



## Fatima Pardo Avila

Basic Life Research Scientist, Structural Biology

### Publications

---

#### PUBLICATIONS

- **Quasi-continuous cotranslational compaction and folding of a multidomain protein.** *bioRxiv : the preprint server for biology*  
Mitsikosta, S., Westerfield, J. M., Pardo-Avila, F., Levitt, M., von Heijne, G., Metola, A.  
2026
- **Integrating computational design with crystallographic validation.** *Methods in enzymology*  
Watson, P. R., Pardo-Avila, F., Hosseinzade, P.  
2025; 723: 111-124
- **Single-residue effects on the behavior of a nascent polypeptide chain inside the ribosome exit tunnel.** *bioRxiv : the preprint server for biology*  
Pardo-Avila, F., Kudva, R., Levitt, M., von Heijne, G.  
2024
- **Probing Interplays between Human XBP1u Translational Arrest Peptide and 80S Ribosome.** *Journal of chemical theory and computation*  
Di Palma, F., Decherchi, S., Pardo-Avila, F., Succi, S., Levitt, M., von Heijne, G., Cavalli, A.  
2021
- **Anchor extension: a structure-guided approach to design cyclic peptides targeting enzyme active sites.** *Nature communications*  
Hosseinzadeh, P., Watson, P. R., Craven, T. W., Li, X., Rettie, S., Pardo-Avila, F., Bera, A. K., Mulligan, V. K., Lu, P., Ford, A. S., Weitzner, B. D., Stewart, L. J., Moyer, et al  
2021; 12 (1): 3384
- **8-oxo-guanine DNA damage induces transcription errors by escaping two distinct fidelity control checkpoints of RNA polymerase II.** *The Journal of biological chemistry*  
Konovalov, K. A., Pardo-Avila, F., Tse, C. K., Oh, J., Wang, D., Huang, X.  
2019
- **De novo design of potent and selective mimics of IL-2 and IL-15** *NATURE*  
Silva, D., Yu, S., Ulge, U. Y., Spangler, J. B., Jude, K. M., Labao-Almeida, C., Ali, L. R., Quijano-Rubio, A., Ruterbusch, M., Leung, I., Biary, T., Crowley, S. J., Marcos, et al  
2019; 565 (7738): 186+
- **De novo design of potent and selective mimics of IL-2 and IL-15.** *Nature*  
Silva, D., Yu, S., Ulge, U. Y., Spangler, J. B., Jude, K. M., Labao-Almeida, C., Ali, L. R., Quijano-Rubio, A., Ruterbusch, M., Leung, I., Biary, T., Crowley, S. J., Marcos, et al  
2019; 565 (7738): 186–91
- **Structural, thermodynamic and catalytic characterization of an ancestral triosephosphate isomerase reveal early evolutionary coupling between monomer association and function.** *The FEBS journal*  
Schulte-Sasse, M., Pardo-Avila, F., Pulido-Mayoral, N. O., Vazquez-Lobo, A., Costas, M., Garcia-Hernandez, E., Rodriguez-Romero, A., Fernandez-Velasco, D. A.  
2018

- **Structure of the 30S ribosomal decoding complex at ambient temperature** *RNA*  
Dao, E., Poitevin, F., Sierra, R. G., Gati, C., Rao, Y., Ciftci, H., Aksit, F., McGurk, A., Obrinski, T., Mgbam, P., Hayes, B., De Lichtenberg, C., Pardo-Avila, et al  
2018; 24 (12): 1667–76
- **The shape of the ribosome exit tunnel affects cotranslational protein folding.** *eLife*  
Kudva, R., Tian, P., Pardo-Avila, F., Carroni, M., Best, R., Bernstein, H. D., von Heijne, G.  
2018; 7
- **The shape of the bacterial ribosome exit tunnel affects cotranslational protein folding** *ELIFE*  
Kudva, R., Tian, P., Pardo-Avila, F., Carroni, M., Best, R. B., Bernstein, H. D., von Heijne, G.  
2018; 7
- **Aminoglycoside ribosome interactions reveal novel conformational states at ambient temperature** *NUCLEIC ACIDS RESEARCH*  
O'Sullivan, M. E., Poitevin, F., Sierra, R. G., Gati, C., Dao, E., Rao, Y., Aksit, F., Ciftci, H., Corsepius, N., Greenhouse, R., Hayes, B., Hunter, M. S., Liang, et al  
2018; 46 (18): 9793–9804
- **Structure of the 30S ribosomal decoding complex at ambient temperature.** *RNA (New York, N.Y.)*  
Dao, E. H., Poitevin, F., Sierra, R. G., Gati, C., Rao, Y., Ciftci, H. I., Aksit, F., McGurk, A., Obrinski, T., Mgbam, P., Hayes, B., DE Lichtenberg, C., Pardo-Avila, et al  
2018
- **Aminoglycoside ribosome interactions reveal novel conformational states at ambient temperature.** *Nucleic acids research*  
O'Sullivan, M. E., Poitevin, F., Sierra, R. G., Gati, C., Dao, E. H., Rao, Y., Aksit, F., Ciftci, H., Corsepius, N., Greenhouse, R., Hayes, B., Hunter, M. S., Liang, et al  
2018
- **Comprehensive computational design of ordered peptide macrocycles** *SCIENCE*  
Hosseinzadeh, P., Bhardwaj, G., Mulligan, V., Shortridge, M. D., Craven, T. W., Pardo-Avila, F., Retti, S. A., Kim, D. E., Silva, D., Ibrahim, Y. M., Webb, I. K., Cort, J. R., Adkins, et al  
2017; 358 (6369): 1461–66
- **Constructing Kinetic Network Models to Elucidate Mechanisms of Functional Conformational Changes of Enzymes and Their Recognition with Ligands** *COMPUTATIONAL APPROACHES FOR STUDYING ENZYME MECHANISM, PT B*  
Zhang, L., Jiang, H., Sheong, F. K., Pardo-Avila, F., Cheung, P. H., Huang, X.  
2016; 578: 343-371
- **Millisecond dynamics of RNA polymerase II translocation at atomic resolution** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Silva, D., Weiss, D. R., Avila, F. P., Da, L., Levitt, M., Wang, D., Huang, X.  
2014; 111 (21): 7665-7670
- **A Two-State Model for the Dynamics of the Pyrophosphate Ion Release in Bacterial RNA Polymerase** *PLOS COMPUTATIONAL BIOLOGY*  
Da, L., Avila, F., Wang, D., Huang, X.  
2013; 9 (4): e1003020