

Use of Computational Tools in Medicinal Chemistry Projects



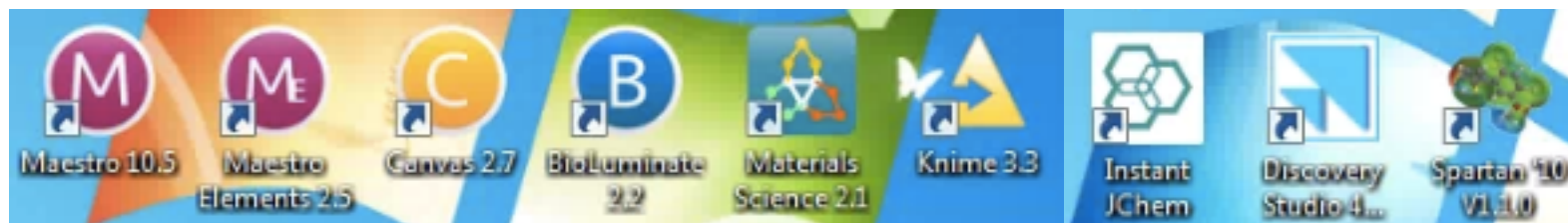
Chaemin Lim
Research Topic Seminar
November 05, 2016



Wipf Group

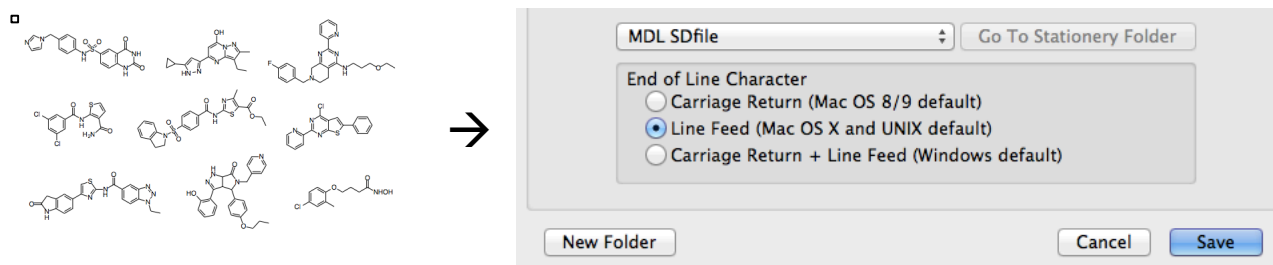
Computational Tools in Wipf Group

- **Instant JChem (Group License) / Instant JChem for Excel**
 - Create, explore and share chemical and non-chemical data
 - Physical-chemical property and molecular descriptor calculations
 - Structure search, substructure filter, property filter (Lead-like filter)
 - List and query management
- **Schrödinger software** - Small Molecule Drug Discovery Suite (7th floor computer)
 - Maestro: All purpose molecular modeling environment. Protein target preparation, ligand preparation, general modeling tools, etc...
 - Canvas: A comprehensive cheminformatics computing environment. Fingerprint-based similarity searching and substructure matching, clustering and diversity selection, chemistry filters, etc...
- **Spartan (University License)**
 - A general purpose modeling tool: provide information about molecular structure, energy, reactivity, selectivity and a wide range of molecular properties
 - Molecular mechanics calculations and quantum chemical calculations



Quick Guide for Instant JChem

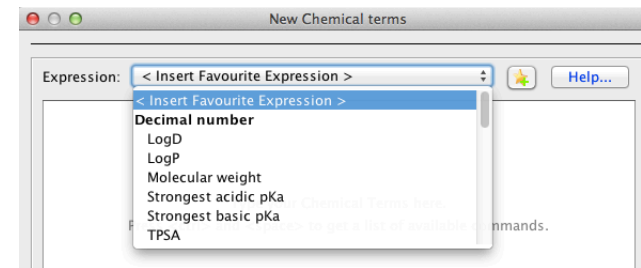
i) Generate SD file: ChemDraw/InstantJChem/DiscoveryStudioViewer, etc...



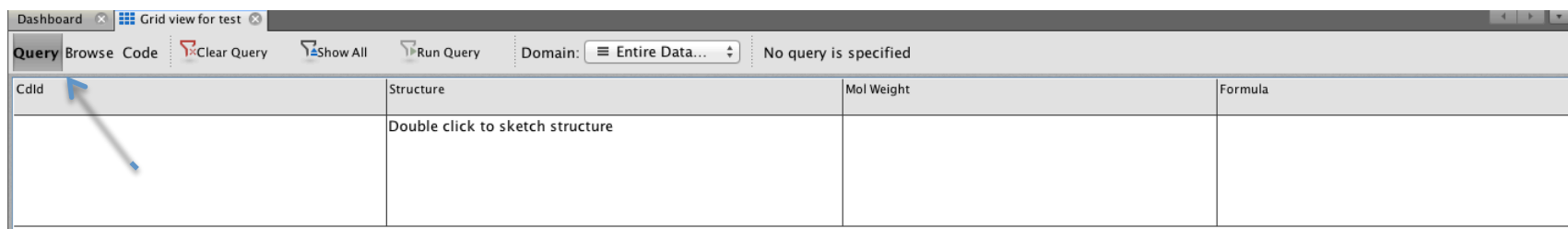
ii) Import File: File – Import file or click the icon



iii) Properties calculation: Click “New Chemical Terms Field”

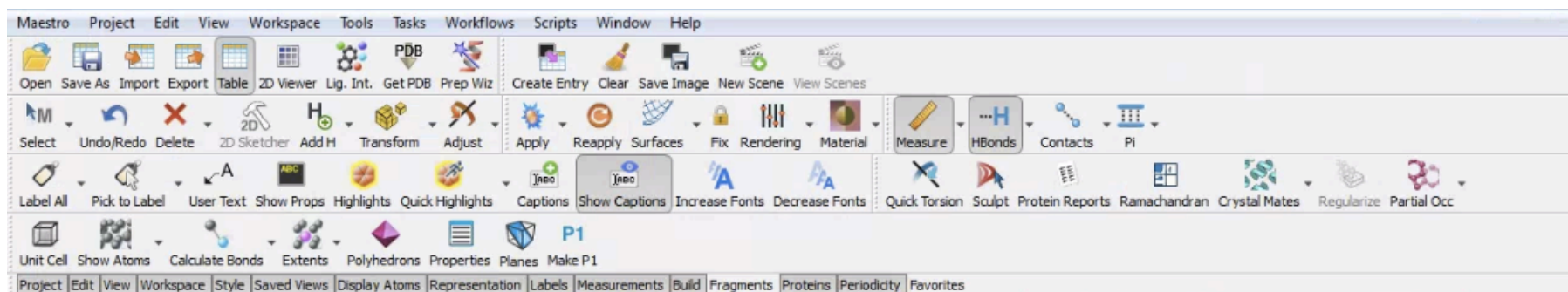


iv) Filter, substructure search: Click Query



Schrodinger Maestro & Canvas

- **Schrödinger software** - Small Molecule Drug Discovery Suite (7th floor computer)
 - **Maestro**: All purpose molecular modeling environment. Protein target preparation, ligand preparation, general modeling tools, etc...
 - Quick guide for docking
 - i) Importing and Editing Molecules with Maestro: Get PDB (from RCSB or import directly from Maestro)
 - ii) Prepare Protein: Protein Preparation Wizard
 - iii) Prepare Ligand: Import compounds as a SD/mol file format (or Draw) then 'Applications – LigPrep'
 - iv) Generate the Grid
 - v) Glide Dock (Rigid docking)



Schrodinger Maestro & Canvas

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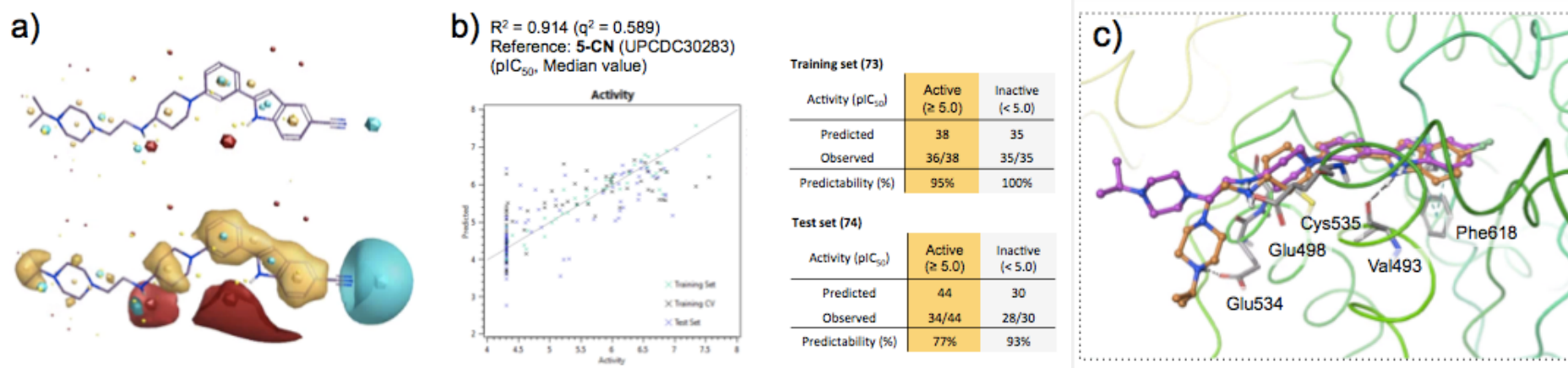
i) Prepare compounds (or download library) as a SD file

ii) Import SD file: if you have multiple structural files, you can select additional options (store each files as as view, remove duplicates, etc...)

iii) Select options

Target 1 – p97 AAA ATPase

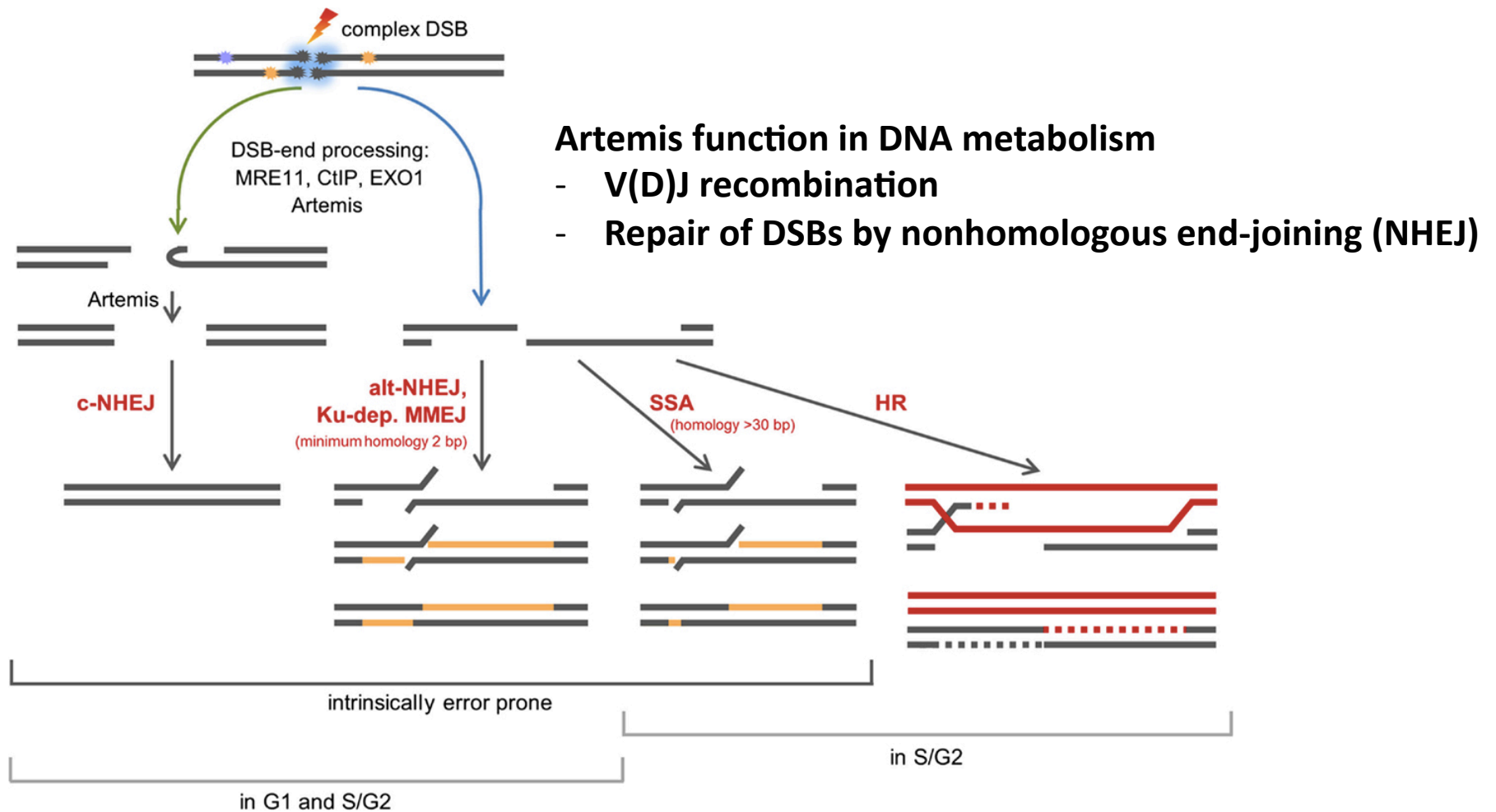
- p97 modulates protein processes related to protein homeostasis in cancer
- Developed a **3D-QSAR model** for a series of 2-phenyl indole analogs based on ca. 150 synthetic compounds with biochemical assay information
- The predicted pIC_{50} from the model correlate well with the observed pIC_{50} ($R^2 = 0.914$, $q^2 = 0.589$) and the phenyl indole orientation of the reference structure was matched by the protein bound conformation from a cryo-EM structure that was subsequently obtained
- **Further optimization of the binding mode** of phenyl indole analogs using docking simulations and a refined protein model.



- A member of the metallo- β -lactamase protein family
 - **Critical for the major pathway of double-strand break repair**
 - **Endonuclease activity** at DNA hairpins and at 5'- and 3'-DNA overhangs of duplex DNA, and this endonucleolytic activity is dependent upon DNA-PKcs
 - Essential for the successful V(D)J recombination in lymphocytes
- Valuable therapeutic target for human acute lymphoblastic lymphoma and leukemia

DNA Double Strand Break (DSB) Repair

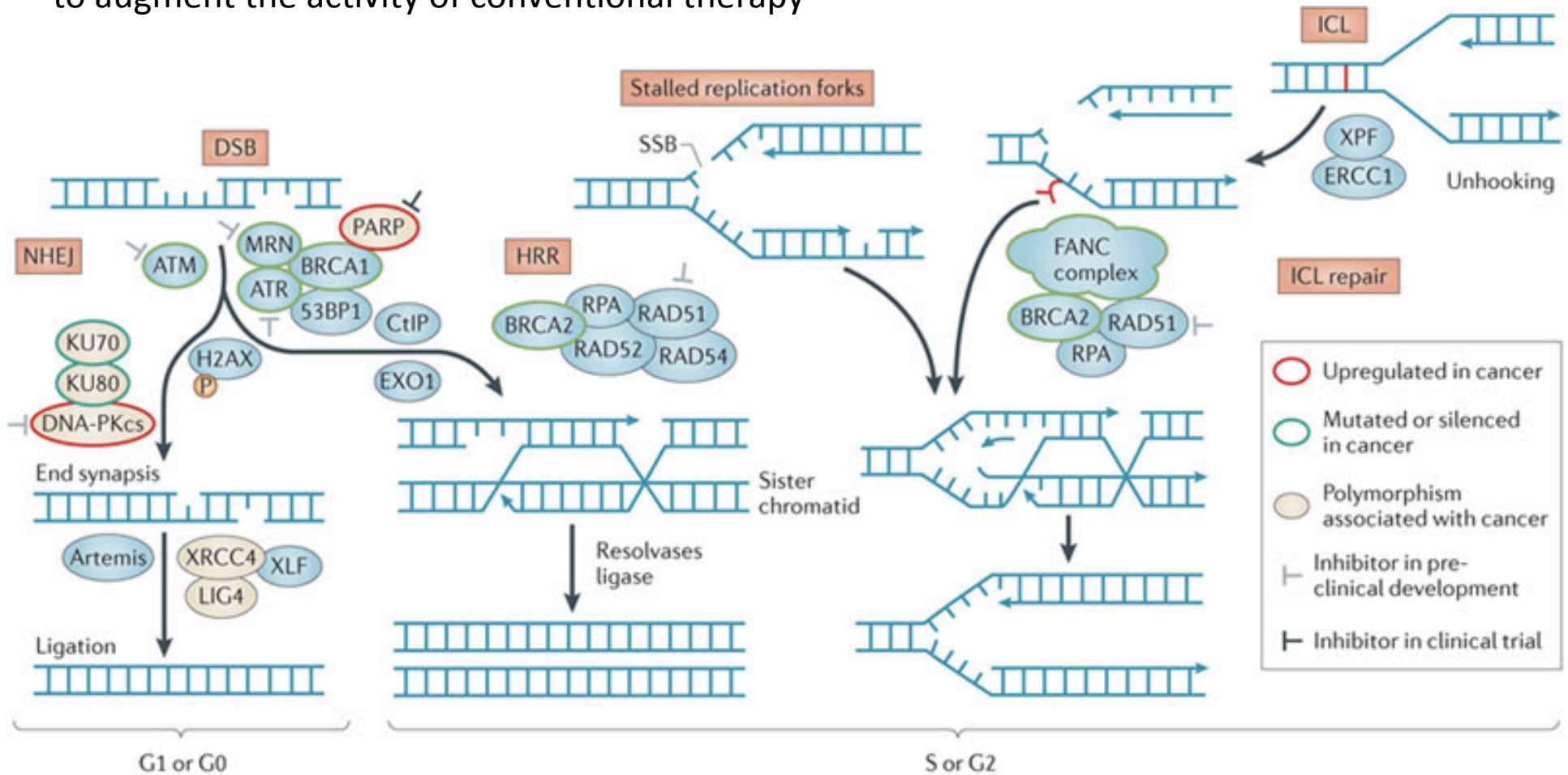
Major pathways of DNA double-strand break repair



Front. Oncol. 6:28. doi: 10.3389/fonc.2016.00028

Therapeutic Targeting of DNA Damage Repair

*Inhibitors of the DDR have been developed to overcome resistance and to augment the activity of conventional therapy



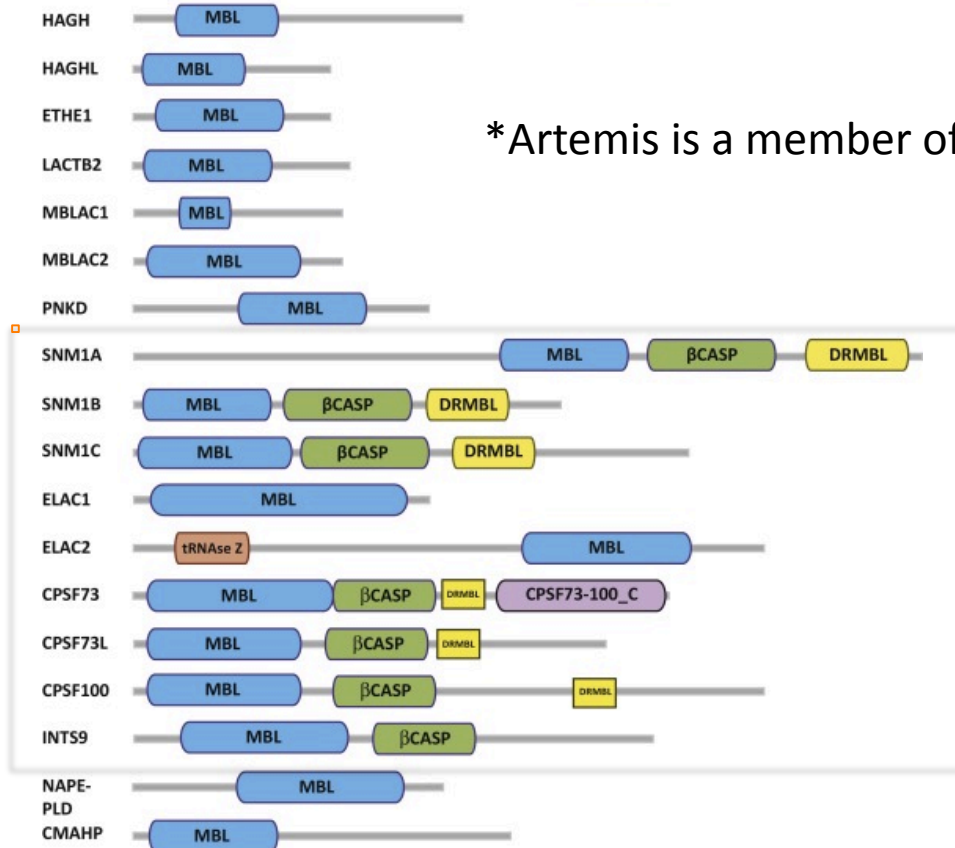
<DNA double-strand break and interstrand crosslink repair>

Nature Reviews | Cancer

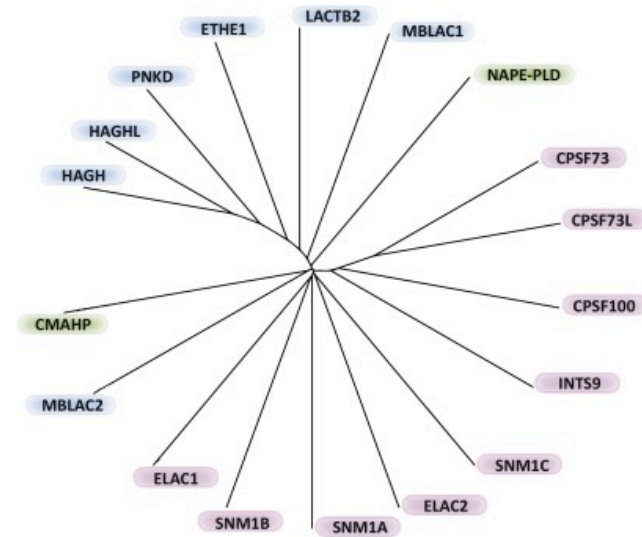
Nature Reviews Cancer 2012, 12, 801-817 | doi:10.1038/nrc3399

Humann Metallo- β -Lactamase Protein Family

- A small family of approximately 18 zinc- and iron-dependent proteins with roles in metabolism and/or detoxification and nucleic acid modification.
- Group 1, The Glyoxalase II Subfamily
- Group 2, **The DNA/RNA Interacting hMBLf Subfamily**
- Group 3, NAPE-PLD and CMAH



*Artemis is a member of the metallo- β -lactamase protein family



In-class Selectivity within β -CASP family

- SNM1 enzymes (SNM1A, SNM1B, and SNM1C (Artemis)) involved in DNA repair pathways

DNA lesion	DNA Repair Pathway	Nucleases	Fold
DSB	Non-homologous end joining (NHEJ)	Mre11	PP2B
		Artemis	MBL
DSB	Homologous recombination (HR)	Mre11	PP2B
DSB	Microhomology-mediated end joining	Mre11	PP2B
ICL	Repair of interstrand crosslinks (ICL)	SNM1A/B	MBL

		Metallo- β -lactamase							
		I	II	III	IV				
Human	SNM1A	FTVDAF	LTHFHSDHYA	ANHCP	ILHTGDFR		1040 aa	SNM1A	
Yeast	SNM1/Pso2	IVVDGF	LSHFHSDHYI	ANHCP	ILHTGDFR		532 aa	SNM1B/Apollo	
Human	SNM1B/Apollo	IAVDFW	LSHFHSDHYT	ANHCP	ILYTGDFR				
Human	SNM1C/Artemis	ISIDRF	LSHCHKDHMK	AGHCP	VLYTGDFR		692 aa	SNM1C/Artemis	
Human	CPSF-73	IMLDCC	ISHFHLDHCG	AGHVL	LLYTGDFR				
<i>E. coli</i>	UlaG	VCVDFW	ATHDHNDHID	AFDRT	LYHSGDSH				
<i>B. cereus</i>	BLM	VLVDSS	ITHAHADRIG	KGHTE	ILVCGCLV				
		β -CASP domain							
		A	B	C					
Human	SNM1A	LYLDTT	EHSSY	IPTVN					
Yeast	SNM1/Pso2	LYLDTT	EHSSF	IPTVN					
Human	SNM1B/Apollo	LYLDNT	DHSSY	VPIVS					
Human	SNM1C/Artemis	VYLDTT	FHSSY	YPNVI					
Human	CPSF-73	LIEST	AHTDY	ILVHG					

Characteristic sequence motifs of DNA nucleases of the MBL/ β -CASP family

Available from: <http://www.intechopen.com/books/dna-repair-on-the-pathways-to-fixing-dna-damage-and-errors/nucleases-of-metallo-beta-lactamase-and-protein-phosphatase-families-in-dna-repair>

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✧ Wipf Group members past and present



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