



Designing potent inhibitors of human P38γ for effective breast cancer therapy

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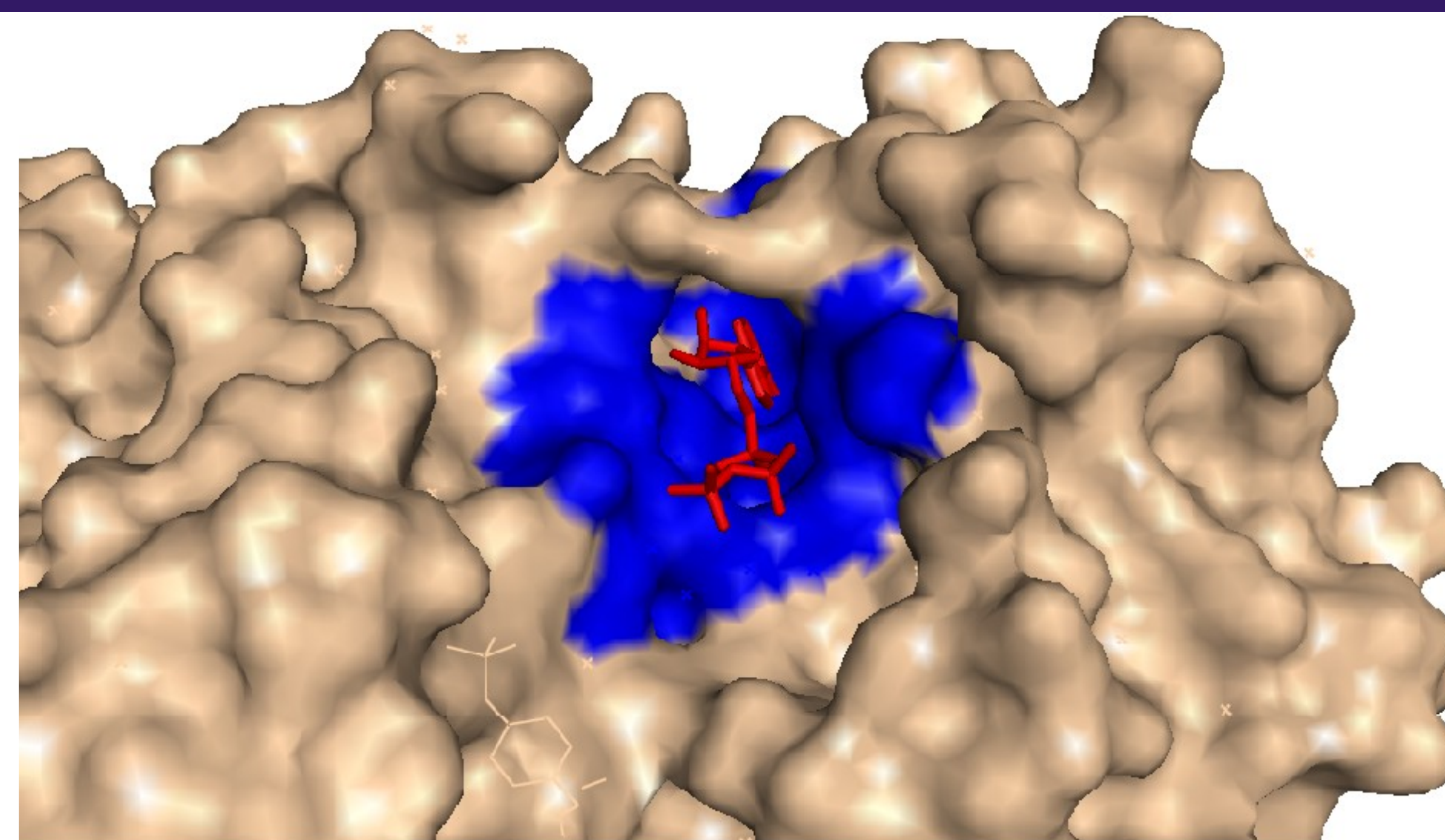
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सत्यमेव जयते

Key points:

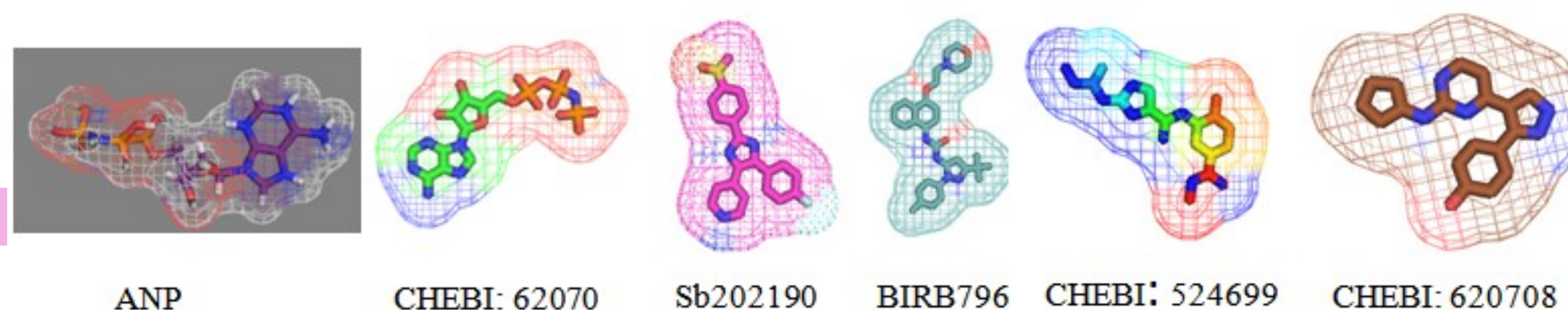
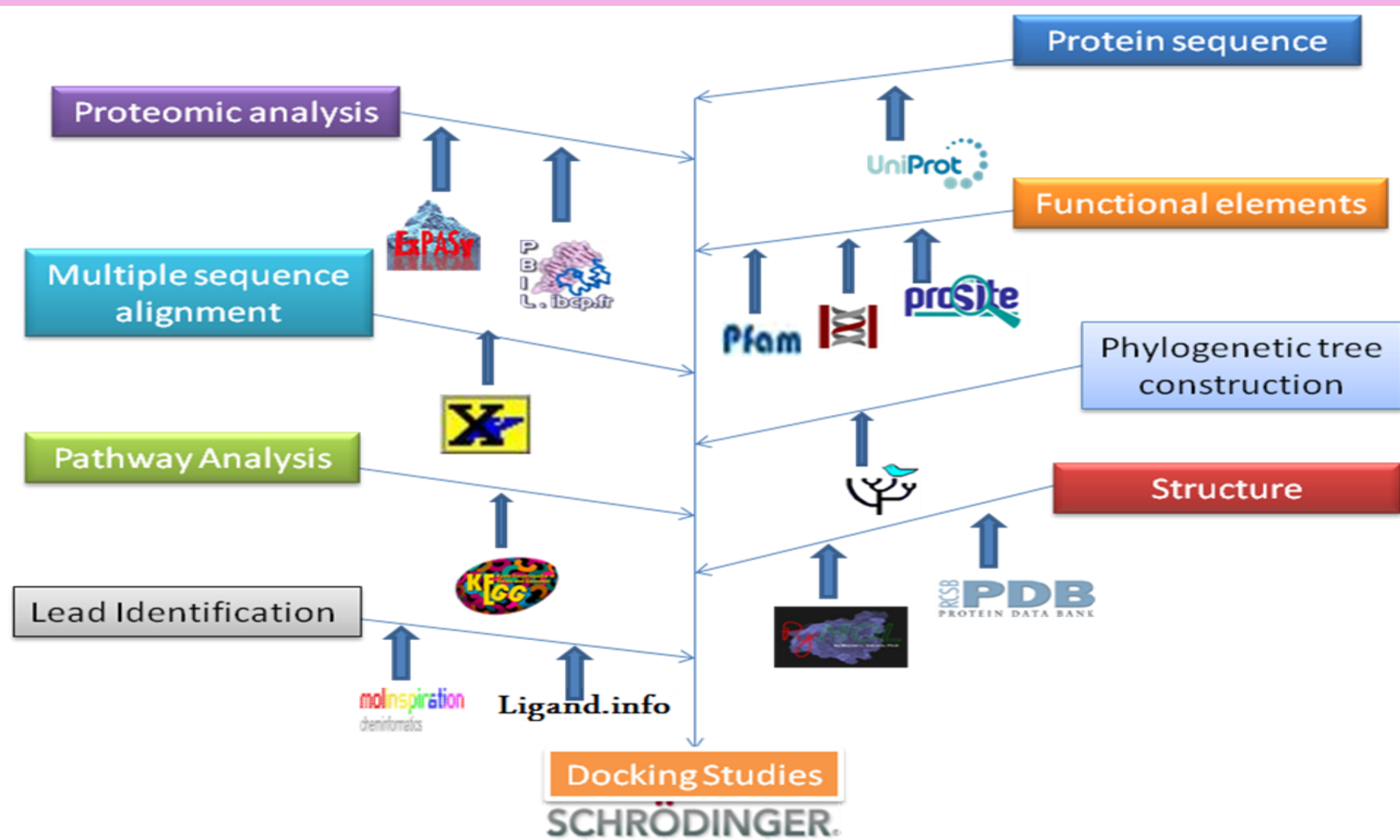
- Oncogenic constitutive enzyme human p38γ is a serine/threonine protein kinase, activated through phosphorylation by environmental stress and pro-inflammatory cytokines responses (Lechner *et al.*, 1996). Over expression of the protein leads to formation of tumorigenesis effectors.
- Human p38γ protein is highly expressed in several human malignant cell lines (Wang *et al.*, 2000; Pillaire *et al.*, 2000), indicating its possible role in tumorigenesis. Human p38γ specifically integrates their antagonistic activity to stimulate cell invasion. Human p38γ over expression increases invasion that is the spread of malignant cells to new sites of the body in ER+ and higher levels in ER- breast cancer cells (Qi *et al.*, 2006).
- Computational method for drug designing was practiced here to explore lead molecules targeting



P38γ-ANP complex
Active sites :
LYS56, PRO110,
MET112, ASP115,
GLY157, ASN158,
ASP171, W2111,
W2039 and
W2152
X-ray
crystallography
Structure
visualized
Through PyMol.

Figure d: X-Ray Crystallography Structure of 1CM8 (surface display, active site residues are coloured and ANP ligand stick display) visualized through pymol.

MATERIALS AND METHODS:



- Docking of the generated lead molecules with the human p38γ protein using Schrodinger software suite 2009 (Maestro 9.0) produced 18 lead molecules, Among the 18 lead molecules, Lead '1' directly blocking five residues forming hydrogen bond with lowest XP G Score: -10.224 kcal /Mol.

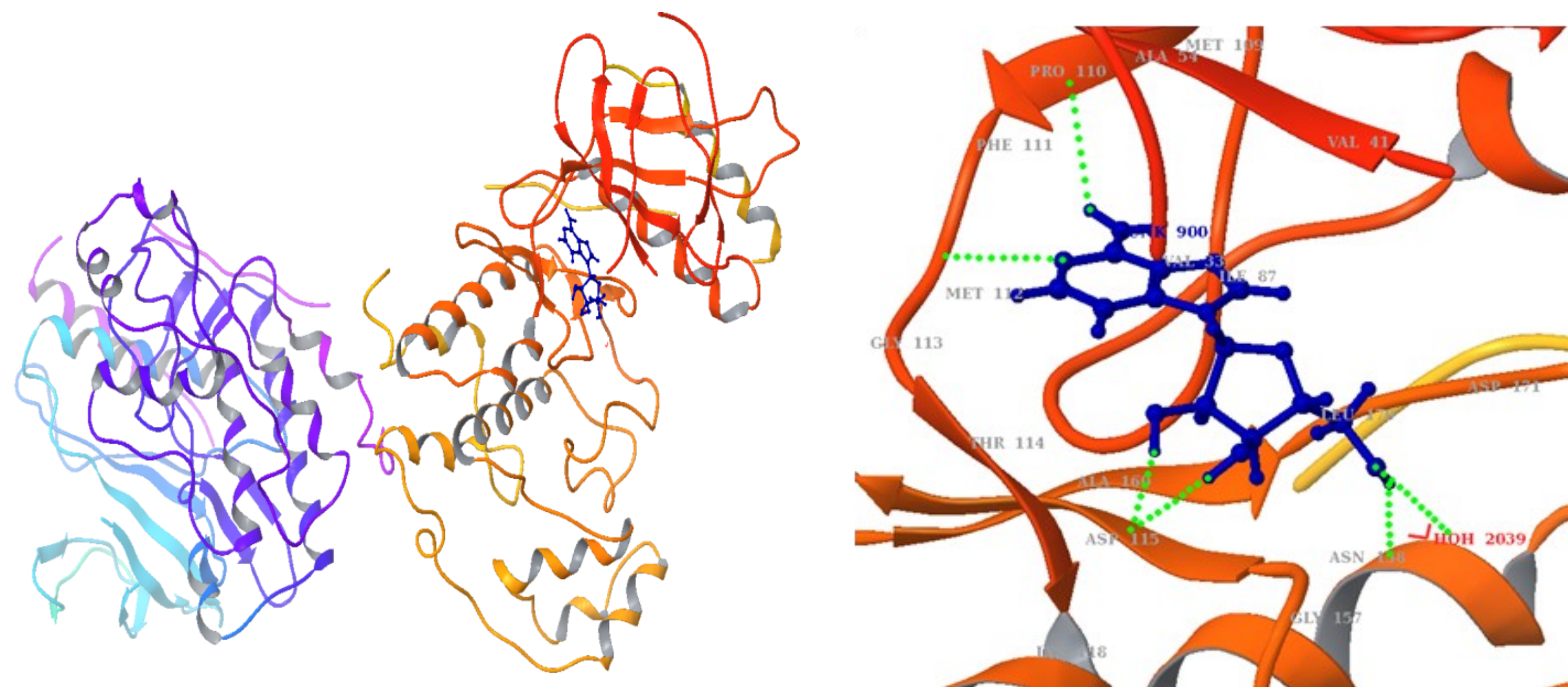
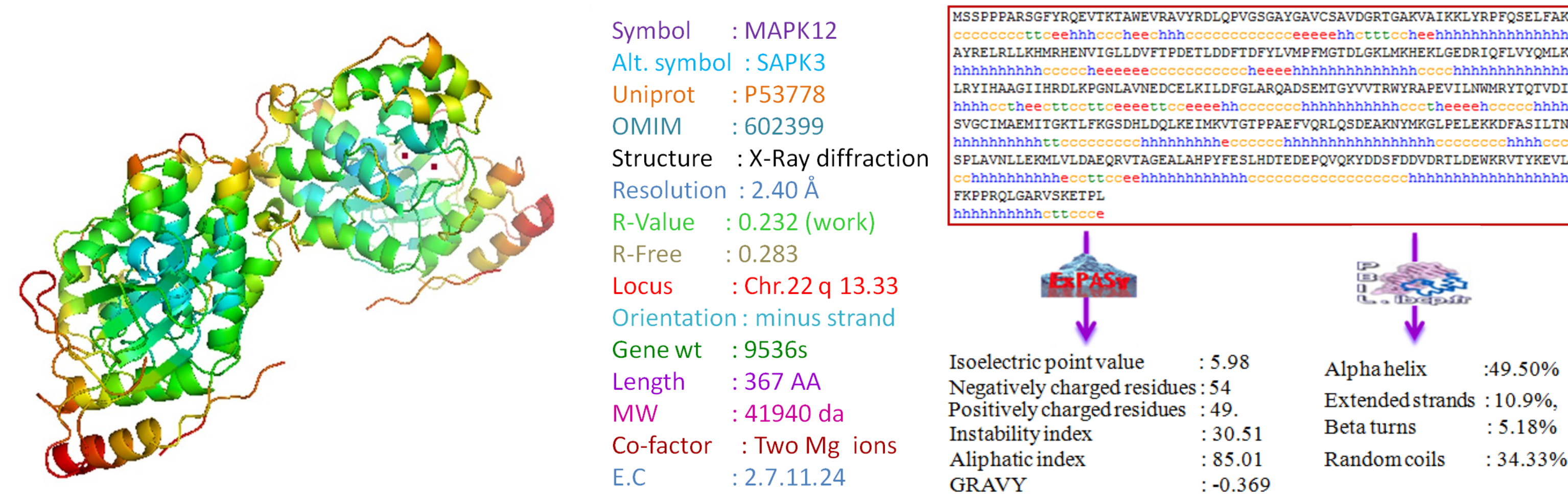


Figure e: Representing the hydrogen bonds of lead '1' with the human p38γ protein.

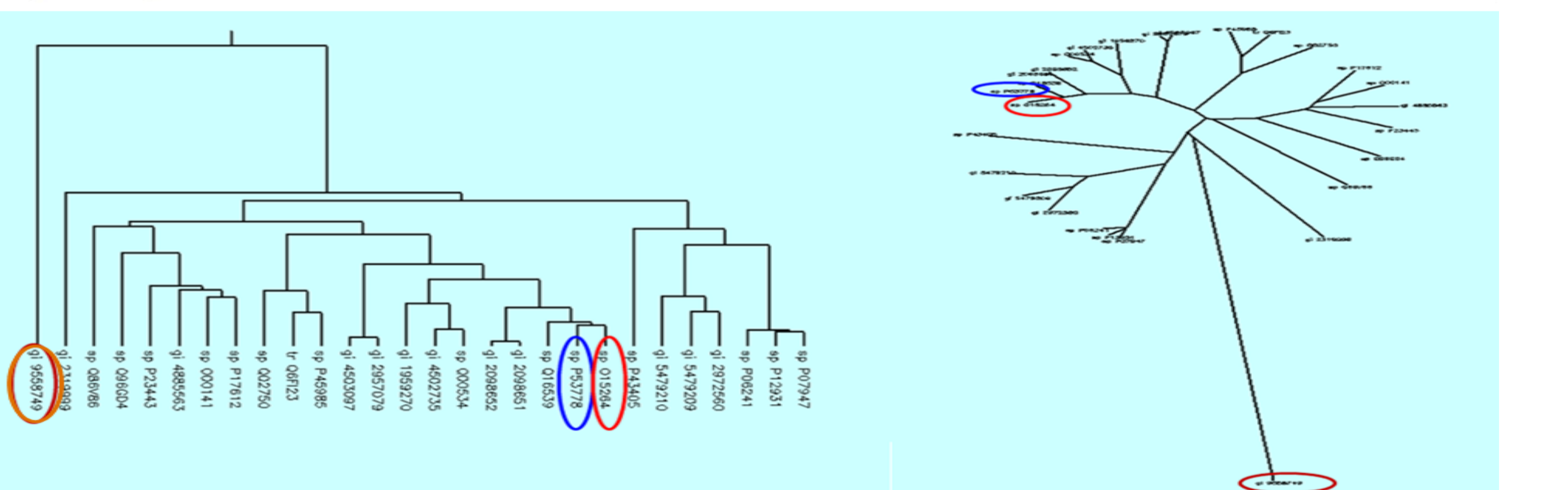
Analysis of binding orientations of the docking complex revealed that four amino acid residues Pro110, Met112, Asp115 (two Hydrogen bonds), Asn158 and W2039 of active site were directly involved in formation of hydrogen bond network for human p38γ protein functional activity inhibition with Lead '1' that complements well with previous crystallographic reports of human p38γ –ANP inhibitor complex.

3-DEAZA-ADENOSINE (Lead '1') was involved in good van der Waal interaction with Lys56 that is highly important for ATP binding and subsequent activation of human p38γ.

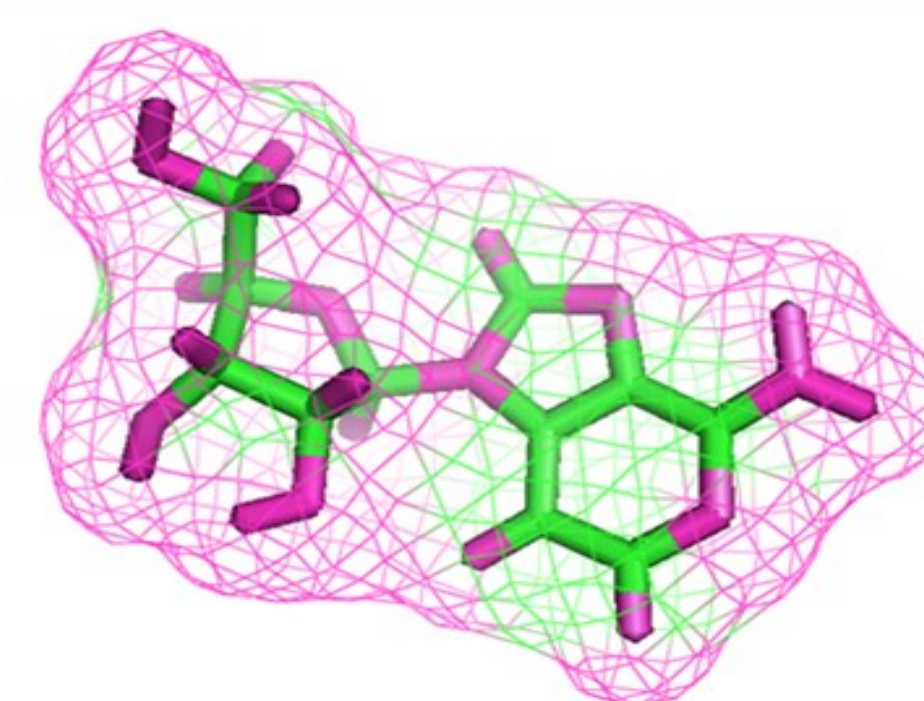
RESULTS AND DISCUSSION:



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>sp|P53778|MK12_HUMAN Mitogen-activated protein kinase 12 OS=Homo sapiens GN=MAPK12 PE=1 SV=3
MSSEPPARSGFFRQEVFKTAMVRVAVYRDLQVGGSSAYGAVCSAVDGRGKAVKELKLYRPFQSELPFR
PFQSELPFAKRAYRELRLKIMRHEAVIGLLVFFPEDETLDETDYLYVMPFMGTDLQKIM
KHEKLGEDRIQFLVYQMLKGLRYIHAAGIITHRDLKPGNLAVNEDCELEKILDFGLARQADS
EMTGYVTRWYRAPEVILNWMRYTQTVDIWSVGCIMAEMITGKTLFKGSDHLDQLKEIMK
VTGTPFAEFVQLQSDKAKNYMKGLEPELEKDFASILTNASLAVNLEKMLVLDLAEQRV
TAGEALAHFYFESLHDTDEDEPQVQKYYDDSEDDVDRTLDLWKRVTYKEVLSFKPFRQLGAR
VSKETEL
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- Rooted tree and Un-rooted tree was constructed by using the UPGMA algorithm of distance based method respectively. Mitogen-activated protein kinase 13 (P38δ) is closely related and Eukaryotic elongation factor 2 kinase (EEF2K) is distantly related respectively to human p38γ protein.



Lead '1'
MOL. WEIGHT : 266.26
Docking Score : -10.224
Docking energy : -72.683

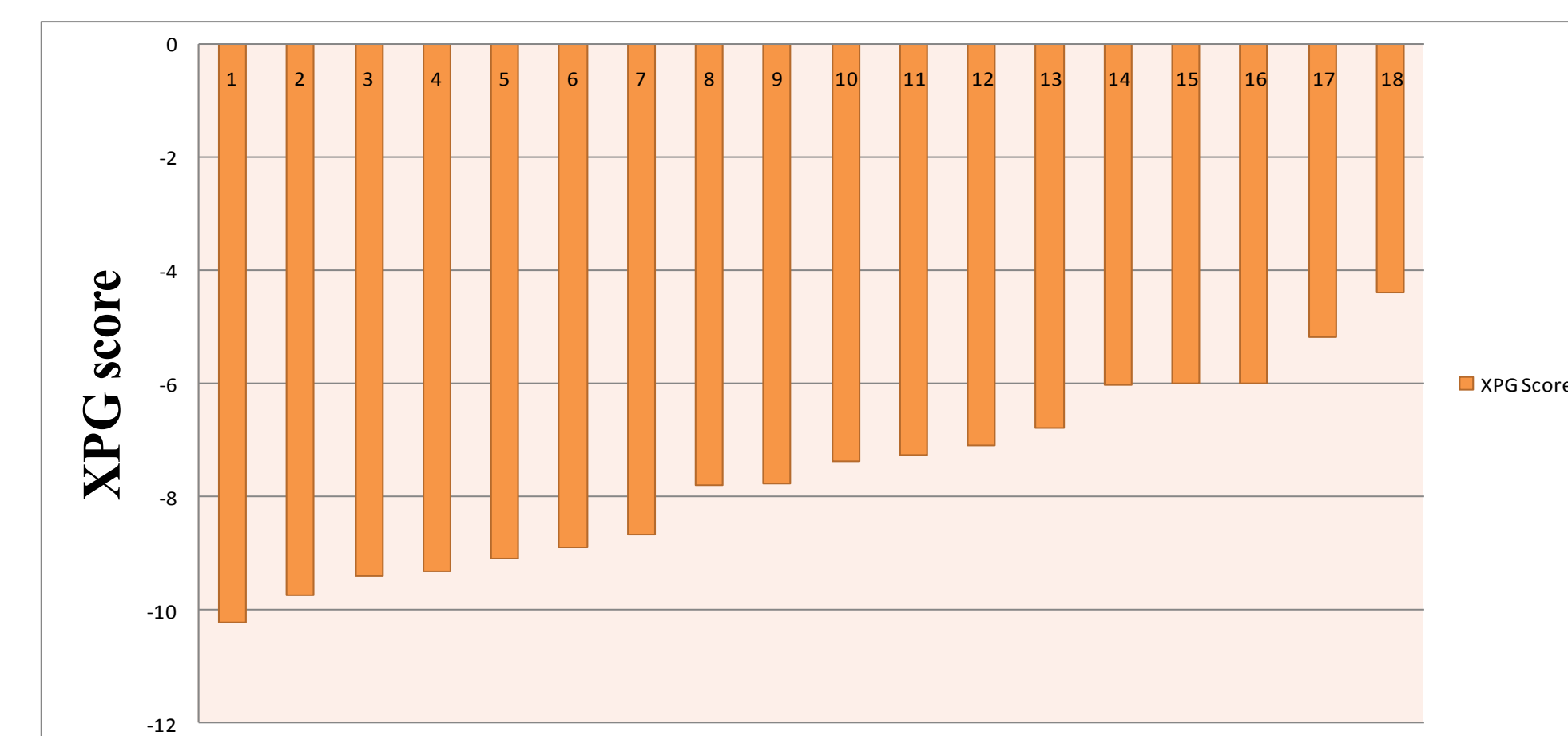


Figure f: Graphical representation of XPG scores

Conclusion:

3-DEAZA-ADENOSINE reports with good docking energy, docking score, stable conformation, orientation and exhibits functional activity inhibition. Thus it might be encouraging for new directions as a drug for human p38γ protein for the novel class treatment of breast cancer.

Acknowledgement:

My deep sense of gratitude to the honorable **Dr. A. Umamaheswari**, Coordinator of BIF & Head of the Department, Bioinformatics, SVIMS for making me a part of her unit and providing all necessary comforts. I am extremely grateful to **DBT**, Ministry of Science and Technology, Govt. of India for providing all the essential facilities to carry out the work.