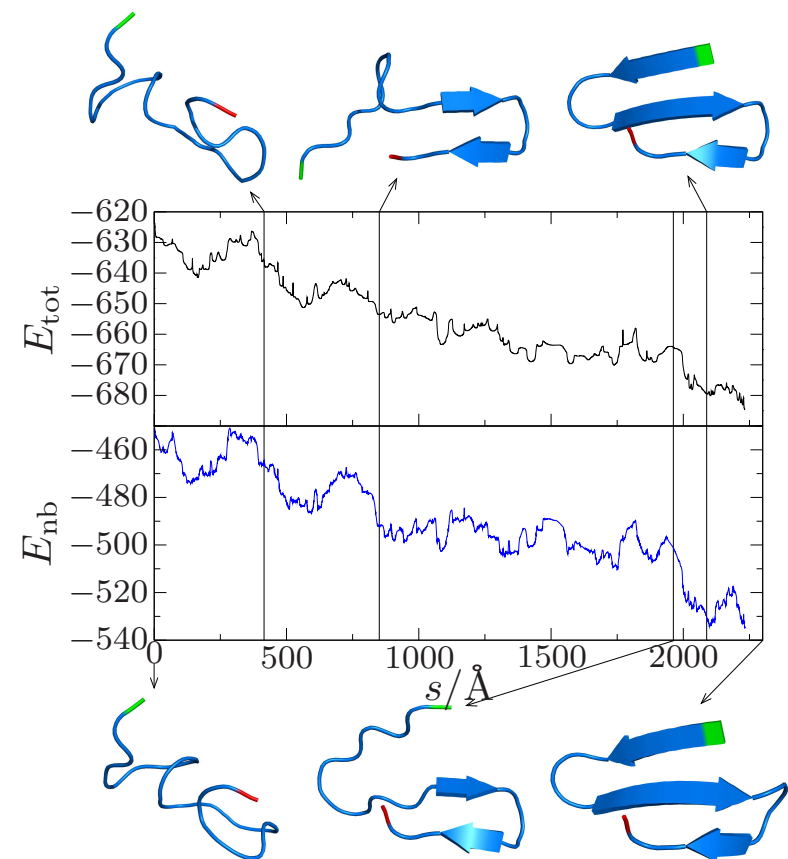


GNNQQNY is a polar heptapeptide from the N-terminal prion-determining region

of the 685 residue yeast prion protein **Sup35**. **Dimer** free energy minima are in-register parallel, **IP**, off-register parallel, **OP**, and antiparallel, **IA**, sheets.

Dimer formation **rates** are estimated as **milliseconds** to **seconds**. Time scale for **interconversion** between dimers ranges from hours to days at 298 K.

Folding of Beta3s



Beta3s is a designed 20-residue peptide with a three-stranded antiparallel β -sheet. Folding with CHARMM19/EEF1 involves **early** formation of the C-terminal hairpin followed by **docking** of the N-terminal strand.

Mean first passage time is **300 ns** at 298 K, consistent with other calculations and the experimental upper bound of 4000 ns (*J. Phys. Chem. B*, **112**, 8760, 2008).

A Connection Between Dynamics and Thermodynamics

The organisation of a PES is governed by its **stationary points**, where Taylor expansions provide local descriptions in terms of **Hessian matrices**.

The organisation of **families** of PES's as a function of **parameters** in the potential is determined by the stationary points that possess additional zero Hessian eigenvalues, known as **non-Morse** points.

Catastrophe theory provides a local representation of the PES around non-Morse points as a function of **both** atomic coordinates and parameters.

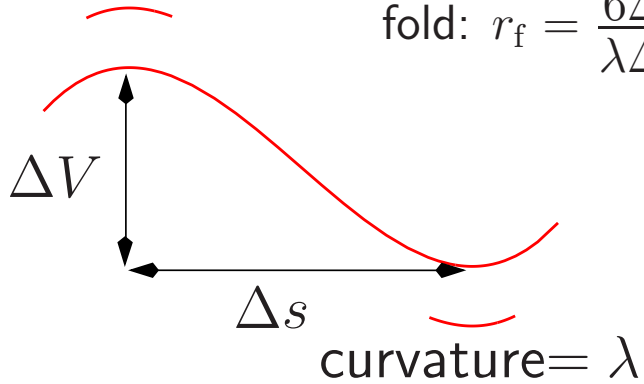
The **splitting lemma** reduces the dimensionality to the **essential** variables, while **transversality** guarantees that the resulting classifications are **universal**.

The simplest one-parameter catastrophes are the **fold**, $f(x) = \frac{1}{3}x^3 + ax$, and the symmetrical **cusp**, $f(x) = \frac{1}{4}x^4 + \frac{1}{2}ax^2$.

Geometries of the **fold** and **cusp** catastrophes.

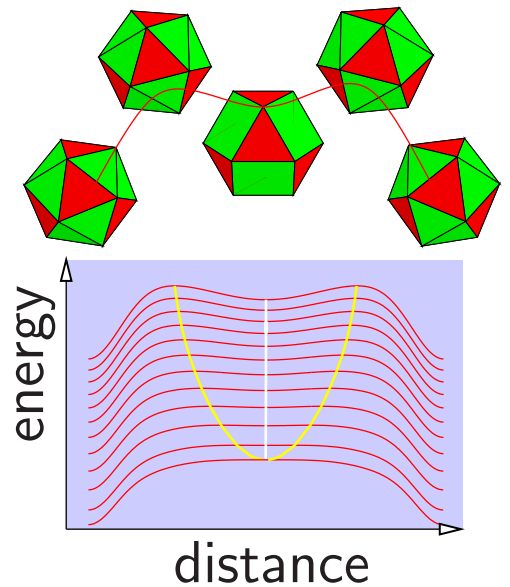
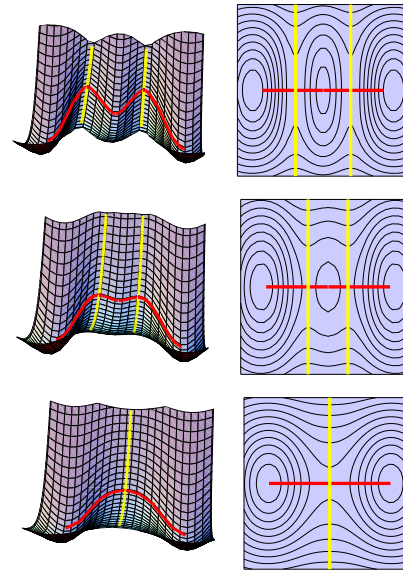
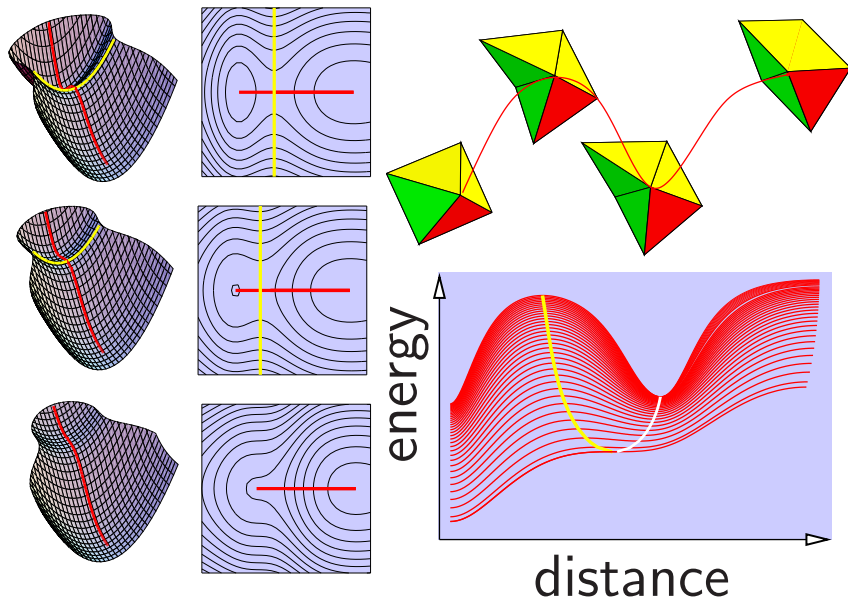
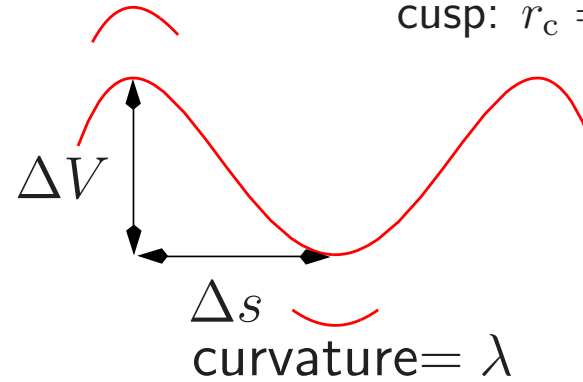
curvature = $-\lambda$

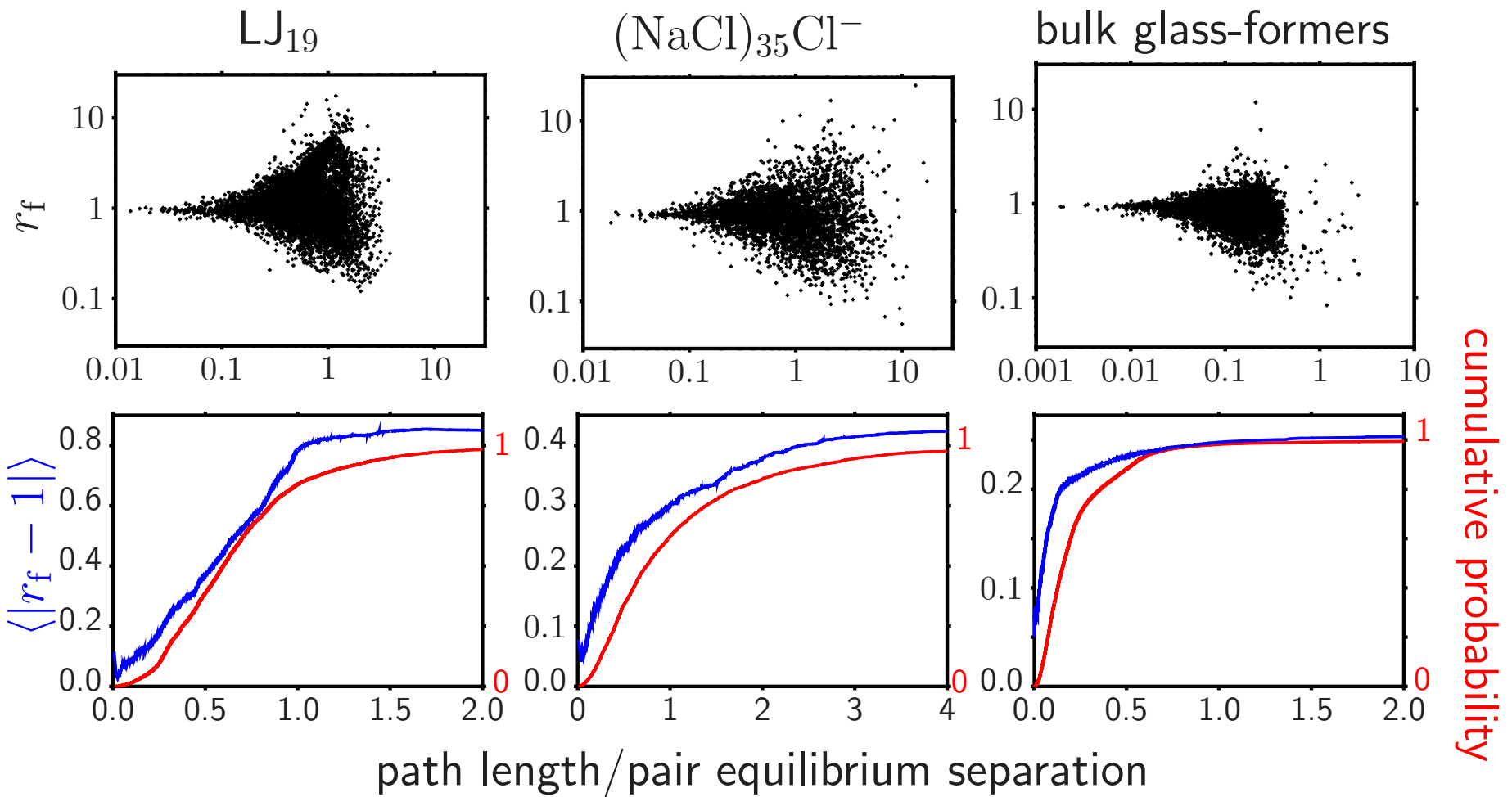
fold: $r_f = \frac{6\Delta V}{\lambda\Delta s^2} = 1$



curvature = -2λ

cusp: $r_c = \frac{4\Delta V}{\lambda\Delta s^2} = 1$





For systems with a fixed potential we effectively have a **snap-shot** of parameter space. On average, r_f remains **close to unity** for many pathways in both model clusters and bulk, providing an explanation for **Hammond's postulate**.