

# Ref Genome update from Princeton

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# Specific Aims of Princeton Sub-Contract

- Generate orthologous clusters on MOD-approved protein sets.
- Use the above results to integrate data from multiple homolog/ortholog detection methods and overlay on PANTHER families.
- Provide the coordination and expert review necessary to enable reliable transfer of GO annotations to newly sequenced genomes.
- *Annotation Tracker to aid in assigning/tracking Ref Genome/PAINT annotation.*

# Software/Data Progress Report: Sven Heinicke

- Orthologous Clusters: Done with 12 Ref Genomes-OrthoMCL, InParanoid, Combined Clusters. Complete PANTHER set: OrthoMCL done, InParanoid in progress
- Annotation Tracker

# Orthologous Clusters: next six months and beyond

- Larger PANTHER set: MultiParanoid issues addressed.
- Keep all data up-to-date and synchronized with PANTHER.
- Other needs?

# Annotation Tracker: next six months and beyond

- Additional new features?

# PAINT Curation Progress Report: Mike Livstone

- Progress so far
- WNTs

# PAINT curation next six months

- Finish WNT, ~ 2 more target areas
- Send WNT protein list to BioGRID curators for genetic/physical interaction curation
- Refine SOPs, continue to identify bottlenecks, etc

# PAINT curation 12 months

- Keep pace with new focused/deeply annotated families, make significant push on previously “done” families (~400)
- Identify areas/rules for automation for going forward