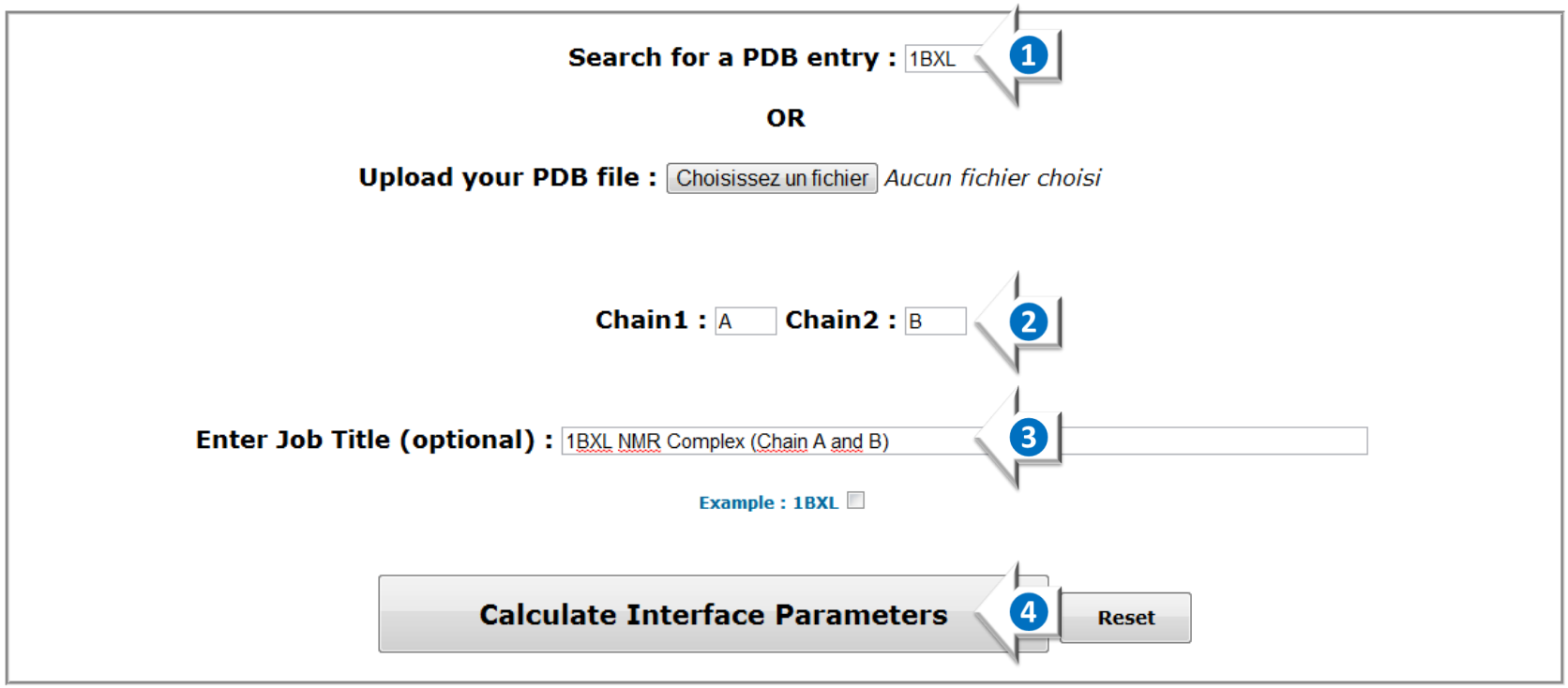
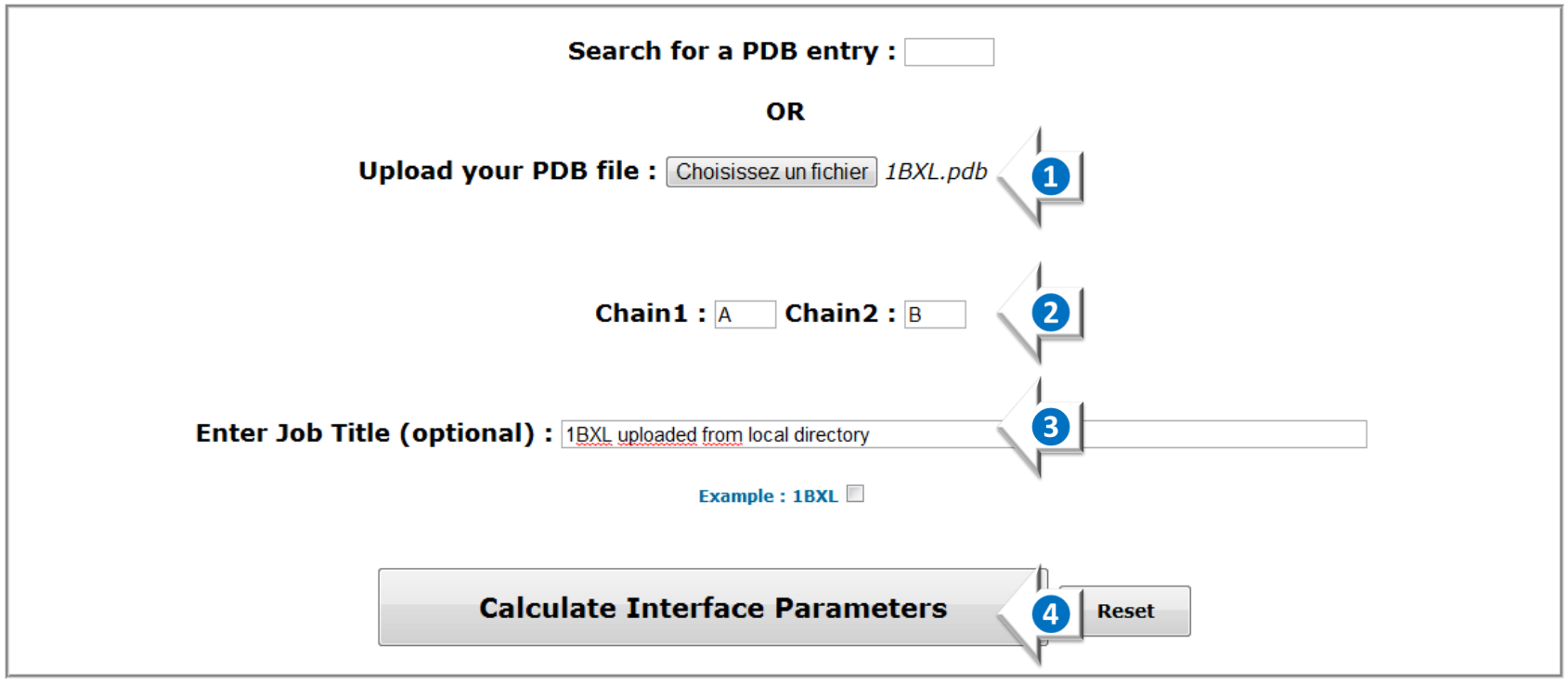
How to Run 2P2I$_{INSPECTOR}$

Using a 4 letter PDB code :



1. Enter a valid PDB code
2. Select two Chains in contact
3. Enter a Job Title (optional)
4. Run 2P2I$_{INSPECTOR}$

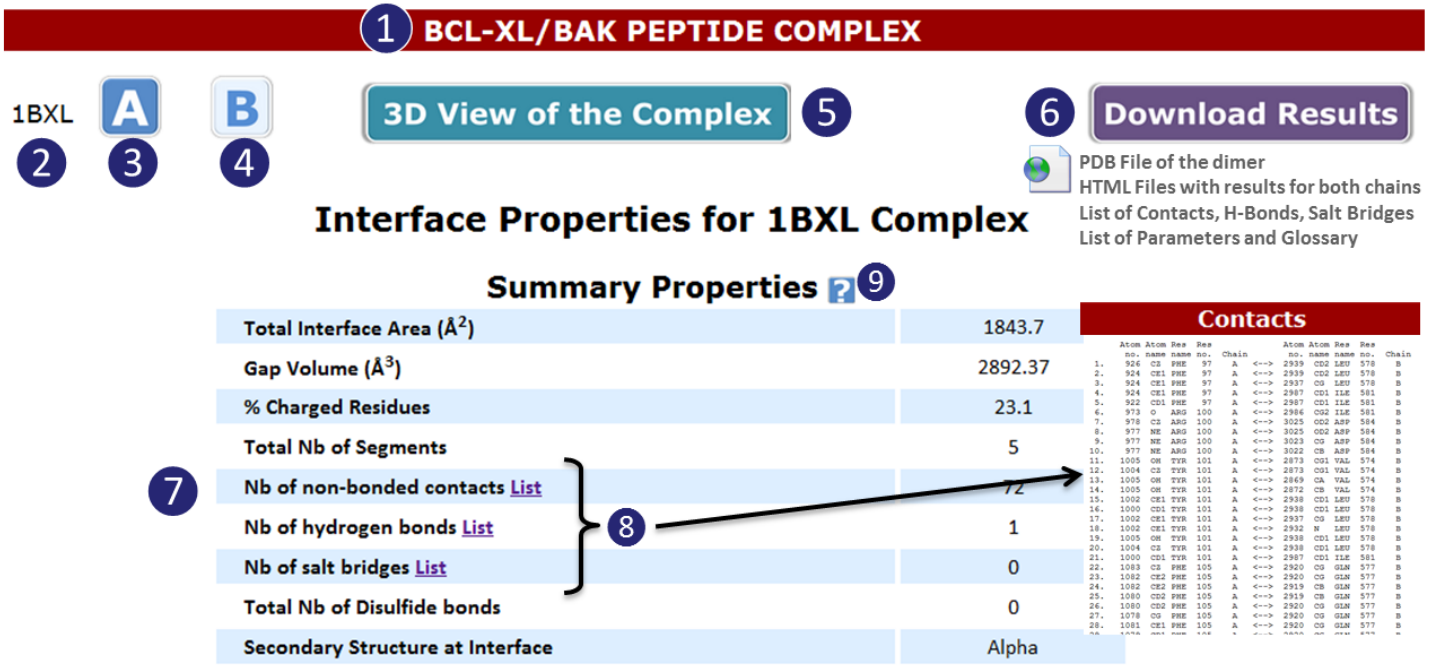
Using a PDB File from a local Directory:



1. Upload a PDB File
2. Select two Chains in contact
3. Enter a Job Title (optional)
4. Run 2P2I$_{INSPECTOR}$

(To see an example simply tick the **1BXL example box** ☑ and run 2P2I$_{INSPECTOR}$

2P2I$_{INSPECTOR}$ Results



1. Job Title
2. PDB Code or PDB Filename
3. 4. Show detailed properties for chain A or B
5. Visualize complex using Jmol applet and customized menus
6. Download Results (2P2Iinspector-results.tgz)
7. Result table for global interface parameters
8. Open popup menus with list of contacts, hydrogen bonds or salt bridges
9. Open a popup menu with parameter definitions

Detailed Properties (by Chain)

SEGMENTS & BASA

Number of Segments	4
Interface Accessible Surface Area	873.4
% Interface Accessible Surface Area	7.2
% Neutral contribution	45.9
% Polar contribution	56.2
% Non polar contribution	43.8
% Charged contribution	27.3

CONTACTS

Number of Non-Bonded	Residues	Atoms
All	13	34
Neutral	5	18
Polar	6	15
Hydrophobic	7	19
Charged	3	6

Detailed Properties (by Chain)

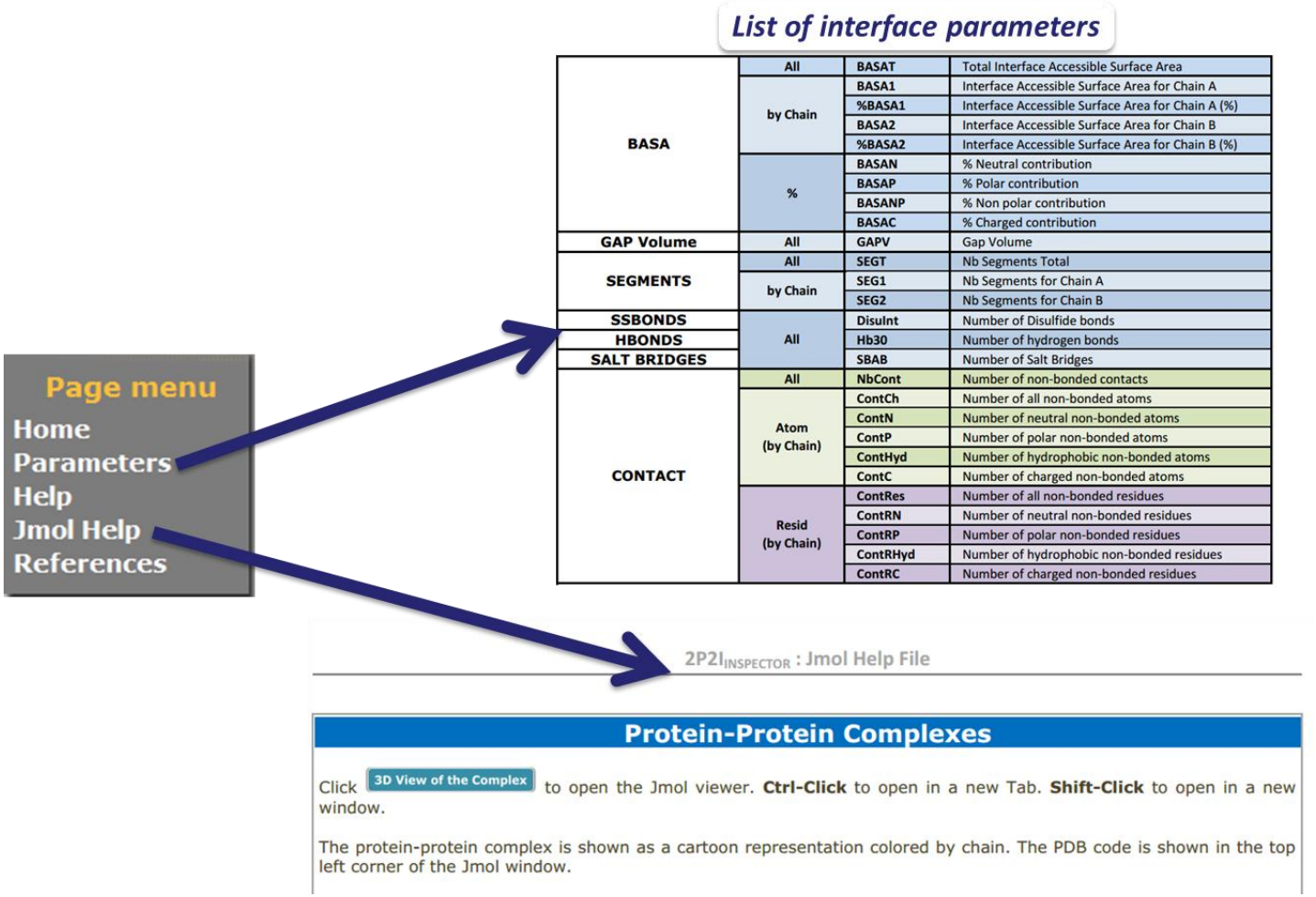
GENERAL PROPERTIES

Properties	Residues	Atoms
% Aromatic	21.7	30.7
% Acidic	8.7	5.4
% Basic	17.4	15.1
% Acyclic	78.3	69.3
% Cyclic	21.7	30.7
% Aliphatic	39.1	41.6
% Small	21.7	12.7
% Medium	4.3	7.8
% Large	73.9	79.5
% Alpha character	78.3	79.5
% Beta character	0.0	0.0
% Coil	8.7	7.2

ATOM PROPERTIES

Atom Types	%
Carbon	34.3
(O)xygen	7.2
(N)itrogen	3.6
(S)ulfur	0.0
Hydrogen	54.8
(P)hosphorus	0.0
Fluor	0.0
N+O+P+S	4.8

List of Parameters and Jmol Help File



BASA	All	BASAT	Total Interface Accessible Surface Area
	by Chain	BASA1	Interface Accessible Surface Area for Chain A
		%BASA1	Interface Accessible Surface Area for Chain A (%)
		BASA2	Interface Accessible Surface Area for Chain B
		%BASA2	Interface Accessible Surface Area for Chain B (%)
	%	BASAN	% Neutral contribution
		BASAP	% Polar contribution
		BASANP	% Non polar contribution
		BASAC	% Charged contribution
GAP Volume	All	GAPV	Gap Volume
SEGMENTS	All	SEGT	Nb Segments Total
	by Chain	SEG1	Nb Segments for Chain A
		SEG2	Nb Segments for Chain B
SSBONDS	All	DisuInt	Number of Disulfide bonds
HBONDS		Hb30	Number of hydrogen bonds
SALT BRIDGES		SBAB	Number of Salt Bridges
CONTACT	All	NbCont	Number of non-bonded contacts
	Atom (by Chain)	ContCh	Number of all non-bonded atoms
		ContN	Number of neutral non-bonded atoms
		ContP	Number of polar non-bonded atoms
		ContHyd	Number of hydrophobic non-bonded atoms
		ContC	Number of charged non-bonded atoms
	Resid (by Chain)	ContRes	Number of all non-bonded residues
		ContRN	Number of neutral non-bonded residues
		ContRP	Number of polar non-bonded residues
		ContRHyd	Number of hydrophobic non-bonded residues
		ContRC	Number of charged non-bonded residues