CURRICULUM VITAE

Prof. Ajay Kumar Saxena
Structural Biology Lab
Jawaharlal Nehru University, School of Life Sciences
New Delhi-110067, INDIA
Ph: 0091-11-26704155, Email:ajaysaxena@mail.jnu.ac.in

Education:

1990-1995 Ph.D. in Structural Biology (Protein Crystallography), AIIMS, India.

Academic appointments:

03/2011- Professor, Structural Biology Section, Jawaharlal Nehru University, New Delhi, India
2005-2011 Associate Professor, Structural Biology Section, Jawaharlal Nehru University, New Delhi, India
1998-2005 Research Fellow, Structural Biology Section, LIG, NIAID, National Institutes of Health, Maryland, USA
1996-1998 Postdoctoral Fellow, Institute of Biophysics & X-ray Structure Re- search, Austrian Academy of Sciences, Austria, Europe

Awards/Fellowships:

2012 Bill & Melinda gates foundation travel award for GRC
2005 NIH/NIAID special performance award
1998-2005 John E. Fogatry International Fellowship, National Institutes of Health, USA
1996-1998 Austrian Academy of Science Fellowship, Government of Austria, Austria
1995-1996 Senior Research Fellowship, Department of Biotechnology, India
1990-1994 Junior Research Fellowship, All India Institute of Medical Sciences, India
1988 National merit scholar

Extramural research funding:

2018-2023 Department of Science and Technology (DST), India.
Title- Development of Single-cell derived clonal spheroids as a tool for drug discovery in cancer research. Co-PI- *Ajay K. Saxena*

2016-2019 Department of Science and Technology (DST), India.
Title- Structural and functional analysis of *M. tuberculosis* EccC+CFP10/ESAT6 complex from ESX-1 virulence factor secretion system. PI-*Ajay K. Saxena*

2013-2016 University Potential of Excellence (JNU) India
Title: Structure and function analysis of P. falciparum Pfs25 and Pfs28 proteins and their complexes with receptors. *PI- Ajay K. Saxena*

2013-2016 Department of Science and Technology (DST), India.
Title- Structure and function analysis of *M. tuberculosis* vaccine candidate EspC protein. *PI-Ajay K. Saxena*

2013-2016 Department of Biotechnology (DBT), India
Project- Structural and functional analysis of *M. tuberculosis* DprE1 and DprE2 enzymes involved in cell wall synthesis. *PI-Ajay K. Saxena & T. P. Singh*

2010-2013 Department of Science and Technology (DST), India.

Project- Structural and functional analysis of ERG oncoprotein: po- tential target to develop prostate cancer drug. *PI-Ajay K. Saxena*

2011-2014 Council of Scientific and Industrial Research (CSIR), India.
Project-Structure analysis of *M. tuberculosis* CarD protein: an essential regulator of rRNA transcription. *PI-Ajay K. Saxena*

2006-2009 Council of Scientific and Industrial Research (CSIR), India.
Project- Structure analysis of the Human Transporter Associated with Antigen Processing (TAP) protein. *PI-Ajay K. Saxena*

Research interests:

- Structural and functional analysis of disease related proteins from *M. tuberculosis*, *Malaria* and *cancer*
- Structure guided drug/vaccine development

Memberships of professional Societies:

- American crystallographic association
- European crystallographic association
- Asian crystallographic association

Adhoc reviewer:

- Nature Commun., PLoS One, BMC crystallography, Sci. Rep., Protein Science, IUCr journals

Undergraduate teaching

- Molecular Biophysics course to M. Phil
- Membrane Biochemistry to M.S.-IV year
- Structural & Molecular Biology course to M.S. (III) year
- Biophysics & Structural Biology course to M.S. (II) year
- Physics for Biologist course to M.S. (I) year
- Bioinformatics course to MS(III) year

Administrative Positions/Activities

- Member-House allotment committee (2018-2020)
- Member-Standing committee on recognized research institutes (2019-2021)
- Member-SCIC (July 26, 2018-2020)
- Member-SLS grievance committee (2019-2021)
- Member-Anti ragging committee, JNU (2019-2021)
- Member-Advisory committee AIRF (Nov 2017-2020)
- Member-purchase committee, SLS (2019-2021)
- Member-Budget and finance committee (2019)
- Member-School level grievance committee (2019)
- Member-Framing rule and disciplinary service in JNU (2018)
- Member-screening committee of selection of participant in HRDC (2018)
- Member- Purchase committee-SLS (2019)

Other Professional Activities

- Concurrent faculty-School of Sanskrit (2019-2021)
- External member, School of System Medicine, JNU (2021-)
- Proctor, Jawaharlal Nehru University (2019-2021)

- Academic Committee Member, IMTECH, Chandigarh, India (2019- 2021)
- Academic Committee Member, NII, New Delhi, India (2017- 2019)
- Academic Committee Member, CCMB, Hyderabad, India (2018- 2020)
- Academic Council Member, JNU, New Delhi (Feb 19, 2020-2022
- LEAP Program participant at JNU, New Delhi and NUS at Singapore (Feb 2019).

Conference organized

- National seminar on Crystallography (NSC-42 in 2012 GIAN course-2017
- Academic staff college refresher course-November 2018
- Summer school program-JNU-2019

No. of Ph. D./M. tech/MS

- Ph. D.- 8 students
- M. Tech.- **1**5 students
- M.S.- 15 students

RESEARCH ACCOMPLISHMENTS

Project 1. Structure-function analysis of *M. tuberculosis* drug/vaccine candidate proteins
The ESX-1 secretion system of *M. tuberculosis* delivers bacterial proteins into host cell during mycobacterial infection. The structure-function analysis of the protein will contribute significantly in designing therapeutics against *M. tuberculosis* disease.

P1. *M. tuberculosis* (i) Rv3868+EspC complex (ii) Rv3870+ Rv3871+ ESAT6 /CFP10 complex (iii) EspR regulator
In current project, we have structurally and functionally characterized the Rv3868 and Rv3870+Rv3871 of ESX-1 section system and their complexes with EspC and ESAT6/CFP10 virulence proteins.

P2. *M. tuberculosis* (i) GmhA/HddA/GimB (ii) DprE1/E2 enzymes involved in cell wall biogenesis
In current project, we have determined the low-resolution structure using SAXS, kinetic structurally and functionally characterized all enzymes (GmhA, HddA and GmhB) involved in GDP-heptose biosynthetic pathway and looking forward for specific inhibitor/drug development.

P3. *M. tuberculosis* (i) Rv0081/MprA/MprB transcription factors (iii) CarD/RNAP complex from stress regulatory system
In current project, we have structural and functionally characterized various transcription factors involved in ESX-1 regulation, stress regulation and dormant stage of mycobacteria.
(1) *Gangwar et. al., 2011, Acta Cryst, F, F67, 83-86* ***(2)*** *Gangwar et. al., 2014, Acta Cryst F, F70, 433-437* ***(3)*** *Gangwar et. al., Acta Cryst F70 (2014) 160-165* ***(4)*** *Meena et. al, 2016, J. Phys. Chem. Biophys. 6:3* ***(5)*** *Karan et. al., 2017, J. Mol. Model 23:241* ***(6)*** *Karan et. al., 2019, Int. J. Biol. Macromol 136 (2019) 676–685* ***(7)*** *Karan et. al., 2020, Scientific Report* ***(8)*** *Gangwar et. al., bioRxiv preprint, 2020* ***(9)*** *Karan et. al., 2021, Int. J. Biol. Macromol 171 (28-36)* ***(10)*** *Arkita et. al., 2021, Int. J. Biol. Macromol 189: 879–889****.***

Project 2. Structure-function analysis *Plasmodium* drug/vaccine candidate proteins:
The malaria vaccine developers around the world are trying to develop all three types of malaria vaccines, pre-erythrocyte, blood stage and transmission blocking. In current project, we are focusing on structural and biochemical studies on following vaccine candidate proteins,

P1. *Plasmodium* P25/P28 proteins and their complexes with transmission blocking antibodies.

In current project, we have functionally and structurally characterized the *Plasmodium* P25 and P28 proteins and their complexes with Fab fragment of transmission blocking antibodies.

(1) *Saxena et. al., Acta Cryst D60 2054, 2004* ***(2)*** *Saxena et. al., Cryst D60 706, 2004* ***(3)*** *Saxena et. al., (Struc. & Mol. Biol) 13(1), 2006* ***(4)*** *Saxena et. al., Eukar. Cell, 6(8), 2007* ***(5)*** *Sharma et. al., J. Mol. Model.15(4), 2009* ***(6)*** *Sharma et. al., J. Mol. Model. 15(3), 2009* ***(7)*** *Saxena et. al., Int. J. Biol. Macromol. 50, 2012.*

P2. *Plasmodium* cysteine proteases (i) Falstatin/Falcipain and (iii) Metacaspase2/ 3 enzymes.

In current project, we have functionally and structurally characterized the *Plasmodium* Falcipain-2/Falcipain-3 and Metacaspase-2/Metacaspase-3 enzymes

(1) *Sudararaj et. al., 2012, PLoS ONE, 7(10)* ***(2)*** *Sudararaj et. al., 2014, PLoS ONE, 9(4)* ***(3)*** *Vandana et. al., 2018, Molecular & Biochemical Parasitology 220: 28–41* ***(4)*** *Ahuja et. al., 2018, BBA-Molecular Cell Research 1865(8): 1148-1159* ***(5)*** *Pant et. al., 2018, Sci. Rep. 8:16193* ***(6)*** *Pasupureddy et. al., 2019, Experimental Parasitology 197:43-50* ***(7)*** *Bhumika et. al., 2019, Int. J. Biol. Macromol. 138: 309-320* ***(8)*** *Vandana et. al., 2021, The Journal of Biochemistry*

Project 3. Structure-function analysis of cancer related proteins

In cancer project, we have expressed, purified, biochemically characterized and solve the x-ray structure of Ergp55-DNA complex. Ergp55 is the most frequent proto-oncogenic alterations in prostate cancer cell and directly involved in prostate cancer. In research projects, we have crystallized and determined the X-ray structure of membrane yeast Sac1, Cdr1p and TAP proteins.

P1. Human antigenic peptide transporter TAP

P2. *C. albicans* Cdr1p multidrug transporter, Yeast Sac-1 enzyme

P3. Human Ergp55 oncoprotein

(1) *Manford et. al., 2010,* The EMBO Journal 29, 1489–1498 ***(2)*** *Gangwar et. al., 2011, Acta Cryst. F68,* 83-86 (***3)*** *Gangwar et. al., 2012, PLoS ONE 7(6), e39850* ***(4)*** *Meena et. al., 2012, Acta Crystallogr. Section F Biol. Crystallogr. F68, 655–658* ***(5)*** *Rawal et. al., 2013, J. Biol. Chem. 288(34), 24480-93* ***(6)*** *Shah et. al., 2015, Sci. Rep., 2015, 5:11211* ***(7)*** *Shah et. Al., 2015 FEMS Yeast Res. 15(5). pii: fov036* ***(8)*** *Rawal et. al., 2016, Sci. Rep. 6:27132* ***(9)*** *Sharma et. al., 2018, Acta Crystallogr. Section F Biol. Crystallogr. F74, 656-663* ***(10)*** *Sukrit et. al., 2020, J. Biomol. Struc. & Dynamics, DOI: 10.1080 /07391102.2020.1838329* (***11)*** *Sukrit et. al., JMIR Bioinformatics Biotechnol 2020 1(1): e19371* ***(12)*** *Sukrit et. al., 2019, J. Biomol. Struc. & Dynamics, 37(16): 4345–4360* ***(13)*** *Sukrit et. al., 2018, Infection and Drug Resistance 11: 1–15.* ***(14)*** *Jawa et al., 2021, Front. Oncol. 11:676948.*

PUBLICATIONS (# corresponding author)

2021

55. Sukrit Srivastava, **Ajay Kumar Saxena**, Michael Kolbe **(2021)** Exploring the structural basis to develop efficient multi-epitope vaccines displaying interaction with HLA and TAP and TLR3 molecules to prevent NIPAH infection, a global threat to human health. *BioRxiV preprint doi: https://doi.org/10.1101/2021.09.17.460735*

54. Jawa Y, Yadav P, Gupta S, Mathan SV, Pandey J, **Saxena AK**, Kateriya S, Tiku AB, Mondal N, Bhattacharya J, Ahmad S, Chaturvedi R, Tyagi RK, Tandon V and Singh RP **(2021)** Current Insights and Advancements in Head and Neck Cancer: Emerging Biomarkers and Therapeutics with cues From Single Cell and 3D Model Omics Profiling. *Front. Oncol. 11:676948.*

53. Arkita Bandhopadhyay and **Ajay K. Saxena# (2021).** Structural and ATPase activity analysis of nucleotide binding domain of Rv3870 enzyme of *M. tuberculosis* ESX-1 system. *Int. J. Biol. Macromol 189: 879–889.*

52. Arkita Bandhopadhyay and **Ajay K. Saxena# (2021).** Structural and biochemical analysis of ATPase activity and EsxAB substrate binding of *M. tuberculosis* EccCb1 enzyme. *BioRxiV preprint doi: https://doi.org/10.1101/2021.05.31.446396.*

51. Vandana, R. Pandey, Srinivasan E., I. Kalia, A. P Singh, **Ajay K. Saxena**, R. Rajaekaran, D. Gupta, K. C. Pandey **(2021).** *P. falciparum* Metacaspases-2 captures its natural substrate in a non-canonical way. *The journal of Biochemistry mvab086, https://doi.org/10.1093/jb/mvab086*

50. Sumita Karan, Ankita Behl, Amin Sagar, Arkita Bandhopadhyay, **Ajay K. Saxena# (2021).** Structural studies on *Mycobacterium tuberculosis HddA* enzyme using small angle X-ray scattering and dynamics simulation techniques, *Int. J. Biol. Macromol.171:28-36.*

2016-2020

49. S. Karan, B. Pratap, Shiv P. Yadav, FNU. Ashish & **Ajay K. Saxena# (2020).** Structural and functional characterization of *M. tuberculosis* sedoheptulose- 7-phosphate isomerase, a critical enzyme involved in lipopolysaccharide biosynthetic pathway. *Nature Sci. Rep. 10(1):20813.*

48. S. P. Gangwar, A. Bandyopadhyay and **Ajay K. Saxena# (2020**). Structural studies on *M. tuberculosis* decaprenyl phosphoryl-β-Dribose epimerase-2 enzyme involved in cell wall biogenesis. *bioRxiv preprint doi: https://doi.org/10.1101/2020.10.15.341941*

47. S. Srivastava, S. Verma, M. Kamthania , D. Agarwal , **Ajay K. Saxena** , M. Kolbe , S. Singh , A. Kotnis , B. Rathi , S. A. Nayar , H-J Shin , K. Vashisht & K. C. Pandey **(2020).** Computationally validated SARS-CoV-2 CTL and HTL Multi-Patch vaccines, designed by reverseepitomics approach, show potential to coverlarge ethnically distributed human population worldwide, *Journal of Biomolecular Structure and Dynamics, DOI: 10.1080 /07391102.2020.1838329*

46. Srivastava, S., Verma, S., Kamthania, M., Kaur, R., Badyal, R.K., **Saxena, A. K.,** Shin, H.J., Kolbe, M. and Pandey, K.C. **(2020).** Structural basis to design multi-epitope vaccines against Novel Coronavirus 19 (COVID19) infection, the ongoing pandemic emergency: an in-silico *approach*.
JMIR Bioinformatics Biotechnol 2020 1(1): e19371.

45. Srivastava, S., Kamthania, M., Kumar Pandey, Kumar R., **Saxena, A. K.,** Saxena, V., Kumar Singh, S., Kumar Sharma, R. and Sharma, N. **(2019).** Design of novel multi-epitope vaccines against severe acute respiratory syndrome validated through multistage molecular interaction and dynamics.
Journal of Biomolecular Structure and Dynamics, 37(16): 4345–4360.

44. Bhumika Kumar, Deepak Singla, Mohammad Kashif, Ruby Sharma, Rajnikant Dixit, Agam P. Singh, **Ajay K. Saxena**, Mohammad Abid, Kailash C. Pandey **(2019).** Metacaspase-3 of Plasmodium falciparum: An atypical trypsin-like serine protease.
Int. J. Biol. Macromol. 138: 309-320.

43. Sumita Karan, Bhanu pratap, Ashish, **Ajay K. Saxena# (2019).** Low-resolution SAXS and structural dynamics analysis on *M. tuberculosis* GmhB enzyme involved in GDP-heptose biosynthetic pathway.
Int. J. Biol. Macromol. 136: 676–685.

42. R. Pasupureddy, S.Verma, A. Pant, R. Sharma, **A. K. Saxena**, R. Dixit, S. Seshadri, K. C. Pandey (**2019**). Crucial residues in falcipains that mediates hemoglobin hydrolysis.
*Experimental Parasitology 197:43-*50*.*

41. A. Pant, R. Kumar, N.Ahmed Wani, S. Verma, R. Sharma, S. Sharma, V. Pande, **A. K. Saxena**, R. Dixit, R.K. Rai and K. C. Pandey **(2018).** Allosteric Site Inhibitor Disrupting Auto-processing of Malarial Cysteine Proteases
Nature Sci. Rep. 8: 16193.

40. S. Srivastava, M. Kamthania, **A. K Saxena**, N. Sharma **(2018).** *In silico* approach to develop a Multi-Epitope Vaccines against MERS Coronavirus satisfying human HLA, TAP and TLR-3 checkpoints
Infection and Drug Resistance 11: 1–15.

39. R. Sharma, S. P. Gangwar, **A. K. Saxena# (2018)**. Comparative structure analysis of ETSi domain of ERG3 and its complex with E74 promoter DNA sequence
Acta Crystallogr. Section F Biol. Crystallogr. F74: 656-663.

38. K. Ahuja, M. A. Beg, R. Sharma, **A. K. Saxena**, N. Naqvi, N. Puri, A. Chaudhury, R. Duncan, P. Salotra, H. Nakhasi, A. Selvapandiyan **(2018).** Importance of threshold expression of a novel trypanosome specific glycosomal protein for the growth of *Leishmania donovani* parasites.
BBA-Molecular Cell Research 1865(8):1148-1159.

37. Vandana, A. P. Singh, J. Singh, R. Sharma, M. Akhter, P. K. Mishrag, **A. K. Saxena**, R. Dixit, B. Rathie, A. Katyalf, K. C. Pandey **(2018).** Biochemical characterization of unusual cysteine protease of *P. falciparum*, metacaspase-2 (MCA-2)
Molecular & Biochemical Parasitology 220: 28–41.

36. S. Karan, V. K. Kashyap, S. Shafi and **A. K. Saxena# (2017**). Structural and inhibition analysis of novel sulfur rich 2-mercapto benzothiazole and 1,2,3- triazole ligands against *Mycobacterium tuberculosis* DprE1 enzyme.
J. Mol. Model. 23:241.

35. M. K. Rawal, A. Banerjee, A. H. Shah, M. F. Khan, S. Sen, **A. K. Saxena**, B. C. Monk, R. D. Cannon, R. Bhatnagar, A. K. Mondal & R. Prasad **(2016**). Newly identified motifs in *Candida albicans* **Cdr1** protein nucleotide binding domains are pleiotropic drug resistance subfamily-specific and functionally asymmetric.
Nature Sci. Rep. 6:27132.

34. S. R. Meena and **A. K. Saxena**# **(2016).** Structure of *E. coli* **GroEL** in substate and ADP unloaded state (**PDB-4HEL)**
J. Phys. Chem. Biophys. 6:3

2011-2015

33. A. H. Shah, M. K. Rawal, **A. K. Saxena,** Mondal, A. and R. Prasad **(2015).** ABC transporter ***Cdr1p*** harbors a critical acid/base pair of between intracel- lular loop and nucleotide-binding domain important for protein trafficking.
FEMS Yeast Res. 15(5). pii: fov036.

32. A. H. Shah, M. K. Rawal, S. Dhamgaye, S. S. Komath, **A. K. Saxena** and R. Prasad **(2015).** Mutational Insight into Intracellular loops defines cross talk between NBDs and ICLs of the yeast ABC transporter ***Cdr1p***
Nature Sci. Rep. 5: 11211.

31. S. Sundararaj, **A. K. Saxena**, R. Sharma, K. Vashisht, S. Sharma, A. Anvikar, R. Dixit, K. C. Pandey **(2014).** Hydrophobic interaction and hydrogen bond within the BC loop are interacting within the active site of ***cysteine proteases*** of ***P. falciparum*** and ***P. vivax***
PLoS ONE, 9(4): e93008.

30. S. P. Gangwar, S. R. Meena and **A. K. Saxena#(2014).** Comparison of differ- ent crystal forms of ESX-1 secreted protein regulator ***EspR*** from *M. tuberculo- sis* and its implication for protein regulator activity **(PDB-4NDW)**
Acta Crystallogr. Section F Biol. Crystallogr. F70, 433-437.

29. S. P. Gangwar, S. R. Meena and **A. K. Saxena#(2014**). Crystal structure of carboxy-terminal domain of *M. tuberculosis* ***CarD*** protein: an essential rRNA transcriptional regulator **(PDB-4KMC).**
Acta Crystallogr. Section F Biol. Crystallogr. F70, 160-165.

28. M. K. Rawal, M. F. Khan, K. Kapoor, N. Goyal, S. Sen, **A. K. Saxena**, A. M. Lynn, Joel D. A., Tyndall, B. C., Monk, R. D. Cannon and R. Prasad (**2013**). Insight into PDR ABC pump drug transport through mutagenesis of **Cdr1p** transmembrane domains
J. Biol. Chem. 288(34),2448093.

27. Gangwar, S. P., Dey, S. and **Saxena, A. K.# (2012).** Structural modeling and DNA binding auto-inhibition analysis of **Ergp55,** a critical transcription factor in prostate cancer.
PLoS ONE 7(6): e39850.

26. S. Sundararaj, D. singh, **A. K. Saxena**, P. S. Sijwali, R. Dixit, K. C. Pandey **(2012).** The ionic and hydrophobic interactions are required for the activation of cysteine proteases of *P. falciparum*.
PLoS ONE 7(10): e7227.

25. **A. K. Saxena# (2012).** Structure of Fab fragment of malaria transmission- blocking antibody 2A8 against ***P. vivax* P25** protein. **(PDB-3S62)**
Int. J. Biol. Macromol. 50, 153-156.

24. Sita R. Meena, S. P. Gangwar and **A. K. Saxena# (2012).** Purification, crystallization and preliminary x-ray crystallographic analysis of ATPase domain of **TAP** in nucleotide free, ADP, vanadate and azide inhibited form.
Acta Crystallogr. Section F Biol. Crystallogr. F68, 655-658.

23. S. P. Gangwar, Sita R. Meena and **A. K. Saxena# (2012).** Purification, crystallization and preliminary X-ray crystallographic analysis ETS domain of **Ergp55** in complex with cfos promoter DNA sequence.
Acta Crystallogr. Section F Biol. Crystallogr. F68, 1333-1336.

22. **A. K. Saxena# (2012).** Structural and functional analysis of key proteins in- volved in **ESX-1** secretion system of *M.tuberculosis:* novel targets for drug de- velopments
J. Anal. Bioanal. Techniques 3, 7 (Conference paper)

21. S. P. Gangwar, S. R. Meena and **A. K. Saxena# (2011).** Cloning, purification, crystallization and preliminary x-ray analysis of **EspR:** a secreted transcrip- tion factor from *M. tuberculosis*.
Acta Crystallogr. Section F Biol. Crystallogr. F67, 83-86.

20. **A. K. Saxena#** and S. P. Gangwar **(2011).** Structural and functional dissection of **Ergp55** oncoprotein.
J. Anal. Bioanal. Techniques 2, 6 (Conference paper)

2006-2010

19. A. Manford, T. Xia, **A. K. Saxena**, C. Stefan, F. Hu, S. D. Emr and Y. Mao (2010). Crystal structure of the yeast **Sac1**: implications for its phosphoinositide phosphatase function **(PDB-3LWT).**
EMBO J. 29(9), 1489-1498.

18. Sharma, B., Ambedkar R. D. and **Saxena, A. K.#** (2009). A very large C-loop in EGF domain IV is characteristic of the *Plasmodium* **P28** family of ookinete surface proteins.
J. Mol. Model 15(3), 309-321.

17. Sharma B., Jaiswal M. K. and **Saxena, A. K.#** (2009). EGF domain II of protein **Pb28** from *P. berghei* interacts with monoclonal transmission blocking anti- body 13.1.
J. Mol. Model 15(4), 369-382.

16. **Saxena, A. K.#**, Yimin, W. and Garboczi, D. N. (2007). *Plasmodium* **P25 and P28** surface proteins: Potential malaria transmission blocking vaccines.
Eukaryotic Cell 6(8), 1260-1265.

15. **Saxena, A. K.#,** Singh, K., Su, H.P., Klein, M. M., Stower, A. W., Saul, A. J., Long, C. and Garboczi, D. N. (2006). *Plasmodium* **P25 and P28**, essential pro- teins for survival of the malaria parasite in the mosquito are tile-like triangular prism **(PDB-1Z27, 1Z1Y, 1Z3G).** *Nature (Struc. & Mol. Biol.) 13(1), 90-91.*

14. C. Chen, **A. K. Saxena**, W. N. Simcoke, D. N. Garboczi, P. L Pedersen and Y. H. Ko (2006). MITOCHONDRIAL ATP SYNTHASE: crystal structure of the catalytic **F1 unit** in a Vanadate-induced transition-like state and implications for mechanism **(PDB-2F43).** *J. Biol. Chem. 281(19), 13777-13783.*

2001-2005

13. **Saxena, A. K.,** Singh, K., Long, C. and Garboczi, D. N. **(2004).** Preparation, crystallization and preliminary x-ray analysis of complex between antibody and *P. vivax* sexual stage 25kDa protein **Pvs25** and malaria transmission- blocking antibody Fab fragment. *Acta Crystallogr. D Biol. Crystallogr. D60, 2054-2057.*

12. **Saxena, A. K.,** Saul, A. and Garboczi, D. N. (**2004**). Crystallization and pre- liminary X-ray analysis of the *P. vivax* sexual stage 25kD protein, **Pvs25**, a transmission-blocking vaccine candidate for malaria. *Acta Crystallogr. D Biol. Crystallogr. D60, 706-708.*

1996-2000

11. **Saxena, A. K.,** Gries A, Schwarzenbacher, R., Kostner, G. M., Laggner, P. and Prassl, R. (**1998).** Crystallization and preliminary X-ray crystallographic stud- ies on **Apolipoprotein-H** from human plasma. *Acta Crystallogr. D Biol. Crystallogr. D54, 1450-1452.*

10. Prassl, R., Chapman, J M., Nigon, F., Sara, M., Eschenburg, S., Betzel, C., **Saxena, A. K.** and Laggner, P. (**1996).** Crystallization and preliminary X-ray analysis of Low Density Lipoprotein **(LDL)** from human plasma. *J. Biol. Chem. 271(46), 28731-28733.*

9. **Saxena, A. K**., Singh, T. P., Peters, K., Fittkau, S., Visanji, M., Wilson, K. S. and Betzel, C. (**1996**). Structure of a ternary complex of **Proteinase K**, Hg and a substrate analogue hexapeptide N-Ac-Pro-Ala-Pro-Phe-Pro-Ala-NH_2 at 2.2-Å resolution **(PDB-1PJ8).** *Proteins, Struc. Funct. & Genet. 25 (2), 195-201.*

8. **Saxena, A. K.,** Singh, T. P., Peters, K., Peters, K., Fittkau, S. and Betzel, C. (**1996**). Strategy to design peptide inhibitors: Structure of the complex of **Proteinase K** with designed octapeptide inhibitor N-Ac-Pro-Ala-Pro-Phe-DAla- (Ala)3-NH_2 at 2.5 Å resolution **(PDB-1PFG).** *Protein Science 5, 2453-2458.*

7. Singh, T. P. Padmanabhan, B. Narula, P**. Saxena, A. K.,** Betzel, C., Sharma, P. and Dey, S. (**1996**). Design of a specific peptide structure and **subtilisin** in- hibitor using dehydro residues.

Adv. Exp. Med. Biol. 379, 11-20.

1990-1995

6. **Saxena, A. K.,** Sharma, P. and Singh, T. P. (1995). Solid-state conformation of model dehydro-Phe containing peptide N-Ac-dehydro-Phe-L-Val-OH/ OCH_3 in various solvents.
Ind. J. Phys. 69A(3), 307-321.

5. Khanna, A., Khandelwal, B. L., **Saxena, A. K., and** Singh, T. P. (1995). Di-chloro methane assisted oxidation of Pt (O) via cleavage of Te-Carbonyl bond of an asymmetric Telluride leading to the formation of Trans-$[PtCl(Ar)(PPh_3)_2]$.
Polyhedron 14, 2705-2710.

4. Singh, A. K., Srivastava, V., Basumatary, J. K., Singh, T. P. and **Saxena, A. K.** (1994). Triphenyl Tellurium (IV) diethyldithiocarbamate: Synthesis and crys- tal structure of new example showing sterically sensitive long Te-S bonds.
Phosphorous Sulfur and Silicon 89, 31-37.

3. **Saxena, A. K.,** Singh, T. P., Betzel, Ch., Visanji, M., Peters, K. and Fittkau, S. (1993). Structure of a ternary complex of **Proteinase K**, Hg^{2+} and substrate analogue hexpeptide N-Ac-Pro-Ala-Pro-Phe-Pro-Ala-NH_2.
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2021 **Saxena A. K. (2021**) Workshop on "*Strategy for future EMBL research in the Life Sciences in Hamburg,* March 29, Hamburg, Germany.

2021 **Saxena, A. K. (2021)** *14th International Symposium on Cancer Prevention and Therapeutics*, Jawaharlal Nehru University, March 16-17, New Delhi, India.

2020 Arkita Bandyopadyay and **Ajay K. Saxena (2020).** *India-EMBO symposium on Microbial heterogeneity and Host tissue Tropism,* 11-15 February, New Delhi.

2019 Ajay K. Saxena **(2019)** Invited talk on Structure and biochemical analysis of Plasmodium cysteine proteases and its complexes with inhibitors/substrates, National, *Indian Society for Parasitology (ISP) and Special Centre for Molecular Medicine (JNU)Global impact of parasitic pathogens*, September 26, JNU, New Delhi.

2019 Sumita Karan and Ajay K. Saxena **(2019)** Structure function analysis of enzymes involved in GDP-heptose biosynthetic pathway, *Biospark,* JNU, New Delhi.

2018 Ruby Sharma, Kailash C. Pandey and **Ajay K. Saxena** (**2018).** Crystal structure and biochemical analysis of *P. falciparum* cysteine protease Inhibitor Falstatin and its complex with cysteine protease (s). *46th National Seminar on Crystallography (NSC), June 2018* at NIMHANS, Bengaluru.

2018 Ruby Sharma, Kailash C. Pandey and **Ajay K. Saxena (2018).** Crystal structure and biochemical analysis of *P. falciparum* cysteine proteases and its complexes with inhibitors/substrates. *Science Day Celebrations* at Jawaharlal Nehru University, New Delhi , 28 Feb, 2018.

2018 Ruby Sharma, Srinivasan Sundararaj, Kailash C. Pandey, **Ajay K. Saxena (2018).** Crystal structure and biochemical analysis of *Plasmodium falciparum* falstatin in complex with *Plasmodium* cysteine proteases FP2 and FP3. Poster presentation at *Science Day Celebrations* at Jawaharlal Nehru University, 28 Feb, New Delhi.

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2015 Shanti P. Gangwar, Ruby Sharma and **Ajay K. Saxena (2015)**. Structural and functional Analysis of human Ergp55 oncoprotein. International Symposium on **"***Current Advances in Radiobiology, Stem Cells and Cancer Research" organised by Cancer Research and Care Academy (CRCA)***,** February 19-21, 2015, School of Life Sciences, Jawaharlal Nehru University, New Delhi.

2015 Ruby Sharma, Shanti P. Gangwar and **Ajay K. Saxena (2015)**. Structural and functional Analysis of human Ergp55 oncoprotein. Poster Presenta- tion (EMP139) *at 56th Association of Microbiologists of India (AMI*) 8-10th December, 2015, Jawaharlal Nehru University, New Delhi.

2015 Ruby Sharma**,** Shanti P. Gangwar and **Ajay K. Saxena.** Structural and functional Analysis of human Ergp55 oncoprotein. Poster Presentation at *International Symposium on Current Advances in Radiobiology, Stem Cells and Cancer Research***,** February 19-21, 2015, School of Life Sciences, Jawaharlal Nehru University, New Delhi.

2015 Shanti P. Gangwar, Ruby Sharma and **Ajay K. Saxena**. Structural and functional Analysis of human Ergp55 oncoprotein. *56th International Conference "Association of Microbiologists of India (AMI) 2015*" 07 -10 December, 2015 at JNU Convention Centre, New Delhi, India.

2014 Ruby Sharma**,** Srinivasan Sundararaj, Kailash C. Pandey and **Ajay K.Saxena (2014)** Mechanism of Interaction of Falstatin, PlasmodiumCyste- ine Protease Inhibitor with Cysteine Protease(s). Poster Presentation at Indo US Conference **a**nd Workshop on *Recent Advances on Structural Bi- ology & Drug Discovery* on Oct 9-11, 2014 at Department of Biotechnology, IIT Roorkee, India.

2013 **Ajay K. Saxena et. al.,** Structure and function analysis of human Ergp55 oncoprotein, a critical transcription factor involved in prostate cancer *American Society of Cell Biology Annual Meeting*" held on December 14-18, 2013, New Orleans, LA, **USA.**

2012 **Ajay K. Saxena *et. al.,*** New insights in understanding the structure and mechanism of *Plasmodium* P25 and P28 proteins. ***Gordon research conference*** on host-parasite interaction, biology of, June 10-15, Salver Regina University, Providence, RI, **USA.**

2012 Shanti P. Gangwar, Sharmistha Dey and **Ajay K. Saxena.** Structural and functional dissection of Ergp55 protein. *National symposium of microbes in Health and Agriculture*, March 12-13, JNU, New Delhi, **India.**

2012 Shanti P. Gangwar, Sita R. Meena and **Ajay K. Saxena.** Structure and functional analysis of key proteins involved in *Mtb* ESX-1 protein export pathway: potential drug targets. *National symposium of microbes in Health and Agriculture*, March 12-13, JNU, New Delhi, **India.** (*Best poster presentation award*)

2011 Shanti P. Gangwar, Sita R. Meena and **Ajay K. Saxena.** Structural and functional analysis of secreted transcription factor EspR of *M. tuberculosis*. *Indo-NIAID Forum on TB drug discovery research*, April 20-21, New Delhi, **India.**

2010 Shanti P. Gangwar, Sita R. Meena and **Ajay K. Saxena.** Structural and functional analysis of EspR: a secreted transcription factor that control *M. tuberculosis* virulence. ***Gordon research Conference*** on Diffraction methods in Structural Biolo- gy, July 18-23, Lewiston, ME, **USA.**

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2010 Sita R. Meena, Shanti P. Gangwar and **Ajay K. Saxena.** Elucidation the mechanism of ATP hydrolysis cycle of the Transporter Associated with Antigen Processing (TAP). *4th International symposium on recent trends in macromolecular structure and function,* January 21-23, Chennai, **India.** (*Best poster presentation award*)

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2007 **Saxena, A. K.,** Sharma, B. and Amabedkar, R. Structure of P25 proteins from *Plasmodia* and their interactions with transmission-blocking antibodies: a molecular modeling and docking study.
One Hundred Years of Tropical Medicine, London, **UK.**

2003 *31st Annual Mid-Atlantic Protein Crystallography Workshop*, Durham, North Carolina, USA, June 22-23, 2003.

2002 *30th Annual Mid-Atlantic Protein Crystallography Workshop*, NCI-Frederick, Maryland, USA, May 3-4, 2002.

2001 *29th Annual Mid-Atlantic Protein Crystallography Workshop*, College of Wil- liam and Mary, Williamsburg, Virginia, USA, May 23-25, 2001.

1999 *Workshop on ABC Transporters and Human Diseases*, Division of Basic Sci- ences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA, Sept. 12-14, 1999.

1999 *Workshop on Membrane Proteins*, 7th Floor, Clark Hall, Cornell University, Ithaca, New York, USA, June 22-23, 1999.

1999 *Mid-Atlantic Workshop,* Centre for Advanced Research in Biotechnology (CARB), Maryland, USA, April 28-30, 1999.

1999 *Second AAPS frontier symposium: Membrane Transporter and Drug Therapy*, National Institute of Health, Bethesda, Maryland, USA, 8-10 April, 1999.

1999 *Gordon Research Conference*: Ligand Recognition and Molecular Gating, Ventura, California, USA, 7-12 March 1999.

1998 *American Crystallographic Association (ACA) Annual Meeting*, Arlington, Virginia, USA, 18-23 July, 1998.

1998 *Mid-Atlantic Workshop John Hopkins University*, Baltimore, Maryland, USA, 11-13June, 1998.

1997 **Saxena, A. K.,** Prassl, R., Chapman, J. M., Sara, M. and Laggner, P.; Crys- tallization and Preliminary X-ray Analysis of Human Plasma Low Densi- ty Lipoprotein.

Seventeenth European Crystallographic Meeting (ECM-17) I. S. T. Lisbon- Portugal, 24- 28 August 1997.

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1995 **Saxena, A. K.,** Betzel, Ch. and Singh, T. P. ; Structures of the complexes of Proteinase K and designed Oligopeptides. *International Seminar-Cum School on Macromolecular Crystallographic Data*, Saha Institute of Nuclear Physics, Calcutta, 16-20 November 1995.

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XXII National Seminar on Crystallography, Indian Association for Cultivation of Science, Jadavpur, Calcutta, 26-28 December 1990. This paper has been adjudged best in the poster session.