Functionally constrained human proteins are less prone to disruption of stability caused by single amino acid substitutions

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Abstract

It is well understood that missense mutations that disrupt protein structural stability are a common pathogenic mechanism in human genetic disease. At a proteome-wide scale, we have quantitated potential disruption of protein stability due to amino acid substitution and show that the most functionally constrained proteins are typically less susceptible to large mutational changes in stability. Mechanistically, this relates to greater intrinsic disorder among constrained proteins, but also to increased B-factors in the ordered regions of constrained proteins. This overall robustness of constrained proteins to the stability effects of mutations partly explains why overtransmission of pathogenic missense variation is less prevalent in genetic disorders characterised with protein truncating variation. From analysis of the predicted protein stability effects of missense genetic variation across all human proteins, we show that the most functionally constrained proteins are depleted of both destabilising ($\Delta\Delta G > 0.5$ kcal/mol) and overly-stabilising ($\Delta\Delta G < -0.5$ kcal/mol) amino acid variation in disease-free populations. Despite this, amino acid substitutions with large stability effects in functionally constrained proteins are still highly prevalent among pathogenic human genetic variation. Importantly, we observe that there are approximately five times more missense variants with large stability effects than there are unambiguous loss-of-function mutations. Missense variants with disruption of stability effects recapitulate the per-gene patterns of functional constraint observed with protein truncating loss-of-function variation, yet their relative abundance abrogates difficulties encountered when estimating functional constraint for the shortest human genes.

Introduction

The pathogenicity effects of missense mutations that result in altered protein stability have been widely accepted for some time[1]. Due to evolutionary trade-offs, most proteins are only marginally stable, yet must function in the busy physiochemical environment of the cell, mixed among proteases that degrade unfolded proteins[2]. Hence, missense mutations that disrupt stability of the encoded protein have potentially large functional consequences. And a large proportion of all possible missense variants have functionally relevant stability effects on the encoded protein[3,4]. The functional effects of these protein mutants range from interfering with correct protein folding to disruption of protein-protein interactions, to affecting cellular localization of the protein[5]. Destabilization of a protein structure underlies the pathogenic mechanism of many and diverse missense mutations that cause genetic disease[6].

Missense mutations with protein stability effects are common - and may be the pathogenic mechanism of a significant minority, or even the majority, of missense substitutions[1]. Mutations that disrupt protein stability can result in complete loss of protein function, but may often simply reduce (hypomorphic mutations) or increase activity (hypermorphic and gain-of-function mutations) from the wild-type level, and in some cases alter the activity of the protein (neomorphic mutations)[7]. Furthermore, at a systems level, the functional impact and/or penetrance of these mutations is dependent also on gene functional constraint, potential haploinsufficiency and the inheritance pattern of the mutant phenotype (including dominance/recessiveness and/or polygenicity)[8,9]. Given these diverse effects of mutations, and that these effects are not readily distinguished at the sequence level, in the context of this study we have chosen a broader term for mutants that affect protein stability as Disruption-of-Stability (DoS) mutants. Here, this term, DoS mutant, makes no assumptions about mechanism, inheritance or penetrance, yet simply indicates that the mutant protein is functionally altered (or disrupted) compared to the wild-type protein, especially if this has deleterious consequences that may lead to the variation becoming subject to purifying selection.

Protein stability is commonly measured as the change in the Gibbs free energy (ΔG) between the native, folded state of a protein and the unfolded state. Hence, the change in stability due to an amino acid substitution can be quantified as the change in ΔG value between the wild-type and variant protein – represented as $\Delta\Delta G$. Protein instability due to mutation may reduce the energetic difference between the folded and unfolded states, thus destabilizing the protein. Or an amino acid substitution may increase the rigidity of the protein, thereby overly stabilizing the protein. Much empirical data has been collected to characterize the relationship between amino acid substitutions and structural stability[10]. This data has been used to train a diversity of accurate computational tools to predict the $\Delta\Delta G$ due to single and/or multiple amino acid substitutions[11], and these may be applied to predict stability changes due to genetic variation at a proteome-wide level.

With human genome sequences collected from increasingly larger numbers of individuals, it has been observed that genes subject to high functional constraint do not display the expected numbers of detrimental variants that are observed among functionally redundant genes[12]. A gene subject to strong functional constraint will harbor many fewer protein Loss-of-Function (pLoF) variants than a functionally redundant gene. To quantitate functional constraint, the 'loss-of-function observed/expected upper bound fraction' (LOEUF) score and the relative rank of LOUEF score among all genes[12] (with genes commonly partitioned bins by decile) has been calculated from the GnomAD dataset[12]. The LOEUF scores calculated from population-scale genome datasets count only the most unambiguous of potential pLoF mutants: nonsense, frameshift and canonical splice donor-acceptor mutants[13]. However, these pLoF mutants are comparatively rare. Estimating functional constraint from these requires very large datasets of genomes, from more than one hundred thousand individuals[12]. And even then, the shortest genes in the genome

may contain very few or no pLoF mutations by chance and remained underpowered for detection of functional constraint[14]. To address this lack of resolution inherent in unambigious pLoF variation, especially in shorter genes, an approach utilizing S_{het} scores has recently been proposed[14]. This employs a population genetics model with machine learning, using gene features derived from auxiliary datasets that are predictive of pLoF constraint, including gene expression information[14]. The inclusion of this auxiliary data better predicts functional constraint for the shortest 25% of human genes, through pooling of information from better-powered genes that are subject to similar constraint[14].

We have previously made exhaustive predictions of the stability effects of all possible amino acid substitutions within all human proteins (www.stabilitysort.org)[15]. Here we investigate the relative depletion of missense variants with high predicted protein stability impacts from genes under strong functional constraint. With this, we identify thresholds at which missense mutations disrupt protein stability and become DoS variants. From these we identify that the most functionally constrained genes in the genome are comparatively more robust to mutational instability than functionally redundant proteins. Also employing these thresholds to count DoS variation, we calculate LOEUF scores using this more frequent mutation type and show this recapitulates known constraint patterns.

Results

The tolerated range of protein stability effects due to missense variation

We computed predictions of protein stability change due to mutation ($\Delta\Delta G$) for all possible single amino acid substitutions in every human protein. We used the MAESTRO tool[16] to predict the stability effect, measured as $\Delta\Delta G$, of all single amino acid substitutions using structural models predicted by AlphaFold2[17]. We chose the MAESTRO tool because of its low computational cost and good predictive performance[11,18]. Furthermore, MAESTRO is available as standalone software, thereby facilitating computation in a parallel, high-performance computing environment. With this exhaustive stability change data we were able to observe the stability variation of variant sets of differing functional types. Figure 1a shows that the set of all possible changes for every residue in every protein ranged from highly destabilizing $\Delta\Delta G$ values above 2.5 kcal/mol to overly stabilizing changes with values below -1.5 kcal/mol. Figure 1a also compares the observed, tolerated stability variation for each of the functional constraint categories (LOEUF deciles) estimated for missense variants from the GnomAD database[12], and stability variation observed among all observed pathogenic, missense mutations from the ClinVar database[19]. As might be expected, the range of $\Delta\Delta G$ values for missense variants observed in the most functionally constrained LOEUF decile (bin 0) is narrower than the range of pathogenic missense variants recorded in ClinVar. The range of tolerated DoS becomes increasingly broad with decreasing functional constraint. Yet, the range $\Delta\Delta G$ values for the least constrained genes (bin 9) is still much narrower than that exhibited by all possible mutants (Figure 1a). Noteworthy is the skew in ClinVar pathogenic variation towards destabilizing variation (higher $\Delta\Delta G$), compared with population variation observed in the GnomAD dataset.

For comparison, Figure 1b shows an additional functional constraint metric, S_{het} has robust performance with shorter genes[20]. As observed among proteins of decreasing LOEUF, the range of tolerated stability variation becomes narrower with increasing selective pressure, though the differentiation of these effect is less pronounced between these categories than for LOEUF decile bins.

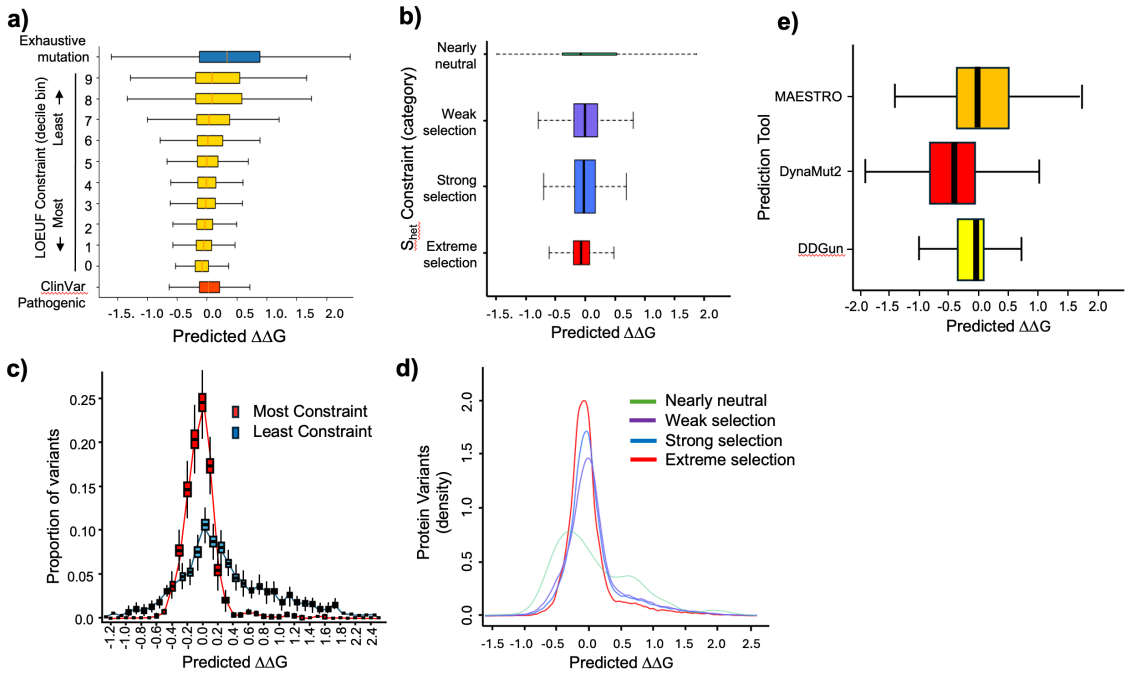

Figure 1. Functional constraint and predicted protein instability due to single amino acid substitutions. **a)** Range of predicted protein instability (ΔΔG) for missense variants of defined functional importance (medians marked in red, bounds of each box are the interquartile range (IQR) and whiskers extend 1.5*IQR from each box). Variant categories are i) ClinVar Pathogenic: all missense change from the ClinVar database with the annotation CLNSIG=Pathogenic, ii) LOEUF Constraint: GnomAD population variation stratified by gene functional constraint (LOEUF) deciles, and iii) Exhaustive mutation: the comprehensive prediction of stability effects for all possible single amino acid substitutions in all human proteins. **b)** Predicted protein instability variation grouped by gene and stratified by S_{het} selection constraint categories. **c)** Comparative depletion of single amino acid variation by predicted ΔΔG between LOEUF constraint categories: most constrained (red; LOUEF bin 0) and least constrained (blue; LOEUF bin 9) in a disease-free cohort (1000 Genomes, Phase 3 release, 3115 individuals). **d)** Comparative depletion of single amino acid variation by predicted ΔΔG between S_{het} selective constraint categories (green: nearly neutral, purple: weak selection, blue: strong selection, red: extreme selection). **e)** Range of ΔΔG values predicted by three widely used tools (MAESTRO, DynaMut2 and DDGun) on the same input set of amino acid substitutions.

Instability thresholds for missense disruption-of-function variants

We were motivated to identify instability thresholds at which the most functionally constrained human proteins no longer harbored presumed-pathogenic destabilizing or stabilizing amino acid variation in population-scale datasets. Our presumption was that among these constrained proteins, variants with large stability effects that affect protein function will become subject to purifying selection and hence be absent from the sequence record of disease-free human populations. To identify stability change thresholds at which missense variation becomes subject to purifying selection, we sought the maximum and minimum values of ΔΔG that were tolerated within the most constrained human proteins (LOUEF bin 0). Figure 1c shows the variation in the predicted ΔΔG of amino acid substitutions observed in a disease-free human population of 3115 individuals (1000 Genomes, Phase 3 release)[21], where observed missense variation in the most- and least constrained LOUEF decile bins (0 and 9, respectively) is plotted separately. The variation observed among the most constrained human proteins (LOEUF bin 0) was presumed to

be almost entirely benign and that from the least constrained proteins (LOEUF bin 9) was assumed to contain a considerable number that are deleterious changes. Figure 1c shows the expected excess of destabilizing and overly-stabilising variation present among LOEUF bin 9 proteins as longer tails extending to higher and lower ΔΔG values. Using this observed depletion of protein instability variation in the most constrained (bin 0) genes, we chose upper and lower ΔΔG cut-offs of 0.5 and -0.5 kcal/mol, respectively. We repeated this threshold-finding analysis with the selection pressure categories defined by S_{het} value. [14]The depletion of missense variation from 'extreme selection' gene category was compared to the 'nearly neutral' category (Figure 1d) and this comparison supports the thresholds chosen above.

Using -0.5< ΔΔG <0.5 thresholds, we calculate a false-discovery rate (FDR) of 6%, for DoS mutants being annotated as benign variants in ClinVar (CLNSIG=Benign). With this same benign variant set, we also obtained comparable FDR values with AlphaMissense pathogenicity scores[22] (4.3% of benign variants called as 'pathogenic') and substantially higher FDR values than with PolyPhen2[23] (14.9% called 'probably damaging') or SIFT[24] (29.9% called 'deleterious'). ΔΔG values alone with these thresholds for DoS variation (-0.5<ΔΔG <0.5) have good performance for detecting missense variation that may cause a disrupted molecular phenotype.

These ΔΔG threshold values (-0.5<ΔΔG <0.5) are narrow compared to those empirically measured[25,26]. For comparison, we replicated ΔΔG predictions for 2419 amino acid substitutions observed across eleven proteins with two additional tools: DynaMut2[27] and DDGun[28]. Both additional tools have been shown to provide similar accuracy to MAESTRO[11]. The predicted values of these additional tools also show a narrower range of predicted ΔΔG values than that observed in empirical data (Figure 1e), lending support to the finding above that at relatively minor predicted instability values, there are observable depletions of missense variants among functionally constrained genes compared to those that are relatively unconstrained.

With the instability thresholds above, 18.4% of all ClinVar pathogenic missense variants (5115/27766=0.184; CLNSIG=Pathogenic) lie outside of these boundaries for tolerated stability of functionally benign mutations.

Proteins subject to strong functional constraint are more robust to mutational instability

We developed an aggregate protein metric, the Instability Heat Score (IHS), to quantitate the susceptibility to mutational stability effects of any given protein, subject to single amino acid substitution mutations. For any given protein, the IHS is the average of the absolute stability change (|ΔΔG|) of all possible substitutions that result in a predicted stability change that lies outside the thresholds determined above (-0.5<ΔΔG<0.5). This metric represents the susceptibility of a given protein to single incident mutations that cause an amino acid substitution. IHS varies considerably between proteins and the distribution of values differ with relative category of functional constraint (Figure 2a). Figures 2b-d show representative heatmaps of proteins that are either more fragile to amino acid substitution (high IHS) or are colder (low IHS). We have generated heatmaps of IHS of all human proteins (available at www.stabilitysort.org). In general, and as expected, proteins are rarely uniformly prone to mutational instability along their length.

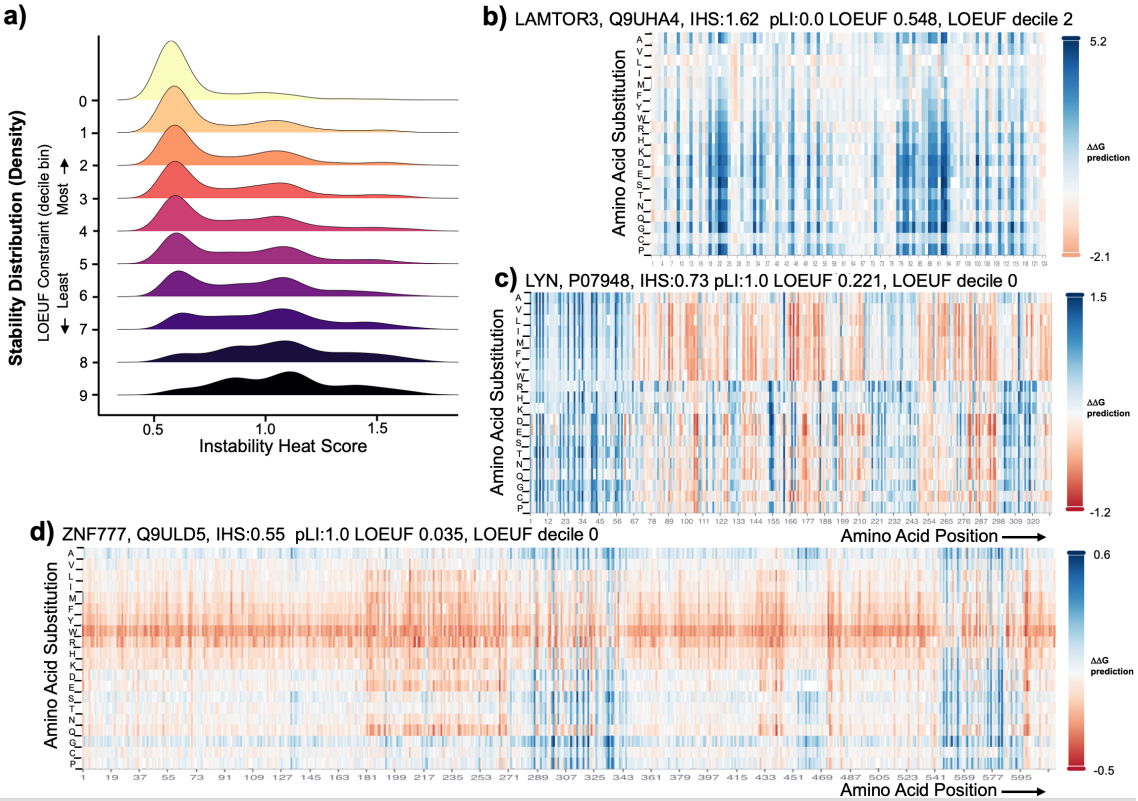

Figure 2. Instability Heat Scores (IHS). **a)** Distribution of IHS by LOEUF functional constraint category (partitioned by LOEUF decile). Representative heat maps of IHS (from www.stabilitysort.org) for **b)** LAMTOR3 (Q9UHA4, IHS:1.62, pLI:0.0, LOEUF:0.548, LOEUF decile:2), **c)** LYN (P07948, IHS:0.73, pLI:1.0, LOEUF:0.221, LOEUF decile:0) and **d)** ZNF777 (Q9ULD5, IHS:0.55, pLI:1.0, LOEUF:0.035, LOEUF decile:0) genes.

We observed that when proteins are partitioned into constraint decile bins by LOEUF that more constrained proteins have broadly lower IHS and therefore are generally less prone to large changes in stability due to missense mutations (Figure 3a). When we included only proteins that have well-powered LOEUF estimates[29] (GnomAD v4.1), the differentiation of IHS with functional constraint is slightly decreased (Figure 3b), yet the overall trend towards generally lower IHS in constrained proteins remains. Seeking a potential mechanism for this trend, we considered the contribution of relative protein disorder with IHS. Figure 3c shows a decrease in structural order (increased intrinsic disorder) quantified by the percentage of the AlphaFold2 model for each structure with pLDDT greater than 70%. Visually, this mirrors lower IHS in constrained protein LOEUF deciles groups.

Quantities such as pLi[30] provide an alternative metric with which to assess the relationship of IHS with functional constraint[31]. The pLi score observed for all human genes has a strongly bimodal distribution[31] as shown in the lower distribution in Figure 3d, with a greater number of genes displaying low functional constraint, as expected[31]. We partitioned genes by low (pLi < 0.5) and high (pLi > 0.5) functional constraint and observed the range of IHS for each category (upper boxplot in Figure 3d). Similar to LOEUF decile grouping, the two pLi groups indicate that the higher constraint genes (pLi > 0.5) have a general property of lower IHS, as indicated by the non-

overlapping notches between the two boxes. This is despite the two categories containing a very large number of genes each, potential diluting any subtle signals present in this information.

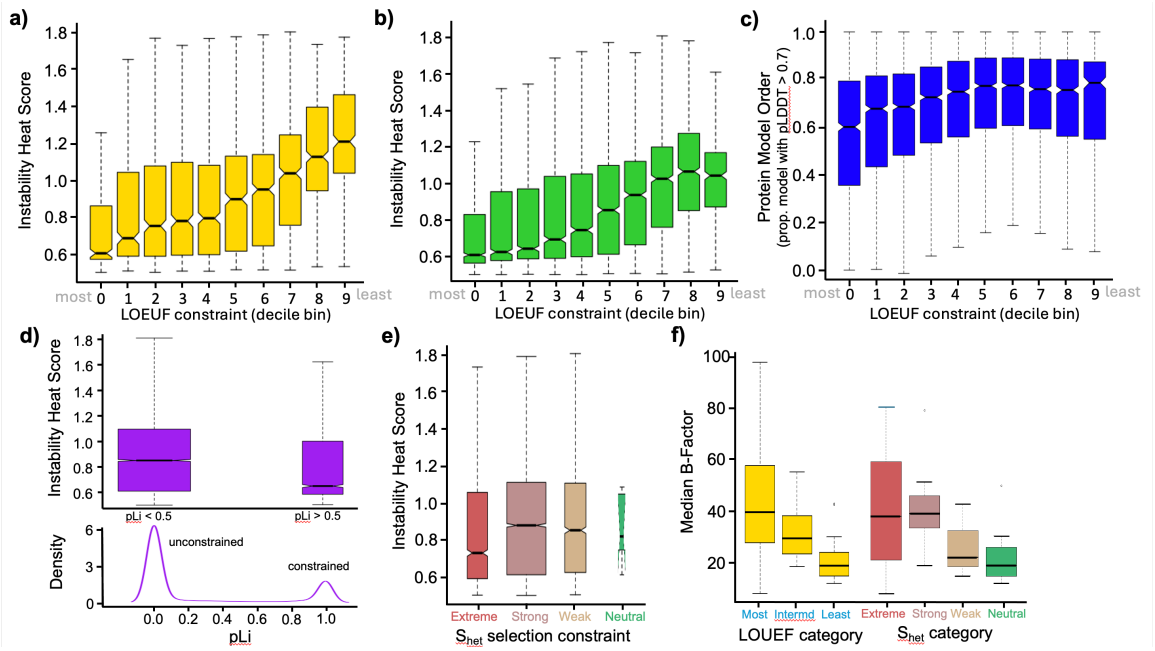

Figure 3. Protein robustness to stability effects of amino acid change with respect to functional constraint category. In all boxplots, the central bar in each box represents the median value of each respective category, the bounds of each box are the interquartile range (IQR), whiskers extend 1.5*IQR from each box and the central notches (where present) represent an approximation of the 95% confidence interval of the median box value. **a)** Observed range of Instability Heat Score (IHS) for all human proteins, grouped by LOEUF functional constraint decile bins (bin 0 is most constrained and bin 9 is least constrained), **b)** observed range of IHS by LOEUF decile bins for all well-powered human proteins, **c)** proportion of protein (AlphaFold2-model) with order greater than pLDDT > 0.7 by LOEUF functional constraint decile bin, **d)** comparative range of IHS for all human genes grouped by low- and high-pLi scores, with respective low and high functional constraint. The width of boxes in the upper plot indicates the relative number of genes present in each category, **e)** observed range of IHS for all human genes partitioned by S_{het} selective constraint categories. Box widths are proportional to the number of genes included in each category. The 'neutral' category in green contains very few genes and has an expanded width by a factor of three to better display the mean and notches for this category only, and **f)** median B-factor for experimentally solved protein structures, grouped by LOEUF and S_{het} constraint categories.

Similarly, we replicated this analysis using the gene selection pressure categories defined by S_{het}[14]. Figure 3e shows boxplots of IHS by S_{het} selection constraint categories (extreme, strong, weak and neutral selection) following the naming scheme of Zeng *et al*[14]. As with the pLi comparison above, the number of genes present in each selection constraint category varies, and there are very few genes that are neutral. However, the median IHS for genes subject to extreme selection is distinctly lower than the strong and weak categories, though the small number of genes in the neutral category yields an inconclusive comparison with other categories.

The broad phenomenon that the most functionally constrained proteins may be less prone to instability by some metrics is recapitulated in the median B-score values of proteins with experimentally solved structures (Figure 3f, Supplementary Data 1). Noteworthy to this investigation is that the experimentally solved structures are frequently only partial structures (see Supplementary Data 1) and do not include intrinsically disordered regions, due to the inherent difficulty with experimental crystallization of these regions. Proteins from the most functionally constrained categories have higher median B-score values than those of the least constrained categories. These proteins in experimentally-solved structures have greater uncertainty (and thus greater movement) of the positions of atoms in the protein crystals. This same trend is also present among gene categories (strong, weak and neutral selection) partitioned by S_{het} score (Figure 3f), though B-factors for proteins in the extreme selection show the broadest variation and encompasses that of all of the other three categories.

We note from Figure 3a that the most constrained proteins (bin 0) have a median IHS of just 0.61. But despite this, the greatest number of pathogenic DoS variants present in ClinVar (CLNSIG=Pathogenic) are also found among these most functionally-constrained proteins, and of these, 20.4% are amino acid substitutions with functionally disruptive stability effects (at threshold $-0.5<\Delta\Delta G<0.5$). Importantly, we variously found no correlation between functional constraint categories and commonly-used predictors of mutation functional effect (CADD, SIFT, PolyPhen2), nor with residue solvent accessibility. We did observe a weak increase in AlphaMissense pathogenicity score with increased functional constraint (data not shown).

Instability Heat Scores and relative pathogenic effect of missense variation

We explored the relevance of protein IHS in the context of missense variation observed in a large phenotype-associated genome dataset, obtained from individuals with autism and their families[32]. This dataset aggregates genomic variation from 63237 individuals and calculates Bayes Factor (BF) values to quantify evidence of phenotypic association from multiple variant classes (protein truncating variation (PTV), missense variation, indels and copy number variation) and modes of inheritance[32]. We used these BF values to investigate covariation with both IHS and predicted $\Delta\Delta G$ scores, at both a per gene and per variant level. The BF dataset strongly indicates that PTV contributes most evidence that implicates the majority of the 72 ASD-linked genes[32]. But intriguingly, for a minority of genes, missense variation provides more than 90% of the evidence that links them to an autism phenotype in proband individuals (eg. PTEN, SLC6A1, DYNC1H1, DEAF1, AP2S1)[32]. The 72 ASD-linked genes are overwhelmingly from the most functionally constrained classes (54 of 72 genes are from the top 10% of most constrained gene class). We find (Figure 4a) that these 72 genes are heavily skewed towards lower IHS and as a group have some of the lowest IHS values in the genome. Furthermore, only three of the 72 ASD-linked genes (DEAF1, PTEN, AP2S1) harbor potential DoS variation is ASD probands (Figure 4a, Supplementary Table 1). Whereas Figure 4b shows this same comparison for all *de novo* variation identified in all genes (both ASD-linked variation and passenger mutations). Comparison between Figure 4a and 4b identifies that, as a group, ASD-associated genes have i) much lower IHS, ii) much narrower range of predicted $\Delta\Delta G$, and iii) comparatively almost no *de novo* variants in ASD-linked genes harbor functionally-important, DoS variation. Two ASD-linked genes (PTEN and AP2S1) are outliers to the above generalizations, having the highest two IHS of the 72 ASD-associated genes, and are two of the least functionally constrained proteins in this set. Supplementary Table 1 provides further information of IHS, LOEUF functional constraint and *de novo* missense mutations observed outside DoS thresholds in ASD probands. Figure 4c shows BF values for PTV and missense variation (MisB and MisA classes, after nomenclature of Fu *et al*[32]) plotted against IHS. This comparison shows that PTEN and AP2S1 have the highest susceptibility to DoS mutations of the 72 ASD-linked genes, and this is reflected in the unusually high contribution of missense variation (BF values from MisB) to detecting this phenotypic association.

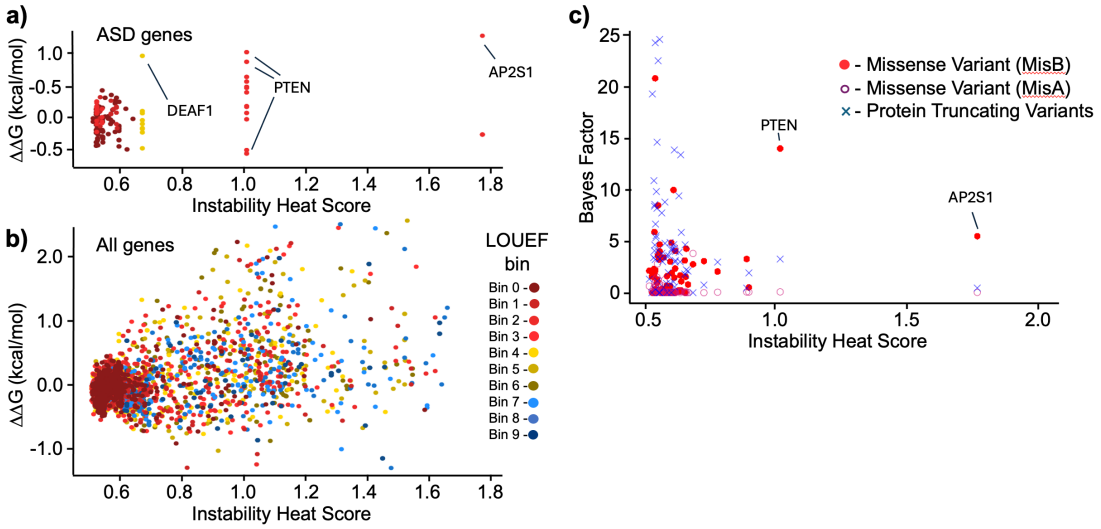

Figure 4. Genes linked to phenotypes in individuals with autism are robust to potential protein instability effects of *de novo* missense variation. **a)** Almost all ASD-linked genes[32] are highly functionally constrained (points colored by LOEUF bin), have lower Instability Heat Score (IHS) and little observed *de novo* genetic variation has stability effects outside the -0.5<ΔΔG<0.5 thresholds that imply functional importance. Whereas **b)** among all observed *de novo* genetic variation present in the same individuals there is a broad range of functional constraint, IHS and stability effects on the encoded proteins, including much that is likely to compromise function. **c)** With Bayes Factor (BF) values for 72 ASD-linked genes, for each of three variant classes (using BF values and nomenclature from Fu *et al*[32]), two proteins (PTEN and AP2S1) display both higher IHS and MisB BF values, and additionally, contain amino acid substitutions in ASD probands with ΔΔG values that imply function DoS variation of these proteins.

Comparison of constraint between pLoF and DoS variation

More point mutations will cause missense variation than will cause nonsense or canonical splicing changes. Hence, DoS variation has the potential to greatly outnumber protein LoF (pLoF) variation, which is presently the gold-standard variation type used to estimate gene functional constraint. Using observed variation from the GnomAD dataset [12], and the DoS thresholds chosen above (-0.5 <ΔΔG < 0.5), there are five times more observed DoS variants per gene (median=35) than pLoF variants (median=7).

We used the set of observed DoS variants per gene from the GnomAD dataset (v4.1) and calculated the expected number of DoS variants[33] to calculate LOEUF scores per human gene (see Materials and Methods). Figure 5a shows that comparion between LOEUF scores calculated with the same methodology, but with either pLoF and DoS variation as input. The range of LOEUF scores calculated from DoS variants is narrower than that calculated with pLoF variants, with few genes having values less than 0.5 or greater than 1.5. When genes are partitioned by LOEUF decile values, Figure 5b shows that the greatest similarity between LOEUF scores calculated from both DoS and protein pLoF variant classes is observed among the most constrained genes and this less so for genes subject to less constraint.

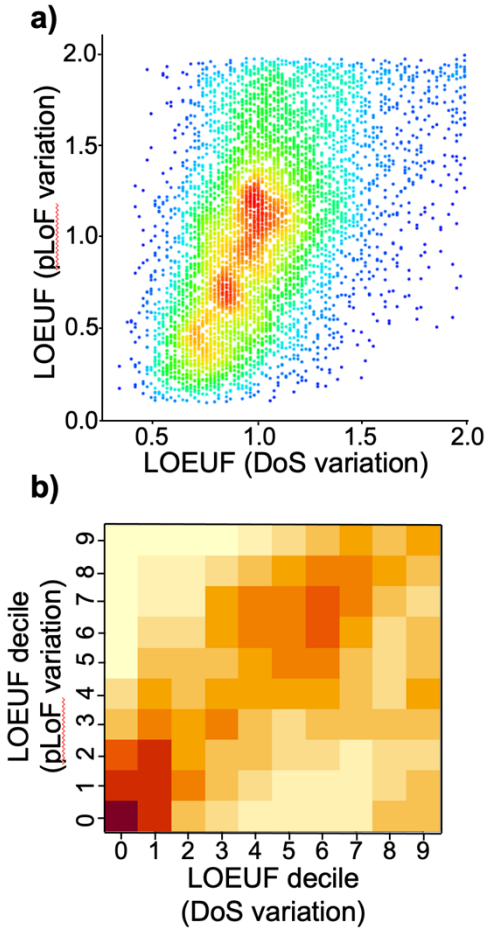

Figure 5. Comparisons of gene-specific LOEUF scores derived from LoF and DoS variant sets, calculated from GnomAD (r4.1) data using EnsEMBL canonical transcripts. **a)** Heat plot of similarity of LOEUF scores between those calculated with pLoF and DoS variation, and **b)** heatmap of similarity of gene identifiers for genes present in each LOEUF decile category, calculated from either pLoF or DoS variation.

Supplementary Data 2 contains a reference dataset of observed and expected variant counts for both pLoF and DoS variation and the LOEUF scores calculated from these for all human genes (EnsEMBL GRCh38 p14) with canonical transcripts having a one-to-one mapping with UniProt identifiers for which an AlphaFold2-predicted structural model exists. Genes in this Supplementary Data have also been annotated with the raw difference in LOUEF scores calculated by pLoF and DoS variation.

Table 1 shows selected genes from Supplementary Data 2 with the largest differences in functional constraint between pLoF and DoS variants. Of note, HLA-B and HLA-DRB1 genes have LOUEF scores calculated with DoS variants that are more than double that calculated with pLoF variation. These genes encode subunits of the T-cell receptor, and missense variation among copies of these genes is integral to recognition of a diversity of antigenic peptides. Many of the genes in Table 1 with the most disparate LOEUF scores are among the shorter genes in the human genome and have few, if any, observed pLoF variants in the GnomAD dataset. Other genes have very few DoS variants, while having relatively larger numbers of clear pLoF variants. Table 1 includes two gene examples of functionally important roles for the gene described and include OMIM identifiers for disease phenotypes that result from pLoF mutations in these genes.

Gene	Length (nt)	Transcript	DoS variation			pLoF variation			OMIM Phenotype-Genotype (MIM numbers)
			Observed Variants	Expected Variants	LOEUF	Observed Variants	Expected Variants	LOEUF	
HLA genes - high missense variants, antigenic diversity									
HLA-DRB1	798	ENST00000360004	78	31.00	2	6	10.24	1.16	
HLA-B	1086	ENST00000412585	128	60.05	2	10	18.59	0.91	
Appear constrained in GnomAD, due to very few observed LoF									
RGS1	627	ENST00000367459	43	29.25	1.86	1	9.39	0.51	
AQP9	885	ENST00000219919	139	81.23	1.94	3	11.72	0.66	
RAD23B	1227	ENST00000358015	84	67.79	1.48	1	20.92	0.23	
PRPS1L1	954	ENST00000506618	103	29.87	2	2	8.01	0.79	
LAMTOR3	372	ENST00000499666	31	23.53	1.76	1	8.66	0.55	
Appear unconstrained in GnomAD, but with penetrant mutant phenotypes									
KLLN	534	ENST00000445946	22	52.18	0.6	3	2.62	1.89	615107, 612105
SDHAF1	345	ENST00000378887	28	66.18	0.58	1	0.91	1.90	619166, 612848

Table 1. Selected genes with greatest LOEUF difference between values calculated with either DoS or pLoF variation

Discussion

From an exhaustive computational mutagenesis experiment and the predictions of the resulting changes to protein stability, we have observed that, in aggregate, the most functionally constrained human proteins are more robust to the stability effects of single amino acid substitutions. That some proteins are structurally more capable of accommodating amino acid substitutions has been the subject of long interest (see [34]). Both the higher intrinsic disorder that typifies constrained, haploinsufficient genes[35] and the higher network centrality of constrained gene[36,37] go some way to explaining this trend. Worth consideration also is the often lethal effect of mutations to essential, constrained proteins and the subsequent high cost to organismal fitness. These effects may have led to selective pressure driving these proteins towards relatively fewer contacts between residues and therefore increased inherent flexibility to amino acid substitution. This is reflected in the higher median B-factors we observed from experimentally solved structures in the most functionally constrained proteins. It is striking how interwoven this property (captured by IHS) is with the overall functional constraint to which a given gene/protein is subject. One important consequence of this will be that fewer missense variants in strongly constrained disease genes will result in pathogenic effects, due to a central pathogenic mechanism of mutation being muted in these genes. Hence, when searching affected cohorts and/or personal genomes for causal mutations, if the phenotype or condition results from alteration or ablation of the function of highly constrained genes, the contribution of missense variation may be slight, and it is important to prioritise other mutation types in these investigations.

While keeping the preceding points in mind, functionally constrained proteins are not impervious to mutation-induced instability. We find that the most functionally constrained proteins disproportionately contain more observed pathogenic variants in the ClinVar database, potentially due to their high functional importance and potential to produce penetrant disease phenotypes. Strikingly, the distribution of pathogenic missense variation recorded in ClinVar is skewed towards destabilizing change, though our data also indicate that stabilizing structural change is just as subject to purifying selection. This underrepresentation of stabilizing pathogenic variation may represent some combination of i) a recording bias, ii) a difference in pathogenic mechanism, or iii) that the disease phenotypes due to this form of variation are milder.

Among genetic disorders that result from disruption of highly functionally constrained genes, our understanding of the contribution of missense variation remains poor, despite these being one of the more predominant forms of observed genetic variation. Here we describe the comparative robustness of constrained proteins to the stability effects of amino acid substitutions. In analysis of the observed de novo missense variation identified in people with autism and their families, we note the predominance of PTV in highly functionally constrained genes (LOEUF bins 0 and 1), yet point out the trend towards both higher IHS, and a greater contribution of missense variation to BF values, among slightly less functionally constrained genes (pLoF LOEUF decile 2 and greater). The prevalent assumption has been that the ambiguity of the functional effects of missense variants obscures true signal. Yet, here we have better characterized one aspect of these ambiguities faced in the interpretation of the functional effect of missense genetic variation.

Sequence conservation metrics are at the core of many tools for the prediction of the functional importance of missense mutations[22–24,38]. In a local, three-dimensional protein structure context, further useful metrics may be derived from identification of areas of evolutionarily constrained sequence that are co-located in the folded protein, but not necessarily adjacent in the primary sequence. The Missense Tolerence Ratio (MTR)[39,40] and Contact Set Missense Tolerance score (COSMIS)[41] are calculated by extension of a sphere of 5 to 8 Angstroms from a given amino acid and quantifying sequence constraint of all the amino acids that project into this local sphere. Interestingly, genes under strong functional constraint show much greater proportions of their encoded protein with constrained regions, calculated by the COSMIS score[41]. This is subtly different to, yet highly compatible with, our finding that functionally constrained proteins are more able to accommodate amino acid substitutions without incurring large structural stability effects.

This work does rely on a single method, MAESTRO, for the exhaustive predictions of mutation stability effects. We replicated a small, representative set of predictions with two other predictors (DynaMut2[27] and DDGun[28]) and the concordance was encouraging, though not exhaustive. The MAESTRO tool has been shown to perform very well and better than Rosetta[42] or FoldX[43] modelling in two comparison studies[11,18]. For exhaustive prediction of stability effects of all possible single amino acid substitutions in the human proteome, one essential consideration was computational expense. For this task, MAESTRO required just 448 CPU days of processor time. Other efficient tools with similar accuracy, such as DynaMut2, require prohibitively more computation time (approximately 7000 CPU years of processor time) to compute a replicate exhaustive prediction set. Though such an exercise to produce this comparative dataset, or improvements in the predictive performance of faster toolsets[18], would facilitate a useful comparison with this data.

All tools used in this study found a narrow range of tolerated stability effects (-0.5 kcal/ml < $\Delta\Delta G$ < 0.5 kcal/mol) of observed missense. The range of tolerated stability effects was similar between functional constrain measures (pLoF LOEUF and S_{het}). The $\Delta\Delta G$ thresholds derived here, that focus on the limits of instability that cause a missense variant to become subject to purifying selection may be very sensitive compared to those that can detect molecular dysfunction from laboratory-based assay. And, indeed, in many contexts the functional perturbation of protein structure may only need to be very slight for it to become subject to purifying selection. Furthermore, in previous work, we have shown that many missense variants at highly conserved sites had no experimentally assayable phenotype, even when they were in disease genes with an expected mutant phenotype[44].

The stability effects of amino acid substitutions on protein structures are known to be universal among the kingdoms of life[45]. However, the magnitude of the functional effects of missense variation is also appreciated to vary among functional classes of genes[8,9,46], and is potentially related to the severity of disease phenotypes and functional constraint to which different genes can produce and are subject to. One area of future work might investigate whether a diversity of appropriate instability ($\Delta\Delta G$) thresholds might be better for different classes of proteins and/or

folds than a single threshold value. One example is that it may be better to have differing ΔΔG thresholds for different protein functional contexts, such as the differences between globular proteins and those embedded in membranes. Further work should seek to refine the thresholds of functional disruption through protein instability, initially by protein functional classifications.

Quantitative estimates of gene functional constraint provide very useful information for interpretation of the importance of coding genetic variation. Here we identify that DoS variation is another reliable source of variation which may be used for calculating a orthogonal metric of functional constraint. Furthermore, the increased resolution provided by missense variant stability effects may mean that that some existing phenotype cohorts are sufficiently large for making population-driven assessments of altered gene constraint in certain phenotypic groups.

Materials and Methods

Datasets

Human population missense variation was obtained from GnomAD[12] v4.1. Canonical transcripts for human genes were obtained from EnsEMBL[47] release GRCh38 p14. Variant calls from disease-free individual genomes were obtained from the 1000 Genomes, Phase 3 release[21]. Confirmed pathogenic and benign missense variants were obtained from the ClinVar database[19] release 230930. Predictions of the stability effects of all possible single amino acid substitutions were made using structural models available from the AlphaFold2 Protein Structure Database[17]. The results of MAESTRO predictions[16] made for all human proteins[15] are available at stabilitysort.org/download/. 11198 *de novo*, missense mutations identified among ASD probands were obtained from Supplementary Table 20 from the original work describing these[32]. Observed and expected pLoF variant counts and LOEUF scores were obtained from GnomAD [12] v4.1. AlphaMissense median pathogenicity scores were obtained from datasets released with this work[22]. S_{het} scores from supplementary data of published work [14].

Toolsets

Predictions of variant functional effect were made with PolyPhen2[23], SIFT[24] and CADD[38], obtained using EnsEMBL Variant Effect Predictor[48].. Predictions of the stability effects of single amino acid substitutions on protein structures were performed with MAESTRO[16], DynaMut2[27] and DDGun[28].

Instability Heat Scores

To quantitate the per protein instability sensitivity to single amino acid changes, we created the Instability Heat Score (IHS). This score is the average of absolute stability change (|ΔΔG|) of all possible amino acid substitutions above the DoS threshold of 0.5:

$$IHS = \frac{1}{S}\sum_{i \in S} |\Delta\Delta Gi|$$

where *S* is the set of all possible amino acid substitutions where the absolute stability change is above the specified ΔΔG threshold of 0.5, and ΔΔG*i* is the stability change associated with the *i*-th possible amino acid substitution.

LOEUF Calculation from DoS variation

To calculate the expected number of DoS variants and the LOEUF score for a given gene, a minor extension was made to existing methodology[12,33]. This methodology was built to estimate

the expected numbers of pLoF mutations for a gene, given a model of the relative trinucleotide mutation frequencies in non-coding regions, calibrated with the numbers of observed synonymous substitutions for that gene. From this, and for potential pLoF sites for a given sequence, the expected number of substitutions for that type may be estimated. In our modification of this approach, we appraised each potential missense substitution for its' predicted effect it on structural stability of a given protein structural model. A substitution is counted as DoS if its' predicted stability effects were greater than defined thresholds ($-0.5 < \Delta\Delta G < 0.5$, see Results). The estimate of expected DoS variants was then used in place of expected pLoF variants in the calculation of LOUEF for each gene. Likewise, for observed variants, the predicted stability effects of each observed missense variant were appraised and counted if outside of the threshold values being applied. A python implementation of this method using DoS variation is available from https://gitlab.com/tdaadt/missensedof.

Data Availability

All datasets used are available in the public domain, including the comprehensive set of stability change predictions for all possible single amino acid substitutions in human proteins (stabilitysort.org/download).

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