**Validating folding energy estimates as a method for variant interpretation**

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**Abstract**

Interpretation of variants of uncertain significance remains a major problem in genomic analysis. Whilst statistical models can be used to predict pathogenicity, they offer no insights into the biophysical mechanism of variant action, and genomic data available for training is biased towards the subpopulations who have access. Protein misfolding has been found to act as a frequent mechanism for loss of gene or domain activity, where it is typically responsible for ~2/3 of disease-causing variants and somatic mutations. The accuracy of energy predictions however has consistently been challenged by highly variable correlation coefficients reported from different proteins, and the unknown impact of alternative structures where available. Here we address this directly through a systematic analysis of mega-scale folding experimental results, enabled by a fully automated predictive pipeline based on FoldX. We find that whilst absolute correlation coefficients are mediocre for three highly studied proteins (PIN1, Spg, and FYN, ranging from 0.29-0.43), the correlation coefficient alone does not capture the full predictive power of the estimates. Specifically, we find a clear linear relationship between experimental and theoretical result, with a small number of outlier residues responsible for reducing the correlation. We show that the quantitative accuracy of predictions can be improved by aggregating estimates taken from different structures, and that the problematic outlier residues can be both empirically and theoretically identified, allowing us to flag low-confidence values. Our findings not only provide a framework for identifying problematic mutations in advance but also offers new insights into potential improvements of the FoldX protocol for more accurate protein stability predictions. Our insights support the use of FoldX in computational saturation screens to support variant analysis.

## Introduction

Genome sequencing is a major tool in the study of human disease. The relentless reduction in cost over time has made these techniques increasingly widely available, having become routine in higher-income countries and starting to become available in lower and middle income countries. With increased uptake of sequencing technologies, interpretation of variants of uncertain significance is a growing problem. This is further challenged by biases intrinsic in available datasets, which have been sampled from relatively small subpopulations at this point, and the intrinsic sparsity and diversity of variants that can arise. Statistical techniques have shown great power in predicting pathogenicity but mechanistic understanding of mutation could address bias issues in existing training sets, and offers the potential for therapeutic design.

Protein misfolding is responsible for the majority of pathogenic missense mutations observed in humans (1,2), and is estimated to be responsible for a loss of activity in two-thirds of variants across multiple long-standing studies (3-5). Experimental assessments of changes in protein stability have historically been labour intensive, time-consuming, and require substantial amounts of purified protein (6). This hinders large-scale studies and the rapid assessment of protein variants. As such, computational methods are invaluable tools in high-throughput studies involving numerous protein variants.

A wide range of tools are now available for calculating folding energies of protein structures, with FoldX (7) and Rosetta (8) leading the field. FoldX specifically is one of the most widely used tools for predicting the effects of mutations on protein folding and stability (9), and has been found to offer similar predictive power to Rosetta at substantially lower computational cost (10). FoldX stability calculations have been used to assess the impact of various disease-linked mutations on the stability of the protein rhodopsin in the retina (11), and missense mutations in E-cadherin on the protein's stability and its role in the hereditary diffuse gastric cancer (12). FoldX has also been effectively used to study the impact of mutations in viral proteins, particularly in the context of SARS-CoV-2. One study combined molecular dynamics simulations with FoldX to predict escape mutations in the virus's receptor-binding domain, finding a positive correlation between predicted binding affinity changes and experimentally observed escape fractions (13). Another study assessed the effects of mutations on the binding interactions between the SARS-CoV-2 spike protein and neutralising antibodies, aiding in the identification of mutations that could impact vaccine efficacy (14).

Whilst FoldX has been successfully applied to a wide range of different biological problems, there remains ongoing questions regarding its predictive power and therefore its suitability for assessing proteins generally. This is highlighted by the wide range of correlation coefficients reported in the literature, for example from 0.2 for the engineered Flavin mononucleotide based Fluorescent Protein (15) to 0.8 for a large set of mutations across multiple proteins (7). Related to this is how the choice of initial structure influences calculations. This has been studied for different structures of COVID spike protein, revealing variation between estimates taken from different structures and the need to aggregate data to establish a consensus (16). Resolving and validating FoldX predictive performance at scale across multiple proteins is fundamental to its adoption in variant interpretation.

Here we present a systematic analysis of FoldX predictions through computational saturation screens applied to a mega-scale study of protein folding stability from Tsuboyama et al (17). This dataset of over 1000 substitutions in seven proteins with large numbers of experimentally determined structures allows us unprecedented validation of predictions generated by the tool. We find that the presence of outliers substitutions, which make up a

small proportion of the overall estimates, distorts the correlations between predictions and measurements, obscuring a clear linear trend. When comparing across alternative structures for a single protein we find estimates for single substitutions are generally consistent, with unimodal distributions well described by the median. Finally using elastic network modelling we find that outlier substitutions are associated with residue positions that are tightly constrained within structures, leading to overestimates. Our results resolve historic contradictions in FoldX performance at scale and show how folding calculations can be used routinely in computational saturation screens.

## Materials and Methods

### Mutein pipeline for automated FoldX ΔΔG calculation

Following the method originated in Shorthouse et al (10) and adapted to a high-performance computing cluster for Hall et al (18), FoldX was used to calculate the ΔΔG values of mutations on a Sun Grid Engine computing cluster. For each gene of interest, the pipeline retrieved all PDB structures from the primary accession code using the UniProt API (19), and additionally the AlphaFold PDB structure (20). For every PDB structure, a parallel FoldX RepairPDB command was run 5 times for steric clash minimisation and optimisation of residue orientations. With further parallelisation, FoldX PositionScan was run on every residue in the relevant chains, for every possible amino acid mutation. The default FoldX settings were used for RepairPDB and PositionScan. The resulting protein residues are aligned to the gene positions resulting in ΔΔG for every possible mutation on all relevant PDB structures for the gene. Code for performing simulations is available at Zenodo (21). All data is included in supplementary information.

### Gene alignment

Structures downloaded by the Mutein pipeline frequently are not aligned to the canonical amino acid sequence for the gene as defined by UniProt. Differences can include first residues (for example, due to the construct used for structural analysis), residue numbering, excised loops, or natural variants. To ensure the structures are aligned to the reference protein sequence, we extract from the datasets the sequence used in the FoldX pipeline for each protein structure and the sequence used in the experimental dataset. Our approach augments BioPython's Pairwise Aligner with additional rules for amino acid matches and substitutions, to refine matches by removing small or misleading alignments, to define valid substitutions, and to detect and filter artificial constructs in the pipeline structures. When a pipeline structure has multiple variations, only the variation with the highest match percentage is retained. The aligned sequence is then mapped to the reference sequence number scheme.

We further take account of amino acid substitutions in the experimental structure compared to the reference when returning the ΔΔG of a substitution elsewhere. Assuming a thermodynamic cycle, we add the ΔΔG of mutating back to the reference sequence to the substitution being studied for that structure so that all energies under study are relative to the same reference sequence. All code used in this study is available as SI.

## Results

### Analysis of PIN1 reveals underlying relationship between theoretical and measured results

PIN1 is a nuclear localised protein responsible for the control of multiple cellular processes, including cell cycle progression and the DNA damage response. It acts as an enzyme catalysing conformational transitions in proteins, initiating changes in protein structure, stability and function (22). It consists of two domains connected by a disordered region; a WW domain that mediates specific protein-protein interactions, and a PpiC domain responsible for catalysis. Of proteins studied in the experimental dataset, PIN1 has the most available structures (Table 1), and so was selected for initial analysis. All structures were found to have different residue numbers (Fig 1A), so were realigned to the UniProt reference sequence before being correlated with experimental data (Fig 1B, S1, materials and methods).

An initial analysis of theoretical estimates and measurements suggests a weak relationship between the two, with a Pearson correlation coefficient equal to 0.28. Visualisation of the scatter plot however reveals a clear linear trend, punctuated by a small number of poorly predicted substitutions (Fig 1C). A linear regression applied to the data confirms the observation, and allows us to highlight outlier substitutions as those that are more than two standard deviations away from the line of best fit. This shows that five substitutions from five residues make up 75% of all the outliers.

The outsized role of individual substitutions raises questions on the nature and origin of variation between different estimates taken from structures that are ostensibly the same. To explore this question for individual substitutions we tested the shapes of the distributions. We found using Hartigan's dip test that the distribution of estimates was unimodal for almost all substitutions (with only two substitutions, F25Y and T29D less than a multiple test corrected p-value threshold of 0.05). Application of the D'Agostino-Pearson test revealed that the majority of these unimodal distributions were not normally distributed (53/60 non-normal), and had a skew apparent from visualisation of individual distributions. The median of these distributions was found to adequately represent the peak of this distribution, and when the median is plotted against experimental energies this is observed to tightly follow the trend of the linear regression resulting in an improved Pearson correlation coefficient of 0.64. These observations raise the question of how much do measures of $\Delta\Delta G$ vary between different structures for well behaved substitutions. For PIN1, a bootstrapping analysis of non-outlier substitutions reveal 95% confidence intervals of -0.173 and +0.176 kcal/mol. Outlier substitutions have a notably broader variance than other substitutions, suggesting that problematic residues can be identified from this distribution and flagged as low confidence predictions.

Finally, to explore the nature of variance across the complete dataset, we performed a principal component analysis of all measured energies. A biplot shows a separation of structures based on the specific experimental construct used in determining the structure (Fig 1D). This has the further effect of separating NMR structures from crystal structures, as a result of using smaller constructs. Given that AlphaFold models are folded using forcefields trained from potentially all available structures, we examined the energies from this model finding that it clustered with full length constructs, but the energies had a weaker correlation with experiment in isolation than the median energies.

### Expansion to a larger protein cohort confirms underlying patterns in prediction

The observations in PIN1 show that FoldX was capable of producing accurate predictions of folding energies, and suggested a process for handling the energy estimates taken from a large number of structures. To validate these insights, we first analysed the predicted energies for FYN and Spg, the proteins from the mega-scale dataset with the next two largest numbers of structures. *FYN* encodes a kinase in the src family (23), whilst *spg* in Streptococcus sp. group G encodes immunoglobulin G-binding protein G (24).

TABLE I
PROBLEMATIC RESIDUES AND MUTATIONS

| Protein | (1) Total Residues | (2) Total Mutations | (3) Problem Residues | (4) Problem Mutations | Problem % Outliers |
|---|---|---|---|---|---|
| PIN1 | 32 | 60 | 5 | 5 | 75% |
| Spg | 54 | 886 | 4 | 40 | 75% |
| FYN | 12 | 71 | 3 | 5 | 83% |
| RplI | 33 | 46 | 2 | 4 | 73% |

Columns 1 and 2 list the total number of individual residues and mutations

Table 1. Distribution of problematic substitutions across proteins under study. “Problem” residues or mutations are defined by those with estimates more than 2 standard deviations away from the line of best fit. A small minority of residues contribute disproportionately to outlier observations, defined as being more than two standard deviations from the line of best fit. THO1, CPA2, PRPF40A are excluded from the analysis as there are insufficient datapoints to identify outliers.

The same patterns observed in PIN1 were recapitulated (Fig 2) for FYN and Spg. Both sets of predicted energies follow a clear line of best fit, with a stronger correlation found between the medians (0.79 for Spg, 0.67 for FYN) than the complete set of predicted energies. In each case a small number of substitutions contributed disproportionately to the outlier energies observed (Table 1). When considering only non-outlier residues, we find comparable 95% confidence intervals across different structures to those see in PIN1 (Spg -0.351, +0.342 kcal/mol, FYN -0.401, +0.485 kcal/mol). These trends were further confirmed when expanding beyond the three initial proteins to the complete datasets (Fig S2). While the automated tool facilitates alignment of all structures of all proteins in the experimental dataset, the level of analysis going forward is limited by the representation of each protein in the experimental dataset. For three of the ten proteins (SUCB, YAP1, VIL1) there are only two or three variants in the experimental assay and hence analysis of these proteins is not taken further.

TABLE II
LINEAR SLOPE COEFFICIENTS

| Protein | (1) Structures | (2) Mutations | (3) All estimated ΔΔG | (4) Median estimated ΔΔG | |
|---|---|---|---|---|---|
| **PIN1** | 78 | 60 | 0.62 | 0.69 | |
| *St. error* | | | *0.029* | *0.11* | |
| **Spg** | 29 | 886 | 1.2 | 0.89 | |
| *St. error* | | | *0.013* | *0.024* | |
| **FYN** | 34 | 71 | 0.97 | 0.93 | |
| *St. error* | | | *0.053* | *0.12* | |
| **CPA2** | 1 | 20 | 0.98 | - | -[b] |
| *St. error* | | | *0.24* | | |
| **PRPF40A** | 4 | 47 | 0.46 | 0.57 | 0.[illegible] |
| *St. error* | | | *0.16* | *0.18* | |
| **RplI** | 5 | 46 | 0.14 | 0.50 | 0.[illegible] |
| *St. error* | | | *0.13* | *0.11* | |
| **THO1** | 3 | 28 | 0.55 | 0.64 | 0.[illegible] |
| *St. error* | | | *0.18* | *0.14* | |

Table 2. Slope and standard error of the slope of the line of best fit calculated from measured and predicted misfolding energies. CPA2 has only one structure available overlapping with the experimental dataset and so is excluded from the median estimates.

The common trends observed for each protein in isolation raises the question whether the trends hold when all predictions aggregated together (Table 2). Examination of the trend lines for different datasets shows that each line of best fit appears to have a distinct slope and intercept. It should be noted however that 95% confidence intervals are considered, all slope coefficients of the other overlap and hence there is no suggestion they follow statistically different models.

### Outlier predictions arise from highly constrained residues

Whilst analysis of the whole cohort reveals fundamental trends that enable predictions, outlier substitutions are a clear problem for a small number of residues. Understanding the origin of these problematic substitutions may suggest methods to address the issues, or flag

hard to predict residues at the point of calculation to users. We therefore studied the origins of the outlier substitutions.

We first sought to conclude whether all substitutions of single residues are poor predictors, or if specific substitutions are problematic. For all proteins other than Spg we cannot draw conclusions on this as the Tsuboyama dataset does not have experimentally observed ΔΔG for all substitutions at a particular residue position (Table 1). For PIN1, FYN and RplI it appears that if a residue is problematic then all substitutions at that point are poor. However, given only select substitutions at these residues are represented in the Tsuboyama dataset this is arguably a sample effect. For Spg however, all substitutions are evenly distributed in variants (Fig S3) and so we can look at the distributions of substitutions in the outliers. Substitutions in the outliers are dominated by bulky aromatic amino acids tyrosine (Y) and phenylalanine (F) as well as bulky polarised amino acid histidine (H) with the count of tyrosine and phenylalanine 4-times and the count of histidine 2-times that of the other amino acids of substitution (Fig S3). With problem mutations categorised by high variance in ΔΔG values we can also identify problem residues across the protein sequence without experimental measurements, increasing the size of our dataset and enabling deeper analysis. As Fig 3A illustrates for PIN1, Spg and FYN the feature of a few residues with large variances in ΔΔG values observed when validating the FoldX pipeline with the experimental dataset above (Fig S4A,C) is a feature for the set of protein structures. Most amino acid substitutions (except alanine (A) and glycine (G)) contribute to the spikes in energies in Fig 3A, with bulky aromatic and basic residues dominating the distribution (Fig 3B).

At this point we hypothesise whether from a full protein perspective you see higher energies in regions of more disorder as for example for PIN1 the most structured well-defined part of the protein appears to be the WW domain (residue positions 1-38). This would be expected to arise if flexible loop regions are poorly packed in the minimised structure. To test this we use MoreRONN scores as a predictive score of disorder. MoreRONN gives a value for every residue in the protein so we can plot the variance in ΔΔG values against the disorder score (Fig 3C). It appears for PIN1 and FYN that more ordered areas have the highest variance in energies, while the reverse is the case for Spg where higher variances are found in the more disordered regions. While permutation tests suggest they are statistically significant individually for PIN1 and Spg these relationships are small in real terms with correlation coefficients less than 0.2. In addition, a Kruskal-Wallis H-test to test if they are from different distributions is not statistically significant. We also note that for Spg only small regions of the protein are resolved and these overlay solely with regions of disorder (Fig S4A), whereas the complete protein for PIN1 and FYN is resolved across structures. As such it is also possible the relationship observed in Fig 3C – suggesting higher variances in ΔΔG values are found in more disordered regions of Spg - is largely a sampling artifact.

Based on these observations, we hypothesised next that problematic residues that are harder for FoldX to predict ΔΔG are in tightly structured regions of the protein. To investigate this we use an Elastic Network Model to find the mode of motions for the protein from the static structure, examining the fastest modes of motion (25,26). These are small localised high frequency vibrations in incredibly tight energy wells, and are believed to represent highly constrained regions. We initially examined the 10 fastest modes for PIN1 and found a significant result using a Chi-squared test (p value = 0.007), suggesting residues with a high variance in energies are not independent of residues in the 10 fastest modes. We next looked to determine how many fast modes of motion best predict residues with high variance in energies. We took from the 30 fastest modes for each protein and plotted the receiver operating characteristic (ROC) curve, to allow us to identify the optimal number of fast modes to consider for each protein. Fig 3D and S4B,D show the ROC curves for PIN1, Spg

and FYN. The area under the curve of the optimal number of fastest modes is 0.74 for the 3 fastest modes for PIN1, 0.76 for the 17 fastest modes for Spg and 0.76 for the 11 fastest modes for FYN. There is however a notable lack of consensus across the proteins for the best number of modes in the classifier (Fig 3E). Together these show that the problematic predictions arise from substitutions to keystone residues in maintaining the protein fold that are not adequately refolded or minimised after computational mutation.

## Conclusions

Protein misfolding is a common mechanism underpinning gene dysfunction through mutation. Accurate and rapid prediction of the impact on protein stability of an amino acid substitution associated with disease allows us to predict pathogenicity and potentially propose new therapeutic interventions. It also offers the opportunity to separate distinct mechanisms of gene dysfunction in heterogeneous datasets such as tumour sequencing (27). Our work presented here is a major validation of FoldX as a tool for prospective calculation of misfolding energies. It rationalises the apparent wide variation in measured correlation coefficients across different proteins, and establishes that the approach is sound for both qualitative and quantitative prediction. We have shown that small numbers of positions are poorly predicted, and that these are in themselves predictable, allowing us to propose strategies to manage them. Our work allows us to estimate the confidence intervals due to variations between structures, finding +/- 0.17 to 0.48 kcal/mol, allowing us to estimate confidence for proteins with fewer or single structures available. Our findings that outlier residues distort analyses further resolves contradictions between studies that reported poor correlation between experimental energies and predictions, alongside studies that showed strong predictive power for individual proteins. These outliers can severely reduce correlations whilst only affecting a small proportion of substitutions. The work also reveals previously unreported insights from inter-protein and inter-structure comparisons. These tantalisingly suggest that different relationships between predicted and measured energies may be associated with different proteins, and that variation between structures of the same protein are principally dependent on construct. Together this underlines the influence of protein environment (including experimental conditions) in determining the fold of a structure.

Despite the new insights gathered here, we acknowledge the limitations of the available data used for validation and the implications for our study. The dataset contains a set of small well-folded proteins, with no oligomers or cofactors. Additionally, it does not represent common protein types including multimeric proteins, DNA binding proteins, and membrane proteins, all of which would be expected to potentially present unique problems that may challenge the forcefield or require alternative options to be selected in the running of FoldX. Nonetheless, our study represents a comprehensive validation of this approach and future experimental datasets will extend our understanding of prediction of misfolding.

Our work also highlights practical issues that may undermine prediction. Estimates are worse where there are few structures available. Outliers tend to be overestimates, and arise from poor repacking in the process of minimising the structure. Future approaches may benefit from using protein dynamics to address both issues. Low-computational cost simulation methods such as CONCOORD or BioEmu could be used rapidly generate large numbers of alternative structures (28,29). Similarly, whilst AlphaFold models did not generate better predictions, refolding each model after mutation with AlphaFold or BioEmu may minimise the impact of poor repacking post mutation. The fundamental trade off here is that ensemble based approaches like Rosetta increase computational time required, and where it has been studied has not greatly altered predictions, and addressing this will require further work.

The results presented here justify the expansion of FoldX adoption and other computational saturation screen based approaches to prediction of changes to protein function through mutation (30,31). In addition to the benefits of mechanistic understanding, rapid and accurate estimation of biophysical properties could offer a new set of features to decorate sequencing datasets and support machine learning approaches. In this light, our study

further justifies the future collection of pre-calculated databases of energies of misfolding as a complement to other public scores of pathogenicity.

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**Data and code availability**

The mutein pipeline is made available through Zenodo (21). All other code and data are shared as supplementary materials.

1. Wang, Z., and J. Moult. 2001. SNPs, protein structure, and disease. *Hum Mutat*. 17(4):263-270, doi: 10.1002/humu.22.
2. Pandey, P., and E. Alexov. 2024. Most Monogenic Disorders Are Caused by Mutations Altering Protein Folding Free Energy. *International Journal of Molecular Sciences*. 25(4):1963, https://www.mdpi.com/1422-0067/25/4/1963.
3. Rennell, D., S. E. Bouvier, L. W. Hardy, and A. R. Poteete. 1991. Systematic mutation of bacteriophage T4 lysozyme. *J Mol Biol*. 222(1):67-88, doi: 10.1016/0022-2836(91)90738-r.
4. Kotler, E., O. Shani, G. Goldfeld, M. Lotan-Pompan, O. Tarcic, A. Gershoni, T. A. Hopf, D. S. Marks, M. Oren, and E. Segal. 2018. A Systematic p53 Mutation Library Links Differential Functional Impact to Cancer Mutation Pattern and Evolutionary Conservation. *Mol Cell*. 71(1):178-190.e178, doi: 10.1016/j.molcel.2018.06.012.
5. Song, H., J. Wu, Y. Tang, Y. Dai, X. Xiang, Y. Li, L. Wu, J. Wu, Y. Liang, Y. Xing, N. Yan, Y. Li, Z. Wang, S. Xiao, J. Li, D. Zheng, X. Chen, H. Fang, C. Ye, Y. Ma, Y. Wu, W. Wu, J. Li, S. Zhang, and M. Lu. 2023. Diverse rescue potencies of p53 mutations to ATO are predetermined by intrinsic mutational properties. *Sci Transl Med*. 15(690):eabn9155, doi: 10.1126/scitranslmed.abn9155.
6. Magliery, T. J. 2015. Protein stability: computation, sequence statistics, and new experimental methods. *Curr Opin Struct Biol*. 33:161-168, doi: 10.1016/j.sbi.2015.09.002.
7. Schymkowitz, J., J. Borg, F. Stricher, R. Nys, F. Rousseau, and L. Serrano. 2005. The FoldX web server: an online force field. *Nucleic Acids Research*. 33(suppl_2):W382-W388, doi: 10.1093/nar/gki387, https://doi.org/10.1093/nar/gki387.
8. Kellogg, E. H., A. Leaver-Fay, and D. Baker. 2011. Role of conformational sampling in computing mutation-induced changes in protein structure and stability. *Proteins*. 79(3):830-838, doi: 10.1002/prot.22921.
9. Sapozhnikov, Y., J. S. Patel, F. M. Ytreberg, and C. R. Miller. 2023. Statistical modeling to quantify the uncertainty of FoldX-predicted protein folding and binding stability. *BMC Bioinformatics*. 24(1):426, doi: 10.1186/s12859-023-05537-0, https://doi.org/10.1186/s12859-023-05537-0.
10. Shorthouse, D., M. W. J. Hall, and B. A. Hall. 2021. Computational Saturation Screen Reveals the Landscape of Mutations in Human Fumarate Hydratase. *Journal of Chemical Information and Modelling*. Articles ASAP:852392, doi: https://doi.org/10.1021/acs.jcim.1c00063, https://www.biorxiv.org/content/biorxiv/early/2019/11/23/852392.full.pdf.
11. Rakoczy, E. P., C. Kiel, R. McKeone, F. Stricher, and L. Serrano. 2011. Analysis of disease-linked rhodopsin mutations based on structure, function, and protein stability calculations. *J Mol Biol*. 405(2):584-606, doi: 10.1016/j.jmb.2010.11.003.
12. Simões-Correia, J., J. Figueiredo, R. Lopes, F. Stricher, C. Oliveira, L. Serrano, and R. Seruca. 2012. E-Cadherin Destabilization Accounts for the Pathogenicity of Missense Mutations in Hereditary Diffuse Gastric Cancer. *PLOS ONE*. 7(3):e33783, doi: 10.1371/journal.pone.0033783, https://doi.org/10.1371/journal.pone.0033783.

13. Barnes, J. E., P. K. Lund-Andersen, J. S. Patel, and F. M. Ytreberg. 2022. The effect of mutations on binding interactions between the SARS-CoV-2 receptor binding domain and neutralizing antibodies B38 and CB6. *Scientific reports*. 12(1):18819, doi: 10.1038/s41598-022-23482-5, https://doi.org/10.1038/s41598-022-23482-5.
14. Dehouck, Y., A. Grosfils, B. Folch, D. Gilis, P. Bogaerts, and M. Rooman. 2009. Fast and accurate predictions of protein stability changes upon mutations using statistical potentials and neural networks: PoPMuSiC-2.0. *Bioinformatics*. 25(19):2537-2543, doi: 10.1093/bioinformatics/btp445, https://doi.org/10.1093/bioinformatics/btp445.
15. Walter, J., S. Hausmann, T. Drepper, M. Puls, T. Eggert, and M. Dihné. 2012. Flavin Mononucleotide-Based Fluorescent Proteins Function in Mammalian Cells without Oxygen Requirement. *PLOS ONE*. 7(9):e43921, doi: 10.1371/journal.pone.0043921, https://doi.org/10.1371/journal.pone.0043921.
16. Mehra, R., and K. P. Kepp. 2022. Structural heterogeneity and precision of implications drawn from cryo-electron microscopy structures: SARS-CoV-2 spike-protein mutations as a test case. *European Biophysics Journal*. 51(7):555-568, doi: 10.1007/s00249-022-01619-8, https://doi.org/10.1007/s00249-022-01619-8.
17. Tsuboyama, K., J. Dauparas, J. Chen, E. Laine, Y. Mohseni Behbahani, J. J. Weinstein, N. M. Mangan, S. Ovchinnikov, and G. J. Rocklin. 2023. Mega-scale experimental analysis of protein folding stability in biology and design. *Nature*. 620(7973):434-444, doi: 10.1038/s41586-023-06328-6, https://doi.org/10.1038/s41586-023-06328-6.
18. Hall, M. W. J., D. Shorthouse, R. Alcraft, P. H. Jones, and B. A. Hall. 2023. Mutations observed in somatic evolution reveal underlying gene mechanisms. *Communications Biology*. 6(1):753, doi: 10.1038/s42003-023-05136-y, https://doi.org/10.1038/s42003-023-05136-y.
19. Ahmad, S., L. Jose da Costa Gonzales, Emily H. Bowler-Barnett, Daniel L. Rice, M. Kim, S. Wijerathne, A. Luciani, S. Kandasaamy, J. Luo, X. Watkins, E. Turner, Maria J. Martin, and C. the UniProt. 2025. The UniProt website API: facilitating programmatic access to protein knowledge. *Nucleic Acids Research*. 53(W1):W547-W553, doi: 10.1093/nar/gkaf394, https://doi.org/10.1093/nar/gkaf394.
20. Varadi, M., S. Anyango, M. Deshpande, S. Nair, C. Natassia, G. Yordanova, D. Yuan, O. Stroe, G. Wood, A. Laydon, A. Žídek, T. Green, K. Tunyasuvunakool, S. Petersen, J. Jumper, E. Clancy, R. Green, A. Vora, M. Lutfi, M. Figurnov, A. Cowie, N. Hobbs, P. Kohli, G. Kleywegt, E. Birney, D. Hassabis, and S. Velankar. 2022. AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models. *Nucleic Acids Research*. 50(D1):D439-D444, doi: 10.1093/nar/gkab1061, https://doi.org/10.1093/nar/gkab1061.
21. Alcraft, R., and B. A. Hall. 2025. https://doi.org/10.5281/zenodo.17182761
22. Ranganathan, R., K. P. Lu, T. Hunter, and J. P. Noel. 1997. Structural and Functional Analysis of the Mitotic Rotamase Pin1 Suggests Substrate Recognition Is Phosphorylation Dependent. *Cell*. 89(6):875-886, doi: https://doi.org/10.1016/S0092-8674(00)80273-1, https://www.sciencedirect.com/science/article/pii/S0092867400802731.
23. Noble, M. E., A. Musacchio, M. Saraste, S. A. Courtneidge, and R. K. Wierenga. 1993. Crystal structure of the SH3 domain in human Fyn; comparison of the three-dimensional structures of SH3 domains in tyrosine kinases and spectrin. *Embo j*. 12(7):2617-2624, doi: 10.2210/pdb1shf/pdb.
24. Johansson, M. U., I.-M. Frick, H. Nilsson, P. J. Kraulis, S. Hober, P. Jonasson, M. Linhult, P.-Å. Nygren, M. Uhlén, L. Björck, T. Drakenberg, S. Forsén, and M. Wikström. 2002. Structure, Specificity, and Mode of Interaction for Bacterial Albumin-binding Modules*. *Journal of Biological Chemistry*. 277(10):8114-8120, doi: https://doi.org/10.1074/jbc.M109943200, https://www.sciencedirect.com/science/article/pii/S0021925819364087.
25. Rader, A. J., G. Anderson, B. Isin, H. G. Khorana, I. Bahar, and J. Klein-Seetharaman. 2004. Identification of core amino acids stabilizing rhodopsin.

*Proceedings of the National Academy of Sciences*. 101(19):7246-7251, doi: 10.1073/pnas.0401429101, https://doi.org/10.1073/pnas.0401429101.

26. Demirel, M. C., A. R. Atilgan, R. L. Jernigan, B. Erman, and I. Bahar. 1998. Identification of kinetically hot residues in proteins. *Protein Sci*. 7(12):2522-2532, doi: 10.1002/pro.5560071205.
27. Shorthouse, D., J. Bradley, S. E. Critchlow, C. Bendtsen, and B. A. Hall. 2022. Heterogeneity of the cancer cell line metabolic landscape. *Molecular Systems Biology*. 18(11):e11006, doi: https://doi.org/10.15252/msb.202211006, https://doi.org/10.15252/msb.202211006.
28. de Groot, B. L., D. M. van Aalten, R. M. Scheek, A. Amadei, G. Vriend, and H. J. Berendsen. 1997. Prediction of protein conformational freedom from distance constraints. *Proteins*. 29(2):240-251, doi: 10.1002/(sici)1097-0134(199710)29:2<240::aid-prot11>3.0.co;2-o.
29. Lewis, S., T. Hempel, J. Jiménez-Luna, M. Gastegger, Y. Xie, A. Y. K. Foong, V. G. Satorras, O. Abdin, B. S. Veeling, I. Zaporozhets, Y. Chen, S. Yang, A. E. Foster, A. Schneuing, J. Nigam, F. Barbero, V. Stimper, A. Campbell, J. Yim, M. Lienen, Y. Shi, S. Zheng, H. Schulz, U. Munir, R. Sordillo, R. Tomioka, C. Clementi, and F. Noé. Scalable emulation of protein equilibrium ensembles with generative deep learning. *Science (New York, N.Y.)*. 389(6761):eadv9817, doi: 10.1126/science.adv9817, https://doi.org/10.1126/science.adv9817.
30. Hall, B. A., K. B. A. Halim, A. Buyan, B. Emmanouil, and M. S. P. Sansom. 2014. Sidekick for Membrane Simulations: Automated Ensemble Molecular Dynamics Simulations of Transmembrane Helices. *Journal of Chemical Theory and Computation*. 10(5):2165-2175, doi: 10.1021/ct500003g, https://doi.org/10.1021/ct500003g.
31. Gerasimavicius, L., B. J. Livesey, and J. A. Marsh. 2022. Loss-of-function, gain-of-function and dominant-negative mutations have profoundly different effects on protein structure. *Nature Communications*. 13(1):3895, doi: 10.1038/s41467-022-31686-6, https://doi.org/10.1038/s41467-022-31686-6.

Figure Legends

Figure 1. Theoretical estimates of PIN1 variant misfolding reveal underlying predictive relationship. A) Before alignment heatmap PIN1 residue matches between FoldX pipeline structures and the reference sequence for PIN1. Black is a residue match, white is a mismatch. B) After alignment heatmap of residue matches between FoldX pipeline structures and the reference gene sequence for PIN1. Dark blue is a residue match, pale blue is a substitution, and blank is either a mismatch or no residue. For PIN1 we can see that residue positions 40-50 are a loop that isn't historically resolved easily, other than in 4 relatively new structures. The percentage of residue matches with the reference gene are noted for each structure on the right-hand side. Any aligned structures with a match percentage less than 5% (e.g. 7AOG to 7BGW, 7NIF to 7OQA for PIN1) are considered to only include the gene of interest in a binding site of an altogether different enzyme and are dropped from the dataset going forward. C) Scatter plot of predicted and measured change in energy of folding (ΔΔG) with linear regression analysis, outlier identification and median energies. When problematic residues are discounted, median energies tighten the linear trend. D) PCA projection of top two components with domain colouring for PIN1, with each structure normalised independently so that PCA reflects variation within local domains, revealing the relationship between experimental construct and folding energy prediction. PIN1 has two resolved domains, the WW domain which is residues 1-38 and the PPIase domain which is residues 50 up to 163. Most structures do not resolve the loop region in between. AlphaFold energy estimates cluster with structures of the full structure.

Figure 2. Linear relationship between theoretical estimates and measured energies is observed for (A) SPG and (B) FYN. Consistent with observations from PIN1, predictions and measurements have a linear relationship, with a handful of outliers reducing the correlation. Visualising the median estimates for each substitution we see that they cluster tightly to the linear trend of the whole cohort. Each gene is found to have a slightly different slope.

Figure 3. Outlier estimates arise from tightly packed residues. A) Visualisation of energy estimates from all predictions reveals that all substitutions to single residues (rather than single substitutions) share outlier estimates. B) Energy spikes in A (>10 kcal/mol) are associated with most amino acid substitutions (except alanine and glycine) and are dominated by bulky aromatic and basic residues. C) Outlier estimates are not found in disordered areas as predicted by MoreRONN. Scatter plot of energy variance against score shows no clear relationship. D) Gaussian network modelling of tightly restrained residues is predictive of outliers in PIN1. ROC curve plots false and true positive rates for different summed squared fluctuations of residues in top 3 modes (AUC=0.74) E) The number of modes needed to predict outlier residues accurately varies between genes. The multiple black curves represent the ROC curves for the first fastest mode up to the 30 fastest modes while the mode in magenta is the mode that maximises the area under the curve (AUC).

Supplementary Figure 1. Alignment plots of other genes in this study

Supplementary Figure 2. Regression analysis applied to other genes A) RPL1 B) THO1 C) PRPF40A D) CPA2

Supplementary Figure 3. Frequency of outlier energy estimates aggregated by amino acid type.

Supplementary Figure 4. A, C) Distribution of FoldX pipeline ΔΔG energies across the full length of structures for SPG and FYN respectively with the MoreRONN disorder score overlaid. B, D) ROC plots for alternative numbers of top modes for SPG and FYN respectively. The multiple black curves represent the ROC curves for the first fastest mode

up to the 30 fastest modes while the mode in magenta is the mode that maximises the area under the curve (AUC).

Figure 1

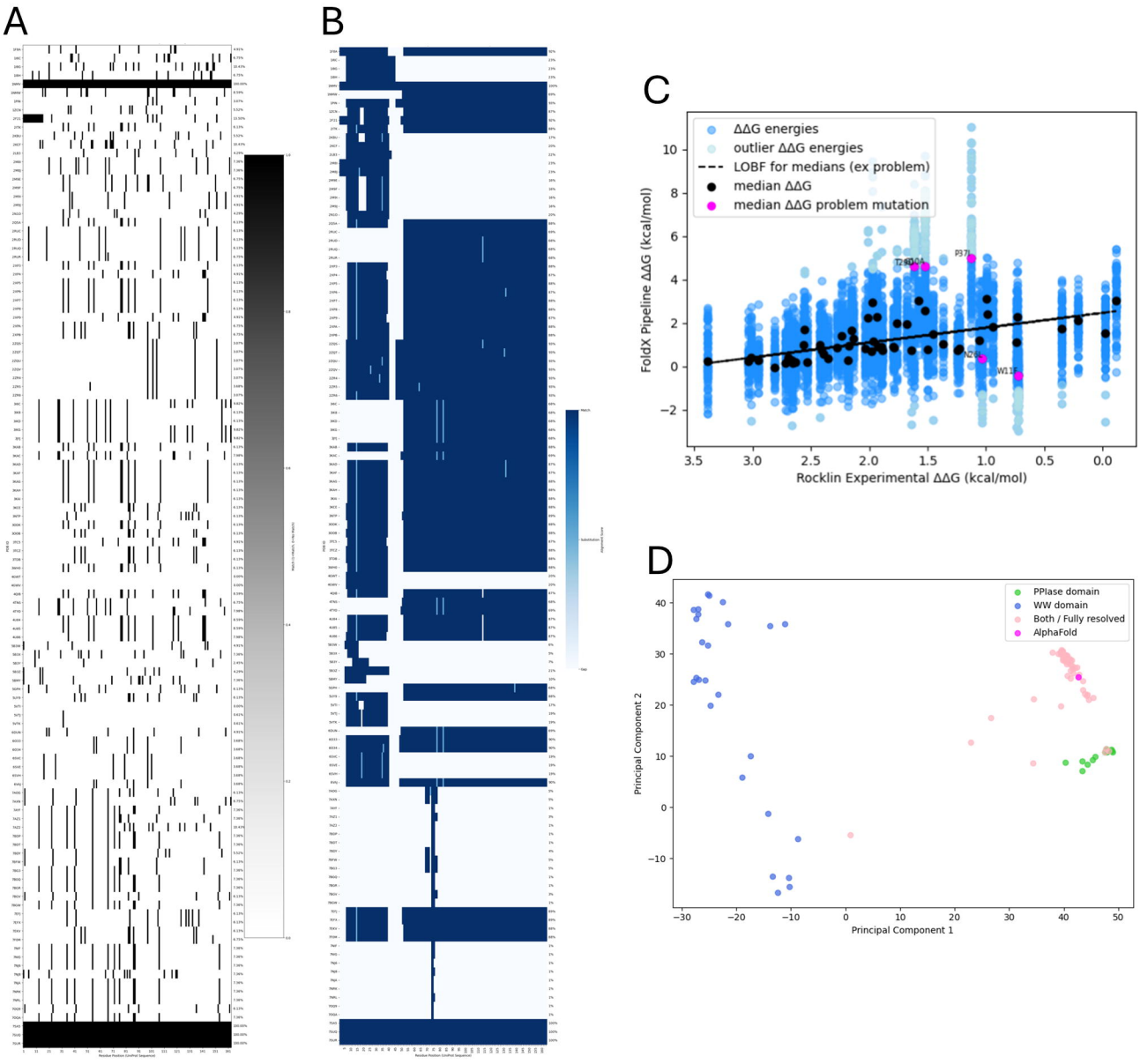
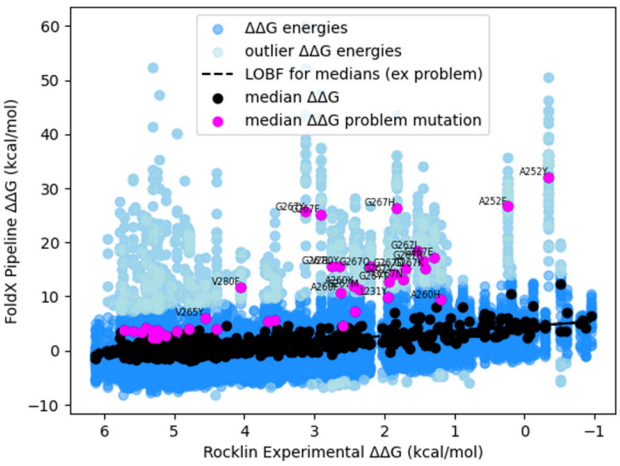

A
B
C
ΔΔG energies
outlier ΔΔG energies
LOBF for medians (ex problem)
median ΔΔG
median ΔΔG problem mutation
FoldX Pipeline ΔΔG (kcal/mol)
Rocklin Experimental ΔΔG (kcal/mol)
D
PPIase domain
WW domain
Both / Fully resolved
AlphaFold
Principal Component 1
Principal Component 2

Figure 2

A


ΔΔG energies
outlier ΔΔG energies
LOBF for medians (ex problem)
median ΔΔG
median ΔΔG problem mutation
FoldX Pipeline ΔΔG (kcal/mol)
Rocklin Experimental ΔΔG (kcal/mol)
A252Y
A252F
G267H
V280F
V265Y
A260H
D231Y

B

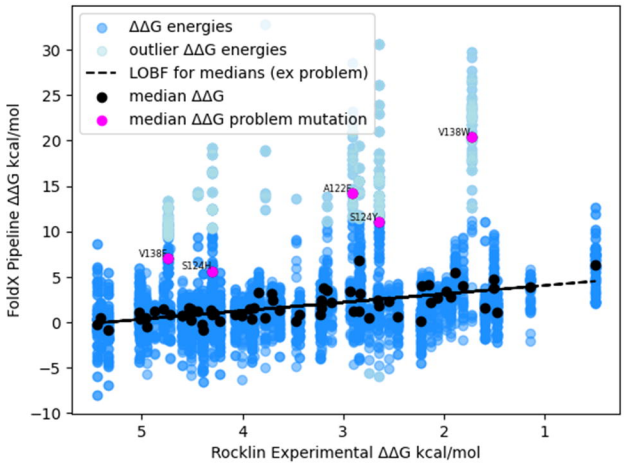

ΔΔG energies
outlier ΔΔG energies
LOBF for medians (ex problem)
median ΔΔG
median ΔΔG problem mutation
FoldX Pipeline ΔΔG kcal/mol
Rocklin Experimental ΔΔG kcal/mol
V138W
A122
S124Y
V138F
S124H

Figure 3

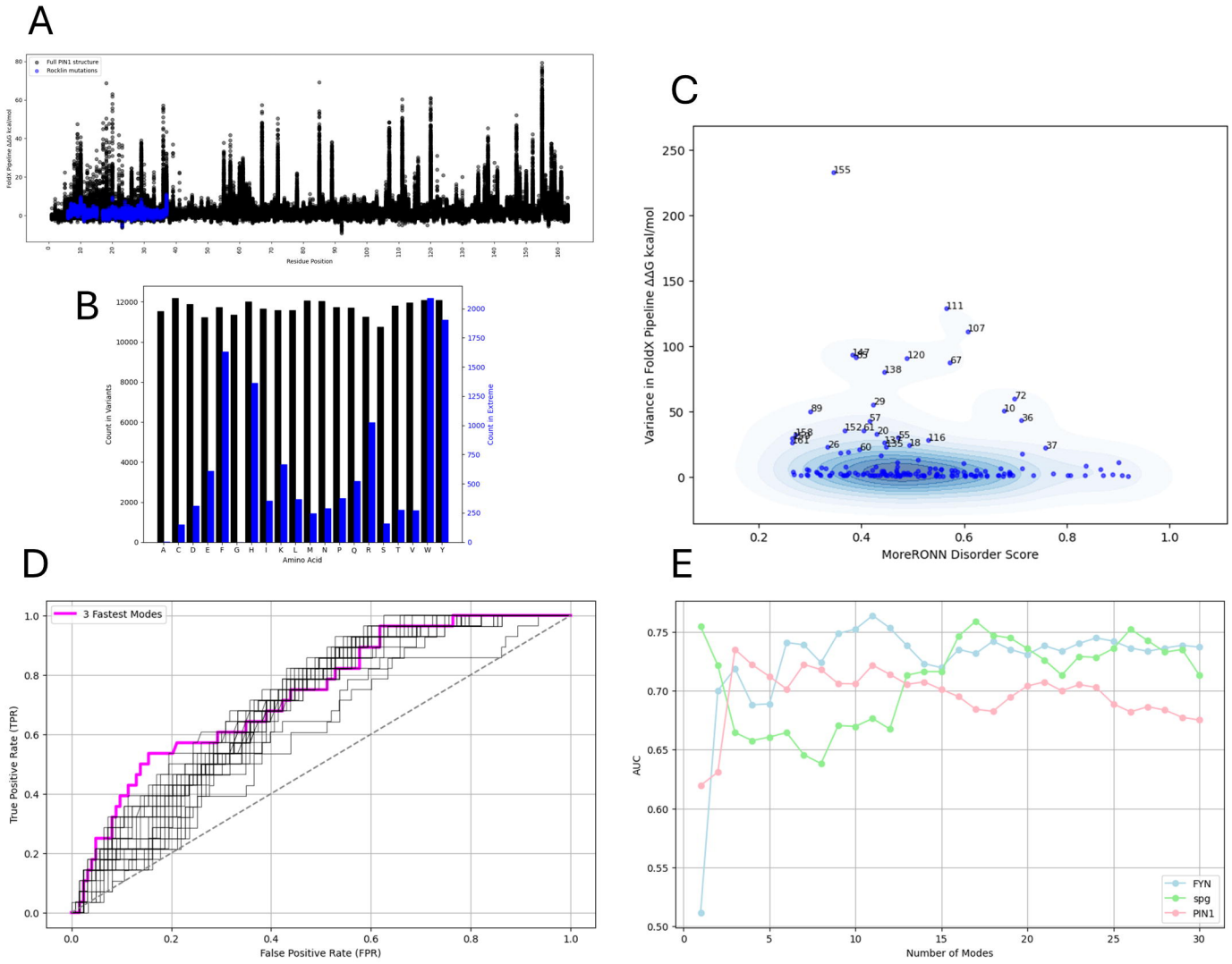

A
Full PIN1 structure
Rocklin mutations
FoldX Pipeline ΔΔG kcal/mol
Residue Position
B
Count in Variants
Count in Extreme
Amino Acid
C
Variance in FoldX Pipeline ΔΔG kcal/mol
MoreRONN Disorder Score
D
3 Fastest Modes
True Positive Rate (TPR)
False Positive Rate (FPR)
E
AUC
Number of Modes
FYN
spg
PIN1

Figure S1

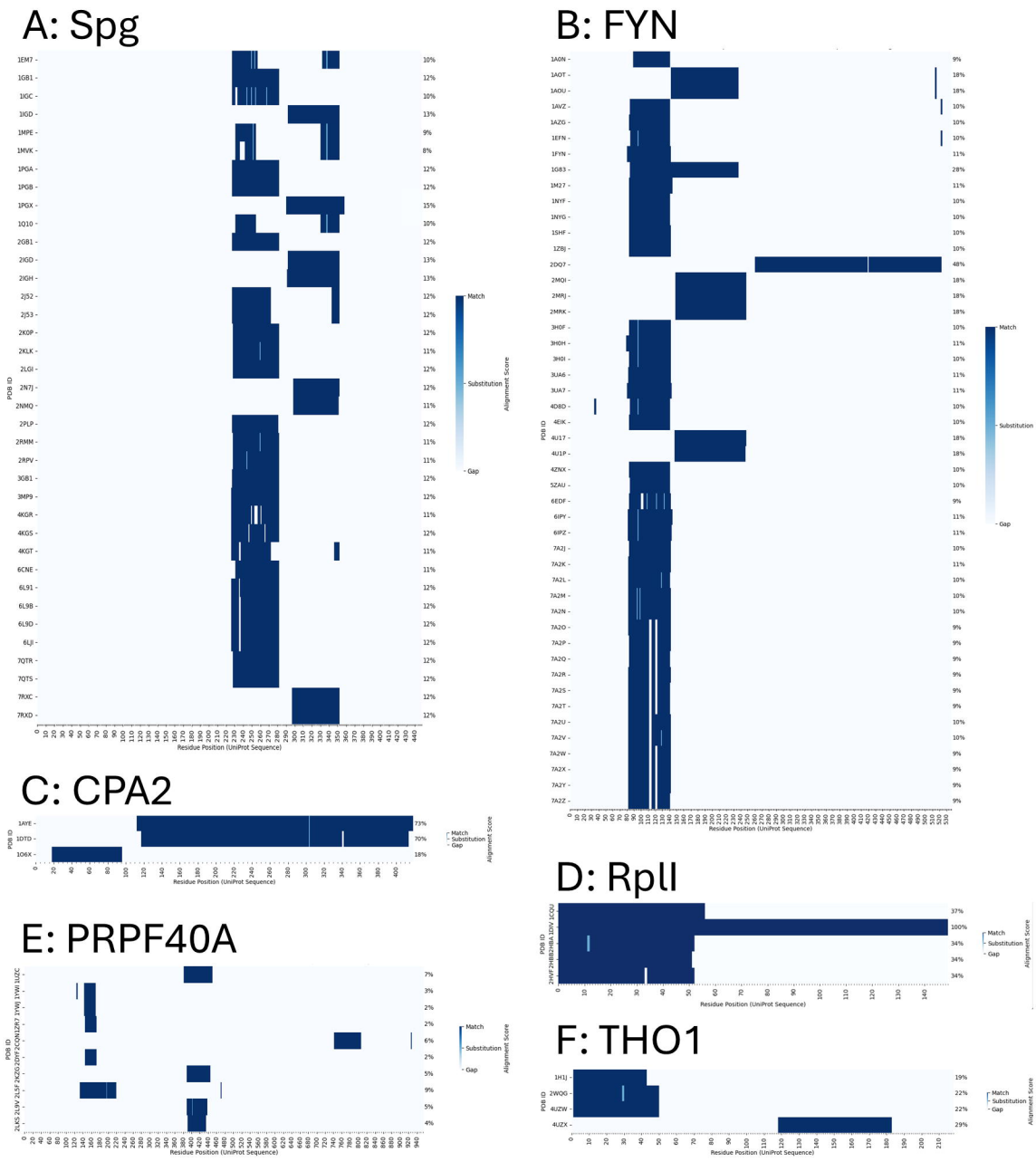

A: Spg
B: FYN
C: CPA2
D: RplI
E: PRPF40A
F: THO1
PDB ID
Residue Position (UniProt Sequence)
Alignment Score
Match
Substitution
Gap

Figure S2

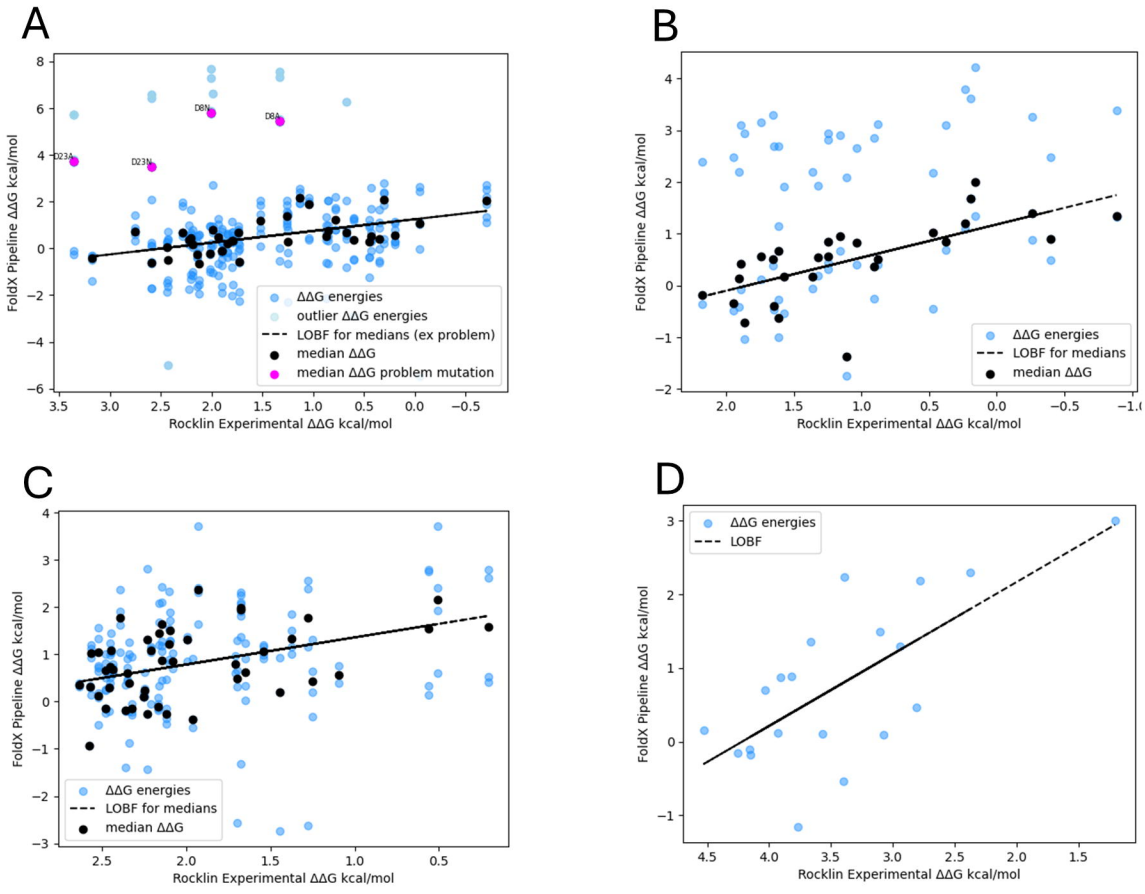

A
FoldX Pipeline ΔΔG kcal/mol
Rocklin Experimental ΔΔG kcal/mol
D23A
D23N
D8N
D8A
ΔΔG energies
outlier ΔΔG energies
LOBF for medians (ex problem)
median ΔΔG
median ΔΔG problem mutation
B
FoldX Pipeline ΔΔG kcal/mol
Rocklin Experimental ΔΔG kcal/mol
ΔΔG energies
LOBF for medians
median ΔΔG
C
FoldX Pipeline ΔΔG kcal/mol
Rocklin Experimental ΔΔG kcal/mol
ΔΔG energies
LOBF for medians
median ΔΔG
D
FoldX Pipeline ΔΔG kcal/mol
Rocklin Experimental ΔΔG kcal/mol
ΔΔG energies
LOBF

Figure S3

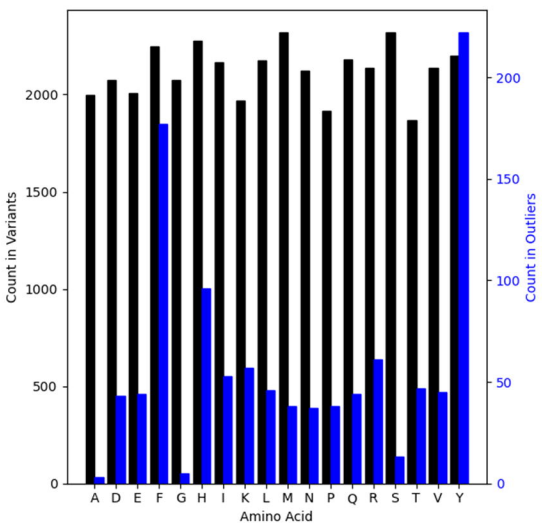
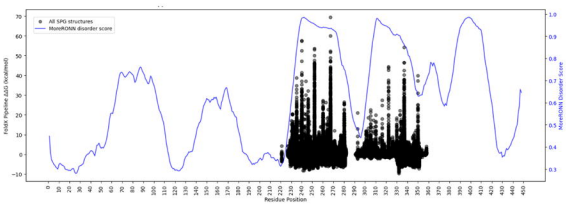
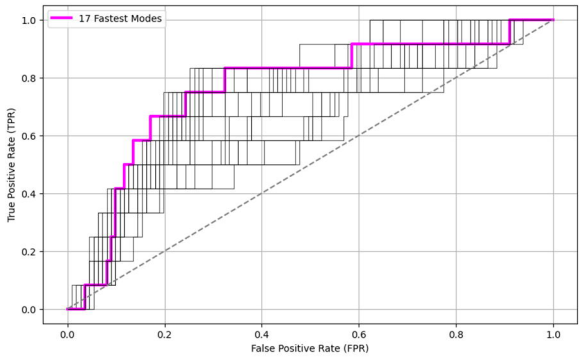

Count in Variants
Count in Outliers
Amino Acid
0
500
1000
1500
2000
0
50
100
150
200
A D E F G H I K L M N P Q R S T V Y

Figure S4

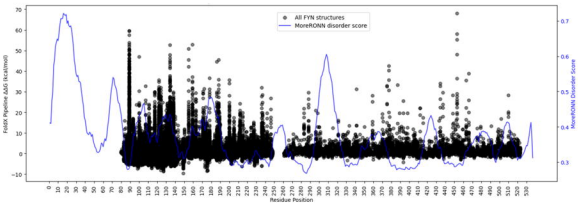
A

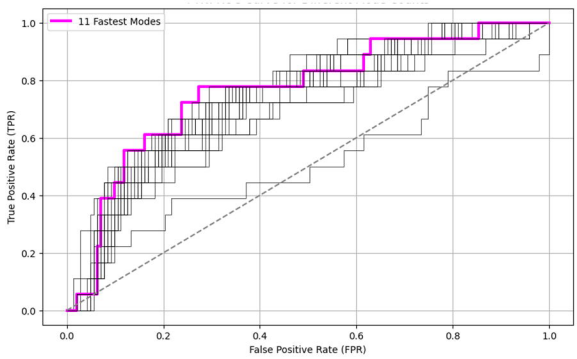



B




C




D