VIEW CONTACTS

DesertScientific
Software

FIRSTLY

WHAT IS VIEWCONTACTS?

Mastering non-covalent interactions

ViewContacts is state-of-the-art software for improved understanding of favourable and unfavourable non-covalent interactions in protein-ligand complexes.

Non-covalent bonds, whilst weak by nature, help to maintain the three dimensional structure of a protein. They are critical in drug discovery because most drugs work by binding non-covalently with the target protein. By studying these non-covalent interactions, you gain insight into the processes in which proteins bind to one another, subsequently improving your targeted drug design. ViewContacts is the new leading tool in this area for your chemists, modellers and crystallographers.

CONTENTS

ADVANTAGES

DATA DRIVEN

Created by industry experts, ViewContacts is accurate and comprehensive at finding many different types of hydrogen bonds, polar interactions and lipophilic contacts in binding sites.

RULE BASED

ViewContacts ensures correct identification of interactions by using an extensive range of rigourously tested rules. These rules form the basis of a superior algorithm, developed from the latest findings in structural biology, molecular modeling, molecular recognition and data mining studies.

VISUALISATION

ViewContacts creates scripts that allow fast and easy exploration of the key protein-ligand interactions determining binding affinity.

HANDLES WATER MOLECULES

Rank scores provide easy identification of bound water molecules for targeting in ligand design experiments.

IDENTIFIES UNFAVOURABLE INTERACTIONS

ViewContacts allows you to detect desolvation penalties that negatively affect target binding.

EASY TO USE

All of your scientists (crystallographers, modellers and medicinal chemists) can make the best use of protein crystal structure data for drug design.

2 INTERACTION TYPES

ViewContacts identifies all commonly occurring non-covalent interaction types such as:

- → hydrogen bonding
- → ionic pairs
- → van der Waals

As well as many less understood types:

- → cation-pi
- → hydrogen bonding to pi-systems
- → σ-hole bonding (halogen bonding)
- → dipolar antiperiplaner interactions
- → pi-stacking
- → pi edge-to-face contacts
- → hydrogen bonding involving CH groups

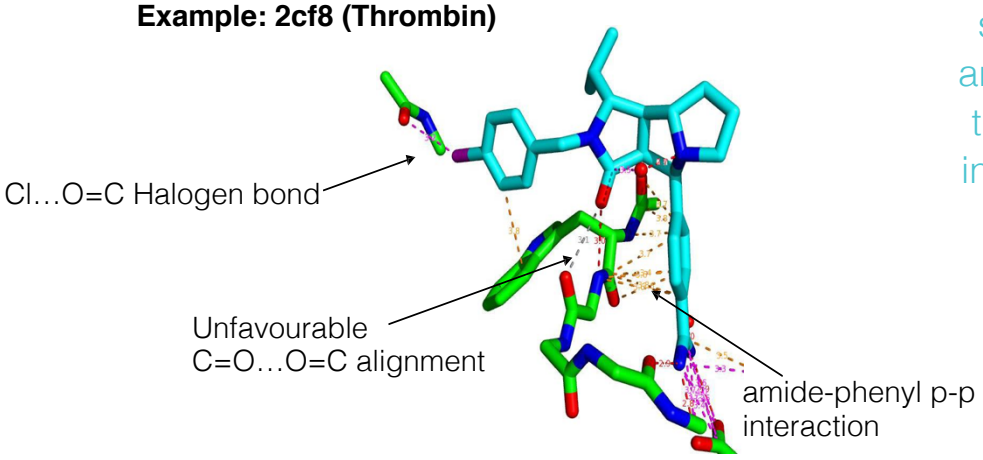
3 PAIR INTERACTION DEFINITIONS

ViewContacts automatically assigns SMARTS-based atom types and detects all favourable and unfavourable interactions (with distance and angle constraints and pruning of redundant contacts).

Classification of Interaction Types

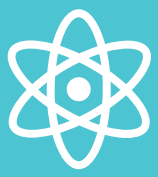
- → hydrogen bonding
- → mental bonding
- → ionic
- → cation-dipole
- → cation-pi
- → dipolarc
- → σ-hole bond
- → h_donor-pi
- → pi-pi
- → van der Waals
- → unfavourable of 1, 2, 3, 6
- → polar and non-polar clashes
- → polar-nonpolar desolvation penalties

Example: 2cf8 (Thrombin)



ViewContacts creates scripts that allow fast and easy exploration of the key protein-ligand interaction determining binding affinity

VIEWCONTACTS FEATURES

any HET group in any domain of any pdb file can be explored	size of viewed binding site can be modified	interactions can be grouped into different schemes
interactions can be sub-divided into weak / strong	all interactions in a binding site can be viewed	buried contacts can be viewed separately from solvated contacts
water mediated hydrogen bonds can be highlighted		results from docking studies can be read easily, with poses stored in sdf files(s)
SMARTS definitions can handle tautomers	scripts create molecular surface, solvent excluded surface, shortcut for viewing temperature factores and more	bond orders from input sdf file, cif library or detected using automated methods
SMARTS definitions and angle and distance constraints can be customised or extended	command line and api resources available	easily linked with our Proasis4 protein structure database and visualisation systems

HANDLING OF WATER MOLECULES

ViewContacts ranks scores to provide easy identification of bound water molecules that can be targeted in ligand design experiments

ViewContacts includes a powerful method for scoring water replacement potential based on the deviation from the ideal tetrahedral coordination of the protein bound water molecules.

$$Rank = \sum_{n}\{(2.80\ A / r_n) + [\sum_{m}\cos(\Theta_{Td} - \Theta_{nm})] / 6\}$$

The ranked scores are:

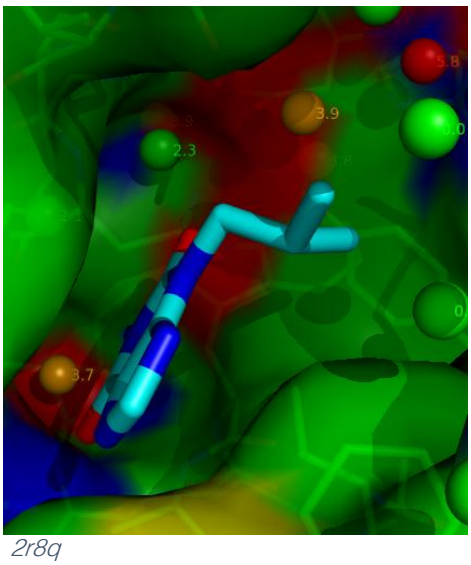
- → 1 ideal H-bond: 1.0
- → 2 ideal H-bonds: 2.3
- → 3 ideal H-bonds: 4.0
- → tetrahedral coordination: 6.0

A maximum of 4 protein contacts are counted (≤2 donors and ≤ 2 acceptors), and any angle less than 60° is rejected

Example: 2r8q (PDE-B1)

Colour-coding of rank score in PyMOL

1. Green: 0 – 2.3 (easy to replace)
2. Amber: 2.3 – 4.0 (possible to replace with suitable polar functionalities)
3. Red: 4.0 – 6.0 (unlikely to replace)



2r8q

IDENTIFICATION OF UNFAVOURABLE INTERACTIONS

ViewContacts allows for the detection of desolvation penalties that negatively affect the binding site

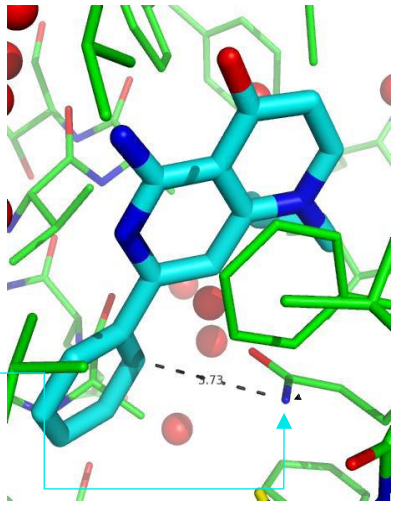
ViewContacts has been built to identify both unfavourable contact pairs and potential desolvation penalties.

Unfavourable contact pairs can arise due to very short contact distances or from repulsive electrostatic forces. Desolvation penalities are detected by placing water molecules around the binding site to test whether a polar atom would be strongly preferred at the location of any apolar ligand atom.

Distances and angles are checked for all polar / apolar interactions and solvent exposure is taken into account when testing for desolvation penalties.

Example: 3hdz (PDE-5)

There is no hydrogen bond partner for this buried N atom in the binding site, so the contact is highlighted as an unfavourable interaction



HARDWARE
& Software Requirements

INDUSTRY STANDARDS

ViewContacts™ software runs under Linux. Server software requirements include:

- → Python – version 2.7 is required
- → Openbabel - latest version 2.3.0 or later is recommended

End users access functionality using:

- → Proasis4
- → ViperWeb
- → Command line scripts
- → API rescources
- → from within PyMOL, MOE, and other third-party applications

Molecular Graphics Visualisation of results using:

- → Proasis4
- → PyMOL
- → MOE
- → Benchware 3D

Contact us:

info@desertsci.com

www.desertsci.com

Evaluation licenses available