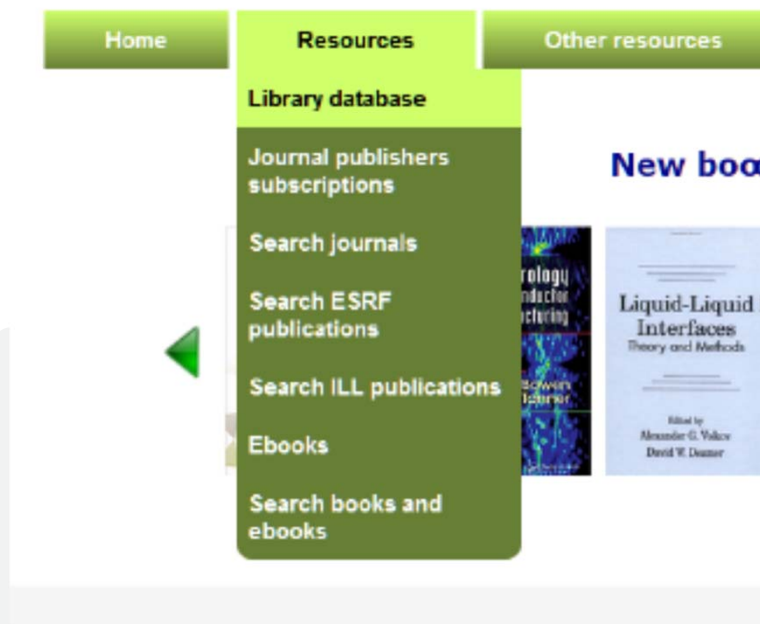


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and or not Authors Country and

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and or not Exact Journal or Serie's title and

and or not Bibliographic Information (journal, book, conference) and

and or not

Document Type

- All
- Publications with ESRF author(s) and describing an ESRF experiment
- Publications without ESRF author(s) and describing an ESRF experiment
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Publication year

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You can search for several beamlines at once:

ESRF publications: Complex search

Beamline or

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Document Type

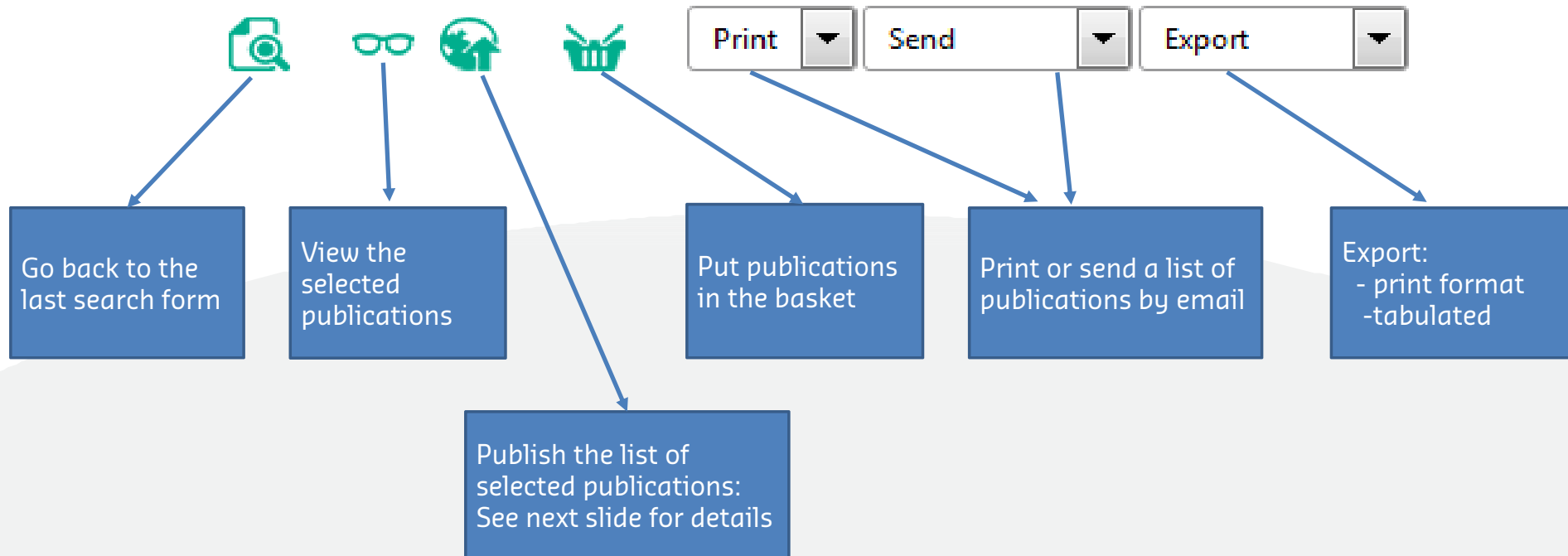
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By clicking on  , you can:

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Only 100 results per page are displayed.

The screenshot shows a search results interface with the following elements:

- Top navigation: Print, Send, Export, 100 Records per page.
- Sorting: Ascending sort, Descending sort, and a plus sign.
- Selection: A "Select all" checkbox.
- Results list (5 items shown):
 - 1. Ababou A., Koronakis V. - Structures of gate loop variants of the AcrB drug efflux pump bound by erythromycin substrate. PloS One **11**, e0159154-1-e0159154-8(2016). DOI. Open Access.
 - 2. Abate F., Cozzi R., Maritan M., Lo Surdo P., Maione D., Malito E., Bottomley M.J. - Crystal structure of FhuD at 1.6 Å resolution: A ferrichrome-binding protein from the animal and human pathogen Staphylococcus pseudintermedius. Acta Crystallographica F **72**, 214-219(2016). DOI.
 - 3. Abd El-Moemen A., Abdel-Mageed A.M., Bansmann J., Parlinska-Wojtan M., Behm R.J., Kucerova G. - Deactivation of Au/CeO2 catalysts during CO oxidation: Influence of pretreatment and reaction conditions. Journal of Catalysis **341**, 160-179(2016). DOI.
 - 4. Abdoulghafour H., Gouze P., Luquot L., Leprovost R. - Characterization and modeling of the alteration of fractured class-G Portland cement during flow of CO2-rich brine. International Journal of Greenhouse Gas Control **48**, 155-170(2016). DOI.
 - 5. Abes M., Koops C.T., Hrkac S.B., McCord J., Urs N. O., Wolff N., Kienle L., Ren W. J., Bouchenoire L., Murphy B.M., Magnussen O.M. - Domain structure and reorientation in CoFe2O4. Physical Review B **93**, 195427-1-195427-7(2016). DOI.
- Footer: 1589 (Total : 1589) Page 1 of 16.

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↓ Ascending sort : ▼ ↑ Descending sort : ▼ +

Ababou A., Koronakis V. - Structures of gate loop variants of the AcrB drug efflux pump bound by erythromycin substrate

1 PloS One **11**, e0159154-1-e0159154-8(2016)  Open Access

DOI

Abate F., Cozzi R., Maritan M., Lo Surdo P., Maione D., Malito E., Bottomley M.J. - Crystal structure of FhuD at 1.6 Å resolution: A ferrichrome-binding protein from the animal and human pathogen *Staphylococcus pseudintermedius*

2 Acta Crystallographica F **72**, 214-219(2016)

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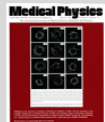
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New Scientist, Issue 3101 J. Phys. Soc. Japan, Issue 9 Physik Journal, Issue 12 Powder Diffraction, Issue 3 Z. Kristallographie, Issue 11 Medical Physics, Issue 10 Reflets de la physique, September

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 **Open Access** Agrawal N., Lehtonen S.I., Uusi-Mäkelä M., Jain P., Viitala S., Määttä J.A.E., Kähkönen N., Azizi L., Riihimäki T.A., Kulomaa M.S., Johnson M.S., Hytönen V.P., Airene T.T. - Molecular features of steroid-binding antidins and their use for assaying serum progesterone
[PloS One](#)  **14**, e0212339-1-e0212339-27 (2019)

Number: ESRF19AG1419

Beamline: ID30A-3

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Facility used: ESRF (Grenoble)

Abstract: Chicken avidin (Avd) and streptavidin from *Streptomyces avidinii* are extensively used in bionanotechnology due to their extremely tight binding to biotin (K-d similar to 10⁻¹⁵ M for chicken Avd). We previously reported engineered Avds known as antidins, which have micro- to nanomolar affinities for steroids, non-natural ligands of Avd. Here, we report the 2.8 angstrom X-ray structure of the sbAvd-2 (1117Y) antidin co-crystallized with progesterone. We describe the creation of new synthetic phage display libraries and report the experimental as well as computational binding analysis of progesterone-binding antidins. We introduce a next-generation antidin with 5 nM binding affinity for progesterone, and demonstrate the use of anti dins for measuring progesterone in serum samples. Our data give insights on how to engineer and alter the binding preferences of Avds and to develop better molecular tools for modern bionanotechnological applications.

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