



Working with sequences,
alignments, and linking to 3D
structure.

ICM-Pro

LOAD AND DISPLAY PROTEIN KINASE STRUCTURES

Load a kinase structure from the PDB.

The screenshot displays the Molsoft ICM software interface. At the top, the title bar reads "2phk Molsoft icm 3.7-2a [NewProject *] (1 object)". The menu bar includes File, Edit, View, BioInfo, Tools, Homology, Chemistry, Docking, MolMechanics, Windows, and Help. The toolbar contains various icons for file operations and visualization. The search bar at the top left contains the text "2phk". Below it, the "Workspace Panel" shows a tree view of objects, with "2phk" selected. A callout box with a blue border and white background points to the search bar and contains the text "1. Enter search string '2phk'". The main 3D view shows a protein structure rendered as a multi-colored ribbon (purple, blue, green, yellow, orange, red). Two ligands are visible: "F ac2" and "F ac4". The terminal window at the bottom shows the following commands and output:

```
Startup> Loading libraries..
Startup> Loading aliases..
Startup> Loading modules.. _macro_bioinfo_rebel_ligedit_docking
...ICM startup file executed...
icm/def> generalSearchFromGUI "PDB Search" "2phk"
Info> PDB index loaded from C:/Program Files/Molsoft LLC/ICM-Pro_17/data/inx/PDB.tab
icm/2phk>
```

The bottom status bar shows "Welcome to ICM" on the left and "6 Mol 1 Obj" on the right. The page number "3" is located in the bottom right corner.

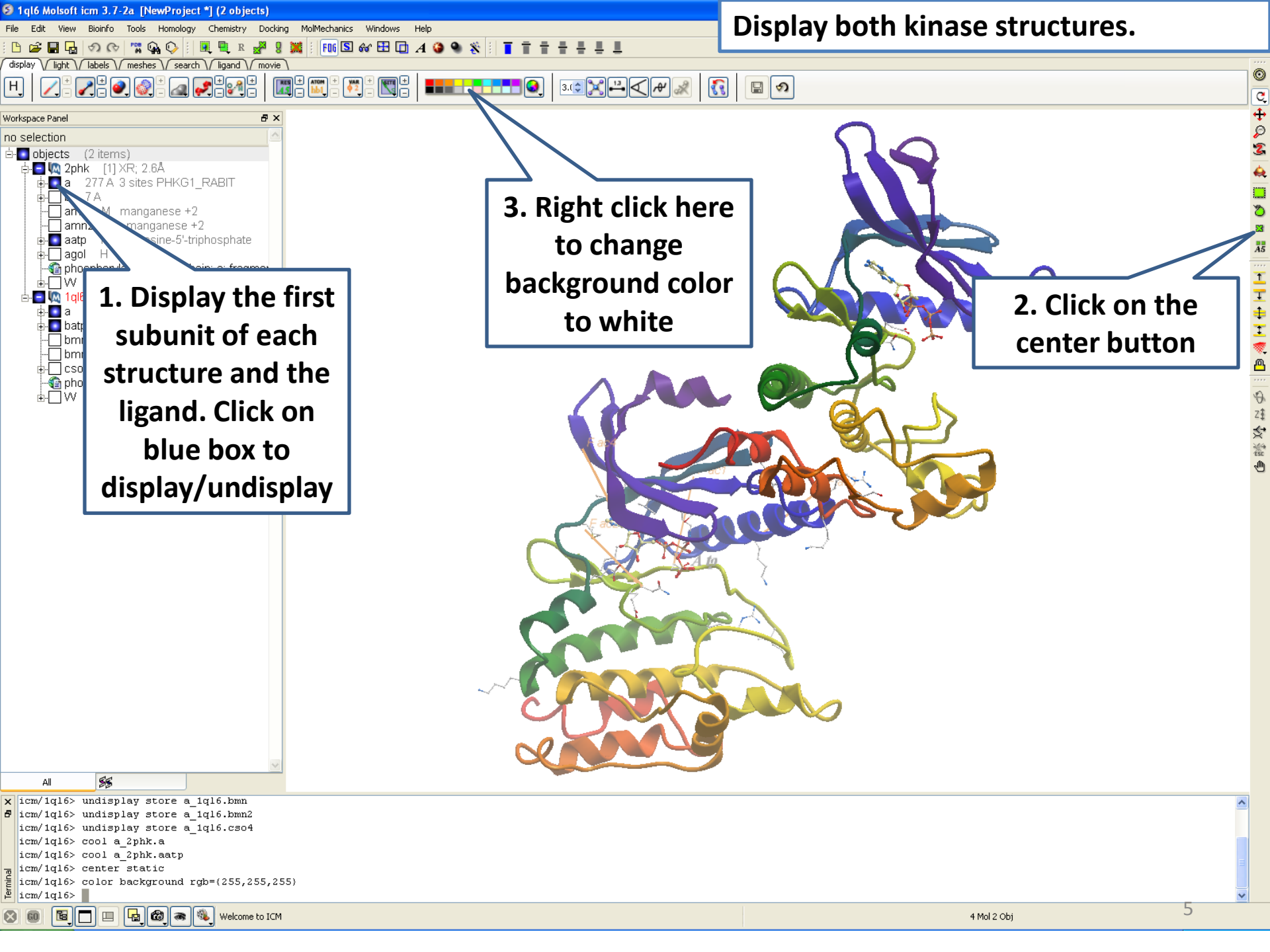
Load another kinase structure from the PDB.

The screenshot displays the Molsoft icm 3.7-2a software interface. The main window shows a 3D ribbon representation of a protein structure, colored in a gradient from purple at the top to orange at the bottom. Several atoms are highlighted with blue spheres and labeled as *Fac1*, *Fac2*, *Fac3*, and *So4*. The interface includes a menu bar at the top with options like File, Edit, View, BioInfo, Tools, Homology, Chemistry, Docking, MolMechanics, Windows, and Help. Below the menu bar is a toolbar with various icons for file operations and viewing. The Workspace Panel on the left shows a tree view of objects, with '1ql6' selected. A callout box points to the search input field in the Workspace Panel, containing the text '1. Enter search string "1ql6"'. The Terminal window at the bottom shows the following commands and output:

```
Startup> Loading aliases..
Startup> Loading modules.. _macro_bioinfo_rebel_ligedit_docking
...ICM startup file executed...
icm/def> generalSearchFromGUI "PDB Search" "2phk"
Info> PDB index loaded from C:/Program Files/Molsoft LLC/ICM-Pro_17/data/inx/PDB.tab
icm/2phk> generalSearchFromGUI "PDB Search" "1ql6"
Warning> [375] 10 missing SEQRES residues (thr ..) before ser [a 11 ]
icm/1ql6>
```

The status bar at the bottom right indicates '5 Mol 1 Obj' and the page number '4'.

Display both kinase structures.



1. Display the first subunit of each structure and the ligand. Click on blue box to display/undisplay

3. Right click here to change background color to white

2. Click on the center button

1. Click and hold

Color each kinase structure ribbon a different color.

The screenshot shows the ICM (Interchangeable Crystallographic Model) software interface. The main window displays a protein structure in a ribbon representation, colored in shades of green and yellow. A context menu is open over the structure, showing options for coloring. The 'color.' option is selected, and the 'object' option is highlighted in the submenu. The 'Workspace Panel' on the left shows a list of objects, including '2phk [1] XR; 2.6Å' and '1ql6 [2] XR; 2.4Å'. The 'Terminal' window at the bottom shows the following commands:

```
icm/1ql6> undisplay store a_1ql6.bmn2
icm/1ql6> undisplay store a_1ql6.cso4
icm/1ql6> cool a_2phk.a
icm/1ql6> cool a_2phk.aatp
icm/1ql6> center static
icm/1ql6> color background rgb=(255,255,255)
icm/1ql6> color Res(a_*.//DD) object ribbon
icm/1ql6>
```

2. Color by Object

```
icm/1ql6> undisplay store a_1ql6.bmn2
icm/1ql6> undisplay store a_1ql6.cso4
icm/1ql6> cool a_2phk.a
icm/1ql6> cool a_2phk.aatp
icm/1ql6> center static
icm/1ql6> color background rgb=(255,255,255)
icm/1ql6> color Res(a_*.//DD) object ribbon
icm/1ql6>
```

Superimpose the kinase structures.

The screenshot displays the ICM (Interchangeable Conformations Manager) software interface. The main window shows two protein structures, 1q16 and 2phk, superimposed in a green ribbon representation. The interface includes a top menu bar, a toolbar, and a Workspace Panel on the left. Three callout boxes provide instructions: 1. Double click here (pointing to the 2phk entry in the Workspace Panel), 2. Press the control key and double click here (pointing to the 1q16 entry), and 3. Press the superimpose button (pointing to the Superimpose icon in the toolbar). A terminal window at the bottom shows the following output:

```
Info> 6 50%Dev=0.5 wRmsd=0.3 Rmsd=0.3 for 60.0% (665 of 1108 atoms)
Info> 7 50%Dev=0.5 wRmsd=0.3 Rmsd=0.3 for 59.9% (664 of 1108 atoms)
Info> 8 50%Dev=0.5 wRmsd=0.3 Rmsd=0.3 for 60.1% (666 of 1108 atoms)
Info> 9 50%Dev=0.5 wRmsd=0.3 Rmsd=0.3 for 60.1% (666 of 1108 atoms)
Info> 666 of 1108 atoms superimposed (i_2out and i_out), rmsd_partial_unweighted=0.348, rmsd_full_weighted=0.261 (r_2out and r_out). Atoms in: as_out and as_2out. Option 'output' for deviat:
icm/1q16> center static
icm/1q16>
```

1. Double click here

2. Press the control key and double click here

3. Press the superimpose button

**EXTRACT SEQUENCES FROM PDB
STRUCTURES AND LOAD NEW
SEQUENCES FROM SWISSPROT**

Extract sequences from PDB.

The screenshot displays the Molsoft icm 3.7-2a interface. The main window shows a protein structure in a ribbon representation, colored in shades of green and yellow. Three callout boxes provide instructions:

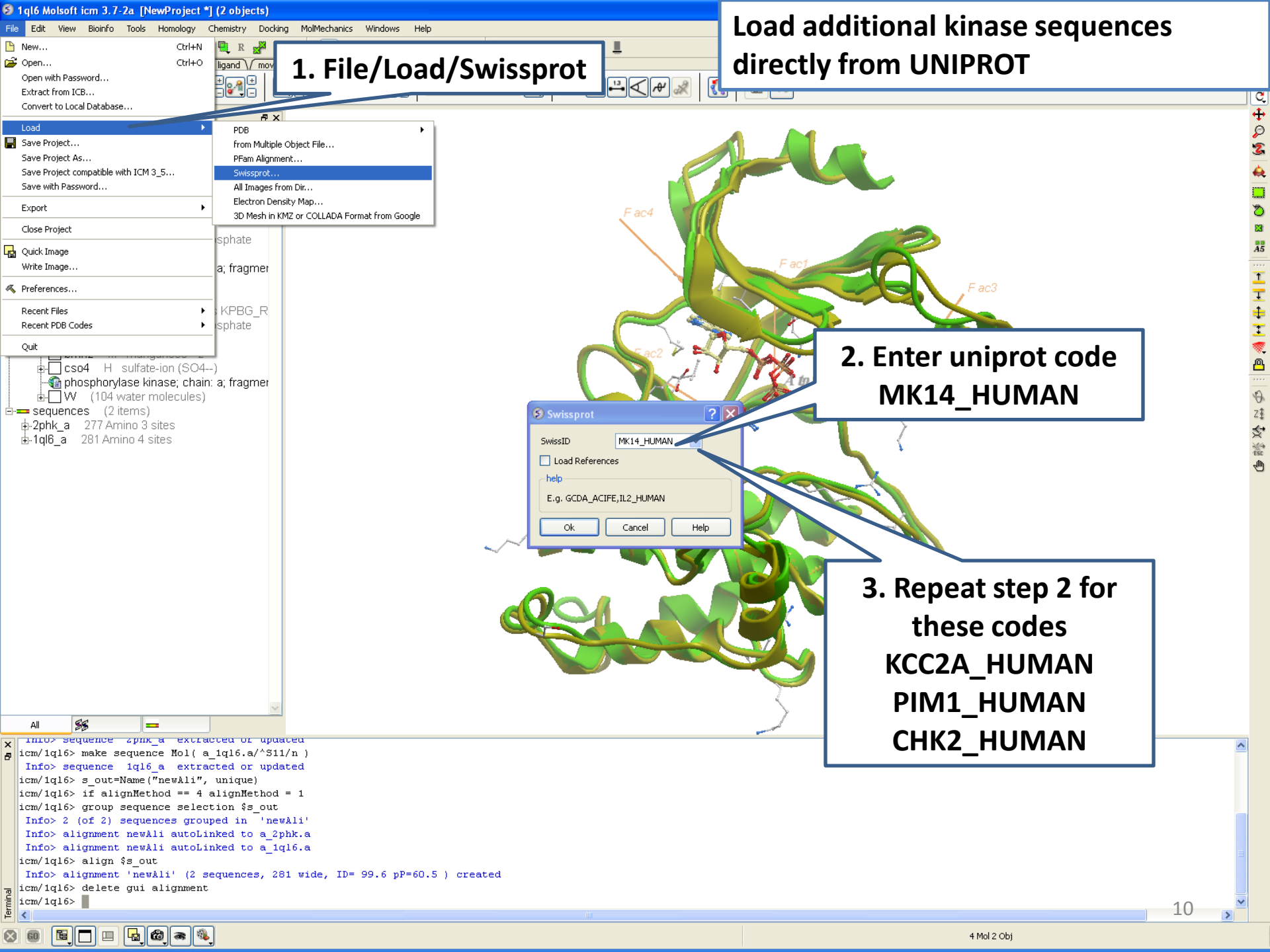
- 1. Right click and select Extract Sequence**: Points to a right-click context menu that is open over the protein structure. The 'Extract Sequence' option is highlighted in blue.
- 2. Right click and select Extract Sequence**: Points to the same 'Extract Sequence' option in the context menu.
- 3. Sequences are listed here**: Points to the 'sequences' section in the Workspace Panel on the left.

The Workspace Panel on the left shows a tree view of objects and sequences. The 'sequences' section lists:

- 2phk_a 277 Amino
- 1ql6_a 281 Amino

The terminal window at the bottom shows the following commands and output:

```
Info> 666 of 1108 atoms superimposed (i_2out and i_out), rmsd_partial_unweighted=0.348, rmsd_full_weighted=0.261 (r_2out and r_out). Atoms in: as_out and as2_out. Option 'output' for deviat:
icm/1ql6> center static
icm/1ql6> make sequence Mol( a_2phk.a/^G14/n )
Info> sequence 2phk_a extracted or updated
icm/1ql6> make sequence Mol( a_1ql6.a/^S11/n )
Info> sequence 1ql6_a extracted or updated
icm/1ql6>
```



1. File/Load/Swissprot

Load additional kinase sequences directly from UNIPROT

2. Enter uniprot code MK14_HUMAN

3. Repeat step 2 for these codes
KCC2A_HUMAN
PIM1_HUMAN
CHK2_HUMAN

- Load
 - PDB
 - From Multiple Object File...
 - PFam Alignment...
 - Swissprot...
 - All Images from Dir...
 - Electron Density Map...
 - 3D Mesh in KMZ or COLLADA Format from Google

Swissprot

SwissID:

Load References

[help](#)

E.g. GCDA_ACIFE,IL2_HUMAN

Ok Cancel Help

```
icm/1q16> info> sequence 2phk_a extracted or updated
icm/1q16> make sequence Mol( a_1q16.a/^S11/n )
Info> sequence 1q16_a extracted or updated
icm/1q16> s_out=Name("newAli", unique)
icm/1q16> if alignMethod == 4 alignMethod = 1
icm/1q16> group sequence selection $s_out
Info> 2 (of 2) sequences grouped in 'newAli'
Info> alignment newAli autoLinked to a_2phk.a
Info> alignment newAli autoLinked to a_1q16.a
icm/1q16> align $s_out
Info> alignment 'newAli' (2 sequences, 281 wide, ID= 99.6 pP=60.5 ) created
icm/1q16> delete gui alignment
icm/1q16>
```

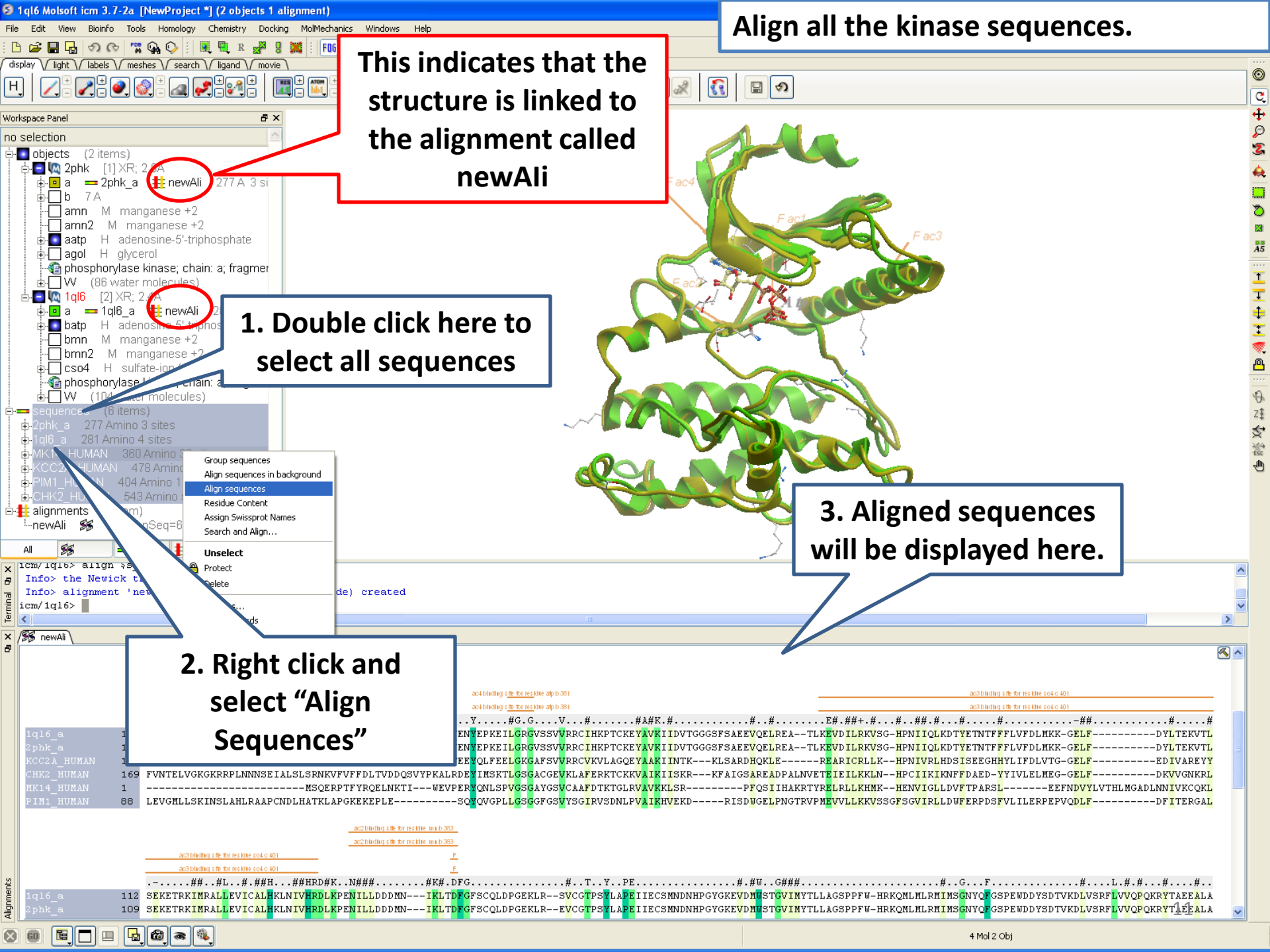
Align all the kinase sequences.

This indicates that the structure is linked to the alignment called newAli

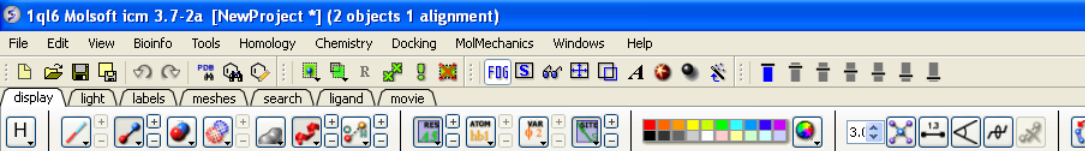
1. Double click here to select all sequences

2. Right click and select "Align Sequences"

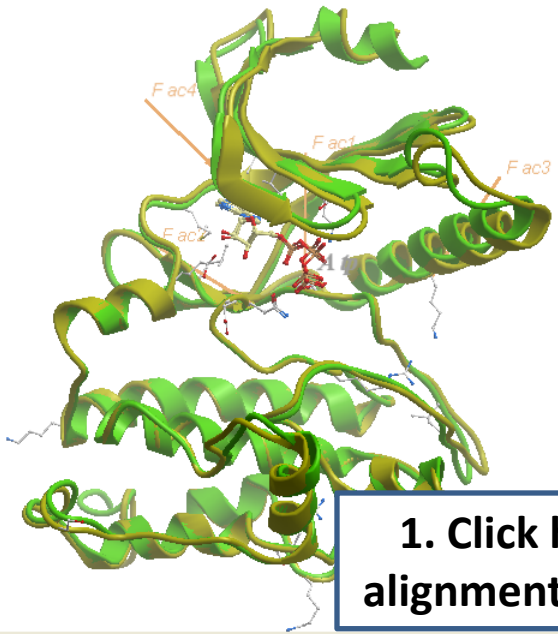
3. Aligned sequences will be displayed here.



LINKING SEQUENCE ALIGNMENT TO STRUCTURE



Color alignment by sequence conservation.



1. Click here to see alignment tools panel.

```
icm/1q16> align %s_out
Info> the Newick tree is saved in s_out
Info> alignment 'newAli' (6 sequences, 717 res.wide) created
icm/1q16>
```

Sequence	Residue	Conservation
1q16_a	1Y.....#G.G...V...#.....#A#K.#.....#..
2phk_a	1GFYEN..EPKEL..R..VSSV..RRC..IHKP..TCKEY..V..I..DVTGGGFSAEVQE
KCC2A_HUMAN	1MATITCTRFTEE..QLFEEL..K..AFSV..RRCV..KVLAGEY..A..IINTR---KLSARDHOK
CHK2_HUMAN	134	DKYRTYSKKHFRIFREVGPKNYSYIAYIEDHSGNGTFVNTLELVGKGRRLPNMNSIEIALSLSRNKVVFVDFLDVDDQSVYPKALRDE..IMSKTLS..SACGE..KLFERKTCCKV..I..IISKR---KFAIGSARE
MK14_HUMAN	1MSQERPTFYRQELNKTI---WEVPER..QNLSPV..S..AYGS..CAAFDTRTKGLRV..V..KLSR---PFQS
PIM1_HUMAN	53	TRSHSHSHSPRHSLRHSPGSGCGSSSGHRPCADILEVGMLLSKINLAHLRAAPCNDLHATKLAPGKEKPELE---SQ..QVGPLLS..S..GFS..YSGIRVSDNLPV..I..HVEKD---RISDUGE

Sequence	Residue	Conservation
1q16_a	56E#.##+.#...#.#...#.....-##.....#.....#
2phk_a	56	LREA--TLK..VD..IL..RKVSG--HPNII..QLK..D..TYE..TNTFF..LVFDL..MKK--GELF-----DYLTEKVTIL
KCC2A_HUMAN	57	LE-----R..ARICRLLK--HPNIVRL..HDSISEEGHHYL..IPDLVTC--GELF-----EDIVAREYYSERDASHCIQQI..EAVLHC..QMGVW..R..RDLPE..LL..LASKLKGAAV..L..A..P..LA..I..EVE--GEQQA
CHK2_HUMAN	264	ADPALNVETI..EIL..KRLN--HPCII..KIKNFDAED--YIVLEL..MEG--GELF-----DKVGNKRLREKATCKLYFYQM..LAVQYL..ENGII..R..RDLPE..VLLSQEEDCLII..IT..F..H..SKIL--GETSL
MK14_HUMAN	62	IIHAKRTYR..LRL..LKHMK--HENVIGLL..DVF..TPARSL-----EEFNVDVYLVTLHMGADLNNIVRCQKL..TDDHVQFLIYQI..RGLKYL..SADII..R..RDLPS..LAV--N..EDCEL..IL..F..LARHTD---DEM
PIM1_HUMAN	171	LPNGTRVPM..VVLL..KKVSSGFSGV..IRLL..D..MFERPDSFVL..IL..RPEPVQDLF-----DFITERGALQELARSPF..VQV..EAVRH..C..G..V..L..R..I..D..E..I..I..I--DLNRGEL..L..I..F..SGALLK---DTV

2. Select Color:conservation.

View options

- title
- consensus
- profile
- sequence offset
- ruler
- order

Comment: 1 2 3

Tree UPGMA

Sync with workspace

Tree only Unaligned

View Differences Horizontal scroll

Strength (50%)

Color: conservation

Selection

Propagate to ALL sequences

By Consensus: X

Select Invert Hide

Preferences

1. Click and hold

Color structure ribbons by alignment.
Dark green = fully conserved.

The screenshot displays the MolMechanics software interface. The main window shows a 3D ribbon representation of a protein structure. A context menu is open over the structure, with the 'alignment' option selected. The menu includes options like 'Unlink Color from Alignment', 'Link Color to Alignment', 'assign sec. structure', 'ribbon', 'smooth ribbon', 'wide ribbon', 'wide smooth ribbon', 'cylinders', 'protein worm', 'DNA worm', 'Display Chain Breaks', 'Display Chain Break Labels', 'undisplay other representations', 'display complete residues', 'select', and 'transparent'. The 'alignment' option is highlighted in blue.

The terminal window shows the following commands and output:

```
Info> the newick tree is saved in s_out
Info> alignment 'newAli' (6 sequences, 717 res.wide) created
icm/1q16> color ribbon Res(a_.*//DD) alignment
icm/1q16>
```

The sequence alignment window shows a multi-sequence alignment of 6 sequences: 1q16_a, 2phk_a, KCC2A_HUMAN, CHK2_HUMAN, MK14_HUMAN, and PIM1_HUMAN. The alignment is shown with a conservation scale at the bottom, ranging from 0 to 1.0. The scale is labeled 'conservation' and has a color gradient from light green to dark green. The alignment is shown with a color gradient from light green to dark green, indicating the level of conservation for each residue across the sequences.

The 'View options' panel on the right shows the following settings:

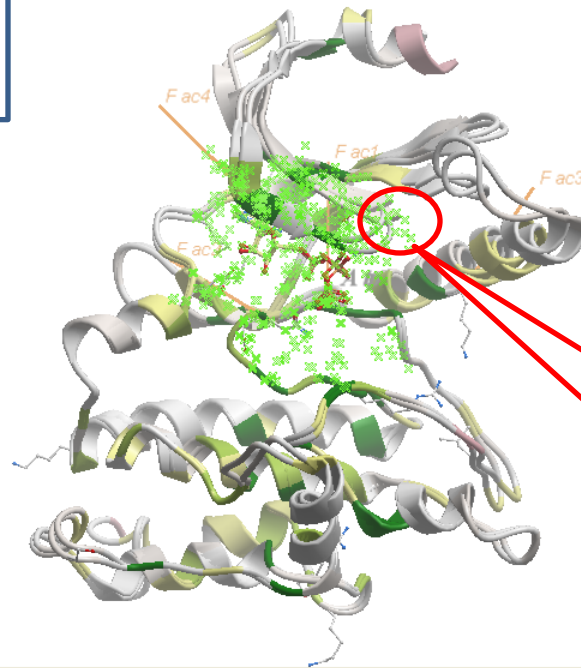
- title:
- consensus:
- profile:
- sequence offset:
- ruler:
- order:
- Comment: 1, 2, 3
- Tree:
- UPGMA:
- Sync with workspace:
- Tree only:
- Unaligned:
- View Differences:
- Unaligned scroll:
- Strength (50%):
- Color: conservation
- Selection: Propagate to ALL sequences
- By Consensus: X
- Select, Invert, Hide buttons
- Preferences:

2. Color by alignment

**IDENTIFY SEQUENCE CONSERVATION IN
LIGAND BINDING POCKET**

Select residues surrounding ligand binding pocket.

1. Right click on ATP ligand in the first object



Green crosses = graphical selection

2. Select/Neighbors

Notice selection is returned to alignment – highlighted in blue

1q16_a	1STHGFYENPEKPELGRVSSVRRRCIHKPTCKEYVVIDVDTGGGSFSAEEVQE
2phk_a	1GEYENPEKPELGRVSSVRRRCIHKPTCKEYVVIDVDTGGGSFSAEEVQE
KCC2A_HUMAN	1KALRDEIMSKTSLACGEGKLAERKTKCKVILIIISKR---KFAIGSARE
CHK2_HUMAN	134	DKYRTYSKKHFRIFREVGPKNISYIAYIEDHSGNGTFTVNTLEVGKGRRLPNNNSEIALSLSPN
MK14_HUMAN	1LPVSSVAYGSCAAFDTRKTGLRVVIVKLSR---PFQS
PIM1_HUMAN	53	TRSHSHSHSP.....LLSSGFGSIVSGIRVSDNLPVILIHVEKD---RISDUGE

1q16_a	56	LREA--TLKVDILRRVSG-HPNIIQLKDYETNTFFLVFDLTKK-GELF-----DYLTEKVTLSSEKTRKIMRAL-EVICALKLNIVHRLPENILLDDDMN---ILDTDFQFSCQLDPGEKLR
2phk_a	53	LREA--TLKVDILRRVSG-HPNIIQLKDYETNTFFLVFDLTKK-GELF-----DYLTEKVTLSSEKTRKIMRAL-EVICALKLNIVHRLPENILLDDDMN---ILDTDFQFSCQLDPGEKLR
KCC2A_HUMAN	57	LE---RARIICRLK--HPNIVRLHDSISEEGHYLIFDLVTG-GELF-----EDIVAREYYSADASHCIQIQI-EAVLHCQMGVVRHDLPENLLASLKGAAVLAAPFLATEVE-GEQQA
CHK2_HUMAN	264	ADPALNVTIEILKKNL--HPCIIKIKNFFDAED--YIVLELMEG-GELF-----DKVGNKRLKEATCKLYFYQM-LAVQYLSNGLIHRDLPEVLLSSQEDCLITDFGHSKIL--GETSL
MK14_HUMAN	62	IIHAKRTYRILRLKHK--HENVIGLLDVPFPARSL-----EFFNDVYLVTHLGMADLNNIVRCQKLTDDHVQFLIYQIRGLKYIESADIIHRDLPSLAV--N-EDCELILDFLARHTD---DEM
PIM1_HUMAN	171	LPNGTRVPMVVLKRVSSGFSVIRLLDWFERPDSFVILIRPEPVQQLF-----DFITERGALQELARSFFVQV-EAVRHCCNGVRLHIDELI--DLNRGELILIPSGALK---DTV

Propagate selection to all sequences in alignment.

Workspace Panel

- 49 Res 3 Mol, 2 Obj
- objects (2 items)
- 2phk [1] XR; 2.6Å
- 1q16 [2] XR; 2.4Å
- sequences (6 items)
- 2phk_a 277 Amino 3 sites
- 1q16_a 281 Amino 4 sites
- MK14_HUMAN 360 Amino 33 sites
- KCC2A_HUMAN 478 Amino 16 sites
- PIM1_HUMAN 404 Amino 11 sites
- CHK2_HUMAN 543 Amino 58 sites

Terminal

```
icm/1q16> alignment 'newAli' (6 sequences, /1/ res.wide) created
icm/1q16> color ribbon Res(a_*/./DD) alignment
icm/1q16> as_graph = Atom( Res(Sphere( a_2phk.aatp/381 (Mol( (a_*/./D | a_*/./DD) ) & !Mol( a_2phk.aatp/381 ) ) ) )
icm/1q16>
```

newAli

1q16_a	1Y.....#G.G...V...#.....#A#K.#.....#.....
2phk_a	1	-----STHGFYENEPKPLRNRVSSVPRCIHKPTCKEYVILIDVTGGGSFSAEEVQE
KCC2A_HUMAN	1	-----GFYENEPKELRNRVSSVPRRCLKPTCKEYVILIDVTGGGSFSAEEVQE
CHK2_HUMAN	134	DKYRTYSKKHFRIFREVGPKNISYIAYIEDHSGNGTFTVNTLEVGKRRRPLNNSSEIALSLSRNKVVFVFDLTVDDOSVPRDIMSRTLSSACGEKLAFLRKTCKKVILIIISKR---KFAIGSARE
MK14_HUMAN	1	-----MSQRRPTN-----WEVPERLNLSPVSGAYGSCAADTRKTGLRVVVKLSR-----PFQS
PIM1_HUMAN	53	TRSHSHSHSPRHLRHSPPSGSGSSSGHRPCADILEVGMLLSKINSLAHLRAAPGNLPLE-----SQVQGPLLPLQFQSYSGIRVSDNLPVLIHVEKD-----RISDWGE

Alignments

1q16_a	5#L.#.###...##HRD#K..N###.....#K#.DFG.....
2phk_a	5	IMRALVEVICALKLNIVHRLLPENILLDDDMN---ILTLDFQFSCQLDPGEKLR
KCC2A_HUMAN	5	IMRALVEVICALKLNIVHRLLPENILLDDDMN---ILTLDFQFSCQLDPGEKLR
CHK2_HUMAN	62	CIQQIEAVLHCGQMGVLRDLPEENLLASLKGAAVLAFLGLATEVE-GEQQA
MK14_HUMAN	2	YFYQMLAVQYLSENGIIRDLPEVLLSSQEDCLILITDFGHSKIL--GETSL
PIM1_HUMAN	171	LPLNGTRVPMVVLKRVSSGFSVIRLLDFERPDSFVILIRPEPVQDLF-----DFITERGALQELARSFVQVLEAVRHCCNGVRLIIDEILLI--DLNRGELIIRISGALLK---DTV

1. Propagate to all sequences

conservation

Propagate to ALL sequences

By Consensus X

Select Invert Hide

Preferences 17

4 Mol 2 Obj

1ql6 Molsoft icm 3.7-2a [NewProject *] (2 objects 1 alignment)

File Edit View BioInfo Tools Homology Chemistry Docking MolMechanics Windows Help

display light labels meshes search ligand movie

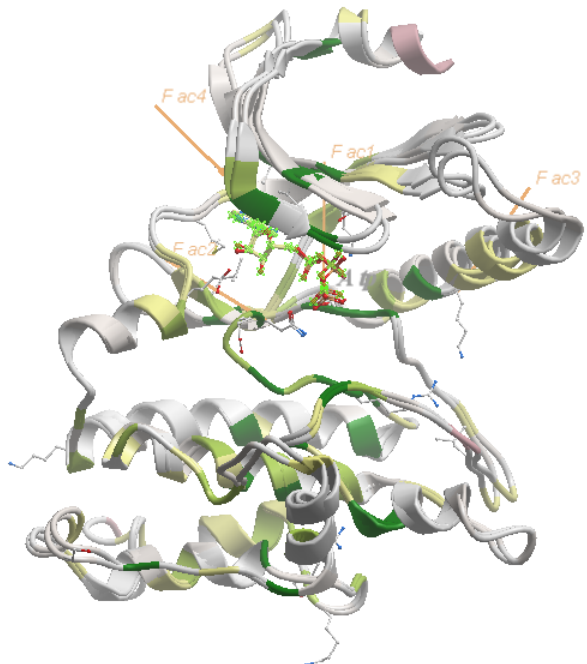
Workspace Panel

1 Mol 1 Obj

- objects (2 items)
 - 2phk [1] XR; 2.6Å
 - a 2phk_a newAli 277 A 3 sites
 - b 7 A
 - amn M manganese +2
 - amn2 M manganese +2
 - aatp H adenosine-5'-triphosphate
 - agol H glycerol
 - phosphorylase kinase; chain: a; fragmer
 - W (86 water molecules)
 - 1ql6 [2] XR; 2.4Å
 - a 1ql6_a newAli 281 A 4 sites
 - bato H adenosine-5'-triphosphate
 - brmn M manganese +2
 - brmn2 M manganese +2
 - cso4 H sulfate-ion (SO4--)
 - phosphorylase kinase; chain: a; fragmer
 - W (104 water molecules)
- sequences (6 items)
 - 2phk_a 277 Amino 3 sites
 - 1ql6_a 281 Amino 4 sites
 - MK14_HUMAN 360 Amino 33 sites
 - KCC2A_HUMAN 478 Amino 16 sites
 - MK14_HUMAN 360 Amino 33 sites
 - CHK2_HUMAN 543 Amino 58 sites
- alignments (1 item)
 - newAli id=27 nSeq=6

All

Display only the residues in the ligand binding pocket.



3. Click again to restore view

2. Hide selection

1. Invert selection

Residue conservation in the ligand binding pocket

```

icm> alignment 'newAli' (6 sequences, /1/ res.wide) created
icm/1ql6> color ribbon Res(a_*/./DD) alignment
icm/1ql6> as_graph = Atom( Res(Sphere( a_2phk.aatp/381 (Mol( (a_*/./D | a_*/./DD) ) & !Mol( a_2phk.aatp/381 ) ) ) ) )
icm/1ql6>
  
```

	#	G	V	A	K	#	...	D	K	N	H	D				
1ql6_a	1	L	R	V	S	S		I	F	D	L	E	E	L	T	F
2phk_a	1	L	R	V	S	S		I	F	D	L	E	E	L	T	F
KCC2A_HUMAN	1	L	K	A	F	S		V	F	D	L	V	E	L	A	L
CHK2_HUMAN	1	L	S	A	C	G		I	L	E	L	M	E	L	T	H
MK14_HUMAN	1	V	S	A	Y	G		I	---	D	X	S	A	L	L	
PII1_HUMAN	1	L	S	G	F	G		I	L	E	R	P	D	E	L	I

View

consensus

seq ruler

Comment UPGMA

Tree

Sync with

Tree only

View Difference

Strength (50%)

Color conservation

Selection

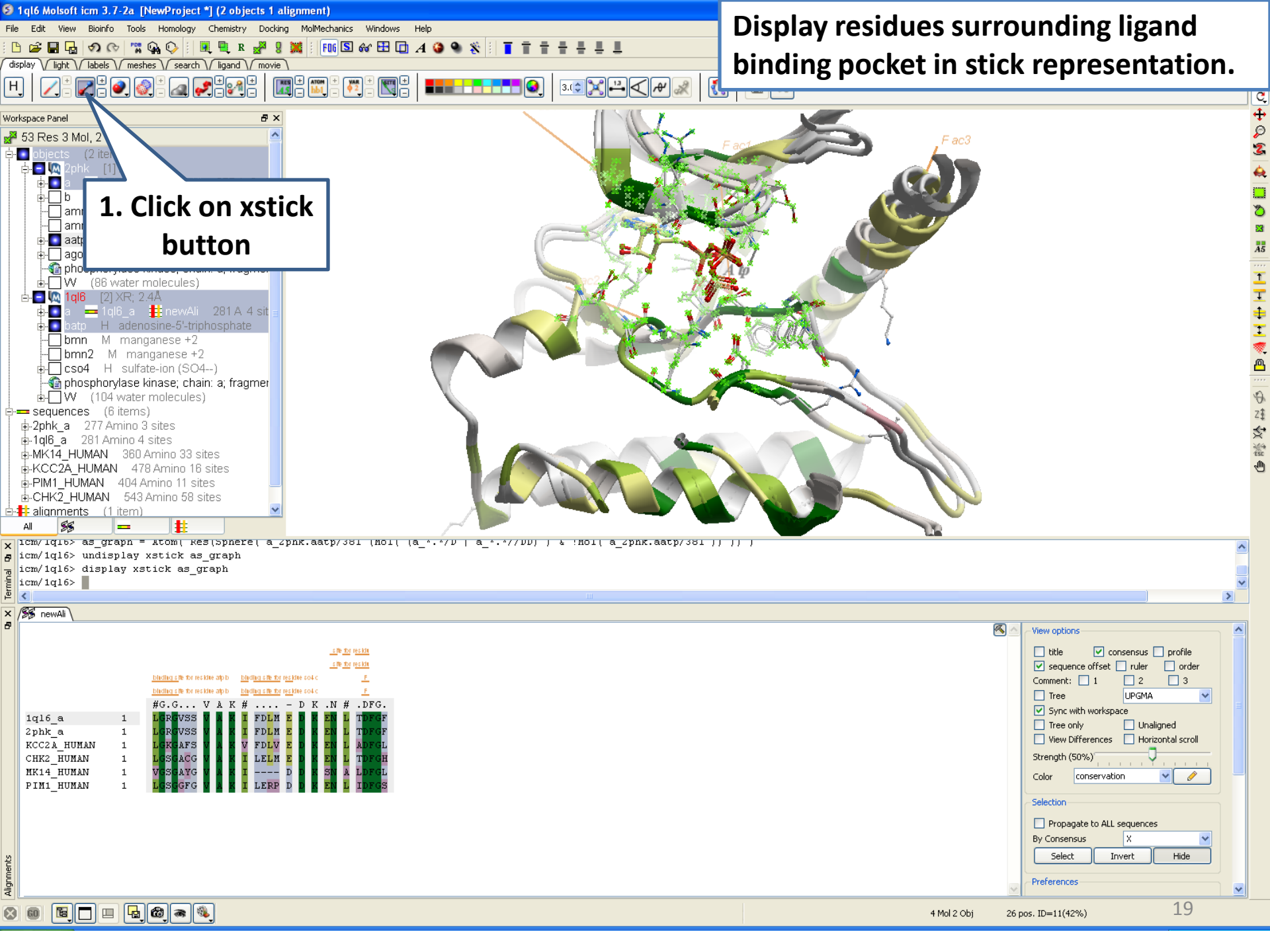
Propagate to ALL sequences

By consensus X

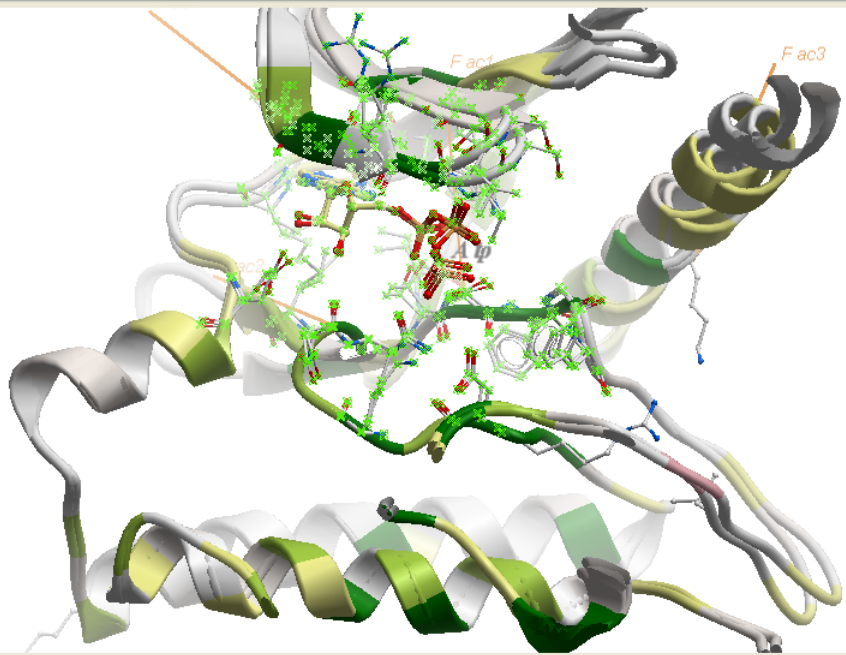
Select Invert Hide

Preferences 18

Display residues surrounding ligand binding pocket in stick representation.



1. Click on xstick button



```
icm/1q16> as_graph = atom( res(sphere( a_2phk.aatp/381 (mol( a_*.*/D | a_*.*/DD ) & mol( a_2phk.aatp/381 ) ) ) )
icm/1q16> undisplay xstick as_graph
icm/1q16> display xstick as_graph
icm/1q16>
```

newAli

	#G	...	V	A	K	#	...	-	D	K	.N	#	.DFG					
1q16_a	1	L	R	V	S	S	I	F	D	L	M	E	E	L	T	F	G	F
2phk_a	1	L	R	V	S	S	I	F	D	L	M	E	E	L	T	F	G	F
KCC2A_HUMAN	1	L	R	A	F	S	V	F	D	L	V	E	E	L	A	D	F	G
CHK2_HUMAN	1	L	S	A	C	G	I	L	E	L	M	E	E	L	T	F	G	H
MK14_HUMAN	1	V	S	A	Y	G	I	---	D	K	S	A	L	D	F	G	L	
PIM1_HUMAN	1	L	S	G	F	G	I	L	E	R	P	D	E	L	T	F	G	

View options

- title
- consensus
- profile
- sequence offset
- ruler
- order
- Comment: 1 2 3
- Tree
- UPGMA
- Sync with workspace
- Tree only
- Unaligned
- View Differences
- Horizontal scroll
- Strength (50%)
- Color: conservation

Selection

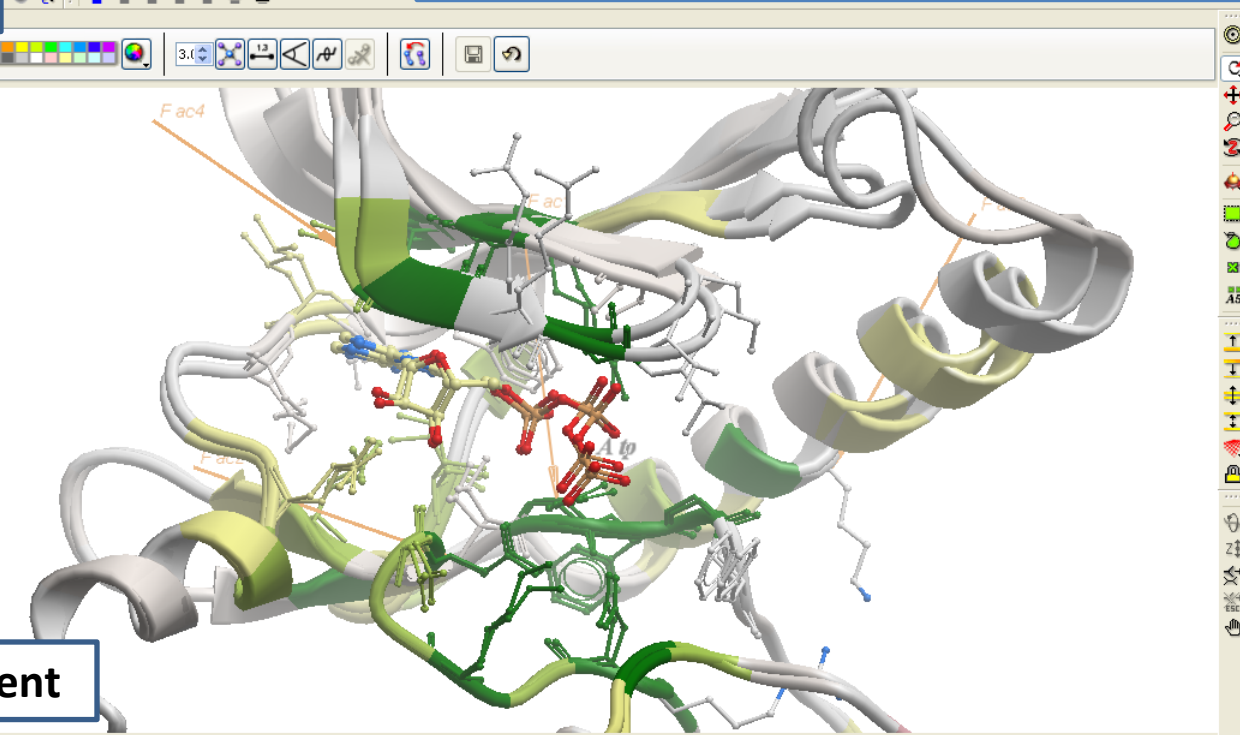
- Propagate to ALL sequences
- By Consensus: X
- Select Invert Hide

Preferences

Color stick by alignment.

1. Click and hold

The screenshot shows the 'objects' panel on the left side of the software interface. A context menu is open over the 'alignment' option. The menu items include: atom type, residue sc, residue, molecule, molecule_C, object, object_C, bfactor, occupancy, accessibility, hydrophobicity, polarity, sec. structure, NtoC, user atom field, user res. field, and alignment. The 'alignment' option is highlighted with a blue box.



2. Color by alignment

```
icm/1ql6> display xstick as_graph
icm/1ql6> center static as_graph
icm/1ql6> color xstick as_graph alignment
icm/1ql6>
```

Alignments

		#G.G... V A K #	...	- D K .N #	.DFG.
1ql6_a	1	L R V S S	I F D L M	E K E N	L T F P G F
2phk_a	1	L R V S S	I F D L M	E K E N	L T F P G F
KCC2A_HUMAN	1	L R K A F S	V F D L V	E K E N	L A D P G L
CHK2_HUMAN	1	L S S A C G	I L E L M	E K E N	L T F P G H
MK14_HUMAN	1	V S S A Y G	A A A I	- - - - D K S S	A L D F G L
PIM1_HUMAN	1	L S S G F G	I L E R P	D E K E N	L T F P G S

View options

- title
- consensus
- profile
- sequence offset
- ruler
- order

Comment: 1 2 3

Tree UPGMA

Sync with workspace

Tree only Unaligned

View Differences Horizontal scroll

Strength (50%)

Color: conservation

Selection

Propagate to ALL sequences

By Consensus: X

Select Invert Hide

Preferences