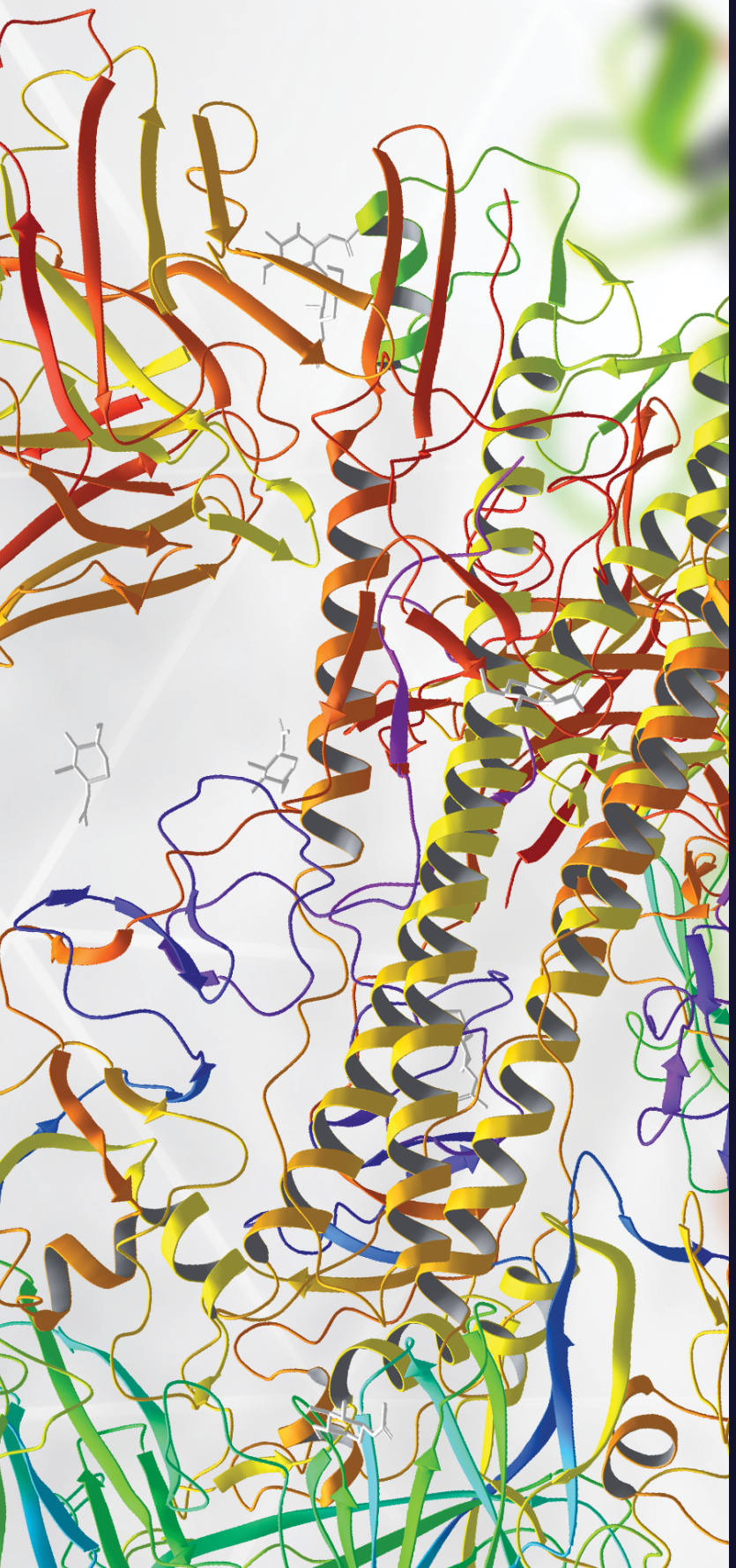
Biologics by Design

Cutting-edge software for modeling multiple biologics modalities, including monoclonal antibodies, vaccine antigens, enzymes, and peptides



Accelerate Research and Development Projects

- Make decisions more confidently through the scientific accuracy of Schrödinger's proven methodologies
- Extend your knowledge base by leveraging the experience of over 200 PhD research scientists at Schrödinger with expertise across computational research areas
- Stay up-to-date with the latest scientific advances with quarterly updates

Maximize the Value of your Computational Software

- Derive benefits quickly through basic and advanced training with Schrödinger scientists, locally on-site or online across the globe
- Conveniently access a comprehensive library of videos, documentation, and step-by-step online training materials
- Enjoy the support of highly-trained support experts, always ready to tackle your scientific and technical challenges

Improve Workflow Efficiency and Streamline Efforts

- Easily follow logically-organized tasks and flexible workflows bringing the power of computational chemistry and biology to advanced and occasional users
- Work efficiently through Schrödinger's unique unified modeling and simulation interface for biologics design

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Antibody Modeling

- Reliable structure prediction from sequence
- Automated intuitive workflows
- Advanced ab initio CDR loop prediction using PRIME
- Antibody humanization by CDR grafting
- Regularly updated and curated antibody database

Liability Prediction

- Rapid protein surface analysis
- Protein aggregation prediction with AggScore
- Chemical liability prediction
- QSAR analysis for biologics

Advanced Protein Engineering

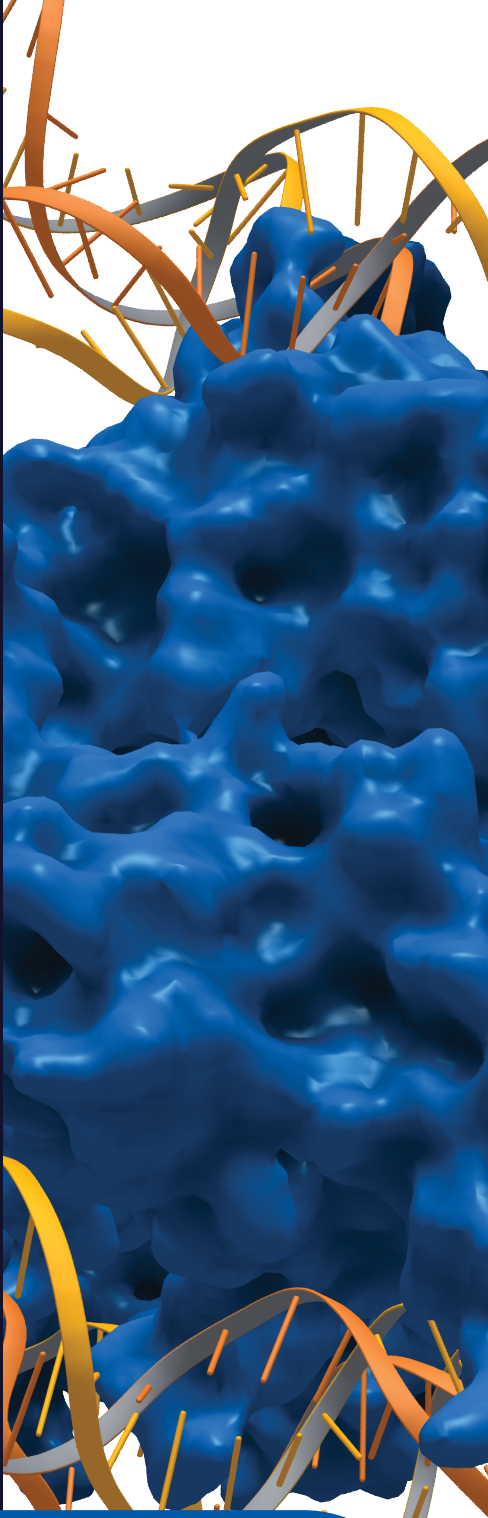
- In silico mutagenesis and scoring
- Cysteine scanning and design of disulfide bridges
- Protein FEP+ for prediction of relative free energy changes
- Fusion protein linker design

Protein Docking

- Well-validated docking code, PIPER
- Proven track record in community-wide blind prediction competitions
- Antibody and Standard (Protein or Nucleic Acid) modes
- Protein-Peptide docking

Comprehensive Protein Modeling

- Advanced tools for sequence alignment, with extensive annotation options
- Complete set of homology modeling tools, including both rapid and high-accuracy methods
- Easy to interpret protein structure quality analysis
- Residue-based analysis of energies, solvent-accessible surface areas, and hydropathy
- Molecular Dynamics simulation using Desmond



Find the solutions you're looking for:

Drug Discovery
Comprehensive solutions, validated across hundreds of targets, to accelerate lead discovery and optimization.

Materials Science
Integrated solutions for atomic-scale simulation of chemical systems to design novel polymers and other products essential to modern life.

Enterprise Informatics with LiveDesign
Breaks down traditional silo walls to unleash the power of real-time collaborative design and project management.

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Request a free trial

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