ESRF BLOCK ALLOCATION GROUP: PROGRESS REPORT

BAG RESPONSIBLE:
PROPOSAL REF.: 39378 (continuation of MX-1627)

SHIFT USAGE SINCE LAST BIANUAL REVIEW:

Allocated:	17	**Cancelled By Users:**	0	**Total Number Of Visits:**	16
Scheduled:	18	**Cancelled By ESRF:**	0	**Total Number Of Visitors:**	18
Used:	18				

COMMENT ON SHIFTS:

BAG PRINCIPAL INVESTIGATORS: (L) = no longer active in the BAG, (N) = new since last review

• L. ESSEN, Philipps-Universitaet Marburg Fachbereich Chemie Hans Meerwein Strasse Marburg/Lahn DE - 35032 MARBURG

• G. KLEBE, Philipps-Universitaet Marburg Institut fuer Pharmazeutische Chemie Marbacher Weg 6 DE - 35032 MARBURG

• K. REUTER, Philipps-Universitaet Marburg Institut fuer Pharmazeutische Chemie Marbacher Weg 6 DE - 35032 MARBURG

• A. HEINE, Philipps-Universitaet Marburg Institut fuer Pharmazeutische Chemie Marbacher Weg 6 DE - 35032 MARBURG

• G. BANGE, Philipps University Marburg LOEWE Zentrum für Synthetische Mikrobiologie Hans-Meerwein-Str DE - 35043 MARBURG

• V. SRINIVASAN, Philipps University Marburg LOEWE Zentrum für Synthetische Mikrobiologie Hans-Meerwein-Str DE - 35043 MARBURG

FROM DATA COLLECTED ON ESRF BEAMLINES SINCE LAST REPORT:

Total number of PDB submissions:	Total number of publications:
23	11

FIVE MOST IMPORTANT PUBLICATIONS directly resulting from data recorded either wholy or partially on ESRF beamlines - (1): ESRF data only, (2): from more than one source

• MinD-like ATPase FlhG effects location and number of bacterial flagella during C-ring assembly | Schuhmacher J.S., Rossmann F., Dempwolff F., Knauer C., Altegoer F., Steinchen W., Dorrich A.K., Klingl A., Stephan M., Linne U., Thormann K.M., Bange G. | Proceedings of the National Academy of Sciences of the USA, vol.112, p.3092-3097, 2015 (1)

• Co-translational capturing of nascent ribosomal proteins by their dedicated chaperones | Pausch P., Singh U., Ahmed Y.L., Pillet B., Murat G., Altegoer F., Stier G., Thoms M., Hurt E., Sinning I., Bange G., Kressler D. | Nature Communications, vol.6, p.7494-1-7494-15, 2015 (1)

• A synthetic adenylation-domain-based tRNA-aminoacylation catalyst | Giessen T.W., Altegoer F., Nebel A.J., Steinbach R.M., Bange G., Marahiel M.A. | Angewandte Chemie International Edition, vol.54, p.2492-2496, 2015 (1)

• Interactions by the fungal Flo11 adhesin depend on a fibronectin type III-like adhesin domain girdled by aromatic bands | Kraushaar T., Brückner S., Veelders M., Rhinow D., Schreiner F., Birke R., Pagenstecher A., Mösch H.U., Essen L.O. | Structure, vol.23, p.1005-1017, 2015 (1)

• Structural and evolutionary aspects of antenna chromophore usage by class II photolyases | Kiontke S., Gnau P., Haselsberger R., Batschauer A., Essen L.O. | Journal of Biological Chemistry, vol.289, p.19659-19669, 2014 (1)

SUMMARY OF THE RESULTS OBTAINED SINCE LAST BIANUAL REVIEW:

Major contributions from the Bange group include: i) crystal structures of the ATPase FlhG that determines place and number of bacterial flagella (Schuhmacher, PNAS, 2015); ii) structure of a t-RNA binding module for the rational design of a new catalyst (Giessen, Ang. Chem. Int. Ed., 2015); iii) A ribosomal chaperone that guides ribosomal protein 10 during ribosome assembly (Pausch, Nature Communications, 2015); iv) structural determination of catalytic mechanism/allosteric regulation of the central pppGpp synthetase RelP (Steinchen, PNAS, 2015, final revision).
Several crystal structures have been determined for flagellar type III secretion (fT3SS)/ biofilm formation (bioF) and bacterial cell division (Div) that are partially submitted to PDB and await publication (e.g., 5DMB, 5DMD). Several structures of fungal effectors (FVF) are finished and await publication.
BioSAXS was successfully applied to several projects: In particular, we could structurally determine: i) several complexes involved the post-transcriptional regulation and targeting of Flagellin to the fT3SS (2 manuscripts in prep./submitted); ii) an essential complex for biofilm formation (in prep.).

Major contributions from the Essen group include the structures of: i) fungal Flo11 adhesin, and flocculin-like adhesins (Kraushaar, Structure, 2015; Kock, 2015, submitted); ii) an engineered, minimal channel porin (Grosse, Biochemistry, 2014); iii) phytochromes and photoreceptors (Kionetke, 2015, JBC; Banerjee, 2015, in rev.). Several more structures await publication (including: animal-like cryptochromes, protein phosphatase PPP5, asymmetric SDH heterotetramer BbsCD).
BioSAXS was successfully applied to determine the models of i) ABfR1 and the ABfR1/DNA; ii) the Aureochrome 1a alone and complexed to AUREO-box DNA (2 manuscripts are in prep.).

Srinivasan could determine structures of the early-acting components of the mitochondrial iron-sulfur cluster (ISC) assembly machinery that synthesizes a [2Fe-2S] cluster on the scaffold protein Isu1 (in preparation). These steps critically rely on the cysteine desulfurase Nfs1-Isd11 (as a sulfur donor), the ferredoxin Yah1 (as electron donor for sulfur reduction), and Yfh1 (frataxin) for the sulfur transfer from Nfs1 to Isu1. BioSAXS was successfully applied to structurally determine the entire ISC biosynthetic complex Nfs1-Isd11, Yah1, Yfh1, and Isu1. The data reveal a first 3D picture of the orientation of these components, and, together with comprehensive biochemical studies, allow the proposal of a mechanism of ISC formation on Isu1 (manuscript in prep.). Furthermore, structural analysis of the central ABC-transporter Atm1 in complex with substrate and/or nucleotides was carried on.

Klebe and coworkers could determine several high-resolution structures of Factor XIII complexed with medically relevant compounds for the development of anti-coagulants (in prep.).

The Reuter group could collect several datasets for t-RNA-guanine transglycosylase (TGT) for the development of Shigelliosis inhibitors.

The Heine group could make significant progress in determining the structure of mQTRT, the non-catalytic subunit of the TGT from mouse, at reasonable resolution (in prep.). Furthermore, they could determine several high-resolution datasets of Proteinkinase A complexed with ligands for inhibitor development (in prep.).

BEAMLINE PERFORMANCE:

We are very positive about the excellent assistance by the beamline staff that was helpful in the case of difficult data collections and hardware issues. The automatic data processing is a great help.

Beamline equipment is world class and we always enjoy measuring at the ESRF.

The recent installation of the MASSIF beamlines is a great advance for high-throughput data collection. We were also impressed that samples that could not be measured during our shifts, were stored and still measured at a later time point. Thank you so much! We will require even more in the near future for the high-throughput structural determination of medically relevant targets.

Negative: The EHO called to hardware problems during late night spoke only poor-English.