

Supplementary Note 1

Differentially conserved frustration networks in the human Ras superfamily

Comparing superfamilies that have a distribution of broader evolutionary distances among their members proves more challenging than for the globin case. The human RAS superfamily comprises a broad range of proteins that despite their sequence and functional diversification, share both a common structural framework and enzymatic activity related to the production of GDP by the hydrolysis of GTP¹. This group of small GTPases play crucial roles in cellular signal transduction pathways, regulating processes such as cell growth, proliferation, and differentiation². The activation of RAS signaling is mediated by guanine nucleotide exchange factors (GEFs), while GTPase-activating proteins (GAPs) facilitate the hydrolysis of GTP to GDP, thereby inactivating RAS³. These proteins exist in two conformational states: an active GTP-bound state capable of binding to effectors to transduce signals and an inactive GDP-bound state. There are 5 RAS subfamilies, i.e. RAS, RHO, RAB, ARF and RAN, that bind to different effectors. The conserved GTP-binding site consists of 5 motifs, named G1 to G5, that contain the core residues essential for the GTPase activity and its associated conformational changes. These motifs have been shown to harbor different SDPs linked to family-specific functionalities¹. Mutations in RAS genes are commonly associated with various human cancers, including colorectal, lung, and pancreatic cancers, highlighting the importance of RAS signaling in oncogenesis⁴. Targeting RAS proteins has been an area of intense research for developing anticancer therapeutics⁵. The understanding of RAS biology and its implications in disease has been greatly advanced by studies utilizing molecular and cellular approaches, as well as animal models⁶.

We retrieved all paralogs within the RAS superfamily in humans¹ and calculated their frustration conservation patterns (see Methods). The RAN family was omitted from our analysis as it contained only one sequence. As a consequence of the high energetic variability within each family, the frustration conservation analysis using the SRFI analysis shows little conservation for the G1-G5 motifs (Supplementary Fig 4) with only a few minimally frustrated and neutral positions being frustrationally conserved ($\text{FrstIC} > 0.5$) across all families. Most of the minimally frustrated positions, i.e.: 14, 19, 20, 53, 56 and 81, are located in the G1 and G3 motifs. Within the G1 and G3 regions, there is relatively more energetic conservation compared to G2, G4, and G5. Additionally, in G4, N and K residues, which play a role in substrate specificity by contacting the oxygen of the purine⁷, are maximally frustrated and conserved. Surprisingly, the T35 residue, present within a loop region in G2, crucial for sensing GTP and binding the Mg²⁺ ion⁷, is conserved in terms of sequence in most members, but no conservation of energy is observed, or if conserved, it is neutral. This lack of frustration conservation is caused by the conformational diversity of the region across the different family members.

Inorder to gain resolution, we explored frustration conservation at the level of residue-residue contacts based on the mutational FI. This index was used instead of the configurational one as we expect functional signals to be more dependent on the amino acids identity than the conformational state of the protein. When mapped onto the reference structures for each RAS family, highly frustrated interactions are localized around the G1-G5 motifs whereas the rest of the fold is mainly enriched in minimally frustrated interactions (Supplementary Fig 5A). To enhance interpretability, we represented the interactions involving only residues that belong to the G1-G5 motifs or that are SDPs in each subfamily as graphs (Supplementary Fig 5B). Despite the large evolutionary distances, it is noticeable the highly connected network of frustrated interactions involving mainly G1 and G4 motifs, undetected when performing the SRFI. More in detail, highly frustrated interactions involving mainly Lys16 (G1), Asp57 (G3) and Lys117 (G4) are present in all four subfamilies. These interactions involve residues that interact with the GTP or the Mg²⁺ ion as well as some residues that interact with other protein partners (Supplementary Fig 6). RHO is the most divergent family as it has an extra helix next to G4,

after which there appears Pro138 (Pro124 in RAS numbering) that participates in many highly frustrated interactions with Lys117 and Lys118. These interactions within RHO are part of a different highly frustrated interaction network from the one containing Lys16 and Asp57.

Beyond similarities, there are energetic differences between the different subfamilies which seem to be related to SDPs (marked with asterisks in Supplementary Fig 4). As an example, SDP 83 (RAS numbering) shows family specific requirements; being neutral or without local frustration conservation at the single residue level but with conserved frustration levels in its interactions with other residues. This SDP is a highly conserved Asp with highly frustrated interactions (Supplementary Fig 5B) in ARF and RAB. In contrast, SDP 83 is a conserved Ser in RHO that establishes minimally frustrated interactions. The SDP identity is not conserved in RAS, having a mixture of both highly frustrated and minimally frustrated interactions (the latter with Val81, another SDP). Other SDPs, e.g. 20, 56 and 81 (RAS numbering) are minimally frustrated with variable identities within the hydrophobic and polar group of amino acids. The change in identity within the SDPs that interact with each other seems to be evolutionarily compensated in each subfamily, possibly finely tuning specific interactions with other residues.

In the case of non-SDP residues, such as the highly conserved residue G60, known to adopt different conformations in the active or inactive state of RAS⁸ its behavior varies across subfamilies. In certain cases, this variability may be attributed to the ability of AlphaFold to capture different conformational states in the protein models, influencing the local structure for equivalent residues in homologous regions and therefore influencing their frustration values. Similarly, T35, which undergoes conformational changes depending on whether it binds with GDT or not⁹, displays both minimally and maximally frustrated contacts across the ARF subfamily and only minimal frustration in the RHO subfamilies. Notably, in RAS and RAB, the contact energy is not conserved at all or, if conserved, it appears to be neutral. Despite expecting similar behavior to that observed in ARF and RHO, considering its mobile nature (as seen in the case of G60), we are limited in capturing differing conformations while analyzing a single protein. As a future endeavor, we could combine FrustraEvo will algorithms that are able to predict conformational ensembles for a given protein instead of just one structure¹⁰.

The differential evolutionary conservation of frustration in the RAS superfamily adds a layer of information that is simply not possible to observe just using SDPs information and that complements existing literature. Moreover, it offers a local energetic perspective of how fully conserved residues in sequences differentially interact with other functional residues, e.g. those in the G1-G5 region, like residue G60 or T35.

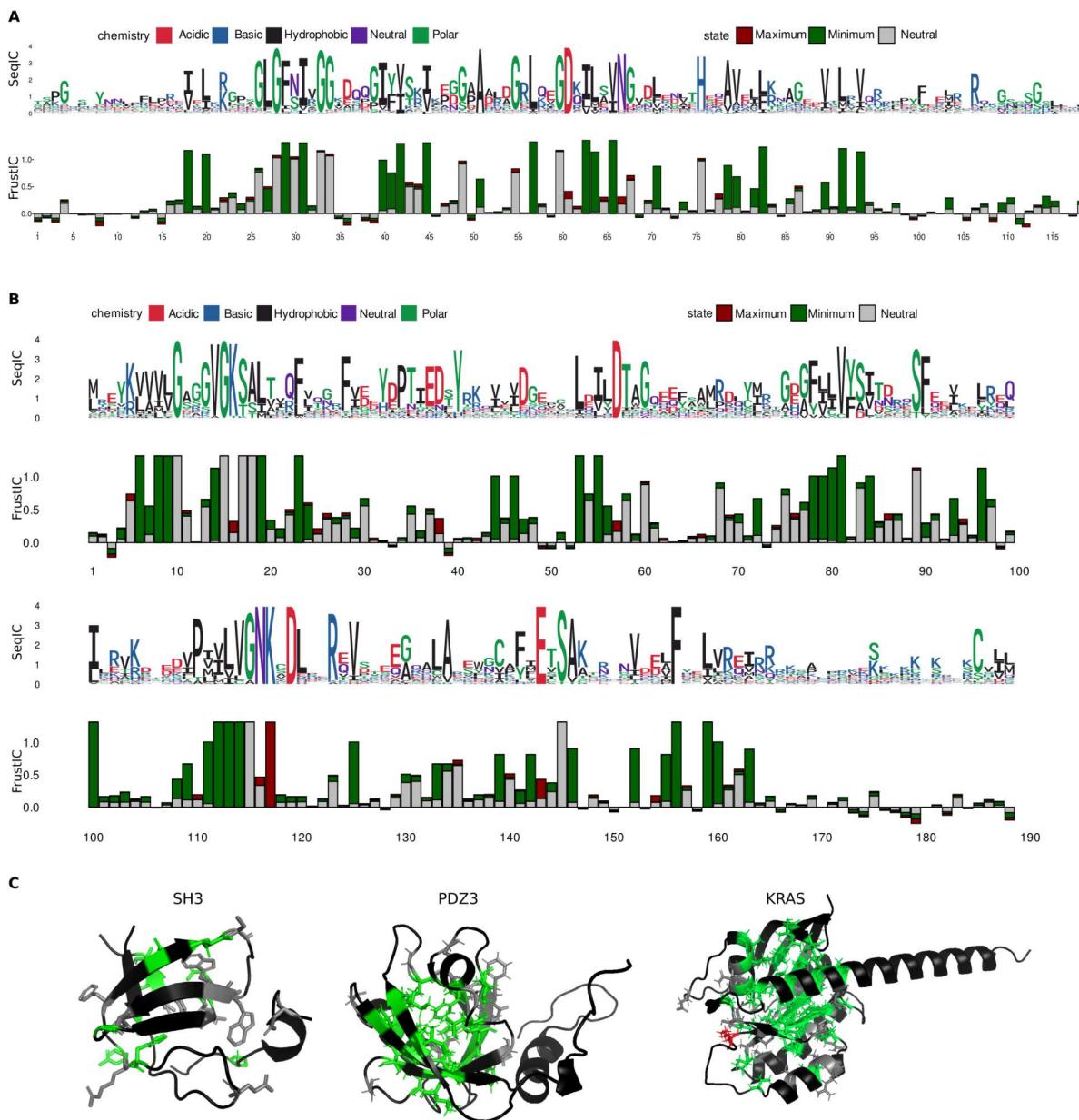
Supplementary Note 2

Unsupervised Analysis of the SARSCov2 Proteome in the context of the entire Beta Coronaviruses phylogeny with FrustraEvo

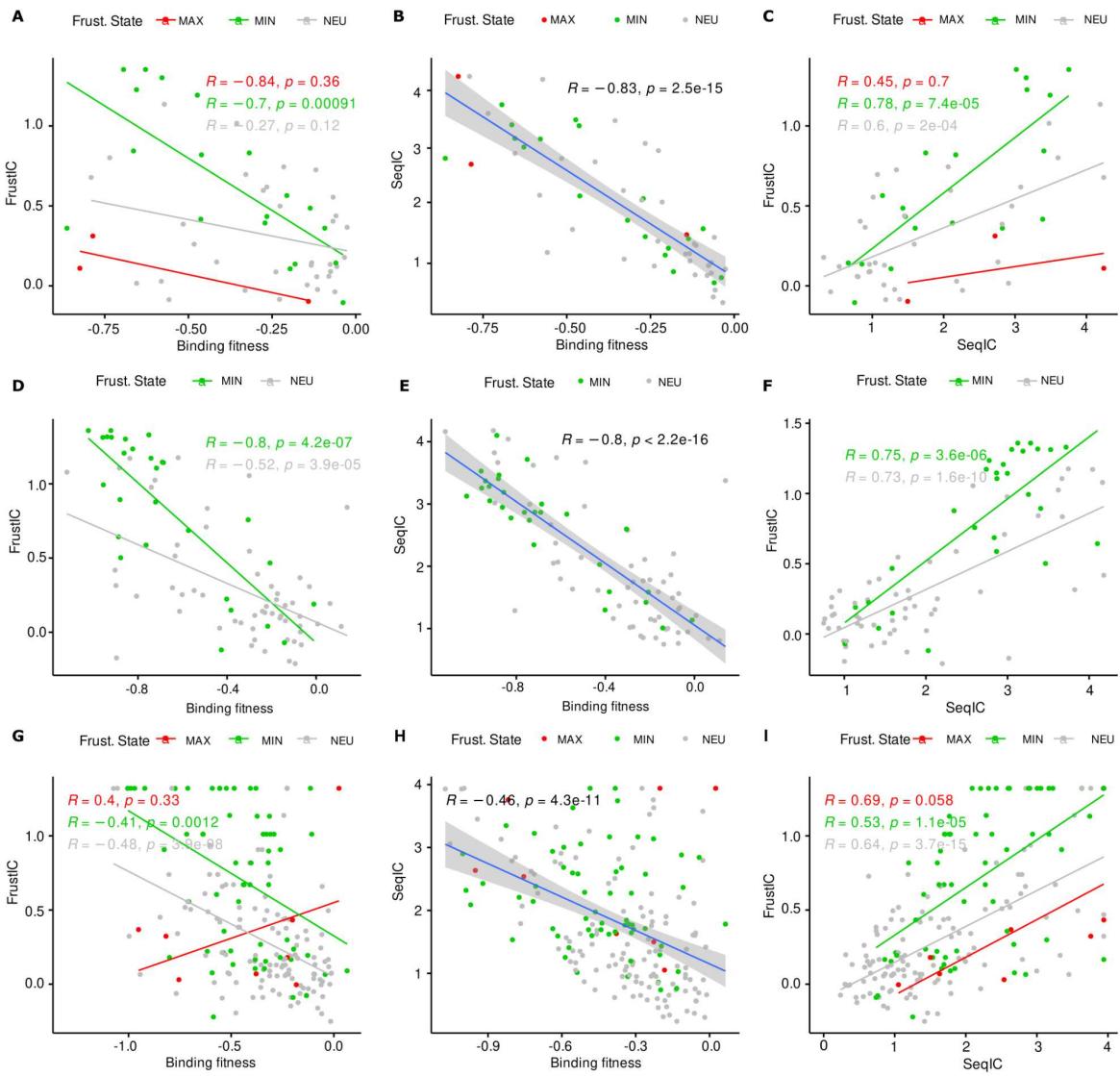
We have used our pipeline to process 29 SARS-CoV-2 proteins or protein domains (see Methods) from which 22 of them passed our quality filters (more than 10 sequences and average pLDDT over aligned positions of the cluster ≥ 80 ; see Methods, Supplementary Fig 7). For each cluster we compared sequence and frustration conservation by calculating the mean SeqIC and FrustIC per position and per cluster. In **Fig. 4A** we observe a significant positive correlation between these values ($r=0.69$, $p\text{value}=2.6\text{e-}14$). Some protein families like cluster 5 in the C-terminal domain of the Nucleoprotein (N_CTerm) deviate from the correlation. These have a lower FrustIC than expected (Supplementary Fig 8). Close inspection of this case shows that this family has regions with low pLDDT scores (Supplementary Fig 9A) regardless of the median for the entire protein being $\text{pLDDT}\geq 80$, which is known to correlate with flexible regions¹¹. Hence the conformation of the region and its frustration values can be heterogeneous and therefore yield lower FrustIC than expected given the sequence diversity in the family. At the same time, however, other factors such as the predicted amount of disordered residues (Supplementary Fig 9B) or the MSA phylogenetic diversity (Supplementary Fig 9C) can also influence the FrustIC and SeqIC relationship. On the other side of the spectrum, we have cases like cluster 2 in the non-structural protein (nsp) 13 (Supplementary Fig 8) for which the analysis of frustration conservation explains much more than expected from the overall correlation with sequence, because at some loci different amino acids can have similar frustration states, e.g. hydrophobic residues in the core of the structure (Supplementary Fig 10). Finally, when assessing full protein families we have found that some proteins, e.g. the C-terminal of the SARS-Unique Domain (SUD_Cterm) of nsp3 (3 subfamilies, FrustIC $\text{sd}=0.042$) or the Envelope (E) protein (2 subfamilies, FrustIC $\text{sd}=0.046$) are very homogeneous in terms of their average FrustIC values across subfamilies while others, e.g. N_Cterm (5 subfamilies, FrustIC $\text{sd}=0.217$), N_Nterm (6 subfamilies, FrustIC $\text{sd}=0.20$) or nsp8 (6 subfamilies, FrustIC $\text{sd}=0.176$), show a large amount of energetic variability across them. Once again, the quality of the models, the phylogenetic variability and flexibility of protein regions are factors that might influence these observations but no clear trend was identified (Supplementary Fig 9). Further information for all the families can be found in Supplementary Table 3 and Supplementary Table 4.

As we were interested in using this type of analysis to detect evolutionary constraints in SARS-CoV-2, we next focused on analyzing the Sarbecovirus subfamily that contains the proteins of this virus. In Fig. 4B we show the proportions for frustratingly conserved (FrustIC >0.5 , either MIN, NEU or MAX frustrated) and non-conserved (FrustIC ≤ 0.5) residues. This type of analysis allows us to rapidly sort proteins according to their frustration conservation level, which ultimately relates to there being different degrees of selective pressure on different proteins of the virus. The proportion of frustratingly conserved residues across proteins is heterogeneous (93.6% in the case of the E protein and up to 48.3% for the N_CTerm domain) reflecting the fact that some proteins are much more constrained by their family features than others. From those that are frustratingly conserved, the majority of residues belong to the neutral (mean = 0.35, $\text{sd} = 0.06$) or minimally frustrated (mean=0.29, $\text{sd} = 0.06$) classes, as expected. An interesting aspect to quantify is how much consistency there is between the Sarbecovirus family and the SARS-CoV-2 proteins. This would let us know to what extent the family restrictions are still present in the virus, whether the restrictions are of a different nature, i.e. stability vs. function, or whether there are novel constraints in the SARS-CoV-2 that were not present in the family. We found 332 residues conserved in the highly frustrated state within the proteome of the SARS-CoV-2 family (Supplementary Table 5) from which 301 residues were also conserved and highly frustrated in SARS-CoV-2 itself. This suggests that the functional signals, related to the presence of highly frustrated interactions in those regions, are coherent both at the family and at the SARS-CoV-2 levels. We found several residues where the frustration

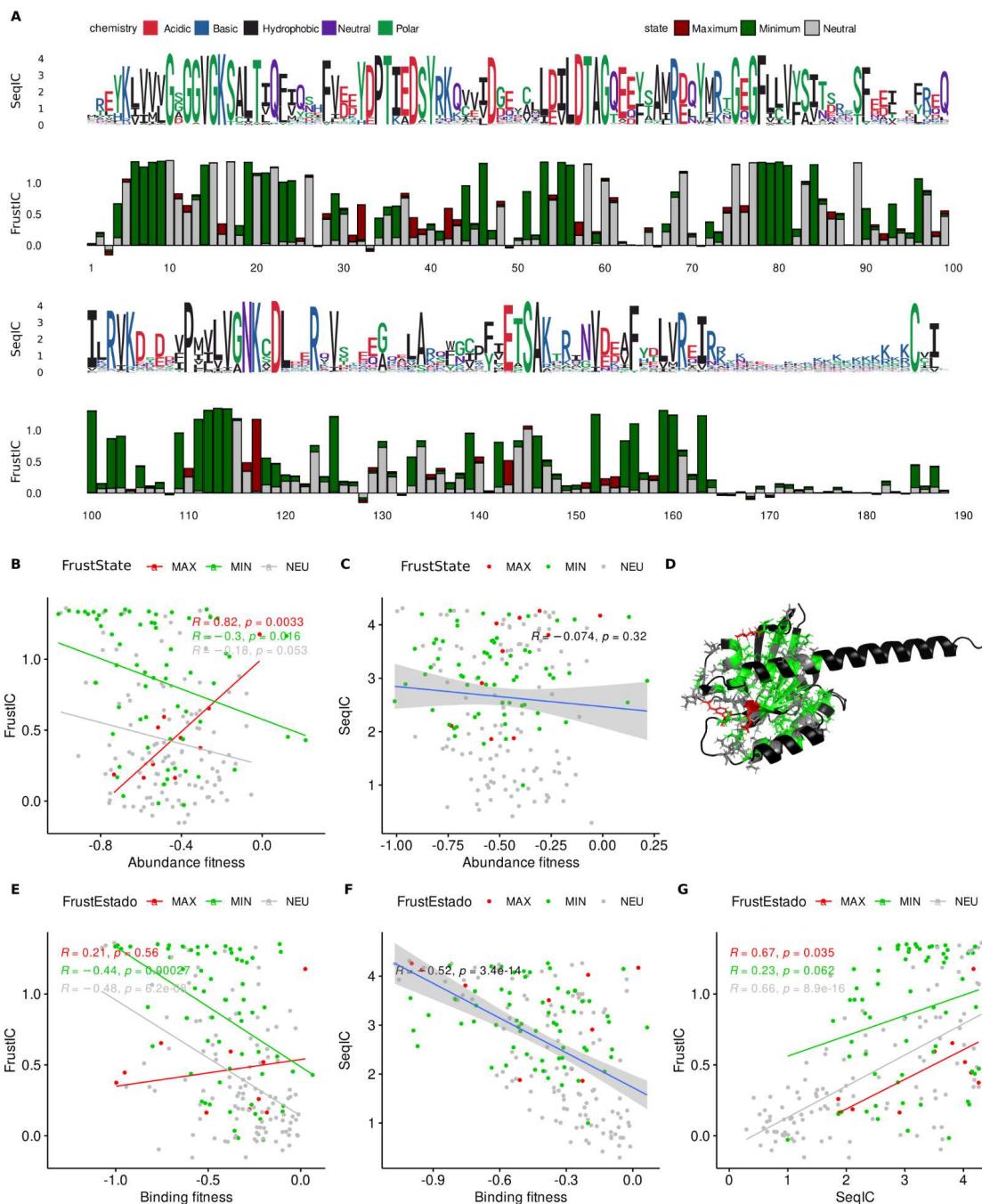
conservation state differs between SARS-CoV-2 and its family. There are 62 residues that are conserved ($\text{FrustIC}>0.5$) in the neutral or minimally frustrated state at the family level but conserved in a highly frustrated state in SARS-CoV-2, suggesting recent gain of function events (Supplementary Table 6). While the majority of these residues are located in proteins that are well studied (Spike n=18, nsp5 n=6), it is noticeable that other less characterized ones contain many of these type of residues as well (nsp2 n=9, nsp3 domains n=9), defining interesting positions for their study (Supplementary Table6). In addition, there are 345 positions that are conserved and highly frustrated in SARS-CoV-2 but that are frustrationally conserved at the family level (Supplementary Table 5).



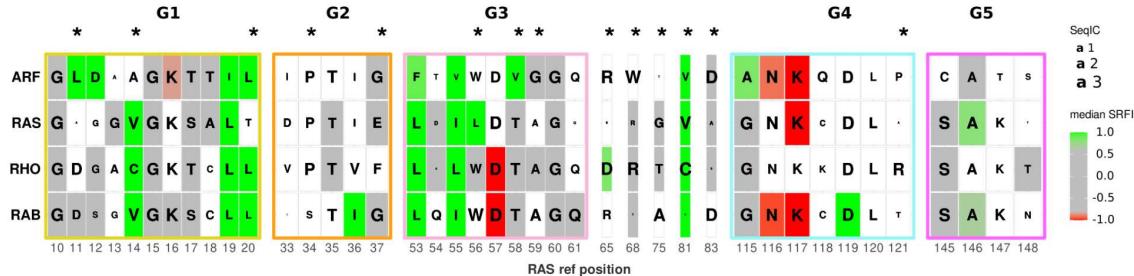
Supplementary Fig. 1. (A) Sequence and Frustration logo plots showing SeqIC and FrustIC values per MSA column respectively for PSD95-PDZ3. The numbering of the plot corresponds to the sequence of reference chain A from PDB 1BE9. Positions containing a gap in the sequences of reference are not considered in the plot. Protein PSD95-PDZ3 has been trimmed to match tested positions for mutation fitness in ¹⁴. (B) Sequence and Frustration logo plots for KRAS calculated with Rojas et al. data. Numbering corresponds to the protein of reference P01116-2. (C) FrustIC results mapped to SH3, PDZ3 and KRAS protein models. Residues with FrustIC<=0.5 are shown in black. Residues with FrustIC>0.5 are coloured according to the frustration state that contributes more information to the overall FrustIC value.



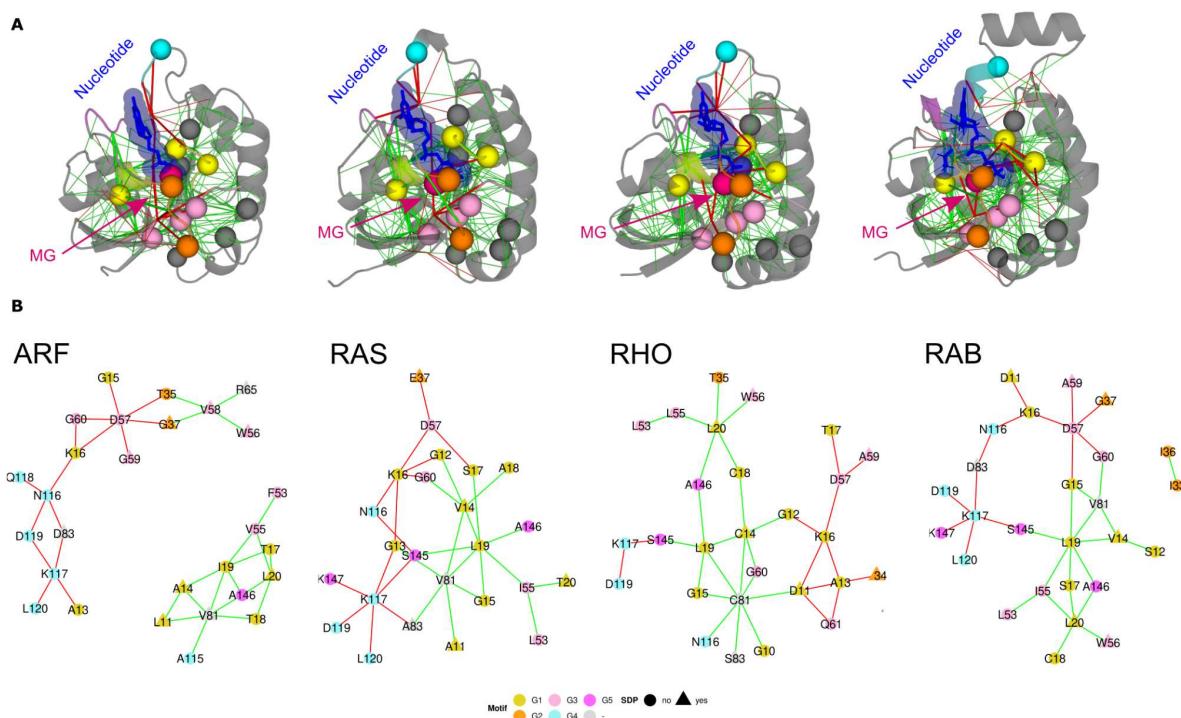
Supplementary Fig. 2. Pearson correlation between FrustIC or SeqIC and binding fitness and FrustIC vs SeqIC in SH3 domain (A, B, C), protein domain PDZ3 (D, E, F) and KRAS protein (G, H, I). P-value corresponds to a two-sided test. Error bands in the correlation plots correspond to a 95% confidence interval.



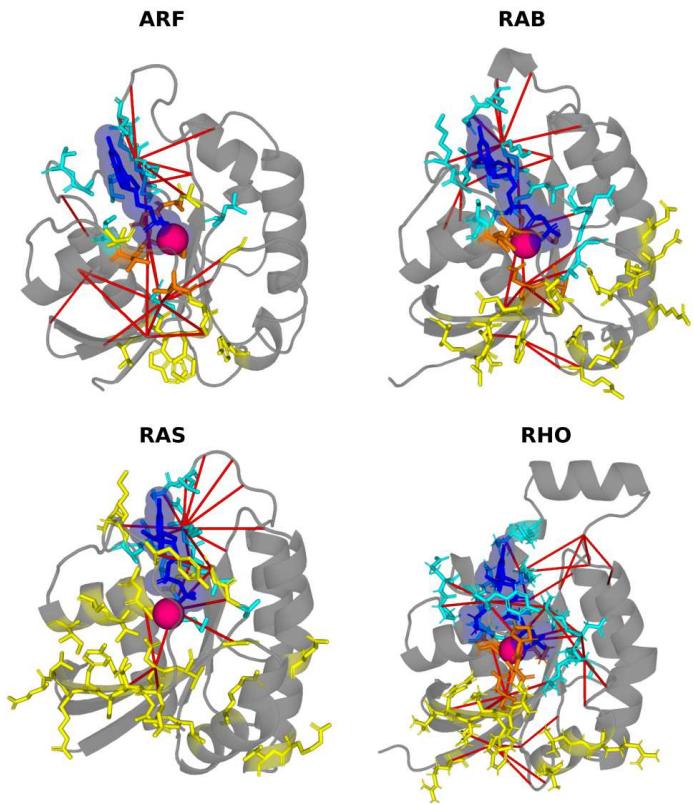
Supplementary Fig. 3. Results of KRAS with automatic retrieval of sequences of the protein family. (A) Sequence and Frustration logo plots for KRAS. Numbering corresponds to the protein of reference P01116-2. Pearson correlation between FrustIC or SeqIC and abundance fitness (B and C) or binding fitness (E and F) and FrustIC vs SeqIC (G). (D) FrustIC results mapped to KRAS proteins models. Residues with $\text{FrustIC} \leq 0.5$ are shown in black. Residues with $\text{FrustIC} > 0.5$ are coloured according to the frustration state that contributes more information to the overall FrustIC value. P-value corresponds to a two-sided test. Error bands in the correlation plots correspond to a 95% confidence interval.



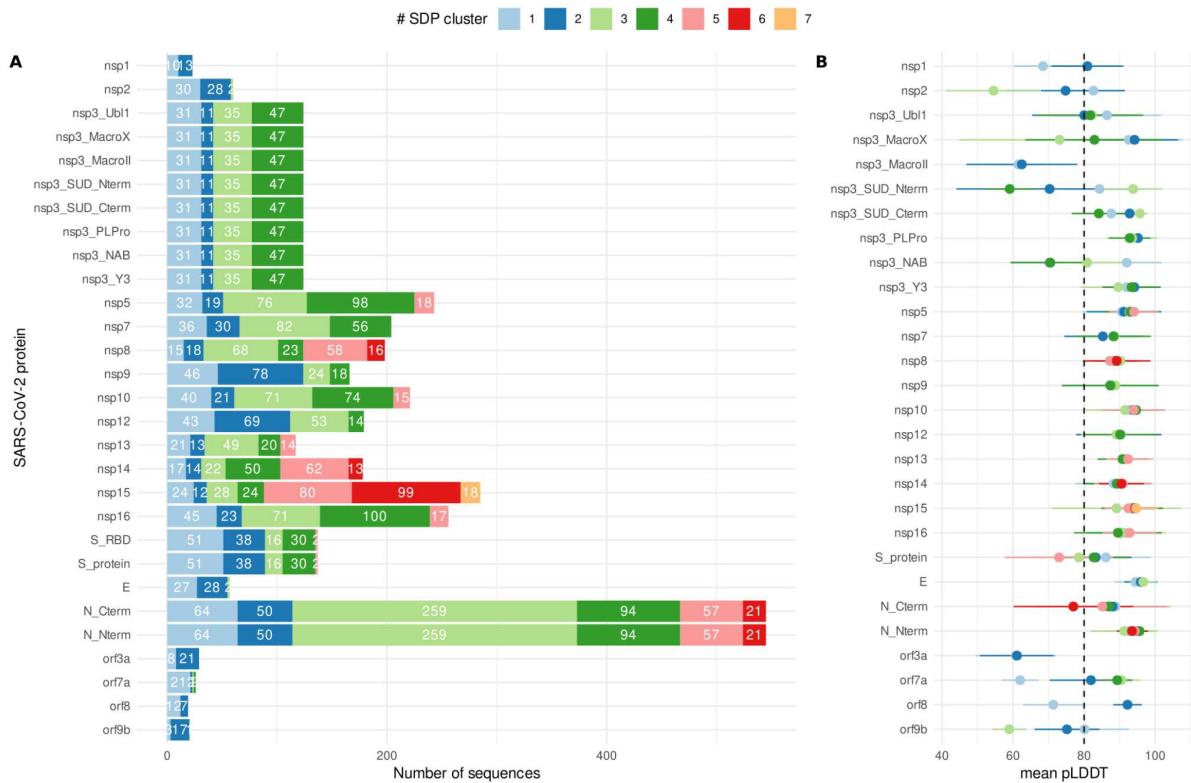
Supplementary Fig 4. Consensus multiple sequence frustration alignment (MSFA) comparing FrustIC and SeqIC results for the G1-G5 motifs and SDPs (marked with asterisks) in each of the subfamilies. Consensus amino acid identities are shown for each family. The size of the letter represents the SeqIC. The background color corresponds, in shades from green through gray to red, to the median single residue frustration index (SRFI) of that position across all structures in the family. White background means that FrustIC ≤ 0.5 .



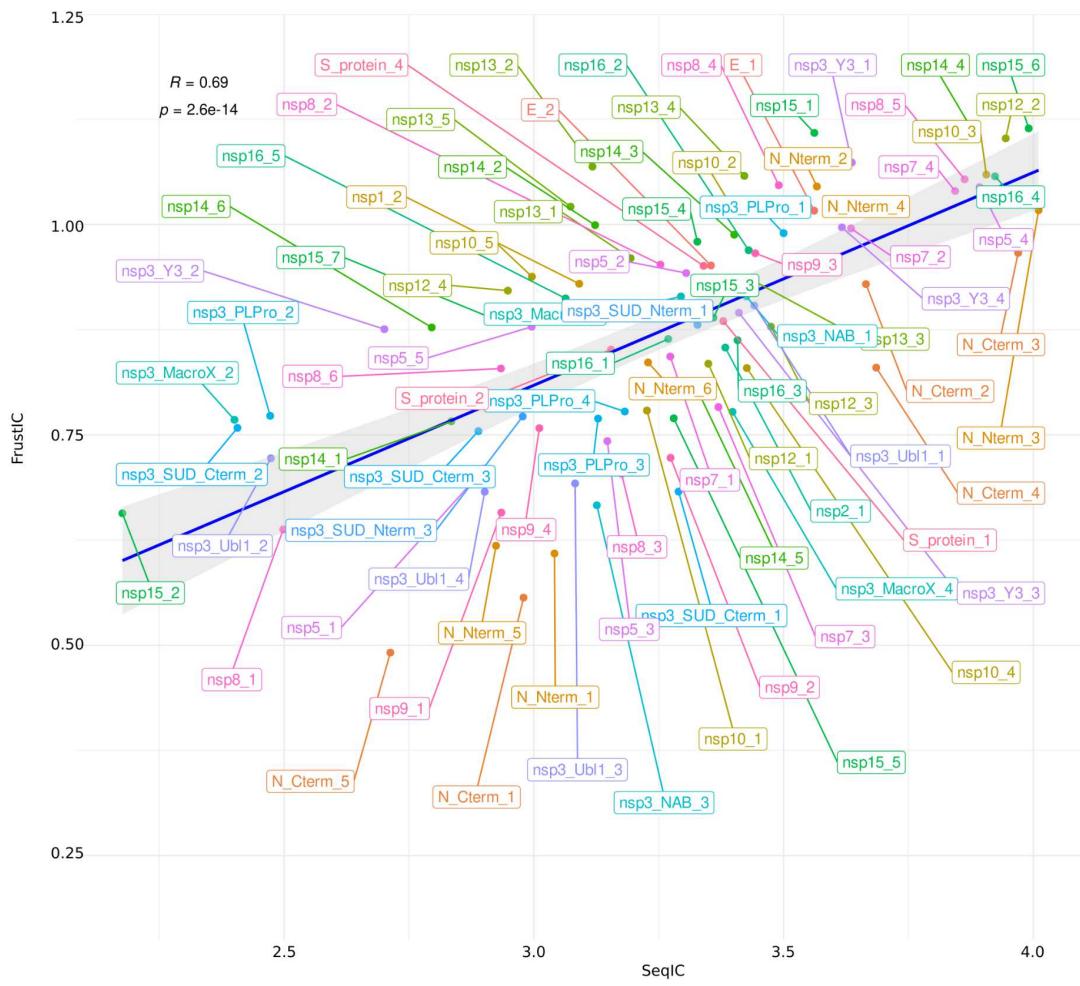
Supplementary Fig 5. Frustration conservation patterns unmask strongly conserved constraints across the Human RAS superfamily. A) Conserved highly frustrated (red lines) and minimally frustrated (green lines) interactions (FrustIC >0.5) according to the mutational FI. C α of SDPs are in globular shape. G1 motif is in yellow, G2 orange, G3 light pink, G4 cyan and G5 in magenta. Structures shown correspond to PDBs 7MGE (ARF), 3TKL (RAB), 121P (RAS) and 6BCB (RHO). B) Networks representing conserved highly frustrated (red lines) or minimally frustrated (green lines) interactions (FrustIC >0.5) between residues within the G1-G5 motifs (circular shape) or SDPs (triangular shape) in at least 50% of the structures of each subfamily. Nodes with triangular shape correspond to SDPs outside the G1-G5 motifs.



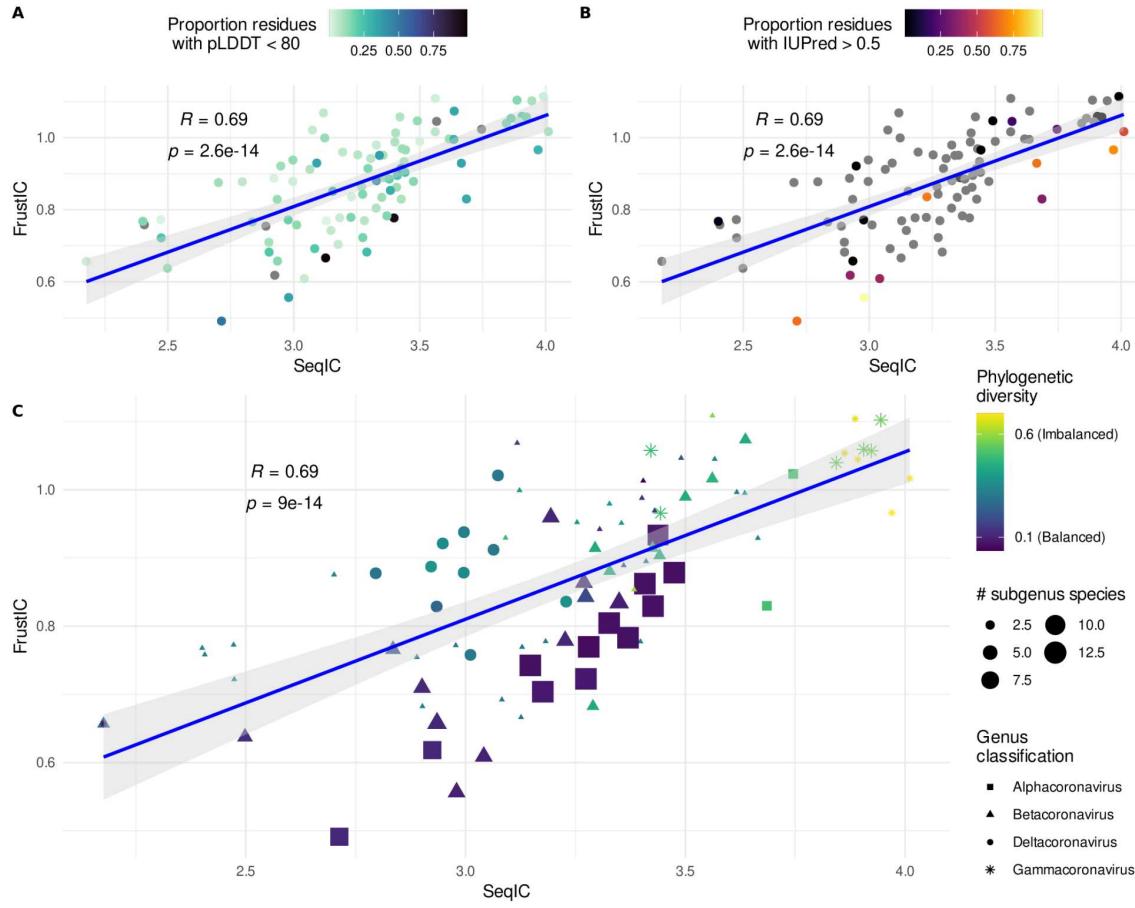
Supplementary Fig. 6. Highly frustrated contacts between residues of the ARF, RAB, RAS or RHO proteins (PDB codes 7MGE, 3TKL, 1XD2 and 6BCB respectively) and the GTP nucleotide (in dark blue and sticks) or the Mg ion (in magenta and spherical shape). Additionally, residues colored in blue or yellow and represented in sticks are residues that interact with the GTP and Mg ligands or a protein partner included in the PDB file respectively (inter-residue distance $\leq 5\text{\AA}$). When they are colored in orange means that they participate in both types of interfaces (protein and ligand).



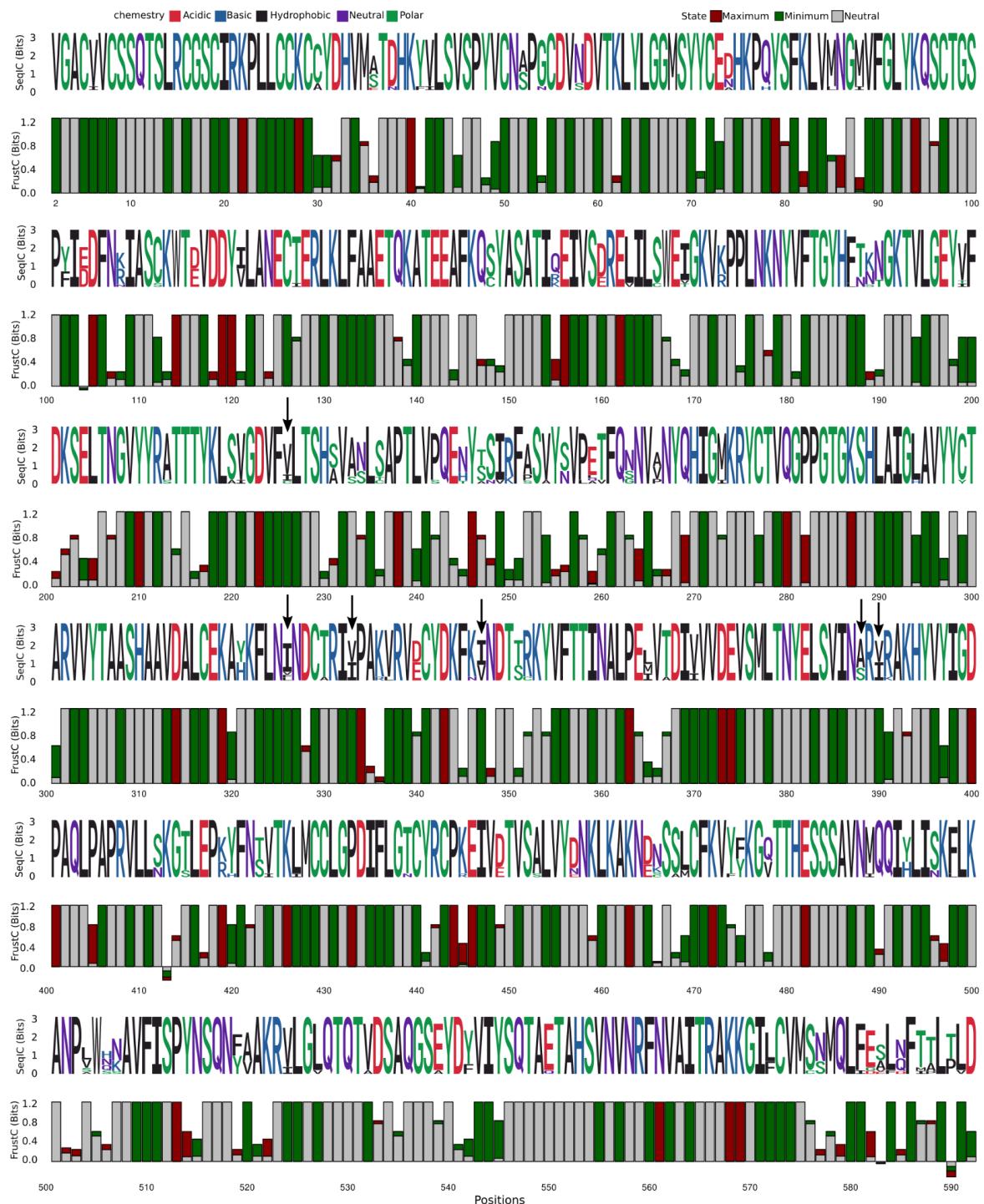
Supplementary Fig. 7. Coronavirus S3Det cluster and AlphaFold2 models quality. (A) Barplot depicting the distribution of sequences per S3Det cluster of all proteins or protein domains considered in the study (see Tables S2 and S3). Clusters with less than 10 sequences were not considered in our analyses. (B) Mean pLDST score per S3Det cluster of each protein or domain. The dashed line at pLDST=80 represents the minimum quality threshold for a cluster to be considered. Below that we considered that the models are of low quality and therefore removed from the analysis.



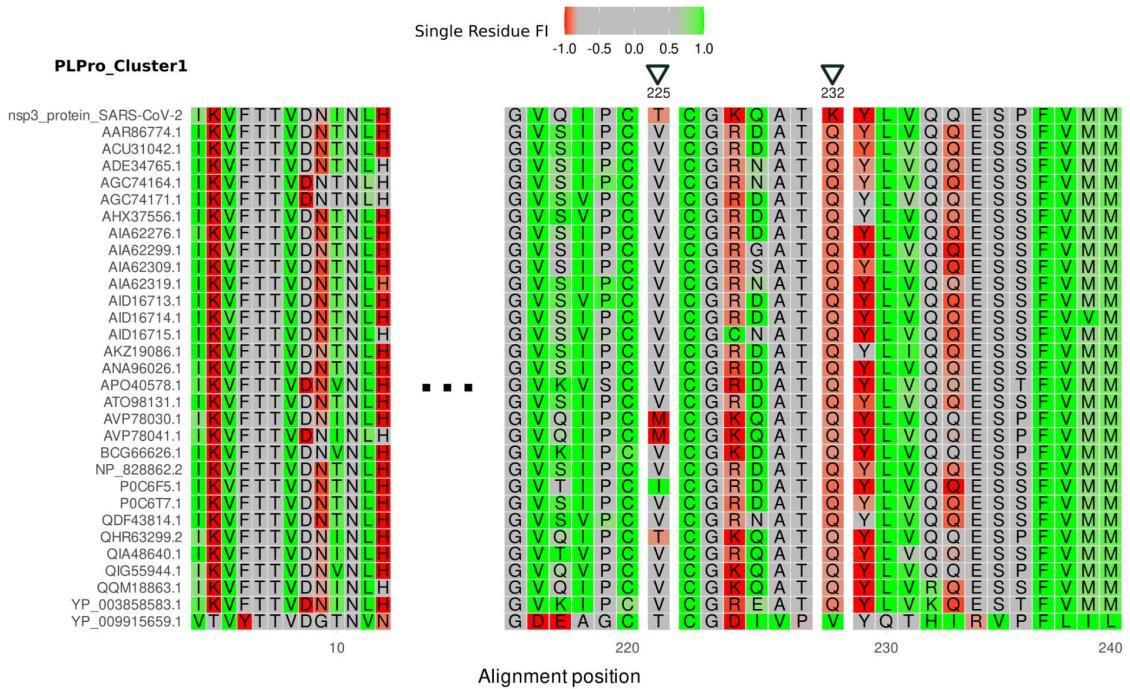
Supplementary Fig. 8. Same correlation plot as in Fig. 5 showing mean FrustIC vs mean SeqIC per S3Det cluster computed for Coronavirus proteins (see Methods) but with all the data points labelled by protein and S3Det cluster.



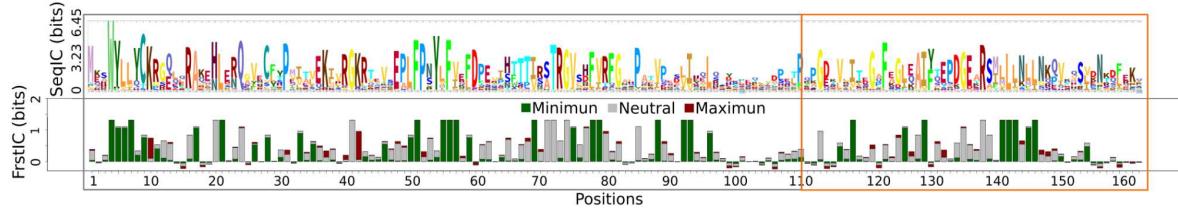
Supplementary Fig. 9. Factors affecting the expected correlation between SeqIC and FrustIC in Coronaviruses. (A) Quality of S3Det clusters models per protein represented by the mean proportion of residues with pLDDT<80 (low quality models). (B) Disorder tendency of S3Det clusters models represented by the mean proportion of residues with IUPred>0.5 (disordered). Grey dots indicate that no residues were found with IUPred> 0.5. (C) Phylogenetic balance represented by the diversity of the subgenus classification within each protein and S3Det cluster (see Methods). The size of the point represents the number of subgenus species represented by the considered sequences. The shape of the point refers to the corresponding genus classification (Alpha, Beta, Gamma or Deltacoronavirus) of all the sequences in each S3Det cluster.



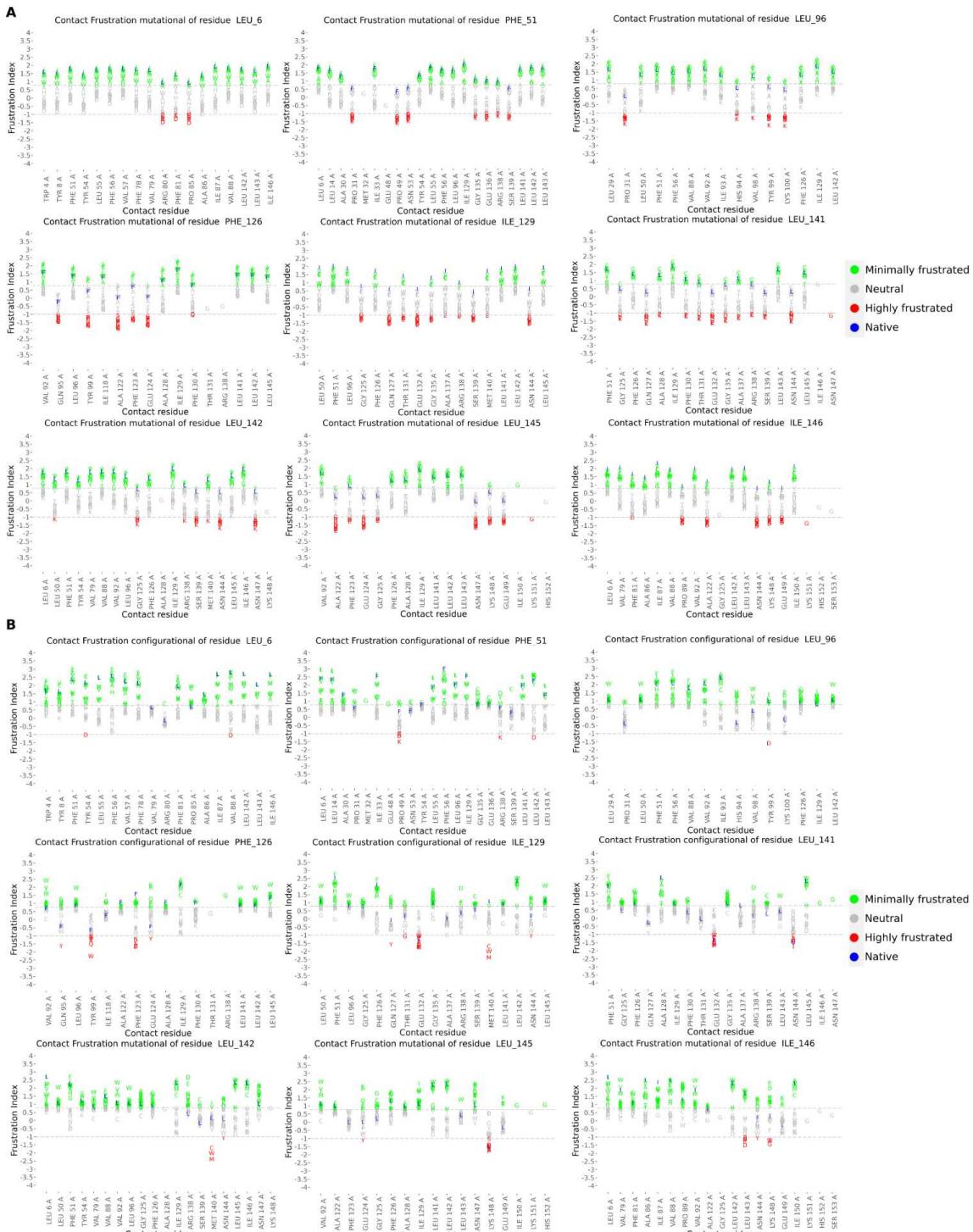
Supplementary Fig. 10. Sequence and Frustration logo plots showing SeqIC and FrustIC values per MSA column respectively for the cluster 2 of Coronavirus protein nsp13. The numbering of the plot corresponds to the sequence of reference AYR18613.1. Positions containing a gap in the sequences of reference are not considered in the plot. Arrows point to examples of hydrophobic residues with lower conservation of SeqIC compared to FrustIC in a minimally frustration state.



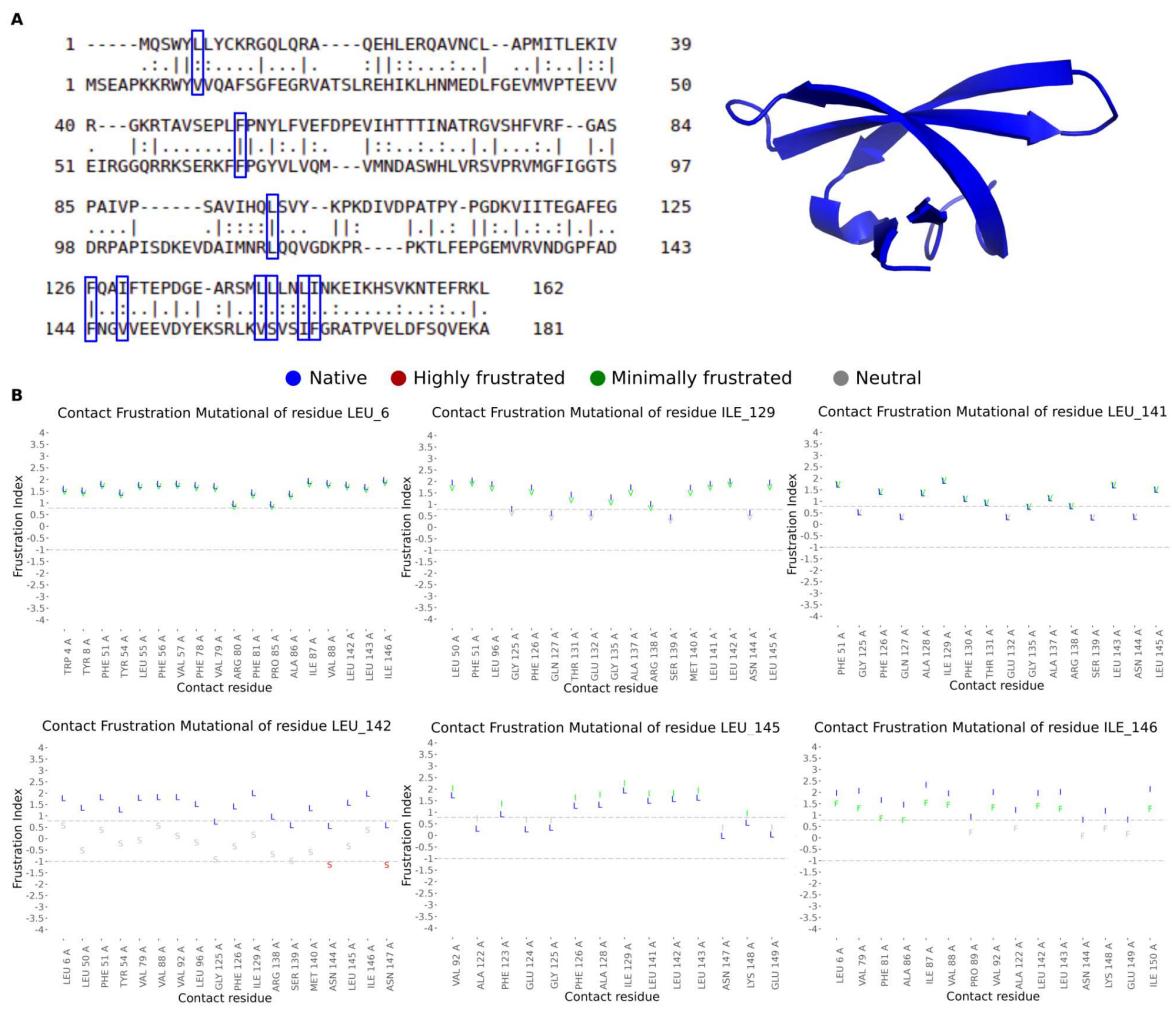
Supplementary Fig. 11. Selected positions of the multiple sequence frustration alignment of PLPro S3Det cluster1 (Sarbecovirus). Highlighted positions, marked in triangle, 221/225 and 228/232 (Alignment position / SARS-CoV-2 numbering) representing interesting examples of change in frustration in the SARS-CoV-2 sequence (first row) compared to the rest of sequences.



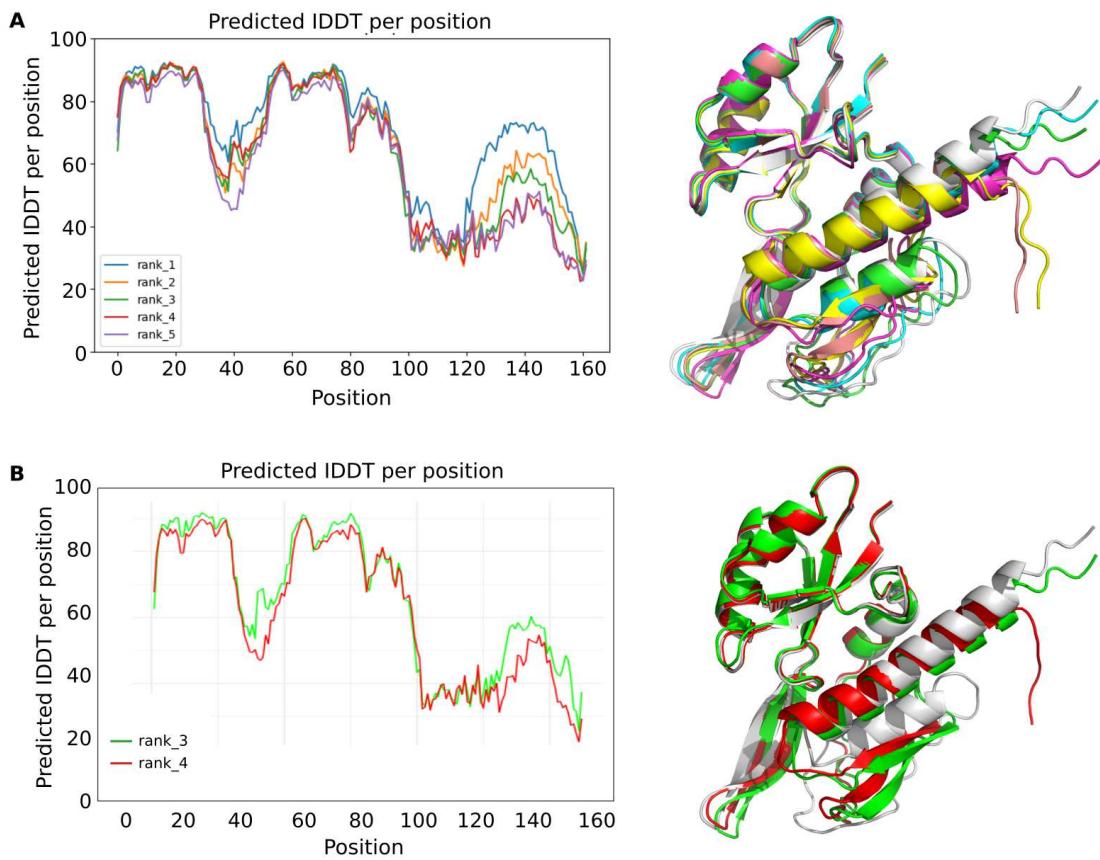
Supplementary Fig. 12. Conservation of local frustration and sequence identity for RfaH family. FrustIC based on the single-residue level frustration index. In green are represented the minimally frustrated; in red highly frustrated contacts; and in gray neutral. In gray box is the non-metamorphic region and in orange box the metamorphic region.



Supplementary Fig. 13. Contact frustration changes upon mutation, for mutational (A) and configurational (B) frustration index, of a specific residue for all canonical amino acids alternatives. X axis: all possible contacts that form the native protein and the mutants are shown. Y axis: frustration values, the canonical amino acids alternatives are represented in letters and coloured based to their frustration value. Native variant appears in blue.



Supplementary Fig. 14. A) Sequence alignment between RFAH and NUSG, in the blue boxes are marked the 9 IR. B) Contact frustration changes for mutational index between native RFAH amino acids and NUSG equivalent positions. X axis: all possible contacts that form the native protein and the mutants are shown. Y axis: frustration values, the amino acids alternatives are represented in letters and coloured based to their frustration value. Native variant appears in blue.



Supplementary Fig. 15. A) AlphaFold2 (AF2) models for RfaH containing 6 mutations with identities extracted from NusG. On the left a structural alignment between the 5 AF2 models of the NusG mutants and the native of RfaH from *E. Coli* is shown. In blue, orange, green, red and magenta are represented the NusG mutants and in white the RfaH from *E. Coli*. On the right the Predicted IDDT values per position for all NusG mutants of the AF2 models are shown. B) AF2 models for the RfaH sequence containing the L142S mutation. On the left are shown an structural alignment between 2 models of AF2 (Rank 3 and Rank 4) and the native of RfaH from *E. Coli*. In green and red the AF2 models and in white the native of RfaH from *E. Coli*. On the right the Predicted IDDT values per position for L142S mutants of the AF2 models are shown.

Supplementary Table 1. Frustration conservation state of relevant functional residues in hemoglobins.

Residue	FrustIC Score	Function
Lys7α	1.02	Forms a salt bridge with Asp74α (conserved and minimally frustrated) (Shaanan, 1983)
Glū27α	0.7	Forms a salt bridge with His112α (not energetically conserved) (Shaanan, 1983)
Glū30α	0.7	Forms a salt bridge with His50α (not energetically conserved) (Shaanan, 1983)
Lys40α	1.29	Lys40α is located in the α1-β2 hair, making a salt bridge with His146 in the β2 chain (His146β2), which in turns establishes an intra chain salt bridge with Asp94β2 (Imai et al., 1989). The salt bridges involving Lys40α and Asp94β2 play a key role in cooperative oxygen binding by hemoglobin.
Tyr42α	1.29	Participates in one of the strongest interactions in the α1-β2 interface, establishing a hydrogen bond with Asp99β2. Absence of this bond is actually observed in an abnormal hemoglobin, and shifts the allosteric equilibrium towards the oxy form, but it does not inhibit formation of the deoxy structure. In their absence the quaternary deoxy structure does not form and all cooperative effects are inhibited (Kavanaugh et al., 2005). Tyr42α is also one of the amino acids that interacts with the heme group in Human hemoglobin (Kavanaugh et al., 2005).
Lys99α	0.84	Form salt bridge with Arg141α. Lys99α leads to anemias when mutated by amino acids that disrupt the protein-protein interactions with AHSP (Mollan et al. 2010).
Ser124α	1.02	When mutated by a Proline (HB Pollicoro) can lead to a disrupted interaction with AHSP due to conformation changes of the interacting helix in α-globin, leading to α-thalassemia (Bisconte et al. 2015).
Asp126α	0.57	Has been reported to play a role in the α1/α2 interface stabilization and has been found in Hb Sassari (Asp->His mutation) leading to a higher oxygen affinity possibly due to perturbations in the equilibrium between the two quaternary states (Sanna et al., 1994).
Lys127α	1.29	Mutation of the neighbor α-Lys127α conserved lead to increased oxygen binding molecules as it happens with the naturally occurring α1/α2 interface in Hb G-Cambodia (Huang et al., 2010).
Tyr140α	0.51	Hb Room increased oxygen affinity and decreased cooperativity (no described symptoms). Tyr140, is involved in the allosteric transition of Hb, which occurs when both α-heme groups become oxygenated tyr140 is expelled from the tyrosine pocket, leading to the rupture of 4 salt bridges that restrict the T-state associated with Arg141 and, therefore, the Hb α1/α2 interface. (Perutz, 1970).
Trp37β	0.59	Mutations in this residue have been shown to produce changes in the tertiary structure of hemoglobin, due to the disruption of intersubunit contacts associated with Trp37 that generate a change in the quaternary structure at the α1β2 interface (Kavanaugh, 1998).
Asn57β	1.29	It was reported as part of a hemoglobin variant known as HB G-Ferrara. It shows an increased of the oxygen affinity observed at acid pH values, may be related to an enhanced dissociation of the molecule into dimers (Giardina et al. 1978).
Glu101β	1.02	Interface with α-globin in human (Fermi 1975) (Shaanan, 1983)
Asn108β	0.7	Interface with α-globin in human (Fermi 1975) (Shaanan, 1983)
Tyr145β	0.68	It has been shown that this residue may be important in electron transfer pathways from reducing agents to the heme of Hb (Puscas, 2018).

Shaanan, B. (1983). Structure of human oxyhaemoglobin at 2°: resolution. *Journal of molecular biology*, 171(1), 31-59.

Imai, K., Tsunehsiige, A., Harano, T., & Harano, K. (1989). Structure-Function Relationships in Hemoglobin Kariva, Lys-40 (C5) α→Glu, with High Oxygen Affinity: Functional role of the salt bridge between lys-40α and the β chain carboxy terminus. *Journal of Biological Chemistry*, 264(19), 11174-11180.

Kavanaugh, J. S., Rogers, P. H., Arnone, A., Hui, H. L., Wierzbza, A., DeYoung, A., ... & Friedman, J. M. (2005). Intersubunit interactions associated with Tyr42α stabilize the quaternary-T tetramer but are not major quaternary constraints in deoxyhemoglobin. *Biochemistry*, 44(10), 3806-3820.

Kavanaugh, J. S., Wiedert, J. A., Rogers, P. H., & Arnone, A. (1998). High-resolution crystal structures of human hemoglobin with mutations at tryptophan 37: structural basis for a high-affinity T-state. *Biochemistry*, 37(13), 4358-4373.

Mollan, T. L., Yu, X., Weiss, M. J., & Olson, J. S. (2010). The role of alpha-hemoglobin stabilizing protein in redox chemistry, denaturation, and hemoglobin assembly. *Antioxidants & redox signaling*, 12(2), 219-231.

Bisconte, M. G., Giardina, R., Scatena, R., Pellegrini, M., Olianas, A., Manca, L., ... & Corda, M. (1994). Functional alterations in adult and fetal hemoglobin Sassari Asp-α126 (Hb)->His. The role of α1 α1α2 contact. *Journal of Biological Chemistry*, 269(28), 18338-18342.

Moore, J. A., Pullon, B. M., Wang, D., & Brennan, S. O. (2021). Hb Walkato c127 (H10) Lys→Gln: HbA1: c. 382A>C: A Novel High Oxygen Affinity Variant. *Hemoglobin*, 45(1), 41-45.

Giardina, B., Brunori, M., Antonini, E., & Tentori, L. (1978). Properties of hemoglobin G. Ferrara (β57 (E1) Asn→Lys). *Biochimica et Biophysica Acta (BBA)-Protein Structure*, 534(1), 1-6.

Fermi, G. (1975). Three-dimensional Fourier synthesis of human deoxyhaemoglobin at 2°: A resolution: refinement of the atomic model. *Journal of Molecular Biology*, 97(2), 237-256.

Puscas, C., Radu, L., Carrascoza, F., Mot, A. C., Amanei, D., Lungu, O., ... & Slaghi-Dumitrescu, R. (2018). The high affinity of small-molecule antioxidants for hemoglobin. *Free Radical Biology and Medicine*, 124, 260-274.

Perutz, M. F. (1970). Stereochemistry of cooperative effects in haemoglobin: haem-haem interaction and the problem of allostery. *Nature*, 228(5273), 726-734.

Supplementary Table 2. Characteristics of the Coronavirus protein families considered in section 5. SARS-CoV-2 proteins that did not have an experimental PDB structure (in red) were discarded from the analysis.

Protein	SARS2 seq length	MSA length	MSA depth	# S3Det clusters	# SDPs	SARS-CoV-2 PDB
nsp1	180	185	24	2	4	7K7P
nsp2	638	699	61	3	51	7MSW
nsp3	1945	3426	124	4	48	7PKU, 7LGO, 6XA9, 7RKG, 6Z5T, 7THH
nsp4	500	625	328	6	5	-
nsp5	306	371	244	5	9	7CBT
nsp6	290	374	190	3	11	-
nsp7	83	89	205	4	3	7BV1
nsp8	198	232	198	6	1	7OZV
nsp9	113	118	166	4	1	7KRI
nsp10	139	153	221	5	1	7C2J
nsp11	13	-	-	-	-	-
nsp12	932	1131	195	2	27	7DTE
nsp13	601	809	127	2	2	7KRN
nsp14	527	591	179	6	10	7EIZ
nsp15	346	423	286	7	2	7N06
nsp16	298	497	257	5	6	7C2J
S	1273	1998	193	5	34	7A92
orf3a	275	287	30	2	8	7KJR
orf3b	57	-	-	-	-	-
E	75	105	58	3	3	7K3G
M	222	485	503	6	2	-
orf6	61	90	24	5	0	-
orf7a	121	137	26	4	0	7CI3
orf7b	43	55	15	3	0	-
N	419	780	547	6	3	7N01, 7ACT
orf8	121	135	19	2	9	7F5F
orf9b	97	98	21	3	4	7KDT
orf9c	73	73	12	2	0	-
orf10	38	38	3	0	0	-

Supplementary Table 3. Summary of AlphaFold2 modeling results for the Coronavirus protein families considered in section 5. Sequences containing 'X' characters or that are too short failed to be modelled and are shown in red.												
Protein or protein domain	# S3Det cluster	# Seqs	PDB_code	Trimmed ref seq length	Trimmed MSA length	Mean pLDDT	Not modelled	ID protein not modelled	Mean FrustIC	SD FrustIC	Mean SeqIC	SD SeqIC
nsp1	1	10				68.38 0	-					
nsp1	2	13	7k7p	116	121	80.93 0	-		0.930	0.383	3.091	0.401
nsp2	1	30				82.62 0	-		0.854	0.442	3.383	0.578
nsp2	2	28				74.74 0	-					
nsp2	3	2	7msw	501	541	54.45 0	-					
nsp3_Ubl1	1	31				85.13 0	-		0.904	0.419	3.441	0.494
nsp3_Ubl1	2	11				79.68 0	-					
nsp3_Ubl1	3	35				82.19 0	-		0.692	0.510	3.083	0.742
nsp3_Ubl1	4	47	7pkv	110	125	81.38 0	-		0.681	0.497	2.903	0.808
nsp3_MacroX	1	31				94.79 0	-		0.914	0.422	3.295	0.659
nsp3_MacroX	2	11				92.92 0	-		0.768	0.484	2.401	0.770
nsp3_MacroX	3	35				78.35 1	AIZ74404.1					
nsp3_MacroX	4	47	6z5t	171	321	82.85 0	-		0.777	0.498	3.398	0.708
nsp3_Macroll	1	31				57.75 0	-					
nsp3_Macroll	2	11				64.11 0	-					
nsp3_Macroll	3	35				- 35	All					
nsp3_Macroll	4	47	model	127	163	- 47	All					
nsp3_SUD_Nterm	1	31				83.49 0	-		0.881	0.426	3.328	0.536
nsp3_SUD_Nterm	2	11				71.88 0	-					
nsp3_SUD_Nterm	3	35				91.66 0	-		0.768	0.475	2.966	0.805
nsp3_SUD_Nterm	4	47	model	263	307	58.17 0	-					
nsp3_SUD_Cterm	1	31				88.81 0	-		0.683	0.366	3.290	0.593
nsp3_SUD_Cterm	2	11				93.13 0	-		0.758	0.429	2.407	0.648
nsp3_SUD_Cterm	3	35				95.71 0	-		0.754	0.515	2.889	0.821
nsp3_SUD_Cterm	4	47	7thh	65	87	83.01 0	-		0.285	0.331	2.983	0.856
nsp3_PLPro	1	31				94.69 0	-		0.990	0.362	3.500	0.460
nsp3_PLPro	2	11				95.06 0	-		0.773	0.440	2.472	0.664
nsp3_PLPro	3	35				93.86 1	AIZ74404.1		0.769	0.476	3.129	0.754
nsp3_PLPro	4	47	6xa9	308	333	92.63 2	AWB14623.1, AFG25759.1		0.778	0.479	3.182	0.776
nsp3_NAB	1	31				88.57 3	ACU31042.1, AAR86774.1, ANA96026.1		0.915	0.422	3.426	0.450
nsp3_NAB	2	11				66.2 0	-					
nsp3_NAB	3	35				78.46 1	QLD98030.1		0.666	0.444	3.126	0.760
nsp3_NAB	4	47	7lgo	112	125	64.57 1	AFG25769.1		0.730	0.466	3.452	0.725
nsp3_Y3	1	31				90.3 0	-		1.074	0.339	3.637	0.320
nsp3_Y3	2	11	7rqg			92.94 0	-		0.876	0.406	2.701	0.460
nsp3_Y3	3	35				88.66 1	QLD98030.1		0.895	0.447	3.411	0.615
nsp3_Y3	4	47		101	104	92.92 0	-		0.997	0.431	3.617	0.537
nsp5	1	32				90.63 0	-		0.710	0.483	2.901	0.822
nsp5	2	19				91.25 0	-		0.942	0.430	3.305	0.502
nsp5	3	76				92.8 0	-		0.743	0.479	3.147	0.874
nsp5	4	98				93.04 0	-		1.044	0.366	3.892	0.450
nsp5	5	18	7cbt	304	347	94.06 0	-		0.878	0.412	2.996	0.623
nsp7	1	36				87.77 0	-		0.843	0.471	3.273	0.643
nsp7	2	30				84.84 1	QEG03810.1		0.995	0.387	3.635	0.349
nsp7	3	82				87.99 0	-		0.783	0.386	3.370	0.692
nsp7	4	56	7bv1	71	77	87.86 0	-		1.040	0.329	3.843	0.308
nsp8	1	15				88.88 0	-		0.638	0.443	2.498	0.649
nsp8	2	18				89.33 0	-		0.952	0.402	3.254	0.496
nsp8	3	68				90.22 0	-		0.704	0.455	3.176	0.755
nsp8	4	23				87.99 0	-		1.047	0.362	3.490	0.423
nsp8	5	58				86.96 0	-		1.054	0.340	3.862	0.376
nsp8	6	16	7ozv	186	220	88.18 0	-		0.829	0.416	2.934	0.572
nsp9	1	46				88.27 0	-		0.658	0.478	2.935	0.795
nsp9	2	78				87.36 0	-		0.723	0.438	3.274	0.806
nsp9	3	24				88.81 0	-		0.966	0.352	3.443	0.308
nsp9	4	18	7kri	112	117	87.41 0	-		0.758	0.428	3.011	0.640
nsp10	1	40				90.44 0	-		0.779	0.489	3.227	0.764
nsp10	2	21				90.84 0	-		1.013	0.376	3.404	0.518
nsp10	3	71				88.43 0	-		1.059	0.331	3.906	0.327
nsp10	4	74				91.7 0	-		0.829	0.458	3.426	0.773
nsp10	5	15	7c2j	121	129	90 0	-		0.938	0.404	2.996	0.603
nsp12	1	43				90.18 1	QLD97932.1		0.835	0.475	3.349	0.750
nsp12	2	69				89.76 0	-		1.102	0.310	3.945	0.292
nsp12	3	53				89.02 0	-		0.878	0.447	3.472	0.720
nsp12	4	14	7dte	925	1007	90.32 0	-		0.921	0.424	2.947	0.616
nsp13	1	21				92.31 0	-		0.960	0.436	3.194	0.648
nsp13	2	13				91.93 0	-		1.069	0.341	3.117	0.340
nsp13	3	49				91.43 0	-		0.934	0.432	3.438	0.715
nsp13	4	20				90.74 0	-		1.058	0.319	3.421	0.304
nsp13	5	14	7km	591	604	92.3 0	-		1.021	0.356	3.074	0.427
nsp14	1	17				88.31 0	-		0.766	0.477	2.835	0.691
nsp14	2	14				89.2 0	-		0.999	0.393	3.123	0.456
nsp14	3	22				90.27 0	-		0.988	0.404	3.401	0.482
nsp14	4	50				89.24 0	-		1.103	0.308	3.886	0.279
nsp14	5	62				90.56 1	QEG03729.1		0.805	0.465	3.327	0.820
nsp14	6	13	7elz	521	554	90.32 0	-		0.878	0.419	2.796	0.602
nsp15	1	24				94.64 0	-		1.109	0.320	3.562	0.376
nsp15	2	12				93.94 0	-		0.657	0.464	2.176	0.688
nsp15	3	28				89.14 0	-		0.889	0.465	3.360	0.620
nsp15	4	24				93.53 0	-		0.980	0.424	3.327	0.606
nsp15	5	80				92.45 1	QEG03729.1		0.770	0.470	3.280	0.816
nsp15	6	99				94.4 0	-		1.114	0.320	3.991	0.333
nsp15	7	18	7n06	344	421	94.64 0	-		0.887	0.411	2.922	0.658
nsp16	1	45				91.56 0	-		0.864	0.471	3.269	0.778
nsp16	2	23				90.18 0	-		0.969	0.422	3.430	0.474
nsp16	3	71				90.89 0	-		0.862	0.465	3.408	0.738
nsp16	4	100				88.57 0	-		1.058	0.372	3.924	0.427
nsp16	5	17	7c2j	296	319	92.64 0	-		0.912	0.406	3.063	0.546
S_protein	1	51				86.12 2	camel_Abu Dhabi_B101, hCoV-OC43_USA_TCNP_00204_2017		0.885	0.444	3.380	0.737
S_protein	2	35				83.26 2	camel_UAE_415915_W4_2015, BtCoV_KW2E-F93_Nyc_spec_GHA_2010		0.850	0.461	3.153	0.784
S_protein	3	16				78.48 1	Bat-CoV_CM705-P13					
S_protein	4	29				82.71 0	-		0.951	0.436	3.340	0.744
S_protein	5	2	7k3g	1148	1539	72.97 0	-					

Supplementary Table 4. Frustration states of SARS-CoV-2 proteins close orthologs (same S3Det cluster), computed with FrustraEvo, and SARS-CoV-2 individual frustration score, computed with FrustratomeR. FrustIC represents the conservation of frustration across the cluster and SRFI is the single residue frustration index of the SARS-CoV-2 sequence. The first column containin amino acids letters corresponds to the consensus amino acid based on the MSA of the cluster while 'SARS2 AA' represents the amino acid appearing in the SARS-CoV-2 protein.

Protein	SARS2 containin g cluster	Protein positio n	MSA consensus AA	FrustIC	Frustraev o state	SARS2 AA	SRFI	Frustratomet er state
nsp2	1	1	R	0.395	MIN	R	0.607	NEU
nsp2	1	2	Y	0.391	NEU	Y	-0.327	NEU
nsp2	1	3	V	1.313	MIN	V	1.36	MIN
nsp2	1	4	D	0.316	MAX	D	-1.097	MAX
nsp2	1	5	N	1.313	MAX	N	-1.071	MAX
nsp2	1	6	N	1.102	NEU	N	-0.89	NEU
nsp2	1	7	F	0.960	MIN	F	1.235	MIN
nsp2	1	8	C	1.313	MIN	C	2.602	MIN
nsp2	1	9	G	1.313	NEU	G	0.015	NEU
nsp2	1	10	P	1.313	NEU	P	-0.541	NEU
nsp2	1	11	D	0.476	NEU	D	-1.25	MAX
nsp2	1	12	G	1.313	NEU	G	-0.082	NEU
nsp2	1	13	Y	1.102	MAX	Y	-0.892	NEU
nsp2	1	14	P	1.102	MAX	P	-1.176	MAX
nsp2	1	15	L	1.313	MIN	L	0.774	NEU
nsp2	1	16	E	0.529	NEU	E	-0.603	NEU
nsp2	1	17	C	1.313	MIN	C	2.89	MIN
nsp2	1	18	I	1.313	MIN	I	1.885	MIN
nsp2	1	19	K	0.960	NEU	K	-0.721	NEU
nsp2	1	20	D	1.102	NEU	D	-0.518	NEU
nsp2	1	21	L	0.663	MIN	L	0.949	MIN
nsp2	1	22	L	0.960	MIN	L	0.908	MIN
nsp2	1	23	A	1.313	NEU	A	0.44	NEU
nsp2	1	24	R	0.960	MIN	R	0.701	NEU
nsp2	1	25	A	0.591	NEU	A	0.538	NEU
nsp2	1	26	G	1.313	NEU	G	-0.81	NEU
nsp2	1	27	K	0.316	NEU	K	-0.976	NEU
nsp2	1	28	S	1.313	NEU	A	0.425	NEU
nsp2	1	29	M	-0.060	MAX	S	0.59	NEU
nsp2	1	30	C	0.844	MIN	C	1.875	MIN
nsp2	1	31	T	0.638	MIN	T	1.268	MIN
nsp2	1	32	L	0.591	NEU	L	0.604	NEU
nsp2	1	33	S	1.102	NEU	S	-0.168	NEU
nsp2	1	34	E	0.432	NEU	E	-0.653	NEU
nsp2	1	35	Q	0.663	NEU	Q	-1.009	MAX
nsp2	1	36	L	1.313	MIN	L	0.838	MIN
nsp2	1	37	D	1.102	NEU	D	0.179	NEU
nsp2	1	38	F	0.316	MAX	F	-0.41	NEU
nsp2	1	39	I	1.313	MIN	I	1.255	MIN

nsp2	1	40	E	0.663	NEU	D	0.289	NEU
nsp2	1	41	S	1.313	NEU	T	-0.663	NEU
nsp2	1	42	K	0.326	MAX	K	-1.188	MAX
nsp2	1	43	R	0.326	NEU	R	1.297	MIN
nsp2	1	44	G	1.313	NEU	G	-0.462	NEU
nsp2	1	45	V	-0.170	MAX	V	-1.087	MAX
nsp2	1	46	Y	1.102	MAX	Y	-2.324	MAX
nsp2	1	47	C	0.746	MIN	C	1.704	MIN
nsp2	1	48	C	1.313	MIN	C	2.088	MIN
nsp2	1	49	R	0.313	MIN	R	0.589	NEU
nsp2	1	50	E	0.663	MAX	E	-1.459	MAX
nsp2	1	51	H	1.313	NEU	H	-0.45	NEU
nsp2	1	52	E	0.331	NEU	E	-0.591	NEU
nsp2	1	53	H	1.313	NEU	H	-0.161	NEU
nsp2	1	54	E	0.663	NEU	E	-0.961	NEU
nsp2	1	55	I	1.313	MIN	I	1.027	MIN
nsp2	1	56	A	1.102	MIN	A	0.601	NEU
nsp2	1	57	W	1.313	MIN	W	0.833	MIN
nsp2	1	58	F	0.222	MIN	Y	0.665	NEU
nsp2	1	59	T	1.313	NEU	T	-0.251	NEU
nsp2	1	60	E	0.752	NEU	E	-0.64	NEU
nsp2	1	61	R	0.844	NEU	R	-0.265	NEU
nsp2	1	62	S	0.960	NEU	S	-0.49	NEU
nsp2	1	63	D	0.844	NEU	E	-0.791	NEU
nsp2	1	64	K	0.663	NEU	K	-0.703	NEU
nsp2	1	65	S	1.313	NEU	S	-0.483	NEU
nsp2	1	66	Y	0.844	MIN	Y	0.635	NEU
nsp2	1	67	E	1.313	NEU	E	-0.682	NEU
nsp2	1	68	H	0.844	MIN	L	1.358	MIN
nsp2	1	69	Q	0.432	MAX	Q	-1.066	MAX
nsp2	1	70	T	1.102	NEU	T	-0.396	NEU
nsp2	1	71	P	0.529	NEU	P	-1.029	MAX
nsp2	1	72	F	1.313	MIN	F	0.769	NEU
nsp2	1	73	E	0.326	NEU	E	0.396	NEU
nsp2	1	74	I	1.313	MIN	I	1.164	MIN
nsp2	1	75	K	0.591	NEU	K	0.408	NEU
nsp2	1	76	S	0.476	NEU	L	1.293	MIN
nsp2	1	77	A	1.313	MIN	A	0.8	MIN
nsp2	1	78	K	0.365	MAX	K	-1.236	MAX
nsp2	1	79	K	1.102	NEU	K	-0.82	NEU
nsp2	1	80	F	1.313	MIN	F	1.086	MIN
nsp2	1	81	D	0.313	MIN	D	0.929	MIN
nsp2	1	82	T	1.313	NEU	T	-0.353	NEU
nsp2	1	83	F	0.844	MIN	F	1.066	MIN
nsp2	1	84	K	0.663	MIN	N	0.735	NEU
nsp2	1	85	G	0.844	NEU	G	-0.788	NEU

nsp2	1	86	E	0.529	NEU	E	-0.116	NEU
nsp2	1	87	C	1.313	MIN	C	1.276	MIN
nsp2	1	88	P	1.313	NEU	P	-0.177	NEU
nsp2	1	89	K	-0.120	NEU	N	-0.95	NEU
nsp2	1	90	F	1.313	MIN	F	1.11	MIN
nsp2	1	91	V	1.313	MIN	V	1.3	MIN
nsp2	1	92	F	1.313	MIN	F	1.303	MIN
nsp2	1	93	P	1.313	MAX	P	-1.238	MAX
nsp2	1	94	L	1.313	MIN	L	1.104	MIN
nsp2	1	95	N	1.102	NEU	N	-0.801	NEU
nsp2	1	96	S	1.313	NEU	S	-0.676	NEU
nsp2	1	97	K	0.395	NEU	I	1.505	MIN
nsp2	1	98	V	1.313	MIN	I	1.213	MIN
nsp2	1	99	K	0.752	NEU	K	-0.989	NEU
nsp2	1	100	V	0.529	MIN	T	-0.409	NEU
nsp2	1	101	I	1.313	MIN	I	1.302	MIN
nsp2	1	102	Q	0.313	NEU	Q	0.062	NEU
nsp2	1	103	P	1.102	NEU	P	-0.509	NEU
nsp2	1	104	R	0.591	NEU	R	0.21	NEU
nsp2	1	105	V	0.960	NEU	V	-0.775	NEU
nsp2	1	106	E	1.102	MIN	E	1.779	MIN
nsp2	1	107	K	1.102	NEU	K	-0.156	NEU
nsp2	1	108	K	0.663	MIN	K	0.24	NEU
nsp2	1	109	K	1.102	MIN	K	1.707	MIN
nsp2	1	110	T	0.395	NEU	L	0.593	NEU
nsp2	1	111	E	1.313	MIN	D	1.343	MIN
nsp2	1	112	G	1.313	NEU	G	-0.022	NEU
nsp2	1	113	F	1.313	MIN	F	1.053	MIN
nsp2	1	114	M	1.313	MIN	M	0.876	MIN
nsp2	1	115	G	0.844	NEU	G	0.582	NEU
nsp2	1	116	R	0.960	NEU	R	-0.291	NEU
nsp2	1	117	I	1.313	MIN	I	1.676	MIN
nsp2	1	118	R	1.313	NEU	R	-0.116	NEU
nsp2	1	119	S	1.313	NEU	S	-0.177	NEU
nsp2	1	120	V	1.313	MIN	V	1.791	MIN
nsp2	1	121	Y	1.313	NEU	Y	-0.665	NEU
nsp2	1	122	P	0.326	NEU	P	0.554	NEU
nsp2	1	123	V	1.313	MIN	V	1.553	MIN
nsp2	1	124	A	1.102	MAX	A	-1.055	MAX
nsp2	1	125	S	0.960	NEU	S	-0.317	NEU
nsp2	1	126	P	1.313	NEU	P	-0.408	NEU
nsp2	1	127	Q	0.299	NEU	N	-0.492	NEU
nsp2	1	128	E	0.746	NEU	E	-0.393	NEU
nsp2	1	129	C	1.313	MIN	C	2.353	MIN
nsp2	1	130	N	0.960	NEU	N	-0.582	NEU
nsp2	1	131	D	0.299	NEU	Q	0.499	NEU

nsp2	1	132	M	0.746	MIN	M	0.919	MIN
nsp2	1	133	H	0.663	NEU	C	2.073	MIN
nsp2	1	134	L	1.313	MIN	L	1.088	MIN
nsp2	1	135	S	1.313	NEU	S	-0.49	NEU
nsp2	1	136	T	0.746	NEU	T	0.077	NEU
nsp2	1	137	L	0.960	MIN	L	1.049	MIN
nsp2	1	138	M	-0.162	MIN	M	-0.572	NEU
nsp2	1	139	K	0.844	MIN	K	1.055	MIN
nsp2	1	140	C	1.313	MIN	C	2.44	MIN
nsp2	1	141	N	0.395	NEU	D	2.281	MIN
nsp2	1	142	H	1.313	MIN	H	1.162	MIN
nsp2	1	143	C	0.591	MIN	C	1.108	MIN
nsp2	1	144	D	0.313	MIN	G	-0.772	NEU
nsp2	1	145	E	0.395	MAX	E	-1.341	MAX
nsp2	1	146	V	0.204	MIN	T	0.428	NEU
nsp2	1	147	S	1.313	NEU	S	0.042	NEU
nsp2	1	148	W	0.017	MIN	W	0.541	NEU
nsp2	1	149	Q	0.238	NEU	Q	-0.236	NEU
nsp2	1	150	T	1.313	NEU	T	-0.339	NEU
nsp2	1	151	C	0.432	MIN	G	-0.695	NEU
nsp2	1	152	D	0.432	NEU	D	-1.264	MAX
nsp2	1	153	F	1.313	MIN	F	1.178	MIN
nsp2	1	154	L	0.476	MIN	V	1.659	MIN
nsp2	1	155	K	1.102	NEU	K	-0.716	NEU
nsp2	1	156	A	1.313	NEU	A	-0.244	NEU
nsp2	1	157	T	1.313	MIN	T	1.028	MIN
nsp2	1	158	C	0.960	MIN	C	1.015	MIN
nsp2	1	159	E	0.395	MAX	E	-0.467	NEU
nsp2	1	160	Q	-0.237	MIN	F	0.677	NEU
nsp2	1	161	C	0.960	MIN	C	0.48	NEU
nsp2	1	162	G	0.960	NEU	G	-1.13	MAX
nsp2	1	163	T	0.432	NEU	T	-0.999	NEU
nsp2	1	164	E	0.432	MIN	E	1.044	MIN
nsp2	1	165	N	1.102	NEU	N	-0.671	NEU
nsp2	1	166	L	0.313	MIN	L	0.032	NEU
nsp2	1	167	V	0.591	MIN	T	-0.157	NEU
nsp2	1	168	C	-0.105	MIN	K	-1.096	MAX
nsp2	1	169	E	0.071	NEU	E	0.938	MIN
nsp2	1	170	G	1.102	NEU	G	-0.056	NEU
nsp2	1	171	P	0.663	NEU	A	0.594	NEU
nsp2	1	172	T	1.313	NEU	T	-0.289	NEU
nsp2	1	173	T	1.313	NEU	T	-0.219	NEU
nsp2	1	174	C	1.313	MIN	C	1.621	MIN
nsp2	1	175	G	1.313	NEU	G	-0.254	NEU
nsp2	1	176	Y	0.476	NEU	Y	-0.173	NEU
nsp2	1	177	L	0.326	NEU	L	0.248	NEU

nsp2	1	178	P	0.395	NEU	P	-0.623	NEU
nsp2	1	179	T	0.154	NEU	Q	-0.06	NEU
nsp2	1	180	N	0.960	NEU	N	-0.93	NEU
nsp2	1	181	A	0.844	NEU	A	0.292	NEU
nsp2	1	182	V	1.313	MIN	V	1.175	MIN
nsp2	1	183	V	1.102	MIN	V	1.29	MIN
nsp2	1	184	K	1.313	MAX	K	-1.497	MAX
nsp2	1	185	M	0.342	MIN	I	1.196	MIN
nsp2	1	186	P	0.591	NEU	Y	-3.026	MAX
nsp2	1	187	C	1.102	MIN	C	1.897	MIN
nsp2	1	188	P	0.529	NEU	P	-0.908	NEU
nsp2	1	189	A	-0.012	NEU	A	-0.946	NEU
nsp2	1	190	C	1.102	MIN	C	1.351	MIN
nsp2	1	191	Q	0.893	NEU	H	-0.413	NEU
nsp2	1	192	D	0.529	MAX	N	-0.887	NEU
nsp2	1	193	P	0.746	MIN	S	-0.55	NEU
nsp2	1	194	E	0.407	NEU	E	-0.229	NEU
nsp2	1	195	I	0.136	NEU	V	0.278	NEU
nsp2	1	196	G	1.313	NEU	G	-0.668	NEU
nsp2	1	197	P	0.663	NEU	P	1.106	MIN
nsp2	1	198	E	0.960	MAX	E	-1.553	MAX
nsp2	1	199	H	1.102	NEU	H	-0.709	NEU
nsp2	1	200	S	1.313	NEU	S	-0.492	NEU
nsp2	1	201	V	0.136	NEU	L	0.695	NEU
nsp2	1	202	A	1.313	NEU	A	-0.227	NEU
nsp2	1	203	D	0.529	NEU	E	-1.559	MAX
nsp2	1	204	Y	0.960	NEU	Y	-0.307	NEU
nsp2	1	205	H	1.313	NEU	H	-0.653	NEU
nsp2	1	206	N	1.313	NEU	N	-0.637	NEU
nsp2	1	207	H	0.114	MIN	E	-1.758	MAX
nsp2	1	208	S	1.313	NEU	S	-0.355	NEU
nsp2	1	209	N	0.391	NEU	G	-0.353	NEU
nsp2	1	210	I	1.313	MIN	L	1.312	MIN
nsp2	1	211	E	0.591	MIN	K	-0.123	NEU
nsp2	1	212	T	1.313	NEU	T	-0.2	NEU
nsp2	1	213	R	0.543	MIN	I	1.521	MIN
nsp2	1	214	L	1.313	NEU	L	-0.182	NEU
nsp2	1	215	R	0.342	NEU	R	-0.432	NEU
nsp2	1	216	K	-0.257	MIN	K	0.083	NEU
nsp2	1	217	G	1.313	NEU	G	-0.003	NEU
nsp2	1	218	G	1.313	NEU	G	-0.82	NEU
nsp2	1	219	R	1.313	NEU	R	-0.774	NEU
nsp2	1	220	T	0.844	NEU	T	-0.084	NEU
nsp2	1	221	K	-0.106	MAX	I	1.304	MIN
nsp2	1	222	C	0.432	MIN	A	0.168	NEU
nsp2	1	223	F	1.102	MIN	F	1.372	MIN

nsp2	1	224	G	1.313	NEU	G	-0.243	NEU
nsp2	1	225	G	1.313	NEU	G	-0.355	NEU
nsp2	1	226	C	1.313	MIN	C	1.405	MIN
nsp2	1	227	V	1.313	MIN	V	1.219	MIN
nsp2	1	228	F	1.313	MIN	F	1.383	MIN
nsp2	1	229	A	1.313	NEU	S	-0.663	NEU
nsp2	1	230	Y	0.476	MAX	Y	-0.713	NEU
nsp2	1	231	V	1.313	MIN	V	1.542	MIN
nsp2	1	232	G	1.313	NEU	G	-0.342	NEU
nsp2	1	233	C	1.313	MIN	C	1.306	MIN
nsp2	1	234	Y	0.893	NEU	H	0.018	NEU
nsp2	1	235	N	1.313	NEU	N	-0.247	NEU
nsp2	1	236	K	0.746	MAX	K	-0.98	NEU
nsp2	1	237	R	0.476	NEU	C	1.647	MIN
nsp2	1	238	A	1.313	NEU	A	0.126	NEU
nsp2	1	239	Y	0.746	NEU	Y	0.446	NEU
nsp2	1	240	W	0.844	NEU	W	0.568	NEU
nsp2	1	241	V	1.313	MIN	V	1.317	MIN
nsp2	1	242	P	1.313	NEU	P	-0.882	NEU
nsp2	1	243	R	1.313	NEU	R	-0.551	NEU
nsp2	1	244	A	1.313	NEU	A	0.387	NEU
nsp2	1	245	S	1.313	NEU	S	-0.418	NEU
nsp2	1	246	A	1.313	NEU	A	0.274	NEU
nsp2	1	247	N	1.313	NEU	N	-0.697	NEU
nsp2	1	248	I	1.313	MIN	I	1.014	MIN
nsp2	1	249	G	0.663	NEU	G	-0.957	NEU
nsp2	1	250	A	0.476	NEU	C	2.014	MIN
nsp2	1	251	N	1.313	NEU	N	-0.711	NEU
nsp2	1	252	H	1.313	NEU	H	-0.413	NEU
nsp2	1	253	T	1.313	NEU	T	-0.406	NEU
nsp2	1	254	G	1.313	NEU	G	-0.342	NEU
nsp2	1	255	I	1.313	MIN	V	0.962	MIN
nsp2	1	256	T	0.395	NEU	V	1.176	MIN
nsp2	1	257	G	1.102	NEU	G	-0.016	NEU
nsp2	1	258	D	0.061	MIN	E	-1.542	MAX
nsp2	1	259	N	1.313	NEU	G	-0.479	NEU
nsp2	1	260	V	0.476	MIN	S	-0.611	NEU
nsp2	1	261	E	0.529	MAX	E	-2.346	MAX
nsp2	1	262	T	0.591	MIN	G	0.065	NEU
nsp2	1	263	L	0.844	MIN	L	0.882	MIN
nsp2	1	264	N	0.529	MAX	N	-0.925	NEU
nsp2	1	265	E	0.960	MAX	D	-1.772	MAX
nsp2	1	266	D	0.529	MAX	N	-0.775	NEU
nsp2	1	267	L	1.313	MIN	L	0.873	MIN
nsp2	1	268	L	0.591	MIN	L	0.565	NEU
nsp2	1	269	E	0.365	NEU	E	-0.475	NEU

nsp2	1	270	I	1.313	MIN	I	1.529	MIN
nsp2	1	271	L	1.313	MIN	L	1.049	MIN
nsp2	1	272	N	0.238	NEU	Q	-0.231	NEU
nsp2	1	273	R	0.071	NEU	K	-1.518	MAX
nsp2	1	274	E	-0.146	NEU	E	0.425	NEU
nsp2	1	275	R	-0.091	NEU	K	-1.622	MAX
nsp2	1	276	V	1.313	MIN	V	1.652	MIN
nsp2	1	277	N	0.529	NEU	N	0.561	NEU
nsp2	1	278	I	1.313	MIN	I	1.405	MIN
nsp2	1	279	N	1.102	NEU	N	-0.682	NEU
nsp2	1	280	I	1.313	MIN	I	2.087	MIN
nsp2	1	281	V	0.529	MIN	V	0.645	NEU
nsp2	1	282	G	1.102	NEU	G	0.051	NEU
nsp2	1	283	D	0.591	NEU	D	0.535	NEU
nsp2	1	284	F	0.395	NEU	F	0.246	NEU
nsp2	1	285	Q	-0.055	MAX	K	1.068	MIN
nsp2	1	286	L	1.313	MIN	L	1.205	MIN
nsp2	1	287	N	0.529	NEU	N	-0.988	NEU
nsp2	1	288	E	0.746	NEU	E	-0.951	NEU
nsp2	1	289	E	0.432	MAX	E	-1.139	MAX
nsp2	1	290	V	1.313	MIN	I	1.649	MIN
nsp2	1	291	A	0.326	MIN	A	0.417	NEU
nsp2	1	292	I	1.313	MIN	I	1.263	MIN
nsp2	1	293	I	1.313	MIN	I	1.534	MIN
nsp2	1	294	L	1.313	MIN	L	1.205	MIN
nsp2	1	295	A	0.432	NEU	A	0.544	NEU
nsp2	1	296	S	1.313	NEU	S	-0.69	NEU
nsp2	1	297	F	1.313	MIN	F	0.884	MIN
nsp2	1	298	S	1.313	NEU	S	-0.732	NEU
nsp2	1	299	A	0.844	NEU	A	0.385	NEU
nsp2	1	300	S	1.313	NEU	S	-0.264	NEU
nsp2	1	301	T	1.102	NEU	T	-0.361	NEU
nsp2	1	302	S	0.960	NEU	S	-0.757	NEU
nsp2	1	303	A	0.395	NEU	A	0.678	NEU
nsp2	1	304	F	0.960	MIN	F	1.06	MIN
nsp2	1	305	I	1.313	MIN	V	1.097	MIN
nsp2	1	306	D	1.313	NEU	E	-0.534	NEU
nsp2	1	307	T	1.313	NEU	T	-0.235	NEU
nsp2	1	308	V	1.313	MIN	V	1.229	MIN
nsp2	1	309	K	0.365	NEU	K	-0.744	NEU
nsp2	1	310	G	1.313	NEU	G	-0.1	NEU
nsp2	1	311	L	1.313	MIN	L	1.092	MIN
nsp2	1	312	D	0.529	MIN	D	-0.385	NEU
nsp2	1	313	Y	0.331	NEU	Y	0.78	MIN
nsp2	1	314	K	0.960	MAX	K	-1.745	MAX
nsp2	1	315	S	0.960	NEU	A	0.749	NEU

nsp2	1	316	F	1.313	MIN	F	0.76	NEU
nsp2	1	317	K	1.313	NEU	K	-0.771	NEU
nsp2	1	318	A	0.154	NEU	Q	-1.226	MAX
nsp2	1	319	I	1.313	MIN	I	2.039	MIN
nsp2	1	320	V	1.313	MIN	V	1.346	MIN
nsp2	1	321	E	1.313	NEU	E	-0.725	NEU
nsp2	1	322	S	1.313	NEU	S	-0.697	NEU
nsp2	1	323	C	1.313	MIN	C	1.787	MIN
nsp2	1	324	G	0.960	NEU	G	-1.004	MAX
nsp2	1	325	N	0.316	MAX	N	-1.207	MAX
nsp2	1	326	Y	0.326	NEU	F	0.433	NEU
nsp2	1	327	K	-0.186	NEU	K	-0.467	NEU
nsp2	1	328	V	1.313	MIN	V	1.307	MIN
nsp2	1	329	T	1.313	NEU	T	0.394	NEU
nsp2	1	330	K	0.844	NEU	K	-0.779	NEU
nsp2	1	331	G	1.313	NEU	G	-0.223	NEU
nsp2	1	332	K	1.102	NEU	K	0.401	NEU
nsp2	1	333	P	0.543	NEU	A	-0.129	NEU
nsp2	1	334	V	0.143	NEU	K	-0.634	NEU
nsp2	1	335	K	0.202	MIN	K	0.94	MIN
nsp2	1	336	G	0.638	NEU	G	-0.111	NEU
nsp2	1	337	A	0.591	NEU	A	-0.696	NEU
nsp2	1	338	W	0.313	MIN	W	0.453	NEU
nsp2	1	339	N	1.313	NEU	N	-0.744	NEU
nsp2	1	340	I	1.313	MIN	I	1.373	MIN
nsp2	1	341	G	0.591	NEU	G	-1.163	MAX
nsp2	1	342	Q	0.960	NEU	E	-0.765	NEU
nsp2	1	343	Q	0.342	NEU	Q	0.564	NEU
nsp2	1	344	K	0.040	MIN	K	1.71	MIN
nsp2	1	345	S	1.313	NEU	S	-0.2	NEU
nsp2	1	346	I	0.746	MIN	I	2.254	MIN
nsp2	1	347	L	1.102	MIN	L	0.799	MIN
nsp2	1	348	T	1.102	NEU	S	-0.434	NEU
nsp2	1	349	P	0.476	NEU	P	-1.138	MAX
nsp2	1	350	L	1.313	MIN	L	1.127	MIN
nsp2	1	351	C	-0.106	MIN	Y	-0.926	NEU
nsp2	1	352	G	0.960	NEU	A	0.369	NEU
nsp2	1	353	F	1.102	MIN	F	0.939	MIN
nsp2	1	354	P	0.501	NEU	A	0.632	NEU
nsp2	1	355	S	1.313	NEU	S	-0.478	NEU
nsp2	1	356	Q	0.432	NEU	E	-0.868	NEU
nsp2	1	357	A	0.844	NEU	A	0.1	NEU
nsp2	1	358	A	0.476	NEU	A	0.471	NEU
nsp2	1	359	G	0.960	NEU	R	-0.402	NEU
nsp2	1	360	V	1.313	MIN	V	1.194	MIN
nsp2	1	361	I	1.313	MIN	V	1.124	MIN

nsp2	1	362	R	1.102	NEU	R	-0.797	NEU
nsp2	1	363	S	1.102	NEU	S	-0.456	NEU
nsp2	1	364	I	1.313	MIN	I	1.251	MIN
nsp2	1	365	F	0.395	MIN	F	0.367	NEU
nsp2	1	366	S	1.313	NEU	S	-0.659	NEU
nsp2	1	367	R	1.313	NEU	R	-0.449	NEU
nsp2	1	368	T	0.893	NEU	T	-0.922	NEU
nsp2	1	369	L	1.313	MIN	L	1.206	MIN
nsp2	1	370	D	0.101	NEU	E	-0.725	NEU
nsp2	1	371	A	0.154	NEU	T	-0.161	NEU
nsp2	1	372	A	0.638	NEU	A	-0.387	NEU
nsp2	1	373	N	0.529	NEU	Q	0.762	NEU
nsp2	1	374	H	0.960	NEU	N	-1.199	MAX
nsp2	1	375	S	0.316	NEU	S	-0.329	NEU
nsp2	1	376	I	1.313	MIN	V	1.021	MIN
nsp2	1	377	P	0.202	NEU	R	1.234	MIN
nsp2	1	378	D	0.529	NEU	V	0.811	MIN
nsp2	1	379	L	1.313	MIN	L	1.423	MIN
nsp2	1	380	Q	0.326	MAX	Q	-0.901	NEU
nsp2	1	381	R	-0.144	NEU	K	-1.288	MAX
nsp2	1	382	A	0.746	MIN	A	0.774	NEU
nsp2	1	383	A	0.432	MIN	A	0.544	NEU
nsp2	1	384	V	0.960	MIN	I	1.682	MIN
nsp2	1	385	T	0.476	NEU	T	0.567	NEU
nsp2	1	386	I	0.960	MIN	I	1.866	MIN
nsp2	1	387	L	1.313	MIN	L	1.337	MIN
nsp2	1	388	D	0.529	MAX	D	-1.21	MAX
nsp2	1	389	G	0.476	NEU	G	-1.255	MAX
nsp2	1	390	I	1.313	MIN	I	1.477	MIN
nsp2	1	391	S	1.102	NEU	S	-0.83	NEU
nsp2	1	392	E	0.529	NEU	Q	-0.351	NEU
nsp2	1	393	Q	0.543	NEU	Y	0.498	NEU
nsp2	1	394	S	1.313	NEU	S	-0.793	NEU
nsp2	1	395	L	0.960	MIN	L	0.753	NEU
nsp2	1	396	R	0.432	MIN	R	0.09	NEU
nsp2	1	397	L	1.313	MIN	L	1.309	MIN
nsp2	1	398	V	1.313	MIN	I	1.298	MIN
nsp2	1	399	D	0.365	NEU	D	-0.954	NEU
nsp2	1	400	A	0.342	MIN	A	0.546	NEU
nsp2	1	401	M	1.313	MIN	M	0.672	NEU
nsp2	1	402	V	0.591	MIN	M	0.79	MIN
nsp2	1	403	Y	0.156	NEU	F	0.326	NEU
nsp2	1	404	T	1.313	NEU	T	-0.326	NEU
nsp2	1	405	S	1.313	NEU	S	-0.708	NEU
nsp2	1	406	D	0.299	NEU	D	-0.152	NEU
nsp2	1	407	L	0.960	MIN	L	1.22	MIN

nsp2	1	408	L	0.461	MIN	A	-1.354	MAX
nsp2	1	409	T	1.102	NEU	T	-0.203	NEU
nsp2	1	410	N	1.102	NEU	N	-0.518	NEU
nsp2	1	411	S	0.529	NEU	N	-1.104	MAX
nsp2	1	412	V	1.313	MIN	L	1.468	MIN
nsp2	1	413	I	1.313	MIN	V	1.058	MIN
nsp2	1	414	V	1.313	MIN	V	1.577	MIN
nsp2	1	415	M	0.529	MIN	M	0.478	NEU
nsp2	1	416	A	0.326	MIN	A	0.581	NEU
nsp2	1	417	Y	0.316	MIN	Y	0.616	NEU
nsp2	1	418	V	1.313	MIN	I	1.341	MIN
nsp2	1	419	T	1.313	NEU	T	-0.275	NEU
nsp2	1	420	G	1.313	NEU	G	-0.774	NEU
nsp2	1	421	G	1.313	NEU	G	-0.689	NEU
nsp2	1	422	L	1.313	MIN	V	1.244	MIN
nsp2	1	423	V	1.313	MIN	V	1.162	MIN
nsp2	1	424	Q	0.591	NEU	Q	-0.883	NEU
nsp2	1	425	Q	0.154	NEU	L	1.533	MIN
nsp2	1	426	T	0.529	NEU	T	-0.39	NEU
nsp2	1	427	S	0.752	NEU	S	-0.481	NEU
nsp2	1	428	Q	0.752	NEU	Q	-0.814	NEU
nsp2	1	429	W	0.391	MIN	W	0.863	MIN
nsp2	1	430	L	1.313	MIN	L	1.345	MIN
nsp2	1	431	S	1.102	NEU	T	-0.043	NEU
nsp2	1	432	N	0.960	NEU	N	-0.71	NEU
nsp2	1	433	L	1.102	MIN	I	2.048	MIN
nsp2	1	434	L	0.529	MIN	F	0.46	NEU
nsp2	1	435	G	0.893	NEU	G	-0.759	NEU
nsp2	1	436	T	0.960	NEU	T	-0.303	NEU
nsp2	1	437	T	0.591	MIN	V	1.532	MIN
nsp2	1	438	V	-0.106	MIN	Y	-1.097	MAX
nsp2	1	439	E	0.365	MIN	E	0.388	NEU
nsp2	1	440	K	0.331	MAX	K	-1.436	MAX
nsp2	1	441	L	1.102	MIN	L	1.329	MIN
nsp2	1	442	K	0.476	NEU	K	-0.579	NEU
nsp2	1	443	P	0.960	NEU	P	-0.882	NEU
nsp2	1	444	V	1.313	MIN	V	1.166	MIN
nsp2	1	445	F	1.313	MIN	L	1.176	MIN
nsp2	1	446	A	0.391	NEU	D	-1.467	MAX
nsp2	1	447	W	0.326	MIN	W	0.64	NEU
nsp2	1	448	I	1.313	MIN	L	1.196	MIN
nsp2	1	449	E	0.844	NEU	E	-0.517	NEU
nsp2	1	450	A	-0.091	NEU	E	-1.108	MAX
nsp2	1	451	K	0.960	NEU	K	-0.123	NEU
nsp2	1	452	L	1.313	MIN	F	0.936	MIN
nsp2	1	453	S	0.281	NEU	K	1.368	MIN

nsp2	1	454	A	0.844	NEU	E	-0.685	NEU
nsp2	1	455	G	1.313	NEU	G	-0.736	NEU
nsp2	1	456	V	1.313	MIN	V	1.399	MIN
nsp2	1	457	E	0.960	NEU	E	-0.575	NEU
nsp2	1	458	F	0.746	MIN	F	0.587	NEU
nsp2	1	459	L	1.313	MIN	L	1.366	MIN
nsp2	1	460	K	0.529	NEU	R	0.659	NEU
nsp2	1	461	D	0.476	MAX	D	-1.443	MAX
nsp2	1	462	A	0.365	MIN	G	-0.612	NEU
nsp2	1	463	W	0.529	MIN	W	0.637	NEU
nsp2	1	464	E	1.102	NEU	E	-0.959	NEU
nsp2	1	465	I	1.313	MIN	I	1.292	MIN
nsp2	1	466	L	1.313	MIN	V	0.983	MIN
nsp2	1	467	K	0.316	MAX	K	-0.795	NEU
nsp2	1	468	F	0.960	MIN	F	1.279	MIN
nsp2	1	469	L	1.313	MIN	I	1.313	MIN
nsp2	1	470	I	0.476	MIN	S	-0.567	NEU
nsp2	1	471	T	0.844	NEU	T	-0.723	NEU
nsp2	1	472	G	0.529	NEU	C	1.721	MIN
nsp2	1	473	V	0.432	MIN	A	0.511	NEU
nsp2	1	474	F	0.746	MIN	C	1.315	MIN
nsp2	1	475	D	0.461	MAX	E	-1.094	MAX
nsp2	1	476	I	1.313	MIN	I	2.116	MIN
nsp2	1	477	V	0.342	NEU	V	1.254	MIN
nsp2	1	478	K	1.313	NEU	G	-0.56	NEU
nsp2	1	479	G	0.960	NEU	G	-0.519	NEU
nsp2	1	480	Q	0.476	NEU	Q	-0.944	NEU
nsp2	1	481	I	1.313	MIN	I	1.124	MIN
nsp2	1	482	Q	-0.193	MAX	V	0.913	MIN
nsp2	1	483	V	0.476	MIN	T	-0.509	NEU
nsp2	1	484	A	0.202	NEU	C	0.676	NEU
nsp2	1	485	S	0.461	NEU	A	0.914	MIN
nsp2	1	486	D	0.844	NEU	K	0.467	NEU
nsp2	1	487	N	0.114	MIN	E	0.496	NEU
nsp2	1	488	I	1.313	MIN	I	1.434	MIN
nsp2	1	489	K	0.844	NEU	K	0.357	NEU
nsp2	1	490	E	0.461	NEU	E	-0.955	NEU
nsp2	1	491	C	0.432	MIN	S	-0.454	NEU
nsp2	1	492	V	1.313	MIN	V	0.964	MIN
nsp2	1	493	K	1.102	NEU	Q	-0.837	NEU
nsp2	1	494	T	0.204	NEU	T	0.081	NEU
nsp2	1	495	F	1.313	MIN	F	0.755	NEU
nsp2	1	496	I	1.102	MIN	F	0.681	NEU
nsp2	1	497	D	-0.237	MIN	K	-2.616	MAX
nsp2	1	498	V	0.960	MIN	L	1.387	MIN
nsp2	1	499	V	1.313	MIN	V	1.058	MIN

nsp2	1	500	N	0.365	MAX	N	-1.041	MAX
nsp2	1	501	K	0.365	NEU	K	-1.669	MAX
nsp2	1	502	A	0.476	MIN	F	1.238	MIN
nsp3_Ubl1	1	1	A	0.767	NEU	A	-0.882	NEU
nsp3_Ubl1	1	2	P	0.037	MIN	P	0.305	NEU
nsp3_Ubl1	1	3	T	0.376	NEU	T	-0.425	NEU
nsp3_Ubl1	1	4	K	-0.147	MAX	K	1.508	MIN
nsp3_Ubl1	1	5	V	0.376	NEU	V	1.172	MIN
nsp3_Ubl1	1	6	T	0.856	NEU	T	0.631	NEU
nsp3_Ubl1	1	7	F	1.109	NEU	F	0.288	NEU
nsp3_Ubl1	1	8	G	1.314	NEU	G	-0.139	NEU
nsp3_Ubl1	1	9	E	1.109	NEU	D	-0.817	NEU
nsp3_Ubl1	1	10	D	1.314	MAX	D	-1.395	MAX
nsp3_Ubl1	1	11	T	0.333	NEU	T	0.152	NEU
nsp3_Ubl1	1	12	V	0.376	NEU	V	0.552	NEU
nsp3_Ubl1	1	13	L	0.767	MIN	I	1.129	MIN
nsp3_Ubl1	1	14	E	0.315	MAX	E	-1.244	MAX
nsp3_Ubl1	1	15	V	1.314	MIN	V	1.407	MIN
nsp3_Ubl1	1	16	Q	0.655	NEU	Q	-0.817	NEU
nsp3_Ubl1	1	17	G	0.491	MAX	G	-1.244	MAX
nsp3_Ubl1	1	18	Y	0.905	MAX	Y	-1.137	MAX
nsp3_Ubl1	1	19	K	0.299	MAX	K	-1.32	MAX
nsp3_Ubl1	1	20	N	0.445	NEU	S	0.063	NEU
nsp3_Ubl1	1	21	V	1.314	MIN	V	1.13	MIN
nsp3_Ubl1	1	22	K	0.321	NEU	N	-0.372	NEU
nsp3_Ubl1	1	23	I	1.314	MIN	I	1.121	MIN
nsp3_Ubl1	1	24	T	1.314	NEU	T	0.117	NEU
nsp3_Ubl1	1	25	F	1.109	MIN	F	0.64	NEU
nsp3_Ubl1	1	26	E	1.109	MAX	E	-1.129	MAX
nsp3_Ubl1	1	27	L	1.314	MIN	L	1.049	MIN
nsp3_Ubl1	1	28	D	1.314	NEU	D	-0.777	NEU
nsp3_Ubl1	1	29	E	1.109	NEU	E	0.47	NEU
nsp3_Ubl1	1	30	R	0.969	MIN	R	1.086	MIN
nsp3_Ubl1	1	31	V	1.314	MIN	I	1.909	MIN
nsp3_Ubl1	1	32	D	1.109	MAX	D	-1.495	MAX
nsp3_Ubl1	1	33	K	1.109	MIN	K	1.296	MIN
nsp3_Ubl1	1	34	V	1.314	MIN	V	1.627	MIN
nsp3_Ubl1	1	35	L	1.314	MIN	L	1.565	MIN
nsp3_Ubl1	1	36	N	0.544	NEU	N	-0.89	NEU
nsp3_Ubl1	1	37	E	1.109	NEU	E	-0.365	NEU
nsp3_Ubl1	1	38	K	0.969	MAX	K	-1.189	MAX
nsp3_Ubl1	1	39	C	1.109	MIN	C	1.18	MIN
nsp3_Ubl1	1	40	S	0.767	NEU	S	0.116	NEU
nsp3_Ubl1	1	41	V	0.333	MIN	A	-0.958	NEU
nsp3_Ubl1	1	42	Y	1.109	NEU	Y	0.415	NEU
nsp3_Ubl1	1	43	T	0.352	NEU	T	-0.848	NEU

nsp3_Ubl1	1	44	V	1.314	MIN	V	1.306	MIN
nsp3_Ubl1	1	45	E	0.491	MAX	E	-1.404	MAX
nsp3_Ubl1	1	46	S	0.256	NEU	L	1.438	MIN
nsp3_Ubl1	1	47	G	0.760	NEU	G	-1.128	MAX
nsp3_Ubl1	1	48	T	1.109	NEU	T	0.23	NEU
nsp3_Ubl1	1	49	E	0.169	MAX	E	-1.972	MAX
nsp3_Ubl1	1	50	V	1.314	MIN	V	1.144	MIN
nsp3_Ubl1	1	51	T	0.856	NEU	N	-0.581	NEU
nsp3_Ubl1	1	52	E	0.445	NEU	E	-1.156	MAX
nsp3_Ubl1	1	53	F	1.314	MIN	F	0.981	MIN
nsp3_Ubl1	1	54	A	0.376	NEU	A	0.654	NEU
nsp3_Ubl1	1	55	C	0.969	MIN	C	1.659	MIN
nsp3_Ubl1	1	56	V	1.314	MIN	V	1.4	MIN
nsp3_Ubl1	1	57	V	1.314	MIN	V	1.306	MIN
nsp3_Ubl1	1	58	A	1.314	NEU	A	0.294	NEU
nsp3_Ubl1	1	59	E	0.856	NEU	D	-0.99	NEU
nsp3_Ubl1	1	60	A	0.491	MIN	A	0.553	NEU
nsp3_Ubl1	1	61	V	1.314	MIN	V	1.523	MIN
nsp3_Ubl1	1	62	V	1.314	MIN	I	0.973	MIN
nsp3_Ubl1	1	63	K	1.314	NEU	K	-0.694	NEU
nsp3_Ubl1	1	64	T	1.314	NEU	T	-0.472	NEU
nsp3_Ubl1	1	65	L	1.314	MIN	L	1.116	MIN
nsp3_Ubl1	1	66	Q	0.445	MAX	Q	-1.148	MAX
nsp3_Ubl1	1	67	P	0.299	MIN	P	0.757	NEU
nsp3_Ubl1	1	68	V	1.314	MIN	V	1.464	MIN
nsp3_Ubl1	1	69	S	1.314	NEU	S	-0.767	NEU
nsp3_Ubl1	1	70	D	0.376	NEU	E	0.651	NEU
nsp3_Ubl1	1	71	L	1.109	MIN	L	0.94	MIN
nsp3_Ubl1	1	72	L	1.314	MIN	L	1.229	MIN
nsp3_Ubl1	1	73	T	0.760	MIN	T	1.068	MIN
nsp3_Ubl1	1	74	N	0.445	NEU	P	0.35	NEU
nsp3_Ubl1	1	75	M	1.314	MIN	L	1.127	MIN
nsp3_Ubl1	1	76	G	1.314	NEU	G	0.236	NEU
nsp3_Ubl1	1	77	I	1.314	MIN	I	1.671	MIN
nsp3_Ubl1	1	78	D	0.333	NEU	D	-1.435	MAX
nsp3_Ubl1	1	79	L	1.314	MIN	L	1.179	MIN
nsp3_Ubl1	1	80	D	1.109	NEU	D	-0.59	NEU
nsp3_Ubl1	1	81	E	0.376	NEU	E	-1.267	MAX
nsp3_Ubl1	1	82	W	1.314	MIN	W	0.754	NEU
nsp3_Ubl1	1	83	S	1.109	NEU	S	-0.779	NEU
nsp3_Ubl1	1	84	V	0.350	MIN	M	-1.602	MAX
nsp3_Ubl1	1	85	A	1.314	NEU	A	0.309	NEU
nsp3_Ubl1	1	86	T	0.905	NEU	T	-0.64	NEU
nsp3_Ubl1	1	87	F	0.407	MIN	Y	0.424	NEU
nsp3_Ubl1	1	88	Y	0.376	MIN	Y	0.022	NEU
nsp3_Ubl1	1	89	L	1.314	MIN	L	1.285	MIN

nsp3_Ubl1	1	90	F	1.314	MIN	F	1.241	MIN
nsp3_Ubl1	1	91	D	0.856	NEU	D	-0.766	NEU
nsp3_Ubl1	1	92	D	0.445	NEU	E	-1.355	MAX
nsp3_Ubl1	1	93	A	0.333	NEU	S	1.283	MIN
nsp3_Ubl1	1	94	G	1.314	NEU	G	0.29	NEU
nsp3_Ubl1	1	95	E	1.314	MAX	E	-1.099	MAX
nsp3_Ubl1	1	96	E	-0.028	MAX	F	1.022	MIN
nsp3_Ubl1	1	97	K	0.856	NEU	K	-0.411	NEU
nsp3_Ubl1	1	98	L	1.314	MIN	L	1.306	MIN
nsp3_Ubl1	1	99	S	0.315	NEU	A	-0.018	NEU
nsp3_Ubl1	1	100	S	1.314	NEU	S	-0.732	NEU
nsp3_Ubl1	1	101	R	0.677	MIN	H	0.302	NEU
nsp3_Ubl1	1	102	M	1.314	MIN	M	0.831	MIN
nsp3_Ubl1	1	103	Y	1.109	NEU	Y	0.512	NEU
nsp3_Ubl1	1	104	C	1.314	MIN	C	1.23	MIN
nsp3_Ubl1	1	105	S	1.314	NEU	S	-0.58	NEU
nsp3_Ubl1	1	106	F	1.109	MIN	F	0.837	MIN
nsp3_Ubl1	1	107	Y	1.109	MAX	Y	-3.043	MAX
nsp3_Ubl1	1	108	P	0.969	MIN	P	1.279	MIN
nsp3_Ubl1	1	109	P	0.445	NEU	P	0.764	NEU
nsp3_Ubl1	1	110	D	1.311	NEU	D	0.189	NEU
nsp3_Ubl1	1	111	E	0.856	MIN	E	0.765	NEU
nsp3_Macro>	1	1	E	-0.147	MIN	E	2.33	MIN
nsp3_Macro>	1	2	V	0.561	NEU	V	-0.859	NEU
nsp3_Macro>	1	3	N	0.133	MAX	N	-1.063	MAX
nsp3_Macro>	1	4	Q	0.856	NEU	S	-0.423	NEU
nsp3_Macro>	1	5	F	0.315	MIN	F	0.642	NEU
nsp3_Macro>	1	6	T	0.856	NEU	S	-0.011	NEU
nsp3_Macro>	1	7	G	0.856	NEU	G	0.248	NEU
nsp3_Macro>	1	8	Y	0.352	MIN	Y	0.522	NEU
nsp3_Macro>	1	9	L	0.856	MIN	L	1.4	MIN
nsp3_Macro>	1	10	K	1.314	NEU	K	-0.37	NEU
nsp3_Macro>	1	11	L	1.314	MIN	L	1.257	MIN
nsp3_Macro>	1	12	T	1.314	NEU	T	-0.283	NEU
nsp3_Macro>	1	13	D	0.760	MIN	D	0.87	MIN
nsp3_Macro>	1	14	N	0.321	NEU	N	-0.83	NEU
nsp3_Macro>	1	15	V	1.314	MIN	V	1.148	MIN
nsp3_Macro>	1	16	A	0.428	NEU	Y	-0.568	NEU
nsp3_Macro>	1	17	I	1.314	MIN	I	1.525	MIN
nsp3_Macro>	1	18	K	1.109	MAX	K	-1.228	MAX
nsp3_Macro>	1	19	C	0.544	MIN	N	-1.012	MAX
nsp3_Macro>	1	20	V	0.445	MIN	A	-0.079	NEU
nsp3_Macro>	1	21	D	0.321	NEU	D	-1.774	MAX
nsp3_Macro>	1	22	I	1.109	MIN	I	1.483	MIN
nsp3_Macro>	1	23	V	1.314	MIN	V	1.427	MIN
nsp3_Macro>	1	24	K	-0.034	MAX	E	0.854	MIN

nsp3_Macro	1	25	E	0.856	NEU	E	-0.572	NEU
nsp3_Macro	1	26	A	0.760	MIN	A	0.628	NEU
nsp3_Macro	1	27	Q	0.491	NEU	K	1.197	MIN
nsp3_Macro	1	28	S	0.544	NEU	K	2.203	MIN
nsp3_Macro	1	29	A	0.352	MIN	V	1.321	MIN
nsp3_Macro	1	30	K	-0.004	NEU	K	0.169	NEU
nsp3_Macro	1	31	P	0.606	NEU	P	-0.817	NEU
nsp3_Macro	1	32	T	0.350	NEU	T	-0.07	NEU
nsp3_Macro	1	33	V	1.314	MIN	V	1.317	MIN
nsp3_Macro	1	34	I	1.314	MIN	V	1.105	MIN
nsp3_Macro	1	35	V	1.314	MIN	V	1.217	MIN
nsp3_Macro	1	36	N	0.969	NEU	N	-0.944	NEU
nsp3_Macro	1	37	A	1.314	NEU	A	0.328	NEU
nsp3_Macro	1	38	A	0.856	NEU	A	0.574	NEU
nsp3_Macro	1	39	N	1.314	NEU	N	-0.908	NEU
nsp3_Macro	1	40	I	0.856	MIN	V	1.231	MIN
nsp3_Macro	1	41	H	0.410	NEU	Y	1.067	MIN
nsp3_Macro	1	42	L	1.314	MIN	L	1.228	MIN
nsp3_Macro	1	43	K	1.314	NEU	K	0.168	NEU
nsp3_Macro	1	44	H	1.109	NEU	H	-0.785	NEU
nsp3_Macro	1	45	G	1.109	NEU	G	-0.339	NEU
nsp3_Macro	1	46	G	1.109	NEU	G	-0.801	NEU
nsp3_Macro	1	47	G	1.314	NEU	G	-0.242	NEU
nsp3_Macro	1	48	V	1.314	MIN	V	1.393	MIN
nsp3_Macro	1	49	A	1.314	NEU	A	0.4	NEU
nsp3_Macro	1	50	G	1.314	NEU	G	0.102	NEU
nsp3_Macro	1	51	A	1.314	NEU	A	0.449	NEU
nsp3_Macro	1	52	L	1.314	MIN	L	1.167	MIN
nsp3_Macro	1	53	N	1.314	NEU	N	-0.503	NEU
nsp3_Macro	1	54	K	1.314	NEU	K	0.047	NEU
nsp3_Macro	1	55	A	1.314	NEU	A	0.093	NEU
nsp3_Macro	1	56	T	1.109	NEU	T	-0.034	NEU
nsp3_Macro	1	57	N	1.314	NEU	N	0.122	NEU
nsp3_Macro	1	58	G	1.314	NEU	N	-0.324	NEU
nsp3_Macro	1	59	A	0.376	MAX	A	-0.618	NEU
nsp3_Macro	1	60	M	1.109	NEU	M	-0.103	NEU
nsp3_Macro	1	61	Q	0.969	NEU	Q	-0.243	NEU
nsp3_Macro	1	62	K	0.144	NEU	V	0.301	NEU
nsp3_Macro	1	63	E	1.109	MAX	E	-1.812	MAX
nsp3_Macro	1	64	S	0.220	MAX	S	-0.789	NEU
nsp3_Macro	1	65	D	-0.215	MIN	D	-1.163	MAX
nsp3_Macro	1	66	D	0.074	NEU	D	-1.354	MAX
nsp3_Macro	1	67	Y	0.760	NEU	Y	0.41	NEU
nsp3_Macro	1	68	I	1.314	MIN	I	2.14	MIN
nsp3_Macro	1	69	K	0.407	MIN	A	-0.219	NEU
nsp3_Macro	1	70	L	0.035	MIN	T	-0.615	NEU

nsp3_Macro	1	71	N	1.109	NEU	N	-0.629	NEU
nsp3_Macro	1	72	G	1.314	NEU	G	-0.214	NEU
nsp3_Macro	1	73	P	0.969	NEU	P	-0.291	NEU
nsp3_Macro	1	74	L	1.314	MIN	L	1.232	MIN
nsp3_Macro	1	75	T	0.428	NEU	K	-1.378	MAX
nsp3_Macro	1	76	V	1.314	MIN	V	1.145	MIN
nsp3_Macro	1	77	G	1.314	NEU	G	-0.365	NEU
nsp3_Macro	1	78	G	1.314	NEU	G	-0.448	NEU
nsp3_Macro	1	79	S	1.314	NEU	S	-0.638	NEU
nsp3_Macro	1	80	C	1.109	MIN	C	1.566	MIN
nsp3_Macro	1	81	L	0.760	MIN	V	0.66	NEU
nsp3_Macro	1	82	L	1.314	MIN	L	1.332	MIN
nsp3_Macro	1	83	S	1.314	NEU	S	-0.365	NEU
nsp3_Macro	1	84	G	1.314	NEU	G	-0.86	NEU
nsp3_Macro	1	85	H	1.314	NEU	H	-0.577	NEU
nsp3_Macro	1	86	N	0.969	NEU	N	0.225	NEU
nsp3_Macro	1	87	L	1.314	MIN	L	1.247	MIN
nsp3_Macro	1	88	A	1.109	NEU	A	0.351	NEU
nsp3_Macro	1	89	K	0.315	MAX	K	-0.266	NEU
nsp3_Macro	1	90	K	0.677	MAX	H	-0.329	NEU
nsp3_Macro	1	91	C	1.314	MIN	C	1.068	MIN
nsp3_Macro	1	92	L	1.314	MIN	L	1.057	MIN
nsp3_Macro	1	93	H	1.314	NEU	H	-0.003	NEU
nsp3_Macro	1	94	V	1.314	MIN	V	1.256	MIN
nsp3_Macro	1	95	V	1.314	MIN	V	1.085	MIN
nsp3_Macro	1	96	G	1.314	NEU	G	-0.279	NEU
nsp3_Macro	1	97	P	0.407	NEU	P	-0.861	NEU
nsp3_Macro	1	98	N	1.314	NEU	N	-0.626	NEU
nsp3_Macro	1	99	L	0.969	MIN	V	1.018	MIN
nsp3_Macro	1	100	N	0.544	NEU	N	-0.12	NEU
nsp3_Macro	1	101	A	1.314	NEU	K	0.419	NEU
nsp3_Macro	1	102	G	0.856	NEU	G	-0.986	NEU
nsp3_Macro	1	103	E	0.856	MAX	E	-0.969	NEU
nsp3_Macro	1	104	D	0.856	MAX	D	-1.241	MAX
nsp3_Macro	1	105	I	1.109	MIN	I	1.71	MIN
nsp3_Macro	1	106	Q	0.412	NEU	Q	-0.214	NEU
nsp3_Macro	1	107	L	0.677	MIN	L	0.403	NEU
nsp3_Macro	1	108	L	1.314	MIN	L	0.914	MIN
nsp3_Macro	1	109	K	0.655	NEU	K	-0.68	NEU
nsp3_Macro	1	110	A	0.969	NEU	S	-0.587	NEU
nsp3_Macro	1	111	A	1.314	MIN	A	0.798	MIN
nsp3_Macro	1	112	Y	1.314	MIN	Y	0.896	MIN
nsp3_Macro	1	113	E	0.480	NEU	E	0.786	MIN
nsp3_Macro	1	114	N	0.969	NEU	N	-0.841	NEU
nsp3_Macro	1	115	F	1.314	MIN	F	1.273	MIN
nsp3_Macro	1	116	N	0.321	NEU	N	-0.895	NEU

nsp3_Macro	1	117	S	1.314	NEU	Q	-0.331	NEU
nsp3_Macro	1	118	Q	1.109	NEU	H	-0.179	NEU
nsp3_Macro	1	119	D	0.191	MAX	E	-0.432	NEU
nsp3_Macro	1	120	V	0.350	MIN	V	1.221	MIN
nsp3_Macro	1	121	L	1.314	MIN	L	1.259	MIN
nsp3_Macro	1	122	L	1.314	MIN	L	1.34	MIN
nsp3_Macro	1	123	A	1.314	NEU	A	0.296	NEU
nsp3_Macro	1	124	P	1.109	MAX	P	-1.037	MAX
nsp3_Macro	1	125	L	1.314	MIN	L	1.125	MIN
nsp3_Macro	1	126	L	1.314	MIN	L	0.972	MIN
nsp3_Macro	1	127	S	1.314	NEU	S	-0.539	NEU
nsp3_Macro	1	128	A	1.314	NEU	A	-0.172	NEU
nsp3_Macro	1	129	G	1.314	NEU	G	-0.415	NEU
nsp3_Macro	1	130	I	1.109	MIN	I	1.739	MIN
nsp3_Macro	1	131	F	1.314	MIN	F	0.947	MIN
nsp3_Macro	1	132	G	1.109	NEU	G	0.433	NEU
nsp3_Macro	1	133	A	0.491	NEU	A	0.708	NEU
nsp3_Macro	1	134	K	1.109	NEU	D	-0.689	NEU
nsp3_Macro	1	135	P	1.314	NEU	P	-0.686	NEU
nsp3_Macro	1	136	L	1.109	MIN	I	1.627	MIN
nsp3_Macro	1	137	Q	0.655	NEU	H	-0.598	NEU
nsp3_Macro	1	138	S	1.314	NEU	S	-0.667	NEU
nsp3_Macro	1	139	L	1.314	MIN	L	1.236	MIN
nsp3_Macro	1	140	K	0.428	NEU	R	0.635	NEU
nsp3_Macro	1	141	V	0.856	MIN	V	1.296	MIN
nsp3_Macro	1	142	C	1.314	MIN	C	1.211	MIN
nsp3_Macro	1	143	V	1.109	MIN	V	1.286	MIN
nsp3_Macro	1	144	E	0.767	NEU	D	0.092	NEU
nsp3_Macro	1	145	T	0.350	NEU	T	-0.347	NEU
nsp3_Macro	1	146	V	1.314	MIN	V	1.115	MIN
nsp3_Macro	1	147	R	0.655	MIN	R	1.529	MIN
nsp3_Macro	1	148	T	0.905	NEU	T	-0.229	NEU
nsp3_Macro	1	149	Q	0.856	NEU	N	-0.911	NEU
nsp3_Macro	1	150	V	1.314	MIN	V	1.217	MIN
nsp3_Macro	1	151	Y	0.606	MIN	Y	0.808	MIN
nsp3_Macro	1	152	I	1.314	MIN	L	1.453	MIN
nsp3_Macro	1	153	A	0.544	NEU	A	0.283	NEU
nsp3_Macro	1	154	V	1.314	MIN	V	1.366	MIN
nsp3_Macro	1	155	N	0.191	NEU	F	-0.662	NEU
nsp3_Macro	1	156	D	0.407	MAX	D	0.279	NEU
nsp3_Macro	1	157	K	0.220	NEU	K	-1.184	MAX
nsp3_Macro	1	158	A	0.299	MIN	N	1.307	MIN
nsp3_Macro	1	159	L	1.109	MIN	L	1.377	MIN
nsp3_Macro	1	160	Y	0.561	MAX	Y	-1.116	MAX
nsp3_Macro	1	161	D	0.350	NEU	D	-0.083	NEU
nsp3_Macro	1	162	Q	0.561	MAX	K	-1.548	MAX

nsp3_Macro	1	163	V	1.314	MIN	L	1.225	MIN
nsp3_Macro	1	164	V	0.969	MIN	V	1.33	MIN
nsp3_Macro	1	165	M	0.376	NEU	S	-0.522	NEU
nsp3_Macro	1	166	D	0.321	NEU	S	-0.682	NEU
nsp3_Macro	1	167	Y	0.445	NEU	F	0.696	NEU
nsp3_Macro	1	168	L	1.102	MIN	L	0.99	MIN
nsp3_Macro	1	169	D	1.313	NEU	E	0.315	NEU
nsp3_Macro	1	170	L	0.606	NEU	M	0.548	NEU
nsp3_Macro	1	171	K	0.376	MIN	K	-0.886	NEU
nsp3_Macro	1	172	P	0.969	NEU	S	0.025	NEU
nsp3_SUD_N	1	1	K	0.844	NEU	K	0.362	NEU
nsp3_SUD_N	1	2	I	0.844	MIN	I	0.603	NEU
nsp3_SUD_N	1	3	K	1.102	MAX	K	-1.564	MAX
nsp3_SUD_N	1	4	A	0.638	NEU	A	0.497	NEU
nsp3_SUD_N	1	5	C	0.663	MIN	C	1.531	MIN
nsp3_SUD_N	1	6	I	1.313	MIN	V	1.387	MIN
nsp3_SUD_N	1	7	E	0.844	MAX	E	-1.049	MAX
nsp3_SUD_N	1	8	E	1.102	NEU	E	-0.727	NEU
nsp3_SUD_N	1	9	V	1.313	MIN	V	1.372	MIN
nsp3_SUD_N	1	10	T	1.313	NEU	T	-0.114	NEU
nsp3_SUD_N	1	11	T	1.102	NEU	T	-0.233	NEU
nsp3_SUD_N	1	12	T	0.969	MIN	T	1.155	MIN
nsp3_SUD_N	1	13	L	1.109	MIN	L	1.527	MIN
nsp3_SUD_N	1	14	E	0.905	MIN	E	1.038	MIN
nsp3_SUD_N	1	15	E	1.314	NEU	E	0.367	NEU
nsp3_SUD_N	1	16	T	0.856	NEU	T	-0.168	NEU
nsp3_SUD_N	1	17	K	0.100	MIN	K	0.739	NEU
nsp3_SUD_N	1	18	F	0.905	NEU	F	-0.751	NEU
nsp3_SUD_N	1	19	L	0.760	MIN	L	0.71	NEU
nsp3_SUD_N	1	20	T	1.109	NEU	T	-0.512	NEU
nsp3_SUD_N	1	21	N	1.109	NEU	E	-0.671	NEU
nsp3_SUD_N	1	22	K	0.969	NEU	N	-0.834	NEU
nsp3_SUD_N	1	23	L	1.109	MIN	L	1.307	MIN
nsp3_SUD_N	1	24	L	1.314	MIN	L	1.435	MIN
nsp3_SUD_N	1	25	L	1.109	MIN	L	1.241	MIN
nsp3_SUD_N	1	26	F	1.314	MIN	Y	0.923	MIN
nsp3_SUD_N	1	27	A	0.321	NEU	I	1.269	MIN
nsp3_SUD_N	1	28	D	1.314	NEU	D	-0.194	NEU
nsp3_SUD_N	1	29	I	1.109	MIN	I	1.444	MIN
nsp3_SUD_N	1	30	N	0.760	NEU	N	0.721	NEU
nsp3_SUD_N	1	31	G	1.109	NEU	G	-0.611	NEU
nsp3_SUD_N	1	32	K	1.109	NEU	N	-0.705	NEU
nsp3_SUD_N	1	33	L	0.969	MIN	L	1.347	MIN
nsp3_SUD_N	1	34	Y	0.191	NEU	H	-0.4	NEU
nsp3_SUD_N	1	35	P	-0.124	NEU	P	-0.94	NEU
nsp3_SUD_N	1	36	D	0.352	MAX	D	-0.991	NEU

nsp3_SUD_N	1	37	S	1.314	NEU	S	-0.676	NEU
nsp3_SUD_N	1	38	Q	0.333	MAX	A	-0.633	NEU
nsp3_SUD_N	1	39	N	0.376	NEU	T	-0.222	NEU
nsp3_SUD_N	1	40	M	1.314	MIN	L	1.529	MIN
nsp3_SUD_N	1	41	L	1.314	MIN	V	1.269	MIN
nsp3_SUD_N	1	42	R	0.123	MIN	S	-0.51	NEU
nsp3_SUD_N	1	43	G	1.314	NEU	D	-0.261	NEU
nsp3_SUD_N	1	44	E	-0.195	NEU	I	1.737	MIN
nsp3_SUD_N	1	45	D	0.767	NEU	D	-0.753	NEU
nsp3_SUD_N	1	46	M	0.315	NEU	I	1.57	MIN
nsp3_SUD_N	1	47	S	0.191	MIN	T	0.452	NEU
nsp3_SUD_N	1	48	F	-0.147	NEU	F	-1.594	MAX
nsp3_SUD_N	1	49	L	1.313	MIN	L	1.368	MIN
nsp3_SUD_N	1	50	E	0.767	NEU	K	0.142	NEU
nsp3_SUD_N	1	51	K	0.154	MAX	K	-0.966	NEU
nsp3_SUD_N	1	52	D	0.085	NEU	D	1.355	MIN
nsp3_SUD_N	1	53	A	0.179	NEU	A	0.889	MIN
nsp3_SUD_N	1	54	P	0.561	NEU	P	0.018	NEU
nsp3_SUD_N	1	55	Y	0.905	NEU	Y	-0.348	NEU
nsp3_SUD_N	1	56	I	1.109	MIN	I	1.659	MIN
nsp3_SUD_N	1	57	V	1.314	MIN	V	1.249	MIN
nsp3_SUD_N	1	58	G	1.314	NEU	G	-0.469	NEU
nsp3_SUD_N	1	59	D	1.109	MAX	D	-1.144	MAX
nsp3_SUD_N	1	60	V	1.314	MIN	V	1.475	MIN
nsp3_SUD_N	1	61	I	1.109	MIN	V	1.403	MIN
nsp3_SUD_N	1	62	T	0.655	NEU	Q	-0.923	NEU
nsp3_SUD_N	1	63	S	0.191	NEU	E	-1.239	MAX
nsp3_SUD_N	1	64	G	0.856	NEU	G	-0.839	NEU
nsp3_SUD_N	1	65	D	0.760	NEU	V	0.911	MIN
nsp3_SUD_N	1	66	I	1.314	MIN	L	1.041	MIN
nsp3_SUD_N	1	67	T	1.314	NEU	T	-0.374	NEU
nsp3_SUD_N	1	68	C	0.677	MIN	A	0.459	NEU
nsp3_SUD_N	1	69	V	1.314	MIN	V	1.151	MIN
nsp3_SUD_N	1	70	V	1.314	MIN	V	1.355	MIN
nsp3_SUD_N	1	71	I	1.314	MIN	I	1.402	MIN
nsp3_SUD_N	1	72	P	0.677	NEU	P	-1.067	MAX
nsp3_SUD_N	1	73	A	0.905	NEU	T	-0.292	NEU
nsp3_SUD_N	1	74	K	-0.070	NEU	K	-1.273	MAX
nsp3_SUD_N	1	75	K	-0.124	NEU	K	-0.896	NEU
nsp3_SUD_N	1	76	A	0.041	MAX	A	-0.658	NEU
nsp3_SUD_N	1	77	G	0.969	NEU	G	0.722	NEU
nsp3_SUD_N	1	78	G	1.314	NEU	G	-0.663	NEU
nsp3_SUD_N	1	79	T	0.856	NEU	T	-0.021	NEU
nsp3_SUD_N	1	80	T	0.856	NEU	T	0.087	NEU
nsp3_SUD_N	1	81	E	0.333	NEU	E	-0.468	NEU
nsp3_SUD_N	1	82	M	0.760	MIN	M	0.651	NEU

nsp3_SUD_N	1	83	L	1.314	MIN	L	1.028	MIN
nsp3_SUD_N	1	84	A	0.960	NEU	A	0.681	NEU
nsp3_SUD_N	1	85	K	0.856	NEU	K	-0.826	NEU
nsp3_SUD_N	1	86	A	1.109	MIN	A	0.942	MIN
nsp3_SUD_N	1	87	L	1.314	MIN	L	1.269	MIN
nsp3_SUD_N	1	88	K	0.445	MAX	R	-0.32	NEU
nsp3_SUD_N	1	89	K	0.376	NEU	K	-1.115	MAX
nsp3_SUD_N	1	90	V	1.314	MIN	V	1.278	MIN
nsp3_SUD_N	1	91	P	0.480	NEU	P	-0.392	NEU
nsp3_SUD_N	1	92	V	0.256	MIN	T	-0.558	NEU
nsp3_SUD_N	1	93	D	-0.028	NEU	D	-1.013	MAX
nsp3_SUD_N	1	94	E	0.561	NEU	N	-0.888	NEU
nsp3_SUD_N	1	95	Y	0.376	MIN	Y	0.334	NEU
nsp3_SUD_N	1	96	I	1.109	MIN	I	1.525	MIN
nsp3_SUD_N	1	97	T	1.314	NEU	T	-0.44	NEU
nsp3_SUD_N	1	98	T	1.109	NEU	T	-0.259	NEU
nsp3_SUD_N	1	99	Y	0.233	MAX	Y	0.614	NEU
nsp3_SUD_N	1	100	P	0.333	NEU	P	-0.904	NEU
nsp3_SUD_N	1	101	G	1.109	NEU	G	-0.195	NEU
nsp3_SUD_N	1	102	Q	1.109	NEU	Q	-1.126	MAX
nsp3_SUD_N	1	103	G	0.352	MIN	G	0.549	NEU
nsp3_SUD_N	1	104	C	0.220	MIN	L	1.166	MIN
nsp3_SUD_N	1	105	A	0.655	NEU	N	-0.795	NEU
nsp3_SUD_N	1	106	G	0.491	NEU	G	-0.583	NEU
nsp3_SUD_N	1	107	Y	-0.044	MAX	Y	-0.895	NEU
nsp3_SUD_N	1	108	T	0.491	MIN	T	0.837	MIN
nsp3_SUD_N	1	109	L	0.856	MIN	V	0.918	MIN
nsp3_SUD_N	1	110	E	0.333	MIN	E	1.544	MIN
nsp3_SUD_N	1	111	E	0.445	NEU	E	-0.118	NEU
nsp3_SUD_N	1	112	A	0.677	NEU	A	0.417	NEU
nsp3_SUD_N	1	113	K	1.109	NEU	K	-0.784	NEU
nsp3_SUD_N	1	114	T	0.856	MIN	T	1.414	MIN
nsp3_SUD_N	1	115	A	0.969	MIN	V	1.47	MIN
nsp3_SUD_N	1	116	L	1.109	MIN	L	1.45	MIN
nsp3_SUD_N	1	117	K	0.606	MAX	K	-1.322	MAX
nsp3_SUD_N	1	118	K	0.315	MAX	K	-1.244	MAX
nsp3_SUD_N	1	119	C	0.856	MIN	C	1.774	MIN
nsp3_SUD_N	1	120	K	0.144	MAX	K	-0.727	NEU
nsp3_SUD_N	1	121	S	1.314	NEU	S	-0.539	NEU
nsp3_SUD_N	1	122	A	0.638	MIN	A	0.733	NEU
nsp3_SUD_N	1	123	F	1.314	MIN	F	1.225	MIN
nsp3_SUD_N	1	124	Y	0.376	NEU	Y	0.731	NEU
nsp3_SUD_N	1	125	V	1.314	MIN	I	1.372	MIN
nsp3_SUD_N	1	126	L	1.314	MIN	L	1.409	MIN
nsp3_SUD_N	1	127	P	0.969	NEU	P	-0.859	NEU
nsp3_SUD_N	1	128	S	1.314	NEU	S	-0.54	NEU

nsp3_SUD_N	1	129	E	0.220	NEU	I	1.215	MIN
nsp3_SUD_N	1	130	T	0.154	NEU	I	-0.467	NEU
nsp3_SUD_N	1	131	P	0.094	NEU	S	0.255	NEU
nsp3_SUD_N	1	132	N	0.491	NEU	N	-0.882	NEU
nsp3_SUD_N	1	133	A	-0.226	NEU	E	-1.249	MAX
nsp3_SUD_N	1	134	K	0.133	MIN	K	1.598	MIN
nsp3_SUD_N	1	135	E	0.154	MAX	Q	-0.979	NEU
nsp3_SUD_N	1	136	E	0.281	NEU	E	-0.431	NEU
nsp3_SUD_N	1	137	I	0.445	MIN	I	1.356	MIN
nsp3_SUD_N	1	138	L	0.856	MIN	L	1.446	MIN
nsp3_SUD_N	1	139	G	1.109	NEU	G	-0.622	NEU
nsp3_SUD_N	1	140	T	1.314	NEU	T	-0.235	NEU
nsp3_SUD_N	1	141	V	1.314	MIN	V	1.698	MIN
nsp3_SUD_N	1	142	S	0.969	NEU	S	-0.535	NEU
nsp3_SUD_N	1	143	W	1.314	NEU	W	0.173	NEU
nsp3_SUD_N	1	144	N	1.314	NEU	N	-0.686	NEU
nsp3_SUD_N	1	145	L	1.314	MIN	L	1.236	MIN
nsp3_SUD_N	1	146	R	1.109	NEU	R	-0.368	NEU
nsp3_SUD_N	1	147	E	0.969	MAX	E	-1.376	MAX
nsp3_SUD_N	1	148	M	1.109	NEU	M	0.212	NEU
nsp3_SUD_N	1	149	L	1.314	MIN	L	1.398	MIN
nsp3_SUD_N	1	150	A	1.109	NEU	A	-0.452	NEU
nsp3_SUD_N	1	151	H	1.314	NEU	H	-0.383	NEU
nsp3_SUD_N	1	152	A	1.314	NEU	A	0.338	NEU
nsp3_SUD_N	1	153	E	0.677	NEU	E	0.543	NEU
nsp3_SUD_N	1	154	E	0.376	NEU	E	0.411	NEU
nsp3_SUD_N	1	155	T	0.352	NEU	T	-0.599	NEU
nsp3_SUD_N	1	156	R	1.314	MIN	R	1.761	MIN
nsp3_SUD_N	1	157	K	0.169	NEU	K	-0.056	NEU
nsp3_SUD_N	1	158	L	1.314	MIN	L	1.235	MIN
nsp3_SUD_N	1	159	M	1.314	MIN	M	0.745	NEU
nsp3_SUD_N	1	160	P	0.631	NEU	P	-0.953	NEU
nsp3_SUD_N	1	161	I	1.314	MIN	V	1.448	MIN
nsp3_SUD_N	1	162	C	0.760	MIN	C	0.674	NEU
nsp3_SUD_N	1	163	M	1.314	MIN	V	1.312	MIN
nsp3_SUD_N	1	164	D	0.760	NEU	E	0.504	NEU
nsp3_SUD_N	1	165	V	0.445	MIN	T	-0.266	NEU
nsp3_SUD_N	1	166	R	0.445	NEU	K	-1.027	MAX
nsp3_SUD_N	1	167	A	0.407	MIN	A	-0.039	NEU
nsp3_SUD_N	1	168	I	1.109	MIN	I	1.988	MIN
nsp3_SUD_N	1	169	M	0.856	MIN	V	1.468	MIN
nsp3_SUD_N	1	170	A	1.109	NEU	S	-0.591	NEU
nsp3_SUD_N	1	171	T	1.314	NEU	T	-0.093	NEU
nsp3_SUD_N	1	172	I	1.314	MIN	I	1.702	MIN
nsp3_SUD_N	1	173	Q	0.655	MAX	Q	-1.146	MAX
nsp3_SUD_N	1	174	R	0.677	NEU	R	-0.916	NEU

nsp3_SUD_N	1	175	K	0.256	MAX	K	-0.569	NEU
nsp3_SUD_N	1	176	Y	0.969	NEU	Y	-0.905	NEU
nsp3_SUD_N	1	177	K	1.109	NEU	K	0.461	NEU
nsp3_SUD_N	1	178	G	1.109	NEU	G	0.238	NEU
nsp3_SUD_N	1	179	I	1.109	MIN	I	2.186	MIN
nsp3_SUD_N	1	180	K	0.677	MAX	K	-1.244	MAX
nsp3_SUD_N	1	181	I	1.109	MIN	I	1.898	MIN
nsp3_SUD_N	1	182	Q	0.606	NEU	Q	-0.752	NEU
nsp3_SUD_N	1	183	E	1.109	MAX	E	-1.075	MAX
nsp3_SUD_N	1	184	G	1.314	NEU	G	-0.097	NEU
nsp3_SUD_N	1	185	I	1.109	MIN	V	0.976	MIN
nsp3_SUD_N	1	186	V	1.314	MIN	V	1.505	MIN
nsp3_SUD_N	1	187	D	1.109	MIN	D	0.736	NEU
nsp3_SUD_N	1	188	Y	1.313	NEU	Y	-0.583	NEU
nsp3_SUD_N	1	189	G	0.969	NEU	G	-0.257	NEU
nsp3_SUD_N	1	190	V	0.491	MIN	A	-0.139	NEU
nsp3_SUD_N	1	191	R	1.314	NEU	R	0.169	NEU
nsp3_SUD_N	1	192	F	1.314	MIN	F	0.76	NEU
nsp3_SUD_N	1	193	F	0.352	NEU	Y	-0.067	NEU
nsp3_SUD_N	1	194	F	1.314	MIN	F	1.148	MIN
nsp3_SUD_N	1	195	Y	0.333	NEU	Y	-0.53	NEU
nsp3_SUD_N	1	196	T	1.314	NEU	T	0.297	NEU
nsp3_SUD_N	1	197	S	1.314	NEU	S	-0.098	NEU
nsp3_SUD_N	1	198	K	0.333	NEU	K	0.906	MIN
nsp3_SUD_N	1	199	E	1.314	NEU	T	-0.28	NEU
nsp3_SUD_N	1	200	P	0.376	NEU	T	0.088	NEU
nsp3_SUD_N	1	201	V	1.314	MIN	V	1.074	MIN
nsp3_SUD_N	1	202	A	0.544	NEU	A	0.676	NEU
nsp3_SUD_N	1	203	S	1.109	NEU	S	0.007	NEU
nsp3_SUD_N	1	204	I	1.314	MIN	L	1.253	MIN
nsp3_SUD_N	1	205	I	1.314	MIN	I	1.245	MIN
nsp3_SUD_N	1	206	T	0.491	NEU	N	1.795	MIN
nsp3_SUD_N	1	207	K	0.445	MAX	T	-0.136	NEU
nsp3_SUD_N	1	208	L	1.314	MIN	L	1.515	MIN
nsp3_SUD_N	1	209	N	0.760	NEU	N	-0.667	NEU
nsp3_SUD_N	1	210	S	0.760	NEU	D	0.026	NEU
nsp3_SUD_N	1	211	L	1.314	MIN	L	1.427	MIN
nsp3_SUD_N	1	212	N	0.321	MIN	N	-0.262	NEU
nsp3_SUD_N	1	213	E	1.109	NEU	E	-0.573	NEU
nsp3_SUD_N	1	214	P	0.376	MAX	T	-0.402	NEU
nsp3_SUD_N	1	215	L	1.314	MIN	L	1.439	MIN
nsp3_SUD_N	1	216	V	1.314	MIN	V	1.17	MIN
nsp3_SUD_N	1	217	T	1.314	NEU	T	-0.323	NEU
nsp3_SUD_N	1	218	M	1.314	NEU	M	0.002	NEU
nsp3_SUD_N	1	219	P	0.491	NEU	P	-1.001	MAX
nsp3_SUD_N	1	220	I	1.314	MIN	L	1.405	MIN

nsp3_SUD_N	1	221	G	1.314	NEU	G	-0.537	NEU
nsp3_SUD_N	1	222	Y	1.109	NEU	Y	-0.195	NEU
nsp3_SUD_N	1	223	V	1.109	MIN	V	1.046	MIN
nsp3_SUD_N	1	224	T	1.314	NEU	T	-0.137	NEU
nsp3_SUD_N	1	225	H	1.314	NEU	H	-0.239	NEU
nsp3_SUD_N	1	226	G	1.109	NEU	G	-0.14	NEU
nsp3_SUD_N	1	227	F	1.314	MIN	L	1.53	MIN
nsp3_SUD_N	1	228	N	0.677	MAX	N	-1.151	MAX
nsp3_SUD_N	1	229	L	1.314	MIN	L	1.297	MIN
nsp3_SUD_N	1	230	E	0.969	MAX	E	-1.122	MAX
nsp3_SUD_N	1	231	E	0.856	MAX	E	-1.146	MAX
nsp3_SUD_N	1	232	A	1.314	NEU	A	0.285	NEU
nsp3_SUD_N	1	233	A	0.606	NEU	A	0.398	NEU
nsp3_SUD_N	1	234	R	1.314	NEU	R	-0.284	NEU
nsp3_SUD_N	1	235	C	0.856	MIN	Y	0.575	NEU
nsp3_SUD_N	1	236	M	1.314	MIN	M	0.868	MIN
nsp3_SUD_N	1	237	R	0.606	NEU	R	-0.932	NEU
nsp3_SUD_N	1	238	S	1.314	NEU	S	-0.983	NEU
nsp3_SUD_N	1	239	L	1.314	MIN	L	1.615	MIN
nsp3_SUD_N	1	240	K	1.314	NEU	K	-0.648	NEU
nsp3_SUD_N	1	241	A	1.314	MIN	V	1.101	MIN
nsp3_SUD_N	1	242	P	0.244	NEU	P	-1.202	MAX
nsp3_SUD_N	1	243	A	0.321	MIN	A	0.802	MIN
nsp3_SUD_N	1	244	V	0.544	MIN	T	-0.128	NEU
nsp3_SUD_N	1	245	V	1.109	MIN	V	1.268	MIN
nsp3_SUD_N	1	246	S	1.109	NEU	S	-0.743	NEU
nsp3_SUD_N	1	247	V	1.314	MIN	V	1.572	MIN
nsp3_SUD_N	1	248	S	1.314	NEU	S	-0.608	NEU
nsp3_SUD_N	1	249	S	1.314	NEU	S	-0.135	NEU
nsp3_SUD_N	1	250	P	0.969	NEU	P	-0.895	NEU
nsp3_SUD_N	1	251	D	1.314	NEU	D	-0.707	NEU
nsp3_SUD_N	1	252	A	0.969	NEU	A	0.163	NEU
nsp3_SUD_N	1	253	V	1.109	MIN	V	1.554	MIN
nsp3_SUD_N	1	254	T	0.767	NEU	T	-0.384	NEU
nsp3_SUD_N	1	255	T	1.314	NEU	A	0.313	NEU
nsp3_SUD_N	1	256	Y	1.109	NEU	Y	0.465	NEU
nsp3_SUD_N	1	257	N	1.109	MAX	N	-1.261	MAX
nsp3_SUD_N	1	258	G	1.109	NEU	G	-0.288	NEU
nsp3_SUD_N	1	259	Y	1.109	MAX	Y	-2.537	MAX
nsp3_SUD_N	1	260	L	1.109	MIN	L	1.023	MIN
nsp3_SUD_N	1	261	T	0.969	NEU	T	-0.311	NEU
nsp3_SUD_N	1	262	S	1.109	NEU	S	-0.736	NEU
nsp3_SUD_N	1	263	S	1.314	NEU	S	-0.07	NEU
nsp3_SUD_N	1	264	S	1.314	NEU	S	0.335	NEU
nsp3_SUD_C	1	1	T	0.321	MIN	T	1.567	MIN
nsp3_SUD_C	1	2	P	0.223	NEU	P	-0.569	NEU

nsp3_SUD_C	1	3	E	0.376	MAX	E	-1.165	MAX
nsp3_SUD_C	1	4	E	0.315	NEU	E	-0.884	NEU
nsp3_SUD_C	1	5	H	0.321	NEU	H	0.568	NEU
nsp3_SUD_C	1	6	F	0.407	NEU	F	-0.313	NEU
nsp3_SUD_C	1	7	I	0.606	MIN	I	2.013	MIN
nsp3_SUD_C	1	8	E	0.299	MAX	E	-1.853	MAX
nsp3_SUD_C	1	9	T	1.314	NEU	T	-0.207	NEU
nsp3_SUD_C	1	10	V	0.969	MIN	I	1.739	MIN
nsp3_SUD_C	1	11	S	0.969	NEU	S	-0.607	NEU
nsp3_SUD_C	1	12	L	0.491	MIN	L	0.985	MIN
nsp3_SUD_C	1	13	A	-0.155	MIN	A	1.014	MIN
nsp3_SUD_C	1	14	G	1.314	NEU	G	-0.377	NEU
nsp3_SUD_C	1	15	S	0.760	NEU	S	-0.665	NEU
nsp3_SUD_C	1	16	Y	0.333	MAX	Y	0.001	NEU
nsp3_SUD_C	1	17	R	0.905	NEU	K	-0.309	NEU
nsp3_SUD_C	1	18	D	0.191	MIN	D	0.783	MIN
nsp3_SUD_C	1	19	W	0.223	NEU	W	0.451	NEU
nsp3_SUD_C	1	20	S	0.905	NEU	S	0.137	NEU
nsp3_SUD_C	1	21	Y	0.054	NEU	Y	-0.564	NEU
nsp3_SUD_C	1	22	S	1.109	NEU	S	-0.118	NEU
nsp3_SUD_C	1	23	G	0.655	NEU	G	-0.305	NEU
nsp3_SUD_C	1	24	Q	0.767	NEU	Q	-0.413	NEU
nsp3_SUD_C	1	25	R	0.256	MIN	S	-0.739	NEU
nsp3_SUD_C	1	26	T	0.856	NEU	T	0.457	NEU
nsp3_SUD_C	1	27	E	0.376	MIN	Q	0.553	NEU
nsp3_SUD_C	1	28	L	0.760	MIN	L	0.564	NEU
nsp3_SUD_C	1	29	G	0.561	NEU	G	0.088	NEU
nsp3_SUD_C	1	30	V	1.109	MIN	I	2.151	MIN
nsp3_SUD_C	1	31	E	0.352	NEU	E	-0.77	NEU
nsp3_SUD_C	1	32	F	0.445	MIN	F	0.787	MIN
nsp3_SUD_C	1	33	L	1.109	MIN	L	1.539	MIN
nsp3_SUD_C	1	34	K	0.677	MAX	K	-0.863	NEU
nsp3_SUD_C	1	35	R	0.760	NEU	R	0.603	NEU
nsp3_SUD_C	1	36	G	1.109	NEU	G	0.066	NEU
nsp3_SUD_C	1	37	D	1.314	MIN	D	1.415	MIN
nsp3_SUD_C	1	38	K	1.109	MAX	K	-1.908	MAX
nsp3_SUD_C	1	39	I	0.480	MIN	S	-0.103	NEU
nsp3_SUD_C	1	40	V	1.109	MIN	V	1.997	MIN
nsp3_SUD_C	1	41	Y	0.352	MAX	Y	-0.171	NEU
nsp3_SUD_C	1	42	H	0.905	NEU	Y	-0.273	NEU
nsp3_SUD_C	1	43	L	0.969	NEU	T	0.224	NEU
nsp3_SUD_C	1	44	E	0.256	NEU	S	0.262	NEU
nsp3_SUD_C	1	45	S	0.480	NEU	N	0.596	NEU
nsp3_SUD_C	1	46	P	0.752	NEU	P	-0.096	NEU
nsp3_SUD_C	1	47	I	0.844	MIN	T	0.639	NEU
nsp3_SUD_C	1	48	E	0.445	NEU	T	0.086	NEU

nsp3_SUD_C	1	49	F	0.544	MIN	F	0.997	MIN
nsp3_SUD_C	1	50	H	0.969	NEU	H	-0.032	NEU
nsp3_SUD_C	1	51	L	0.969	MIN	L	1.467	MIN
nsp3_SUD_C	1	52	D	0.491	NEU	D	0.47	NEU
nsp3_SUD_C	1	53	G	1.109	NEU	G	-0.412	NEU
nsp3_SUD_C	1	54	E	0.856	MAX	E	-1.628	MAX
nsp3_SUD_C	1	55	V	0.969	MIN	V	1.04	MIN
nsp3_SUD_C	1	56	L	0.969	MIN	I	1.786	MIN
nsp3_SUD_C	1	57	P	-0.226	NEU	T	0.979	MIN
nsp3_SUD_C	1	58	L	0.655	MIN	F	0.454	NEU
nsp3_SUD_C	1	59	D	0.856	MIN	D	0.592	NEU
nsp3_SUD_C	1	60	K	0.760	MAX	N	-1.139	MAX
nsp3_SUD_C	1	61	L	1.109	MIN	L	1.533	MIN
nsp3_SUD_C	1	62	K	0.376	MAX	K	-0.928	NEU
nsp3_SUD_C	1	63	S	0.407	NEU	T	0.766	NEU
nsp3_SUD_C	1	64	L	0.760	MIN	L	0.959	MIN
nsp3_SUD_C	1	65	L	1.109	MIN	L	1.545	MIN
nsp3_SUD_C	1	66	S	1.313	NEU	S	0.086	NEU
nsp3_PLPro	1	1	I	1.314	MIN	I	0.83	MIN
nsp3_PLPro	1	2	K	1.109	MAX	K	-1.119	MAX
nsp3_PLPro	1	3	V	1.314	MIN	V	1.02	MIN
nsp3_PLPro	1	4	F	1.109	NEU	F	0.052	NEU
nsp3_PLPro	1	5	T	1.314	NEU	T	-0.479	NEU
nsp3_PLPro	1	6	T	1.314	NEU	T	-0.082	NEU
nsp3_PLPro	1	7	V	1.109	MIN	V	1.927	MIN
nsp3_PLPro	1	8	D	0.480	NEU	D	-0.65	NEU
nsp3_PLPro	1	9	N	1.314	NEU	N	-0.828	NEU
nsp3_PLPro	1	10	T	0.856	MIN	I	0.975	MIN
nsp3_PLPro	1	11	N	1.109	NEU	N	-0.256	NEU
nsp3_PLPro	1	12	L	1.314	MIN	L	1.153	MIN
nsp3_PLPro	1	13	H	0.491	MAX	H	-1.08	MAX
nsp3_PLPro	1	14	T	1.314	NEU	T	-0.584	NEU
nsp3_PLPro	1	15	Q	0.856	NEU	Q	-0.952	NEU
nsp3_PLPro	1	16	I	1.314	MIN	V	1.356	MIN
nsp3_PLPro	1	17	V	1.314	MIN	V	1.694	MIN
nsp3_PLPro	1	18	D	0.352	MIN	D	0.942	MIN
nsp3_PLPro	1	19	M	0.074	NEU	M	-1.577	MAX
nsp3_PLPro	1	20	S	1.109	MIN	S	0.828	MIN
nsp3_PLPro	1	21	M	1.109	MAX	M	-1.53	MAX
nsp3_PLPro	1	22	T	1.109	NEU	T	-0.252	NEU
nsp3_PLPro	1	23	Y	0.856	MIN	Y	0.713	NEU
nsp3_PLPro	1	24	G	1.314	NEU	G	-0.396	NEU
nsp3_PLPro	1	25	Q	1.314	NEU	Q	0.262	NEU
nsp3_PLPro	1	26	Q	0.856	NEU	Q	-0.763	NEU
nsp3_PLPro	1	27	F	1.314	MIN	F	0.757	NEU
nsp3_PLPro	1	28	G	1.314	NEU	G	-0.685	NEU

nsp3_PLPro	1	29	P	1.314	NEU	P	0.364	NEU
nsp3_PLPro	1	30	T	0.856	NEU	T	-0.142	NEU
nsp3_PLPro	1	31	Y	0.856	NEU	Y	-0.125	NEU
nsp3_PLPro	1	32	L	1.314	MIN	L	1.165	MIN
nsp3_PLPro	1	33	D	0.969	NEU	D	-0.778	NEU
nsp3_PLPro	1	34	G	1.314	NEU	G	-0.362	NEU
nsp3_PLPro	1	35	A	0.144	MIN	A	0.606	NEU
nsp3_PLPro	1	36	D	0.905	NEU	D	0.352	NEU
nsp3_PLPro	1	37	V	1.314	MIN	V	1.415	MIN
nsp3_PLPro	1	38	T	1.314	NEU	T	-0.072	NEU
nsp3_PLPro	1	39	K	1.314	NEU	K	0.387	NEU
nsp3_PLPro	1	40	I	1.109	MIN	I	1.656	MIN
nsp3_PLPro	1	41	K	1.314	NEU	K	0.251	NEU
nsp3_PLPro	1	42	P	0.544	NEU	P	-0.467	NEU
nsp3_PLPro	1	43	H	0.352	NEU	H	0.41	NEU
nsp3_PLPro	1	44	V	-0.084	MIN	N	-1.48	MAX
nsp3_PLPro	1	45	N	0.969	NEU	S	-0.026	NEU
nsp3_PLPro	1	46	H	1.314	NEU	H	-0.336	NEU
nsp3_PLPro	1	47	E	1.109	MIN	E	1.626	MIN
nsp3_PLPro	1	48	G	0.969	NEU	G	-0.474	NEU
nsp3_PLPro	1	49	K	0.445	MAX	K	-1.091	MAX
nsp3_PLPro	1	50	T	1.109	NEU	T	-0.135	NEU
nsp3_PLPro	1	51	F	1.314	MIN	F	1.289	MIN
nsp3_PLPro	1	52	F	0.905	MIN	Y	0.878	MIN
nsp3_PLPro	1	53	V	1.314	MIN	V	1.104	MIN
nsp3_PLPro	1	54	L	1.109	MIN	L	1.14	MIN
nsp3_PLPro	1	55	P	0.677	MAX	P	-1.435	MAX
nsp3_PLPro	1	56	S	0.445	NEU	N	0.06	NEU
nsp3_PLPro	1	57	D	0.445	NEU	D	-0.896	NEU
nsp3_PLPro	1	58	D	0.969	MIN	D	1.785	MIN
nsp3_PLPro	1	59	T	0.760	MIN	T	0.921	MIN
nsp3_PLPro	1	60	L	1.314	MIN	L	1.058	MIN
nsp3_PLPro	1	61	R	1.109	MIN	R	1.593	MIN
nsp3_PLPro	1	62	S	0.677	NEU	V	1.714	MIN
nsp3_PLPro	1	63	E	0.445	MAX	E	-0.962	NEU
nsp3_PLPro	1	64	A	0.969	NEU	A	0.5	NEU
nsp3_PLPro	1	65	F	0.856	NEU	F	-0.155	NEU
nsp3_PLPro	1	66	E	1.109	NEU	E	-0.886	NEU
nsp3_PLPro	1	67	Y	0.631	MAX	Y	-1.651	MAX
nsp3_PLPro	1	68	Y	0.969	NEU	Y	-0.765	NEU
nsp3_PLPro	1	69	H	1.109	NEU	H	-0.085	NEU
nsp3_PLPro	1	70	T	1.109	NEU	T	-0.633	NEU
nsp3_PLPro	1	71	L	0.606	NEU	T	-0.339	NEU
nsp3_PLPro	1	72	D	1.314	NEU	D	0.014	NEU
nsp3_PLPro	1	73	E	0.856	NEU	P	0.019	NEU
nsp3_PLPro	1	74	S	1.109	MIN	S	1.542	MIN

nsp3_PLPro	1	75	F	1.109	MIN	F	1.038	MIN
nsp3_PLPro	1	76	L	1.314	MIN	L	1.524	MIN
nsp3_PLPro	1	77	G	1.314	NEU	G	0.159	NEU
nsp3_PLPro	1	78	R	1.314	NEU	R	-0.011	NEU
nsp3_PLPro	1	79	Y	1.314	NEU	Y	0.05	NEU
nsp3_PLPro	1	80	M	0.767	MIN	M	0.851	MIN
nsp3_PLPro	1	81	S	1.314	NEU	S	-0.469	NEU
nsp3_PLPro	1	82	A	1.314	NEU	A	0.458	NEU
nsp3_PLPro	1	83	L	1.314	MIN	L	1.397	MIN
nsp3_PLPro	1	84	N	1.314	NEU	N	-0.334	NEU
nsp3_PLPro	1	85	H	1.314	NEU	H	-0.398	NEU
nsp3_PLPro	1	86	T	1.109	NEU	T	-0.305	NEU
nsp3_PLPro	1	87	K	1.109	NEU	K	-0.886	NEU
nsp3_PLPro	1	88	K	0.760	MIN	K	1.084	MIN
nsp3_PLPro	1	89	W	0.491	NEU	W	-1.088	MAX
nsp3_PLPro	1	90	K	1.109	MAX	K	-1.15	MAX
nsp3_PLPro	1	91	F	0.445	MIN	Y	-1.22	MAX
nsp3_PLPro	1	92	P	1.109	MAX	P	-1.635	MAX
nsp3_PLPro	1	93	Q	1.314	MAX	Q	-1.338	MAX
nsp3_PLPro	1	94	V	1.314	MIN	V	1.226	MIN
nsp3_PLPro	1	95	G	0.544	NEU	N	-1.074	MAX
nsp3_PLPro	1	96	G	1.314	NEU	G	-0.64	NEU
nsp3_PLPro	1	97	L	1.314	MIN	L	1.288	MIN
nsp3_PLPro	1	98	T	1.109	NEU	T	-0.267	NEU
nsp3_PLPro	1	99	S	0.969	NEU	S	-0.691	NEU
nsp3_PLPro	1	100	I	1.314	MIN	I	2.035	MIN
nsp3_PLPro	1	101	K	1.109	MAX	K	-1.319	MAX
nsp3_PLPro	1	102	W	1.314	MAX	W	-1.646	MAX
nsp3_PLPro	1	103	A	0.905	NEU	A	-0.857	NEU
nsp3_PLPro	1	104	D	1.314	NEU	D	0.148	NEU
nsp3_PLPro	1	105	N	0.856	MAX	N	-1.024	MAX
nsp3_PLPro	1	106	N	1.109	NEU	N	-0.79	NEU
nsp3_PLPro	1	107	C	1.314	MIN	C	2.011	MIN
nsp3_PLPro	1	108	Y	0.445	MIN	Y	0.506	NEU
nsp3_PLPro	1	109	L	1.314	MIN	L	1.538	MIN
nsp3_PLPro	1	110	S	1.314	NEU	A	0.454	NEU
nsp3_PLPro	1	111	S	1.314	NEU	T	-0.264	NEU
nsp3_PLPro	1	112	V	0.606	MIN	A	0.558	NEU
nsp3_PLPro	1	113	L	1.314	MIN	L	1.362	MIN
nsp3_PLPro	1	114	L	1.314	MIN	L	1.366	MIN
nsp3_PLPro	1	115	A	1.109	NEU	T	-0.02	NEU
nsp3_PLPro	1	116	L	1.314	MIN	L	1.392	MIN
nsp3_PLPro	1	117	Q	0.352	MAX	Q	-0.859	NEU
nsp3_PLPro	1	118	Q	1.109	NEU	Q	-0.759	NEU
nsp3_PLPro	1	119	I	1.314	MIN	I	1.588	MIN
nsp3_PLPro	1	120	E	1.109	MIN	E	1.422	MIN

nsp3_PLPro	1	121	V	1.314	MIN	L	1.368	MIN
nsp3_PLPro	1	122	K	0.407	MIN	K	0.266	NEU
nsp3_PLPro	1	123	F	1.109	MIN	F	1.058	MIN
nsp3_PLPro	1	124	N	0.333	NEU	N	-0.021	NEU
nsp3_PLPro	1	125	A	1.314	NEU	P	-0.804	NEU
nsp3_PLPro	1	126	P	1.314	NEU	P	-0.307	NEU
nsp3_PLPro	1	127	A	0.445	NEU	A	-0.131	NEU
nsp3_PLPro	1	128	L	1.314	MIN	L	1.407	MIN
nsp3_PLPro	1	129	Q	0.606	MAX	Q	-1.01	MAX
nsp3_PLPro	1	130	E	0.677	NEU	D	-0.817	NEU
nsp3_PLPro	1	131	A	1.314	MIN	A	0.737	NEU
nsp3_PLPro	1	132	Y	1.314	NEU	Y	-0.938	NEU
nsp3_PLPro	1	133	Y	1.109	MAX	Y	-2.306	MAX
nsp3_PLPro	1	134	R	1.314	NEU	R	0.036	NEU
nsp3_PLPro	1	135	A	1.314	NEU	A	0.51	NEU
nsp3_PLPro	1	136	R	1.314	NEU	R	-0.024	NEU
nsp3_PLPro	1	137	A	1.109	NEU	A	0.254	NEU
nsp3_PLPro	1	138	G	1.314	NEU	G	-0.253	NEU
nsp3_PLPro	1	139	D	1.109	NEU	E	-0.736	NEU
nsp3_PLPro	1	140	A	0.856	MIN	A	0.587	NEU
nsp3_PLPro	1	141	A	1.314	NEU	A	0.189	NEU
nsp3_PLPro	1	142	N	0.969	NEU	N	-0.863	NEU
nsp3_PLPro	1	143	F	1.109	MIN	F	0.674	NEU
nsp3_PLPro	1	144	C	1.314	MIN	C	1.382	MIN
nsp3_PLPro	1	145	A	1.109	NEU	A	0.433	NEU
nsp3_PLPro	1	146	L	1.314	MIN	L	1.364	MIN
nsp3_PLPro	1	147	I	1.109	MIN	I	1.444	MIN
nsp3_PLPro	1	148	L	1.314	MIN	L	1.732	MIN
nsp3_PLPro	1	149	A	0.677	NEU	A	0.569	NEU
nsp3_PLPro	1	150	Y	0.969	MAX	Y	-1.764	MAX
nsp3_PLPro	1	151	S	0.256	NEU	C	0.585	NEU
nsp3_PLPro	1	152	N	0.767	NEU	N	-0.065	NEU
nsp3_PLPro	1	153	K	1.314	NEU	K	-0.832	NEU
nsp3_PLPro	1	154	T	0.655	NEU	T	0.247	NEU
nsp3_PLPro	1	155	V	0.969	MIN	V	1.18	MIN
nsp3_PLPro	1	156	G	1.314	NEU	G	-0.317	NEU
nsp3_PLPro	1	157	E	0.350	NEU	E	-1.145	MAX
nsp3_PLPro	1	158	L	1.314	NEU	L	0.126	NEU
nsp3_PLPro	1	159	G	0.376	MAX	G	-1.288	MAX
nsp3_PLPro	1	160	D	1.314	NEU	D	-0.627	NEU
nsp3_PLPro	1	161	V	1.109	MIN	V	1.305	MIN
nsp3_PLPro	1	162	R	0.544	MIN	R	0.941	MIN
nsp3_PLPro	1	163	E	-0.004	NEU	E	-0.757	NEU
nsp3_PLPro	1	164	T	1.314	NEU	T	-0.427	NEU
nsp3_PLPro	1	165	M	0.677	NEU	M	0.54	NEU
nsp3_PLPro	1	166	T	0.561	NEU	S	-0.694	NEU

nsp3_PLPro	1	167	H	1.314	NEU	Y	-0.653	NEU
nsp3_PLPro	1	168	L	1.314	MIN	L	1.534	MIN
nsp3_PLPro	1	169	L	1.314	MIN	F	1.333	MIN
nsp3_PLPro	1	170	Q	1.109	MAX	Q	-1.171	MAX
nsp3_PLPro	1	171	H	1.314	NEU	H	0.253	NEU
nsp3_PLPro	1	172	A	0.445	MIN	A	0.755	NEU
nsp3_PLPro	1	173	N	1.314	MIN	N	1.715	MIN
nsp3_PLPro	1	174	L	1.314	MIN	L	1.378	MIN
nsp3_PLPro	1	175	E	-0.177	NEU	D	2.217	MIN
nsp3_PLPro	1	176	S	1.109	NEU	S	0.429	NEU
nsp3_PLPro	1	177	A	0.299	NEU	C	2.423	MIN
nsp3_PLPro	1	178	K	0.969	NEU	K	-0.571	NEU
nsp3_PLPro	1	179	R	0.760	NEU	R	0.555	NEU
nsp3_PLPro	1	180	V	0.544	MIN	V	0.53	NEU
nsp3_PLPro	1	181	L	1.314	MIN	L	1.214	MIN
nsp3_PLPro	1	182	N	0.365	MAX	N	-0.872	NEU
nsp3_PLPro	1	183	V	1.314	MIN	V	0.872	MIN
nsp3_PLPro	1	184	V	1.109	MIN	V	0.551	NEU
nsp3_PLPro	1	185	C	1.314	MIN	C	1.929	MIN
nsp3_PLPro	1	186	K	0.969	MIN	K	0.796	MIN
nsp3_PLPro	1	187	H	0.350	NEU	T	-1.035	MAX
nsp3_PLPro	1	188	C	1.109	MIN	C	1.405	MIN
nsp3_PLPro	1	189	G	1.314	NEU	G	-0.535	NEU
nsp3_PLPro	1	190	Q	1.109	NEU	Q	0.23	NEU
nsp3_PLPro	1	191	K	1.314	NEU	Q	0.09	NEU
nsp3_PLPro	1	192	T	0.760	NEU	Q	-0.722	NEU
nsp3_PLPro	1	193	T	1.314	NEU	T	-0.026	NEU
nsp3_PLPro	1	194	T	0.491	MIN	T	0.46	NEU
nsp3_PLPro	1	195	L	1.109	MIN	L	1.568	MIN
nsp3_PLPro	1	196	T	0.677	NEU	K	0.143	NEU
nsp3_PLPro	1	197	G	1.314	NEU	G	-0.444	NEU
nsp3_PLPro	1	198	V	1.314	MIN	V	1.313	MIN
nsp3_PLPro	1	199	E	0.333	NEU	E	-0.587	NEU
nsp3_PLPro	1	200	A	1.314	NEU	A	0.238	NEU
nsp3_PLPro	1	201	V	1.314	MIN	V	1.247	MIN
nsp3_PLPro	1	202	M	0.299	NEU	M	-0.964	NEU
nsp3_PLPro	1	203	Y	0.856	NEU	Y	0.038	NEU
nsp3_PLPro	1	204	M	0.969	MAX	M	-1.395	MAX
nsp3_PLPro	1	205	G	1.109	NEU	G	-0.086	NEU
nsp3_PLPro	1	206	T	1.314	NEU	T	-0.243	NEU
nsp3_PLPro	1	207	L	1.109	MIN	L	1.201	MIN
nsp3_PLPro	1	208	S	1.314	NEU	S	-0.393	NEU
nsp3_PLPro	1	209	Y	0.856	NEU	Y	0.451	NEU
nsp3_PLPro	1	210	D	0.544	MIN	E	1.226	MIN
nsp3_PLPro	1	211	N	0.352	NEU	Q	-0.843	NEU
nsp3_PLPro	1	212	L	1.314	MIN	F	0.987	MIN

nsp3_PLPro	1	213	K	1.109	NEU	K	-0.235	NEU
nsp3_PLPro	1	214	T	0.969	NEU	K	-0.366	NEU
nsp3_PLPro	1	215	G	1.314	NEU	G	-0.461	NEU
nsp3_PLPro	1	216	V	1.109	MIN	V	1.589	MIN
nsp3_PLPro	1	217	S	0.561	MIN	Q	0.411	NEU
nsp3_PLPro	1	218	I	1.109	MIN	I	2.553	MIN
nsp3_PLPro	1	219	P	0.445	NEU	P	0.423	NEU
nsp3_PLPro	1	220	C	1.314	MIN	C	1.407	MIN
nsp3_PLPro	1	221	V	0.767	NEU	T	-0.88	NEU
nsp3_PLPro	1	222	C	1.314	MIN	C	1.415	MIN
nsp3_PLPro	1	223	G	1.314	NEU	G	-0.233	NEU
nsp3_PLPro	1	224	R	0.256	NEU	K	-1.29	MAX
nsp3_PLPro	1	225	D	0.969	MIN	Q	1.171	MIN
nsp3_PLPro	1	226	A	1.109	NEU	A	0.144	NEU
nsp3_PLPro	1	227	T	1.314	NEU	T	0.102	NEU
nsp3_PLPro	1	228	Q	0.905	NEU	K	-1.325	MAX
nsp3_PLPro	1	229	Y	0.321	MAX	Y	-1.132	MAX
nsp3_PLPro	1	230	L	1.109	MIN	L	1.247	MIN
nsp3_PLPro	1	231	V	1.109	MIN	V	1.273	MIN
nsp3_PLPro	1	232	Q	0.856	NEU	Q	0.25	NEU
nsp3_PLPro	1	233	Q	0.905	NEU	Q	-0.474	NEU
nsp3_PLPro	1	234	E	1.109	NEU	E	0.172	NEU
nsp3_PLPro	1	235	S	1.109	NEU	S	-0.593	NEU
nsp3_PLPro	1	236	S	1.314	NEU	P	-0.438	NEU
nsp3_PLPro	1	237	F	1.314	MIN	F	1.243	MIN
nsp3_PLPro	1	238	V	1.314	MIN	V	1.385	MIN
nsp3_PLPro	1	239	M	1.314	MIN	M	0.846	MIN
nsp3_PLPro	1	240	M	1.314	MIN	M	0.88	MIN
nsp3_PLPro	1	241	S	1.314	NEU	S	-0.579	NEU
nsp3_PLPro	1	242	A	0.561	MIN	A	0.57	NEU
nsp3_PLPro	1	243	P	1.109	NEU	P	-0.627	NEU
nsp3_PLPro	1	244	P	1.109	NEU	P	-0.769	NEU
nsp3_PLPro	1	245	A	1.109	NEU	A	0.096	NEU
nsp3_PLPro	1	246	E	0.544	NEU	Q	-0.668	NEU
nsp3_PLPro	1	247	Y	1.109	NEU	Y	-0.316	NEU
nsp3_PLPro	1	248	K	0.333	NEU	E	1.712	MIN
nsp3_PLPro	1	249	L	1.109	MIN	L	1.543	MIN
nsp3_PLPro	1	250	Q	0.631	NEU	K	0.134	NEU
nsp3_PLPro	1	251	Q	1.314	NEU	H	0.229	NEU
nsp3_PLPro	1	252	G	1.109	NEU	G	-0.357	NEU
nsp3_PLPro	1	253	T	0.606	NEU	T	-1.152	MAX
nsp3_PLPro	1	254	F	1.314	MIN	F	1.349	MIN
nsp3_PLPro	1	255	L	1.109	MIN	T	-0.381	NEU
nsp3_PLPro	1	256	C	1.314	MIN	C	1.226	MIN
nsp3_PLPro	1	257	A	0.606	NEU	A	0.679	NEU
nsp3_PLPro	1	258	N	1.314	NEU	S	-0.582	NEU

nsp3_PLPro	1	259	E	0.856	MAX	E	-1.103	MAX
nsp3_PLPro	1	260	Y	0.631	NEU	Y	-0.675	NEU
nsp3_PLPro	1	261	T	1.109	NEU	T	-0.061	NEU
nsp3_PLPro	1	262	G	0.856	MIN	G	0.635	NEU
nsp3_PLPro	1	263	N	0.905	NEU	N	-0.204	NEU
nsp3_PLPro	1	264	Y	0.491	NEU	Y	-1.079	MAX
nsp3_PLPro	1	265	Q	0.969	NEU	Q	-0.325	NEU
nsp3_PLPro	1	266	C	1.109	MIN	C	1.806	MIN
nsp3_PLPro	1	267	G	1.314	NEU	G	0.015	NEU
nsp3_PLPro	1	268	H	1.314	NEU	H	0.465	NEU
nsp3_PLPro	1	269	Y	0.677	NEU	Y	-0.833	NEU
nsp3_PLPro	1	270	T	1.109	NEU	K	-0.375	NEU
nsp3_PLPro	1	271	H	1.314	NEU	H	-0.597	NEU
nsp3_PLPro	1	272	I	1.314	MIN	I	1.497	MIN
nsp3_PLPro	1	273	T	0.969	NEU	T	-0.233	NEU
nsp3_PLPro	1	274	A	0.349	NEU	S	-0.5	NEU
nsp3_PLPro	1	275	K	0.352	NEU	K	-1.028	MAX
nsp3_PLPro	1	276	E	0.037	MIN	E	-0.073	NEU
nsp3_PLPro	1	277	T	0.969	NEU	T	0.248	NEU
nsp3_PLPro	1	278	L	1.314	MIN	L	0.832	MIN
nsp3_PLPro	1	279	Y	1.314	NEU	Y	-0.74	NEU
nsp3_PLPro	1	280	R	0.174	NEU	C	0.915	MIN
nsp3_PLPro	1	281	I	1.314	MIN	I	1.43	MIN
nsp3_PLPro	1	282	D	0.321	MIN	D	-0.227	NEU
nsp3_PLPro	1	283	G	1.314	NEU	G	-0.373	NEU
nsp3_PLPro	1	284	A	1.314	NEU	A	0.196	NEU
nsp3_PLPro	1	285	H	0.220	NEU	L	1.079	MIN
nsp3_PLPro	1	286	L	1.314	MIN	L	0.981	MIN
nsp3_PLPro	1	287	T	1.314	NEU	T	-0.28	NEU
nsp3_PLPro	1	288	K	0.407	MAX	K	0.09	NEU
nsp3_PLPro	1	289	M	0.491	MIN	S	-0.531	NEU
nsp3_PLPro	1	290	S	0.677	NEU	S	-0.096	NEU
nsp3_PLPro	1	291	E	1.109	MIN	E	1.257	MIN
nsp3_PLPro	1	292	Y	0.767	NEU	Y	-0.314	NEU
nsp3_PLPro	1	293	K	0.256	NEU	K	0.745	NEU
nsp3_PLPro	1	294	G	1.314	NEU	G	-0.364	NEU
nsp3_PLPro	1	295	P	0.767	MAX	P	-1.496	MAX
nsp3_PLPro	1	296	V	1.314	MIN	I	1.225	MIN
nsp3_PLPro	1	297	T	1.314	NEU	T	-0.438	NEU
nsp3_PLPro	1	298	D	0.350	MAX	D	-0.972	NEU
nsp3_PLPro	1	299	V	1.109	MIN	V	1.324	MIN
nsp3_PLPro	1	300	F	1.314	MIN	F	1.383	MIN
nsp3_PLPro	1	301	Y	1.314	MIN	Y	0.702	NEU
nsp3_PLPro	1	302	K	1.109	NEU	K	-0.776	NEU
nsp3_PLPro	1	303	E	1.109	MAX	E	-1.209	MAX
nsp3_PLPro	1	304	T	0.969	NEU	N	-0.123	NEU

nsp3_PLPro	1	305	S	1.109	NEU	S	0.492	NEU
nsp3_PLPro	1	306	Y	1.109	MAX	Y	-2.668	MAX
nsp3_PLPro	1	307	T	0.220	NEU	T	0.342	NEU
nsp3_PLPro	1	308	T	1.314	NEU	T	0.022	NEU
nsp3_PLPro	1	309	T	0.352	MIN	T	0.888	MIN
nsp3_NAB	1	1	Y	1.309	MAX	F	-1.332	MAX
nsp3_NAB	1	2	T	1.087	NEU	T	0.065	NEU
nsp3_NAB	1	3	E	0.346	NEU	E	-1.118	MAX
nsp3_NAB	1	4	Q	1.087	NEU	Q	-0.459	NEU
nsp3_NAB	1	5	P	1.309	NEU	P	0.157	NEU
nsp3_NAB	1	6	I	1.309	MIN	I	1.638	MIN
nsp3_NAB	1	7	D	0.602	NEU	D	-0.864	NEU
nsp3_NAB	1	8	L	1.309	MIN	L	1.483	MIN
nsp3_NAB	1	9	V	0.938	MIN	V	0.837	MIN
nsp3_NAB	1	10	P	0.369	NEU	P	-0.95	NEU
nsp3_NAB	1	11	T	1.309	NEU	N	-0.75	NEU
nsp3_NAB	1	12	Q	1.309	NEU	Q	-0.489	NEU
nsp3_NAB	1	13	P	1.309	NEU	P	-0.376	NEU
nsp3_NAB	1	14	L	0.446	NEU	Y	-2.936	MAX
nsp3_NAB	1	15	P	0.938	NEU	P	0.453	NEU
nsp3_NAB	1	16	N	0.313	NEU	N	-0.762	NEU
nsp3_NAB	1	17	A	0.170	MAX	A	-1.134	MAX
nsp3_NAB	1	18	S	1.309	NEU	S	-0.341	NEU
nsp3_NAB	1	19	F	0.363	MIN	F	0.566	NEU
nsp3_NAB	1	20	D	0.718	NEU	D	-0.766	NEU
nsp3_NAB	1	21	N	0.938	NEU	N	-0.438	NEU
nsp3_NAB	1	22	F	1.309	MIN	F	1.232	MIN
nsp3_NAB	1	23	K	1.087	NEU	K	-0.682	NEU
nsp3_NAB	1	24	L	1.309	MIN	F	0.891	MIN
nsp3_NAB	1	25	T	0.560	MIN	V	1.813	MIN
nsp3_NAB	1	26	C	1.087	MIN	C	1.452	MIN
nsp3_NAB	1	27	S	1.309	NEU	D	-0.799	NEU
nsp3_NAB	1	28	N	0.938	NEU	N	-0.454	NEU
nsp3_NAB	1	29	T	0.170	NEU	I	2.187	MIN
nsp3_NAB	1	30	K	1.087	MIN	K	1.388	MIN
nsp3_NAB	1	31	F	1.309	MIN	F	1.493	MIN
nsp3_NAB	1	32	A	1.309	MIN	A	1.075	MIN
nsp3_NAB	1	33	D	0.131	MIN	D	-0.299	NEU
nsp3_NAB	1	34	D	0.818	NEU	D	-0.889	NEU
nsp3_NAB	1	35	L	1.309	MIN	L	1.25	MIN
nsp3_NAB	1	36	N	1.309	NEU	N	-0.857	NEU
nsp3_NAB	1	37	Q	0.938	NEU	Q	-0.567	NEU
nsp3_NAB	1	38	M	0.867	MIN	L	1.13	MIN
nsp3_NAB	1	39	T	0.938	NEU	T	0.03	NEU
nsp3_NAB	1	40	G	1.087	NEU	G	-0.457	NEU
nsp3_NAB	1	41	F	-0.029	NEU	Y	-2.077	MAX

nsp3_NAB	1	42	K	0.404	MIN	K	0.989	MIN
nsp3_NAB	1	43	K	0.560	MAX	K	-0.841	NEU
nsp3_NAB	1	44	P	0.111	MIN	P	0.847	MIN
nsp3_NAB	1	45	A	1.087	NEU	A	0.446	NEU
nsp3_NAB	1	46	S	0.404	NEU	S	0.813	MIN
nsp3_NAB	1	47	R	0.404	MIN	R	0.603	NEU
nsp3_NAB	1	48	E	1.087	NEU	E	-0.13	NEU
nsp3_NAB	1	49	L	1.309	MIN	L	1.111	MIN
nsp3_NAB	1	50	S	0.632	NEU	K	-0.28	NEU
nsp3_NAB	1	51	V	1.309	MIN	V	1.465	MIN
nsp3_NAB	1	52	T	1.309	NEU	T	-0.547	NEU
nsp3_NAB	1	53	F	1.309	MIN	F	0.944	MIN
nsp3_NAB	1	54	F	1.087	MIN	F	0.894	MIN
nsp3_NAB	1	55	P	1.309	NEU	P	-0.698	NEU
nsp3_NAB	1	56	D	0.446	MAX	D	-0.943	NEU
nsp3_NAB	1	57	L	1.309	MIN	L	1.159	MIN
nsp3_NAB	1	58	N	0.720	NEU	N	0.405	NEU
nsp3_NAB	1	59	G	1.309	NEU	G	-0.875	NEU
nsp3_NAB	1	60	D	0.124	NEU	D	0.513	NEU
nsp3_NAB	1	61	V	1.309	MIN	V	1.347	MIN
nsp3_NAB	1	62	V	1.309	MIN	V	1.232	MIN
nsp3_NAB	1	63	A	1.309	NEU	A	0.372	NEU
nsp3_NAB	1	64	I	1.309	MIN	I	1.4	MIN
nsp3_NAB	1	65	D	1.309	NEU	D	-0.118	NEU
nsp3_NAB	1	66	Y	1.309	MIN	Y	0.755	NEU
nsp3_NAB	1	67	R	0.718	NEU	K	-0.335	NEU
nsp3_NAB	1	68	H	1.087	NEU	H	-0.117	NEU
nsp3_NAB	1	69	Y	0.421	MAX	Y	-1.072	MAX
nsp3_NAB	1	70	S	0.632	NEU	T	0.264	NEU
nsp3_NAB	1	71	A	0.343	MIN	P	-0.738	NEU
nsp3_NAB	1	72	S	1.087	NEU	S	-0.308	NEU
nsp3_NAB	1	73	F	1.309	MIN	F	1.098	MIN
nsp3_NAB	1	74	K	0.938	NEU	K	-0.686	NEU
nsp3_NAB	1	75	K	0.632	NEU	K	-1.03	MAX
nsp3_NAB	1	76	G	1.309	NEU	G	0.066	NEU
nsp3_NAB	1	77	A	0.560	NEU	A	0.532	NEU
nsp3_NAB	1	78	K	1.309	MAX	K	-1.39	MAX
nsp3_NAB	1	79	L	1.309	MIN	L	1.03	MIN
nsp3_NAB	1	80	L	0.938	MIN	L	1.166	MIN
nsp3_NAB	1	81	H	1.087	MIN	H	0.614	NEU
nsp3_NAB	1	82	K	0.313	NEU	K	-0.95	NEU
nsp3_NAB	1	83	P	1.087	NEU	P	-0.843	NEU
nsp3_NAB	1	84	I	1.309	MIN	I	1.205	MIN
nsp3_NAB	1	85	V	1.309	MIN	V	1.192	MIN
nsp3_NAB	1	86	W	1.309	MIN	W	0.86	MIN
nsp3_NAB	1	87	H	1.309	NEU	H	0.121	NEU

nsp3_NAB	1	88	I	1.087	MIN	V	1.354	MIN
nsp3_NAB	1	89	N	0.938	NEU	N	-0.084	NEU
nsp3_NAB	1	90	Q	0.343	MAX	N	-0.622	NEU
nsp3_NAB	1	91	T	0.242	NEU	A	0.422	NEU
nsp3_NAB	1	92	T	0.938	NEU	T	-0.004	NEU
nsp3_NAB	1	93	N	0.498	NEU	N	-0.744	NEU
nsp3_NAB	1	94	K	0.324	MIN	K	0.792	MIN
nsp3_NAB	1	95	T	1.309	NEU	A	0.002	NEU
nsp3_NAB	1	96	T	1.087	NEU	T	-0.053	NEU
nsp3_NAB	1	97	Y	-0.023	MAX	Y	-2.579	MAX
nsp3_NAB	1	98	K	1.087	NEU	K	-0.364	NEU
nsp3_NAB	1	99	P	1.087	NEU	P	-0.276	NEU
nsp3_NAB	1	100	N	0.404	NEU	N	-0.954	NEU
nsp3_NAB	1	101	T	0.632	NEU	T	-0.254	NEU
nsp3_NAB	1	102	W	0.498	NEU	W	-1.204	MAX
nsp3_NAB	1	103	C	1.309	MIN	C	1.909	MIN
nsp3_NAB	1	104	L	1.309	MIN	I	1.208	MIN
nsp3_NAB	1	105	R	1.309	NEU	R	-0.568	NEU
nsp3_NAB	1	106	C	1.309	MIN	C	1.86	MIN
nsp3_NAB	1	107	L	1.309	MIN	L	1.076	MIN
nsp3_NAB	1	108	W	0.818	MIN	W	0.921	MIN
nsp3_NAB	1	109	S	1.309	NEU	S	0.483	NEU
nsp3_NAB	1	110	T	1.087	NEU	T	-0.496	NEU
nsp3_NAB	1	111	K	-0.247	MAX	K	-1.14	MAX
nsp3_NAB	1	112	P	1.087	MIN	P	1.788	MIN
nsp3_NAB	1	113	V	0.242	MAX	V	-1.105	MAX
nsp3_Y3	1	1	H	0.544	MIN	Q	-0.033	NEU
nsp3_Y3	1	2	S	0.191	MAX	S	-1.35	MAX
nsp3_Y3	1	3	D	0.349	NEU	D	-1.26	MAX
nsp3_Y3	1	4	L	0.969	MIN	I	1.048	MIN
nsp3_Y3	1	5	E	0.760	MAX	E	-1.155	MAX
nsp3_Y3	1	6	V	1.314	MIN	V	1.109	MIN
nsp3_Y3	1	7	T	1.314	NEU	T	-0.253	NEU
nsp3_Y3	1	8	G	1.314	NEU	G	-0.863	NEU
nsp3_Y3	1	9	D	1.109	MAX	D	-1.83	MAX
nsp3_Y3	1	10	S	1.314	NEU	S	-0.749	NEU
nsp3_Y3	1	11	C	1.109	MIN	C	1.06	MIN
nsp3_Y3	1	12	N	1.109	NEU	N	-0.876	NEU
nsp3_Y3	1	13	N	1.109	NEU	N	-0.661	NEU
nsp3_Y3	1	14	F	0.491	MIN	Y	0.306	NEU
nsp3_Y3	1	15	M	1.314	MIN	M	1.099	MIN
nsp3_Y3	1	16	L	1.314	MIN	L	1.485	MIN
nsp3_Y3	1	17	T	1.314	NEU	T	0.019	NEU
nsp3_Y3	1	18	Y	1.314	MAX	Y	-3.679	MAX
nsp3_Y3	1	19	N	1.314	MAX	N	-1.082	MAX
nsp3_Y3	1	20	K	0.315	NEU	K	0.025	NEU

nsp3_Y3	1	21	V	1.314	MIN	V	0.892	MIN
nsp3_Y3	1	22	E	1.314	MIN	E	2.329	MIN
nsp3_Y3	1	23	N	0.376	NEU	N	0.621	NEU
nsp3_Y3	1	24	M	1.314	NEU	M	-0.103	NEU
nsp3_Y3	1	25	T	1.109	MIN	T	0.877	MIN
nsp3_Y3	1	26	P	1.314	NEU	P	-0.623	NEU
nsp3_Y3	1	27	R	0.544	NEU	R	-0.998	NEU
nsp3_Y3	1	28	D	1.314	MAX	D	-1.2	MAX
nsp3_Y3	1	29	L	1.314	MIN	L	1.37	MIN
nsp3_Y3	1	30	G	1.314	NEU	G	-0.483	NEU
nsp3_Y3	1	31	A	1.109	NEU	A	0.13	NEU
nsp3_Y3	1	32	C	1.109	MIN	C	1.623	MIN
nsp3_Y3	1	33	I	1.314	MIN	I	1.834	MIN
nsp3_Y3	1	34	D	0.407	NEU	D	-1.037	MAX
nsp3_Y3	1	35	C	1.314	MIN	C	1.535	MIN
nsp3_Y3	1	36	N	1.314	NEU	S	-0.549	NEU
nsp3_Y3	1	37	A	1.314	NEU	A	0.145	NEU
nsp3_Y3	1	38	R	1.314	NEU	R	-0.58	NEU
nsp3_Y3	1	39	H	1.314	NEU	H	-0.037	NEU
nsp3_Y3	1	40	I	1.314	MIN	I	1.91	MIN
nsp3_Y3	1	41	N	1.314	NEU	N	-0.745	NEU
nsp3_Y3	1	42	A	0.491	NEU	A	0.443	NEU
nsp3_Y3	1	43	Q	0.905	NEU	Q	0.114	NEU
nsp3_Y3	1	44	V	1.314	MIN	V	1.295	MIN
nsp3_Y3	1	45	A	1.314	NEU	A	0.175	NEU
nsp3_Y3	1	46	K	0.969	NEU	K	-0.035	NEU
nsp3_Y3	1	47	S	1.109	NEU	S	-0.708	NEU
nsp3_Y3	1	48	H	1.314	NEU	H	-0.342	NEU
nsp3_Y3	1	49	N	0.169	NEU	N	0.755	NEU
nsp3_Y3	1	50	V	1.109	MIN	I	1.913	MIN
nsp3_Y3	1	51	S	1.314	NEU	A	-0.402	NEU
nsp3_Y3	1	52	L	1.314	MIN	L	1.457	MIN
nsp3_Y3	1	53	I	1.314	MIN	I	0.894	MIN
nsp3_Y3	1	54	W	0.407	MIN	W	0.524	NEU
nsp3_Y3	1	55	N	1.314	NEU	N	-0.231	NEU
nsp3_Y3	1	56	V	1.314	MIN	V	1.415	MIN
nsp3_Y3	1	57	K	1.109	MAX	K	-1.292	MAX
nsp3_Y3	1	58	D	1.314	NEU	D	-0.935	NEU
nsp3_Y3	1	59	Y	0.491	NEU	F	0.904	MIN
nsp3_Y3	1	60	M	0.856	NEU	M	0.38	NEU
nsp3_Y3	1	61	S	1.109	NEU	S	-0.089	NEU
nsp3_Y3	1	62	L	0.969	MIN	L	0.862	MIN
nsp3_Y3	1	63	S	1.314	NEU	S	-0.06	NEU
nsp3_Y3	1	64	E	1.109	MIN	E	1.138	MIN
nsp3_Y3	1	65	Q	1.314	NEU	Q	0.18	NEU
nsp3_Y3	1	66	L	1.314	MIN	L	1.109	MIN

nsp3_Y3	1	67	R	1.314	NEU	R	-0.142	NEU
nsp3_Y3	1	68	K	0.969	MAX	K	-1.672	MAX
nsp3_Y3	1	69	Q	1.314	MAX	Q	-1.044	MAX
nsp3_Y3	1	70	I	1.314	MIN	I	1.622	MIN
nsp3_Y3	1	71	R	0.969	MAX	R	-1.149	MAX
nsp3_Y3	1	72	S	1.314	NEU	S	-0.285	NEU
nsp3_Y3	1	73	A	1.314	NEU	A	0.331	NEU
nsp3_Y3	1	74	A	0.407	NEU	A	0.48	NEU
nsp3_Y3	1	75	K	0.905	MAX	K	-1.947	MAX
nsp3_Y3	1	76	K	1.109	MAX	K	-1.145	MAX
nsp3_Y3	1	77	N	0.969	MAX	N	-1.024	MAX
nsp3_Y3	1	78	N	1.109	MIN	N	0.597	NEU
nsp3_Y3	1	79	I	1.314	MIN	L	1.186	MIN
nsp3_Y3	1	80	P	1.314	NEU	P	-0.662	NEU
nsp3_Y3	1	81	F	1.314	MIN	F	0.88	MIN
nsp3_Y3	1	82	R	0.407	NEU	K	-1.285	MAX
nsp3_Y3	1	83	L	1.314	MIN	L	1.291	MIN
nsp3_Y3	1	84	T	1.314	NEU	T	-0.369	NEU
nsp3_Y3	1	85	C	1.109	NEU	C	-0.476	NEU
nsp3_Y3	1	86	A	0.491	NEU	A	0.538	NEU
nsp3_Y3	1	87	T	1.109	NEU	T	-0.216	NEU
nsp3_Y3	1	88	T	1.109	NEU	T	-0.057	NEU
nsp3_Y3	1	89	R	1.109	NEU	R	-0.092	NEU
nsp3_Y3	1	90	Q	0.544	NEU	Q	-1.122	MAX
nsp3_Y3	1	91	V	0.445	MAX	V	-0.963	NEU
nsp3_Y3	1	92	V	1.109	MIN	V	1.409	MIN
nsp3_Y3	1	93	N	0.299	NEU	N	-1.12	MAX
nsp3_Y3	1	94	V	1.314	MIN	V	1.396	MIN
nsp3_Y3	1	95	I	1.314	MIN	V	0.888	MIN
nsp3_Y3	1	96	T	1.314	NEU	T	-0.091	NEU
nsp3_Y3	1	97	T	1.314	NEU	T	-0.055	NEU
nsp3_Y3	1	98	K	1.314	MAX	K	-1.414	MAX
nsp3_Y3	1	99	I	1.314	MIN	I	1.34	MIN
nsp3_Y3	1	100	S	1.314	NEU	A	-0.777	NEU
nsp3_Y3	1	101	L	1.314	MIN	L	1.024	MIN
nsp3_Y3	1	102	K	0.856	MIN	K	0.857	MIN
nsp5	1	1	S	0.772	NEU	S	-0.174	NEU
nsp5	1	2	G	0.341	MAX	G	-0.989	NEU
nsp5	1	3	L	1.316	MIN	F	1.17	MIN
nsp5	1	4	V	0.319	NEU	R	0.752	NEU
nsp5	1	5	K	-0.006	NEU	K	-1.734	MAX
nsp5	1	6	M	0.341	NEU	M	0.561	NEU
nsp5	1	7	A	0.781	NEU	A	-1.104	MAX
nsp5	1	8	H	0.498	NEU	F	0.78	MIN
nsp5	1	9	P	0.341	NEU	P	-1.017	MAX
nsp5	1	10	S	1.316	NEU	S	-0.618	NEU

nsp5	1	11	G	1.316	NEU	G	-0.783	NEU
nsp5	1	12	A	0.578	NEU	K	-0.541	NEU
nsp5	1	13	V	1.316	MIN	V	1.1	MIN
nsp5	1	14	E	1.316	MAX	E	-1.127	MAX
nsp5	1	15	P	0.671	NEU	G	-0.582	NEU
nsp5	1	16	C	1.316	MIN	C	1.493	MIN
nsp5	1	17	M	1.316	MIN	M	0.792	MIN
nsp5	1	18	V	1.316	MIN	V	1.185	MIN
nsp5	1	19	Q	0.867	NEU	Q	-0.557	NEU
nsp5	1	20	V	1.316	MIN	V	1.104	MIN
nsp5	1	21	T	0.781	NEU	T	0.148	NEU
nsp5	1	22	C	1.115	MIN	C	0.944	MIN
nsp5	1	23	G	1.316	NEU	G	-0.865	NEU
nsp5	1	24	S	0.316	MIN	T	0.96	MIN
nsp5	1	25	M	0.867	NEU	T	-0.385	NEU
nsp5	1	26	T	1.316	NEU	T	-0.001	NEU
nsp5	1	27	L	1.316	MIN	L	0.721	NEU
nsp5	1	28	N	0.691	NEU	N	-0.811	NEU
nsp5	1	29	G	1.316	NEU	G	-0.387	NEU
nsp5	1	30	L	1.316	MIN	L	1.2	MIN
nsp5	1	31	W	0.979	NEU	W	0.334	NEU
nsp5	1	32	L	1.316	MIN	L	1.196	MIN
nsp5	1	33	D	0.772	MAX	D	-1.276	MAX
nsp5	1	34	N	0.979	MAX	D	-1.071	MAX
nsp5	1	35	Y	0.341	MIN	V	1.279	MIN
nsp5	1	36	V	1.316	MIN	V	1.163	MIN
nsp5	1	37	Y	0.867	MIN	Y	0.671	NEU
nsp5	1	38	C	1.316	MIN	C	1.392	MIN
nsp5	1	39	P	1.115	MAX	P	-1.083	MAX
nsp5	1	40	R	1.316	NEU	R	-0.453	NEU
nsp5	1	41	H	1.316	NEU	H	-0.069	NEU
nsp5	1	42	V	1.316	MIN	V	1.201	MIN
nsp5	1	43	M	0.200	MIN	I	0.956	MIN
nsp5	1	44	C	1.314	MIN	C	2.102	MIN
nsp5	1	45	P	0.352	NEU	T	0.914	MIN
nsp5	1	46	A	0.407	NEU	S	-0.638	NEU
nsp5	1	47	D	0.302	NEU	E	-0.186	NEU
nsp5	1	48	Q	-0.006	NEU	D	-0.864	NEU
nsp5	1	49	L	0.369	MIN	M	-0.834	NEU
nsp5	1	50	L	-0.050	NEU	L	-0.343	NEU
nsp5	1	51	D	0.194	MIN	N	0.727	NEU
nsp5	1	52	P	0.319	MAX	P	-1.128	MAX
nsp5	1	53	N	0.505	NEU	N	-0.73	NEU
nsp5	1	54	Y	0.319	NEU	Y	0.212	NEU
nsp5	1	55	D	0.361	MAX	E	-1.505	MAX
nsp5	1	56	A	0.558	NEU	D	-0.291	NEU

nsp5	1	57	L	0.388	MIN	L	0.822	MIN
nsp5	1	58	L	0.558	MIN	L	1.45	MIN
nsp5	1	59	I	0.236	NEU	I	-0.354	NEU
nsp5	1	60	S	1.115	NEU	R	0.357	NEU
nsp5	1	61	M	0.118	MIN	K	-1.424	MAX
nsp5	1	62	T	0.772	NEU	S	-0.06	NEU
nsp5	1	63	N	0.361	MAX	N	-1.037	MAX
nsp5	1	64	H	0.505	NEU	H	0.207	NEU
nsp5	1	65	S	0.781	NEU	N	-0.833	NEU
nsp5	1	66	F	1.316	MIN	F	1.383	MIN
nsp5	1	67	H	0.327	MIN	L	0.017	NEU
nsp5	1	68	V	1.316	MIN	V	1.197	MIN
nsp5	1	69	V	0.498	NEU	Q	-0.802	NEU
nsp5	1	70	G	0.180	NEU	A	0.316	NEU
nsp5	1	71	A	1.109	NEU	G	-0.681	NEU
nsp5	1	72	P	0.361	NEU	N	0.639	NEU
nsp5	1	73	A	0.317	NEU	V	1.433	MIN
nsp5	1	74	N	0.025	NEU	Q	-0.426	NEU
nsp5	1	75	L	1.316	MIN	L	1.057	MIN
nsp5	1	76	R	1.115	NEU	R	0.093	NEU
nsp5	1	77	V	1.316	MIN	V	1.216	MIN
nsp5	1	78	I	0.319	MIN	I	-0.194	NEU
nsp5	1	79	G	0.979	NEU	G	-0.785	NEU
nsp5	1	80	H	1.316	NEU	H	-0.221	NEU
nsp5	1	81	S	0.302	NEU	S	0.169	NEU
nsp5	1	82	M	1.115	MIN	M	1.111	MIN
nsp5	1	83	Q	-0.193	NEU	Q	-1.208	MAX
nsp5	1	84	G	0.867	NEU	N	-0.813	NEU
nsp5	1	85	T	0.558	NEU	C	1.591	MIN
nsp5	1	86	L	1.316	MIN	V	0.86	MIN
nsp5	1	87	L	1.316	MIN	L	1.327	MIN
nsp5	1	88	K	0.361	MAX	K	-1.374	MAX
nsp5	1	89	L	1.316	MIN	L	1.066	MIN
nsp5	1	90	T	1.115	NEU	K	-0.607	NEU
nsp5	1	91	V	1.316	MIN	V	1.328	MIN
nsp5	1	92	D	0.671	NEU	D	0.255	NEU
nsp5	1	93	S	0.147	NEU	T	-0.431	NEU
nsp5	1	94	A	-0.090	NEU	A	-0.987	NEU
nsp5	1	95	N	0.361	MAX	N	-1.016	MAX
nsp5	1	96	P	0.236	NEU	P	-0.215	NEU
nsp5	1	97	K	0.236	NEU	K	-0.666	NEU
nsp5	1	98	T	1.316	NEU	T	-0.455	NEU
nsp5	1	99	P	1.316	NEU	P	-0.462	NEU
nsp5	1	100	A	0.302	NEU	K	0.061	NEU
nsp5	1	101	Y	0.867	MIN	Y	0.604	NEU
nsp5	1	102	T	0.558	NEU	K	-1.425	MAX

nsp5	1	103	F	0.772	MIN	F	0.672	NEU
nsp5	1	104	T	0.327	NEU	V	1.289	MIN
nsp5	1	105	T	0.302	NEU	R	1.286	MIN
nsp5	1	106	V	0.979	MIN	I	1.293	MIN
nsp5	1	107	K	0.369	MAX	Q	-1.019	MAX
nsp5	1	108	P	0.097	NEU	P	-0.93	NEU
nsp5	1	109	G	1.316	NEU	G	-0.342	NEU
nsp5	1	110	Q	0.097	NEU	Q	-0.831	NEU
nsp5	1	111	S	0.916	NEU	T	-0.056	NEU
nsp5	1	112	F	1.316	MIN	F	1.368	MIN
nsp5	1	113	S	1.316	NEU	S	-0.58	NEU
nsp5	1	114	V	1.316	MIN	V	1.248	MIN
nsp5	1	115	L	1.316	MIN	L	0.884	MIN
nsp5	1	116	A	1.115	NEU	A	0.375	NEU
nsp5	1	117	C	0.979	MIN	C	2.024	MIN
nsp5	1	118	Y	0.505	MAX	Y	-2.864	MAX
nsp5	1	119	N	0.558	NEU	N	0.295	NEU
nsp5	1	120	G	1.316	NEU	G	-0.131	NEU
nsp5	1	121	R	0.317	NEU	S	0.119	NEU
nsp5	1	122	P	0.153	MAX	P	-0.835	NEU
nsp5	1	123	T	0.772	NEU	S	-0.566	NEU
nsp5	1	124	G	1.316	NEU	G	-0.457	NEU
nsp5	1	125	V	0.090	MIN	V	1.43	MIN
nsp5	1	126	Y	0.620	NEU	Y	-0.349	NEU
nsp5	1	127	T	1.115	NEU	Q	-0.792	NEU
nsp5	1	128	V	1.316	MIN	C	1.888	MIN
nsp5	1	129	V	0.044	NEU	A	0.491	NEU
nsp5	1	130	M	1.115	MIN	M	1.028	MIN
nsp5	1	131	R	0.388	MIN	R	-0.522	NEU
nsp5	1	132	P	0.361	MAX	P	-1.333	MAX
nsp5	1	133	N	0.273	NEU	N	-0.755	NEU
nsp5	1	134	G	0.097	NEU	F	1.383	MIN
nsp5	1	135	T	0.979	NEU	T	-0.362	NEU
nsp5	1	136	I	1.316	MIN	I	1.167	MIN
nsp5	1	137	K	0.057	NEU	K	-1.103	MAX
nsp5	1	138	G	1.316	NEU	G	-0.521	NEU
nsp5	1	139	S	1.316	NEU	S	0.234	NEU
nsp5	1	140	F	1.316	MIN	F	1.274	MIN
nsp5	1	141	L	0.578	MIN	L	0.734	NEU
nsp5	1	142	C	0.558	MIN	N	-0.679	NEU
nsp5	1	143	G	1.316	NEU	G	-0.5	NEU
nsp5	1	144	S	1.316	NEU	S	-0.542	NEU
nsp5	1	145	C	1.316	MIN	C	2.409	MIN
nsp5	1	146	G	1.316	NEU	G	-0.291	NEU
nsp5	1	147	S	1.316	NEU	S	-0.615	NEU
nsp5	1	148	V	0.505	MIN	V	1.182	MIN

nsp5	1	149	G	1.316	NEU	G	-0.478	NEU
nsp5	1	150	Y	0.361	MIN	F	1.199	MIN
nsp5	1	151	T	-0.032	NEU	N	-0.839	NEU
nsp5	1	152	K	-0.251	NEU	I	1.711	MIN
nsp5	1	153	E	0.044	MAX	D	-0.13	NEU
nsp5	1	154	G	0.558	NEU	Y	-1.047	MAX
nsp5	1	155	N	0.505	NEU	D	1.644	MIN
nsp5	1	156	V	-0.006	MIN	C	1.823	MIN
nsp5	1	157	I	1.316	MIN	V	1.064	MIN
nsp5	1	158	N	0.459	MAX	S	-0.429	NEU
nsp5	1	159	F	1.316	MIN	F	1.228	MIN
nsp5	1	160	C	1.316	MIN	C	1.78	MIN
nsp5	1	161	Y	1.316	NEU	Y	0.517	NEU
nsp5	1	162	M	0.647	MIN	M	1.198	MIN
nsp5	1	163	H	1.316	NEU	H	-0.368	NEU
nsp5	1	164	Q	0.316	NEU	H	-0.092	NEU
nsp5	1	165	M	0.273	NEU	M	0.281	NEU
nsp5	1	166	E	1.115	MAX	E	-1.844	MAX
nsp5	1	167	L	0.316	MIN	L	1.246	MIN
nsp5	1	168	P	-0.259	NEU	P	0.775	NEU
nsp5	1	169	N	0.388	NEU	T	-0.264	NEU
nsp5	1	170	G	0.317	MAX	G	-1.091	MAX
nsp5	1	171	T	0.505	NEU	V	1.816	MIN
nsp5	1	172	H	1.316	NEU	H	-0.447	NEU
nsp5	1	173	T	1.115	NEU	A	0.407	NEU
nsp5	1	174	G	1.316	NEU	G	-0.331	NEU
nsp5	1	175	S	0.979	NEU	T	-0.479	NEU
nsp5	1	176	D	0.327	NEU	D	-1.232	MAX
nsp5	1	177	F	1.316	MIN	L	1.16	MIN
nsp5	1	178	D	-0.020	NEU	E	-1.747	MAX
nsp5	1	179	G	1.316	NEU	G	-0.273	NEU
nsp5	1	180	N	0.361	NEU	N	-0.133	NEU
nsp5	1	181	F	0.236	NEU	F	1.271	MIN
nsp5	1	182	Y	0.979	MAX	Y	-2.777	MAX
nsp5	1	183	G	1.316	NEU	G	-0.726	NEU
nsp5	1	184	P	-0.020	NEU	P	0.669	NEU
nsp5	1	185	F	0.341	NEU	F	1.48	MIN
nsp5	1	186	E	0.041	MIN	V	0.815	MIN
nsp5	1	187	D	0.341	NEU	D	-0.858	NEU
nsp5	1	188	R	0.867	NEU	R	0.205	NEU
nsp5	1	189	Q	0.459	MIN	Q	0.668	NEU
nsp5	1	190	V	0.341	MIN	T	0.776	NEU
nsp5	1	191	H	0.044	MAX	A	-1.588	MAX
nsp5	1	192	Q	0.979	NEU	Q	-0.82	NEU
nsp5	1	193	A	-0.063	NEU	A	-1.444	MAX
nsp5	1	194	A	0.505	MIN	A	0.848	MIN

nsp5	1	195	L	-0.104	NEU	G	0.208	NEU
nsp5	1	196	T	0.388	MIN	T	0.073	NEU
nsp5	1	197	D	0.206	MIN	D	0.558	NEU
nsp5	1	198	K	-0.104	MAX	T	-0.043	NEU
nsp5	1	199	T	0.316	MIN	T	-0.121	NEU
nsp5	1	200	C	1.115	MIN	I	1.153	MIN
nsp5	1	201	T	1.316	NEU	T	-0.198	NEU
nsp5	1	202	V	0.620	MIN	V	1.464	MIN
nsp5	1	203	N	0.459	MAX	N	-1.043	MAX
nsp5	1	204	V	1.316	MIN	V	1.26	MIN
nsp5	1	205	V	1.316	MIN	L	1.25	MIN
nsp5	1	206	A	0.772	NEU	A	0.307	NEU
nsp5	1	207	W	1.316	NEU	W	0.215	NEU
nsp5	1	208	L	1.316	MIN	L	1.43	MIN
nsp5	1	209	Y	1.316	NEU	Y	-0.272	NEU
nsp5	1	210	A	0.459	NEU	A	0.155	NEU
nsp5	1	211	A	1.115	NEU	A	0.418	NEU
nsp5	1	212	V	1.316	MIN	V	1.418	MIN
nsp5	1	213	L	1.314	MIN	I	1.526	MIN
nsp5	1	214	N	0.760	NEU	N	-0.9	NEU
nsp5	1	215	G	1.314	NEU	G	-0.595	NEU
nsp5	1	216	C	-0.090	MIN	D	-0.883	NEU
nsp5	1	217	N	-0.001	MAX	R	-0.944	NEU
nsp5	1	218	W	0.147	MIN	W	-0.007	NEU
nsp5	1	219	F	0.316	MIN	F	1.028	MIN
nsp5	1	220	V	1.115	MIN	L	0.535	NEU
nsp5	1	221	K	0.118	NEU	N	-1.074	MAX
nsp5	1	222	P	0.153	NEU	R	1.376	MIN
nsp5	1	223	N	0.781	NEU	F	-0.691	NEU
nsp5	1	224	R	0.916	NEU	T	-0.167	NEU
nsp5	1	225	T	0.420	NEU	T	-0.497	NEU
nsp5	1	226	S	0.772	NEU	T	-0.36	NEU
nsp5	1	227	V	0.255	MIN	L	0.889	MIN
nsp5	1	228	A	0.781	NEU	N	0.087	NEU
nsp5	1	229	D	0.781	NEU	D	-0.796	NEU
nsp5	1	230	F	0.867	MIN	F	0.717	NEU
nsp5	1	231	N	0.361	MAX	N	-0.998	NEU
nsp5	1	232	E	0.025	MAX	L	0.032	NEU
nsp5	1	233	W	0.153	NEU	V	1.214	MIN
nsp5	1	234	A	1.115	NEU	A	0.163	NEU
nsp5	1	235	M	-0.152	MIN	M	0.106	NEU
nsp5	1	236	K	0.505	NEU	K	-1.19	MAX
nsp5	1	237	N	0.916	NEU	Y	-0.699	NEU
nsp5	1	238	Q	0.620	NEU	N	-0.166	NEU
nsp5	1	239	F	0.342	MIN	Y	-0.952	NEU
nsp5	1	240	T	0.620	NEU	E	-1.061	MAX

nsp5	1	241	E	0.361	MAX	P	-1.113	MAX
nsp5	1	242	F	1.316	MIN	L	1.199	MIN
nsp5	1	243	T	0.558	MIN	T	-0.199	NEU
nsp5	1	244	G	0.558	NEU	Q	-1.059	MAX
nsp5	1	245	T	0.429	NEU	D	-1.142	MAX
nsp5	1	246	-	1.265	NEU	H	-0.194	NEU
nsp5	1	247	-	1.265	MIN	V	1.367	MIN
nsp5	1	248	Q	0.498	NEU	D	0.085	NEU
nsp5	1	249	A	0.319	NEU	I	1.625	MIN
nsp5	1	250	L	1.316	MIN	L	1.032	MIN
nsp5	1	251	D	0.388	MAX	G	-0.603	NEU
nsp5	1	252	P	0.062	NEU	P	-0.779	NEU
nsp5	1	253	L	1.316	MIN	L	1.3	MIN
nsp5	1	254	A	0.420	MIN	S	-0.718	NEU
nsp5	1	255	A	0.153	MIN	A	-0.482	NEU
nsp5	1	256	K	0.459	MAX	Q	-0.978	NEU
nsp5	1	257	T	1.316	NEU	T	-0.387	NEU
nsp5	1	258	G	0.620	NEU	G	-0.778	NEU
nsp5	1	259	V	1.316	MIN	I	1.628	MIN
nsp5	1	260	S	0.578	NEU	A	0.47	NEU
nsp5	1	261	V	1.115	MIN	V	1.281	MIN
nsp5	1	262	E	0.498	MAX	L	1.384	MIN
nsp5	1	263	Q	0.327	NEU	D	-0.698	NEU
nsp5	1	264	M	1.115	MIN	M	0.675	NEU
nsp5	1	265	L	1.316	MIN	C	0.91	MIN
nsp5	1	266	Y	0.244	NEU	A	-0.001	NEU
nsp5	1	267	A	0.319	NEU	S	-0.793	NEU
nsp5	1	268	L	1.115	MIN	L	1.291	MIN
nsp5	1	269	K	1.316	MAX	K	-1.537	MAX
nsp5	1	270	Q	-0.211	NEU	E	-2.078	MAX
nsp5	1	271	-	1.265	MIN	L	1.43	MIN
nsp5	1	272	L	1.316	MIN	L	1.558	MIN
nsp5	1	273	S	0.369	NEU	Q	-1.611	MAX
nsp5	1	274	N	0.153	NEU	N	-0.011	NEU
nsp5	1	275	G	0.327	NEU	G	-1.507	MAX
nsp5	1	276	F	0.979	MIN	M	0.792	MIN
nsp5	1	277	Q	-0.090	NEU	N	1.107	MIN
nsp5	1	278	G	0.327	MAX	G	-0.515	NEU
nsp5	1	279	K	0.341	NEU	R	-0.026	NEU
nsp5	1	280	T	0.429	NEU	T	0.021	NEU
nsp5	1	281	I	1.316	MIN	I	1.457	MIN
nsp5	1	282	L	1.316	MIN	L	0.951	MIN
nsp5	1	283	G	0.578	MAX	G	-0.647	NEU
nsp5	1	284	S	0.671	NEU	S	-0.59	NEU
nsp5	1	285	T	0.498	NEU	A	-0.295	NEU
nsp5	1	286	M	0.182	NEU	L	1.108	MIN

nsp5	1	287	L	1.316	MIN	L	1.555	MIN
nsp5	1	288	E	1.316	MAX	E	-1.235	MAX
nsp5	1	289	D	0.420	MAX	D	-1.236	MAX
nsp5	1	290	E	0.429	NEU	E	-1.351	MAX
nsp5	1	291	F	0.327	MIN	F	1.18	MIN
nsp5	1	292	T	1.316	NEU	T	-0.52	NEU
nsp5	1	293	P	0.772	MAX	P	-1.084	MAX
nsp5	1	294	E	-0.178	MAX	F	1.241	MIN
nsp5	1	295	D	0.691	NEU	D	-0.348	NEU
nsp5	1	296	V	1.316	MIN	V	1.077	MIN
nsp5	1	297	N	-0.178	MAX	V	1.288	MIN
nsp5	1	298	M	0.498	NEU	R	0.144	NEU
nsp5	1	299	Q	0.772	MAX	Q	-0.987	NEU
nsp5	1	300	M	0.691	MIN	C	1.163	MIN
nsp5	1	301	M	0.867	NEU	S	-0.487	NEU
nsp5	1	302	G	1.316	NEU	G	-0.425	NEU
nsp5	1	303	V	0.772	MIN	V	0.302	NEU
nsp5	1	304	V	0.147	MIN	T	-0.063	NEU
nsp5	1	305	M	-0.099	NEU	F	-0.075	NEU
nsp7	1	1	K	0.442	NEU	K	-0.319	NEU
nsp7	1	2	L	0.403	MIN	M	-0.851	NEU
nsp7	1	3	T	0.610	NEU	S	-0.283	NEU
nsp7	1	4	D	0.403	NEU	D	0.304	NEU
nsp7	1	5	L	1.321	MIN	V	1.137	MIN
nsp7	1	6	K	1.138	MAX	K	-1.143	MAX
nsp7	1	7	C	1.138	MIN	C	1.802	MIN
nsp7	1	8	T	1.321	NEU	T	-0.254	NEU
nsp7	1	9	S	1.321	NEU	S	-0.822	NEU
nsp7	1	10	V	1.321	MIN	V	1.272	MIN
nsp7	1	11	V	1.321	MIN	V	1.174	MIN
nsp7	1	12	L	1.321	MIN	L	0.92	MIN
nsp7	1	13	L	1.321	MIN	L	0.951	MIN
nsp7	1	14	S	1.321	NEU	S	-0.748	NEU
nsp7	1	15	V	1.321	MIN	V	1.325	MIN
nsp7	1	16	L	1.138	MIN	L	1.087	MIN
nsp7	1	17	Q	1.011	MAX	Q	-1.308	MAX
nsp7	1	18	Q	0.341	NEU	Q	-1.028	MAX
nsp7	1	19	L	1.321	MIN	L	1.098	MIN
nsp7	1	20	H	0.433	MIN	R	1.192	MIN
nsp7	1	21	L	1.321	MIN	V	1.255	MIN
nsp7	1	22	E	-0.094	MAX	E	-0.915	NEU
nsp7	1	23	A	0.907	NEU	S	-0.265	NEU
nsp7	1	24	N	0.323	NEU	S	-0.991	NEU
nsp7	1	25	S	1.321	NEU	S	-0.818	NEU
nsp7	1	26	K	0.557	MAX	K	-1.622	MAX
nsp7	1	27	A	0.377	NEU	L	1.251	MIN

nsp7	1	28	W	1.138	NEU	W	-0.553	NEU
nsp7	1	29	A	0.740	NEU	A	0.617	NEU
nsp7	1	30	H	0.610	NEU	Q	-0.882	NEU
nsp7	1	31	C	1.321	MIN	C	1.119	MIN
nsp7	1	32	V	1.321	MIN	V	0.856	MIN
nsp7	1	33	K	-0.049	NEU	Q	0.419	NEU
nsp7	1	34	L	1.011	MIN	L	1.091	MIN
nsp7	1	35	H	1.321	NEU	H	-0.106	NEU
nsp7	1	36	N	1.321	MAX	N	-1.172	MAX
nsp7	1	37	D	0.330	NEU	D	-1.427	MAX
nsp7	1	38	I	1.321	MIN	I	1.36	MIN
nsp7	1	39	L	0.907	NEU	L	-0.565	NEU
nsp7	1	40	A	-0.210	NEU	L	-1.1	MAX
nsp7	1	41	A	0.907	NEU	A	-0.274	NEU
nsp7	1	42	T	0.433	NEU	K	1.012	MIN
nsp7	1	43	D	0.610	MAX	D	-1.507	MAX
nsp7	1	44	P	0.377	MAX	T	-0.364	NEU
nsp7	1	45	T	1.321	NEU	T	-0.34	NEU
nsp7	1	46	E	0.180	MAX	E	-0.354	NEU
nsp7	1	47	A	0.510	NEU	A	0.14	NEU
nsp7	1	48	F	0.468	NEU	F	0.203	NEU
nsp7	1	49	E	1.138	MAX	E	-1.624	MAX
nsp7	1	50	K	0.341	MAX	K	-0.981	NEU
nsp7	1	51	F	1.321	MIN	M	0.714	NEU
nsp7	1	52	V	1.011	MIN	V	0.878	MIN
nsp7	1	53	S	0.377	NEU	S	-0.695	NEU
nsp7	1	54	L	1.321	MIN	L	1.186	MIN
nsp7	1	55	L	1.321	MIN	L	1.067	MIN
nsp7	1	56	A	1.138	NEU	S	-0.664	NEU
nsp7	1	57	T	0.377	NEU	V	1.299	MIN
nsp7	1	58	L	1.321	MIN	L	1.054	MIN
nsp7	1	59	M	0.330	MIN	L	0.827	MIN
nsp7	1	60	S	1.321	NEU	S	-0.303	NEU
nsp7	1	61	F	1.138	MIN	M	1.016	MIN
nsp7	1	62	S	0.280	NEU	Q	-1.115	MAX
nsp7	1	63	G	1.138	NEU	G	-0.487	NEU
nsp7	1	64	N	0.671	NEU	A	0.099	NEU
nsp7	1	65	V	1.321	MIN	V	1.232	MIN
nsp7	1	66	D	-0.064	MAX	D	-0.531	NEU
nsp7	1	67	L	1.321	MIN	I	1.009	MIN
nsp7	1	68	E	0.212	MAX	N	0.055	NEU
nsp7	1	69	A	0.376	NEU	K	0.45	NEU
nsp7	1	70	L	1.321	MIN	L	0.993	MIN
nsp7	1	71	A	0.610	MIN	C	2.491	MIN
nsp7	1	72	S	0.194	NEU	E	2.043	MIN
nsp8	1	1	F	0.294	MIN	F	1.311	MIN

nsp8	1	2	S	0.565	NEU	S	-0.555	NEU
nsp8	1	3	N	-0.008	NEU	S	1.005	MIN
nsp8	1	4	L	0.911	MIN	L	1.278	MIN
nsp8	1	5	P	1.265	NEU	P	-0.302	NEU
nsp8	1	6	S	1.265	NEU	S	-0.74	NEU
nsp8	1	7	Y	0.698	NEU	Y	0.054	NEU
nsp8	1	8	V	0.911	MIN	A	0.545	NEU
nsp8	1	9	A	0.359	NEU	A	0.502	NEU
nsp8	1	10	Y	0.911	NEU	F	0.375	NEU
nsp8	1	11	E	0.698	NEU	A	0.345	NEU
nsp8	1	12	N	0.565	NEU	T	0.268	NEU
nsp8	1	13	A	0.911	NEU	A	0.524	NEU
nsp8	1	14	Q	-0.022	NEU	Q	-0.845	NEU
nsp8	1	15	K	-0.008	NEU	E	-1.252	MAX
nsp8	1	16	A	0.565	MIN	A	0.688	NEU
nsp8	1	17	Y	0.359	NEU	Y	-0.353	NEU
nsp8	1	18	D	0.268	NEU	E	-1.369	MAX
nsp8	1	19	Q	-0.008	NEU	Q	-1.202	MAX
nsp8	1	20	A	1.265	MIN	A	0.795	MIN
nsp8	1	21	V	0.294	MIN	V	0.454	NEU
nsp8	1	22	A	0.428	NEU	A	-0.785	NEU
nsp8	1	23	N	0.359	NEU	N	-0.526	NEU
nsp8	1	24	G	0.911	NEU	G	-0.635	NEU
nsp8	1	25	D	0.268	NEU	D	-1.041	MAX
nsp8	1	26	S	1.265	NEU	S	-0.695	NEU
nsp8	1	27	E	-0.135	NEU	E	-0.29	NEU
nsp8	1	28	S	1.265	NEU	V	-0.298	NEU
nsp8	1	29	V	0.268	MIN	V	0.865	MIN
nsp8	1	30	L	1.265	MIN	L	1.12	MIN
nsp8	1	31	K	0.543	MAX	K	-1.474	MAX
nsp8	1	32	A	0.268	NEU	K	-1.822	MAX
nsp8	1	33	L	0.911	MIN	L	1.349	MIN
nsp8	1	34	K	1.265	MAX	K	-1.405	MAX
nsp8	1	35	K	1.265	MAX	K	-2.147	MAX
nsp8	1	36	A	-0.008	MIN	S	-0.706	NEU
nsp8	1	37	M	0.268	MIN	L	1.219	MIN
nsp8	1	38	N	0.346	NEU	N	0.602	NEU
nsp8	1	39	V	0.543	MIN	V	0.299	NEU
nsp8	1	40	A	0.294	NEU	A	0.648	NEU
nsp8	1	41	K	0.911	NEU	K	-0.713	NEU
nsp8	1	42	S	0.698	NEU	S	0.235	NEU
nsp8	1	43	V	0.268	NEU	E	-0.781	NEU
nsp8	1	44	L	0.911	MIN	F	1.152	MIN
nsp8	1	45	D	0.911	NEU	D	-0.592	NEU
nsp8	1	46	R	-0.008	NEU	R	-0.255	NEU
nsp8	1	47	D	0.911	MAX	D	-1.526	MAX

nsp8	1	48	A	0.698	MIN	A	0.782	MIN
nsp8	1	49	A	1.265	NEU	A	-0.864	NEU
nsp8	1	50	M	0.543	NEU	M	0.355	NEU
nsp8	1	51	Q	-0.301	NEU	Q	-1.029	MAX
nsp8	1	52	R	0.911	NEU	R	-0.748	NEU
nsp8	1	53	K	0.698	MAX	K	-1.175	MAX
nsp8	1	54	L	0.428	MIN	L	1.489	MIN
nsp8	1	55	E	0.346	NEU	E	0.433	NEU
nsp8	1	56	R	0.268	MAX	K	-1.229	MAX
nsp8	1	57	M	0.294	NEU	M	0.513	NEU
nsp8	1	58	A	0.294	MIN	A	0.933	MIN
nsp8	1	59	D	0.698	NEU	D	-0.677	NEU
nsp8	1	60	Q	-0.008	NEU	Q	-0.608	NEU
nsp8	1	61	A	0.346	MIN	A	0.693	NEU
nsp8	1	62	M	0.698	NEU	M	0.388	NEU
nsp8	1	63	T	0.346	NEU	T	0.596	NEU
nsp8	1	64	Q	0.034	NEU	Q	-0.896	NEU
nsp8	1	65	M	0.543	MIN	M	0.567	NEU
nsp8	1	66	Y	0.268	MAX	Y	-2.64	MAX
nsp8	1	67	K	1.265	MAX	K	-1.732	MAX
nsp8	1	68	Q	0.698	MAX	Q	-1.194	MAX
nsp8	1	69	A	0.911	NEU	A	0.142	NEU
nsp8	1	70	R	1.265	MIN	R	1.675	MIN
nsp8	1	71	A	1.265	NEU	S	-0.521	NEU
nsp8	1	72	E	0.346	MIN	E	0.56	NEU
nsp8	1	73	D	1.265	MIN	D	1.039	MIN
nsp8	1	74	K	0.428	MAX	K	-1.391	MAX
nsp8	1	75	R	-0.073	MIN	R	1.364	MIN
nsp8	1	76	A	0.543	NEU	A	0.028	NEU
nsp8	1	77	K	0.106	NEU	K	-0.594	NEU
nsp8	1	78	V	0.911	MIN	V	1.163	MIN
nsp8	1	79	T	0.268	NEU	T	0.164	NEU
nsp8	1	80	S	1.265	NEU	S	-0.75	NEU
nsp8	1	81	A	0.543	MIN	A	0.828	MIN
nsp8	1	82	M	0.911	MIN	M	0.604	NEU
nsp8	1	83	Q	1.265	NEU	Q	-0.805	NEU
nsp8	1	84	T	0.911	NEU	T	0.148	NEU
nsp8	1	85	M	0.698	NEU	M	0.161	NEU
nsp8	1	86	L	1.265	MIN	L	1.473	MIN
nsp8	1	87	F	0.911	MIN	F	0.729	NEU
nsp8	1	88	N	1.265	NEU	T	0.326	NEU
nsp8	1	89	M	0.294	MIN	M	0.324	NEU
nsp8	1	90	L	1.265	MIN	L	1.127	MIN
nsp8	1	91	R	0.543	NEU	R	0.515	NEU
nsp8	1	92	R	-0.022	MIN	K	0.329	NEU
nsp8	1	93	L	1.265	MIN	L	1.243	MIN

nsp8	1	94	D	0.911	NEU	D	-0.717	NEU
nsp8	1	95	N	1.265	NEU	N	-0.197	NEU
nsp8	1	96	D	0.034	MIN	D	0.593	NEU
nsp8	1	97	A	-0.008	NEU	A	0.142	NEU
nsp8	1	98	L	1.265	MIN	L	0.975	MIN
nsp8	1	99	N	1.265	NEU	N	0.548	NEU
nsp8	1	100	N	0.428	MIN	N	1.554	MIN
nsp8	1	101	I	1.265	MIN	I	1.486	MIN
nsp8	1	102	I	0.911	MIN	I	1.315	MIN
nsp8	1	103	N	0.212	MIN	N	1.19	MIN
nsp8	1	104	N	0.346	NEU	N	-0.409	NEU
nsp8	1	105	A	0.911	MIN	A	0.758	NEU
nsp8	1	106	R	-0.008	MIN	R	1.167	MIN
nsp8	1	107	N	0.359	NEU	D	-0.703	NEU
nsp8	1	108	G	0.294	NEU	G	-1.007	MAX
nsp8	1	109	C	0.543	NEU	C	0.185	NEU
nsp8	1	110	V	1.265	MIN	V	1.278	MIN
nsp8	1	111	P	0.268	NEU	P	-1.129	MAX
nsp8	1	112	L	1.265	MIN	L	0.847	MIN
nsp8	1	113	N	1.265	NEU	N	-0.466	NEU
nsp8	1	114	I	0.911	MIN	I	1.244	MIN
nsp8	1	115	I	1.265	MIN	I	1.406	MIN
nsp8	1	116	P	0.543	NEU	P	-0.46	NEU
nsp8	1	117	L	0.294	MIN	L	1.169	MIN
nsp8	1	118	T	0.911	NEU	T	-0.457	NEU
nsp8	1	119	A	0.911	NEU	T	-0.313	NEU
nsp8	1	120	A	0.698	NEU	A	-0.288	NEU
nsp8	1	121	N	-0.022	MIN	A	0.606	NEU
nsp8	1	122	K	0.428	MAX	K	-0.987	NEU
nsp8	1	123	L	1.265	MIN	L	1.527	MIN
nsp8	1	124	M	0.543	MIN	M	0.822	MIN
nsp8	1	125	V	1.265	MIN	V	1.253	MIN
nsp8	1	126	V	1.265	MIN	V	1.667	MIN
nsp8	1	127	V	1.265	MIN	I	1.318	MIN
nsp8	1	128	P	1.265	NEU	P	-0.399	NEU
nsp8	1	129	D	0.346	MAX	D	-0.842	NEU
nsp8	1	130	Y	-0.135	NEU	Y	-0.738	NEU
nsp8	1	131	S	0.346	MIN	N	1.305	MIN
nsp8	1	132	V	0.294	MIN	T	-0.073	NEU
nsp8	1	133	Y	0.428	NEU	Y	-0.03	NEU
nsp8	1	134	K	0.294	NEU	K	1.114	MIN
nsp8	1	135	N	0.023	NEU	N	-0.166	NEU
nsp8	1	136	T	0.698	NEU	T	-0.421	NEU
nsp8	1	137	C	1.265	MIN	C	1.078	MIN
nsp8	1	138	T	-0.008	NEU	D	-0.127	NEU
nsp8	1	139	G	0.268	NEU	G	-0.052	NEU

nsp8	1	140	P	0.346	MAX	T	-0.193	NEU
nsp8	1	141	T	0.428	NEU	T	-0.116	NEU
nsp8	1	142	L	1.265	MIN	F	0.877	MIN
nsp8	1	143	T	0.911	NEU	T	-0.202	NEU
nsp8	1	144	Y	0.565	NEU	Y	-0.472	NEU
nsp8	1	145	A	0.565	NEU	A	-0.221	NEU
nsp8	1	146	G	0.106	NEU	S	0.918	MIN
nsp8	1	147	A	0.911	NEU	A	0.289	NEU
nsp8	1	148	L	0.346	MIN	L	0.83	MIN
nsp8	1	149	W	0.268	MIN	W	0.546	NEU
nsp8	1	150	D	0.543	MAX	E	-0.912	NEU
nsp8	1	151	V	1.265	MIN	I	1.917	MIN
nsp8	1	152	Q	0.294	NEU	Q	-0.6	NEU
nsp8	1	153	Q	0.543	NEU	Q	-0.969	NEU
nsp8	1	154	V	1.265	MIN	V	1.423	MIN
nsp8	1	155	V	0.428	MIN	V	1.398	MIN
nsp8	1	156	D	0.698	MAX	D	-1.37	MAX
nsp8	1	157	A	1.265	NEU	A	-0.176	NEU
nsp8	1	158	D	0.543	NEU	D	0.269	NEU
nsp8	1	159	G	0.911	NEU	S	-0.676	NEU
nsp8	1	160	K	0.565	NEU	K	-0.412	NEU
nsp8	1	161	I	-0.008	NEU	I	1.785	MIN
nsp8	1	162	V	1.265	MIN	V	1.316	MIN
nsp8	1	163	N	-0.022	NEU	Q	-1.34	MAX
nsp8	1	164	L	0.212	MIN	L	0.841	MIN
nsp8	1	165	S	0.698	NEU	S	-0.217	NEU
nsp8	1	166	D	0.268	NEU	E	-1.923	MAX
nsp8	1	167	I	1.265	MIN	I	2.308	MIN
nsp8	1	168	T	0.294	MIN	S	1.133	MIN
nsp8	1	169	R	0.273	NEU	M	-0.256	NEU
nsp8	1	170	D	0.034	NEU	D	0.735	NEU
nsp8	1	171	N	0.543	NEU	N	-0.308	NEU
nsp8	1	172	S	1.258	NEU	S	-0.609	NEU
nsp8	1	173	P	0.060	NEU	P	0.601	NEU
nsp8	1	174	N	0.666	MIN	N	0.991	MIN
nsp8	1	175	L	0.887	MIN	L	1.449	MIN
nsp8	1	176	A	0.034	MAX	A	-1.176	MAX
nsp8	1	177	W	0.543	NEU	W	0.662	NEU
nsp8	1	178	P	0.543	NEU	P	-0.975	NEU
nsp8	1	179	L	1.265	MIN	L	1.333	MIN
nsp8	1	180	V	0.698	MIN	I	1.31	MIN
nsp8	1	181	V	1.265	MIN	V	1.326	MIN
nsp8	1	182	T	1.265	NEU	T	-0.087	NEU
nsp8	1	183	A	1.265	MIN	A	0.761	NEU
nsp8	1	184	L	0.268	MIN	L	1.487	MIN
nsp8	1	185	R	0.911	NEU	R	-0.794	NEU

nsp8	1	186	A	0.508	NEU	A	0.005	NEU
nsp8	1	187	N	0.060	NEU	N	-0.845	NEU
nsp9	1	1	N	1.330	NEU	N	-0.418	NEU
nsp9	1	2	N	0.335	NEU	N	-1.064	MAX
nsp9	1	3	E	-0.203	NEU	E	-0.678	NEU
nsp9	1	4	L	0.771	NEU	L	-0.841	NEU
nsp9	1	5	M	0.008	NEU	S	-0.496	NEU
nsp9	1	6	P	0.115	NEU	P	-0.774	NEU
nsp9	1	7	Q	0.574	NEU	V	0.605	NEU
nsp9	1	8	G	0.219	NEU	A	-1.379	MAX
nsp9	1	9	L	1.330	MIN	L	1.517	MIN
nsp9	1	10	K	0.219	NEU	R	0.828	MIN
nsp9	1	11	T	0.982	NEU	Q	-0.953	NEU
nsp9	1	12	M	-0.153	MIN	M	0.498	NEU
nsp9	1	13	V	0.056	NEU	S	-0.411	NEU
nsp9	1	14	V	1.330	MIN	C	1.109	MIN
nsp9	1	15	N	0.771	NEU	A	-0.152	NEU
nsp9	1	16	A	0.331	MIN	A	0.733	NEU
nsp9	1	17	G	1.330	NEU	G	-0.327	NEU
nsp9	1	18	P	-0.203	NEU	T	-0.038	NEU
nsp9	1	19	D	0.005	NEU	T	-0.525	NEU
nsp9	1	20	Q	0.056	NEU	Q	-1.046	MAX
nsp9	1	21	T	-0.011	NEU	T	0.618	NEU
nsp9	1	22	-	0.169	MIN	A	-0.707	NEU
nsp9	1	23	C	0.982	MIN	C	0.783	MIN
nsp9	1	24	N	0.581	MIN	T	0.131	NEU
nsp9	1	25	T	0.056	NEU	D	0.026	NEU
nsp9	1	26	-	1.258	NEU	D	-0.495	NEU
nsp9	1	27	P	0.624	NEU	N	-0.603	NEU
nsp9	1	28	T	0.771	NEU	A	0.05	NEU
nsp9	1	29	L	0.443	MIN	L	1.123	MIN
nsp9	1	30	A	0.364	NEU	A	0.397	NEU
nsp9	1	31	Y	0.443	NEU	Y	0.531	NEU
nsp9	1	32	Y	0.364	NEU	Y	0.194	NEU
nsp9	1	33	N	1.179	NEU	N	-0.802	NEU
nsp9	1	34	P	0.363	NEU	T	0.158	NEU
nsp9	1	35	V	0.342	MIN	T	-0.255	NEU
nsp9	1	36	Q	0.189	MIN	K	1.573	MIN
nsp9	1	37	G	0.419	NEU	G	0.202	NEU
nsp9	1	38	G	0.260	NEU	G	0.478	NEU
nsp9	1	39	R	0.352	NEU	R	0.429	NEU
nsp9	1	40	M	0.331	MIN	F	1.49	MIN
nsp9	1	41	V	1.330	MIN	V	1.844	MIN
nsp9	1	42	M	1.179	MIN	L	1.324	MIN
nsp9	1	43	A	1.330	NEU	A	0.121	NEU
nsp9	1	44	I	1.330	MIN	L	1.552	MIN

nsp9	1	45	L	1.330	MIN	L	1.307	MIN
nsp9	1	46	S	0.771	NEU	S	-0.815	NEU
nsp9	1	47	D	0.502	NEU	D	0.942	MIN
nsp9	1	48	N	-0.004	MIN	L	1.018	MIN
nsp9	1	49	D	0.663	MAX	Q	-0.844	NEU
nsp9	1	50	G	0.467	NEU	D	-0.499	NEU
nsp9	1	51	L	1.330	MIN	L	1.103	MIN
nsp9	1	52	K	-0.041	MAX	K	-1.748	MAX
nsp9	1	53	Y	0.342	NEU	W	0.089	NEU
nsp9	1	54	A	0.397	MIN	A	0.599	NEU
nsp9	1	55	K	0.471	MAX	R	-0.07	NEU
nsp9	1	56	V	1.330	MIN	F	0.972	MIN
nsp9	1	57	E	0.330	MIN	P	0.708	NEU
nsp9	1	58	K	0.229	NEU	K	-1.758	MAX
nsp9	1	59	S	0.574	MIN	S	0.715	NEU
nsp9	1	60	D	0.116	NEU	D	2.477	MIN
nsp9	1	61	G	-0.179	MIN	G	2.005	MIN
nsp9	1	62	-	1.250	MIN	T	0.716	NEU
nsp9	1	63	G	0.364	NEU	G	1.497	MIN
nsp9	1	64	F	0.335	MIN	T	0.119	NEU
nsp9	1	65	V	1.330	MIN	I	1.646	MIN
nsp9	1	66	V	0.028	NEU	Y	-1.385	MAX
nsp9	1	67	L	0.834	MIN	T	-0.175	NEU
nsp9	1	68	E	0.834	NEU	E	-0.477	NEU
nsp9	1	69	L	1.179	MIN	L	1.319	MIN
nsp9	1	70	Q	0.833	NEU	E	-0.808	NEU
nsp9	1	71	P	1.330	NEU	P	-0.814	NEU
nsp9	1	72	P	0.834	MAX	P	-1.013	MAX
nsp9	1	73	C	1.330	MIN	C	2.089	MIN
nsp9	1	74	K	0.364	NEU	R	-0.412	NEU
nsp9	1	75	F	0.419	NEU	F	0.695	NEU
nsp9	1	76	L	0.364	MIN	V	0.572	NEU
nsp9	1	77	I	0.771	MIN	T	0.119	NEU
nsp9	1	78	A	-0.097	MAX	D	1.653	MIN
nsp9	1	79	G	0.331	MIN	T	0.194	NEU
nsp9	1	80	P	0.077	MIN	P	1.254	MIN
nsp9	1	81	K	0.471	MIN	K	0.118	NEU
nsp9	1	82	G	1.179	NEU	G	0.252	NEU
nsp9	1	83	P	0.208	NEU	P	-1.693	MAX
nsp9	1	84	K	0.342	NEU	K	-0.164	NEU
nsp9	1	85	I	1.179	MIN	V	0.997	MIN
nsp9	1	86	K	0.342	MAX	K	-1.326	MAX
nsp9	1	87	Y	0.443	NEU	Y	0.802	MIN
nsp9	1	88	L	1.179	MIN	L	1.526	MIN
nsp9	1	89	Y	0.903	MIN	Y	0.551	NEU
nsp9	1	90	F	1.330	MIN	F	1.348	MIN

nsp9	1	91	V	0.714	MIN	I	1.312	MIN
nsp9	1	92	K	0.568	MAX	K	-1.055	MAX
nsp9	1	93	G	1.330	NEU	G	-0.562	NEU
nsp9	1	94	L	1.330	MIN	L	1.294	MIN
nsp9	1	95	N	0.714	NEU	N	0.117	NEU
nsp9	1	96	N	0.834	NEU	N	1.008	MIN
nsp9	1	97	L	0.714	NEU	L	-0.777	NEU
nsp9	1	98	H	0.663	NEU	N	-0.819	NEU
nsp9	1	99	R	1.330	NEU	R	-0.536	NEU
nsp9	1	100	G	1.330	NEU	G	-0.63	NEU
nsp9	1	101	Q	-0.130	NEU	M	0.742	NEU
nsp9	1	102	V	1.330	MIN	V	1.199	MIN
nsp9	1	103	L	1.330	MIN	L	1.395	MIN
nsp9	1	104	G	1.179	NEU	G	-0.215	NEU
nsp9	1	105	T	1.330	NEU	S	-0.804	NEU
nsp9	1	106	I	1.330	MIN	L	1.296	MIN
nsp9	1	107	A	0.834	NEU	A	0.231	NEU
nsp9	1	108	A	0.922	NEU	A	-0.072	NEU
nsp9	1	109	T	0.771	NEU	T	0.078	NEU
nsp9	1	110	V	0.903	MIN	V	1.379	MIN
nsp9	1	111	R	0.397	MIN	R	1.566	MIN
nsp9	1	112	L	0.771	MIN	L	1.277	MIN
nsp9	1	113	Q	1.072	NEU	Q	-0.736	NEU
nsp10	1	1	A	0.020	NEU	A	0.676	NEU
nsp10	1	2	F	0.476	NEU	F	0.699	NEU
nsp10	1	3	A	0.691	NEU	A	0.657	NEU
nsp10	1	4	V	0.715	NEU	V	0.627	NEU
nsp10	1	5	D	0.856	NEU	D	-0.754	NEU
nsp10	1	6	P	0.137	MAX	A	0.728	NEU
nsp10	1	7	A	0.126	NEU	A	0.634	NEU
nsp10	1	8	K	0.341	NEU	K	-1.146	MAX
nsp10	1	9	A	1.325	NEU	A	0.125	NEU
nsp10	1	10	Y	1.039	NEU	Y	-0.368	NEU
nsp10	1	11	K	-0.177	NEU	K	-1.161	MAX
nsp10	1	12	D	0.656	NEU	D	-0.464	NEU
nsp10	1	13	Y	-0.124	MAX	Y	-1.115	MAX
nsp10	1	14	L	0.325	MIN	L	-0.184	NEU
nsp10	1	15	N	0.355	NEU	A	0.049	NEU
nsp10	1	16	S	1.156	NEU	S	0.08	NEU
nsp10	1	17	G	1.039	NEU	G	-0.415	NEU
nsp10	1	18	G	1.325	NEU	G	-0.173	NEU
nsp10	1	19	A	-0.036	NEU	Q	-1.261	MAX
nsp10	1	20	P	1.039	NEU	P	-0.563	NEU
nsp10	1	21	I	1.325	MIN	I	1.66	MIN
nsp10	1	22	T	0.872	NEU	T	-0.063	NEU
nsp10	1	23	N	1.325	NEU	N	-0.15	NEU

nsp10	1	24	C	1.325	MIN	C	1.77	MIN
nsp10	1	25	V	1.325	MIN	V	0.786	MIN
nsp10	1	26	K	1.156	NEU	K	-0.301	NEU
nsp10	1	27	M	1.156	MIN	M	0.736	NEU
nsp10	1	28	L	1.156	NEU	L	-0.618	NEU
nsp10	1	29	T	0.354	NEU	C	2.427	MIN
nsp10	1	30	P	0.872	NEU	T	0.226	NEU
nsp10	1	31	H	-0.215	NEU	H	0.544	NEU
nsp10	1	32	T	0.656	NEU	T	0.516	NEU
nsp10	1	33	G	1.156	NEU	G	0.146	NEU
nsp10	1	34	T	0.415	NEU	T	0.683	NEU
nsp10	1	35	G	1.325	NEU	G	0.157	NEU
nsp10	1	36	I	0.415	MIN	Q	-0.526	NEU
nsp10	1	37	A	1.325	NEU	A	0.281	NEU
nsp10	1	38	I	1.325	MIN	I	0.94	MIN
nsp10	1	39	T	0.656	NEU	T	0.651	NEU
nsp10	1	40	V	0.203	MIN	V	1.48	MIN
nsp10	1	41	K	-0.030	NEU	T	1.033	MIN
nsp10	1	42	P	0.941	NEU	P	-0.396	NEU
nsp10	1	43	E	0.349	NEU	E	-0.916	NEU
nsp10	1	44	A	1.156	NEU	A	-0.483	NEU
nsp10	1	45	N	0.354	MIN	N	0.733	NEU
nsp10	1	46	A	-0.205	NEU	M	-0.556	NEU
nsp10	1	47	D	0.396	NEU	D	-0.652	NEU
nsp10	1	48	Q	1.325	NEU	Q	-0.904	NEU
nsp10	1	49	E	0.781	NEU	E	-0.862	NEU
nsp10	1	50	S	1.325	NEU	S	-0.542	NEU
nsp10	1	51	F	1.325	MIN	F	0.975	MIN
nsp10	1	52	G	1.325	NEU	G	-0.133	NEU
nsp10	1	53	G	1.325	NEU	G	-0.006	NEU
nsp10	1	54	A	1.156	NEU	A	0.347	NEU
nsp10	1	55	S	1.325	NEU	S	-0.334	NEU
nsp10	1	56	C	1.325	MIN	C	1.184	MIN
nsp10	1	57	C	1.325	MIN	C	1.783	MIN
nsp10	1	58	L	1.325	MIN	L	1.329	MIN
nsp10	1	59	Y	0.261	MAX	Y	-0.483	NEU
nsp10	1	60	C	1.325	MIN	C	1.163	MIN
nsp10	1	61	R	1.156	NEU	R	-0.598	NEU
nsp10	1	62	C	1.325	MIN	C	1.3	MIN
nsp10	1	63	H	1.325	NEU	H	-0.261	NEU
nsp10	1	64	I	1.325	MIN	I	2.531	MIN
nsp10	1	65	E	-0.114	NEU	D	0.702	NEU
nsp10	1	66	H	0.781	NEU	H	0.144	NEU
nsp10	1	67	P	0.288	MIN	P	0.404	NEU
nsp10	1	68	D	0.444	NEU	N	-0.232	NEU
nsp10	1	69	V	-0.118	MIN	P	1.113	MIN

nsp10	1	70	S	0.288	NEU	K	0.198	NEU
nsp10	1	71	G	0.856	NEU	G	-0.368	NEU
nsp10	1	72	V	0.556	NEU	F	-1.308	MAX
nsp10	1	73	C	1.325	MIN	C	1.779	MIN
nsp10	1	74	K	0.341	MIN	D	0.941	MIN
nsp10	1	75	Y	0.715	MIN	L	1.095	MIN
nsp10	1	76	K	0.656	MAX	K	-1.804	MAX
nsp10	1	77	G	1.325	NEU	G	-0.641	NEU
nsp10	1	78	K	0.656	MAX	K	-1.469	MAX
nsp10	1	79	F	1.039	MIN	Y	0.563	NEU
nsp10	1	80	V	1.325	MIN	V	0.985	MIN
nsp10	1	81	Q	1.325	NEU	Q	-0.835	NEU
nsp10	1	82	I	1.325	MIN	I	0.88	MIN
nsp10	1	83	P	0.715	NEU	P	-0.942	NEU
nsp10	1	84	T	0.476	NEU	T	0.423	NEU
nsp10	1	85	Q	0.184	NEU	T	-0.417	NEU
nsp10	1	86	C	0.468	MIN	C	1.791	MIN
nsp10	1	87	V	0.341	NEU	A	0.163	NEU
nsp10	1	88	N	0.691	NEU	N	0.515	NEU
nsp10	1	89	D	0.556	MAX	D	-1.11	MAX
nsp10	1	90	P	1.325	NEU	P	-0.629	NEU
nsp10	1	91	V	1.325	MIN	V	1.221	MIN
nsp10	1	92	G	1.325	NEU	G	-0.487	NEU
nsp10	1	93	F	1.325	MIN	F	1.331	MIN
nsp10	1	94	C	0.514	MIN	T	-0.511	NEU
nsp10	1	95	L	1.325	MIN	L	1.13	MIN
nsp10	1	96	R	0.007	NEU	K	0.17	NEU
nsp10	1	97	N	0.656	MAX	N	-1.152	MAX
nsp10	1	98	T	0.325	MIN	T	-0.114	NEU
nsp10	1	99	V	0.856	NEU	V	0.402	NEU
nsp10	1	100	C	1.325	MIN	C	1.338	MIN
nsp10	1	101	N	0.941	NEU	T	-0.615	NEU
nsp10	1	102	V	0.415	MIN	V	1.116	MIN
nsp10	1	103	C	1.325	MIN	C	1.083	MIN
nsp10	1	104	Q	0.514	NEU	G	-0.583	NEU
nsp10	1	105	M	0.415	NEU	M	0.304	NEU
nsp10	1	106	W	0.856	MIN	W	0.805	MIN
nsp10	1	107	K	-0.012	MAX	K	-1.258	MAX
nsp10	1	108	G	1.325	NEU	G	0.069	NEU
nsp10	1	109	Y	0.370	NEU	Y	-0.835	NEU
nsp10	1	110	G	1.325	NEU	G	-0.198	NEU
nsp10	1	111	C	1.325	MIN	C	1.348	MIN
nsp10	1	112	N	0.781	NEU	S	-0.771	NEU
nsp10	1	113	C	1.325	MIN	C	1.457	MIN
nsp10	1	114	D	-0.042	NEU	D	1.659	MIN
nsp10	1	115	S	0.370	NEU	Q	1.077	MIN

nsp10	1	116	L	1.032	MIN	L	0.895	MIN
nsp10	1	117	R	0.012	NEU	R	1.633	MIN
nsp10	1	118	E	0.347	NEU	E	0.077	NEU
nsp10	1	119	P	0.199	NEU	P	0.564	NEU
nsp10	1	120	M	0.764	NEU	M	0.069	NEU
nsp10	1	121	L	0.705	NEU	L	-0.876	NEU
nsp10	1	122	Q	1.032	NEU	Q	0.796	MIN
nsp12	1	1	-	0.121	MIN	A	0.553	NEU
nsp12	1	2	T	0.368	NEU	Q	-0.874	NEU
nsp12	1	3	N	0.539	MIN	S	0.456	NEU
nsp12	1	4	F	1.032	MIN	F	1.182	MIN
nsp12	1	5	L	1.152	MIN	L	1.397	MIN
nsp12	1	6	N	0.856	NEU	N	-0.549	NEU
nsp12	1	7	R	1.039	NEU	R	-0.172	NEU
nsp12	1	8	V	1.156	MIN	V	1.097	MIN
nsp12	1	9	R	0.781	NEU	C	2.173	MIN
nsp12	1	10	G	1.039	NEU	G	-0.202	NEU
nsp12	1	11	T	0.618	NEU	V	-0.451	NEU
nsp12	1	12	S	0.514	NEU	S	-0.175	NEU
nsp12	1	13	V	0.494	NEU	A	-1.027	MAX
nsp12	1	14	A	0.182	MIN	A	0.267	NEU
nsp12	1	15	R	1.325	MIN	R	2.494	MIN
nsp12	1	16	L	1.325	MIN	L	1.403	MIN
nsp12	1	17	V	-0.114	MIN	T	-0.109	NEU
nsp12	1	18	P	1.325	NEU	P	-0.277	NEU
nsp12	1	19	C	0.618	MIN	C	0.212	NEU
nsp12	1	20	A	0.656	NEU	G	0.621	NEU
nsp12	1	21	S	0.332	NEU	T	-0.795	NEU
nsp12	1	22	G	0.715	NEU	G	0.16	NEU
nsp12	1	23	L	0.603	MIN	T	-0.581	NEU
nsp12	1	24	S	-0.003	NEU	S	0.651	NEU
nsp12	1	25	T	0.656	NEU	T	-0.666	NEU
nsp12	1	26	D	1.325	MAX	D	-1.349	MAX
nsp12	1	27	V	1.325	MIN	V	1.532	MIN
nsp12	1	28	V	1.325	NEU	V	-0.749	NEU
nsp12	1	29	L	0.096	MIN	Y	-0.842	NEU
nsp12	1	30	R	1.325	NEU	R	-0.684	NEU
nsp12	1	31	A	1.325	NEU	A	0.076	NEU
nsp12	1	32	F	0.415	MIN	F	0.991	MIN
nsp12	1	33	D	1.325	MAX	D	-1.206	MAX
nsp12	1	34	I	1.325	MIN	I	1.426	MIN
nsp12	1	35	C	-0.083	MIN	Y	-2.325	MAX
nsp12	1	36	N	0.332	MAX	N	-1.634	MAX
nsp12	1	37	A	0.577	NEU	D	0	NEU
nsp12	1	38	K	0.781	MIN	K	0.827	MIN
nsp12	1	39	V	0.327	NEU	V	1.003	MIN

nsp12	1	40	A	1.325	NEU	A	-0.602	NEU
nsp12	1	41	G	1.325	NEU	G	-0.397	NEU
nsp12	1	42	I	1.325	MIN	F	0.785	MIN
nsp12	1	43	G	1.325	NEU	A	0.206	NEU
nsp12	1	44	L	0.106	MIN	K	-1.407	MAX
nsp12	1	45	H	-0.219	MAX	F	0.319	NEU
nsp12	1	46	Y	-0.191	MIN	L	1.196	MIN
nsp12	1	47	K	1.325	MAX	K	-1.77	MAX
nsp12	1	48	T	-0.126	NEU	T	-0.012	NEU
nsp12	1	49	N	0.941	NEU	N	0.18	NEU
nsp12	1	50	C	0.476	MIN	C	1.406	MIN
nsp12	1	51	C	1.325	MIN	C	2.261	MIN
nsp12	1	52	R	1.325	NEU	R	-0.531	NEU
nsp12	1	53	F	1.156	MIN	F	1.354	MIN
nsp12	1	54	Q	-0.233	MAX	Q	-0.842	NEU
nsp12	1	55	E	0.355	NEU	E	-1.035	MAX
nsp12	1	56	L	0.476	MIN	K	0.786	MIN
nsp12	1	57	D	0.055	NEU	D	-0.074	NEU
nsp12	1	58	E	0.577	MIN	E	1.311	MIN
nsp12	1	59	D	-0.248	MAX	D	1.059	MIN
nsp12	1	60	G	1.156	NEU	D	1.614	MIN
nsp12	1	61	N	-0.036	NEU	N	0.823	MIN
nsp12	1	62	K	0.319	NEU	L	-0.357	NEU
nsp12	1	63	L	1.156	NEU	I	-0.8	NEU
nsp12	1	64	D	1.156	NEU	D	-0.571	NEU
nsp12	1	65	S	1.039	NEU	S	-0.781	NEU
nsp12	1	66	Y	1.039	MIN	Y	0.949	MIN
nsp12	1	67	F	1.325	MIN	F	1.037	MIN
nsp12	1	68	V	1.325	MIN	V	1.313	MIN
nsp12	1	69	V	1.325	MIN	V	1.204	MIN
nsp12	1	70	K	0.514	MAX	K	-1.654	MAX
nsp12	1	71	R	1.325	NEU	R	-0.558	NEU
nsp12	1	72	H	0.341	NEU	H	1.328	MIN
nsp12	1	73	T	0.603	NEU	T	0.069	NEU
nsp12	1	74	L	1.039	NEU	F	-0.336	NEU
nsp12	1	75	E	0.442	NEU	S	0.605	NEU
nsp12	1	76	N	0.656	NEU	N	-0.085	NEU
nsp12	1	77	Y	0.941	MAX	Y	-2.568	MAX
nsp12	1	78	N	-0.030	NEU	Q	0.661	NEU
nsp12	1	79	L	0.137	NEU	H	1.117	MIN
nsp12	1	80	E	0.656	MAX	E	-1.389	MAX
nsp12	1	81	K	0.216	NEU	E	-1.451	MAX
nsp12	1	82	E	0.441	NEU	T	0.349	NEU
nsp12	1	83	C	1.156	MIN	I	2.032	MIN
nsp12	1	84	Y	0.872	NEU	Y	0.094	NEU
nsp12	1	85	E	0.288	MIN	N	-0.834	NEU

nsp12	1	86	L	0.415	MIN	L	1.307	MIN
nsp12	1	87	L	0.856	MIN	L	1.396	MIN
nsp12	1	88	K	0.552	NEU	K	-1.192	MAX
nsp12	1	89	D	0.514	NEU	D	0.189	NEU
nsp12	1	90	C	0.872	MIN	C	1.173	MIN
nsp12	1	91	G	0.055	MIN	P	1.165	MIN
nsp12	1	92	V	0.332	MIN	A	0.104	NEU
nsp12	1	93	V	1.325	MIN	V	0.964	MIN
nsp12	1	94	A	0.715	MIN	A	0.791	MIN
nsp12	1	95	E	0.514	NEU	K	-0.709	NEU
nsp12	1	96	H	1.325	NEU	H	-0.283	NEU
nsp12	1	97	D	1.325	NEU	D	-0.43	NEU
nsp12	1	98	F	0.856	NEU	F	-0.542	NEU
nsp12	1	99	F	1.325	MIN	F	1.758	MIN
nsp12	1	100	T	-0.057	NEU	K	-1.944	MAX
nsp12	1	101	F	1.325	MIN	F	1.453	MIN
nsp12	1	102	D	-0.068	MIN	R	1.522	MIN
nsp12	1	103	V	1.039	MIN	I	2.194	MIN
nsp12	1	104	D	-0.101	NEU	D	0.981	MIN
nsp12	1	105	G	0.514	NEU	G	-0.484	NEU
nsp12	1	106	S	-0.169	MIN	D	-1.452	MAX
nsp12	1	107	M	0.114	NEU	M	0.629	NEU
nsp12	1	108	V	0.328	MIN	V	0.833	MIN
nsp12	1	109	P	1.164	NEU	P	-0.099	NEU
nsp12	1	110	H	1.327	NEU	H	0.143	NEU
nsp12	1	111	I	0.735	MIN	I	0.581	NEU
nsp12	1	112	V	0.386	MIN	S	-0.468	NEU
nsp12	1	113	R	1.164	NEU	R	-0.694	NEU
nsp12	1	114	Q	0.463	NEU	Q	-0.965	NEU
nsp12	1	115	R	0.211	NEU	R	0.766	NEU
nsp12	1	116	L	1.050	MIN	L	1.124	MIN
nsp12	1	117	T	1.327	NEU	T	-0.303	NEU
nsp12	1	118	K	0.353	MIN	K	0.917	MIN
nsp12	1	119	Y	0.434	NEU	Y	0.015	NEU
nsp12	1	120	T	1.327	NEU	T	-0.187	NEU
nsp12	1	121	M	0.386	MIN	M	0.836	MIN
nsp12	1	122	A	0.327	MIN	A	0.468	NEU
nsp12	1	123	D	0.535	MAX	D	-1.066	MAX
nsp12	1	124	L	1.327	MIN	L	1.567	MIN
nsp12	1	125	V	1.327	MIN	V	1.155	MIN
nsp12	1	126	Y	1.164	NEU	Y	-0.168	NEU
nsp12	1	127	A	0.408	NEU	A	-0.19	NEU
nsp12	1	128	L	1.327	MIN	L	1.326	MIN
nsp12	1	129	R	1.327	NEU	R	-0.489	NEU
nsp12	1	130	H	1.327	NEU	H	-0.157	NEU
nsp12	1	131	F	0.353	NEU	F	0.574	NEU

nsp12	1	132	D	0.497	NEU	D	0.388	NEU
nsp12	1	133	R	0.030	NEU	E	-0.732	NEU
nsp12	1	134	N	0.677	MIN	G	0.356	NEU
nsp12	1	135	N	0.327	MIN	N	0.23	NEU
nsp12	1	136	C	1.326	MIN	C	1.9	MIN
nsp12	1	137	E	0.368	MIN	D	0.946	MIN
nsp12	1	138	T	0.209	MIN	T	-0.048	NEU
nsp12	1	139	L	1.327	MIN	L	1.397	MIN
nsp12	1	140	K	0.027	MAX	K	-0.857	NEU
nsp12	1	141	E	0.578	NEU	E	-0.567	NEU
nsp12	1	142	I	1.327	MIN	I	2.054	MIN
nsp12	1	143	L	1.327	MIN	L	1.485	MIN
nsp12	1	144	V	0.386	MIN	V	0.345	NEU
nsp12	1	145	L	0.239	NEU	T	0.423	NEU
nsp12	1	146	Y	0.735	NEU	Y	0.417	NEU
nsp12	1	147	G	0.158	NEU	N	0.25	NEU
nsp12	1	148	C	0.408	MIN	C	1.852	MIN
nsp12	1	149	C	1.327	MIN	C	2.059	MIN
nsp12	1	150	D	0.361	MAX	D	-1.287	MAX
nsp12	1	151	E	-0.083	NEU	D	-0.587	NEU
nsp12	1	152	S	0.386	MIN	D	1.264	MIN
nsp12	1	153	Y	0.423	MAX	Y	-2.179	MAX
nsp12	1	154	F	0.463	MIN	F	0.194	NEU
nsp12	1	155	D	1.050	NEU	N	0.088	NEU
nsp12	1	156	K	0.192	NEU	K	0.905	MIN
nsp12	1	157	K	0.677	MIN	K	1.014	MIN
nsp12	1	158	D	0.408	NEU	D	0.18	NEU
nsp12	1	159	W	0.386	NEU	W	-0.879	NEU
nsp12	1	160	Y	0.161	MAX	Y	-1.199	MAX
nsp12	1	161	D	1.327	NEU	D	-0.407	NEU
nsp12	1	162	F	0.535	MIN	F	1.102	MIN
nsp12	1	163	V	1.050	MIN	V	1.098	MIN
nsp12	1	164	E	0.714	NEU	E	0.149	NEU
nsp12	1	165	N	1.327	NEU	N	-0.637	NEU
nsp12	1	166	P	1.164	NEU	P	-0.489	NEU
nsp12	1	167	D	0.434	NEU	D	0.69	NEU
nsp12	1	168	I	1.327	MIN	I	1.898	MIN
nsp12	1	169	I	1.327	MIN	L	1.225	MIN
nsp12	1	170	N	0.408	MIN	R	0.773	NEU
nsp12	1	171	V	1.327	MIN	V	1.257	MIN
nsp12	1	172	Y	1.050	NEU	Y	0.22	NEU
nsp12	1	173	H	0.535	MAX	A	0.306	NEU
nsp12	1	174	K	0.800	NEU	N	-0.294	NEU
nsp12	1	175	L	1.327	MIN	L	1.395	MIN
nsp12	1	176	G	1.327	NEU	G	-0.788	NEU
nsp12	1	177	E	0.126	NEU	E	-0.958	NEU

nsp12	1	178	I	0.341	NEU	R	-0.095	NEU
nsp12	1	179	V	1.327	MIN	V	1.297	MIN
nsp12	1	180	R	0.386	NEU	R	-0.443	NEU
nsp12	1	181	R	0.386	NEU	Q	-1.157	MAX
nsp12	1	182	A	1.327	NEU	A	-0.142	NEU
nsp12	1	183	L	1.050	MIN	L	1.128	MIN
nsp12	1	184	L	0.955	MIN	L	1.039	MIN
nsp12	1	185	N	0.577	NEU	K	-1.317	MAX
nsp12	1	186	T	0.873	NEU	T	-0.463	NEU
nsp12	1	187	V	0.353	MIN	V	1.633	MIN
nsp12	1	188	K	0.126	NEU	Q	-0.837	NEU
nsp12	1	189	F	0.677	MIN	F	0.746	NEU
nsp12	1	190	A	0.463	MIN	C	0.959	MIN
nsp12	1	191	D	0.304	NEU	D	0.746	NEU
nsp12	1	192	A	0.890	NEU	A	0.348	NEU
nsp12	1	193	M	0.624	MIN	M	0.701	NEU
nsp12	1	194	V	0.677	MIN	R	-0.465	NEU
nsp12	1	195	E	0.328	NEU	N	-0.459	NEU
nsp12	1	196	A	0.199	MIN	A	0.719	NEU
nsp12	1	197	G	1.327	NEU	G	-0.004	NEU
nsp12	1	198	L	1.327	MIN	I	1.383	MIN
nsp12	1	199	V	1.327	MIN	V	1.184	MIN
nsp12	1	200	G	1.327	NEU	G	-0.451	NEU
nsp12	1	201	V	1.327	MIN	V	1.719	MIN
nsp12	1	202	L	1.327	MIN	L	0.972	MIN
nsp12	1	203	T	1.327	NEU	T	-0.364	NEU
nsp12	1	204	L	1.327	MIN	L	1.175	MIN
nsp12	1	205	D	1.164	MAX	D	-1.331	MAX
nsp12	1	206	N	1.050	NEU	N	-0.958	NEU
nsp12	1	207	Q	0.341	NEU	Q	-1.013	MAX
nsp12	1	208	D	0.368	NEU	D	-0.961	NEU
nsp12	1	209	L	1.327	MIN	L	1.362	MIN
nsp12	1	210	N	-0.072	MIN	N	1.043	MIN
nsp12	1	211	G	1.327	NEU	G	-0.481	NEU
nsp12	1	212	K	0.535	NEU	N	-0.051	NEU
nsp12	1	213	W	0.604	NEU	W	0.463	NEU
nsp12	1	214	Y	0.714	MAX	Y	-2.02	MAX
nsp12	1	215	D	0.497	NEU	D	-0.868	NEU
nsp12	1	216	F	0.328	MIN	F	0.494	NEU
nsp12	1	217	G	1.327	NEU	G	-0.504	NEU
nsp12	1	218	D	1.164	NEU	D	0.165	NEU
nsp12	1	219	F	1.327	MIN	F	1.297	MIN
nsp12	1	220	V	1.327	MIN	I	2.184	MIN
nsp12	1	221	I	-0.080	MIN	Q	-0.648	NEU
nsp12	1	222	T	0.873	NEU	T	-0.369	NEU
nsp12	1	223	A	0.034	NEU	T	0.521	NEU

nsp12	1	224	P	0.333	MAX	P	-0.458	NEU
nsp12	1	225	G	0.497	NEU	G	0.701	NEU
nsp12	1	226	C	0.577	NEU	S	-0.121	NEU
nsp12	1	227	G	1.327	NEU	G	-0.041	NEU
nsp12	1	228	V	1.327	MIN	V	1.673	MIN
nsp12	1	229	A	0.126	NEU	P	-1.118	MAX
nsp12	1	230	V	1.327	MIN	V	1.388	MIN
nsp12	1	231	V	0.341	MIN	V	1.488	MIN
nsp12	1	232	D	0.735	MAX	D	-0.63	NEU
nsp12	1	233	S	1.327	NEU	S	-0.577	NEU
nsp12	1	234	Y	0.333	MIN	Y	0.666	NEU
nsp12	1	235	Y	1.327	NEU	Y	-0.426	NEU
nsp12	1	236	S	1.327	NEU	S	-0.288	NEU
nsp12	1	237	Y	0.368	NEU	L	1.11	MIN
nsp12	1	238	L	0.333	NEU	L	1.344	MIN
nsp12	1	239	M	1.327	MIN	M	0.951	MIN
nsp12	1	240	P	1.327	MAX	P	-1.051	MAX
nsp12	1	241	M	1.164	MIN	I	1.312	MIN
nsp12	1	242	L	0.535	MIN	L	1.298	MIN
nsp12	1	243	T	1.327	NEU	T	-0.293	NEU
nsp12	1	244	M	0.408	MIN	L	1.246	MIN
nsp12	1	245	T	0.386	NEU	T	-0.325	NEU
nsp12	1	246	H	0.873	NEU	R	-0.84	NEU
nsp12	1	247	A	0.368	NEU	A	-0.425	NEU
nsp12	1	248	L	1.327	MIN	L	1.53	MIN
nsp12	1	249	A	0.192	MAX	T	-0.146	NEU
nsp12	1	250	A	1.003	NEU	A	-0.316	NEU
nsp12	1	251	E	1.164	NEU	E	0.06	NEU
nsp12	1	252	L	0.100	MIN	S	-0.666	NEU
nsp12	1	253	H	0.080	NEU	H	0.952	MIN
nsp12	1	254	-	0.120	MIN	V	1.292	MIN
nsp12	1	255	D	1.308	MIN	D	1.775	MIN
nsp12	1	256	-	-0.179	NEU	T	0.796	MIN
nsp12	1	257	D	-0.148	NEU	D	-0.932	NEU
nsp12	1	258	L	0.735	MIN	L	1.116	MIN
nsp12	1	259	N	0.100	NEU	T	0.301	NEU
nsp12	1	260	K	-0.087	NEU	K	-0.415	NEU
nsp12	1	261	P	0.735	NEU	P	0.061	NEU
nsp12	1	262	Y	0.088	NEU	Y	-2.69	MAX
nsp12	1	263	R	0.353	NEU	I	1.529	MIN
nsp12	1	264	E	0.027	MIN	K	0.482	NEU
nsp12	1	265	W	0.677	MIN	W	0.972	MIN
nsp12	1	266	D	0.192	MAX	D	-0.708	NEU
nsp12	1	267	L	0.463	NEU	L	0.454	NEU
nsp12	1	268	V	0.103	NEU	L	0.583	NEU
nsp12	1	269	Q	0.423	NEU	K	0.286	NEU

nsp12	1	270	Y	0.800	MIN	Y	0.639	NEU
nsp12	1	271	D	0.535	MAX	D	-0.895	NEU
nsp12	1	272	F	0.136	MIN	F	1.001	MIN
nsp12	1	273	T	0.497	NEU	T	0.595	NEU
nsp12	1	274	D	0.796	NEU	E	0.981	MIN
nsp12	1	275	Y	0.368	MAX	E	-0.248	NEU
nsp12	1	276	K	0.624	MAX	R	-0.477	NEU
nsp12	1	277	L	0.535	MIN	L	0.72	NEU
nsp12	1	278	E	0.345	NEU	K	1.59	MIN
nsp12	1	279	L	1.327	MIN	L	1.246	MIN
nsp12	1	280	F	0.955	MIN	F	0.955	MIN
nsp12	1	281	N	0.353	NEU	D	-0.23	NEU
nsp12	1	282	K	0.341	NEU	R	-1.049	MAX
nsp12	1	283	Y	1.164	MAX	Y	-1.384	MAX
nsp12	1	284	F	0.535	MIN	F	0.598	NEU
nsp12	1	285	K	0.463	NEU	K	-0.623	NEU
nsp12	1	286	H	0.873	NEU	Y	0.778	NEU
nsp12	1	287	W	1.327	MAX	W	-1.458	MAX
nsp12	1	288	D	0.276	NEU	D	-0.014	NEU
nsp12	1	289	M	0.209	NEU	Q	-0.709	NEU
nsp12	1	290	T	0.463	NEU	T	-0.576	NEU
nsp12	1	291	Y	1.164	MAX	Y	-1.918	MAX
nsp12	1	292	H	0.955	MIN	H	0.704	NEU
nsp12	1	293	P	0.955	NEU	P	-0.017	NEU
nsp12	1	294	N	0.497	NEU	N	-0.907	NEU
nsp12	1	295	C	0.386	MIN	C	1.672	MIN
nsp12	1	296	V	0.955	MIN	V	1.407	MIN
nsp12	1	297	N	0.577	NEU	N	0.516	NEU
nsp12	1	298	C	1.327	MIN	C	1.609	MIN
nsp12	1	299	A	-0.043	NEU	L	0.133	NEU
nsp12	1	300	D	1.050	NEU	D	-0.114	NEU
nsp12	1	301	D	1.327	NEU	D	-0.428	NEU
nsp12	1	302	R	0.873	NEU	R	0.131	NEU
nsp12	1	303	C	1.327	MIN	C	2.307	MIN
nsp12	1	304	I	1.164	MIN	I	2.124	MIN
nsp12	1	305	L	1.327	MIN	L	1.195	MIN
nsp12	1	306	H	1.327	NEU	H	-0.595	NEU
nsp12	1	307	C	1.327	MIN	C	1.608	MIN
nsp12	1	308	A	1.164	MIN	A	0.652	NEU
nsp12	1	309	N	1.327	MAX	N	-1.149	MAX
nsp12	1	310	F	1.327	MIN	F	1.37	MIN
nsp12	1	311	N	0.368	MAX	N	-0.835	NEU
nsp12	1	312	I	1.327	MIN	V	0.943	MIN
nsp12	1	313	L	1.327	MIN	L	1.264	MIN
nsp12	1	314	F	1.164	MIN	F	1.191	MIN
nsp12	1	315	S	0.873	NEU	S	-0.424	NEU

nsp12	1	316	M	0.677	MIN	T	-0.335	NEU
nsp12	1	317	V	0.535	MIN	V	1.113	MIN
nsp12	1	318	L	0.463	MIN	F	0.094	NEU
nsp12	1	319	P	1.003	NEU	P	-0.328	NEU
nsp12	1	320	N	-0.080	NEU	P	0.827	MIN
nsp12	1	321	T	1.327	NEU	T	-0.138	NEU
nsp12	1	322	C	0.327	MIN	S	-0.319	NEU
nsp12	1	323	F	0.333	NEU	F	0.975	MIN
nsp12	1	324	G	1.327	NEU	G	-0.314	NEU
nsp12	1	325	P	0.955	NEU	P	-0.896	NEU
nsp12	1	326	L	1.327	MIN	L	0.838	MIN
nsp12	1	327	V	1.327	MIN	V	1.802	MIN
nsp12	1	328	R	0.577	NEU	R	-0.787	NEU
nsp12	1	329	K	0.408	MAX	K	-1.649	MAX
nsp12	1	330	I	1.327	MIN	I	2.061	MIN
nsp12	1	331	F	0.463	NEU	F	0.401	NEU
nsp12	1	332	V	1.327	MIN	V	1.496	MIN
nsp12	1	333	D	0.577	NEU	D	0.085	NEU
nsp12	1	334	G	1.327	NEU	G	-0.037	NEU
nsp12	1	335	V	1.327	MIN	V	0.684	NEU
nsp12	1	336	P	0.873	NEU	P	-0.668	NEU
nsp12	1	337	F	1.164	MIN	F	0.709	NEU
nsp12	1	338	V	1.327	MIN	V	1.657	MIN
nsp12	1	339	V	1.327	MIN	V	1.175	MIN
nsp12	1	340	S	1.327	NEU	S	-0.571	NEU
nsp12	1	341	I	0.386	MIN	T	-0.334	NEU
nsp12	1	342	G	1.327	NEU	G	-0.586	NEU
nsp12	1	343	Y	0.955	MIN	Y	0.714	NEU
nsp12	1	344	H	1.327	NEU	H	-0.142	NEU
nsp12	1	345	Y	0.333	MIN	F	1.141	MIN
nsp12	1	346	K	0.386	MAX	R	-0.567	NEU
nsp12	1	347	E	1.327	MAX	E	-1.416	MAX
nsp12	1	348	L	1.327	MIN	L	1.215	MIN
nsp12	1	349	G	1.327	NEU	G	-0.369	NEU
nsp12	1	350	V	1.327	MIN	V	1.177	MIN
nsp12	1	351	V	1.327	MIN	V	1.142	MIN
nsp12	1	352	M	0.463	NEU	H	-0.558	NEU
nsp12	1	353	N	1.050	NEU	N	-0.955	NEU
nsp12	1	354	M	0.199	MAX	Q	0.265	NEU
nsp12	1	355	D	1.327	MIN	D	1.764	MIN
nsp12	1	356	V	0.624	MIN	V	0.238	NEU
nsp12	1	357	D	0.714	NEU	N	-0.605	NEU
nsp12	1	358	T	-0.024	NEU	L	0.896	MIN
nsp12	1	359	H	0.328	MIN	H	0.762	NEU
nsp12	1	360	R	0.222	NEU	S	-0.469	NEU
nsp12	1	361	Y	0.114	MAX	S	0.585	NEU

nsp12	1	362	R	1.327	MIN	R	2.058	MIN
nsp12	1	363	L	1.327	MIN	L	1.137	MIN
nsp12	1	364	S	1.164	NEU	S	-0.179	NEU
nsp12	1	365	L	0.735	MIN	F	0.329	NEU
nsp12	1	366	K	0.577	NEU	K	-1.319	MAX
nsp12	1	367	E	1.327	NEU	E	-0.855	NEU
nsp12	1	368	L	1.327	MIN	L	1.268	MIN
nsp12	1	369	L	0.497	MIN	L	1.572	MIN
nsp12	1	370	V	0.624	MIN	V	1.381	MIN
nsp12	1	371	Y	1.327	NEU	Y	0.391	NEU
nsp12	1	372	A	0.497	NEU	A	0.269	NEU
nsp12	1	373	A	0.624	NEU	A	0.448	NEU
nsp12	1	374	D	1.327	MAX	D	-1.116	MAX
nsp12	1	375	P	0.873	NEU	P	-0.982	NEU
nsp12	1	376	A	0.497	MIN	A	0.739	NEU
nsp12	1	377	M	1.327	MIN	M	0.847	MIN
nsp12	1	378	H	1.164	NEU	H	-0.495	NEU
nsp12	1	379	V	0.677	MIN	A	0.514	NEU
nsp12	1	380	A	1.164	NEU	A	0.241	NEU
nsp12	1	381	S	1.327	NEU	S	-0.705	NEU
nsp12	1	382	A	0.535	NEU	G	-0.72	NEU
nsp12	1	383	N	1.164	NEU	N	-0.501	NEU
nsp12	1	384	A	0.423	NEU	L	1.288	MIN
nsp12	1	385	L	1.164	MIN	L	1.342	MIN
nsp12	1	386	L	0.239	NEU	L	-0.568	NEU
nsp12	1	387	D	-0.087	MAX	D	-1.079	MAX
nsp12	1	388	L	0.955	MIN	K	1.198	MIN
nsp12	1	389	R	0.382	MIN	R	1.562	MIN
nsp12	1	390	T	1.327	NEU	T	-0.479	NEU
nsp12	1	391	C	0.027	NEU	T	0.166	NEU
nsp12	1	392	C	1.164	MIN	C	1.554	MIN
nsp12	1	393	F	0.677	MIN	F	0.419	NEU
nsp12	1	394	S	1.327	NEU	S	-0.779	NEU
nsp12	1	395	V	1.327	MIN	V	1.673	MIN
nsp12	1	396	A	0.353	NEU	A	0.865	MIN
nsp12	1	397	A	0.434	NEU	A	0.529	NEU
nsp12	1	398	L	1.050	MIN	L	0.461	NEU
nsp12	1	399	T	1.050	NEU	T	0.283	NEU
nsp12	1	400	T	0.201	NEU	N	-0.127	NEU
nsp12	1	401	G	0.380	NEU	N	-0.519	NEU
nsp12	1	402	V	0.800	MIN	V	1.042	MIN
nsp12	1	403	T	-0.249	MIN	A	-1.015	MAX
nsp12	1	404	F	0.327	MIN	F	1.057	MIN
nsp12	1	405	Q	0.735	NEU	Q	-0.919	NEU
nsp12	1	406	T	0.184	NEU	T	0.17	NEU
nsp12	1	407	V	0.800	MIN	V	1.368	MIN

nsp12	1	408	K	0.434	MIN	K	0.611	NEU
nsp12	1	409	P	0.434	NEU	P	-0.684	NEU
nsp12	1	410	G	1.327	NEU	G	-0.359	NEU
nsp12	1	411	N	0.535	NEU	N	-0.966	NEU
nsp12	1	412	F	1.327	MIN	F	1.455	MIN
nsp12	1	413	N	1.327	NEU	N	-0.54	NEU
nsp12	1	414	Q	0.497	NEU	K	-1.03	MAX
nsp12	1	415	D	1.327	NEU	D	-0.589	NEU
nsp12	1	416	F	1.327	MIN	F	1.218	MIN
nsp12	1	417	Y	1.327	NEU	Y	-0.145	NEU
nsp12	1	418	D	0.368	MAX	D	-1.043	MAX
nsp12	1	419	F	0.577	NEU	F	-0.339	NEU
nsp12	1	420	A	0.368	MIN	A	0.366	NEU
nsp12	1	421	V	1.164	MIN	V	0.825	MIN
nsp12	1	422	S	0.677	NEU	S	-0.169	NEU
nsp12	1	423	K	0.318	MAX	K	-1.133	MAX
nsp12	1	424	G	1.050	NEU	G	-0.615	NEU
nsp12	1	425	F	1.050	MIN	F	0.656	NEU
nsp12	1	426	F	1.164	MIN	F	1.009	MIN
nsp12	1	427	K	1.327	MAX	K	-1.78	MAX
nsp12	1	428	E	1.327	NEU	E	-0.83	NEU
nsp12	1	429	G	1.327	NEU	G	-0.157	NEU
nsp12	1	430	S	1.327	NEU	S	-0.945	NEU
nsp12	1	431	S	0.497	MIN	S	0.87	MIN
nsp12	1	432	V	1.327	MIN	V	1.254	MIN
nsp12	1	433	D	0.368	NEU	E	-0.03	NEU
nsp12	1	434	L	1.327	MIN	L	0.757	NEU
nsp12	1	435	K	0.778	NEU	K	-0.174	NEU
nsp12	1	436	H	1.327	NEU	H	-0.517	NEU
nsp12	1	437	F	1.327	MIN	F	1.423	MIN
nsp12	1	438	F	1.327	MIN	F	1.3	MIN
nsp12	1	439	F	-0.166	NEU	F	0.274	NEU
nsp12	1	440	A	0.800	NEU	A	-0.91	NEU
nsp12	1	441	Q	1.327	NEU	Q	-0.72	NEU
nsp12	1	442	D	0.624	NEU	D	-0.966	NEU
nsp12	1	443	G	1.164	NEU	G	-0.715	NEU
nsp12	1	444	N	1.164	NEU	N	-0.172	NEU
nsp12	1	445	A	1.327	NEU	A	0.265	NEU
nsp12	1	446	A	0.955	MIN	A	0.781	MIN
nsp12	1	447	I	0.873	MIN	I	0.913	MIN
nsp12	1	448	T	1.327	NEU	S	-0.127	NEU
nsp12	1	449	D	1.327	NEU	D	-0.468	NEU
nsp12	1	450	Y	1.164	MIN	Y	0.81	MIN
nsp12	1	451	N	1.164	NEU	D	-0.401	NEU
nsp12	1	452	Y	0.677	MAX	Y	0.12	NEU
nsp12	1	453	Y	1.050	MIN	Y	1.471	MIN

nsp12	1	454	R	0.126	NEU	R	-0.423	NEU
nsp12	1	455	Y	0.184	NEU	Y	0.432	NEU
nsp12	1	456	N	0.955	NEU	N	-0.895	NEU
nsp12	1	457	L	0.535	NEU	L	0.24	NEU
nsp12	1	458	P	1.327	MAX	P	-1.196	MAX
nsp12	1	459	T	1.327	NEU	T	-0.183	NEU
nsp12	1	460	M	1.327	MIN	M	0.894	MIN
nsp12	1	461	C	1.327	MIN	C	1.441	MIN
nsp12	1	462	D	0.735	MAX	D	-0.979	NEU
nsp12	1	463	I	1.327	MIN	I	0.963	MIN
nsp12	1	464	K	0.497	MAX	R	0.207	NEU
nsp12	1	465	Q	0.624	NEU	Q	-0.849	NEU
nsp12	1	466	L	0.624	MIN	L	1.308	MIN
nsp12	1	467	L	1.327	MIN	L	0.992	MIN
nsp12	1	468	F	0.386	MIN	F	1.231	MIN
nsp12	1	469	V	0.535	MIN	V	1.285	MIN
nsp12	1	470	L	1.327	MIN	V	1.382	MIN
nsp12	1	471	E	0.386	NEU	E	-1.16	MAX
nsp12	1	472	V	1.327	MIN	V	1.239	MIN
nsp12	1	473	V	1.327	MIN	V	1.262	MIN
nsp12	1	474	D	0.463	MAX	D	-1.202	MAX
nsp12	1	475	K	1.003	NEU	K	-0.519	NEU
nsp12	1	476	Y	1.164	NEU	Y	0.044	NEU
nsp12	1	477	F	0.735	MIN	F	0.865	MIN
nsp12	1	478	E	0.368	MIN	D	0.351	NEU
nsp12	1	479	I	1.327	MIN	C	1.593	MIN
nsp12	1	480	Y	1.327	MIN	Y	0.779	NEU
nsp12	1	481	D	0.873	MIN	D	0.746	NEU
nsp12	1	482	G	1.327	NEU	G	-0.219	NEU
nsp12	1	483	G	1.327	NEU	G	-0.541	NEU
nsp12	1	484	C	1.327	MIN	C	1.725	MIN
nsp12	1	485	I	1.327	MIN	I	0.866	MIN
nsp12	1	486	N	-0.009	NEU	N	0.611	NEU
nsp12	1	487	A	1.327	NEU	A	-0.276	NEU
nsp12	1	488	S	1.050	NEU	N	-0.374	NEU
nsp12	1	489	Q	0.408	MAX	Q	-1.06	MAX
nsp12	1	490	V	1.327	MIN	V	1.378	MIN
nsp12	1	491	I	1.164	NEU	I	0.131	NEU
nsp12	1	492	V	1.327	MIN	V	1.192	MIN
nsp12	1	493	N	-0.051	NEU	N	-0.365	NEU
nsp12	1	494	N	1.164	MIN	N	0.886	MIN
nsp12	1	495	Y	0.341	MAX	L	1.533	MIN
nsp12	1	496	D	1.327	MIN	D	2.369	MIN
nsp12	1	497	K	0.497	MAX	K	-1.32	MAX
nsp12	1	498	S	1.327	NEU	S	-0.014	NEU
nsp12	1	499	A	1.327	NEU	A	-0.063	NEU

nsp12	1	500	G	1.327	NEU	G	-0.066	NEU
nsp12	1	501	Y	0.333	MIN	F	1.045	MIN
nsp12	1	502	P	1.327	NEU	P	-0.971	NEU
nsp12	1	503	F	1.327	MIN	F	1.288	MIN
nsp12	1	504	N	1.327	NEU	N	-0.588	NEU
nsp12	1	505	K	0.873	MAX	K	-1.644	MAX
nsp12	1	506	F	0.677	MIN	W	-2.508	MAX
nsp12	1	507	G	1.327	NEU	G	-0.357	NEU
nsp12	1	508	K	1.327	MAX	K	-1.633	MAX
nsp12	1	509	A	1.327	NEU	A	0.391	NEU
nsp12	1	510	R	1.327	MIN	R	2.132	MIN
nsp12	1	511	L	1.327	MIN	L	1.217	MIN
nsp12	1	512	Y	0.328	MAX	Y	-1.223	MAX
nsp12	1	513	Y	1.327	NEU	Y	-0.177	NEU
nsp12	1	514	E	1.327	NEU	D	-0.392	NEU
nsp12	1	515	S	1.327	NEU	S	-0.865	NEU
nsp12	1	516	L	0.161	MIN	M	0.248	NEU
nsp12	1	517	S	0.955	NEU	S	0.493	NEU
nsp12	1	518	Y	0.327	NEU	Y	-2.366	MAX
nsp12	1	519	E	1.164	NEU	E	-0.831	NEU
nsp12	1	520	E	1.164	MAX	D	-1.104	MAX
nsp12	1	521	Q	1.327	NEU	Q	-0.848	NEU
nsp12	1	522	D	1.327	MAX	D	-1.734	MAX
nsp12	1	523	E	0.353	NEU	A	0.378	NEU
nsp12	1	524	L	1.164	MIN	L	1.297	MIN
nsp12	1	525	F	0.141	NEU	F	0.652	NEU
nsp12	1	526	A	0.955	NEU	A	0.386	NEU
nsp12	1	527	Y	0.604	MAX	Y	-2.1	MAX
nsp12	1	528	T	1.327	NEU	T	-0.347	NEU
nsp12	1	529	K	0.333	NEU	K	-0.643	NEU
nsp12	1	530	R	1.327	MIN	R	1.013	MIN
nsp12	1	531	N	0.577	MAX	N	-1.061	MAX
nsp12	1	532	V	1.327	MIN	V	1.101	MIN
nsp12	1	533	L	1.164	MIN	I	0.534	NEU
nsp12	1	534	P	0.341	MAX	P	-0.895	NEU
nsp12	1	535	T	1.327	NEU	T	-0.161	NEU
nsp12	1	536	I	1.164	MIN	I	1.047	MIN
nsp12	1	537	T	1.327	NEU	T	-0.11	NEU
nsp12	1	538	Q	1.327	NEU	Q	-0.753	NEU
nsp12	1	539	M	1.327	MIN	M	0.788	MIN
nsp12	1	540	N	0.873	NEU	N	-0.926	NEU
nsp12	1	541	L	1.327	MIN	L	1.362	MIN
nsp12	1	542	K	0.735	NEU	K	-0.092	NEU
nsp12	1	543	Y	0.365	MAX	Y	-2.148	MAX
nsp12	1	544	A	1.327	NEU	A	-0.61	NEU
nsp12	1	545	I	1.327	MIN	I	0.994	MIN

nsp12	1	546	S	1.327	NEU	S	-0.736	NEU
nsp12	1	547	A	0.955	MAX	A	-1.242	MAX
nsp12	1	548	K	1.327	MAX	K	-2.122	MAX
nsp12	1	549	N	1.327	NEU	N	-0.254	NEU
nsp12	1	550	R	0.955	NEU	R	0.28	NEU
nsp12	1	551	A	1.164	NEU	A	-0.461	NEU
nsp12	1	552	R	1.327	NEU	R	-0.074	NEU
nsp12	1	553	T	1.327	NEU	T	-0.471	NEU
nsp12	1	554	V	0.341	NEU	V	0.279	NEU
nsp12	1	555	A	0.955	MIN	A	0.706	NEU
nsp12	1	556	G	1.327	NEU	G	-0.102	NEU
nsp12	1	557	V	1.327	MIN	V	1.348	MIN
nsp12	1	558	S	1.327	NEU	S	-0.5	NEU
nsp12	1	559	I	1.327	MIN	I	1.415	MIN
nsp12	1	560	L	1.327	MIN	C	1.543	MIN
nsp12	1	561	S	1.327	NEU	S	-0.617	NEU
nsp12	1	562	T	1.327	NEU	T	-0.302	NEU
nsp12	1	563	M	0.386	NEU	M	0.161	NEU
nsp12	1	564	T	1.327	NEU	T	-0.217	NEU
nsp12	1	565	N	1.327	NEU	N	-0.791	NEU
nsp12	1	566	R	1.327	NEU	R	-0.797	NEU
nsp12	1	567	Q	0.800	NEU	Q	-0.908	NEU
nsp12	1	568	F	-0.225	NEU	F	1.076	MIN
nsp12	1	569	H	1.327	NEU	H	0.015	NEU
nsp12	1	570	Q	0.386	NEU	Q	-0.904	NEU
nsp12	1	571	K	1.327	MAX	K	-1.983	MAX
nsp12	1	572	M	1.327	MIN	L	0.998	MIN
nsp12	1	573	L	1.327	MIN	L	1.561	MIN
nsp12	1	574	K	1.164	MAX	K	-1.028	MAX
nsp12	1	575	S	1.327	NEU	S	-0.461	NEU
nsp12	1	576	I	1.327	MIN	I	1.686	MIN
nsp12	1	577	A	0.800	MIN	A	0.777	NEU
nsp12	1	578	A	0.497	MAX	A	-1.149	MAX
nsp12	1	579	T	1.327	NEU	T	-0.484	NEU
nsp12	1	580	R	0.327	MIN	R	0.676	NEU
nsp12	1	581	G	0.873	NEU	G	-0.73	NEU
nsp12	1	582	A	0.341	NEU	A	0.403	NEU
nsp12	1	583	T	1.327	NEU	T	-0.557	NEU
nsp12	1	584	V	1.327	MIN	V	1.233	MIN
nsp12	1	585	V	1.327	MIN	V	1.237	MIN
nsp12	1	586	I	1.327	MIN	I	1.479	MIN
nsp12	1	587	G	1.164	NEU	G	-0.595	NEU
nsp12	1	588	T	1.327	NEU	T	-0.307	NEU
nsp12	1	589	T	1.327	NEU	S	0.275	NEU
nsp12	1	590	K	1.327	NEU	K	0.278	NEU
nsp12	1	591	F	0.873	MIN	F	0.815	MIN

nsp12	1	592	Y	1.164	MAX	Y	-1.528	MAX
nsp12	1	593	G	1.327	NEU	G	-0.306	NEU
nsp12	1	594	G	1.327	NEU	G	-0.387	NEU
nsp12	1	595	W	1.327	NEU	W	-0.636	NEU
nsp12	1	596	D	0.577	NEU	H	-0.243	NEU
nsp12	1	597	D	0.353	MIN	N	-0.214	NEU
nsp12	1	598	M	0.353	MIN	M	0.62	NEU
nsp12	1	599	L	1.327	MIN	L	1.486	MIN
nsp12	1	600	R	-0.105	NEU	K	-1.576	MAX
nsp12	1	601	T	1.327	NEU	T	-0.204	NEU
nsp12	1	602	L	1.327	MIN	V	1.128	MIN
nsp12	1	603	Y	0.333	MIN	Y	0.444	NEU
nsp12	1	604	K	0.353	MAX	S	0.019	NEU
nsp12	1	605	D	0.535	MIN	D	1.389	MIN
nsp12	1	606	V	1.327	MIN	V	1.101	MIN
nsp12	1	607	D	0.353	MIN	E	0.451	NEU
nsp12	1	608	N	0.382	NEU	N	-0.357	NEU
nsp12	1	609	P	1.327	NEU	P	-0.316	NEU
nsp12	1	610	H	0.063	NEU	H	-0.284	NEU
nsp12	1	611	L	1.327	MIN	L	1.076	MIN
nsp12	1	612	M	1.327	MIN	M	0.904	MIN
nsp12	1	613	G	1.327	NEU	G	-0.482	NEU
nsp12	1	614	W	0.442	NEU	W	-0.178	NEU
nsp12	1	615	D	0.027	NEU	D	-1.707	MAX
nsp12	1	616	Y	0.470	MAX	Y	0.864	MIN
nsp12	1	617	P	0.873	NEU	P	-0.203	NEU
nsp12	1	618	K	0.735	NEU	K	-0.371	NEU
nsp12	1	619	C	1.327	MIN	C	1.531	MIN
nsp12	1	620	D	1.327	NEU	D	-0.275	NEU
nsp12	1	621	R	1.164	NEU	R	-0.505	NEU
nsp12	1	622	A	0.955	NEU	A	0.461	NEU
nsp12	1	623	M	0.368	NEU	M	0.52	NEU
nsp12	1	624	P	0.333	NEU	P	-1.004	MAX
nsp12	1	625	N	0.577	MAX	N	-1.034	MAX
nsp12	1	626	M	0.577	MIN	M	0.554	NEU
nsp12	1	627	L	1.327	MIN	L	1.072	MIN
nsp12	1	628	R	1.327	NEU	R	-0.747	NEU
nsp12	1	629	I	1.327	MIN	I	1.939	MIN
nsp12	1	630	F	1.327	MIN	M	0.832	MIN
nsp12	1	631	A	1.327	NEU	A	0.388	NEU
nsp12	1	632	S	0.577	NEU	S	-0.925	NEU
nsp12	1	633	L	1.327	MIN	L	1.314	MIN
nsp12	1	634	V	1.327	MIN	V	1.217	MIN
nsp12	1	635	L	1.164	MIN	L	1.035	MIN
nsp12	1	636	A	1.327	NEU	A	0.274	NEU
nsp12	1	637	R	1.050	MIN	R	1.263	MIN

nsp12	1	638	K	0.463	NEU	K	-1.231	MAX
nsp12	1	639	H	1.327	NEU	H	0.115	NEU
nsp12	1	640	S	0.368	NEU	T	-0.66	NEU
nsp12	1	641	T	0.677	NEU	T	-0.079	NEU
nsp12	1	642	C	1.327	MIN	C	1.291	MIN
nsp12	1	643	C	1.327	MIN	C	1.348	MIN
nsp12	1	644	S	0.497	NEU	S	0.14	NEU
nsp12	1	645	Q	0.313	NEU	L	0.421	NEU
nsp12	1	646	S	1.327	NEU	S	-0.737	NEU
nsp12	1	647	D	0.105	NEU	H	-0.762	NEU
nsp12	1	648	R	1.327	NEU	R	-0.631	NEU
nsp12	1	649	F	1.164	MIN	F	1.241	MIN
nsp12	1	650	Y	-0.001	MIN	Y	1.016	MIN
nsp12	1	651	R	0.577	MIN	R	0.149	NEU
nsp12	1	652	L	1.327	MIN	L	1.068	MIN
nsp12	1	653	A	1.327	MIN	A	0.691	NEU
nsp12	1	654	N	0.386	NEU	N	-1.008	MAX
nsp12	1	655	E	1.050	MAX	E	-1.211	MAX
nsp12	1	656	C	1.327	MIN	C	1.879	MIN
nsp12	1	657	A	1.327	NEU	A	0.401	NEU
nsp12	1	658	Q	1.327	NEU	Q	-0.887	NEU
nsp12	1	659	V	0.368	MIN	V	0.672	NEU
nsp12	1	660	L	1.050	NEU	L	0.336	NEU
nsp12	1	661	S	1.327	NEU	S	-0.398	NEU
nsp12	1	662	E	0.800	NEU	E	-0.865	NEU
nsp12	1	663	I	0.368	MIN	M	0.704	NEU
nsp12	1	664	V	1.327	MIN	V	1.567	MIN
nsp12	1	665	L	1.164	MIN	M	1.006	MIN
nsp12	1	666	C	1.164	MIN	C	1.61	MIN
nsp12	1	667	G	1.327	NEU	G	-0.416	NEU
nsp12	1	668	G	1.327	NEU	G	-0.466	NEU
nsp12	1	669	G	0.386	NEU	S	-0.558	NEU
nsp12	1	670	Y	0.368	MIN	L	1.314	MIN
nsp12	1	671	Y	0.368	NEU	Y	0.569	NEU
nsp12	1	672	V	1.327	MIN	V	1.487	MIN
nsp12	1	673	K	1.327	MAX	K	-1.289	MAX
nsp12	1	674	P	0.386	MAX	P	-1.133	MAX
nsp12	1	675	G	1.327	NEU	G	-0.168	NEU
nsp12	1	676	G	1.164	NEU	G	-0.216	NEU
nsp12	1	677	T	1.327	NEU	T	-0.147	NEU
nsp12	1	678	S	1.164	NEU	S	-0.643	NEU
nsp12	1	679	S	1.327	NEU	S	-0.254	NEU
nsp12	1	680	G	1.327	NEU	G	-0.521	NEU
nsp12	1	681	D	1.164	MAX	D	-1.269	MAX
nsp12	1	682	A	1.003	NEU	A	0.08	NEU
nsp12	1	683	T	1.327	NEU	T	-0.18	NEU

nsp12	1	684	T	1.164	NEU	T	-0.179	NEU
nsp12	1	685	A	0.890	NEU	A	0.12	NEU
nsp12	1	686	Y	0.800	MIN	Y	0.685	NEU
nsp12	1	687	A	1.164	NEU	A	0.259	NEU
nsp12	1	688	N	1.327	NEU	N	-0.635	NEU
nsp12	1	689	S	1.164	NEU	S	-0.774	NEU
nsp12	1	690	V	1.164	MIN	V	1.596	MIN
nsp12	1	691	F	1.327	MIN	F	1.273	MIN
nsp12	1	692	N	1.164	NEU	N	-0.721	NEU
nsp12	1	693	I	1.327	MIN	I	1.243	MIN
nsp12	1	694	C	1.327	MIN	C	1.048	MIN
nsp12	1	695	Q	1.045	NEU	Q	-0.781	NEU
nsp12	1	696	A	1.327	NEU	A	0.39	NEU
nsp12	1	697	V	0.577	MIN	V	1.414	MIN
nsp12	1	698	T	1.327	NEU	T	-0.192	NEU
nsp12	1	699	A	1.164	NEU	A	0.397	NEU
nsp12	1	700	N	0.577	MAX	N	-1.117	MAX
nsp12	1	701	V	1.164	MIN	V	1.32	MIN
nsp12	1	702	C	0.368	NEU	N	-0.543	NEU
nsp12	1	703	A	0.873	NEU	A	0.379	NEU
nsp12	1	704	L	1.327	MIN	L	1.161	MIN
nsp12	1	705	M	1.003	MIN	L	1.045	MIN
nsp12	1	706	S	1.327	NEU	S	-0.58	NEU
nsp12	1	707	C	0.535	MIN	T	-0.294	NEU
nsp12	1	708	N	1.164	NEU	D	-0.498	NEU
nsp12	1	709	G	0.955	NEU	G	-0.632	NEU
nsp12	1	710	N	1.050	NEU	N	0.13	NEU
nsp12	1	711	K	0.328	NEU	K	0.74	NEU
nsp12	1	712	I	1.327	MIN	I	1.814	MIN
nsp12	1	713	E	-0.133	NEU	A	-0.812	NEU
nsp12	1	714	D	0.423	NEU	D	-1.059	MAX
nsp12	1	715	L	0.237	NEU	K	-1.923	MAX
nsp12	1	716	Y	0.031	MAX	Y	-1.575	MAX
nsp12	1	717	I	1.327	MIN	V	1.283	MIN
nsp12	1	718	R	0.333	NEU	R	0.129	NEU
nsp12	1	719	D	1.327	NEU	N	-0.517	NEU
nsp12	1	720	L	0.955	MIN	L	1.427	MIN
nsp12	1	721	Q	0.368	MAX	Q	-0.984	NEU
nsp12	1	722	K	0.027	NEU	H	0.223	NEU
nsp12	1	723	R	0.136	NEU	R	0.303	NEU
nsp12	1	724	L	1.327	MIN	L	1.305	MIN
nsp12	1	725	Y	0.199	NEU	Y	0.709	NEU
nsp12	1	726	S	-0.105	NEU	E	-1.322	MAX
nsp12	1	727	N	0.058	NEU	C	2.144	MIN
nsp12	1	728	V	1.327	MIN	L	1.153	MIN
nsp12	1	729	Y	0.333	MAX	Y	-1.242	MAX

nsp12	1	730	R	0.624	NEU	R	0.496	NEU
nsp12	1	731	S	0.796	NEU	N	-0.396	NEU
nsp12	1	732	D	0.386	MIN	R	1.896	MIN
nsp12	1	733	T	-0.152	MIN	D	1.393	MIN
nsp12	1	734	V	0.242	MIN	V	1.141	MIN
nsp12	1	735	D	0.408	NEU	D	-0.436	NEU
nsp12	1	736	P	0.304	NEU	T	-0.352	NEU
nsp12	1	737	K	-0.183	MIN	D	0.038	NEU
nsp12	1	738	F	0.333	NEU	F	1.081	MIN
nsp12	1	739	V	1.327	MIN	V	1.138	MIN
nsp12	1	740	D	0.249	NEU	N	-0.342	NEU
nsp12	1	741	E	0.677	MAX	E	-1.132	MAX
nsp12	1	742	Y	0.624	NEU	F	1.098	MIN
nsp12	1	743	Y	0.677	NEU	Y	-0.401	NEU
nsp12	1	744	A	0.735	NEU	A	-0.116	NEU
nsp12	1	745	F	0.386	MIN	Y	0.209	NEU
nsp12	1	746	L	1.327	MIN	L	1.343	MIN
nsp12	1	747	N	1.164	NEU	R	-0.301	NEU
nsp12	1	748	K	1.327	NEU	K	0.051	NEU
nsp12	1	749	H	1.327	NEU	H	-0.211	NEU
nsp12	1	750	F	1.327	MIN	F	1.222	MIN
nsp12	1	751	S	1.327	NEU	S	-0.593	NEU
nsp12	1	752	M	0.735	MIN	M	0.779	NEU
nsp12	1	753	M	1.050	MIN	M	0.899	MIN
nsp12	1	754	I	1.327	MIN	I	1.134	MIN
nsp12	1	755	L	1.327	MIN	L	1.025	MIN
nsp12	1	756	S	1.327	NEU	S	-0.511	NEU
nsp12	1	757	D	0.434	NEU	D	-1.352	MAX
nsp12	1	758	D	1.327	MAX	D	-1.357	MAX
nsp12	1	759	G	1.327	NEU	A	0.408	NEU
nsp12	1	760	V	1.327	MIN	V	1.076	MIN
nsp12	1	761	V	1.327	MIN	V	1.229	MIN
nsp12	1	762	C	1.327	MIN	C	1.558	MIN
nsp12	1	763	Y	0.735	NEU	F	1.248	MIN
nsp12	1	764	N	0.873	NEU	N	-0.997	NEU
nsp12	1	765	S	1.327	NEU	S	-0.203	NEU
nsp12	1	766	D	0.434	MIN	T	0.117	NEU
nsp12	1	767	Y	0.128	NEU	Y	-0.625	NEU
nsp12	1	768	A	1.164	NEU	A	-0.239	NEU
nsp12	1	769	S	-0.074	NEU	S	-0.023	NEU
nsp12	1	770	K	1.327	NEU	Q	-0.873	NEU
nsp12	1	771	G	1.327	NEU	G	-0.669	NEU
nsp12	1	772	Y	-0.087	MIN	L	1.123	MIN
nsp12	1	773	I	1.327	MIN	V	1.134	MIN
nsp12	1	774	A	1.327	NEU	A	-0.058	NEU
nsp12	1	775	N	1.327	NEU	S	-0.503	NEU

nsp12	1	776	I	1.327	MIN	I	1.027	MIN
nsp12	1	777	Q	0.100	MIN	K	-0.227	NEU
nsp12	1	778	N	0.469	NEU	N	-0.4	NEU
nsp12	1	779	F	1.327	MIN	F	1.004	MIN
nsp12	1	780	K	1.327	NEU	K	-0.88	NEU
nsp12	1	781	E	0.577	MAX	S	-0.459	NEU
nsp12	1	782	V	0.497	MIN	V	1.393	MIN
nsp12	1	783	L	1.327	MIN	L	1.018	MIN
nsp12	1	784	Y	1.327	MAX	Y	-1.842	MAX
nsp12	1	785	Y	0.677	MIN	Y	0.985	MIN
nsp12	1	786	Q	0.341	NEU	Q	-1.149	MAX
nsp12	1	787	N	0.577	NEU	N	-0.965	NEU
nsp12	1	788	N	0.434	NEU	N	-0.889	NEU
nsp12	1	789	V	1.327	MIN	V	1.496	MIN
nsp12	1	790	F	0.624	NEU	F	0.269	NEU
nsp12	1	791	M	0.955	NEU	M	0.037	NEU
nsp12	1	792	S	1.327	NEU	S	-0.98	NEU
nsp12	1	793	E	1.164	NEU	E	-0.086	NEU
nsp12	1	794	A	1.327	NEU	A	-0.115	NEU
nsp12	1	795	K	0.735	MAX	K	-1.257	MAX
nsp12	1	796	C	1.327	MIN	C	1.624	MIN
nsp12	1	797	W	1.327	MAX	W	-1.321	MAX
nsp12	1	798	V	0.735	MIN	T	-0.332	NEU
nsp12	1	799	E	1.050	MAX	E	-1.551	MAX
nsp12	1	800	P	0.735	NEU	T	0.307	NEU
nsp12	1	801	D	0.365	NEU	D	0.02	NEU
nsp12	1	802	I	1.327	MIN	L	1.178	MIN
nsp12	1	803	T	0.318	NEU	T	0.032	NEU
nsp12	1	804	K	0.497	MIN	K	1.49	MIN
nsp12	1	805	G	1.327	NEU	G	-0.384	NEU
nsp12	1	806	P	1.327	NEU	P	-0.719	NEU
nsp12	1	807	H	0.800	NEU	H	0.64	NEU
nsp12	1	808	E	1.050	NEU	E	-0.204	NEU
nsp12	1	809	F	0.497	MIN	F	0.769	NEU
nsp12	1	810	C	1.327	MIN	C	1.476	MIN
nsp12	1	811	S	1.327	NEU	S	0.149	NEU
nsp12	1	812	Q	1.327	NEU	Q	-0.403	NEU
nsp12	1	813	H	1.164	MIN	H	1.153	MIN
nsp12	1	814	T	1.327	NEU	T	-0.098	NEU
nsp12	1	815	M	0.463	MIN	M	0.665	NEU
nsp12	1	816	L	0.434	MIN	L	1.193	MIN
nsp12	1	817	V	1.327	MIN	V	1.441	MIN
nsp12	1	818	K	0.328	MIN	K	0.491	NEU
nsp12	1	819	M	0.161	NEU	Q	-0.852	NEU
nsp12	1	820	G	0.368	MIN	G	0.709	NEU
nsp12	1	821	G	0.353	NEU	D	0.753	NEU

nsp12	1	822	D	0.800	NEU	D	-0.84	NEU
nsp12	1	823	Y	0.276	NEU	Y	-1.617	MAX
nsp12	1	824	V	0.497	MIN	V	1.759	MIN
nsp12	1	825	Y	-0.249	MIN	Y	0.324	NEU
nsp12	1	826	L	1.327	MIN	L	1.364	MIN
nsp12	1	827	P	0.408	MAX	P	-0.73	NEU
nsp12	1	828	Y	1.327	MIN	Y	0.75	NEU
nsp12	1	829	P	1.327	MAX	P	-1.842	MAX
nsp12	1	830	D	0.535	NEU	D	0.214	NEU
nsp12	1	831	P	1.327	NEU	P	-0.875	NEU
nsp12	1	832	S	1.327	NEU	S	-0.576	NEU
nsp12	1	833	R	0.955	NEU	R	-0.565	NEU
nsp12	1	834	I	1.327	MIN	I	1.191	MIN
nsp12	1	835	L	1.327	MIN	L	1.169	MIN
nsp12	1	836	G	1.327	NEU	G	-0.355	NEU
nsp12	1	837	A	0.735	NEU	A	0.521	NEU
nsp12	1	838	G	1.164	NEU	G	-0.415	NEU
nsp12	1	839	C	1.327	MIN	C	1.256	MIN
nsp12	1	840	F	1.327	MIN	F	1.236	MIN
nsp12	1	841	V	1.050	MIN	V	1.857	MIN
nsp12	1	842	D	0.624	NEU	D	-0.321	NEU
nsp12	1	843	D	0.873	NEU	D	-0.705	NEU
nsp12	1	844	L	1.164	NEU	I	0.011	NEU
nsp12	1	845	L	0.735	NEU	V	0.185	NEU
nsp12	1	846	K	0.209	NEU	K	0.96	MIN
nsp12	1	847	T	1.327	NEU	T	-0.253	NEU
nsp12	1	848	D	0.677	MAX	D	-1.071	MAX
nsp12	1	849	G	1.327	NEU	G	-0.823	NEU
nsp12	1	850	T	0.328	MIN	T	0.33	NEU
nsp12	1	851	L	0.333	NEU	L	-0.283	NEU
nsp12	1	852	M	1.327	MIN	M	1.24	MIN
nsp12	1	853	I	1.327	MIN	I	1.48	MIN
nsp12	1	854	E	0.327	NEU	E	-0.803	NEU
nsp12	1	855	R	1.327	NEU	R	-0.764	NEU
nsp12	1	856	F	1.164	MIN	F	1.066	MIN
nsp12	1	857	V	1.327	MIN	V	1.374	MIN
nsp12	1	858	S	0.434	MAX	S	-1.17	MAX
nsp12	1	859	L	1.327	MIN	L	1.32	MIN
nsp12	1	860	A	0.624	NEU	A	0.514	NEU
nsp12	1	861	I	1.327	MIN	I	1.538	MIN
nsp12	1	862	D	0.408	NEU	D	-0.863	NEU
nsp12	1	863	A	0.463	NEU	A	0.524	NEU
nsp12	1	864	Y	1.327	NEU	Y	-0.719	NEU
nsp12	1	865	P	1.327	NEU	P	-0.357	NEU
nsp12	1	866	L	1.327	MIN	L	1.565	MIN
nsp12	1	867	T	0.386	NEU	T	-0.85	NEU

nsp12	1	868	K	0.955	MAX	K	-1.532	MAX
nsp12	1	869	H	1.164	NEU	H	0.415	NEU
nsp12	1	870	E	0.677	NEU	P	0.506	NEU
nsp12	1	871	N	0.577	NEU	N	-0.403	NEU
nsp12	1	872	P	0.341	MIN	Q	-0.219	NEU
nsp12	1	873	E	0.955	MAX	E	-1.694	MAX
nsp12	1	874	Y	0.463	NEU	Y	-1.258	MAX
nsp12	1	875	Q	0.386	NEU	A	0.063	NEU
nsp12	1	876	N	0.353	MAX	D	-1.069	MAX
nsp12	1	877	V	1.327	MIN	V	1.154	MIN
nsp12	1	878	F	0.535	MIN	F	0.807	MIN
nsp12	1	879	W	-0.219	NEU	H	0.167	NEU
nsp12	1	880	V	1.327	MIN	L	1.163	MIN
nsp12	1	881	Y	0.434	MIN	Y	0.654	NEU
nsp12	1	882	L	1.327	MIN	L	1.368	MIN
nsp12	1	883	Q	-0.133	MAX	Q	-1.121	MAX
nsp12	1	884	Y	1.050	MIN	Y	0.858	MIN
nsp12	1	885	I	1.327	MIN	I	1.255	MIN
nsp12	1	886	K	0.341	MAX	R	0.078	NEU
nsp12	1	887	K	0.222	NEU	K	1.203	MIN
nsp12	1	888	L	1.327	MIN	L	1.214	MIN
nsp12	1	889	Y	1.327	NEU	H	-0.242	NEU
nsp12	1	890	N	0.027	MIN	D	0.923	MIN
nsp12	1	891	D	1.327	NEU	E	-0.729	NEU
nsp12	1	892	L	1.327	MIN	L	1.18	MIN
nsp12	1	893	T	1.327	NEU	T	0.027	NEU
nsp12	1	894	G	0.890	NEU	G	-0.017	NEU
nsp12	1	895	H	-0.185	MIN	H	0.278	NEU
nsp12	1	896	M	1.050	MIN	M	0.958	MIN
nsp12	1	897	L	0.873	MIN	L	0.87	MIN
nsp12	1	898	D	1.164	NEU	D	-0.782	NEU
nsp12	1	899	S	1.327	NEU	M	0.136	NEU
nsp12	1	900	Y	0.890	NEU	Y	0.316	NEU
nsp12	1	901	S	1.327	NEU	S	-0.517	NEU
nsp12	1	902	V	1.164	MIN	V	1.725	MIN
nsp12	1	903	M	-0.144	NEU	M	-0.617	NEU
nsp12	1	904	L	0.624	MIN	L	0.599	NEU
nsp12	1	905	S	0.442	NEU	T	0.255	NEU
nsp12	1	906	T	0.313	NEU	N	1.588	MIN
nsp12	1	907	D	-0.196	MIN	D	1.364	MIN
nsp12	1	908	N	0.353	NEU	N	1.414	MIN
nsp12	1	909	G	0.434	NEU	T	0.529	NEU
nsp12	1	910	Q	0.030	NEU	S	0.39	NEU
nsp12	1	911	K	0.333	MIN	R	1.466	MIN
nsp12	1	912	F	0.239	MIN	Y	-0.765	NEU
nsp12	1	913	W	0.353	MIN	W	0.712	NEU

nsp12	1	914	E	0.368	NEU	E	-1.271	MAX
nsp12	1	915	E	0.423	NEU	P	0.269	NEU
nsp12	1	916	S	-0.156	NEU	E	-1.222	MAX
nsp12	1	917	F	0.735	NEU	F	0.616	NEU
nsp12	1	918	Y	1.164	NEU	Y	-0.527	NEU
nsp12	1	919	K	0.380	NEU	E	-0.777	NEU
nsp12	1	920	N	0.075	NEU	A	0.79	MIN
nsp12	1	921	M	0.341	MIN	M	1.055	MIN
nsp12	1	922	Y	0.890	MIN	Y	0.854	MIN
nsp12	1	923	L	-0.072	MIN	T	0.259	NEU
nsp12	1	924	R	-0.249	MIN	P	-1.208	MAX
nsp12	1	925	S	0.624	NEU	H	0.031	NEU
nsp12	1	926	A	0.873	NEU	T	0.478	NEU
nsp13	1	1	V	1.292	MIN	V	1.798	MIN
nsp13	1	2	G	1.292	NEU	G	-0.199	NEU
nsp13	1	3	S	1.292	NEU	A	0.137	NEU
nsp13	1	4	C	1.292	MIN	C	1.724	MIN
nsp13	1	5	V	1.292	MIN	V	1.217	MIN
nsp13	1	6	V	1.292	MIN	L	1.011	MIN
nsp13	1	7	C	1.292	MIN	C	1.565	MIN
nsp13	1	8	N	0.307	NEU	N	-0.772	NEU
nsp13	1	9	S	1.292	NEU	S	-0.264	NEU
nsp13	1	10	Q	1.292	NEU	Q	-0.473	NEU
nsp13	1	11	T	1.292	NEU	T	-0.583	NEU
nsp13	1	12	S	1.292	NEU	S	-0.571	NEU
nsp13	1	13	L	1.292	MIN	L	1.004	MIN
nsp13	1	14	R	1.292	NEU	R	-0.678	NEU
nsp13	1	15	C	1.292	MIN	C	1.353	MIN
nsp13	1	16	G	1.292	NEU	G	-0.411	NEU
nsp13	1	17	T	1.292	NEU	A	-0.163	NEU
nsp13	1	18	C	1.292	MIN	C	1.587	MIN
nsp13	1	19	I	1.292	MIN	I	0.857	MIN
nsp13	1	20	R	1.292	NEU	R	-0.836	NEU
nsp13	1	21	R	1.292	MAX	R	-1.389	MAX
nsp13	1	22	P	1.292	NEU	P	-0.835	NEU
nsp13	1	23	F	1.292	MIN	F	1.376	MIN
nsp13	1	24	L	1.292	MIN	L	1.059	MIN
nsp13	1	25	C	1.292	MIN	C	1.664	MIN
nsp13	1	26	C	1.292	MIN	C	1.66	MIN
nsp13	1	27	K	1.292	MAX	K	-1.38	MAX
nsp13	1	28	C	1.292	MIN	C	1.619	MIN
nsp13	1	29	C	1.292	MIN	C	2.043	MIN
nsp13	1	30	Y	1.292	MIN	Y	1.085	MIN
nsp13	1	31	D	1.292	NEU	D	-0.778	NEU
nsp13	1	32	H	1.292	NEU	H	0.041	NEU
nsp13	1	33	V	1.292	MIN	V	1.184	MIN

nsp13	1	34	I	0.839	MIN	I	1.708	MIN
nsp13	1	35	S	0.590	NEU	S	0.283	NEU
nsp13	1	36	T	1.292	NEU	T	-0.459	NEU
nsp13	1	37	T	0.307	NEU	S	-0.266	NEU
nsp13	1	38	H	1.292	NEU	H	0.001	NEU
nsp13	1	39	K	1.292	MAX	K	-1.105	MAX
nsp13	1	40	L	-0.264	NEU	L	0.615	NEU
nsp13	1	41	V	1.292	MIN	V	1.164	MIN
nsp13	1	42	L	1.292	MIN	L	0.687	NEU
nsp13	1	43	S	1.292	NEU	S	-0.555	NEU
nsp13	1	44	V	0.839	MIN	V	1.952	MIN
nsp13	1	45	S	1.292	NEU	N	0.178	NEU
nsp13	1	46	P	1.292	NEU	P	-0.958	NEU
nsp13	1	47	Y	0.374	MIN	Y	0.597	NEU
nsp13	1	48	V	1.292	MIN	V	0.722	NEU
nsp13	1	49	C	1.292	MIN	C	2.079	MIN
nsp13	1	50	N	1.016	NEU	N	-0.675	NEU
nsp13	1	51	A	0.743	NEU	A	-0.322	NEU
nsp13	1	52	P	0.701	MIN	P	0.886	MIN
nsp13	1	53	G	1.292	NEU	G	-0.268	NEU
nsp13	1	54	C	1.292	MIN	C	1.33	MIN
nsp13	1	55	D	0.590	NEU	D	-0.699	NEU
nsp13	1	56	V	1.292	MIN	V	1.854	MIN
nsp13	1	57	A	1.292	NEU	T	-0.702	NEU
nsp13	1	58	D	0.374	NEU	D	-0.942	NEU
nsp13	1	59	V	1.292	MIN	V	1.276	MIN
nsp13	1	60	T	1.292	NEU	T	-0.667	NEU
nsp13	1	61	Q	0.374	MAX	Q	-0.761	NEU
nsp13	1	62	L	1.292	MIN	L	1.311	MIN
nsp13	1	63	Y	0.500	NEU	Y	0.727	NEU
nsp13	1	64	L	1.292	MIN	L	1.061	MIN
nsp13	1	65	G	1.292	NEU	G	0.158	NEU
nsp13	1	66	G	1.292	NEU	G	-0.298	NEU
nsp13	1	67	M	1.292	NEU	M	-0.09	NEU
nsp13	1	68	S	1.292	NEU	S	0.313	NEU
nsp13	1	69	Y	1.292	MIN	Y	0.706	NEU
nsp13	1	70	Y	0.071	MIN	Y	0.438	NEU
nsp13	1	71	C	1.292	MIN	C	2.073	MIN
nsp13	1	72	K	0.091	MAX	K	-2.009	MAX
nsp13	1	73	D	1.016	NEU	S	0.127	NEU
nsp13	1	74	H	0.839	MIN	H	1.14	MIN
nsp13	1	75	K	0.294	NEU	K	-1.219	MAX
nsp13	1	76	P	1.292	NEU	P	-0.755	NEU
nsp13	1	77	P	0.294	MIN	P	1.62	MIN
nsp13	1	78	I	0.307	NEU	I	0.427	NEU
nsp13	1	79	S	1.292	NEU	S	-0.564	NEU

nsp13	1	80	F	1.292	MIN	F	1.028	MIN
nsp13	1	81	P	1.292	NEU	P	0.232	NEU
nsp13	1	82	L	1.292	MIN	L	1.069	MIN
nsp13	1	83	C	1.292	MIN	C	1.918	MIN
nsp13	1	84	A	1.292	NEU	A	-0.347	NEU
nsp13	1	85	N	0.294	MIN	N	1.134	MIN
nsp13	1	86	G	1.292	NEU	G	-0.593	NEU
nsp13	1	87	Q	0.294	NEU	Q	0.371	NEU
nsp13	1	88	V	1.292	MIN	V	1.233	MIN
nsp13	1	89	F	1.292	MIN	F	1.282	MIN
nsp13	1	90	G	1.292	NEU	G	-0.249	NEU
nsp13	1	91	L	1.292	MIN	L	0.724	NEU
nsp13	1	92	Y	1.292	NEU	Y	0.185	NEU
nsp13	1	93	K	1.292	MAX	K	-1.471	MAX
nsp13	1	94	N	1.292	NEU	N	-0.93	NEU
nsp13	1	95	M	0.500	NEU	T	0.06	NEU
nsp13	1	96	C	1.292	MIN	C	2.365	MIN
nsp13	1	97	T	0.374	NEU	V	0.651	NEU
nsp13	1	98	G	1.292	NEU	G	-0.106	NEU
nsp13	1	99	S	1.292	NEU	S	-0.36	NEU
nsp13	1	100	P	0.126	NEU	D	-1.69	MAX
nsp13	1	101	S	0.500	NEU	N	-0.978	NEU
nsp13	1	102	V	0.701	MIN	V	1.146	MIN
nsp13	1	103	T	0.743	NEU	T	-0.189	NEU
nsp13	1	104	D	0.334	MAX	D	-1.286	MAX
nsp13	1	105	F	1.292	MIN	F	1.433	MIN
nsp13	1	106	N	0.374	MAX	N	-1.007	MAX
nsp13	1	107	R	1.292	NEU	A	0.289	NEU
nsp13	1	108	L	1.292	MIN	I	1.215	MIN
nsp13	1	109	A	1.292	NEU	A	0.012	NEU
nsp13	1	110	T	1.292	NEU	T	-0.215	NEU
nsp13	1	111	C	1.292	MIN	C	1.04	MIN
nsp13	1	112	D	1.292	NEU	D	-0.625	NEU
nsp13	1	113	W	1.016	MAX	W	-1.118	MAX
nsp13	1	114	S	1.292	NEU	T	0.164	NEU
nsp13	1	115	N	0.374	NEU	N	-0.392	NEU
nsp13	1	116	S	0.177	NEU	A	0.904	MIN
nsp13	1	117	G	0.307	MAX	G	-0.679	NEU
nsp13	1	118	D	1.016	MAX	D	-1.134	MAX
nsp13	1	119	Y	0.429	MAX	Y	-0.568	NEU
nsp13	1	120	I	0.334	NEU	I	1.621	MIN
nsp13	1	121	L	1.292	MIN	L	1.196	MIN
nsp13	1	122	A	1.292	NEU	A	0.275	NEU
nsp13	1	123	N	0.701	NEU	N	-1.055	MAX
nsp13	1	124	T	0.374	NEU	T	-0.228	NEU
nsp13	1	125	T	0.374	NEU	C	2.089	MIN

nsp13	1	126	T	1.292	NEU	T	0.265	NEU
nsp13	1	127	E	1.292	NEU	E	-0.688	NEU
nsp13	1	128	R	1.016	NEU	R	-0.347	NEU
nsp13	1	129	L	1.292	MIN	L	1.336	MIN
nsp13	1	130	K	0.374	NEU	K	-1.077	MAX
nsp13	1	131	L	1.292	MIN	L	1.577	MIN
nsp13	1	132	F	1.292	MIN	F	1.181	MIN
nsp13	1	133	A	1.292	MIN	A	0.988	MIN
nsp13	1	134	A	1.292	MIN	A	0.844	MIN
nsp13	1	135	E	0.839	NEU	E	-0.983	NEU
nsp13	1	136	T	1.292	NEU	T	-0.319	NEU
nsp13	1	137	L	1.292	MIN	L	1.621	MIN
nsp13	1	138	R	0.294	NEU	K	0.34	NEU
nsp13	1	139	A	1.292	MIN	A	0.818	MIN
nsp13	1	140	T	0.569	NEU	T	-0.267	NEU
nsp13	1	141	E	1.292	NEU	E	-0.382	NEU
nsp13	1	142	E	1.292	NEU	E	-0.683	NEU
nsp13	1	143	A	0.500	NEU	T	-0.299	NEU
nsp13	1	144	S	1.292	NEU	F	0.192	NEU
nsp13	1	145	K	0.429	NEU	K	0.588	NEU
nsp13	1	146	Q	0.177	NEU	L	1.12	MIN
nsp13	1	147	S	1.292	NEU	S	-0.177	NEU
nsp13	1	148	Y	0.374	MIN	Y	0.907	MIN
nsp13	1	149	A	1.016	NEU	G	-0.442	NEU
nsp13	1	150	I	0.500	MIN	I	1.317	MIN
nsp13	1	151	A	1.292	NEU	A	-0.319	NEU
nsp13	1	152	T	0.590	NEU	T	-0.28	NEU
nsp13	1	153	V	1.292	MIN	V	1.135	MIN
nsp13	1	154	K	0.307	NEU	R	-0.256	NEU
nsp13	1	155	E	0.294	MAX	E	-1.08	MAX
nsp13	1	156	V	1.292	MIN	V	1.191	MIN
nsp13	1	157	L	0.590	MIN	L	1.204	MIN
nsp13	1	158	S	1.292	NEU	S	-0.343	NEU
nsp13	1	159	D	0.307	NEU	D	0.999	MIN
nsp13	1	160	R	0.374	NEU	R	-1.038	MAX
nsp13	1	161	E	0.307	MAX	E	-1.058	MAX
nsp13	1	162	L	1.292	MIN	L	1.215	MIN
nsp13	1	163	I	0.429	MIN	H	-0.508	NEU
nsp13	1	164	L	1.292	MIN	L	1.345	MIN
nsp13	1	165	S	-0.149	MIN	S	-0.849	NEU
nsp13	1	166	W	0.701	NEU	W	-0.944	NEU
nsp13	1	167	E	0.701	NEU	E	0.387	NEU
nsp13	1	168	V	0.294	NEU	V	0.875	MIN
nsp13	1	169	G	1.292	NEU	G	-0.122	NEU
nsp13	1	170	K	1.292	NEU	K	-0.278	NEU
nsp13	1	171	P	1.016	NEU	P	0.155	NEU

nsp13	1	172	R	1.292	NEU	R	0.269	NEU
nsp13	1	173	P	1.292	NEU	P	-0.591	NEU
nsp13	1	174	P	0.500	NEU	P	-0.174	NEU
nsp13	1	175	L	1.292	MIN	L	1.04	MIN
nsp13	1	176	N	1.292	NEU	N	-0.249	NEU
nsp13	1	177	R	1.292	NEU	R	-0.483	NEU
nsp13	1	178	N	1.292	MIN	N	1.355	MIN
nsp13	1	179	Y	1.292	NEU	Y	-0.186	NEU
nsp13	1	180	V	0.839	MIN	V	1.319	MIN
nsp13	1	181	F	1.292	MIN	F	0.982	MIN
nsp13	1	182	T	1.292	NEU	T	-0.137	NEU
nsp13	1	183	G	1.292	NEU	G	-0.176	NEU
nsp13	1	184	Y	1.016	MIN	Y	0.654	NEU
nsp13	1	185	H	0.334	NEU	R	0.536	NEU
nsp13	1	186	I	0.839	MIN	V	1.736	MIN
nsp13	1	187	T	0.500	MIN	T	0.513	NEU
nsp13	1	188	K	1.016	NEU	K	-0.232	NEU
nsp13	1	189	N	1.292	NEU	N	-0.329	NEU
nsp13	1	190	S	1.292	NEU	S	-0.762	NEU
nsp13	1	191	K	1.292	NEU	K	-0.373	NEU
nsp13	1	192	V	0.839	MIN	V	1.655	MIN
nsp13	1	193	Q	1.292	NEU	Q	-0.466	NEU
nsp13	1	194	L	1.292	MIN	I	1.574	MIN
nsp13	1	195	G	1.292	NEU	G	-0.019	NEU
nsp13	1	196	E	0.590	NEU	E	-0.942	NEU
nsp13	1	197	Y	0.307	MIN	Y	0.639	NEU
nsp13	1	198	I	0.374	MIN	T	-0.448	NEU
nsp13	1	199	F	0.590	MIN	F	0.635	NEU
nsp13	1	200	E	1.292	NEU	E	-0.783	NEU
nsp13	1	201	K	0.429	NEU	K	-0.66	NEU
nsp13	1	202	G	0.307	NEU	G	-0.676	NEU
nsp13	1	203	D	1.292	MIN	D	1.023	MIN
nsp13	1	204	Y	0.590	MAX	Y	-2.634	MAX
nsp13	1	205	G	1.016	NEU	G	-0.757	NEU
nsp13	1	206	D	1.016	NEU	D	-0.29	NEU
nsp13	1	207	A	0.294	MIN	A	0.254	NEU
nsp13	1	208	V	1.292	MIN	V	1.015	MIN
nsp13	1	209	S	0.334	NEU	V	0.393	NEU
nsp13	1	210	Y	0.374	NEU	Y	0.018	NEU
nsp13	1	211	R	0.500	MIN	R	1.145	MIN
nsp13	1	212	S	1.292	NEU	G	-0.301	NEU
nsp13	1	213	S	1.292	NEU	T	-0.252	NEU
nsp13	1	214	T	1.292	NEU	T	-0.185	NEU
nsp13	1	215	T	0.429	NEU	T	0.79	MIN
nsp13	1	216	Y	0.307	MAX	Y	-2.253	MAX
nsp13	1	217	K	1.292	MIN	K	1.313	MIN

nsp13	1	218	L	1.292	MIN	L	0.988	MIN
nsp13	1	219	N	0.701	NEU	N	-0.347	NEU
nsp13	1	220	V	1.292	MIN	V	1.677	MIN
nsp13	1	221	G	1.292	NEU	G	-0.566	NEU
nsp13	1	222	D	0.374	MAX	D	-0.909	NEU
nsp13	1	223	Y	1.292	MIN	Y	0.787	MIN
nsp13	1	224	F	1.292	MIN	F	1.019	MIN
nsp13	1	225	V	1.292	MIN	V	1.351	MIN
nsp13	1	226	L	1.292	MIN	L	1.032	MIN
nsp13	1	227	T	1.292	NEU	T	-0.361	NEU
nsp13	1	228	S	1.292	NEU	S	-0.796	NEU
nsp13	1	229	H	1.292	NEU	H	0.379	NEU
nsp13	1	230	S	1.016	NEU	T	0.267	NEU
nsp13	1	231	V	1.292	MIN	V	0.852	MIN
nsp13	1	232	A	0.334	NEU	M	-0.542	NEU
nsp13	1	233	P	0.839	NEU	P	-0.693	NEU
nsp13	1	234	L	1.292	MIN	L	1.287	MIN
nsp13	1	235	S	0.500	NEU	S	0.236	NEU
nsp13	1	236	A	1.292	NEU	A	-0.113	NEU
nsp13	1	237	P	1.292	MAX	P	-1.542	MAX
nsp13	1	238	T	1.292	NEU	T	-0.518	NEU
nsp13	1	239	L	0.429	MIN	L	0.571	NEU
nsp13	1	240	V	1.292	MIN	V	1.235	MIN
nsp13	1	241	P	1.016	NEU	P	0.275	NEU
nsp13	1	242	Q	0.701	NEU	Q	-0.252	NEU
nsp13	1	243	E	0.374	MAX	E	-0.345	NEU
nsp13	1	244	R	0.329	NEU	H	0.043	NEU
nsp13	1	245	Y	0.334	MAX	Y	-1.827	MAX
nsp13	1	246	V	0.307	NEU	V	0.837	MIN
nsp13	1	247	K	0.307	NEU	R	0.048	NEU
nsp13	1	248	I	1.292	MIN	I	1.369	MIN
nsp13	1	249	T	0.374	NEU	T	0.438	NEU
nsp13	1	250	G	1.292	NEU	G	0.158	NEU
nsp13	1	251	L	1.292	MIN	L	1.229	MIN
nsp13	1	252	Y	0.500	MAX	Y	-1.754	MAX
nsp13	1	253	P	1.292	NEU	P	-0.556	NEU
nsp13	1	254	T	1.016	NEU	T	-0.582	NEU
nsp13	1	255	L	0.307	NEU	L	-0.641	NEU
nsp13	1	256	N	1.292	NEU	N	-0.338	NEU
nsp13	1	257	V	1.292	MIN	I	1.672	MIN
nsp13	1	258	P	0.429	NEU	S	-0.479	NEU
nsp13	1	259	E	0.307	MAX	D	-0.325	NEU
nsp13	1	260	E	1.016	NEU	E	-0.983	NEU
nsp13	1	261	F	0.701	MIN	F	0.645	NEU
nsp13	1	262	A	0.500	NEU	S	-0.676	NEU
nsp13	1	263	S	1.292	NEU	S	-0.425	NEU

nsp13	1	264	N	0.500	NEU	N	-0.986	NEU
nsp13	1	265	V	1.292	MIN	V	0.921	MIN
nsp13	1	266	A	-0.264	NEU	A	-0.355	NEU
nsp13	1	267	N	1.016	NEU	N	-0.476	NEU
nsp13	1	268	Y	0.307	NEU	Y	-0.217	NEU
nsp13	1	269	Q	0.307	NEU	Q	-0.999	NEU
nsp13	1	270	K	0.500	MAX	K	-1.359	MAX
nsp13	1	271	V	0.500	MIN	V	1.51	MIN
nsp13	1	272	G	1.292	NEU	G	-0.526	NEU
nsp13	1	273	M	0.429	MIN	M	0.964	MIN
nsp13	1	274	S	0.126	NEU	Q	-1.546	MAX
nsp13	1	275	K	0.294	NEU	K	-0.88	NEU
nsp13	1	276	Y	0.590	NEU	Y	0.164	NEU
nsp13	1	277	V	0.334	NEU	S	-0.516	NEU
nsp13	1	278	T	1.292	NEU	T	-0.494	NEU
nsp13	1	279	V	1.292	MIN	L	1.073	MIN
nsp13	1	280	Q	0.500	NEU	Q	-1.001	MAX
nsp13	1	281	G	1.292	NEU	G	-0.051	NEU
nsp13	1	282	P	0.590	MAX	P	-1.017	MAX
nsp13	1	283	P	1.292	NEU	P	-0.33	NEU
nsp13	1	284	G	1.292	NEU	G	0.245	NEU
nsp13	1	285	T	1.292	NEU	T	-0.251	NEU
nsp13	1	286	G	1.292	NEU	G	0.063	NEU
nsp13	1	287	K	1.292	MAX	K	-1.325	MAX
nsp13	1	288	S	1.292	NEU	S	-0.706	NEU
nsp13	1	289	H	0.429	NEU	H	-0.305	NEU
nsp13	1	290	F	1.292	MIN	F	1.308	MIN
nsp13	1	291	A	0.590	MIN	A	0.698	NEU
nsp13	1	292	I	1.292	MIN	I	1.462	MIN
nsp13	1	293	G	1.292	NEU	G	-0.379	NEU
nsp13	1	294	L	1.292	MIN	L	1.311	MIN
nsp13	1	295	A	1.292	NEU	A	0.508	NEU
nsp13	1	296	L	1.292	MIN	L	1.34	MIN
nsp13	1	297	Y	1.292	MIN	Y	0.948	MIN
nsp13	1	298	Y	1.016	NEU	Y	0.352	NEU
nsp13	1	299	P	1.016	NEU	P	-0.818	NEU
nsp13	1	300	S	1.292	NEU	S	-0.793	NEU
nsp13	1	301	A	1.292	MIN	A	0.798	MIN
nsp13	1	302	R	0.500	NEU	R	-0.275	NEU
nsp13	1	303	I	1.292	MIN	I	1.438	MIN
nsp13	1	304	V	1.292	MIN	V	1.26	MIN
nsp13	1	305	Y	0.307	NEU	Y	0.609	NEU
nsp13	1	306	T	1.292	NEU	T	-0.49	NEU
nsp13	1	307	A	1.292	NEU	A	0.093	NEU
nsp13	1	308	C	1.292	MIN	C	1.363	MIN
nsp13	1	309	S	1.292	NEU	S	-0.832	NEU

nsp13	1	310	H	1.292	NEU	H	-0.065	NEU
nsp13	1	311	A	1.292	NEU	A	-0.053	NEU
nsp13	1	312	A	1.292	NEU	A	-0.153	NEU
nsp13	1	313	V	1.292	MIN	V	1.09	MIN
nsp13	1	314	D	1.292	MAX	D	-1.358	MAX
nsp13	1	315	A	1.292	NEU	A	0.196	NEU
nsp13	1	316	L	1.292	MIN	L	1.187	MIN
nsp13	1	317	C	1.292	MIN	C	1.14	MIN
nsp13	1	318	E	0.701	NEU	E	-0.829	NEU
nsp13	1	319	K	1.292	MAX	K	-1.653	MAX
nsp13	1	320	A	0.429	NEU	A	0.569	NEU
nsp13	1	321	F	0.701	MIN	L	0.936	MIN
nsp13	1	322	K	0.500	NEU	K	-0.065	NEU
nsp13	1	323	Y	0.590	MAX	Y	-1.658	MAX
nsp13	1	324	L	1.292	MIN	L	1.521	MIN
nsp13	1	325	P	0.374	NEU	P	-1.356	MAX
nsp13	1	326	I	1.292	MIN	I	1.047	MIN
nsp13	1	327	A	0.429	NEU	D	0.717	NEU
nsp13	1	328	K	0.294	NEU	K	-0.748	NEU
nsp13	1	329	C	1.292	MIN	C	1.784	MIN
nsp13	1	330	S	1.292	NEU	S	-0.735	NEU
nsp13	1	331	R	1.292	NEU	R	-0.701	NEU
nsp13	1	332	I	1.292	MIN	I	1.182	MIN
nsp13	1	333	I	1.292	MIN	I	1.266	MIN
nsp13	1	334	P	0.334	MAX	P	-1.733	MAX
nsp13	1	335	A	0.374	MAX	A	-0.883	NEU
nsp13	1	336	K	-0.118	NEU	R	-0.309	NEU
nsp13	1	337	A	0.701	MIN	A	0.66	NEU
nsp13	1	338	R	1.292	MIN	R	1.31	MIN
nsp13	1	339	V	1.292	MIN	V	1.349	MIN
nsp13	1	340	E	1.292	NEU	E	-0.039	NEU
nsp13	1	341	C	1.292	MIN	C	1.175	MIN
nsp13	1	342	F	0.307	MIN	F	1.236	MIN
nsp13	1	343	D	0.701	MAX	D	-1.61	MAX
nsp13	1	344	K	1.292	NEU	K	-0.964	NEU
nsp13	1	345	F	1.016	MIN	F	0.612	NEU
nsp13	1	346	K	0.429	NEU	K	0.631	NEU
nsp13	1	347	V	1.016	MIN	V	0.615	NEU
nsp13	1	348	N	1.016	MAX	N	-1.085	MAX
nsp13	1	349	E	0.374	NEU	S	-0.714	NEU
nsp13	1	350	T	0.500	NEU	T	-0.717	NEU
nsp13	1	351	N	0.701	NEU	L	-0.236	NEU
nsp13	1	352	S	1.016	NEU	E	-0.62	NEU
nsp13	1	353	Q	1.292	NEU	Q	-0.117	NEU
nsp13	1	354	Y	0.429	NEU	Y	0.602	NEU
nsp13	1	355	V	1.292	MIN	V	1.209	MIN

nsp13	1	356	F	1.292	MIN	F	1.47	MIN
nsp13	1	357	S	0.429	NEU	C	1.184	MIN
nsp13	1	358	T	1.292	NEU	T	-0.251	NEU
nsp13	1	359	I	1.292	MIN	V	1.358	MIN
nsp13	1	360	N	0.429	NEU	N	-1.218	MAX
nsp13	1	361	A	0.429	NEU	A	0.558	NEU
nsp13	1	362	L	1.292	MIN	L	1.24	MIN
nsp13	1	363	P	0.701	MAX	P	-0.964	NEU
nsp13	1	364	E	0.374	NEU	E	-0.224	NEU
nsp13	1	365	T	1.292	NEU	T	-0.31	NEU
nsp13	1	366	T	0.839	NEU	T	-0.54	NEU
nsp13	1	367	A	0.701	MIN	A	0.894	MIN
nsp13	1	368	D	1.292	NEU	D	-0.662	NEU
nsp13	1	369	I	1.292	MIN	I	1.18	MIN
nsp13	1	370	L	1.292	MIN	V	1.251	MIN
nsp13	1	371	V	1.292	MIN	V	1.288	MIN
nsp13	1	372	V	1.292	MIN	F	1.306	MIN
nsp13	1	373	D	1.292	MAX	D	-1.309	MAX
nsp13	1	374	E	1.292	MAX	E	-1.246	MAX
nsp13	1	375	V	1.292	MIN	I	1.37	MIN
nsp13	1	376	S	1.292	NEU	S	-0.304	NEU
nsp13	1	377	M	1.292	NEU	M	0.159	NEU
nsp13	1	378	C	1.292	MIN	A	0.657	NEU
nsp13	1	379	T	1.292	NEU	T	-0.339	NEU
nsp13	1	380	N	1.292	NEU	N	-0.83	NEU
nsp13	1	381	Y	0.500	MIN	Y	0.649	NEU
nsp13	1	382	D	1.292	MAX	D	-1.378	MAX
nsp13	1	383	L	1.292	MIN	L	1.233	MIN
nsp13	1	384	S	1.292	NEU	S	-0.711	NEU
nsp13	1	385	I	0.701	MIN	V	1.369	MIN
nsp13	1	386	I	1.292	MIN	V	1.317	MIN
nsp13	1	387	N	1.292	NEU	N	-0.952	NEU
nsp13	1	388	A	1.292	NEU	A	-0.221	NEU
nsp13	1	389	R	1.292	NEU	R	-0.097	NEU
nsp13	1	390	V	1.292	MIN	L	1.214	MIN
nsp13	1	391	R	1.292	MIN	R	1.538	MIN
nsp13	1	392	A	1.292	NEU	A	0.512	NEU
nsp13	1	393	K	0.500	NEU	K	-0.761	NEU
nsp13	1	394	H	1.292	NEU	H	-0.413	NEU
nsp13	1	395	I	0.429	MIN	Y	-0.325	NEU
nsp13	1	396	V	1.292	MIN	V	1.166	MIN
nsp13	1	397	Y	0.839	MIN	Y	0.698	NEU
nsp13	1	398	V	1.292	MIN	I	1.373	MIN
nsp13	1	399	G	1.292	NEU	G	-0.114	NEU
nsp13	1	400	D	1.292	MAX	D	-1.233	MAX
nsp13	1	401	P	0.334	NEU	P	-1.215	MAX

nsp13	1	402	A	1.292	NEU	A	0.451	NEU
nsp13	1	403	Q	1.292	NEU	Q	-0.486	NEU
nsp13	1	404	L	1.292	MIN	L	0.606	NEU
nsp13	1	405	P	1.292	MAX	P	-1.297	MAX
nsp13	1	406	A	1.292	NEU	A	0.335	NEU
nsp13	1	407	P	1.292	NEU	P	-0.743	NEU
nsp13	1	408	R	1.292	NEU	R	-0.224	NEU
nsp13	1	409	T	1.292	MIN	T	0.857	MIN
nsp13	1	410	L	0.500	MIN	L	0.966	MIN
nsp13	1	411	L	0.701	MIN	L	0.896	MIN
nsp13	1	412	T	1.292	NEU	T	0.257	NEU
nsp13	1	413	K	0.334	NEU	K	-0.454	NEU
nsp13	1	414	G	0.307	MAX	G	-1.205	MAX
nsp13	1	415	T	0.839	NEU	T	0.34	NEU
nsp13	1	416	L	0.839	MIN	L	1.144	MIN
nsp13	1	417	E	0.500	MAX	E	-1.205	MAX
nsp13	1	418	P	0.294	NEU	P	-1.123	MAX
nsp13	1	419	E	1.292	MAX	E	-1.574	MAX
nsp13	1	420	N	-0.283	NEU	Y	0.828	MIN
nsp13	1	421	F	1.292	MIN	F	0.968	MIN
nsp13	1	422	N	0.307	NEU	N	-0.971	NEU
nsp13	1	423	S	1.292	NEU	S	-0.513	NEU
nsp13	1	424	V	1.292	MIN	V	1.147	MIN
nsp13	1	425	C	0.307	MIN	C	2.583	MIN
nsp13	1	426	R	0.294	MAX	R	-0.99	NEU
nsp13	1	427	L	1.016	MIN	L	1.074	MIN
nsp13	1	428	M	0.429	NEU	M	0.728	NEU
nsp13	1	429	C	0.374	MIN	K	-1.891	MAX
nsp13	1	430	N	-0.064	NEU	T	0.033	NEU
nsp13	1	431	L	1.292	MIN	I	1.53	MIN
nsp13	1	432	G	0.374	NEU	G	0.576	NEU
nsp13	1	433	P	0.374	NEU	P	-0.883	NEU
nsp13	1	434	D	0.839	NEU	D	-0.734	NEU
nsp13	1	435	I	0.500	MIN	M	0.383	NEU
nsp13	1	436	F	1.292	MIN	F	0.91	MIN
nsp13	1	437	L	1.292	MIN	L	1.117	MIN
nsp13	1	438	G	0.500	NEU	G	-0.274	NEU
nsp13	1	439	T	0.334	NEU	T	-0.188	NEU
nsp13	1	440	C	1.292	MIN	C	1.786	MIN
nsp13	1	441	Y	-0.253	MIN	R	-0.058	NEU
nsp13	1	442	R	0.307	NEU	R	-0.965	NEU
nsp13	1	443	C	1.292	MIN	C	1.453	MIN
nsp13	1	444	P	1.292	MAX	P	-1.336	MAX
nsp13	1	445	K	0.334	MAX	A	0.496	NEU
nsp13	1	446	E	1.292	MAX	E	-1.202	MAX
nsp13	1	447	I	1.292	MIN	I	1.063	MIN

nsp13	1	448	V	1.292	MIN	V	1.124	MIN
nsp13	1	449	D	0.839	NEU	D	-1.026	MAX
nsp13	1	450	T	1.292	NEU	T	-0.284	NEU
nsp13	1	451	V	1.292	MIN	V	1.353	MIN
nsp13	1	452	S	1.292	NEU	S	-0.368	NEU
nsp13	1	453	A	1.292	NEU	A	-0.253	NEU
nsp13	1	454	L	1.292	MIN	L	1.033	MIN
nsp13	1	455	V	1.292	MIN	V	1.135	MIN
nsp13	1	456	Y	1.016	NEU	Y	0.443	NEU
nsp13	1	457	D	1.292	NEU	D	-0.445	NEU
nsp13	1	458	N	1.292	NEU	N	-0.624	NEU
nsp13	1	459	K	0.307	NEU	K	-0.467	NEU
nsp13	1	460	L	1.292	MIN	L	0.977	MIN
nsp13	1	461	K	0.334	NEU	K	0.043	NEU
nsp13	1	462	A	1.292	NEU	A	-0.505	NEU
nsp13	1	463	K	0.334	MAX	H	0.47	NEU
nsp13	1	464	K	1.292	MAX	K	-1.426	MAX
nsp13	1	465	E	-0.227	MIN	D	-1.087	MAX
nsp13	1	466	K	-0.020	MAX	K	-1.154	MAX
nsp13	1	467	S	1.292	NEU	S	-0.492	NEU
nsp13	1	468	G	1.292	NEU	A	-0.862	NEU
nsp13	1	469	Q	1.292	NEU	Q	-0.775	NEU
nsp13	1	470	C	1.292	MIN	C	1.259	MIN
nsp13	1	471	F	0.701	MIN	F	1.327	MIN
nsp13	1	472	K	1.292	MAX	K	-1.244	MAX
nsp13	1	473	I	1.292	MIN	M	0.899	MIN
nsp13	1	474	L	0.500	MIN	F	1.025	MIN
nsp13	1	475	Y	1.292	MIN	Y	0.874	MIN
nsp13	1	476	K	1.016	NEU	K	-0.101	NEU
nsp13	1	477	G	1.016	NEU	G	-0.459	NEU
nsp13	1	478	S	0.429	NEU	V	0.044	NEU
nsp13	1	479	V	0.500	MIN	I	0.925	MIN
nsp13	1	480	T	1.292	NEU	T	-0.223	NEU
nsp13	1	481	H	0.429	NEU	H	-0.835	NEU
nsp13	1	482	D	0.429	NEU	D	-0.796	NEU
nsp13	1	483	A	0.294	NEU	V	-0.847	NEU
nsp13	1	484	S	1.292	NEU	S	-0.371	NEU
nsp13	1	485	S	1.292	NEU	S	-0.375	NEU
nsp13	1	486	A	0.839	MIN	A	0.674	NEU
nsp13	1	487	I	1.292	MIN	I	1.084	MIN
nsp13	1	488	N	0.500	NEU	N	-1.013	MAX
nsp13	1	489	R	1.016	NEU	R	-0.606	NEU
nsp13	1	490	P	1.016	MAX	P	-1.294	MAX
nsp13	1	491	Q	1.292	NEU	Q	-0.847	NEU
nsp13	1	492	L	1.292	MIN	I	1.443	MIN
nsp13	1	493	G	1.292	NEU	G	-0.607	NEU

nsp13	1	494	F	1.292	MIN	V	1.11	MIN
nsp13	1	495	V	1.292	MIN	V	1.238	MIN
nsp13	1	496	K	0.334	MAX	R	-0.717	NEU
nsp13	1	497	E	0.590	NEU	E	-0.658	NEU
nsp13	1	498	F	1.292	MIN	F	1.366	MIN
nsp13	1	499	L	1.292	MIN	L	1.645	MIN
nsp13	1	500	T	0.839	NEU	T	0.275	NEU
nsp13	1	501	A	1.292	NEU	R	0.413	NEU
nsp13	1	502	N	0.590	NEU	N	-0.878	NEU
nsp13	1	503	P	0.701	MAX	P	-1.496	MAX
nsp13	1	504	A	-0.201	NEU	A	-0.912	NEU
nsp13	1	505	W	1.292	NEU	W	0.222	NEU
nsp13	1	506	S	0.701	NEU	R	-0.602	NEU
nsp13	1	507	K	0.374	NEU	K	-0.787	NEU
nsp13	1	508	A	1.292	NEU	A	0.402	NEU
nsp13	1	509	V	1.292	MIN	V	1.146	MIN
nsp13	1	510	F	1.292	MIN	F	1.223	MIN
nsp13	1	511	I	1.292	MIN	I	1.284	MIN
nsp13	1	512	S	1.292	NEU	S	-0.473	NEU
nsp13	1	513	P	1.292	MAX	P	-1.335	MAX
nsp13	1	514	Y	0.294	MAX	Y	0.199	NEU
nsp13	1	515	N	1.292	MIN	N	0.926	MIN
nsp13	1	516	S	1.016	NEU	S	-0.986	NEU
nsp13	1	517	Q	1.292	NEU	Q	-0.771	NEU
nsp13	1	518	N	1.292	NEU	N	-0.237	NEU
nsp13	1	519	A	1.016	NEU	A	-0.794	NEU
nsp13	1	520	V	1.292	MIN	V	1.247	MIN
nsp13	1	521	A	1.016	NEU	A	0.516	NEU
nsp13	1	522	R	1.292	NEU	S	-0.269	NEU
nsp13	1	523	S	1.292	NEU	K	-0.718	NEU
nsp13	1	524	M	0.701	MIN	I	1.668	MIN
nsp13	1	525	L	1.292	MIN	L	1.352	MIN
nsp13	1	526	G	1.292	NEU	G	0.022	NEU
nsp13	1	527	L	1.292	MIN	L	1.366	MIN
nsp13	1	528	P	1.292	NEU	P	0.069	NEU
nsp13	1	529	T	1.292	NEU	T	-0.247	NEU
nsp13	1	530	Q	1.292	NEU	Q	-0.764	NEU
nsp13	1	531	T	1.292	NEU	T	0.236	NEU
nsp13	1	532	V	1.292	MIN	V	1.272	MIN
nsp13	1	533	D	1.292	NEU	D	-0.799	NEU
nsp13	1	534	S	1.292	NEU	S	-0.262	NEU
nsp13	1	535	S	1.292	NEU	S	-0.77	NEU
nsp13	1	536	Q	1.292	NEU	Q	-0.8	NEU
nsp13	1	537	G	1.292	NEU	G	-0.697	NEU
nsp13	1	538	S	1.292	NEU	S	-0.124	NEU
nsp13	1	539	E	1.292	NEU	E	0.178	NEU

nsp13	1	540	Y	0.500	NEU	Y	-0.422	NEU
nsp13	1	541	D	-0.283	NEU	D	-0.552	NEU
nsp13	1	542	Y	0.374	MIN	Y	0.566	NEU
nsp13	1	543	V	1.292	MIN	V	1.264	MIN
nsp13	1	544	I	1.292	MIN	I	1.574	MIN
nsp13	1	545	F	1.292	MIN	F	1.215	MIN
nsp13	1	546	C	0.374	MIN	T	-0.389	NEU
nsp13	1	547	Q	1.016	NEU	Q	-0.972	NEU
nsp13	1	548	T	1.292	NEU	T	-0.064	NEU
nsp13	1	549	A	1.292	NEU	T	-0.038	NEU
nsp13	1	550	D	1.292	NEU	E	-0.333	NEU
nsp13	1	551	T	1.292	NEU	T	0.083	NEU
nsp13	1	552	A	0.334	MAX	A	-0.865	NEU
nsp13	1	553	H	1.292	NEU	H	0.518	NEU
nsp13	1	554	A	1.292	NEU	S	-0.342	NEU
nsp13	1	555	N	0.374	NEU	C	2.092	MIN
nsp13	1	556	N	1.292	NEU	N	-0.345	NEU
nsp13	1	557	V	1.292	MIN	V	1.225	MIN
nsp13	1	558	N	1.292	NEU	N	-0.669	NEU
nsp13	1	559	R	1.292	NEU	R	-0.318	NEU
nsp13	1	560	F	1.292	MIN	F	1.148	MIN
nsp13	1	561	N	1.292	MAX	N	-1.114	MAX
nsp13	1	562	V	1.292	MIN	V	1.177	MIN
nsp13	1	563	A	0.429	MIN	A	0.631	NEU
nsp13	1	564	I	1.292	MIN	I	1.386	MIN
nsp13	1	565	T	1.292	NEU	T	-0.592	NEU
nsp13	1	566	R	1.292	NEU	R	-0.624	NEU
nsp13	1	567	A	1.292	NEU	A	0.263	NEU
nsp13	1	568	K	0.307	MAX	K	-1.284	MAX
nsp13	1	569	K	-0.253	MAX	V	1.407	MIN
nsp13	1	570	G	1.292	NEU	G	-0.39	NEU
nsp13	1	571	I	1.292	MIN	I	1.185	MIN
nsp13	1	572	L	1.292	MIN	L	1.257	MIN
nsp13	1	573	C	1.292	MIN	C	1.113	MIN
nsp13	1	574	V	1.292	MIN	I	1.39	MIN
nsp13	1	575	M	0.701	MIN	M	0.536	NEU
nsp13	1	576	S	1.292	NEU	S	-0.648	NEU
nsp13	1	577	D	0.307	MAX	D	-1.805	MAX
nsp13	1	578	Q	-0.227	MAX	R	1.21	MIN
nsp13	1	579	A	0.701	NEU	D	-0.065	NEU
nsp13	1	580	L	1.016	MIN	L	0.946	MIN
nsp13	1	581	F	0.294	MIN	Y	-0.171	NEU
nsp13	1	582	D	0.500	NEU	D	0.278	NEU
nsp13	1	583	S	0.086	NEU	K	-1.032	MAX
nsp13	1	584	L	1.292	MIN	L	1.378	MIN
nsp13	1	585	Q	0.334	NEU	Q	-0.913	NEU

nsp13	1	586	F	1.292	MIN	F	1.349	MIN
nsp13	1	587	T	0.435	NEU	T	-0.33	NEU
nsp13	1	588	E	0.590	NEU	S	-0.452	NEU
nsp13	1	589	L	1.292	MIN	L	1.524	MIN
nsp13	1	590	S	0.143	NEU	E	-0.57	NEU
nsp13	1	591	V	0.590	MIN	I	1.501	MIN
nsp13	1	592	N	0.091	MIN	P	-0.108	NEU
nsp14	1	1	E	0.754	NEU	E	-0.954	NEU
nsp14	1	2	N	0.012	MIN	N	0.577	NEU
nsp14	1	3	V	0.190	NEU	V	0.528	NEU
nsp14	1	4	T	0.279	NEU	T	-0.293	NEU
nsp14	1	5	G	1.276	NEU	G	0.243	NEU
nsp14	1	6	L	1.276	MIN	L	0.642	NEU
nsp14	1	7	F	0.604	MIN	F	1.049	MIN
nsp14	1	8	K	0.604	MAX	K	-1.044	MAX
nsp14	1	9	D	0.298	NEU	D	-1.017	MAX
nsp14	1	10	C	1.276	MIN	C	1.65	MIN
nsp14	1	11	S	0.604	NEU	S	-0.718	NEU
nsp14	1	12	K	-0.208	NEU	K	-0.911	NEU
nsp14	1	13	A	-0.107	NEU	V	0.801	MIN
nsp14	1	14	E	0.299	NEU	I	-0.527	NEU
nsp14	1	15	T	0.604	NEU	T	0.048	NEU
nsp14	1	16	G	1.201	NEU	G	-0.172	NEU
nsp14	1	17	L	0.339	MIN	L	0.332	NEU
nsp14	1	18	H	0.953	NEU	H	0.22	NEU
nsp14	1	19	P	1.276	NEU	P	-0.85	NEU
nsp14	1	20	A	0.754	NEU	T	-0.699	NEU
nsp14	1	21	Y	0.279	NEU	Q	-0.661	NEU
nsp14	1	22	A	0.489	NEU	A	-1.473	MAX
nsp14	1	23	P	0.442	NEU	P	0.244	NEU
nsp14	1	24	T	1.276	NEU	T	-0.375	NEU
nsp14	1	25	F	0.190	NEU	H	0.12	NEU
nsp14	1	26	L	0.339	MIN	L	0.479	NEU
nsp14	1	27	S	0.636	NEU	S	-1.124	MAX
nsp14	1	28	V	1.276	MIN	V	1.274	MIN
nsp14	1	29	D	1.276	NEU	D	-0.224	NEU
nsp14	1	30	D	0.299	MIN	T	0.328	NEU
nsp14	1	31	K	-0.208	NEU	K	0.74	NEU
nsp14	1	32	F	0.953	MIN	F	0.557	NEU
nsp14	1	33	K	1.276	NEU	K	-0.131	NEU
nsp14	1	34	L	0.279	MIN	T	-0.37	NEU
nsp14	1	35	N	0.299	NEU	E	2.093	MIN
nsp14	1	36	G	0.023	NEU	G	-0.381	NEU
nsp14	1	37	L	0.489	NEU	L	0.359	NEU
nsp14	1	38	C	0.953	MIN	C	0.653	NEU
nsp14	1	39	V	0.953	MIN	V	1.334	MIN

nsp14	1	40	H	0.953	NEU	D	-0.042	NEU
nsp14	1	41	F	0.489	MIN	I	1.165	MIN
nsp14	1	42	D	-0.103	NEU	P	0.471	NEU
nsp14	1	43	T	0.636	NEU	G	-0.085	NEU
nsp14	1	44	I	0.489	MIN	I	1.535	MIN
nsp14	1	45	E	0.953	NEU	P	0.327	NEU
nsp14	1	46	K	0.489	MIN	K	1.152	MIN
nsp14	1	47	Q	0.012	NEU	D	-0.271	NEU
nsp14	1	48	M	0.110	NEU	M	-0.278	NEU
nsp14	1	49	P	0.402	NEU	T	-0.011	NEU
nsp14	1	50	Y	0.012	MIN	Y	-0.698	NEU
nsp14	1	51	R	-0.246	NEU	R	-0.384	NEU
nsp14	1	52	R	0.299	NEU	R	0.268	NEU
nsp14	1	53	L	1.276	MIN	L	0.916	MIN
nsp14	1	54	I	1.276	MIN	I	1.117	MIN
nsp14	1	55	S	1.276	NEU	S	-0.616	NEU
nsp14	1	56	M	0.299	MIN	M	1.165	MIN
nsp14	1	57	M	0.604	MIN	M	0.224	NEU
nsp14	1	58	G	0.754	NEU	G	-0.069	NEU
nsp14	1	59	F	1.276	MIN	F	1.111	MIN
nsp14	1	60	K	-0.246	MAX	K	-1.767	MAX
nsp14	1	61	F	0.279	NEU	M	-0.2	NEU
nsp14	1	62	D	0.953	MIN	N	0.82	MIN
nsp14	1	63	Y	-0.126	MIN	Y	-1.639	MAX
nsp14	1	64	Q	0.953	NEU	Q	0.451	NEU
nsp14	1	65	V	0.953	MIN	V	1.253	MIN
nsp14	1	66	P	0.299	NEU	N	1.03	MIN
nsp14	1	67	G	0.953	NEU	G	-0.607	NEU
nsp14	1	68	Y	-0.107	MAX	Y	1.367	MIN
nsp14	1	69	P	1.276	NEU	P	-0.652	NEU
nsp14	1	70	K	0.299	NEU	N	-0.981	NEU
nsp14	1	71	L	0.279	MIN	M	-0.008	NEU
nsp14	1	72	F	1.276	MIN	F	1.27	MIN
nsp14	1	73	I	1.276	MIN	I	2.129	MIN
nsp14	1	74	T	0.279	NEU	T	0.623	NEU
nsp14	1	75	R	1.276	NEU	R	-0.013	NEU
nsp14	1	76	E	1.276	NEU	E	-0.563	NEU
nsp14	1	77	E	0.754	NEU	E	-0.147	NEU
nsp14	1	78	A	1.276	NEU	A	0.343	NEU
nsp14	1	79	I	1.276	MIN	I	1.378	MIN
nsp14	1	80	K	0.279	MIN	R	0.509	NEU
nsp14	1	81	E	0.279	NEU	H	-0.253	NEU
nsp14	1	82	V	1.276	MIN	V	1.27	MIN
nsp14	1	83	R	1.276	NEU	R	-0.842	NEU
nsp14	1	84	G	1.276	NEU	A	0.416	NEU
nsp14	1	85	W	1.276	NEU	W	0.541	NEU

nsp14	1	86	I	1.276	MIN	I	1.246	MIN
nsp14	1	87	G	1.276	NEU	G	-0.53	NEU
nsp14	1	88	F	1.276	MIN	F	1.203	MIN
nsp14	1	89	D	1.276	MAX	D	-1.343	MAX
nsp14	1	90	V	1.276	MIN	V	1.15	MIN
nsp14	1	91	E	1.276	MAX	E	-1.312	MAX
nsp14	1	92	G	0.953	NEU	G	-0.249	NEU
nsp14	1	93	A	0.299	NEU	C	1.792	MIN
nsp14	1	94	H	1.276	NEU	H	-0.424	NEU
nsp14	1	95	A	0.489	MIN	A	0.991	MIN
nsp14	1	96	C	0.279	NEU	T	-0.403	NEU
nsp14	1	97	G	0.953	NEU	R	-0.648	NEU
nsp14	1	98	P	0.023	NEU	E	-0.365	NEU
nsp14	1	99	A	0.754	NEU	A	0.386	NEU
nsp14	1	100	V	0.754	MIN	V	1.147	MIN
nsp14	1	101	G	0.299	NEU	G	-0.65	NEU
nsp14	1	102	T	1.276	NEU	T	-0.257	NEU
nsp14	1	103	N	1.276	NEU	N	-0.702	NEU
nsp14	1	104	L	1.276	MIN	L	1.178	MIN
nsp14	1	105	P	1.276	NEU	P	-0.903	NEU
nsp14	1	106	L	1.276	MIN	L	1.069	MIN
nsp14	1	107	Q	0.953	NEU	Q	-0.901	NEU
nsp14	1	108	I	1.276	MIN	L	1.221	MIN
nsp14	1	109	G	1.276	NEU	G	-0.815	NEU
nsp14	1	110	F	1.276	MIN	F	1.228	MIN
nsp14	1	111	S	1.276	NEU	S	-0.679	NEU
nsp14	1	112	T	0.953	NEU	T	-0.227	NEU
nsp14	1	113	G	0.339	NEU	G	-0.986	NEU
nsp14	1	114	V	0.953	MIN	V	1.41	MIN
nsp14	1	115	N	0.953	NEU	N	-0.808	NEU
nsp14	1	116	F	0.953	MIN	L	0.894	MIN
nsp14	1	117	V	1.276	MIN	V	1.129	MIN
nsp14	1	118	V	0.279	MIN	A	0.479	NEU
nsp14	1	119	T	0.299	NEU	V	1.189	MIN
nsp14	1	120	P	0.754	NEU	P	-0.855	NEU
nsp14	1	121	T	0.953	NEU	T	-0.6	NEU
nsp14	1	122	G	1.276	NEU	G	-0.449	NEU
nsp14	1	123	Y	-0.107	MAX	Y	-1.225	MAX
nsp14	1	124	V	1.276	MIN	V	0.96	MIN
nsp14	1	125	D	0.636	NEU	D	-0.883	NEU
nsp14	1	126	T	0.953	NEU	T	0.227	NEU
nsp14	1	127	E	0.023	MAX	P	0.377	NEU
nsp14	1	128	S	0.190	NEU	N	-0.045	NEU
nsp14	1	129	G	0.442	NEU	N	0.689	NEU
nsp14	1	130	T	0.953	NEU	T	0.083	NEU
nsp14	1	131	E	0.402	NEU	D	-0.129	NEU

nsp14	1	132	F	0.299	MIN	F	0.2	NEU
nsp14	1	133	A	0.754	NEU	S	-0.311	NEU
nsp14	1	134	R	0.953	NEU	R	-0.691	NEU
nsp14	1	135	V	1.276	MIN	V	1.234	MIN
nsp14	1	136	V	0.636	NEU	S	-0.596	NEU
nsp14	1	137	A	0.279	MIN	A	0.604	NEU
nsp14	1	138	K	0.299	NEU	K	-1.56	MAX
nsp14	1	139	P	0.754	NEU	P	-0.611	NEU
nsp14	1	140	P	0.299	NEU	P	0.798	MIN
nsp14	1	141	P	0.953	MIN	P	0.992	MIN
nsp14	1	142	G	1.276	NEU	G	0.033	NEU
nsp14	1	143	D	0.953	MIN	D	2.192	MIN
nsp14	1	144	Q	0.953	NEU	Q	-0.632	NEU
nsp14	1	145	F	0.953	MIN	F	1.13	MIN
nsp14	1	146	K	0.299	MIN	K	0.722	NEU
nsp14	1	147	H	0.442	MIN	H	0.82	MIN
nsp14	1	148	L	1.276	MIN	L	0.924	MIN
nsp14	1	149	I	0.953	MIN	I	1.723	MIN
nsp14	1	150	P	0.279	NEU	P	0.645	NEU
nsp14	1	151	L	1.276	MIN	L	0.884	MIN
nsp14	1	152	M	0.604	MIN	M	0.718	NEU
nsp14	1	153	R	0.442	NEU	Y	0.249	NEU
nsp14	1	154	K	0.279	NEU	K	-1.259	MAX
nsp14	1	155	G	1.276	NEU	G	-0.47	NEU
nsp14	1	156	E	0.012	MIN	L	1.338	MIN
nsp14	1	157	P	0.754	MAX	P	-1.148	MAX
nsp14	1	158	W	0.279	MIN	W	0.522	NEU
nsp14	1	159	N	0.953	NEU	N	-0.029	NEU
nsp14	1	160	V	0.754	MIN	V	1.363	MIN
nsp14	1	161	V	1.276	MIN	V	1.372	MIN
nsp14	1	162	R	1.276	NEU	R	-0.622	NEU
nsp14	1	163	K	0.023	NEU	I	1.679	MIN
nsp14	1	164	R	0.299	NEU	K	-1.471	MAX
nsp14	1	165	I	1.276	MIN	I	1.458	MIN
nsp14	1	166	V	1.276	MIN	V	1.137	MIN
nsp14	1	167	E	0.299	NEU	Q	-1.366	MAX
nsp14	1	168	M	0.754	MIN	M	0.561	NEU
nsp14	1	169	L	0.754	MIN	L	1.334	MIN
nsp14	1	170	C	0.604	NEU	S	-0.8	NEU
nsp14	1	171	D	0.299	NEU	D	-0.205	NEU
nsp14	1	172	T	1.276	NEU	T	-0.271	NEU
nsp14	1	173	L	1.276	MIN	L	1.539	MIN
nsp14	1	174	D	0.953	NEU	K	0.34	NEU
nsp14	1	175	G	1.276	NEU	N	-0.403	NEU
nsp14	1	176	V	1.276	MIN	L	1.219	MIN
nsp14	1	177	S	1.276	NEU	S	-0.51	NEU

nsp14	1	178	D	0.299	MIN	D	0.355	NEU
nsp14	1	179	R	0.953	NEU	R	-0.863	NEU
nsp14	1	180	V	1.276	MIN	V	1.103	MIN
nsp14	1	181	V	0.279	MIN	V	1.143	MIN
nsp14	1	182	F	1.276	MIN	F	1.442	MIN
nsp14	1	183	V	1.276	MIN	V	1.257	MIN
nsp14	1	184	T	0.299	NEU	L	1.055	MIN
nsp14	1	185	W	1.276	MIN	W	0.94	MIN
nsp14	1	186	A	1.276	NEU	A	-0.783	NEU
nsp14	1	187	H	1.276	NEU	H	-0.201	NEU
nsp14	1	188	G	1.276	NEU	G	-0.691	NEU
nsp14	1	189	F	0.953	NEU	F	0.08	NEU
nsp14	1	190	E	1.276	MAX	E	-1.544	MAX
nsp14	1	191	L	1.276	MIN	L	1.405	MIN
nsp14	1	192	T	1.276	NEU	T	-0.163	NEU
nsp14	1	193	T	1.276	NEU	S	-0.78	NEU
nsp14	1	194	M	0.299	MIN	M	0.414	NEU
nsp14	1	195	H	0.279	NEU	K	-1.295	MAX
nsp14	1	196	Y	0.953	NEU	Y	-0.63	NEU
nsp14	1	197	F	1.276	MIN	F	1.343	MIN
nsp14	1	198	V	0.339	MIN	V	1.305	MIN
nsp14	1	199	K	0.489	MAX	K	-1.171	MAX
nsp14	1	200	I	0.754	MIN	I	1.92	MIN
nsp14	1	201	G	1.276	NEU	G	0.023	NEU
nsp14	1	202	P	0.254	NEU	P	-0.258	NEU
nsp14	1	203	E	0.339	NEU	E	0.148	NEU
nsp14	1	204	R	0.279	NEU	R	0.913	MIN
nsp14	1	205	T	0.953	NEU	T	-0.946	NEU
nsp14	1	206	C	1.276	MIN	C	1.677	MIN
nsp14	1	207	C	0.953	MIN	C	1.271	MIN
nsp14	1	208	L	-0.220	MIN	L	0.72	NEU
nsp14	1	209	C	1.276	MIN	C	0.821	MIN
nsp14	1	210	D	0.279	MIN	D	0.936	MIN
nsp14	1	211	K	0.953	NEU	R	-0.39	NEU
nsp14	1	212	R	0.953	MIN	R	2.259	MIN
nsp14	1	213	A	1.276	NEU	A	-0.079	NEU
nsp14	1	214	T	0.190	NEU	T	-0.941	NEU
nsp14	1	215	C	0.953	MIN	C	1.435	MIN
nsp14	1	216	F	0.402	MIN	F	1.338	MIN
nsp14	1	217	S	0.953	NEU	S	-0.626	NEU
nsp14	1	218	S	1.276	NEU	T	0.222	NEU
nsp14	1	219	V	0.023	NEU	A	-1.002	MAX
nsp14	1	220	Y	1.276	NEU	S	-0.224	NEU
nsp14	1	221	D	0.279	NEU	D	-1.126	MAX
nsp14	1	222	A	1.276	NEU	T	-0.077	NEU
nsp14	1	223	Y	-0.246	NEU	Y	0.753	NEU

nsp14	1	224	A	1.276	NEU	A	-0.066	NEU
nsp14	1	225	C	1.276	MIN	C	2.325	MIN
nsp14	1	226	W	0.953	NEU	W	-0.107	NEU
nsp14	1	227	S	0.953	NEU	H	-0.825	NEU
nsp14	1	228	H	1.276	NEU	H	-0.209	NEU
nsp14	1	229	H	0.953	NEU	S	-0.673	NEU
nsp14	1	230	G	0.279	MIN	I	2.356	MIN
nsp14	1	231	G	0.953	NEU	G	-0.916	NEU
nsp14	1	232	A	0.604	NEU	F	0.582	NEU
nsp14	1	233	D	0.279	MAX	D	-1.172	MAX
nsp14	1	234	Y	0.279	MIN	Y	0.487	NEU
nsp14	1	235	V	1.276	MIN	V	1.088	MIN
nsp14	1	236	Y	1.276	MIN	Y	0.73	NEU
nsp14	1	237	N	0.299	NEU	N	-1.038	MAX
nsp14	1	238	P	0.299	NEU	P	-0.951	NEU
nsp14	1	239	F	1.276	MIN	F	1.458	MIN
nsp14	1	240	L	1.276	MIN	M	0.743	NEU
nsp14	1	241	V	1.276	MIN	I	1.226	MIN
nsp14	1	242	D	0.402	MAX	D	-1.159	MAX
nsp14	1	243	V	1.276	MIN	V	1.266	MIN
nsp14	1	244	Q	1.276	NEU	Q	-0.804	NEU
nsp14	1	245	Q	0.754	NEU	Q	-0.88	NEU
nsp14	1	246	W	1.276	NEU	W	0.398	NEU
nsp14	1	247	G	1.276	NEU	G	-0.525	NEU
nsp14	1	248	Y	-0.220	MIN	F	1.308	MIN
nsp14	1	249	V	1.276	NEU	T	0.446	NEU
nsp14	1	250	G	1.276	NEU	G	-0.29	NEU
nsp14	1	251	N	0.279	NEU	N	0.714	NEU
nsp14	1	252	L	1.276	MIN	L	1.025	MIN
nsp14	1	253	Q	1.276	NEU	Q	-0.058	NEU
nsp14	1	254	S	0.489	NEU	S	0.389	NEU
nsp14	1	255	N	0.402	NEU	N	-1.088	MAX
nsp14	1	256	H	0.402	NEU	H	0.284	NEU
nsp14	1	257	D	0.604	NEU	D	0.134	NEU
nsp14	1	258	N	-0.057	NEU	L	0.286	NEU
nsp14	1	259	V	0.055	MIN	Y	-2.137	MAX
nsp14	1	260	C	1.276	MIN	C	1.241	MIN
nsp14	1	261	D	0.279	MIN	Q	-0.378	NEU
nsp14	1	262	V	0.953	MIN	V	1.25	MIN
nsp14	1	263	H	0.489	MIN	H	0.864	MIN
nsp14	1	264	G	0.279	NEU	G	-0.518	NEU
nsp14	1	265	G	0.299	NEU	N	-1.06	MAX
nsp14	1	266	A	1.276	MAX	A	-1.24	MAX
nsp14	1	267	H	0.953	MIN	H	0.709	NEU
nsp14	1	268	V	0.953	NEU	V	-0.079	NEU
nsp14	1	269	A	0.279	MIN	A	0.497	NEU

nsp14	1	270	S	1.276	NEU	S	-0.752	NEU
nsp14	1	271	C	-0.103	MIN	C	0.864	MIN
nsp14	1	272	D	0.953	MAX	D	-1.062	MAX
nsp14	1	273	A	1.276	NEU	A	0.198	NEU
nsp14	1	274	I	0.953	MIN	I	1.135	MIN
nsp14	1	275	M	1.276	NEU	M	-0.122	NEU
nsp14	1	276	T	1.276	NEU	T	-0.187	NEU
nsp14	1	277	R	1.276	NEU	R	-0.789	NEU
nsp14	1	278	C	1.276	MIN	C	1.657	MIN
nsp14	1	279	L	1.276	MIN	L	1.03	MIN
nsp14	1	280	A	1.276	NEU	A	0.046	NEU
nsp14	1	281	I	1.276	MIN	V	1.234	MIN
nsp14	1	282	H	1.276	NEU	H	-0.033	NEU
nsp14	1	283	D	1.276	NEU	E	-0.532	NEU
nsp14	1	284	C	1.276	MIN	C	1.267	MIN
nsp14	1	285	F	1.276	MIN	F	1.341	MIN
nsp14	1	286	V	1.276	MIN	V	1.528	MIN
nsp14	1	287	K	0.489	NEU	K	-0.047	NEU
nsp14	1	288	E	-0.126	MIN	R	1.616	MIN
nsp14	1	289	V	1.276	MIN	V	1.533	MIN
nsp14	1	290	N	0.442	NEU	D	-0.354	NEU
nsp14	1	291	W	0.254	NEU	W	-1.862	MAX
nsp14	1	292	D	0.299	MIN	T	0.38	NEU
nsp14	1	293	V	1.276	MIN	I	1.803	MIN
nsp14	1	294	E	0.299	MIN	E	1.182	MIN
nsp14	1	295	Y	0.117	NEU	Y	-1.454	MAX
nsp14	1	296	P	0.489	MIN	P	0.529	NEU
nsp14	1	297	I	0.754	MIN	I	1.467	MIN
nsp14	1	298	I	1.276	MIN	I	1.417	MIN
nsp14	1	299	A	0.489	NEU	G	-1.091	MAX
nsp14	1	300	D	0.754	NEU	D	-0.664	NEU
nsp14	1	301	E	0.489	MAX	E	-1.102	MAX
nsp14	1	302	L	0.442	MIN	L	1.099	MIN
nsp14	1	303	A	0.754	NEU	K	-0.198	NEU
nsp14	1	304	I	1.276	MIN	I	1.418	MIN
nsp14	1	305	N	1.276	NEU	N	-0.694	NEU
nsp14	1	306	K	-0.126	NEU	A	0.508	NEU
nsp14	1	307	A	0.489	NEU	A	0.462	NEU
nsp14	1	308	C	1.276	MIN	C	1.188	MIN
nsp14	1	309	R	1.276	NEU	R	-0.562	NEU
nsp14	1	310	K	0.298	NEU	K	-1.079	MAX
nsp14	1	311	V	1.276	MIN	V	1.186	MIN
nsp14	1	312	Q	0.339	MAX	Q	-1.079	MAX
nsp14	1	313	R	0.489	NEU	H	-0.244	NEU
nsp14	1	314	M	0.339	MIN	M	0.485	NEU
nsp14	1	315	V	0.754	MIN	V	1.5	MIN

nsp14	1	316	L	1.276	MIN	V	1.281	MIN
nsp14	1	317	K	0.754	MAX	K	-1.273	MAX
nsp14	1	318	A	0.953	NEU	A	0.551	NEU
nsp14	1	319	A	0.953	MIN	A	0.555	NEU
nsp14	1	320	L	0.953	MIN	L	1.587	MIN
nsp14	1	321	L	-0.171	MIN	L	1.533	MIN
nsp14	1	322	A	0.402	NEU	A	0.608	NEU
nsp14	1	323	D	-0.126	MIN	D	-1.174	MAX
nsp14	1	324	K	0.012	MIN	K	0.429	NEU
nsp14	1	325	F	0.953	MIN	F	0.772	NEU
nsp14	1	326	P	0.279	NEU	P	-1.177	MAX
nsp14	1	327	T	0.299	NEU	V	1.092	MIN
nsp14	1	328	I	1.276	MIN	L	1.182	MIN
nsp14	1	329	H	0.489	NEU	H	0.066	NEU
nsp14	1	330	D	0.339	MAX	D	-1.458	MAX
nsp14	1	331	I	1.276	MIN	I	1.107	MIN
nsp14	1	332	G	1.276	NEU	G	-0.141	NEU
nsp14	1	333	N	1.276	NEU	N	-0.696	NEU
nsp14	1	334	P	0.279	NEU	P	-0.914	NEU
nsp14	1	335	K	1.276	MAX	K	-1.576	MAX
nsp14	1	336	A	0.339	MIN	A	-0.322	NEU
nsp14	1	337	I	0.489	NEU	I	0.48	NEU
nsp14	1	338	K	0.339	NEU	K	-1.034	MAX
nsp14	1	339	C	0.953	MIN	C	1.509	MIN
nsp14	1	340	V	-0.246	MIN	V	1.136	MIN
nsp14	1	341	G	0.934	NEU	P	-0.944	NEU
nsp14	1	342	V	0.316	MIN	Q	-0.031	NEU
nsp14	1	343	A	0.636	NEU	A	0.338	NEU
nsp14	1	344	V	0.754	MIN	D	0.87	MIN
nsp14	1	345	V	0.279	NEU	V	1.228	MIN
nsp14	1	346	N	0.190	NEU	E	-0.892	NEU
nsp14	1	347	W	0.953	NEU	W	-0.003	NEU
nsp14	1	348	K	0.604	NEU	K	-0.674	NEU
nsp14	1	349	F	0.489	NEU	F	-0.012	NEU
nsp14	1	350	Y	-0.107	MAX	Y	0.753	NEU
nsp14	1	351	D	0.754	NEU	D	-1.269	MAX
nsp14	1	352	A	0.754	NEU	A	0.141	NEU
nsp14	1	353	K	0.190	NEU	Q	-0.65	NEU
nsp14	1	354	P	1.276	NEU	P	0.513	NEU
nsp14	1	355	V	1.276	MIN	C	0.936	MIN
nsp14	1	356	V	0.279	NEU	S	0.394	NEU
nsp14	1	357	D	0.110	NEU	D	-0.962	NEU
nsp14	1	358	-	0.637	MAX	K	-1.476	MAX
nsp14	1	359	-	0.637	MAX	A	-1.08	MAX
nsp14	1	360	-	0.637	MAX	Y	-2.014	MAX
nsp14	1	361	K	0.299	NEU	K	1.081	MIN

nsp14	1	362	V	0.953	MIN	I	1.053	MIN
nsp14	1	363	E	0.953	NEU	E	0.161	NEU
nsp14	1	364	E	0.953	NEU	E	-0.767	NEU
nsp14	1	365	L	0.953	MIN	L	0.926	MIN
nsp14	1	366	H	0.110	NEU	F	-0.731	NEU
nsp14	1	367	Y	0.953	NEU	Y	-0.33	NEU
nsp14	1	368	S	0.754	NEU	S	0.013	NEU
nsp14	1	369	Y	0.489	MAX	Y	-2.88	MAX
nsp14	1	370	A	-0.290	MAX	A	-1.071	MAX
nsp14	1	371	T	0.754	NEU	T	-0.224	NEU
nsp14	1	372	H	1.276	NEU	H	-0.333	NEU
nsp14	1	373	K	0.754	NEU	S	-0.586	NEU
nsp14	1	374	D	0.604	MIN	D	0.628	NEU
nsp14	1	375	Q	-0.304	MIN	K	0.395	NEU
nsp14	1	376	F	0.279	NEU	F	0.869	MIN
nsp14	1	377	K	0.023	MIN	T	0.193	NEU
nsp14	1	378	D	0.015	NEU	D	-0.877	NEU
nsp14	1	379	G	1.276	NEU	G	-0.393	NEU
nsp14	1	380	L	1.276	MIN	V	1.21	MIN
nsp14	1	381	C	0.279	NEU	C	1.468	MIN
nsp14	1	382	L	1.276	MIN	L	0.938	MIN
nsp14	1	383	F	1.276	MIN	F	1.279	MIN
nsp14	1	384	W	0.279	NEU	W	0.663	NEU
nsp14	1	385	N	1.276	NEU	N	-0.58	NEU
nsp14	1	386	C	1.276	MIN	C	0.992	MIN
nsp14	1	387	N	0.279	NEU	N	-0.963	NEU
nsp14	1	388	V	1.276	MIN	V	1.23	MIN
nsp14	1	389	D	0.754	MAX	D	-1.218	MAX
nsp14	1	390	C	0.279	MIN	R	0.236	NEU
nsp14	1	391	Y	0.402	MIN	Y	0.56	NEU
nsp14	1	392	P	0.299	MAX	P	-1.014	MAX
nsp14	1	393	A	-0.304	MIN	A	-1.164	MAX
nsp14	1	394	N	0.604	NEU	N	-1.002	MAX
nsp14	1	395	A	1.276	NEU	S	-0.693	NEU
nsp14	1	396	L	1.276	MIN	I	1.36	MIN
nsp14	1	397	V	1.276	MIN	V	1.307	MIN
nsp14	1	398	C	1.276	MIN	C	1.141	MIN
nsp14	1	399	R	1.276	NEU	R	-0.355	NEU
nsp14	1	400	F	1.276	MIN	F	1.21	MIN
nsp14	1	401	D	0.298	NEU	D	0.037	NEU
nsp14	1	402	T	1.276	NEU	T	-0.367	NEU
nsp14	1	403	R	1.276	MIN	R	2.185	MIN
nsp14	1	404	V	1.276	NEU	V	-0.109	NEU
nsp14	1	405	L	0.953	NEU	L	-0.529	NEU
nsp14	1	406	S	1.276	NEU	S	-0.572	NEU
nsp14	1	407	K	-0.103	MAX	N	0.93	MIN

nsp14	1	408	L	1.276	MIN	L	0.774	NEU
nsp14	1	409	N	1.276	NEU	N	-0.873	NEU
nsp14	1	410	L	1.276	MIN	L	0.976	MIN
nsp14	1	411	P	0.339	MIN	P	0.932	MIN
nsp14	1	412	G	1.276	NEU	G	-0.191	NEU
nsp14	1	413	C	1.276	MIN	C	1.593	MIN
nsp14	1	414	N	0.279	MAX	D	-1.486	MAX
nsp14	1	415	G	1.276	NEU	G	0.129	NEU
nsp14	1	416	G	1.276	NEU	G	-0.244	NEU
nsp14	1	417	S	1.276	NEU	S	-0.01	NEU
nsp14	1	418	L	1.276	MIN	L	0.898	MIN
nsp14	1	419	Y	0.953	NEU	Y	-0.653	NEU
nsp14	1	420	V	1.276	MIN	V	1.166	MIN
nsp14	1	421	N	1.276	NEU	N	-0.823	NEU
nsp14	1	422	K	0.754	NEU	K	-0.306	NEU
nsp14	1	423	H	1.276	NEU	H	-0.018	NEU
nsp14	1	424	A	1.276	NEU	A	0.499	NEU
nsp14	1	425	F	1.276	MIN	F	1.158	MIN
nsp14	1	426	H	1.276	NEU	H	-0.392	NEU
nsp14	1	427	T	1.276	NEU	T	-0.368	NEU
nsp14	1	428	P	0.754	NEU	P	0.035	NEU
nsp14	1	429	A	0.604	NEU	A	0.157	NEU
nsp14	1	430	F	0.254	NEU	F	-0.233	NEU
nsp14	1	431	D	1.276	NEU	D	0.167	NEU
nsp14	1	432	K	0.953	MAX	K	-1.534	MAX
nsp14	1	433	S	0.489	NEU	S	-0.26	NEU
nsp14	1	434	A	1.276	NEU	A	-0.217	NEU
nsp14	1	435	F	1.276	NEU	F	-0.441	NEU
nsp14	1	436	V	0.023	NEU	V	1.041	MIN
nsp14	1	437	N	0.604	NEU	N	0.131	NEU
nsp14	1	438	L	1.276	MIN	L	1.127	MIN
nsp14	1	439	K	0.953	MAX	K	-2.131	MAX
nsp14	1	440	P	0.299	NEU	Q	-1.008	MAX
nsp14	1	441	L	1.276	MIN	L	1.407	MIN
nsp14	1	442	P	1.276	NEU	P	-0.601	NEU
nsp14	1	443	F	0.604	NEU	F	0.209	NEU
nsp14	1	444	F	1.276	MIN	F	0.932	MIN
nsp14	1	445	Y	0.953	MIN	Y	0.612	NEU
nsp14	1	446	Y	0.953	MIN	Y	0.544	NEU
nsp14	1	447	S	0.953	NEU	S	-0.117	NEU
nsp14	1	448	D	0.754	NEU	D	0.511	NEU
nsp14	1	449	T	0.953	NEU	S	0.006	NEU
nsp14	1	450	P	0.279	MIN	P	0.981	MIN
nsp14	1	451	C	1.276	MIN	C	2.492	MIN
nsp14	1	452	E	0.254	NEU	E	0.745	NEU
nsp14	1	453	S	-0.148	MIN	S	0.061	NEU

nsp14	1	454	A	0.023	NEU	H	1.089	MIN
nsp14	1	455	G	0.023	NEU	G	0.024	NEU
nsp14	1	456	G	0.316	NEU	K	-0.03	NEU
nsp14	1	457	Q	-0.246	MAX	Q	-0.505	NEU
nsp14	1	458	V	0.190	NEU	V	-0.209	NEU
nsp14	1	459	V	0.299	MIN	V	0.75	NEU
nsp14	1	460	S	0.254	NEU	S	-0.741	NEU
nsp14	1	461	D	0.299	MAX	D	-0.403	NEU
nsp14	1	462	V	1.276	MIN	I	2.018	MIN
nsp14	1	463	D	0.110	NEU	D	-0.327	NEU
nsp14	1	464	Y	0.442	NEU	Y	0.125	NEU
nsp14	1	465	V	1.276	MIN	V	1.278	MIN
nsp14	1	466	P	1.276	NEU	P	-0.718	NEU
nsp14	1	467	L	1.276	MIN	L	1.066	MIN
nsp14	1	468	K	0.190	NEU	K	-0.091	NEU
nsp14	1	469	S	1.276	NEU	S	-0.465	NEU
nsp14	1	470	N	0.953	NEU	A	-1.108	MAX
nsp14	1	471	V	0.023	MIN	T	-0.564	NEU
nsp14	1	472	C	1.276	MIN	C	1.857	MIN
nsp14	1	473	I	1.276	MIN	I	1.155	MIN
nsp14	1	474	T	1.276	NEU	T	-0.764	NEU
nsp14	1	475	R	0.604	NEU	R	1.205	MIN
nsp14	1	476	C	1.276	MIN	C	1.493	MIN
nsp14	1	477	N	0.489	MAX	N	-1.028	MAX
nsp14	1	478	L	1.276	MIN	L	1.15	MIN
nsp14	1	479	G	0.953	NEU	G	-1.204	MAX
nsp14	1	480	G	1.276	NEU	G	-0.496	NEU
nsp14	1	481	A	0.604	NEU	A	0.511	NEU
nsp14	1	482	V	1.276	MIN	V	1.511	MIN
nsp14	1	483	C	1.276	MIN	C	2.177	MIN
nsp14	1	484	K	0.754	NEU	R	-0.186	NEU
nsp14	1	485	K	0.110	NEU	H	0.905	MIN
nsp14	1	486	H	0.754	NEU	H	0.007	NEU
nsp14	1	487	A	0.953	NEU	A	0.127	NEU
nsp14	1	488	D	-0.126	NEU	N	-0.939	NEU
nsp14	1	489	E	0.754	MAX	E	-1.311	MAX
nsp14	1	490	Y	1.276	NEU	Y	-0.171	NEU
nsp14	1	491	R	0.279	NEU	R	0.298	NEU
nsp14	1	492	Q	-0.057	NEU	L	0.175	NEU
nsp14	1	493	F	0.279	MIN	Y	-0.204	NEU
nsp14	1	494	L	1.276	MIN	L	1.109	MIN
nsp14	1	495	E	0.953	NEU	D	-0.456	NEU
nsp14	1	496	A	0.442	NEU	A	0.421	NEU
nsp14	1	497	Y	1.276	NEU	Y	0.124	NEU
nsp14	1	498	N	0.299	MAX	N	-0.832	NEU
nsp14	1	499	T	0.754	NEU	M	0.064	NEU

nsp14	1	500	M	0.754	MIN	M	0.803	MIN
nsp14	1	501	I	0.953	MIN	I	1.565	MIN
nsp14	1	502	S	0.953	NEU	S	-0.469	NEU
nsp14	1	503	A	1.276	NEU	A	0.329	NEU
nsp14	1	504	G	1.276	NEU	G	-0.395	NEU
nsp14	1	505	F	1.276	MIN	F	1.193	MIN
nsp14	1	506	T	1.276	NEU	S	-0.029	NEU
nsp14	1	507	L	1.276	MIN	L	1.149	MIN
nsp14	1	508	W	0.604	MIN	W	0.589	NEU
nsp14	1	509	V	1.276	MIN	V	1.294	MIN
nsp14	1	510	Y	-0.171	NEU	Y	0.564	NEU
nsp14	1	511	K	0.604	MAX	K	-1.55	MAX
nsp14	1	512	Q	0.442	NEU	Q	-0.475	NEU
nsp14	1	513	F	0.489	MIN	F	0.596	NEU
nsp14	1	514	D	0.754	MAX	D	-1.348	MAX
nsp14	1	515	T	0.279	MIN	T	-0.377	NEU
nsp14	1	516	Y	0.012	MIN	Y	-0.573	NEU
nsp14	1	517	N	0.279	MIN	N	0.718	NEU
nsp14	1	518	L	1.276	MIN	L	1.187	MIN
nsp14	1	519	W	0.190	NEU	W	-1.113	MAX
nsp14	1	520	S	0.953	NEU	N	-0.315	NEU
nsp14	1	521	T	0.953	NEU	T	-0.342	NEU
nsp14	1	522	F	1.276	MIN	F	1.219	MIN
nsp15	1	1	S	1.301	NEU	S	-0.345	NEU
nsp15	1	2	L	1.301	MIN	L	0.961	MIN
nsp15	1	3	E	0.563	MAX	E	-1.091	MAX
nsp15	1	4	N	1.301	NEU	N	-0.382	NEU
nsp15	1	5	V	1.301	MIN	V	1.468	MIN
nsp15	1	6	A	1.301	MIN	A	0.86	MIN
nsp15	1	7	Y	0.260	MAX	F	0.956	MIN
nsp15	1	8	N	1.301	NEU	N	-0.499	NEU
nsp15	1	9	V	1.301	MIN	V	1.32	MIN
nsp15	1	10	V	1.301	MIN	V	1.557	MIN
nsp15	1	11	N	1.301	NEU	N	-0.638	NEU
nsp15	1	12	K	0.321	MAX	K	-1.016	MAX
nsp15	1	13	G	1.301	NEU	G	-0.701	NEU
nsp15	1	14	H	1.301	NEU	H	-0.87	NEU
nsp15	1	15	F	1.051	NEU	F	0.216	NEU
nsp15	1	16	D	1.301	MIN	D	2.041	MIN
nsp15	1	17	G	0.651	NEU	G	-1.142	MAX
nsp15	1	18	Q	1.301	NEU	Q	0.108	NEU
nsp15	1	19	Q	0.126	NEU	Q	-0.104	NEU
nsp15	1	20	G	0.651	NEU	G	-1.157	MAX
nsp15	1	21	E	1.301	MAX	E	-1.433	MAX
nsp15	1	22	A	0.490	NEU	V	1.32	MIN
nsp15	1	23	P	0.321	MAX	P	-1.385	MAX

nsp15	1	24	V	1.301	MIN	V	1.29	MIN
nsp15	1	25	S	0.651	MAX	S	-1.087	MAX
nsp15	1	26	I	1.301	MIN	I	1.62	MIN
nsp15	1	27	I	1.301	MIN	I	1.642	MIN
nsp15	1	28	N	1.301	NEU	N	-0.483	NEU
nsp15	1	29	N	0.490	NEU	N	-0.987	NEU
nsp15	1	30	A	1.301	NEU	T	0.083	NEU
nsp15	1	31	V	1.301	MIN	V	1.549	MIN
nsp15	1	32	Y	1.301	NEU	Y	-0.493	NEU
nsp15	1	33	T	1.301	NEU	T	-0.224	NEU
nsp15	1	34	K	1.301	NEU	K	-0.801	NEU
nsp15	1	35	V	1.301	MIN	V	1.415	MIN
nsp15	1	36	D	0.757	NEU	D	-0.702	NEU
nsp15	1	37	G	1.301	NEU	G	-0.29	NEU
nsp15	1	38	V	0.412	MIN	V	1.087	MIN
nsp15	1	39	D	1.301	NEU	D	-0.771	NEU
nsp15	1	40	V	1.301	MIN	V	1.602	MIN
nsp15	1	41	E	0.430	MAX	E	-0.803	NEU
nsp15	1	42	I	1.301	MIN	L	1.167	MIN
nsp15	1	43	F	1.301	MIN	F	1.041	MIN
nsp15	1	44	E	1.301	NEU	E	-0.247	NEU
nsp15	1	45	N	1.301	NEU	N	-0.267	NEU
nsp15	1	46	K	1.301	MIN	K	2.021	MIN
nsp15	1	47	T	1.301	NEU	T	-0.677	NEU
nsp15	1	48	T	1.051	NEU	T	-0.391	NEU
nsp15	1	49	L	1.301	MIN	L	1.077	MIN
nsp15	1	50	P	1.301	NEU	P	-0.44	NEU
nsp15	1	51	V	1.301	MIN	V	1.085	MIN
nsp15	1	52	N	1.301	MAX	N	-1.096	MAX
nsp15	1	53	V	1.301	MIN	V	1.228	MIN
nsp15	1	54	A	1.301	NEU	A	-0.023	NEU
nsp15	1	55	F	1.301	MIN	F	0.714	NEU
nsp15	1	56	E	1.301	NEU	E	-0.883	NEU
nsp15	1	57	L	1.301	MIN	L	1.327	MIN
nsp15	1	58	W	1.301	NEU	W	0.245	NEU
nsp15	1	59	A	1.301	NEU	A	0.471	NEU
nsp15	1	60	K	1.301	MAX	K	-1.201	MAX
nsp15	1	61	R	1.301	NEU	R	-0.743	NEU
nsp15	1	62	N	0.804	MAX	N	-1.145	MAX
nsp15	1	63	I	0.490	NEU	I	0.311	NEU
nsp15	1	64	K	0.301	MIN	K	0.593	NEU
nsp15	1	65	P	0.490	MAX	P	-1.198	MAX
nsp15	1	66	V	1.301	MIN	V	1.147	MIN
nsp15	1	67	P	1.301	NEU	P	-0.848	NEU
nsp15	1	68	E	0.887	MAX	E	-1.069	MAX
nsp15	1	69	I	1.301	MIN	V	1.617	MIN

nsp15	1	70	K	1.301	NEU	K	-0.546	NEU
nsp15	1	71	I	1.301	MIN	I	1.4	MIN
nsp15	1	72	L	1.301	MIN	L	1.144	MIN
nsp15	1	73	N	0.757	NEU	N	-0.948	NEU
nsp15	1	74	N	0.563	NEU	N	-0.982	NEU
nsp15	1	75	L	1.301	MIN	L	1.141	MIN
nsp15	1	76	G	1.301	NEU	G	-0.647	NEU
nsp15	1	77	V	1.301	MIN	V	1.364	MIN
nsp15	1	78	D	1.301	NEU	D	-0.398	NEU
nsp15	1	79	I	1.301	MIN	I	1.084	MIN
nsp15	1	80	A	1.301	NEU	A	0.043	NEU
nsp15	1	81	A	0.430	MIN	A	0.618	NEU
nsp15	1	82	N	0.321	NEU	N	-1.059	MAX
nsp15	1	83	T	1.301	NEU	T	-0.141	NEU
nsp15	1	84	V	1.301	MIN	V	1.169	MIN
nsp15	1	85	I	1.301	MIN	I	1.923	MIN
nsp15	1	86	W	1.301	NEU	W	-0.177	NEU
nsp15	1	87	D	0.887	NEU	D	-0.744	NEU
nsp15	1	88	Y	0.757	MAX	Y	-2.957	MAX
nsp15	1	89	K	0.887	MIN	K	1.55	MIN
nsp15	1	90	R	1.301	NEU	R	-0.211	NEU
nsp15	1	91	E	1.301	NEU	D	0.288	NEU
nsp15	1	92	A	1.051	NEU	A	-0.563	NEU
nsp15	1	93	P	0.651	NEU	P	-1.051	MAX
nsp15	1	94	A	1.051	NEU	A	0.028	NEU
nsp15	1	95	H	1.301	NEU	H	-0.164	NEU
nsp15	1	96	V	1.301	MIN	I	1.552	MIN
nsp15	1	97	S	1.301	NEU	S	-0.703	NEU
nsp15	1	98	T	1.301	NEU	T	-0.287	NEU
nsp15	1	99	I	1.301	MIN	I	1.949	MIN
nsp15	1	100	G	1.301	NEU	G	-0.312	NEU
nsp15	1	101	V	1.301	MIN	V	1.067	MIN
nsp15	1	102	C	1.051	MIN	C	0.631	NEU
nsp15	1	103	T	1.051	NEU	S	0.189	NEU
nsp15	1	104	M	1.301	NEU	M	0.03	NEU
nsp15	1	105	T	1.301	NEU	T	-0.531	NEU
nsp15	1	106	D	1.301	MAX	D	-1.161	MAX
nsp15	1	107	I	1.301	MIN	I	2.076	MIN
nsp15	1	108	A	1.301	NEU	A	0.3	NEU
nsp15	1	109	K	1.051	MIN	K	1.528	MIN
nsp15	1	110	K	1.301	NEU	K	-0.569	NEU
nsp15	1	111	P	1.301	NEU	P	-0.59	NEU
nsp15	1	112	T	0.563	NEU	T	-0.569	NEU
nsp15	1	113	E	1.051	NEU	E	-0.177	NEU
nsp15	1	114	S	0.887	NEU	T	-0.736	NEU
nsp15	1	115	A	0.563	NEU	I	1.363	MIN

nsp15	1	116	C	1.301	MIN	C	1.805	MIN
nsp15	1	117	S	0.516	NEU	A	-0.864	NEU
nsp15	1	118	S	1.051	NEU	P	-0.255	NEU
nsp15	1	119	L	1.301	MIN	L	0.975	MIN
nsp15	1	120	T	1.051	NEU	T	-0.2	NEU
nsp15	1	121	V	1.301	MIN	V	1.22	MIN
nsp15	1	122	L	1.301	MIN	F	1.267	MIN
nsp15	1	123	F	1.051	MIN	F	0.883	MIN
nsp15	1	124	D	1.301	NEU	D	-0.772	NEU
nsp15	1	125	G	1.301	NEU	G	-0.503	NEU
nsp15	1	126	R	1.301	MIN	R	1.843	MIN
nsp15	1	127	V	0.757	MIN	V	0.8	MIN
nsp15	1	128	E	1.051	MIN	D	1.009	MIN
nsp15	1	129	G	1.301	NEU	G	-0.16	NEU
nsp15	1	130	Q	1.301	NEU	Q	-0.744	NEU
nsp15	1	131	V	1.051	MIN	V	1.349	MIN
nsp15	1	132	D	1.301	MIN	D	1.476	MIN
nsp15	1	133	L	1.051	MIN	L	0.913	MIN
nsp15	1	134	F	1.301	MIN	F	0.886	MIN
nsp15	1	135	R	1.051	NEU	R	-0.507	NEU
nsp15	1	136	N	0.804	NEU	N	-0.376	NEU
nsp15	1	137	A	0.651	NEU	A	0.497	NEU
nsp15	1	138	R	1.301	NEU	R	-0.344	NEU
nsp15	1	139	N	0.887	MAX	N	-1.021	MAX
nsp15	1	140	G	1.301	NEU	G	-0.549	NEU
nsp15	1	141	V	1.301	MIN	V	1.259	MIN
nsp15	1	142	L	1.051	MIN	L	0.654	NEU
nsp15	1	143	I	1.301	MIN	I	1.23	MIN
nsp15	1	144	T	1.301	NEU	T	-0.422	NEU
nsp15	1	145	E	1.051	MIN	E	1.8	MIN
nsp15	1	146	G	0.143	NEU	G	0.772	NEU
nsp15	1	147	S	0.516	NEU	S	0.577	NEU
nsp15	1	148	V	1.301	MIN	V	1.466	MIN
nsp15	1	149	K	1.301	NEU	K	-0.689	NEU
nsp15	1	150	G	1.051	NEU	G	-0.714	NEU
nsp15	1	151	L	1.301	MIN	L	1.027	MIN
nsp15	1	152	T	-0.025	NEU	Q	-1.192	MAX
nsp15	1	153	P	0.490	NEU	P	-0.71	NEU
nsp15	1	154	S	1.301	NEU	S	0.182	NEU
nsp15	1	155	K	0.260	MAX	V	-0.004	NEU
nsp15	1	156	G	1.301	NEU	G	-0.334	NEU
nsp15	1	157	P	1.301	NEU	P	-0.084	NEU
nsp15	1	158	A	-0.084	NEU	K	-1.228	MAX
nsp15	1	159	Q	1.301	NEU	Q	-0.401	NEU
nsp15	1	160	A	1.301	NEU	A	-0.023	NEU
nsp15	1	161	S	1.301	NEU	S	-0.045	NEU

nsp15	1	162	V	1.301	MIN	L	1.084	MIN
nsp15	1	163	N	0.301	NEU	N	-0.909	NEU
nsp15	1	164	G	1.301	NEU	G	0.222	NEU
nsp15	1	165	V	1.301	MIN	V	1.217	MIN
nsp15	1	166	T	0.321	NEU	T	0.72	NEU
nsp15	1	167	L	1.301	MIN	L	1.257	MIN
nsp15	1	168	I	0.887	NEU	I	0.031	NEU
nsp15	1	169	G	1.301	NEU	G	-0.898	NEU
nsp15	1	170	E	0.301	MIN	E	1.801	MIN
nsp15	1	171	S	0.306	MIN	A	-0.496	NEU
nsp15	1	172	V	1.051	MIN	V	1.395	MIN
nsp15	1	173	K	1.051	MIN	K	1.504	MIN
nsp15	1	174	T	1.301	NEU	T	-0.099	NEU
nsp15	1	175	Q	1.051	NEU	Q	0.188	NEU
nsp15	1	176	F	0.651	MIN	F	0.065	NEU
nsp15	1	177	N	0.887	NEU	N	-0.942	NEU
nsp15	1	178	Y	1.051	MIN	Y	0.649	NEU
nsp15	1	179	F	0.563	MIN	Y	-0.606	NEU
nsp15	1	180	K	1.301	MAX	K	-1.394	MAX
nsp15	1	181	K	1.301	MAX	K	-1.376	MAX
nsp15	1	182	V	1.301	MIN	V	1.476	MIN
nsp15	1	183	D	1.051	NEU	D	-0.364	NEU
nsp15	1	184	G	1.301	NEU	G	-0.238	NEU
nsp15	1	185	I	0.757	MIN	V	0.535	NEU
nsp15	1	186	I	1.301	MIN	V	1.13	MIN
nsp15	1	187	Q	0.651	NEU	Q	-1.055	MAX
nsp15	1	188	Q	1.301	NEU	Q	0.461	NEU
nsp15	1	189	L	1.301	MIN	L	1.218	MIN
nsp15	1	190	P	1.301	NEU	P	0.174	NEU
nsp15	1	191	E	1.301	NEU	E	-0.749	NEU
nsp15	1	192	T	1.301	NEU	T	-0.248	NEU
nsp15	1	193	Y	1.301	NEU	Y	0.351	NEU
nsp15	1	194	F	1.051	NEU	F	-0.471	NEU
nsp15	1	195	T	1.301	NEU	T	-0.107	NEU
nsp15	1	196	Q	1.301	NEU	Q	-0.716	NEU
nsp15	1	197	S	1.301	NEU	S	-0.12	NEU
nsp15	1	198	R	0.887	MIN	R	0.972	MIN
nsp15	1	199	D	0.360	NEU	N	0.111	NEU
nsp15	1	200	L	1.301	MIN	L	1.241	MIN
nsp15	1	201	E	0.887	NEU	Q	-0.514	NEU
nsp15	1	202	D	0.651	MIN	E	0.958	MIN
nsp15	1	203	F	1.301	NEU	F	0.283	NEU
nsp15	1	204	K	1.301	MIN	K	1.702	MIN
nsp15	1	205	P	1.301	NEU	P	-0.451	NEU
nsp15	1	206	R	0.563	MIN	R	0.555	NEU
nsp15	1	207	S	1.301	NEU	S	-0.487	NEU

nsp15	1	208	Q	0.430	MIN	Q	0.169	NEU
nsp15	1	209	M	1.301	MIN	M	1.065	MIN
nsp15	1	210	E	1.301	NEU	E	-0.801	NEU
nsp15	1	211	T	0.887	MIN	I	1.486	MIN
nsp15	1	212	D	1.301	MAX	D	-1.466	MAX
nsp15	1	213	F	1.301	MIN	F	0.744	NEU
nsp15	1	214	L	1.301	MIN	L	1.337	MIN
nsp15	1	215	E	0.887	MAX	E	-1.613	MAX
nsp15	1	216	L	1.301	NEU	L	-0.125	NEU
nsp15	1	217	A	1.301	NEU	A	-0.581	NEU
nsp15	1	218	M	1.301	MIN	M	0.856	MIN
nsp15	1	219	D	1.301	MAX	D	-1.365	MAX
nsp15	1	220	E	1.301	NEU	E	-0.832	NEU
nsp15	1	221	F	1.301	MIN	F	0.701	NEU
nsp15	1	222	I	1.301	MIN	I	1.573	MIN
nsp15	1	223	Q	0.563	NEU	E	-0.968	NEU
nsp15	1	224	R	0.757	NEU	R	0.558	NEU
nsp15	1	225	Y	1.301	NEU	Y	-0.401	NEU
nsp15	1	226	K	0.887	MIN	K	1.034	MIN
nsp15	1	227	L	1.301	MIN	L	0.801	MIN
nsp15	1	228	E	1.301	NEU	E	-0.218	NEU
nsp15	1	229	G	0.887	NEU	G	-0.87	NEU
nsp15	1	230	Y	0.887	NEU	Y	-0.967	NEU
nsp15	1	231	A	1.301	NEU	A	0.47	NEU
nsp15	1	232	F	1.301	MIN	F	0.886	MIN
nsp15	1	233	E	1.301	MAX	E	-1.147	MAX
nsp15	1	234	H	1.051	NEU	H	-0.914	NEU
nsp15	1	235	I	1.051	MIN	I	1.236	MIN
nsp15	1	236	V	1.301	MIN	V	1.258	MIN
nsp15	1	237	Y	1.301	MAX	Y	-1.748	MAX
nsp15	1	238	G	1.301	NEU	G	-0.499	NEU
nsp15	1	239	D	1.301	NEU	D	-0.554	NEU
nsp15	1	240	F	1.301	NEU	F	-0.526	NEU
nsp15	1	241	S	1.051	MIN	S	0.705	NEU
nsp15	1	242	H	1.301	NEU	H	-0.069	NEU
nsp15	1	243	G	1.301	NEU	S	-0.389	NEU
nsp15	1	244	Q	1.301	NEU	Q	0.362	NEU
nsp15	1	245	L	1.301	MIN	L	0.822	MIN
nsp15	1	246	G	1.301	NEU	G	-0.653	NEU
nsp15	1	247	G	1.301	NEU	G	-0.517	NEU
nsp15	1	248	L	1.301	MIN	L	1.22	MIN
nsp15	1	249	H	1.301	NEU	H	-0.313	NEU
nsp15	1	250	L	1.301	MIN	L	1.328	MIN
nsp15	1	251	M	1.301	MIN	L	1.389	MIN
nsp15	1	252	I	1.301	MIN	I	1.459	MIN
nsp15	1	253	G	1.301	NEU	G	-0.465	NEU

nsp15	1	254	L	1.301	MIN	L	1.321	MIN
nsp15	1	255	A	1.301	NEU	A	0.484	NEU
nsp15	1	256	K	1.301	MAX	K	-1.465	MAX
nsp15	1	257	R	1.051	NEU	R	-0.676	NEU
nsp15	1	258	S	1.051	NEU	F	0.872	MIN
nsp15	1	259	Q	1.301	NEU	K	-0.525	NEU
nsp15	1	260	D	1.301	MIN	E	1.703	MIN
nsp15	1	261	S	1.301	NEU	S	-0.007	NEU
nsp15	1	262	P	0.651	MIN	P	0.966	MIN
nsp15	1	263	L	1.301	MIN	F	0.915	MIN
nsp15	1	264	K	0.757	NEU	E	-1.196	MAX
nsp15	1	265	L	1.301	MIN	L	1.209	MIN
nsp15	1	266	E	0.430	NEU	E	-1.455	MAX
nsp15	1	267	D	0.887	NEU	D	-0.754	NEU
nsp15	1	268	F	0.064	NEU	F	0.906	MIN
nsp15	1	269	I	0.757	MIN	I	0.8	MIN
nsp15	1	270	P	0.490	NEU	P	-0.958	NEU
nsp15	1	271	M	0.757	NEU	M	-0.698	NEU
nsp15	1	272	D	1.051	NEU	D	-0.648	NEU
nsp15	1	273	S	1.301	NEU	S	-0.855	NEU
nsp15	1	274	T	1.301	NEU	T	-0.096	NEU
nsp15	1	275	V	1.301	MIN	V	1.031	MIN
nsp15	1	276	K	0.563	NEU	K	-0.956	NEU
nsp15	1	277	N	1.301	NEU	N	-0.894	NEU
nsp15	1	278	Y	0.651	MIN	Y	0.631	NEU
nsp15	1	279	F	1.051	NEU	F	0.572	NEU
nsp15	1	280	I	1.301	MIN	I	1.14	MIN
nsp15	1	281	T	1.301	NEU	T	-0.096	NEU
nsp15	1	282	D	0.757	MAX	D	-1.134	MAX
nsp15	1	283	A	1.301	MAX	A	-1.171	MAX
nsp15	1	284	Q	0.757	NEU	Q	0.466	NEU
nsp15	1	285	T	1.301	NEU	T	0.336	NEU
nsp15	1	286	G	1.301	NEU	G	-0.079	NEU
nsp15	1	287	S	1.051	NEU	S	0.222	NEU
nsp15	1	288	S	1.301	NEU	S	-0.713	NEU
nsp15	1	289	K	1.301	MAX	K	-1.484	MAX
nsp15	1	290	C	1.301	MIN	C	1.513	MIN
nsp15	1	291	V	1.301	MIN	V	0.727	NEU
nsp15	1	292	C	1.301	MIN	C	1.15	MIN
nsp15	1	293	S	1.301	NEU	S	-0.518	NEU
nsp15	1	294	V	1.301	MIN	V	1.176	MIN
nsp15	1	295	I	1.301	MIN	I	1.305	MIN
nsp15	1	296	D	1.301	NEU	D	-0.81	NEU
nsp15	1	297	L	1.301	MIN	L	1.315	MIN
nsp15	1	298	L	1.301	MIN	L	0.927	MIN
nsp15	1	299	L	1.301	MIN	L	1.128	MIN

nsp15	1	300	D	1.301	MAX	D	-1.315	MAX
nsp15	1	301	D	1.301	MAX	D	-1.504	MAX
nsp15	1	302	F	1.301	MIN	F	1.124	MIN
nsp15	1	303	V	1.301	MIN	V	1.48	MIN
nsp15	1	304	E	1.301	MAX	E	-1.352	MAX
nsp15	1	305	I	1.301	MIN	I	1.515	MIN
nsp15	1	306	I	1.301	MIN	I	1.402	MIN
nsp15	1	307	K	1.301	NEU	K	-0.672	NEU
nsp15	1	308	S	1.301	NEU	S	-0.841	NEU
nsp15	1	309	Q	1.301	NEU	Q	-0.942	NEU
nsp15	1	310	D	0.430	MAX	D	-1.093	MAX
nsp15	1	311	L	1.301	MIN	L	1.352	MIN
nsp15	1	312	S	1.301	MIN	S	1.002	MIN
nsp15	1	313	V	1.301	MIN	V	1.534	MIN
nsp15	1	314	V	0.430	MIN	V	0.676	NEU
nsp15	1	315	S	1.301	NEU	S	-0.726	NEU
nsp15	1	316	K	1.301	MAX	K	-1.19	MAX
nsp15	1	317	V	0.887	NEU	V	0.291	NEU
nsp15	1	318	V	1.301	MIN	V	1.386	MIN
nsp15	1	319	K	0.804	NEU	K	-0.72	NEU
nsp15	1	320	V	1.301	MIN	V	1.186	MIN
nsp15	1	321	T	0.306	MIN	T	0.844	MIN
nsp15	1	322	I	1.301	MIN	I	1.369	MIN
nsp15	1	323	D	1.301	NEU	D	-0.854	NEU
nsp15	1	324	Y	1.301	NEU	Y	0.436	NEU
nsp15	1	325	A	1.051	NEU	T	0.065	NEU
nsp15	1	326	E	1.301	NEU	E	0.339	NEU
nsp15	1	327	I	1.301	MIN	I	1.158	MIN
nsp15	1	328	S	1.301	NEU	S	-0.913	NEU
nsp15	1	329	F	1.301	MIN	F	0.766	NEU
nsp15	1	330	M	1.301	NEU	M	-0.232	NEU
nsp15	1	331	L	1.301	MIN	L	1.197	MIN
nsp15	1	332	W	1.301	MAX	W	-1.348	MAX
nsp15	1	333	C	1.301	MIN	C	1.943	MIN
nsp15	1	334	K	1.301	NEU	K	-0.884	NEU
nsp15	1	335	D	0.804	NEU	D	-0.667	NEU
nsp15	1	336	G	1.301	NEU	G	-0.535	NEU
nsp15	1	337	H	1.051	MIN	H	0.962	MIN
nsp15	1	338	V	1.301	MIN	V	1.091	MIN
nsp15	1	339	E	1.301	NEU	E	-0.833	NEU
nsp15	1	340	T	1.301	NEU	T	-0.449	NEU
nsp15	1	341	F	1.301	MIN	F	0.959	MIN
nsp15	1	342	Y	1.301	NEU	Y	-0.088	NEU
nsp15	1	343	P	1.301	NEU	P	-0.939	NEU
nsp15	1	344	K	1.301	MAX	K	-1.309	MAX
nsp15	1	345	L	1.301	MIN	L	0.855	MIN

nsp16	1	1	S	0.462	NEU	S	-0.214	NEU
nsp16	1	2	Q	1.175	NEU	Q	-0.7	NEU
nsp16	1	3	D	0.052	NEU	A	-0.86	NEU
nsp16	1	4	W	0.346	MAX	W	-1.723	MAX
nsp16	1	5	K	0.613	NEU	Q	-0.865	NEU
nsp16	1	6	P	0.372	NEU	P	-1.204	MAX
nsp16	1	7	G	1.329	NEU	G	-0.494	NEU
nsp16	1	8	V	0.132	MIN	V	1.311	MIN
nsp16	1	9	A	1.329	NEU	A	-0.032	NEU
nsp16	1	10	M	1.175	MIN	M	0.708	NEU
nsp16	1	11	P	0.607	NEU	P	-0.667	NEU
nsp16	1	12	N	1.175	NEU	N	-0.692	NEU
nsp16	1	13	L	1.329	MIN	L	1.409	MIN
nsp16	1	14	Y	0.557	NEU	Y	-0.963	NEU
nsp16	1	15	K	0.332	NEU	K	-0.652	NEU
nsp16	1	16	V	0.434	NEU	M	-0.096	NEU
nsp16	1	17	Q	0.329	MAX	Q	-1.09	MAX
nsp16	1	18	N	0.236	NEU	R	0.149	NEU
nsp16	1	19	M	-0.077	NEU	M	-0.773	NEU
nsp16	1	20	L	0.251	MIN	L	0.8	MIN
nsp16	1	21	L	0.332	NEU	L	0.831	MIN
nsp16	1	22	E	1.067	MAX	E	-1.485	MAX
nsp16	1	23	P	0.329	MIN	K	1.811	MIN
nsp16	1	24	C	1.329	MIN	C	1.414	MIN
nsp16	1	25	D	0.004	NEU	D	1.274	MIN
nsp16	1	26	L	1.175	NEU	L	0.383	NEU
nsp16	1	27	H	1.022	NEU	Q	-0.364	NEU
nsp16	1	28	N	0.462	NEU	N	-0.951	NEU
nsp16	1	29	Y	1.329	MAX	Y	-2.597	MAX
nsp16	1	30	G	1.329	NEU	G	0.244	NEU
nsp16	1	31	Q	0.492	MAX	D	-1.198	MAX
nsp16	1	32	S	0.346	NEU	S	-0.662	NEU
nsp16	1	33	A	0.221	MIN	A	0.379	NEU
nsp16	1	34	R	0.434	NEU	T	-0.796	NEU
nsp16	1	35	L	0.411	MIN	L	1.326	MIN
nsp16	1	36	P	1.175	NEU	P	-0.739	NEU
nsp16	1	37	K	0.676	NEU	K	-0.964	NEU
nsp16	1	38	G	1.329	NEU	G	-0.07	NEU
nsp16	1	39	I	0.462	MIN	I	1.741	MIN
nsp16	1	40	M	0.411	NEU	M	-0.564	NEU
nsp16	1	41	M	1.329	NEU	M	0.141	NEU
nsp16	1	42	N	0.976	NEU	N	-0.716	NEU
nsp16	1	43	V	1.329	MIN	V	1.404	MIN
nsp16	1	44	A	0.462	MIN	A	0.819	MIN
nsp16	1	45	K	0.462	MAX	K	-1.633	MAX
nsp16	1	46	Y	0.896	NEU	Y	-0.45	NEU

nsp16	1	47	T	1.329	NEU	T	-0.286	NEU
nsp16	1	48	Q	0.332	NEU	Q	-0.859	NEU
nsp16	1	49	L	1.329	MIN	L	1.303	MIN
nsp16	1	50	C	0.826	MIN	C	1.415	MIN
nsp16	1	51	Q	1.067	NEU	Q	-0.525	NEU
nsp16	1	52	Y	0.234	NEU	Y	0.621	NEU
nsp16	1	53	L	1.329	MIN	L	1.372	MIN
nsp16	1	54	N	1.329	NEU	N	-0.094	NEU
nsp16	1	55	T	1.175	NEU	T	-0.811	NEU
nsp16	1	56	C	1.175	MIN	L	1.433	MIN
nsp16	1	57	T	1.329	NEU	T	-0.537	NEU
nsp16	1	58	L	1.329	MIN	L	1.205	MIN
nsp16	1	59	A	1.329	NEU	A	0.241	NEU
nsp16	1	60	V	1.175	MIN	V	1.081	MIN
nsp16	1	61	P	1.329	MAX	P	-1.368	MAX
nsp16	1	62	A	1.175	NEU	Y	-0.234	NEU
nsp16	1	63	N	1.329	NEU	N	-0.586	NEU
nsp16	1	64	M	1.175	MIN	M	0.92	MIN
nsp16	1	65	R	1.329	NEU	R	-0.552	NEU
nsp16	1	66	V	1.329	MIN	V	1.157	MIN
nsp16	1	67	I	1.329	MIN	I	1.62	MIN
nsp16	1	68	H	1.329	NEU	H	-0.374	NEU
nsp16	1	69	F	1.329	MIN	F	1.454	MIN
nsp16	1	70	G	1.329	NEU	G	-0.067	NEU
nsp16	1	71	A	1.329	NEU	A	-0.121	NEU
nsp16	1	72	G	1.175	NEU	G	0.046	NEU
nsp16	1	73	S	1.067	NEU	S	-0.569	NEU
nsp16	1	74	D	0.527	MIN	D	0.745	NEU
nsp16	1	75	K	0.492	MAX	K	-1.283	MAX
nsp16	1	76	G	1.329	NEU	G	0.236	NEU
nsp16	1	77	V	1.329	MIN	V	1.411	MIN
nsp16	1	78	A	-0.033	NEU	A	-0.777	NEU
nsp16	1	79	P	0.762	NEU	P	-0.916	NEU
nsp16	1	80	G	1.329	NEU	G	-0.813	NEU
nsp16	1	81	T	1.329	NEU	T	-0.449	NEU
nsp16	1	82	A	0.896	NEU	A	-0.286	NEU
nsp16	1	83	V	1.329	MIN	V	1.177	MIN
nsp16	1	84	L	1.329	MIN	L	1.34	MIN
nsp16	1	85	R	0.492	NEU	R	-0.18	NEU
nsp16	1	86	Q	0.896	NEU	Q	-0.737	NEU
nsp16	1	87	W	0.358	NEU	W	0.76	NEU
nsp16	1	88	L	1.329	MIN	L	1.286	MIN
nsp16	1	89	P	0.411	MAX	P	-0.989	NEU
nsp16	1	90	T	0.042	NEU	T	-0.379	NEU
nsp16	1	91	D	0.896	NEU	G	-0.309	NEU
nsp16	1	92	A	1.329	NEU	T	-0.254	NEU

nsp16	1	93	L	1.175	MIN	L	1.231	MIN
nsp16	1	94	L	1.329	MIN	L	1.284	MIN
nsp16	1	95	V	1.329	MIN	V	1.166	MIN
nsp16	1	96	D	1.067	MAX	D	-1.075	MAX
nsp16	1	97	N	0.372	MAX	S	-0.558	NEU
nsp16	1	98	D	1.329	MAX	D	-1.518	MAX
nsp16	1	99	L	0.654	NEU	L	-0.267	NEU
nsp16	1	100	N	0.349	NEU	N	-0.214	NEU
nsp16	1	101	D	0.234	NEU	D	-0.713	NEU
nsp16	1	102	F	-0.054	NEU	F	-0.224	NEU
nsp16	1	103	V	0.332	MIN	V	0.506	NEU
nsp16	1	104	S	1.329	NEU	S	-0.693	NEU
nsp16	1	105	D	1.175	NEU	D	-0.617	NEU
nsp16	1	106	A	0.372	NEU	A	0.396	NEU
nsp16	1	107	D	1.329	MAX	D	-1.413	MAX
nsp16	1	108	S	0.329	MIN	S	-0.749	NEU
nsp16	1	109	T	1.175	NEU	T	-0.408	NEU
nsp16	1	110	L	0.896	MIN	L	1.197	MIN
nsp16	1	111	I	-0.137	NEU	I	1.631	MIN
nsp16	1	112	G	1.329	NEU	G	-0.627	NEU
nsp16	1	113	D	0.826	MAX	D	-1.22	MAX
nsp16	1	114	C	1.329	MIN	C	1.617	MIN
nsp16	1	115	A	-0.241	NEU	A	-1.268	MAX
nsp16	1	116	T	0.372	NEU	T	0.501	NEU
nsp16	1	117	V	1.329	MIN	V	1.441	MIN
nsp16	1	118	H	0.404	NEU	H	0.293	NEU
nsp16	1	119	T	0.411	NEU	T	-0.457	NEU
nsp16	1	120	A	0.404	NEU	A	-0.556	NEU
nsp16	1	121	N	0.745	NEU	N	-0.738	NEU
nsp16	1	122	K	0.492	NEU	K	-0.542	NEU
nsp16	1	123	W	1.329	MIN	W	0.742	NEU
nsp16	1	124	D	1.175	MAX	D	-1.072	MAX
nsp16	1	125	L	1.329	MIN	L	1.165	MIN
nsp16	1	126	I	1.329	MIN	I	1.352	MIN
nsp16	1	127	I	1.329	MIN	I	1.574	MIN
nsp16	1	128	S	1.329	NEU	S	-0.738	NEU
nsp16	1	129	D	1.329	NEU	D	-0.831	NEU
nsp16	1	130	M	1.329	MIN	M	0.978	MIN
nsp16	1	131	Y	0.826	MAX	Y	-3.116	MAX
nsp16	1	132	D	0.118	MIN	D	1.883	MIN
nsp16	1	133	P	0.319	NEU	P	-1.023	MAX
nsp16	1	134	K	0.826	MIN	K	1.262	MIN
nsp16	1	135	T	1.175	NEU	T	0.144	NEU
nsp16	1	136	K	0.349	NEU	K	0.429	NEU
nsp16	1	137	N	0.527	MIN	N	0.593	NEU
nsp16	1	138	V	0.826	NEU	V	-0.281	NEU

nsp16	1	139	T	0.236	NEU	T	0.112	NEU
nsp16	1	140	G	0.506	NEU	K	0.77	NEU
nsp16	1	141	E	-0.254	MIN	E	-1.857	MAX
nsp16	1	142	N	0.372	MAX	N	-1.026	MAX
nsp16	1	143	D	0.276	NEU	D	0.159	NEU
nsp16	1	144	S	1.329	NEU	S	0.015	NEU
nsp16	1	145	K	1.067	MAX	K	-1.575	MAX
nsp16	1	146	E	0.411	MAX	E	-1.294	MAX
nsp16	1	147	G	0.411	NEU	G	-0.277	NEU
nsp16	1	148	F	1.329	MIN	F	0.835	MIN
nsp16	1	149	F	1.175	MIN	F	0.891	MIN
nsp16	1	150	T	0.492	NEU	T	-0.108	NEU
nsp16	1	151	Y	1.175	NEU	Y	-0.025	NEU
nsp16	1	152	L	1.329	MIN	I	1.551	MIN
nsp16	1	153	C	0.527	MIN	C	1.26	MIN
nsp16	1	154	G	1.175	NEU	G	-0.389	NEU
nsp16	1	155	F	1.329	MIN	F	1.444	MIN
nsp16	1	156	I	1.329	MIN	I	1.219	MIN
nsp16	1	157	K	0.434	MAX	Q	-1.451	MAX
nsp16	1	158	Q	0.565	NEU	Q	-0.996	NEU
nsp16	1	159	K	1.329	MAX	K	-1.367	MAX
nsp16	1	160	L	1.329	MIN	L	1.249	MIN
nsp16	1	161	A	0.462	MIN	A	0.743	NEU
nsp16	1	162	L	1.329	MIN	L	1.475	MIN
nsp16	1	163	G	1.329	NEU	G	-0.484	NEU
nsp16	1	164	G	1.329	NEU	G	-0.566	NEU
nsp16	1	165	S	1.329	NEU	S	-0.609	NEU
nsp16	1	166	V	1.175	MIN	V	1.329	MIN
nsp16	1	167	A	1.329	NEU	A	0.459	NEU
nsp16	1	168	I	1.329	MIN	I	1.378	MIN
nsp16	1	169	K	1.175	MAX	K	-1.151	MAX
nsp16	1	170	I	1.329	MIN	I	1.801	MIN
nsp16	1	171	T	0.705	NEU	T	0.341	NEU
nsp16	1	172	E	1.329	NEU	E	-0.347	NEU
nsp16	1	173	H	0.211	NEU	H	0.732	NEU
nsp16	1	174	S	1.329	NEU	S	-0.592	NEU
nsp16	1	175	W	0.762	MAX	W	-1.558	MAX
nsp16	1	176	S	1.329	NEU	N	-0.481	NEU
nsp16	1	177	A	0.976	NEU	A	-0.58	NEU
nsp16	1	178	D	0.372	NEU	D	-0.8	NEU
nsp16	1	179	L	1.329	MIN	L	1.347	MIN
nsp16	1	180	Y	0.170	NEU	Y	-0.613	NEU
nsp16	1	181	K	0.293	NEU	K	-0.568	NEU
nsp16	1	182	L	1.067	MIN	L	1.423	MIN
nsp16	1	183	M	0.338	NEU	M	0.782	MIN
nsp16	1	184	G	1.329	NEU	G	-0.266	NEU

nsp16	1	185	H	0.042	NEU	H	-0.307	NEU
nsp16	1	186	F	1.329	MIN	F	1.031	MIN
nsp16	1	187	A	0.509	NEU	A	0.243	NEU
nsp16	1	188	W	1.175	NEU	W	0.172	NEU
nsp16	1	189	W	1.175	NEU	W	0.126	NEU
nsp16	1	190	T	1.329	NEU	T	-0.381	NEU
nsp16	1	191	A	0.372	MIN	A	0.175	NEU
nsp16	1	192	F	1.329	MIN	F	1.126	MIN
nsp16	1	193	C	1.329	MIN	V	1.275	MIN
nsp16	1	194	T	1.329	NEU	T	-0.474	NEU
nsp16	1	195	N	1.329	NEU	N	-0.842	NEU
nsp16	1	196	V	0.390	MIN	V	0.964	MIN
nsp16	1	197	N	1.329	NEU	N	-0.736	NEU
nsp16	1	198	A	1.175	NEU	A	0.091	NEU
nsp16	1	199	S	1.329	NEU	S	-0.634	NEU
nsp16	1	200	S	0.434	NEU	S	0.148	NEU
nsp16	1	201	S	1.329	NEU	S	-0.192	NEU
nsp16	1	202	E	1.067	NEU	E	-0.939	NEU
nsp16	1	203	A	1.329	NEU	A	0.377	NEU
nsp16	1	204	F	1.329	MIN	F	1.315	MIN
nsp16	1	205	L	1.329	MIN	L	1.281	MIN
nsp16	1	206	I	1.329	MIN	I	1.369	MIN
nsp16	1	207	G	1.329	NEU	G	-0.531	NEU
nsp16	1	208	V	1.329	MIN	C	1.573	MIN
nsp16	1	209	N	0.705	NEU	N	-0.886	NEU
nsp16	1	210	Y	0.826	MIN	Y	0.738	NEU
nsp16	1	211	L	1.175	MIN	L	1.117	MIN
nsp16	1	212	G	1.175	NEU	G	-0.802	NEU
nsp16	1	213	K	-0.011	NEU	K	-1.447	MAX
nsp16	1	214	-	0.319	MIN	P	-0.905	NEU
nsp16	1	215	K	0.222	NEU	R	-0.504	NEU
nsp16	1	216	E	0.409	NEU	E	-0.521	NEU
nsp16	1	217	Q	0.251	MIN	Q	0.564	NEU
nsp16	1	218	I	1.329	MIN	I	1.277	MIN
nsp16	1	219	D	0.434	NEU	D	-0.222	NEU
nsp16	1	220	G	1.329	NEU	G	-0.447	NEU
nsp16	1	221	Y	0.199	MAX	Y	-1.08	MAX
nsp16	1	222	A	-0.128	NEU	V	1.453	MIN
nsp16	1	223	M	0.571	NEU	M	-0.517	NEU
nsp16	1	224	H	1.329	NEU	H	-0.393	NEU
nsp16	1	225	A	0.462	MIN	A	0.673	NEU
nsp16	1	226	N	0.762	MAX	N	-1.129	MAX
nsp16	1	227	Y	1.329	NEU	Y	-0.564	NEU
nsp16	1	228	I	1.329	MIN	I	0.869	MIN
nsp16	1	229	F	1.329	NEU	F	-0.672	NEU
nsp16	1	230	W	0.462	MAX	W	-1.828	MAX

nsp16	1	231	R	1.329	NEU	R	-0.699	NEU
nsp16	1	232	N	0.358	NEU	N	-0.386	NEU
nsp16	1	233	S	1.175	NEU	T	-0.855	NEU
nsp16	1	234	T	1.329	NEU	N	-0.853	NEU
nsp16	1	235	P	0.293	NEU	P	-0.119	NEU
nsp16	1	236	M	0.372	NEU	I	1.474	MIN
nsp16	1	237	Q	-0.071	NEU	Q	-0.791	NEU
nsp16	1	238	L	0.976	MIN	L	0.853	MIN
nsp16	1	239	S	1.329	NEU	S	-0.176	NEU
nsp16	1	240	S	0.914	NEU	S	-0.719	NEU
nsp16	1	241	Y	0.329	MAX	Y	-0.677	NEU
nsp16	1	242	S	1.329	NEU	S	-0.615	NEU
nsp16	1	243	L	1.329	MIN	L	0.929	MIN
nsp16	1	244	F	0.349	MIN	F	1.131	MIN
nsp16	1	245	D	0.762	NEU	D	0.459	NEU
nsp16	1	246	L	0.358	NEU	M	-0.436	NEU
nsp16	1	247	S	0.462	MIN	S	1.197	MIN
nsp16	1	248	K	0.896	MIN	K	1.129	MIN
nsp16	1	249	F	1.329	MIN	F	0.947	MIN
nsp16	1	250	P	0.390	NEU	P	0.636	NEU
nsp16	1	251	L	1.329	MIN	L	1.431	MIN
nsp16	1	252	K	0.527	NEU	K	0.44	NEU
nsp16	1	253	L	0.607	MIN	L	1.197	MIN
nsp16	1	254	K	0.390	MAX	R	-0.718	NEU
nsp16	1	255	G	1.329	NEU	G	-0.386	NEU
nsp16	1	256	T	1.329	NEU	T	-0.337	NEU
nsp16	1	257	P	0.346	NEU	A	0.308	NEU
nsp16	1	258	V	1.329	MIN	V	1.125	MIN
nsp16	1	259	M	1.329	MIN	M	0.912	MIN
nsp16	1	260	S	0.824	NEU	S	0.369	NEU
nsp16	1	261	L	1.329	MIN	L	1.273	MIN
nsp16	1	262	K	-0.147	NEU	K	-1.4	MAX
nsp16	1	263	E	0.762	NEU	E	-0.548	NEU
nsp16	1	264	S	0.332	MIN	G	-0.481	NEU
nsp16	1	265	Q	1.175	NEU	Q	-0.312	NEU
nsp16	1	266	I	1.329	MIN	I	1.967	MIN
nsp16	1	267	N	0.565	MAX	N	-1.343	MAX
nsp16	1	268	E	0.332	MAX	D	-0.949	NEU
nsp16	1	269	L	1.175	NEU	M	-0.135	NEU
nsp16	1	270	V	1.329	MIN	I	1.613	MIN
nsp16	1	271	L	0.174	MIN	L	1.302	MIN
nsp16	1	272	S	0.896	NEU	S	-0.261	NEU
nsp16	1	273	L	1.329	MIN	L	1.306	MIN
nsp16	1	274	L	1.329	MIN	L	1.182	MIN
nsp16	1	275	S	0.976	NEU	S	-0.181	NEU
nsp16	1	276	K	0.157	NEU	K	-1.818	MAX

nsp16	1	277	G	1.329	NEU	G	-0.323	NEU
nsp16	1	278	R	1.175	NEU	R	-0.659	NEU
nsp16	1	279	L	1.329	MIN	L	1.359	MIN
nsp16	1	280	L	1.329	MIN	I	1.422	MIN
nsp16	1	281	I	1.329	MIN	I	1.586	MIN
nsp16	1	282	R	1.329	NEU	R	-0.209	NEU
nsp16	1	283	D	0.329	MAX	E	-1	MAX
nsp16	1	284	N	0.372	NEU	N	0.491	NEU
nsp16	1	285	N	0.754	NEU	N	0.106	NEU
nsp16	1	286	-	0.083	NEU	R	1.762	MIN
nsp16	1	287	L	1.316	MIN	V	1.098	MIN
nsp16	1	288	V	0.620	NEU	V	-0.221	NEU
nsp16	1	289	V	1.316	MIN	I	1.778	MIN
nsp16	1	290	S	1.316	NEU	S	-0.61	NEU
nsp16	1	291	S	0.927	NEU	S	-0.702	NEU
nsp16	1	292	D	0.494	NEU	D	0.34	NEU
nsp16	1	293	V	1.172	MIN	V	1.195	MIN
nsp16	1	294	L	0.204	NEU	L	1.454	MIN
nsp16	1	295	V	0.383	MIN	V	1.503	MIN
nsp16	1	296	N	-0.011	NEU	N	-0.989	NEU
nsp16	1	297	N	0.382	NEU	N	-0.676	NEU
S_protein	4	1	Q	0.818	NEU	Q	-0.567	NEU
S_protein	4	2	C	-0.267	NEU	C	3.138	MIN
S_protein	4	3	G	0.329	NEU	V	1.23	MIN
S_protein	4	4	T	0.543	NEU	N	1.506	MIN
S_protein	4	5	F	1.311	MIN	L	1.409	MIN
S_protein	4	6	S	0.736	NEU	T	0.28	NEU
S_protein	4	7	D	0.186	NEU	T	0.134	NEU
S_protein	4	8	K	-0.180	MIN	R	1.704	MIN
S_protein	4	9	P	0.621	NEU	T	0.989	MIN
S_protein	4	10	Q	-0.175	NEU	Q	0.634	NEU
S_protein	4	11	P	0.831	NEU	L	-0.829	NEU
S_protein	4	12	K	0.133	NEU	P	0.887	MIN
S_protein	4	13	L	0.312	NEU	P	0.043	NEU
S_protein	4	14	T	0.306	NEU	A	-1.001	MAX
S_protein	4	15	Q	0.524	NEU	Y	-1.029	MAX
S_protein	4	16	V	0.220	MIN	T	-0.436	NEU
S_protein	4	17	S	0.736	NEU	N	-0.653	NEU
S_protein	4	18	S	1.311	NEU	S	-0.773	NEU
S_protein	4	19	S	1.095	NEU	F	1.595	MIN
S_protein	4	20	R	0.276	NEU	T	-0.486	NEU
S_protein	4	21	R	1.095	NEU	R	-0.586	NEU
S_protein	4	22	G	1.311	NEU	G	-0.511	NEU
S_protein	4	23	V	1.311	MIN	V	1.36	MIN
S_protein	4	24	Y	0.312	MAX	Y	-1.893	MAX
S_protein	4	25	Y	0.732	NEU	Y	0.729	NEU

S_protein	4	26	P	0.133	NEU	P	-0.643	NEU
S_protein	4	27	D	1.095	NEU	D	-0.21	NEU
S_protein	4	28	D	1.095	NEU	K	-0.679	NEU
S_protein	4	29	I	0.648	MIN	V	-0.138	NEU
S_protein	4	30	F	-0.105	MIN	F	-1.085	MAX
S_protein	4	31	R	1.311	NEU	R	-0.566	NEU
S_protein	4	32	S	1.311	NEU	S	-0.442	NEU
S_protein	4	33	D	0.220	NEU	S	-0.216	NEU
S_protein	4	34	V	0.514	MIN	V	1.114	MIN
S_protein	4	35	L	0.576	MIN	L	0.867	MIN
S_protein	4	36	H	0.576	NEU	H	0.162	NEU
S_protein	4	37	L	1.095	MIN	S	-0.479	NEU
S_protein	4	38	T	0.576	NEU	T	-0.16	NEU
S_protein	4	39	Q	1.311	NEU	Q	0.109	NEU
S_protein	4	40	D	0.831	NEU	D	-0.997	NEU
S_protein	4	41	Y	0.386	MIN	L	0.911	MIN
S_protein	4	42	F	1.311	MIN	F	1.22	MIN
S_protein	4	43	L	1.311	MIN	L	0.987	MIN
S_protein	4	44	P	0.949	MAX	P	-1.73	MAX
S_protein	4	45	F	1.311	MIN	F	1.224	MIN
S_protein	4	46	N	0.064	NEU	F	0.944	MIN
S_protein	4	47	S	1.311	NEU	S	-0.389	NEU
S_protein	4	48	N	0.481	NEU	N	-0.44	NEU
S_protein	4	49	V	1.311	MIN	V	1.455	MIN
S_protein	4	50	T	1.095	NEU	T	-0.548	NEU
S_protein	4	51	Q	0.732	NEU	W	0.625	NEU
S_protein	4	52	Y	0.333	NEU	F	1.423	MIN
S_protein	4	53	F	0.019	MIN	H	-0.74	NEU
S_protein	4	54	S	1.311	NEU	A	0.548	NEU
S_protein	4	55	L	0.524	MIN	I	0.965	MIN
S_protein	4	56	N	0.441	NEU	H	-0.68	NEU
S_protein	4	57	V	0.064	NEU	V	0.333	NEU
S_protein	4	58	D	0.026	NEU	S	0.29	NEU
S_protein	4	60	-	0.971	NEU	T	0.183	NEU
S_protein	4	61	-	-0.178	NEU	N	-0.477	NEU
S_protein	4	62	-	0.048	NEU	G	0.159	NEU
S_protein	4	63	-	-0.250	NEU	T	0.816	MIN
S_protein	4	64	-	-0.071	MIN	K	-1.149	MAX
S_protein	4	65	Y	0.428	MAX	R	-0.353	NEU
S_protein	4	66	F	0.736	MIN	F	1.283	MIN
S_protein	4	67	D	0.418	NEU	D	-0.736	NEU
S_protein	4	68	N	0.514	MAX	N	-1	MAX
S_protein	4	69	P	0.418	NEU	P	-1.089	MAX
S_protein	4	70	I	0.386	MIN	V	1.125	MIN
S_protein	4	71	L	1.311	MIN	L	1.062	MIN
S_protein	4	72	P	0.648	MAX	P	-1.858	MAX

S_protein	4	73	F	1.311	MIN	F	1.223	MIN
S_protein	4	74	G	0.312	NEU	N	-0.782	NEU
S_protein	4	75	D	0.333	NEU	D	-1.102	MAX
S_protein	4	76	G	1.311	NEU	G	-0.389	NEU
S_protein	4	77	V	1.311	MIN	V	1.259	MIN
S_protein	4	78	Y	0.831	MIN	Y	0.617	NEU
S_protein	4	79	F	1.311	MIN	F	1.332	MIN
S_protein	4	80	A	0.949	NEU	A	0.534	NEU
S_protein	4	81	A	1.095	NEU	S	-0.67	NEU
S_protein	4	82	T	0.949	NEU	T	-0.359	NEU
S_protein	4	83	E	0.514	NEU	E	-0.768	NEU
S_protein	4	84	K	0.514	MAX	K	-0.212	NEU
S_protein	4	85	S	1.311	NEU	S	-0.643	NEU
S_protein	4	86	N	0.382	NEU	N	-0.233	NEU
S_protein	4	87	V	1.095	MIN	I	1.261	MIN
S_protein	4	88	I	1.311	MIN	I	1.206	MIN
S_protein	4	89	R	1.311	NEU	R	-0.8	NEU
S_protein	4	90	G	1.311	NEU	G	-0.438	NEU
S_protein	4	91	W	0.831	MIN	W	0.661	NEU
S_protein	4	92	I	1.311	MIN	I	1.328	MIN
S_protein	4	93	F	1.311	MIN	F	1.416	MIN
S_protein	4	94	G	1.311	NEU	G	-0.694	NEU
S_protein	4	95	S	1.311	NEU	T	-0.004	NEU
S_protein	4	96	T	0.949	MIN	T	1.286	MIN
S_protein	4	97	M	1.311	MIN	L	1.009	MIN
S_protein	4	98	D	0.576	MAX	D	0.003	NEU
S_protein	4	99	N	0.648	NEU	S	-0.322	NEU
S_protein	4	100	T	0.078	MIN	K	0.481	NEU
S_protein	4	101	T	1.311	NEU	T	0.341	NEU
S_protein	4	102	Q	1.311	NEU	Q	-0.857	NEU
S_protein	4	103	S	1.311	NEU	S	-0.821	NEU
S_protein	4	104	A	0.354	NEU	L	1.279	MIN
S_protein	4	105	I	1.311	MIN	L	1.091	MIN
S_protein	4	106	I	1.311	MIN	I	1.894	MIN
S_protein	4	107	V	1.095	MIN	V	1.214	MIN
S_protein	4	108	N	0.461	NEU	N	-0.862	NEU
S_protein	4	109	N	0.319	MAX	N	-1.193	MAX
S_protein	4	110	S	1.095	NEU	A	0.186	NEU
S_protein	4	111	T	0.461	NEU	T	0.064	NEU
S_protein	4	112	H	1.311	NEU	N	-0.831	NEU
S_protein	4	113	I	0.831	MIN	V	1.657	MIN
S_protein	4	114	V	0.949	MIN	V	1.363	MIN
S_protein	4	115	I	1.311	MIN	I	1.75	MIN
S_protein	4	116	R	0.418	NEU	K	-1.185	MAX
S_protein	4	117	V	0.461	MIN	V	1.27	MIN
S_protein	4	118	C	1.311	MIN	C	1.764	MIN

S_protein	4	119	N	0.306	NEU	E	-1.512	MAX
S_protein	4	120	F	1.311	MIN	F	1.371	MIN
S_protein	4	121	N	-0.030	NEU	Q	0.108	NEU
S_protein	4	122	L	1.311	MIN	F	1.396	MIN
S_protein	4	123	C	1.311	MIN	C	2.119	MIN
S_protein	4	124	K	0.418	MAX	N	0.033	NEU
S_protein	4	125	E	0.371	MAX	D	-0.796	NEU
S_protein	4	126	P	0.732	NEU	P	-0.93	NEU
S_protein	4	127	M	1.095	MIN	F	1.518	MIN
S_protein	4	128	F	0.461	MIN	L	1.223	MIN
S_protein	4	129	T	0.371	NEU	G	-0.635	NEU
S_protein	4	130	V	1.095	MIN	V	1.231	MIN
S_protein	4	131	S	0.198	NEU	Y	-1.839	MAX
S_protein	4	132	K	-0.180	NEU	Y	-2.29	MAX
S_protein	4	133	G	0.421	NEU	H	0.582	NEU
S_protein	4	134	T	0.880	NEU	K	-0.609	NEU
S_protein	4	135	Q	0.594	NEU	N	1.085	MIN
S_protein	4	136	T	-0.047	NEU	N	-0.638	NEU
S_protein	4	137	K	1.095	NEU	K	-0.221	NEU
S_protein	4	138	S	1.095	NEU	S	-0.342	NEU
S_protein	4	139	W	-0.050	NEU	W	-2.036	MAX
S_protein	4	146	V	1.311	MIN	V	1.243	MIN
S_protein	4	147	Y	0.576	MIN	Y	0.496	NEU
S_protein	4	148	Q	0.026	NEU	S	-0.164	NEU
S_protein	4	149	N	1.095	NEU	S	-0.315	NEU
S_protein	4	150	A	0.736	NEU	A	-0.222	NEU
S_protein	4	151	F	0.187	MIN	N	-0.427	NEU
S_protein	4	152	N	0.461	NEU	N	-0.83	NEU
S_protein	4	153	C	1.311	MIN	C	1.963	MIN
S_protein	4	154	T	1.311	NEU	T	-0.082	NEU
S_protein	4	155	Y	-0.061	NEU	F	0.99	MIN
S_protein	4	156	D	0.094	NEU	E	-0.774	NEU
S_protein	4	157	R	-0.061	NEU	Y	-0.598	NEU
S_protein	4	158	V	0.461	MIN	V	0.696	NEU
S_protein	4	159	S	0.465	NEU	S	0.621	NEU
S_protein	4	160	K	0.312	MAX	Q	-1.315	MAX
S_protein	4	161	S	0.276	NEU	P	-1.423	MAX
S_protein	4	162	F	-0.127	NEU	F	0.053	NEU
S_protein	4	163	Q	0.333	NEU	L	1.006	MIN
S_protein	4	164	L	0.354	NEU	M	-0.204	NEU
S_protein	4	165	D	0.312	NEU	D	0.496	NEU
S_protein	4	166	T	0.162	MIN	L	1.185	MIN
S_protein	4	167	A	0.371	NEU	E	-0.54	NEU
S_protein	4	168	E	-0.030	NEU	G	-0.251	NEU
S_protein	4	169	K	0.576	MIN	K	1.777	MIN
S_protein	4	170	T	0.133	NEU	Q	-0.817	NEU

S_protein	4	171	G	0.621	NEU	G	-0.647	NEU
S_protein	4	172	N	-0.030	NEU	N	-0.987	NEU
S_protein	4	173	F	1.095	MIN	F	0.868	MIN
S_protein	4	174	K	0.333	NEU	K	0.307	NEU
S_protein	4	175	H	0.949	NEU	N	0.257	NEU
S_protein	4	176	L	1.311	MIN	L	1.098	MIN
S_protein	4	177	R	0.732	NEU	R	-0.141	NEU
S_protein	4	178	E	0.732	MAX	E	-0.896	NEU
S_protein	4	179	F	0.382	MIN	F	1.21	MIN
S_protein	4	180	V	1.311	MIN	V	1.168	MIN
S_protein	4	181	F	1.311	MIN	F	1.438	MIN
S_protein	4	182	K	0.576	MAX	K	-1.173	MAX
S_protein	4	183	N	0.732	NEU	N	-0.917	NEU
S_protein	4	184	K	0.026	NEU	I	1.767	MIN
S_protein	4	185	D	0.831	MAX	D	-1.397	MAX
S_protein	4	186	G	1.311	NEU	G	-0.55	NEU
S_protein	4	187	F	0.461	MIN	Y	-0.776	NEU
S_protein	4	188	L	1.311	MIN	F	1.019	MIN
S_protein	4	189	Y	0.514	NEU	K	-1.119	MAX
S_protein	4	190	V	1.311	MIN	I	1.725	MIN
S_protein	4	191	Y	0.220	NEU	Y	0.627	NEU
S_protein	4	192	S	0.648	NEU	S	-0.692	NEU
S_protein	4	193	G	0.369	NEU	K	-1.112	MAX
S_protein	4	194	Y	0.319	NEU	H	-0.505	NEU
S_protein	4	195	T	1.095	NEU	T	-0.135	NEU
S_protein	4	196	P	0.333	NEU	P	1.211	MIN
S_protein	4	197	I	0.949	MIN	I	1.314	MIN
S_protein	4	198	N	0.648	MIN	N	1.119	MIN
S_protein	4	199	L	1.095	MIN	L	1.315	MIN
S_protein	4	200	V	0.276	NEU	V	-0.168	NEU
S_protein	4	201	R	0.441	NEU	R	-1.085	MAX
S_protein	4	202	G	0.648	NEU	D	-0.92	NEU
S_protein	4	203	L	1.311	MIN	L	1.277	MIN
S_protein	4	204	P	1.095	NEU	P	-1.002	MAX
S_protein	4	205	S	0.481	NEU	Q	-0.797	NEU
S_protein	4	206	G	1.095	NEU	G	-0.214	NEU
S_protein	4	207	F	0.354	NEU	F	0.386	NEU
S_protein	4	208	S	0.949	NEU	S	-0.611	NEU
S_protein	4	209	V	0.461	MIN	A	0.382	NEU
S_protein	4	210	L	1.311	MIN	L	1.105	MIN
S_protein	4	211	K	0.418	MAX	E	-0.808	NEU
S_protein	4	212	P	1.311	NEU	P	0.069	NEU
S_protein	4	213	I	1.311	MIN	L	1.413	MIN
S_protein	4	214	L	0.732	MIN	V	1.536	MIN
S_protein	4	215	K	0.312	NEU	D	-0.055	NEU
S_protein	4	216	L	1.311	MIN	L	1.286	MIN

S_protein	4	217	P	0.382	NEU	P	0.999	MIN
S_protein	4	218	L	1.311	MIN	I	1.316	MIN
S_protein	4	219	G	1.311	NEU	G	-0.113	NEU
S_protein	4	220	I	1.311	MIN	I	1.446	MIN
S_protein	4	221	N	0.333	MIN	N	0.154	NEU
S_protein	4	222	I	1.311	MIN	I	1.305	MIN
S_protein	4	223	T	1.311	NEU	T	0.042	NEU
S_protein	4	224	S	0.064	NEU	R	-0.81	NEU
S_protein	4	225	F	0.831	MIN	F	1.351	MIN
S_protein	4	226	R	0.514	NEU	Q	-0.801	NEU
S_protein	4	227	V	0.461	MIN	T	-0.476	NEU
S_protein	4	228	V	1.311	MIN	L	1.49	MIN
S_protein	4	229	M	0.949	MIN	L	1.207	MIN
S_protein	4	230	T	0.514	NEU	A	0.542	NEU
S_protein	4	231	M	0.461	MIN	L	1.327	MIN
S_protein	4	232	F	0.514	MIN	H	-0.015	NEU
S_protein	4	233	S	0.524	NEU	R	-0.324	NEU
S_protein	4	240	P	-0.171	NEU	D	0.348	NEU
S_protein	4	241	T	0.133	NEU	S	0.244	NEU
S_protein	4	242	T	0.153	NEU	S	1.144	MIN
S_protein	4	243	S	0.804	NEU	S	0.16	NEU
S_protein	4	244	N	0.332	NEU	G	0.054	NEU
S_protein	4	245	F	0.153	MIN	W	0.58	NEU
S_protein	4	246	L	0.144	NEU	T	-0.168	NEU
S_protein	4	247	T	0.033	NEU	A	0.44	NEU
S_protein	4	248	E	0.129	NEU	G	-0.451	NEU
S_protein	4	249	A	0.880	NEU	A	-0.864	NEU
S_protein	4	250	A	1.095	NEU	A	0.127	NEU
S_protein	4	251	A	0.949	NEU	A	-0.047	NEU
S_protein	4	252	Y	0.319	MIN	Y	0.716	NEU
S_protein	4	253	F	0.949	MIN	Y	0.416	NEU
S_protein	4	254	V	1.311	MIN	V	1.401	MIN
S_protein	4	255	G	1.311	NEU	G	-0.395	NEU
S_protein	4	256	Y	1.311	NEU	Y	-0.824	NEU
S_protein	4	257	L	1.311	MIN	L	0.913	MIN
S_protein	4	258	K	0.648	MAX	Q	-0.893	NEU
S_protein	4	259	P	0.418	NEU	P	-0.182	NEU
S_protein	4	260	T	0.648	NEU	R	-0.502	NEU
S_protein	4	261	T	1.095	NEU	T	-0.33	NEU
S_protein	4	262	F	1.311	MIN	F	1.416	MIN
S_protein	4	263	M	0.576	MIN	L	0.981	MIN
S_protein	4	264	L	1.311	MIN	L	1.278	MIN
S_protein	4	265	K	0.949	NEU	K	-1.083	MAX
S_protein	4	266	F	1.311	MIN	Y	0.839	MIN
S_protein	4	267	N	0.261	NEU	N	0.466	NEU
S_protein	4	268	E	0.198	MAX	E	-0.813	NEU

S_protein	4	269	N	0.312	NEU	N	1.309	MIN
S_protein	4	270	G	1.311	NEU	G	-0.195	NEU
S_protein	4	271	T	1.311	NEU	T	-0.36	NEU
S_protein	4	272	I	0.949	MIN	I	1.665	MIN
S_protein	4	273	T	0.354	NEU	T	0.091	NEU
S_protein	4	274	D	0.831	NEU	D	-0.988	NEU
S_protein	4	275	A	0.576	MIN	A	0.865	MIN
S_protein	4	276	V	1.311	MIN	V	1.112	MIN
S_protein	4	277	D	0.514	MAX	D	-1.053	MAX
S_protein	4	278	C	1.095	MIN	C	2.363	MIN
S_protein	4	279	S	1.095	NEU	A	0.421	NEU
S_protein	4	280	Q	0.831	NEU	L	1.06	MIN
S_protein	4	281	N	0.949	MAX	D	-1.499	MAX
S_protein	4	282	P	1.311	NEU	P	-0.97	NEU
S_protein	4	283	L	1.311	MIN	L	1.316	MIN
S_protein	4	284	A	1.095	NEU	S	-0.189	NEU
S_protein	4	285	E	1.311	NEU	E	-0.809	NEU
S_protein	4	286	L	0.831	MIN	T	-0.154	NEU
S_protein	4	287	K	0.319	MAX	K	-1.141	MAX
S_protein	4	288	C	1.311	MIN	C	1.854	MIN
S_protein	4	289	T	1.311	NEU	T	0.28	NEU
S_protein	4	290	L	0.648	MIN	L	1.157	MIN
S_protein	4	291	K	0.354	NEU	K	-0.695	NEU
S_protein	4	292	S	1.095	NEU	S	-0.979	NEU
S_protein	4	293	F	0.418	NEU	F	0.214	NEU
S_protein	4	294	N	1.095	MIN	T	0.833	MIN
S_protein	4	295	V	1.311	MIN	V	1.395	MIN
S_protein	4	296	D	0.306	NEU	E	-1.524	MAX
S_protein	4	297	K	0.732	NEU	K	-0.813	NEU
S_protein	4	298	G	1.311	NEU	G	-0.439	NEU
S_protein	4	299	I	1.311	MIN	I	1.321	MIN
S_protein	4	300	Y	1.311	NEU	Y	-0.612	NEU
S_protein	4	301	Q	1.311	NEU	Q	-0.428	NEU
S_protein	4	302	T	1.311	NEU	T	0.029	NEU
S_protein	4	303	S	1.311	NEU	S	-0.606	NEU
S_protein	4	304	N	1.311	NEU	N	-0.772	NEU
S_protein	4	305	F	1.311	MIN	F	1.305	MIN
S_protein	4	306	R	0.831	NEU	R	0.43	NEU
S_protein	4	307	V	1.311	MIN	V	1.21	MIN
S_protein	4	308	S	-0.005	NEU	Q	-0.052	NEU
S_protein	4	309	P	0.514	NEU	P	-0.977	NEU
S_protein	4	310	T	0.949	NEU	T	-0.669	NEU
S_protein	4	311	Q	0.481	NEU	E	-0.861	NEU
S_protein	4	312	E	0.732	MAX	S	-0.648	NEU
S_protein	4	313	V	1.311	MIN	I	1.267	MIN
S_protein	4	314	V	1.095	MIN	V	1.089	MIN

S_protein	4	315	R	1.311	NEU	R	-0.532	NEU
S_protein	4	316	F	1.311	MIN	F	1.386	MIN
S_protein	4	317	P	1.095	NEU	P	-0.148	NEU
S_protein	4	318	N	1.311	NEU	N	-0.047	NEU
S_protein	4	319	I	1.311	MIN	I	0.918	MIN
S_protein	4	320	T	1.311	NEU	T	-0.486	NEU
S_protein	4	321	N	0.949	NEU	N	-0.817	NEU
S_protein	4	322	L	0.354	MIN	L	1.408	MIN
S_protein	4	323	C	1.311	MIN	C	1.537	MIN
S_protein	4	324	P	0.648	NEU	P	-0.877	NEU
S_protein	4	325	F	1.311	MIN	F	1.177	MIN
S_protein	4	326	D	0.648	NEU	G	-0.41	NEU
S_protein	4	327	E	0.319	NEU	E	-0.776	NEU
S_protein	4	328	V	1.311	MIN	V	1.141	MIN
S_protein	4	329	F	1.311	MIN	F	1.261	MIN
S_protein	4	330	N	0.312	MIN	N	-0.52	NEU
S_protein	4	331	A	0.831	NEU	A	0.493	NEU
S_protein	4	332	T	1.311	NEU	T	-0.125	NEU
S_protein	4	333	R	0.319	MIN	R	0.325	NEU
S_protein	4	334	F	1.311	MIN	F	1.258	MIN
S_protein	4	335	P	0.382	NEU	A	0.47	NEU
S_protein	4	336	S	1.311	NEU	S	-0.678	NEU
S_protein	4	337	V	1.311	MIN	V	1.292	MIN
S_protein	4	338	Y	0.949	NEU	Y	0.099	NEU
S_protein	4	339	A	1.311	NEU	A	0.368	NEU
S_protein	4	340	W	0.418	MIN	W	0.546	NEU
S_protein	4	341	E	0.648	NEU	N	-0.737	NEU
S_protein	4	342	R	1.311	MIN	R	1.304	MIN
S_protein	4	343	T	0.648	NEU	K	-0.598	NEU
S_protein	4	344	K	0.354	NEU	R	1.626	MIN
S_protein	4	345	I	1.311	MIN	I	1.143	MIN
S_protein	4	346	S	1.311	NEU	S	-0.206	NEU
S_protein	4	347	D	0.319	MAX	N	-0.794	NEU
S_protein	4	348	C	1.311	MIN	C	1.556	MIN
S_protein	4	349	V	1.311	MIN	V	1.113	MIN
S_protein	4	350	A	1.311	NEU	A	0.18	NEU
S_protein	4	351	D	1.311	MAX	D	-1.057	MAX
S_protein	4	352	Y	1.311	NEU	Y	-0.428	NEU
S_protein	4	353	T	0.354	NEU	S	1.405	MIN
S_protein	4	354	V	0.382	MIN	V	0.594	NEU
S_protein	4	355	L	1.311	MIN	L	1.209	MIN
S_protein	4	356	Y	1.311	NEU	Y	0.504	NEU
S_protein	4	357	N	0.648	NEU	N	-0.669	NEU
S_protein	4	358	S	1.311	NEU	S	-0.532	NEU
S_protein	4	359	T	1.311	NEU	A	-0.341	NEU
S_protein	4	360	S	0.831	NEU	S	-0.32	NEU

S_protein	4	361	F	1.311	MIN	F	1.184	MIN
S_protein	4	362	S	1.311	NEU	S	-0.574	NEU
S_protein	4	363	T	1.311	NEU	T	-0.378	NEU
S_protein	4	364	F	1.311	MIN	F	1.679	MIN
S_protein	4	365	K	0.949	MAX	K	-1.243	MAX
S_protein	4	366	C	1.311	MIN	C	1.553	MIN
S_protein	4	367	Y	1.311	MIN	Y	1.015	MIN
S_protein	4	368	G	1.311	NEU	G	-0.7	NEU
S_protein	4	369	V	1.311	MIN	V	1.322	MIN
S_protein	4	370	S	1.311	NEU	S	-0.292	NEU
S_protein	4	371	P	0.648	NEU	P	-0.56	NEU
S_protein	4	372	S	1.095	NEU	T	-0.68	NEU
S_protein	4	373	K	0.732	NEU	K	-0.92	NEU
S_protein	4	374	L	1.311	MIN	L	1.241	MIN
S_protein	4	375	I	0.319	MIN	N	-0.582	NEU
S_protein	4	376	D	1.095	MIN	D	0.528	NEU
S_protein	4	377	L	1.311	MIN	L	0.992	MIN
S_protein	4	378	C	1.311	MIN	C	2.304	MIN
S_protein	4	379	F	1.311	MIN	F	1.231	MIN
S_protein	4	380	T	1.311	NEU	T	-0.19	NEU
S_protein	4	381	S	1.095	NEU	N	-0.998	NEU
S_protein	4	382	V	1.311	MIN	V	1.204	MIN
S_protein	4	383	Y	0.576	NEU	Y	-0.907	NEU
S_protein	4	384	A	1.311	MIN	A	0.781	MIN
S_protein	4	385	D	0.576	MAX	D	-0.898	NEU
S_protein	4	386	T	0.831	NEU	S	-0.643	NEU
S_protein	4	387	F	1.311	MIN	F	1.189	MIN
S_protein	4	388	L	1.311	MIN	V	1.359	MIN
S_protein	4	389	I	1.311	MIN	I	1.087	MIN
S_protein	4	390	R	0.354	NEU	R	-0.149	NEU
S_protein	4	391	G	0.514	NEU	G	-0.403	NEU
S_protein	4	392	S	0.831	NEU	D	0.334	NEU
S_protein	4	393	E	1.311	NEU	E	-0.834	NEU
S_protein	4	394	V	1.311	MIN	V	1.391	MIN
S_protein	4	395	R	1.311	MIN	R	1.395	MIN
S_protein	4	396	Q	0.312	MAX	Q	-0.943	NEU
S_protein	4	397	V	1.311	MIN	I	1.692	MIN
S_protein	4	398	A	1.311	NEU	A	-0.264	NEU
S_protein	4	399	P	0.831	MAX	P	-1.034	MAX
S_protein	4	400	G	1.095	NEU	G	0.078	NEU
S_protein	4	401	Q	0.312	NEU	Q	-0.936	NEU
S_protein	4	402	T	1.311	MIN	T	0.727	NEU
S_protein	4	403	G	1.311	NEU	G	-0.48	NEU
S_protein	4	404	V	0.461	NEU	K	0.441	NEU
S_protein	4	405	I	1.311	MIN	I	1.509	MIN
S_protein	4	406	A	1.311	NEU	A	-0.354	NEU

S_protein	4	407	D	0.514	NEU	D	0.589	NEU
S_protein	4	408	Y	0.319	MAX	Y	-1.229	MAX
S_protein	4	409	N	0.333	MAX	N	-1.062	MAX
S_protein	4	410	Y	1.311	NEU	Y	-0.779	NEU
S_protein	4	411	K	0.312	MAX	K	-0.644	NEU
S_protein	4	412	L	1.311	MIN	L	0.97	MIN
S_protein	4	413	P	0.312	NEU	P	0.764	NEU
S_protein	4	414	D	0.949	NEU	D	-0.701	NEU
S_protein	4	415	D	1.311	NEU	D	-0.246	NEU
S_protein	4	416	F	1.311	MIN	F	1.362	MIN
S_protein	4	417	T	0.514	NEU	T	-0.297	NEU
S_protein	4	418	G	1.311	NEU	G	-0.324	NEU
S_protein	4	419	C	1.311	MIN	C	1.049	MIN
S_protein	4	420	V	1.311	MIN	V	1.329	MIN
S_protein	4	421	I	1.311	MIN	I	1.218	MIN
S_protein	4	422	A	0.418	NEU	A	0.391	NEU
S_protein	4	423	W	0.514	MIN	W	0.561	NEU
S_protein	4	424	N	1.311	NEU	N	-0.272	NEU
S_protein	4	425	T	1.311	NEU	S	-0.702	NEU
S_protein	4	426	A	0.736	NEU	N	0.007	NEU
S_protein	4	427	K	0.129	MIN	N	0.366	NEU
S_protein	4	428	Q	0.880	NEU	L	-0.127	NEU
S_protein	4	429	D	0.514	NEU	D	-0.491	NEU
S_protein	4	430	A	1.095	NEU	S	-0.271	NEU
S_protein	4	431	G	0.880	NEU	K	-0.813	NEU
S_protein	4	432	-	-0.079	NEU	V	-0.135	NEU
S_protein	4	433	-	0.790	NEU	G	0.187	NEU
S_protein	4	434	-	1.217	NEU	G	0.199	NEU
S_protein	4	435	-	1.217	NEU	N	-0.208	NEU
S_protein	4	436	-	0.254	NEU	Y	-0.495	NEU
S_protein	4	437	N	0.648	NEU	N	-0.157	NEU
S_protein	4	438	Y	0.319	NEU	Y	0.576	NEU
S_protein	4	439	Y	-0.227	MAX	L	0.869	MIN
S_protein	4	440	Y	0.354	NEU	Y	0.534	NEU
S_protein	4	441	R	1.311	NEU	R	-0.862	NEU
S_protein	4	442	S	0.386	NEU	L	1.208	MIN
S_protein	4	443	H	0.220	NEU	F	-0.341	NEU
S_protein	4	444	R	0.831	MIN	R	1.072	MIN
S_protein	4	445	K	-0.216	MIN	K	0.531	NEU
S_protein	4	446	T	0.949	NEU	S	0.067	NEU
S_protein	4	447	K	0.949	MIN	N	0.42	NEU
S_protein	4	448	L	0.831	NEU	L	-0.036	NEU
S_protein	4	449	K	0.386	NEU	K	-0.011	NEU
S_protein	4	450	P	1.311	NEU	P	-0.476	NEU
S_protein	4	451	F	1.311	MAX	F	-1.291	MAX
S_protein	4	452	E	0.732	MIN	E	0.171	NEU

S_protein	4	453	R	1.311	NEU	R	-0.385	NEU
S_protein	4	454	D	0.461	NEU	D	-0.967	NEU
S_protein	4	455	L	1.311	MIN	I	1.385	MIN
S_protein	4	456	S	0.354	MIN	S	0.805	MIN
S_protein	4	457	S	0.949	NEU	T	-0.292	NEU
S_protein	4	458	D	0.033	NEU	E	0.075	NEU
S_protein	4	459	E	0.418	MIN	I	1.559	MIN
S_protein	4	460	-	-0.210	MIN	Y	-1.945	MAX
S_protein	4	461	-	0.052	MIN	Q	-1.177	MAX
S_protein	4	462	-	0.859	NEU	A	0.166	NEU
S_protein	4	463	-	0.254	MIN	G	-0.754	NEU
S_protein	4	464	-	0.471	NEU	S	0.678	NEU
S_protein	4	465	-	0.859	NEU	T	-0.73	NEU
S_protein	4	466	-	0.289	MIN	P	0.792	MIN
S_protein	4	467	-	0.859	MIN	C	-0.214	NEU
S_protein	4	468	-	0.011	MAX	N	-1.032	MAX
S_protein	4	469	-	0.471	NEU	G	-0.603	NEU
S_protein	4	471	-	-0.064	NEU	E	-1.541	MAX
S_protein	4	472	-	0.254	NEU	G	-1.293	MAX
S_protein	4	473	-	0.279	NEU	F	0.976	MIN
S_protein	4	474	N	0.354	NEU	N	-0.538	NEU
S_protein	4	475	G	0.333	MIN	C	0.72	NEU
S_protein	4	476	V	0.144	NEU	Y	0.084	NEU
S_protein	4	477	R	0.094	MIN	F	0.967	MIN
S_protein	4	478	T	0.319	NEU	P	-1.055	MAX
S_protein	4	479	L	0.648	MIN	L	1.219	MIN
S_protein	4	480	S	0.949	NEU	Q	-1.128	MAX
S_protein	4	481	T	1.311	NEU	S	-0.596	NEU
S_protein	4	482	Y	0.648	NEU	Y	-1.035	MAX
S_protein	4	483	D	0.037	NEU	G	0.799	MIN
S_protein	4	484	F	0.319	MIN	F	0.532	NEU
S_protein	4	485	Y	-0.061	MAX	Q	-0.641	NEU
S_protein	4	486	P	0.064	NEU	P	-1.385	MAX
S_protein	4	487	T	0.064	NEU	T	0.867	MIN
S_protein	4	488	V	0.129	MIN	N	-0.585	NEU
S_protein	4	489	P	0.461	NEU	G	0.291	NEU
S_protein	4	490	V	0.333	MIN	V	0.05	NEU
S_protein	4	491	G	-0.163	MIN	G	0.245	NEU
S_protein	4	492	Y	0.382	NEU	Y	-0.492	NEU
S_protein	4	493	Q	0.732	NEU	Q	-0.701	NEU
S_protein	4	494	A	0.019	MIN	P	-1.326	MAX
S_protein	4	495	T	0.333	NEU	Y	0.78	MIN
S_protein	4	496	R	1.311	NEU	R	-0.707	NEU
S_protein	4	497	V	1.311	MIN	V	1.304	MIN
S_protein	4	498	V	1.311	MIN	V	1.321	MIN
S_protein	4	499	V	1.311	MIN	V	1.429	MIN

S_protein	4	500	L	1.311	MIN	L	1.394	MIN
S_protein	4	501	S	1.311	NEU	S	-0.599	NEU
S_protein	4	502	F	1.311	MIN	F	1.345	MIN
S_protein	4	503	E	1.095	MAX	E	-0.932	NEU
S_protein	4	504	L	1.311	MIN	L	1.024	MIN
S_protein	4	505	L	1.311	MIN	L	1.098	MIN
S_protein	4	506	N	0.198	NEU	H	0.319	NEU
S_protein	4	507	A	0.333	MAX	A	-1.017	MAX
S_protein	4	508	P	0.736	NEU	P	0.613	NEU
S_protein	4	509	A	1.311	NEU	A	0.234	NEU
S_protein	4	510	T	1.311	NEU	T	-0.333	NEU
S_protein	4	511	V	1.311	MIN	V	1.298	MIN
S_protein	4	512	C	1.311	MIN	C	1.575	MIN
S_protein	4	513	G	1.311	NEU	G	-0.466	NEU
S_protein	4	514	P	0.831	MAX	P	-0.949	NEU
S_protein	4	515	K	0.312	MAX	K	-1.153	MAX
S_protein	4	516	L	0.576	MIN	K	-0.311	NEU
S_protein	4	517	S	1.311	NEU	S	-0.683	NEU
S_protein	4	518	T	1.311	NEU	T	-0.028	NEU
S_protein	4	519	D	0.514	NEU	N	-1.344	MAX
S_protein	4	520	L	1.311	MIN	L	1.422	MIN
S_protein	4	521	V	1.311	MIN	V	0.985	MIN
S_protein	4	522	K	0.514	MAX	K	-1.033	MAX
S_protein	4	523	N	0.576	MAX	N	-1.255	MAX
S_protein	4	524	Q	0.648	NEU	K	-1.262	MAX
S_protein	4	525	C	1.311	MIN	C	2.825	MIN
S_protein	4	526	V	1.311	MIN	V	1.106	MIN
S_protein	4	527	N	0.831	NEU	N	-0.658	NEU
S_protein	4	528	F	1.311	MIN	F	0.917	MIN
S_protein	4	529	N	0.949	NEU	N	-0.899	NEU
S_protein	4	530	F	1.311	MIN	F	1.507	MIN
S_protein	4	531	N	0.831	MAX	N	-1.051	MAX
S_protein	4	532	G	1.311	NEU	G	-0.416	NEU
S_protein	4	533	L	1.311	MIN	L	1.137	MIN
S_protein	4	534	K	1.095	NEU	T	-0.029	NEU
S_protein	4	535	G	1.311	NEU	G	-0.47	NEU
S_protein	4	536	T	1.095	NEU	T	-0.815	NEU
S_protein	4	537	G	1.311	NEU	G	-0.157	NEU
S_protein	4	538	V	1.311	MIN	V	1.249	MIN
S_protein	4	539	L	1.311	MIN	L	1.222	MIN
S_protein	4	540	T	1.311	NEU	T	0.024	NEU
S_protein	4	541	P	1.095	NEU	E	-0.234	NEU
S_protein	4	542	S	1.311	NEU	S	-0.89	NEU
S_protein	4	543	S	1.311	NEU	N	0.189	NEU
S_protein	4	544	K	1.311	NEU	K	-0.508	NEU
S_protein	4	545	R	0.382	MIN	K	0.365	NEU

S_protein	4	546	F	1.311	MIN	F	1.179	MIN
S_protein	4	547	Q	0.949	NEU	L	1.292	MIN
S_protein	4	548	S	0.354	MIN	P	1.296	MIN
S_protein	4	549	F	0.461	NEU	F	0.889	MIN
S_protein	4	550	Q	1.311	NEU	Q	-0.367	NEU
S_protein	4	551	Q	1.095	MAX	Q	-1.219	MAX
S_protein	4	552	F	1.311	MIN	F	0.898	MIN
S_protein	4	553	G	1.311	NEU	G	-0.347	NEU
S_protein	4	554	R	1.095	MIN	R	1.145	MIN
S_protein	4	555	D	1.095	MAX	D	-0.988	NEU
S_protein	4	556	V	0.648	NEU	I	-0.152	NEU
S_protein	4	557	S	1.311	NEU	A	-0.544	NEU
S_protein	4	558	D	1.311	MIN	D	1.591	MIN
S_protein	4	559	F	1.311	NEU	T	-0.108	NEU
S_protein	4	560	T	1.095	NEU	T	-0.257	NEU
S_protein	4	561	D	1.095	NEU	D	-0.348	NEU
S_protein	4	562	S	1.311	NEU	A	0.285	NEU
S_protein	4	563	V	1.311	MIN	V	1.279	MIN
S_protein	4	564	R	1.311	NEU	R	-0.166	NEU
S_protein	4	565	D	0.382	NEU	D	-1.019	MAX
S_protein	4	566	P	1.311	MAX	P	-1.059	MAX
S_protein	4	567	Q	1.095	NEU	Q	0.202	NEU
S_protein	4	568	T	1.095	MIN	T	0.733	NEU
S_protein	4	569	L	1.095	NEU	L	-0.518	NEU
S_protein	4	570	E	0.418	NEU	E	0.087	NEU
S_protein	4	571	I	0.461	MIN	I	1.929	MIN
S_protein	4	572	L	1.311	MIN	L	1.182	MIN
S_protein	4	573	D	1.311	NEU	D	-0.711	NEU
S_protein	4	574	I	1.311	MIN	I	1.468	MIN
S_protein	4	575	S	1.311	NEU	T	0.067	NEU
S_protein	4	576	P	0.949	NEU	P	-1.052	MAX
S_protein	4	577	C	1.311	MIN	C	2.004	MIN
S_protein	4	578	S	1.311	NEU	S	-0.579	NEU
S_protein	4	579	F	0.831	MIN	F	1.881	MIN
S_protein	4	580	G	1.311	NEU	G	-0.329	NEU
S_protein	4	581	G	1.311	NEU	G	-0.222	NEU
S_protein	4	582	V	1.311	MIN	V	1.414	MIN
S_protein	4	583	S	1.311	NEU	S	-0.88	NEU
S_protein	4	584	V	1.311	MIN	V	1.419	MIN
S_protein	4	585	I	1.311	MIN	I	1.292	MIN
S_protein	4	586	T	1.311	NEU	T	-0.306	NEU
S_protein	4	587	P	1.311	NEU	P	-0.485	NEU
S_protein	4	588	G	1.311	NEU	G	-0.856	NEU
S_protein	4	589	T	1.095	NEU	T	0.459	NEU
S_protein	4	590	N	0.333	MIN	N	0.526	NEU
S_protein	4	591	A	0.162	MAX	T	0.473	NEU

S_protein	4	592	S	1.311	NEU	S	-0.67	NEU
S_protein	4	593	S	0.621	NEU	N	-1.049	MAX
S_protein	4	594	E	0.949	NEU	Q	-1.005	MAX
S_protein	4	595	V	1.311	MIN	V	1.3	MIN
S_protein	4	596	A	1.311	NEU	A	-0.295	NEU
S_protein	4	597	V	1.311	MIN	V	1.31	MIN
S_protein	4	598	L	1.311	MIN	L	1.213	MIN
S_protein	4	599	Y	1.311	NEU	Y	-0.003	NEU
S_protein	4	600	Q	1.311	NEU	Q	-0.797	NEU
S_protein	4	601	D	1.311	NEU	D	0.194	NEU
S_protein	4	602	V	1.311	MIN	V	1.264	MIN
S_protein	4	603	N	1.095	NEU	N	-1.012	MAX
S_protein	4	604	C	1.311	MIN	C	1.679	MIN
S_protein	4	605	T	0.312	NEU	T	-1.362	MAX
S_protein	4	606	D	0.312	NEU	E	-1.47	MAX
S_protein	4	607	V	1.311	MIN	V	1.476	MIN
S_protein	4	608	P	0.514	MAX	P	-1.098	MAX
S_protein	4	609	T	0.514	NEU	V	1.814	MIN
S_protein	4	610	A	0.576	MIN	A	0.539	NEU
S_protein	4	611	I	1.311	MIN	I	1.863	MIN
S_protein	4	612	H	0.333	MIN	H	0.42	NEU
S_protein	4	613	A	0.648	NEU	A	0.523	NEU
S_protein	4	614	D	0.621	NEU	D	0.389	NEU
S_protein	4	615	Q	0.949	NEU	Q	-0.512	NEU
S_protein	4	616	L	1.311	MIN	L	1.225	MIN
S_protein	4	617	T	1.311	NEU	T	0.394	NEU
S_protein	4	618	P	0.514	MAX	P	-1.09	MAX
S_protein	4	619	A	0.198	NEU	T	0.189	NEU
S_protein	4	620	W	1.095	MIN	W	0.946	MIN
S_protein	4	621	R	0.732	NEU	R	-0.817	NEU
S_protein	4	622	V	0.949	MIN	V	1.119	MIN
S_protein	4	623	Y	0.621	NEU	Y	-0.655	NEU
S_protein	4	624	S	0.949	NEU	S	-0.337	NEU
S_protein	4	625	T	0.831	NEU	T	-0.415	NEU
S_protein	4	626	G	0.621	NEU	G	0.385	NEU
S_protein	4	627	V	-0.175	NEU	S	-0.54	NEU
S_protein	4	628	N	0.133	NEU	N	-0.94	NEU
S_protein	4	629	V	1.095	MIN	V	1.454	MIN
S_protein	4	630	F	1.095	MIN	F	1.59	MIN
S_protein	4	631	Q	1.311	MAX	Q	-1.7	MAX
S_protein	4	632	T	1.311	NEU	T	-0.441	NEU
S_protein	4	633	Q	0.949	NEU	R	1.383	MIN
S_protein	4	634	A	1.311	MIN	A	0.59	NEU
S_protein	4	635	G	1.311	NEU	G	-0.432	NEU
S_protein	4	636	C	1.311	MIN	C	0.839	MIN
S_protein	4	637	L	1.311	MIN	L	1.27	MIN

S_protein	4	638	I	1.311	MIN	I	1.982	MIN
S_protein	4	639	G	1.311	NEU	G	-0.596	NEU
S_protein	4	640	A	1.311	NEU	A	0.388	NEU
S_protein	4	641	E	0.831	MAX	E	-1.22	MAX
S_protein	4	642	H	1.095	NEU	H	-0.286	NEU
S_protein	4	643	V	0.736	MIN	V	0.944	MIN
S_protein	4	644	N	0.514	NEU	N	0.218	NEU
S_protein	4	645	A	1.095	NEU	N	-0.814	NEU
S_protein	4	646	S	1.311	NEU	S	-0.7	NEU
S_protein	4	647	Y	1.311	MIN	Y	0.611	NEU
S_protein	4	648	E	0.461	MAX	E	-1.183	MAX
S_protein	4	649	C	1.311	MIN	C	1.339	MIN
S_protein	4	650	D	0.312	NEU	D	0.22	NEU
S_protein	4	651	I	1.311	MIN	I	1.153	MIN
S_protein	4	652	P	1.311	NEU	P	-0.471	NEU
S_protein	4	653	I	1.311	MIN	I	1.555	MIN
S_protein	4	654	G	1.311	NEU	G	-0.352	NEU
S_protein	4	655	A	1.311	MIN	A	0.953	MIN
S_protein	4	656	G	1.311	NEU	G	-0.276	NEU
S_protein	4	657	I	1.311	MIN	I	1.509	MIN
S_protein	4	658	C	1.311	MIN	C	0.807	MIN
S_protein	4	659	A	0.949	MIN	A	0.636	NEU
S_protein	4	660	S	1.311	NEU	S	-0.912	NEU
S_protein	4	661	Y	0.133	MAX	Y	0.298	NEU
S_protein	4	662	H	1.095	NEU	Q	-0.768	NEU
S_protein	4	663	T	1.087	NEU	T	0.231	NEU
S_protein	4	664	A	0.498	NEU	Q	-0.18	NEU
S_protein	4	665	S	1.095	NEU	T	0.641	NEU
S_protein	4	666	T	0.261	NEU	N	1.115	MIN
S_protein	4	671	L	0.133	NEU	A	-1.273	MAX
S_protein	4	672	R	0.261	NEU	R	-1.229	MAX
S_protein	4	673	S	0.319	MIN	S	0.375	NEU
S_protein	4	674	T	0.648	NEU	V	-0.553	NEU
S_protein	4	675	G	0.481	NEU	A	-0.916	NEU
S_protein	4	676	Q	0.880	NEU	S	-0.167	NEU
S_protein	4	677	K	1.095	NEU	Q	-0.091	NEU
S_protein	4	678	S	1.311	NEU	S	-0.115	NEU
S_protein	4	679	I	1.311	MIN	I	1.305	MIN
S_protein	4	680	V	1.311	MIN	I	0.645	NEU
S_protein	4	681	A	1.095	NEU	A	0.521	NEU
S_protein	4	682	Y	1.095	MIN	Y	0.926	MIN
S_protein	4	683	T	1.311	NEU	T	-0.735	NEU
S_protein	4	684	M	1.095	MIN	M	0.708	NEU
S_protein	4	685	S	1.311	NEU	S	-0.521	NEU
S_protein	4	686	L	1.311	MIN	L	1.063	MIN
S_protein	4	687	G	1.311	NEU	G	-0.172	NEU

S_protein	4	688	A	0.949	NEU	A	-0.45	NEU
S_protein	4	689	E	0.382	MAX	E	-1.099	MAX
S_protein	4	690	N	0.418	MAX	N	-1.202	MAX
S_protein	4	691	S	0.514	NEU	S	0.334	NEU
S_protein	4	692	I	0.382	MIN	V	1.001	MIN
S_protein	4	693	A	0.333	NEU	A	-1.364	MAX
S_protein	4	694	Y	1.311	MAX	Y	-2.493	MAX
S_protein	4	695	A	0.064	NEU	S	0.642	NEU
S_protein	4	696	N	1.311	NEU	N	-0.646	NEU
S_protein	4	697	N	0.319	MAX	N	-0.676	NEU
S_protein	4	698	S	1.095	NEU	S	0.175	NEU
S_protein	4	699	I	1.311	MIN	I	1.791	MIN
S_protein	4	700	A	0.732	NEU	A	-0.599	NEU
S_protein	4	701	I	1.311	MIN	I	1.107	MIN
S_protein	4	702	P	1.311	MAX	P	-1.261	MAX
S_protein	4	703	T	0.949	NEU	T	-0.281	NEU
S_protein	4	704	N	1.311	NEU	N	-0.623	NEU
S_protein	4	705	F	1.311	MIN	F	1.436	MIN
S_protein	4	706	S	1.311	NEU	T	0.072	NEU
S_protein	4	707	I	1.311	MIN	I	1.344	MIN
S_protein	4	708	S	1.311	NEU	S	-0.638	NEU
S_protein	4	709	V	1.311	MIN	V	1.182	MIN
S_protein	4	710	T	1.311	NEU	T	-0.069	NEU
S_protein	4	711	T	1.311	NEU	T	-0.312	NEU
S_protein	4	712	E	1.311	MAX	E	-1.301	MAX
S_protein	4	713	V	1.311	MIN	I	1.372	MIN
S_protein	4	714	M	1.311	MIN	L	1.231	MIN
S_protein	4	715	P	1.311	MAX	P	-1.297	MAX
S_protein	4	716	V	1.311	MIN	V	1.213	MIN
S_protein	4	717	S	1.311	NEU	S	-0.424	NEU
S_protein	4	718	M	1.095	MIN	M	0.643	NEU
S_protein	4	719	A	1.311	NEU	T	-0.255	NEU
S_protein	4	720	K	1.095	NEU	K	0.269	NEU
S_protein	4	721	T	1.311	NEU	T	-0.147	NEU
S_protein	4	722	S	1.311	NEU	S	-0.778	NEU
S_protein	4	723	V	1.311	MIN	V	1.067	MIN
S_protein	4	724	D	1.311	NEU	D	-0.222	NEU
S_protein	4	725	C	1.311	MIN	C	1.261	MIN
S_protein	4	726	T	1.311	NEU	T	-0.785	NEU
S_protein	4	727	M	1.311	MAX	M	-1.245	MAX
S_protein	4	728	Y	0.514	NEU	Y	0.388	NEU
S_protein	4	729	I	1.311	MIN	I	1.948	MIN
S_protein	4	730	C	1.311	MIN	C	1.025	MIN
S_protein	4	731	G	1.311	NEU	G	-0.284	NEU
S_protein	4	732	D	0.831	NEU	D	0.408	NEU
S_protein	4	733	S	1.311	NEU	S	-0.075	NEU

S_protein	4	734	T	-0.204	NEU	T	-0.898	NEU
S_protein	4	735	E	1.311	MAX	E	-1.242	MAX
S_protein	4	736	C	1.311	MIN	C	1.076	MIN
S_protein	4	737	S	1.311	NEU	S	-0.46	NEU
S_protein	4	738	N	0.418	NEU	N	-0.944	NEU
S_protein	4	739	L	1.311	MIN	L	1.049	MIN
S_protein	4	740	L	1.311	MIN	L	1.362	MIN
S_protein	4	741	L	1.311	MIN	L	1.684	MIN
S_protein	4	742	Q	1.311	NEU	Q	-0.822	NEU
S_protein	4	743	Y	1.311	NEU	Y	0.267	NEU
S_protein	4	744	G	1.095	MAX	G	-1.031	MAX
S_protein	4	745	S	1.311	NEU	S	-0.059	NEU
S_protein	4	746	F	1.311	MIN	F	0.992	MIN
S_protein	4	747	C	1.311	MIN	C	1.943	MIN
S_protein	4	748	T	1.311	NEU	T	-0.342	NEU
S_protein	4	749	Q	1.311	NEU	Q	-0.099	NEU
S_protein	4	750	L	1.311	MIN	L	1.405	MIN
S_protein	4	751	N	0.312	NEU	N	-1.041	MAX
S_protein	4	752	R	1.311	NEU	R	-0.49	NEU
S_protein	4	753	A	0.461	NEU	A	0.43	NEU
S_protein	4	754	L	1.311	MIN	L	1.336	MIN
S_protein	4	755	S	1.311	NEU	T	-0.043	NEU
S_protein	4	756	G	1.311	NEU	G	-0.743	NEU
S_protein	4	757	I	1.311	MIN	I	1.531	MIN
S_protein	4	758	A	0.461	NEU	A	0.548	NEU
S_protein	4	759	V	0.418	NEU	V	0.2	NEU
S_protein	4	760	E	0.514	NEU	E	-0.47	NEU
S_protein	4	761	Q	0.831	NEU	Q	-0.783	NEU
S_protein	4	762	D	0.831	NEU	D	-0.635	NEU
S_protein	4	763	K	0.514	NEU	K	0.459	NEU
S_protein	4	764	N	0.648	MAX	N	-1.044	MAX
S_protein	4	765	T	1.311	NEU	T	-0.153	NEU
S_protein	4	766	Q	0.831	MAX	Q	-1.131	MAX
S_protein	4	767	E	1.311	NEU	E	-0.467	NEU
S_protein	4	768	V	1.311	MIN	V	1.444	MIN
S_protein	4	769	F	1.311	MIN	F	0.957	MIN
S_protein	4	770	A	1.311	NEU	A	0.136	NEU
S_protein	4	771	Q	0.354	MAX	Q	-0.928	NEU
S_protein	4	772	V	0.831	MIN	V	1.506	MIN
S_protein	4	773	K	1.311	NEU	K	-0.369	NEU
S_protein	4	774	Q	0.831	MAX	Q	-1.147	MAX
S_protein	4	775	M	0.648	NEU	I	1.817	MIN
S_protein	4	776	Y	0.732	NEU	Y	-1.14	MAX
S_protein	4	777	K	0.312	MIN	K	0.786	MIN
S_protein	4	778	T	1.311	NEU	T	-0.129	NEU
S_protein	4	779	P	1.311	NEU	P	-0.679	NEU

S_protein	4	780	A	0.732	NEU	P	0.739	NEU
S_protein	4	781	I	0.949	NEU	I	0.195	NEU
S_protein	4	782	K	1.311	NEU	K	-0.748	NEU
S_protein	4	783	D	0.949	MAX	D	-1.195	MAX
S_protein	4	784	F	1.311	MIN	F	1.346	MIN
S_protein	4	785	G	1.311	NEU	G	-0.616	NEU
S_protein	4	786	G	1.311	NEU	G	-0.09	NEU
S_protein	4	787	F	1.311	MIN	F	1.197	MIN
S_protein	4	788	N	0.732	MIN	N	0.566	NEU
S_protein	4	789	F	1.311	MIN	F	1.248	MIN
S_protein	4	790	S	1.311	NEU	S	-0.706	NEU
S_protein	4	791	Q	1.311	NEU	Q	-0.86	NEU
S_protein	4	792	I	1.311	MIN	I	1.386	MIN
S_protein	4	793	L	1.311	MIN	L	0.874	MIN
S_protein	4	794	P	1.311	MAX	P	-1.605	MAX
S_protein	4	795	D	0.333	MIN	D	1.101	MIN
S_protein	4	796	P	0.949	NEU	P	0.376	NEU
S_protein	4	797	S	0.064	MIN	S	1.292	MIN
S_protein	4	798	K	1.095	MIN	K	0.642	NEU
S_protein	4	799	P	1.095	MIN	P	1.163	MIN
S_protein	4	800	T	1.311	NEU	S	0.17	NEU
S_protein	4	801	K	0.831	MIN	K	1.127	MIN
S_protein	4	802	R	1.311	MIN	R	1.123	MIN
S_protein	4	803	S	1.311	NEU	S	-0.928	NEU
S_protein	4	804	F	1.311	NEU	F	-0.945	NEU
S_protein	4	805	I	1.311	MIN	I	1.344	MIN
S_protein	4	806	E	1.311	MAX	E	-1.225	MAX
S_protein	4	807	D	1.311	NEU	D	-0.414	NEU
S_protein	4	808	L	1.311	MIN	L	0.579	NEU
S_protein	4	809	L	1.311	MIN	L	1.357	MIN
S_protein	4	810	F	0.576	NEU	F	-0.458	NEU
S_protein	4	811	N	1.311	NEU	N	-0.623	NEU
S_protein	4	812	K	0.949	MAX	K	-1.057	MAX
S_protein	4	813	V	1.311	MIN	V	1.302	MIN
S_protein	4	814	T	1.311	NEU	T	0.323	NEU
S_protein	4	815	L	1.311	MIN	L	1.104	MIN
S_protein	4	816	A	0.133	NEU	A	0.288	NEU
S_protein	4	817	D	-0.240	MIN	D	-1.273	MAX
S_protein	4	818	A	0.418	NEU	A	0.412	NEU
S_protein	4	819	G	1.311	NEU	G	-0.321	NEU
S_protein	4	820	F	1.095	MIN	F	0.717	NEU
S_protein	4	821	M	0.382	NEU	I	1.78	MIN
S_protein	4	822	K	0.831	NEU	K	-0.992	NEU
S_protein	4	823	Q	0.831	MAX	Q	-1.149	MAX
S_protein	4	824	Y	0.261	MIN	Y	-1.804	MAX
S_protein	4	825	G	0.949	NEU	G	-0.383	NEU

S_protein	4	826	E	0.276	NEU	D	-0.158	NEU
S_protein	4	827	C	1.311	MIN	C	3.029	MIN
S_protein	4	828	L	0.576	MIN	L	0.371	NEU
S_protein	4	829	G	1.095	NEU	G	-0.981	NEU
S_protein	4	830	D	-0.047	MIN	D	-1.064	MAX
S_protein	4	831	I	0.648	MIN	I	0.53	NEU
S_protein	4	832	N	0.524	MIN	A	-1.027	MAX
S_protein	4	833	A	1.311	NEU	A	-0.654	NEU
S_protein	4	834	R	1.095	NEU	R	-0.373	NEU
S_protein	4	835	D	0.949	NEU	D	-0.915	NEU
S_protein	4	836	L	1.095	MIN	L	0.412	NEU
S_protein	4	837	I	1.311	MIN	I	1.676	MIN
S_protein	4	838	C	1.311	MIN	C	3.017	MIN
S_protein	4	839	A	1.095	NEU	A	0.307	NEU
S_protein	4	840	Q	1.311	NEU	Q	-0.869	NEU
S_protein	4	841	K	1.311	MAX	K	-1.257	MAX
S_protein	4	842	F	1.311	MIN	F	1.29	MIN
S_protein	4	843	N	1.311	MAX	N	-1.107	MAX
S_protein	4	844	G	0.648	NEU	G	-0.809	NEU
S_protein	4	845	L	1.311	MIN	L	1.228	MIN
S_protein	4	846	T	1.311	NEU	T	0.074	NEU
S_protein	4	847	V	1.311	MIN	V	1.288	MIN
S_protein	4	848	L	1.311	MIN	L	1.253	MIN
S_protein	4	849	P	0.732	NEU	P	-0.448	NEU
S_protein	4	850	P	0.732	NEU	P	-0.82	NEU
S_protein	4	851	L	1.311	NEU	L	-0.107	NEU
S_protein	4	852	L	1.311	MIN	L	1.137	MIN
S_protein	4	853	T	1.311	NEU	T	-0.085	NEU
S_protein	4	854	D	1.311	NEU	D	-0.767	NEU
S_protein	4	855	E	0.736	NEU	E	1.367	MIN
S_protein	4	856	M	1.311	NEU	M	0.39	NEU
S_protein	4	857	I	1.311	MIN	I	1.472	MIN
S_protein	4	858	A	0.949	MIN	A	0.429	NEU
S_protein	4	859	A	1.311	NEU	Q	-0.808	NEU
S_protein	4	860	Y	1.311	NEU	Y	0.204	NEU
S_protein	4	861	T	1.311	NEU	T	-0.361	NEU
S_protein	4	862	A	0.949	MIN	S	-0.679	NEU
S_protein	4	863	A	0.732	NEU	A	0.39	NEU
S_protein	4	864	L	1.311	MIN	L	1.159	MIN
S_protein	4	865	V	1.311	MIN	L	1.106	MIN
S_protein	4	866	S	1.311	NEU	A	0.385	NEU
S_protein	4	867	G	1.311	NEU	G	-0.543	NEU
S_protein	4	868	T	1.311	NEU	T	-0.165	NEU
S_protein	4	869	A	0.949	NEU	I	1.426	MIN
S_protein	4	870	T	1.311	NEU	T	-0.033	NEU
S_protein	4	871	A	1.095	NEU	S	-0.446	NEU

S_protein	4	872	G	1.311	NEU	G	-0.635	NEU
S_protein	4	873	W	0.354	MAX	W	-1.423	MAX
S_protein	4	874	T	1.311	NEU	T	0.152	NEU
S_protein	4	875	F	1.311	MIN	F	0.999	MIN
S_protein	4	876	G	1.311	NEU	G	-0.483	NEU
S_protein	4	877	A	1.311	NEU	A	0.186	NEU
S_protein	4	878	G	0.461	NEU	G	0.661	NEU
S_protein	4	879	A	0.371	NEU	A	0.558	NEU
S_protein	4	880	A	0.732	NEU	A	-0.604	NEU
S_protein	4	881	L	1.311	MIN	L	1.352	MIN
S_protein	4	882	Q	1.311	NEU	Q	0.321	NEU
S_protein	4	883	I	1.311	MIN	I	1.127	MIN
S_protein	4	884	P	1.311	NEU	P	-0.459	NEU
S_protein	4	885	F	1.311	MIN	F	1.308	MIN
S_protein	4	886	A	1.311	NEU	A	0.111	NEU
S_protein	4	887	M	1.311	NEU	M	-0.166	NEU
S_protein	4	888	Q	0.831	NEU	Q	-0.748	NEU
S_protein	4	889	M	1.311	NEU	M	0.176	NEU
S_protein	4	890	A	1.311	NEU	A	0.359	NEU
S_protein	4	891	Y	1.311	MAX	Y	-2.849	MAX
S_protein	4	892	R	1.311	NEU	R	-0.463	NEU
S_protein	4	893	F	1.311	MIN	F	0.996	MIN
S_protein	4	894	N	1.311	NEU	N	-0.795	NEU
S_protein	4	895	G	1.311	NEU	G	0.371	NEU
S_protein	4	896	I	1.311	MIN	I	2.014	MIN
S_protein	4	897	G	1.095	MIN	G	0.612	NEU
S_protein	4	898	V	1.311	MIN	V	1.34	MIN
S_protein	4	899	T	1.095	NEU	T	0.49	NEU
S_protein	4	900	Q	1.311	MAX	Q	-1.191	MAX
S_protein	4	901	N	1.311	NEU	N	-0.878	NEU
S_protein	4	902	V	1.311	MIN	V	1.414	MIN
S_protein	4	903	L	1.311	MIN	L	1.37	MIN
S_protein	4	904	Y	1.311	MAX	Y	-2.111	MAX
S_protein	4	905	E	0.576	MIN	E	-0.335	NEU
S_protein	4	906	N	1.311	MAX	N	-1.126	MAX
S_protein	4	907	Q	1.311	NEU	Q	-0.86	NEU
S_protein	4	908	K	1.311	NEU	K	-0.019	NEU
S_protein	4	909	Q	0.514	NEU	L	1.079	MIN
S_protein	4	910	I	1.311	MIN	I	1.601	MIN
S_protein	4	911	A	1.311	NEU	A	-0.144	NEU
S_protein	4	912	N	1.095	NEU	N	-0.531	NEU
S_protein	4	913	Q	1.311	NEU	Q	-0.755	NEU
S_protein	4	914	F	1.311	MIN	F	1.214	MIN
S_protein	4	915	N	1.311	NEU	N	-0.372	NEU
S_protein	4	916	K	0.648	MAX	S	-0.055	NEU
S_protein	4	917	A	1.311	MIN	A	0.602	NEU

S_protein	4	918	I	1.311	MIN	I	1.562	MIN
S_protein	4	919	S	0.732	NEU	G	-0.496	NEU
S_protein	4	920	Q	0.732	NEU	K	-1.131	MAX
S_protein	4	921	I	1.311	MIN	I	1.455	MIN
S_protein	4	922	Q	0.648	NEU	Q	-1.037	MAX
S_protein	4	923	E	0.732	NEU	D	1.023	MIN
S_protein	4	924	S	1.311	NEU	S	-0.582	NEU
S_protein	4	925	L	1.311	MIN	L	1.591	MIN
S_protein	4	926	T	0.648	MIN	S	0.099	NEU
S_protein	4	927	T	1.311	MIN	S	1.212	MIN
S_protein	4	928	T	0.333	MIN	T	0.427	NEU
S_protein	4	929	S	1.311	NEU	A	0.382	NEU
S_protein	4	930	T	1.095	MIN	S	0.949	MIN
S_protein	4	931	A	1.311	NEU	A	-0.058	NEU
S_protein	4	932	L	1.311	MIN	L	1.486	MIN
S_protein	4	933	G	1.311	NEU	G	-0.701	NEU
S_protein	4	934	K	1.311	NEU	K	-0.867	NEU
S_protein	4	935	L	1.311	MIN	L	1.201	MIN
S_protein	4	936	Q	1.311	NEU	Q	-0.559	NEU
S_protein	4	937	D	1.311	NEU	D	0.446	NEU
S_protein	4	938	V	1.311	MIN	V	1.118	MIN
S_protein	4	939	V	1.311	MIN	V	1.152	MIN
S_protein	4	940	N	1.311	NEU	N	0.265	NEU
S_protein	4	941	Q	1.311	MAX	Q	-1.1	MAX
S_protein	4	942	N	0.831	NEU	N	-0.907	NEU
S_protein	4	943	A	1.311	MIN	A	0.954	MIN
S_protein	4	944	Q	0.481	NEU	Q	0.501	NEU
S_protein	4	945	A	1.311	NEU	A	-0.719	NEU
S_protein	4	946	L	1.311	MIN	L	1.483	MIN
S_protein	4	947	N	0.648	NEU	N	-0.816	NEU
S_protein	4	948	T	1.311	NEU	T	0.438	NEU
S_protein	4	949	L	1.311	MIN	L	1.548	MIN
S_protein	4	950	V	1.311	MIN	V	1.09	MIN
S_protein	4	951	K	1.311	MAX	K	-2.084	MAX
S_protein	4	952	Q	0.732	NEU	Q	-0.855	NEU
S_protein	4	953	L	1.311	MIN	L	0.923	MIN
S_protein	4	954	S	1.311	NEU	S	-0.069	NEU
S_protein	4	955	S	1.311	NEU	S	-0.153	NEU
S_protein	4	956	N	1.311	NEU	N	0.166	NEU
S_protein	4	957	F	1.311	NEU	F	0.437	NEU
S_protein	4	958	G	1.311	NEU	G	-0.96	NEU
S_protein	4	959	A	1.311	NEU	A	0.144	NEU
S_protein	4	960	I	1.311	MIN	I	1.032	MIN
S_protein	4	961	S	1.311	NEU	S	-0.573	NEU
S_protein	4	962	S	1.311	NEU	S	0.281	NEU
S_protein	4	963	V	0.319	MIN	V	0.736	NEU

S_protein	4	964	L	1.311	MIN	L	1.395	MIN
S_protein	4	965	N	1.095	NEU	N	-0.925	NEU
S_protein	4	966	D	1.311	MIN	D	0.748	NEU
S_protein	4	967	I	1.311	MIN	I	1.878	MIN
S_protein	4	968	L	1.311	MIN	L	1.183	MIN
S_protein	4	969	S	1.311	MIN	S	1.028	MIN
S_protein	4	970	R	1.311	MIN	R	1.982	MIN
S_protein	4	971	L	1.311	MIN	L	1.241	MIN
S_protein	4	972	D	1.311	MAX	D	-1.569	MAX
S_protein	4	973	K	1.095	MIN	K	1.859	MIN
S_protein	4	974	V	1.095	MIN	V	1.172	MIN
S_protein	4	975	E	1.095	NEU	E	0.53	NEU
S_protein	4	976	A	1.095	MIN	A	0.698	NEU
S_protein	4	977	E	0.949	NEU	E	-0.946	NEU
S_protein	4	978	V	1.311	MIN	V	1.495	MIN
S_protein	4	979	Q	1.311	NEU	Q	-0.763	NEU
S_protein	4	980	I	1.311	MIN	I	1.335	MIN
S_protein	4	981	D	1.311	MAX	D	-1.441	MAX
S_protein	4	982	R	1.311	NEU	R	-0.563	NEU
S_protein	4	983	L	1.311	MIN	L	1.143	MIN
S_protein	4	984	I	1.311	MIN	I	1.147	MIN
S_protein	4	985	T	1.311	NEU	T	0.236	NEU
S_protein	4	986	G	0.333	NEU	G	-0.995	NEU
S_protein	4	987	R	1.311	NEU	R	-0.399	NEU
S_protein	4	988	L	1.311	MIN	L	1.208	MIN
S_protein	4	989	Q	1.311	NEU	Q	-0.072	NEU
S_protein	4	990	S	1.311	NEU	S	0.124	NEU
S_protein	4	991	L	1.311	MIN	L	1.082	MIN
S_protein	4	992	Q	1.311	NEU	Q	-0.936	NEU
S_protein	4	993	T	1.311	MIN	T	1.346	MIN
S_protein	4	994	Y	1.311	NEU	Y	-0.751	NEU
S_protein	4	995	V	1.311	MIN	V	1.252	MIN
S_protein	4	996	T	1.311	NEU	T	0.048	NEU
S_protein	4	997	Q	1.311	NEU	Q	-0.658	NEU
S_protein	4	998	Q	1.311	NEU	Q	-0.851	NEU
S_protein	4	999	L	1.311	MIN	L	1.507	MIN
S_protein	4	1000	I	1.311	MIN	I	1.164	MIN
S_protein	4	1001	R	1.311	NEU	R	-0.073	NEU
S_protein	4	1002	A	1.311	MIN	A	0.765	NEU
S_protein	4	1003	A	1.311	NEU	A	0.177	NEU
S_protein	4	1004	E	1.095	NEU	E	-0.26	NEU
S_protein	4	1005	I	1.311	MIN	I	1.211	MIN
S_protein	4	1006	R	0.382	MIN	R	0.659	NEU
S_protein	4	1007	A	1.311	NEU	A	0.196	NEU
S_protein	4	1008	S	1.311	NEU	S	-0.851	NEU
S_protein	4	1009	A	1.311	MIN	A	0.637	NEU

S_protein	4	1010	N	1.095	NEU	N	-0.888	NEU
S_protein	4	1011	L	1.311	MIN	L	1.294	MIN
S_protein	4	1012	A	1.311	MIN	A	1.051	MIN
S_protein	4	1013	A	1.311	MIN	A	0.947	MIN
S_protein	4	1014	T	1.311	NEU	T	-0.021	NEU
S_protein	4	1015	K	1.095	NEU	K	-0.831	NEU
S_protein	4	1016	M	0.648	MIN	M	0.777	NEU
S_protein	4	1017	S	1.311	NEU	S	-0.717	NEU
S_protein	4	1018	E	0.648	NEU	E	0.242	NEU
S_protein	4	1019	C	1.311	MIN	C	1.857	MIN
S_protein	4	1020	V	1.311	MIN	V	1.232	MIN
S_protein	4	1021	L	1.311	MIN	L	1.35	MIN
S_protein	4	1022	G	1.311	NEU	G	-0.883	NEU
S_protein	4	1023	Q	1.311	NEU	Q	-0.476	NEU
S_protein	4	1024	S	1.311	NEU	S	0.037	NEU
S_protein	4	1025	K	1.311	NEU	K	-0.443	NEU
S_protein	4	1026	R	1.311	MIN	R	2.032	MIN
S_protein	4	1027	V	1.311	NEU	V	-0.505	NEU
S_protein	4	1028	D	1.311	MIN	D	2.962	MIN
S_protein	4	1029	F	1.311	NEU	F	-0.816	NEU
S_protein	4	1030	C	1.311	MIN	C	1.539	MIN
S_protein	4	1031	G	1.311	NEU	G	-0.379	NEU
S_protein	4	1032	K	0.732	MAX	K	-1.45	MAX
S_protein	4	1033	G	1.311	NEU	G	-0.696	NEU
S_protein	4	1034	Y	0.648	MAX	Y	-1.149	MAX
S_protein	4	1035	H	0.831	NEU	H	0.253	NEU
S_protein	4	1036	L	1.311	MIN	L	1.203	MIN
S_protein	4	1037	M	1.311	MAX	M	-1.511	MAX
S_protein	4	1038	S	1.311	NEU	S	-0.571	NEU
S_protein	4	1039	F	1.311	MIN	F	1.573	MIN
S_protein	4	1040	P	0.354	MAX	P	-0.99	NEU
S_protein	4	1041	Q	1.311	NEU	Q	-0.838	NEU
S_protein	4	1042	A	0.831	NEU	S	-0.601	NEU
S_protein	4	1043	A	0.319	MIN	A	0.595	NEU
S_protein	4	1044	P	1.095	NEU	P	-0.919	NEU
S_protein	4	1045	H	1.311	NEU	H	-0.264	NEU
S_protein	4	1046	G	1.311	NEU	G	-0.467	NEU
S_protein	4	1047	V	1.311	MIN	V	1.167	MIN
S_protein	4	1048	V	1.311	MIN	V	1.213	MIN
S_protein	4	1049	F	1.311	MIN	F	1.865	MIN
S_protein	4	1050	L	1.311	MIN	L	1.304	MIN
S_protein	4	1051	H	1.311	NEU	H	0.044	NEU
S_protein	4	1052	V	1.311	MIN	V	1.192	MIN
S_protein	4	1053	T	1.311	NEU	T	-0.259	NEU
S_protein	4	1054	Y	1.311	MIN	Y	0.818	MIN
S_protein	4	1055	V	1.311	MIN	V	1.385	MIN

S_protein	4	1056	P	1.311	NEU	P	-0.555	NEU
S_protein	4	1057	S	0.831	NEU	A	0.895	MIN
S_protein	4	1058	Q	1.311	NEU	Q	-0.366	NEU
S_protein	4	1059	E	0.576	NEU	E	-1.022	MAX
S_protein	4	1060	R	0.382	NEU	K	-1.358	MAX
S_protein	4	1061	N	1.311	NEU	N	-0.47	NEU
S_protein	4	1062	F	1.311	MIN	F	1.269	MIN
S_protein	4	1063	T	1.311	NEU	T	-0.255	NEU
S_protein	4	1064	T	1.311	NEU	T	-0.287	NEU
S_protein	4	1065	A	1.311	NEU	A	-0.101	NEU
S_protein	4	1066	P	0.949	NEU	P	-0.863	NEU
S_protein	4	1067	A	1.095	NEU	A	0.544	NEU
S_protein	4	1068	I	1.311	MIN	I	1.048	MIN
S_protein	4	1069	C	1.311	MIN	C	1.613	MIN
S_protein	4	1070	H	1.311	NEU	H	-0.771	NEU
S_protein	4	1071	E	0.621	NEU	D	1.014	MIN
S_protein	4	1072	G	1.311	NEU	G	0.221	NEU
S_protein	4	1073	K	0.732	NEU	K	-0.692	NEU
S_protein	4	1074	A	1.311	MIN	A	0.719	NEU
S_protein	4	1075	Y	1.311	NEU	H	-0.477	NEU
S_protein	4	1076	F	1.311	MIN	F	1.298	MIN
S_protein	4	1077	P	0.949	MAX	P	-1	MAX
S_protein	4	1078	R	1.311	NEU	R	-0.761	NEU
S_protein	4	1079	E	0.418	NEU	E	0.784	MIN
S_protein	4	1080	G	1.311	NEU	G	-0.521	NEU
S_protein	4	1081	V	1.311	MIN	V	1.382	MIN
S_protein	4	1082	F	1.311	MIN	F	1.36	MIN
S_protein	4	1083	V	1.311	MIN	V	1.735	MIN
S_protein	4	1084	S	0.418	NEU	S	-0.578	NEU
S_protein	4	1085	N	1.095	NEU	N	-0.815	NEU
S_protein	4	1086	G	1.311	NEU	G	-0.359	NEU
S_protein	4	1087	T	0.949	NEU	T	-0.238	NEU
S_protein	4	1088	S	0.949	NEU	H	0.29	NEU
S_protein	4	1089	W	0.319	MIN	W	0.966	MIN
S_protein	4	1090	F	1.311	MIN	F	1.05	MIN
S_protein	4	1091	I	1.311	MIN	V	1.431	MIN
S_protein	4	1092	T	1.311	NEU	T	-0.17	NEU
S_protein	4	1093	Q	0.949	NEU	Q	-1.055	MAX
S_protein	4	1094	R	1.311	NEU	R	-0.293	NEU
S_protein	4	1095	N	1.095	NEU	N	-0.929	NEU
S_protein	4	1096	F	1.311	MIN	F	1.18	MIN
S_protein	4	1097	Y	0.418	MAX	Y	-3.363	MAX
S_protein	4	1098	S	1.311	NEU	E	-0.825	NEU
S_protein	4	1099	P	0.949	NEU	P	-0.473	NEU
S_protein	4	1100	Q	1.311	NEU	Q	-0.126	NEU
S_protein	4	1101	I	0.732	MIN	I	2.249	MIN

S_protein	4	1102	I	1.311	MIN	I	1.24	MIN
S_protein	4	1103	T	1.311	NEU	T	-0.735	NEU
S_protein	4	1104	T	1.311	NEU	T	0.064	NEU
S_protein	4	1105	D	1.095	NEU	D	0.411	NEU
S_protein	4	1106	N	0.831	NEU	N	-0.928	NEU
S_protein	4	1107	T	1.311	NEU	T	-0.38	NEU
S_protein	4	1108	F	0.949	MIN	F	0.607	NEU
S_protein	4	1109	V	1.095	MIN	V	1.329	MIN
S_protein	4	1110	S	0.382	NEU	S	-0.853	NEU
S_protein	4	1111	G	0.831	NEU	G	-0.882	NEU
S_protein	4	1112	N	1.311	NEU	N	-0.593	NEU
S_protein	4	1113	C	0.461	MIN	C	0.694	NEU
S_protein	4	1114	D	1.095	NEU	D	0.223	NEU
S_protein	4	1115	V	1.311	MIN	V	0.772	NEU
S_protein	4	1116	V	1.311	MIN	V	1.327	MIN
S_protein	4	1117	I	1.311	MIN	I	2.454	MIN
S_protein	4	1118	G	1.311	NEU	G	-0.815	NEU
S_protein	4	1119	I	1.311	MIN	I	1.64	MIN
S_protein	4	1120	I	1.311	MIN	V	0.726	NEU
S_protein	4	1121	N	1.311	MAX	N	-1.039	MAX
S_protein	4	1122	N	1.311	MAX	N	-1.357	MAX
S_protein	4	1123	T	1.311	NEU	T	-0.432	NEU
S_protein	4	1124	V	1.311	MIN	V	1.222	MIN
S_protein	4	1125	Y	0.831	NEU	Y	0.635	NEU
S_protein	4	1126	D	1.311	MAX	D	-1.457	MAX
S_protein	4	1127	P	1.311	NEU	P	0.338	NEU
S_protein	4	1128	L	1.311	NEU	L	-0.671	NEU
S_protein	4	1129	Q	0.949	NEU	Q	0.274	NEU
S_protein	4	1130	P	-0.142	NEU	P	-0.06	NEU
S_protein	4	1131	E	0.319	NEU	E	-1.006	MAX
S_protein	4	1132	L	0.461	NEU	L	-0.305	NEU
S_protein	4	1133	D	0.319	NEU	D	0.575	NEU
S_protein	4	1134	S	0.461	MIN	S	0.695	NEU
S_protein	4	1135	F	1.311	NEU	F	-0.74	NEU
S_protein	4	1136	K	0.514	MIN	K	1.622	MIN
S_protein	4	1137	E	1.095	NEU	E	-0.272	NEU
S_protein	4	1138	E	1.311	NEU	E	0.247	NEU
S_protein	4	1139	L	1.311	MIN	L	1.32	MIN
S_protein	4	1140	D	1.311	NEU	D	-0.531	NEU
S_protein	4	1141	K	0.949	NEU	K	0.162	NEU
S_protein	4	1142	Y	0.576	MAX	Y	-1.438	MAX
S_protein	4	1143	F	1.311	NEU	F	-0.118	NEU
S_protein	4	1144	K	1.311	MIN	K	0.93	MIN
S_protein	4	1145	N	1.311	NEU	N	-0.377	NEU
S_protein	4	1146	H	1.311	MIN	H	0.741	NEU
S_protein	4	1147	T	1.311	NEU	T	-0.206	NEU

S_protein	4	1148	S	1.311	NEU	S	0.099	NEU
S_protein	4	1149	P	0.949	NEU	P	-0.43	NEU
E	1	1	E	1.079	MAX	E	-1.954	MAX
E	1	2	T	0.582	MAX	T	-1.045	MAX
E	1	3	G	1.308	MAX	G	-1.753	MAX
E	1	4	T	1.308	NEU	T	0.367	NEU
E	1	5	L	1.079	NEU	L	-0.785	NEU
E	1	6	I	1.308	MIN	I	0.773	NEU
E	1	7	V	1.308	MIN	V	0.758	NEU
E	1	8	N	1.308	MAX	N	-2.152	MAX
E	1	9	S	0.853	MAX	S	-1.71	MAX
E	1	10	V	1.308	MIN	V	0.652	NEU
E	1	11	L	0.927	MIN	L	0.728	NEU
E	1	12	L	0.582	NEU	L	0.511	NEU
E	1	13	F	0.804	NEU	F	0.463	NEU
E	1	14	L	0.927	MIN	L	0.616	NEU
E	1	15	A	0.927	NEU	A	0.425	NEU
E	1	16	F	0.927	NEU	F	0.385	NEU
E	1	17	V	0.702	MIN	V	0.584	NEU
E	1	18	V	0.927	MIN	V	0.781	MIN
E	1	19	F	1.308	NEU	F	0.134	NEU
E	1	20	L	0.431	NEU	L	0.528	NEU
E	1	21	L	1.079	MIN	L	0.717	NEU
E	1	22	V	1.079	MIN	V	0.804	MIN
E	1	23	T	0.436	MAX	T	-1.193	MAX
E	1	24	L	0.927	NEU	L	0.507	NEU
E	1	25	A	1.308	NEU	A	0.374	NEU
E	1	26	I	0.853	MIN	I	0.743	NEU
E	1	27	L	1.308	MIN	L	0.673	NEU
E	1	28	T	0.927	NEU	T	-0.994	NEU
E	1	29	A	1.308	NEU	A	0.307	NEU
E	1	30	L	1.079	MIN	L	0.684	NEU
E	1	31	R	1.308	MAX	R	-2.162	MAX
N_Nterm	1	1	N	-0.050	NEU	N	1.141	MIN
N_Nterm	1	2	N	0.713	NEU	T	-0.6	NEU
N_Nterm	1	3	V	0.553	MIN	A	-0.641	NEU
N_Nterm	1	4	S	1.338	NEU	S	-0.722	NEU
N_Nterm	1	5	W	0.565	NEU	W	-0.014	NEU
N_Nterm	1	6	F	1.222	MIN	F	1.447	MIN
N_Nterm	1	7	T	0.795	NEU	T	-0.086	NEU
N_Nterm	1	8	P	0.840	NEU	A	0.331	NEU
N_Nterm	1	9	L	1.338	MIN	L	1.654	MIN
N_Nterm	1	10	T	0.216	NEU	T	-0.008	NEU
N_Nterm	1	11	Q	0.442	NEU	Q	-1.225	MAX
N_Nterm	1	12	H	0.396	MIN	H	0.959	MIN
N_Nterm	1	13	G	0.345	MIN	G	1.098	MIN

N_Nterm	1	14	K	1.138	MIN	K	1.569	MIN
N_Nterm	1	15	Q	0.195	NEU	E	0.313	NEU
N_Nterm	1	16	P	0.345	MIN	D	2.43	MIN
N_Nterm	1	17	L	1.138	MIN	L	1.59	MIN
N_Nterm	1	18	R	-0.026	MIN	K	1.694	MIN
N_Nterm	1	19	F	1.338	MIN	F	0.93	MIN
N_Nterm	1	20	P	0.125	NEU	P	-0.251	NEU
N_Nterm	1	21	R	0.394	MIN	R	1.116	MIN
N_Nterm	1	22	G	1.338	NEU	G	-0.258	NEU
N_Nterm	1	23	Q	0.879	NEU	Q	-0.416	NEU
N_Nterm	1	24	G	0.795	NEU	G	-0.354	NEU
N_Nterm	1	25	V	1.338	MIN	V	2.03	MIN
N_Nterm	1	26	P	1.338	NEU	P	-0.857	NEU
N_Nterm	1	27	I	1.222	MIN	I	2.63	MIN
N_Nterm	1	28	N	1.138	NEU	N	-0.592	NEU
N_Nterm	1	29	A	0.238	MAX	T	-0.302	NEU
N_Nterm	1	30	N	0.339	MIN	N	-0.024	NEU
N_Nterm	1	31	S	0.461	MIN	S	-0.101	NEU
N_Nterm	1	32	T	0.170	NEU	S	1.064	MIN
N_Nterm	1	33	P	0.101	NEU	P	0.448	NEU
N_Nterm	1	34	D	0.290	NEU	D	-0.455	NEU
N_Nterm	1	35	Q	0.394	NEU	D	-0.455	NEU
N_Nterm	1	36	N	0.623	NEU	Q	-0.474	NEU
N_Nterm	1	37	H	0.527	NEU	I	1.895	MIN
N_Nterm	1	38	G	1.338	NEU	G	-0.257	NEU
N_Nterm	1	39	Y	1.338	MIN	Y	0.892	MIN
N_Nterm	1	40	W	1.338	MIN	Y	0.884	MIN
N_Nterm	1	41	R	0.396	NEU	R	-0.428	NEU
N_Nterm	1	42	R	1.107	NEU	R	-0.014	NEU
N_Nterm	1	43	Q	1.138	NEU	A	-1.489	MAX
N_Nterm	1	44	D	0.279	NEU	T	0.244	NEU
N_Nterm	1	45	R	0.091	NEU	R	1.005	MIN
N_Nterm	1	46	K	-0.182	NEU	R	1.717	MIN
N_Nterm	1	47	F	0.435	MIN	I	2.296	MIN
N_Nterm	1	48	N	0.020	NEU	R	1.512	MIN
N_Nterm	1	49	K	-0.201	NEU	G	0.746	NEU
N_Nterm	1	50	G	0.364	NEU	G	0.416	NEU
N_Nterm	1	51	-	0.336	NEU	D	2.387	MIN
N_Nterm	1	52	G	0.356	MIN	G	1.361	MIN
N_Nterm	1	53	K	0.347	MAX	K	0.378	NEU
N_Nterm	1	54	M	0.205	NEU	M	0.843	MIN
N_Nterm	1	55	K	-0.186	MIN	K	-0.585	NEU
N_Nterm	1	56	Q	0.234	NEU	D	1.865	MIN
N_Nterm	1	57	L	0.345	NEU	L	0.149	NEU
N_Nterm	1	58	A	0.240	NEU	S	0.597	NEU
N_Nterm	1	59	P	0.461	MAX	P	-0.127	NEU

N_Nterm	1	60	R	1.138	NEU	R	-0.078	NEU
N_Nterm	1	61	W	1.338	MIN	W	1.015	MIN
N_Nterm	1	62	Y	0.553	MIN	Y	0.614	NEU
N_Nterm	1	63	F	1.338	MIN	F	1.844	MIN
N_Nterm	1	64	Y	1.222	MIN	Y	0.778	NEU
N_Nterm	1	65	Y	-0.050	MAX	Y	-1.303	MAX
N_Nterm	1	66	T	0.527	NEU	L	1.539	MIN
N_Nterm	1	67	G	1.338	NEU	G	0.071	NEU
N_Nterm	1	68	T	1.338	NEU	T	-0.176	NEU
N_Nterm	1	69	G	1.338	NEU	G	-0.673	NEU
N_Nterm	1	70	P	0.085	MAX	P	-1.325	MAX
N_Nterm	1	71	E	0.061	NEU	E	-1.022	MAX
N_Nterm	1	72	A	1.138	NEU	A	-0.63	NEU
N_Nterm	1	73	D	0.023	NEU	G	0.161	NEU
N_Nterm	1	74	L	0.840	MIN	L	1.781	MIN
N_Nterm	1	75	P	0.425	MIN	P	-0.079	NEU
N_Nterm	1	76	F	0.353	MIN	Y	0.735	NEU
N_Nterm	1	77	G	0.503	NEU	G	-0.516	NEU
N_Nterm	1	78	T	0.753	NEU	A	-0.013	NEU
N_Nterm	1	79	V	0.238	NEU	N	-0.343	NEU
N_Nterm	1	80	K	0.216	NEU	K	-0.875	NEU
N_Nterm	1	81	D	0.943	MIN	D	1.299	MIN
N_Nterm	1	82	G	0.324	NEU	G	-0.536	NEU
N_Nterm	1	83	I	1.338	MIN	I	1.582	MIN
N_Nterm	1	84	V	0.733	MIN	I	2.112	MIN
N_Nterm	1	85	W	0.339	NEU	W	0.064	NEU
N_Nterm	1	86	V	1.338	MIN	V	1.676	MIN
N_Nterm	1	87	G	0.130	NEU	A	-0.544	NEU
N_Nterm	1	88	E	0.181	MAX	T	-0.325	NEU
N_Nterm	1	89	E	0.425	MIN	E	0.976	MIN
N_Nterm	1	90	G	1.001	NEU	G	-0.315	NEU
N_Nterm	1	91	A	-0.060	NEU	A	-0.103	NEU
N_Nterm	1	92	N	0.338	MIN	L	0.803	MIN
N_Nterm	1	93	N	0.425	MIN	N	-0.532	NEU
N_Nterm	1	94	A	-0.197	NEU	T	-0.331	NEU
N_Nterm	1	95	P	0.503	NEU	P	-0.385	NEU
N_Nterm	1	96	-	0.249	MIN	K	-1.358	MAX
N_Nterm	1	97	S	0.451	NEU	D	-1.114	MAX
N_Nterm	1	98	D	0.410	NEU	H	1.446	MIN
N_Nterm	1	99	F	0.364	MIN	I	1.12	MIN
N_Nterm	1	100	G	1.338	NEU	G	-0.052	NEU
N_Nterm	1	101	T	1.338	NEU	T	-0.069	NEU
N_Nterm	1	102	R	1.138	NEU	R	-0.454	NEU
N_Nterm	1	103	N	0.890	MIN	N	0.896	MIN
N_Nterm	1	104	P	0.875	NEU	P	-0.231	NEU
N_Nterm	1	105	N	0.341	MIN	A	-0.547	NEU

N_Nterm	1	106	N	1.338	MIN	N	1.635	MIN
N_Nterm	1	107	D	0.567	MIN	N	0.47	NEU
N_Nterm	1	108	A	-0.105	MAX	A	-1.204	MAX
N_Nterm	1	109	A	1.338	NEU	A	-0.264	NEU
N_Nterm	1	110	I	1.219	MIN	I	2.2	MIN
N_Nterm	1	111	V	0.108	MIN	V	2.256	MIN
N_Nterm	1	112	T	0.375	MIN	L	1.615	MIN
N_Nterm	1	113	Q	1.132	NEU	Q	-0.523	NEU
N_Nterm	1	114	L	0.783	MIN	L	1.109	MIN
N_Nterm	1	115	A	0.629	NEU	P	0.113	NEU
N_Nterm	1	116	P	0.829	NEU	Q	-0.459	NEU
N_Nterm	1	117	G	1.100	NEU	G	0.102	NEU
N_Nterm	1	118	T	0.614	NEU	T	0.524	NEU
N_Nterm	1	119	-	-0.021	NEU	T	0.761	NEU
N_Nterm	1	120	L	1.222	MIN	L	1.728	MIN
N_Nterm	1	121	P	-0.176	NEU	P	-0.926	NEU
N_Nterm	1	122	K	-0.213	MIN	K	1.477	MIN
N_Nterm	1	123	G	-0.102	NEU	G	1.188	MIN
N_Nterm	1	124	F	1.222	MIN	F	1.316	MIN
N_Nterm	1	125	Y	0.037	NEU	Y	-1.231	MAX
N_Cterm	1	1	T	0.350	NEU	T	0.42	NEU
N_Cterm	1	2	K	0.803	NEU	K	-0.908	NEU
N_Cterm	1	3	K	0.111	NEU	K	-0.425	NEU
N_Cterm	1	4	D	0.829	NEU	S	-0.116	NEU
N_Cterm	1	5	A	0.408	NEU	A	0.422	NEU
N_Cterm	1	6	A	1.065	NEU	A	0.232	NEU
N_Cterm	1	7	A	0.205	MIN	E	2.542	MIN
N_Cterm	1	8	A	0.642	NEU	A	0.064	NEU
N_Cterm	1	9	A	0.796	NEU	S	-0.218	NEU
N_Cterm	1	10	K	0.356	MIN	K	2.012	MIN
N_Cterm	1	11	K	0.452	NEU	K	0.338	NEU
N_Cterm	1	12	L	0.890	NEU	P	-0.311	NEU
N_Cterm	1	13	R	0.803	NEU	R	0.005	NEU
N_Cterm	1	14	H	1.138	NEU	Q	-0.305	NEU
N_Cterm	1	15	K	0.442	NEU	K	-0.045	NEU
N_Cterm	1	16	R	0.676	NEU	R	-0.698	NEU
N_Cterm	1	17	T	0.943	MIN	T	0.877	MIN
N_Cterm	1	18	A	1.001	NEU	A	-0.683	NEU
N_Cterm	1	19	T	1.065	NEU	T	0.112	NEU
N_Cterm	1	20	K	-0.115	NEU	K	-1.116	MAX
N_Cterm	1	21	G	0.867	NEU	A	-0.36	NEU
N_Cterm	1	22	Y	0.026	NEU	Y	-2.427	MAX
N_Cterm	1	23	N	0.499	NEU	N	-0.675	NEU
N_Cterm	1	24	V	0.443	MIN	V	1.632	MIN
N_Cterm	1	25	T	0.890	NEU	T	0.141	NEU
N_Cterm	1	26	Q	-0.026	MAX	Q	-1.397	MAX

N_Cterm	1	27	A	0.102	NEU	A	-0.457	NEU
N_Cterm	1	28	F	0.125	NEU	F	-0.691	NEU
N_Cterm	1	29	G	0.943	NEU	G	-0.612	NEU
N_Cterm	1	30	R	0.481	NEU	R	-0.063	NEU
N_Cterm	1	31	R	0.481	MIN	R	0.701	NEU
N_Cterm	1	32	G	0.753	MIN	G	0.621	NEU
N_Cterm	1	33	P	0.581	MIN	P	0.946	MIN
N_Cterm	1	34	G	0.119	NEU	E	1.044	MIN
N_Cterm	1	35	D	0.176	NEU	Q	0.514	NEU
N_Cterm	1	36	L	0.139	MIN	T	0.838	MIN
N_Cterm	1	37	Q	1.058	NEU	Q	-0.065	NEU
N_Cterm	1	38	G	1.338	NEU	G	-0.056	NEU
N_Cterm	1	39	N	0.601	NEU	N	0.641	NEU
N_Cterm	1	40	F	0.527	MIN	F	0.698	NEU
N_Cterm	1	41	G	0.713	NEU	G	-0.5	NEU
N_Cterm	1	42	D	0.373	NEU	D	-0.07	NEU
N_Cterm	1	43	L	0.172	NEU	Q	-0.861	NEU
N_Cterm	1	44	E	0.394	NEU	E	0.084	NEU
N_Cterm	1	45	L	0.111	MIN	L	0.689	NEU
N_Cterm	1	46	L	0.503	MIN	I	1.115	MIN
N_Cterm	1	47	K	1.001	MIN	R	1.757	MIN
N_Cterm	1	48	L	0.339	NEU	Q	-0.977	NEU
N_Cterm	1	49	G	1.338	NEU	G	-0.102	NEU
N_Cterm	1	50	T	0.443	NEU	T	-0.031	NEU
N_Cterm	1	51	D	0.335	MIN	D	1.112	MIN
N_Cterm	1	52	D	-0.214	MIN	Y	-2	MAX
N_Cterm	1	53	P	0.338	MIN	K	1.1	MIN
N_Cterm	1	54	R	0.527	MIN	H	-0.116	NEU
N_Cterm	1	55	W	-0.236	MIN	W	-1.111	MAX
N_Cterm	1	56	P	1.338	NEU	P	0.008	NEU
N_Cterm	1	57	Q	0.829	NEU	Q	-0.848	NEU
N_Cterm	1	58	I	0.345	MIN	I	1.693	MIN
N_Cterm	1	59	A	0.943	MIN	A	0.766	NEU
N_Cterm	1	60	Q	1.065	NEU	Q	0.031	NEU
N_Cterm	1	61	L	1.065	MIN	F	1.281	MIN
N_Cterm	1	62	A	1.222	NEU	A	0.102	NEU
N_Cterm	1	63	P	0.425	NEU	P	1.013	MIN
N_Cterm	1	64	S	0.713	NEU	S	0.005	NEU
N_Cterm	1	65	A	0.318	MIN	A	0.647	NEU
N_Cterm	1	66	S	0.581	NEU	S	0.3	NEU
N_Cterm	1	67	A	1.138	NEU	A	0.365	NEU
N_Cterm	1	68	F	1.065	MIN	F	1.307	MIN
N_Cterm	1	69	L	0.325	MIN	F	0.926	MIN
N_Cterm	1	70	G	0.384	NEU	G	0.108	NEU
N_Cterm	1	71	M	0.279	MIN	M	1.095	MIN
N_Cterm	1	72	S	1.338	NEU	S	-0.301	NEU

N_Cterm	1	73	H	0.693	NEU	R	-0.039	NEU
N_Cterm	1	74	F	0.753	MIN	I	2.276	MIN
N_Cterm	1	75	K	0.061	NEU	G	0.161	NEU
N_Cterm	1	76	L	0.461	MIN	M	0.695	NEU
N_Cterm	1	77	R	0.338	MIN	E	0.688	NEU
N_Cterm	1	78	H	-0.065	NEU	V	2.228	MIN
N_Cterm	1	79	E	0.040	NEU	T	1.012	MIN
N_Cterm	1	80	S	0.481	NEU	P	0.87	MIN
N_Cterm	1	81	D	0.198	NEU	S	0.248	NEU
N_Cterm	1	82	A	0.365	NEU	G	0.14	NEU
N_Cterm	1	83	T	0.585	NEU	T	0.345	NEU
N_Cterm	1	84	W	-0.188	MAX	W	-2.128	MAX
N_Cterm	1	85	L	1.338	MIN	L	1.503	MIN
N_Cterm	1	86	R	0.364	NEU	T	0.628	NEU
N_Cterm	1	87	Y	0.461	NEU	Y	-0.547	NEU
N_Cterm	1	88	S	0.713	NEU	T	0.781	MIN
N_Cterm	1	89	G	0.713	NEU	G	0.495	NEU
N_Cterm	1	90	A	0.470	NEU	A	-0.936	NEU
N_Cterm	1	91	I	1.138	MIN	I	2.163	MIN
N_Cterm	1	92	K	-0.045	MIN	K	1.776	MIN
N_Cterm	1	93	L	1.065	MIN	L	0.881	MIN
N_Cterm	1	94	D	0.020	MIN	D	1.571	MIN
N_Cterm	1	95	K	0.187	MIN	D	-0.546	NEU
N_Cterm	1	96	K	0.396	MIN	K	0.867	MIN
N_Cterm	1	97	D	0.350	NEU	D	0.748	NEU
N_Cterm	1	98	P	0.890	MIN	P	1.034	MIN
N_Cterm	1	99	N	0.339	NEU	N	0.948	MIN
N_Cterm	1	100	Y	0.112	MAX	F	-0.891	NEU
N_Cterm	1	101	K	0.527	NEU	K	0.351	NEU
N_Cterm	1	102	K	-0.006	NEU	D	-1.142	MAX
N_Cterm	1	103	W	0.713	NEU	Q	-0.867	NEU
N_Cterm	1	104	L	0.503	MIN	V	1.585	MIN
N_Cterm	1	105	E	-0.040	NEU	I	-1.229	MAX
N_Cterm	1	106	L	0.481	MIN	L	-0.143	NEU
N_Cterm	1	107	L	1.107	MIN	L	1.278	MIN
N_Cterm	1	108	E	0.180	MAX	N	-1.232	MAX
N_Cterm	1	109	E	0.124	NEU	K	-0.58	NEU
N_Cterm	1	110	N	1.065	NEU	H	0.099	NEU
N_Cterm	1	111	I	1.338	MIN	I	1.599	MIN
N_Cterm	1	112	D	1.065	MIN	D	1.895	MIN
N_Cterm	1	113	A	0.950	NEU	A	-0.708	NEU
N_Cterm	1	114	Y	0.803	MAX	Y	-3.488	MAX
N_Cterm	1	115	K	0.461	MIN	K	0.974	MIN
N_Cterm	1	116	T	1.001	NEU	T	-0.514	NEU
N_Cterm	1	117	F	0.542	NEU	F	-0.771	NEU
N_Cterm	1	118	P	0.127	MIN	P	0.309	NEU

Supplementary Table 5A: Amino acid positions that are frustratingly conserved in the SARS-CoV-2 containing subfamilies (FrustIC>0.5 and their most informative frustration state is the highly frustrated one). For full table, check Supplementary Table 4.

Protein	SARS2 containing cluster	Protein position	MSA consensus AA	FrustIC	Frustraevo state	SARS2 AA	SRFI	Frustratometer state
N_Nterm	1	43 Q	1.138 NEU	A	-1.489	MAX		
S_protein	4	15 Q	0.524 NEU	Y	-1.029	MAX		
S_protein	4	189 Y	0.514 NEU	K	-1.119	MAX		
S_protein	4	204 P	1.095 NEU	P	-1.002	MAX		
S_protein	4	265 K	0.949 NEU	K	-1.083	MAX		
S_protein	4	480 S	0.949 NEU	Q	-1.128	MAX		
S_protein	4	482 Y	0.648 NEU	Y	-1.035	MAX		
S_protein	4	519 D	0.514 NEU	N	-1.344	MAX		
S_protein	4	524 Q	0.648 NEU	K	-1.262	MAX		
S_protein	4	576 P	0.949 NEU	P	-1.052	MAX		
S_protein	4	593 S	0.621 NEU	N	-1.049	MAX		
S_protein	4	594 E	0.949 NEU	Q	-1.005	MAX		
S_protein	4	603 N	1.095 NEU	N	-1.012	MAX		
S_protein	4	776 Y	0.732 NEU	Y	-1.14	MAX		
S_protein	4	832 N	0.524 MIN	A	-1.027	MAX		
S_protein	4	920 Q	0.732 NEU	K	-1.131	MAX		
S_protein	4	922 Q	0.648 NEU	Q	-1.037	MAX		
S_protein	4	1059 E	0.576 NEU	E	-1.022	MAX		
S_protein	4	1093 Q	0.949 NEU	Q	-1.055	MAX		
nsp10	1	72 V	0.556 NEU	F	-1.308	MAX		
nsp12	1	88 K	0.552 NEU	K	-1.192	MAX		
nsp12	1	185 N	0.577 NEU	K	-1.317	MAX		
nsp12	1	366 K	0.577 NEU	K	-1.319	MAX		
nsp12	1	506 F	0.677 MIN	W	-2.508	MAX		
nsp13	1	123 N	0.701 NEU	N	-1.055	MAX		
nsp13	1	280 Q	0.500 NEU	Q	-1.001	MAX		
nsp13	1	449 D	0.839 NEU	D	-1.026	MAX		
nsp13	1	488 N	0.500 NEU	N	-1.013	MAX		
nsp14	1	27 S	0.636 NEU	S	-1.124	MAX		
nsp14	1	351 D	0.754 NEU	D	-1.269	MAX		
nsp14	1	394 N	0.604 NEU	N	-1.002	MAX		
nsp14	1	470 N	0.953 NEU	A	-1.108	MAX		
nsp14	1	479 G	0.953 NEU	G	-1.204	MAX		
nsp15	1	17 G	0.651 NEU	G	-1.142	MAX		
nsp15	1	20 G	0.651 NEU	G	-1.157	MAX		
nsp15	1	93 P	0.651 NEU	P	-1.051	MAX		
nsp15	1	187 Q	0.651 NEU	Q	-1.055	MAX		
nsp15	1	264 K	0.757 NEU	E	-1.196	MAX		
nsp2	1	35 Q	0.663 NEU	Q	-1.009	MAX		
nsp2	1	71 P	0.529 NEU	P	-1.029	MAX		
nsp2	1	162 G	0.960 NEU	G	-1.13	MAX		
nsp2	1	186 P	0.591 NEU	Y	-3.026	MAX		
nsp2	1	203 D	0.529 NEU	E	-1.559	MAX		
nsp2	1	324 G	0.960 NEU	G	-1.004	MAX		
nsp2	1	341 G	0.591 NEU	G	-1.163	MAX		
nsp2	1	374 H	0.960 NEU	N	-1.199	MAX		
nsp2	1	411 S	0.529 NEU	N	-1.104	MAX		
nsp3_MacroX	1	19 C	0.544 MIN	N	-1.012	MAX		
nsp3_NAB	1	75 K	0.632 NEU	K	-1.03	MAX		
nsp3_PLPro	1	95 G	0.544 NEU	N	-1.074	MAX		
nsp3_PLPro	1	228 Q	0.905 NEU	K	-1.325	MAX		
nsp3_PLPro	1	253 T	0.606 NEU	T	-1.152	MAX		
nsp3_SUD_Nt	1	72 P	0.677 NEU	P	-1.067	MAX		
nsp3_SUD_Nt	1	102 Q	1.109 NEU	Q	-1.126	MAX		
nsp3_Ubl1	1	47 G	0.760 NEU	G	-1.128	MAX		
nsp3_Y3	1	90 Q	0.544 NEU	Q	-1.122	MAX		
nsp5	1	7 A	0.781 NEU	A	-1.104	MAX		
nsp5	1	102 T	0.558 NEU	K	-1.425	MAX		
nsp5	1	154 G	0.558 NEU	Y	-1.047	MAX		
nsp5	1	236 K	0.505 NEU	K	-1.19	MAX		
nsp5	1	240 T	0.620 NEU	E	-1.061	MAX		
nsp5	1	244 G	0.558 NEU	Q	-1.059	MAX		

Supplementary Table 5B: Frequency of frustratingly conserved positions per protein.

Protein	Count	Protein length	Norm (Count/Protein length)
nsp5	6	306	0.02
nsp15	5	346	0.014
nsp2	9	638	0.014
S_protein	18	1273	0.014
nsp3_PLPro	3	308	0.01
nsp3_Y3	1	101	0.01
nsp14	5	527	0.009
nsp3_NAB	1	112	0.009
nsp3_Ubl1	1	110	0.009
N_Nterm	1	124	0.008
nsp3_SUD_Nt	2	263	0.008
nsp10	1	139	0.007
nsp13	4	601	0.007
nsp3_MacroX	1	171	0.006
nsp12	4	932	0.004

Supplementary Table 6. Non-redundant dataset of the 21 mammalian hemoglobins used in section 3.

PDB ID	Organism	Cell Type	Bound/Unbound state
1fsx	Bos taurus (Bovine)	Mammalia	Deoxy
3d4x	Felis catus (Cat) (<i>Felis silvestris catus</i>)	Mammalia	Deoxy
2dn1	Homo sapiens (Human)	Mammalia	Deoxy
3vre	Mammuthus primigenius (Siberian woolly mammoth)	Mammalia	Deoxy
3d1a	Capra hircus (Goat)	Mammalia	Methemoglobin
2dhb	Equus caballus (Horse)	Mammalia	Not clear
3fh9	Pteropus giganteus (Indian flying fox)	Mammalia	Not clear
3gou	Canis lupus familiaris (Dog)	Mammalia	Oxy
3cy5	Bubalus bubalis (Domestic water buffalo)	Mammalia	Oxy
3gdj	Camelus dromedarius (Dromedary) (Arabian camel)	Mammalia	Oxy
3a0g	Cavia porcellus (Guinea pig)	Mammalia	Oxy
2b7h	Cerdocyon thous	Mammalia	Oxy
1fhj	Chrysocyon brachyurus (Maned wolf)	Mammalia	Oxy
1s0h	Equus asinus (Donkey) (<i>Equus africanus asinus</i>)	Mammalia	Oxy
4yu3	Helogale parvula	Mammalia	Oxy
3lqd	Lepus europaeus (European hare)	Mammalia	Oxy
1hds	Odocoileus virginianus	Mammalia	Oxy
2rao	Oryctolagus cuniculus (Rabbit)	Mammalia	Oxy
2qu0	Ovis aries (Sheep)	Mammalia	Oxy
3dht	Rattus norvegicus (Rat)	Mammalia	Oxy
1qpw	Sus scrofa (Pig)	Mammalia	Oxy

Supplementary References

1. Rojas, A. M., Fuentes, G., Rausell, A. & Valencia, A. The Ras protein superfamily: evolutionary tree and role of conserved amino acids. *J. Cell Biol.* **196**, 189–201 (2012).
2. Cox, A. D. & Der, C. J. Ras history: The saga continues. *Small GTPases* **1**, 2–27 (2010).
3. Pylayeva-Gupta, Y., Grabocka, E. & Bar-Sagi, D. RAS oncogenes: weaving a tumorigenic web. *Nat. Rev. Cancer* **11**, 761–774 (2011).
4. Stephen, A. G., Esposito, D., Bagni, R. K. & McCormick, F. Dragging ras back in the ring. *Cancer Cell* **25**, 272–281 (2014).
5. McCormick, F. KRAS as a Therapeutic Target. *Clin. Cancer Res.* **21**, 1797–1801 (2015).
6. Cox, A. D., Fesik, S. W., Kimmelman, A. C., Luo, J. & Der, C. J. Drugging the undruggable RAS: Mission possible? *Nat. Rev. Drug Discov.* **13**, 828–851 (2014).
7. Wittinghofer, A. *Ras Superfamily Small G Proteins: Biology and Mechanisms 1+2*. (Springer, 2014).
8. Macara, I. G. The ras superfamily of molecular switches. *Cell. Signal.* **3**, 179–187 (1991).
9. Spoerner, M., Herrmann, C., Vetter, I. R., Kalbitzer, H. R. & Wittinghofer, A. Dynamic properties of the Ras switch I region and its importance for binding to effectors. *Proc. Natl. Acad. Sci. U. S. A.* **98**, 4944–4949 (2001).
10. Faidon Brotzakis, Z., Zhang, S. & Vendruscolo, M. AlphaFold Prediction of Structural Ensembles of Disordered Proteins. *bioRxiv* 2023.01.19.524720 (2023) doi:10.1101/2023.01.19.524720.
11. Piovesan, D., Monzon, A. M. & Tosatto, S. C. E. Intrinsic protein disorder and conditional folding in AlphaFoldDB. *Protein Sci.* **31**, e4466 (2022).