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Original Article

Mutation near the binding interfaces at α-hemoglobin stabilizing protein is highly pathogenic

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Abstract: Aggregation of free alpha-hemoglobin proteins forms harmful reactive oxygen radicals during the development of normal erythroid cell, which can be prevented by a chaperone, alpha hemoglobin stabilizing protein (AHSP). Mutations at the *AHSP* gene may affect its interacting ability with other globin proteins. Various state-of-the-art tools have been extensively used to identify the most deleterious nsSNPs at the AHSP and their pathogenic effect during AHSP-globin interaction. Comprehensive analysis revealed that the V56G of the AHS protein is the most pathogenic amino acid substitution, agreed consistently and significantly (*P=1.27E-13*) by all the state-of-the-art tools (PROVEAN <-2.5, SIFT=0, SNAP2 >50, SNPs&GO >0.5, PolyPhen >0.5, FATHMM >0.6, PANTHER <-3, VEST P<0.05) and protein-protein interaction analysis. The V56G exists near the hot spot and was found to be the highly pathogenic and it forms an extra helix on mutation. The unchaperoned HBA2 and KLF1 proteins with the AHSP mutant (V56G) chains denote the non-interactive nature. Binding energies were significantly varied upon highly deleterious mutation at *AHSP* and/or *HBA1* gene. The study endorses the mutated AHSP protein, p.val56Gly for detailed confirmatory wet lab analysis.

Keywords: α-Hemoglobin stabilizing protein (AHSP), nsSNPs, bioinformatics, protein-protein interaction, globin genes, mutation, molecular modeling, interface residues, interaction sites

Introduction

Aggregation of free alpha-globin proteins forms toxic reactive oxygen radicals, the phenomenon is prevented by a chaperone, alpha hemoglobin stabilizing protein (AHSP) during the development of normal erythroid cell [1, 2]. In beta-thalassemia patents lack/reduced synthesis of β globin chains leaving free alpha globin protein, which can causes mature red cells hemolysis and premature death of erythroid precursors [2, 3]. Alpha-globin/non-alpha globin protein imbalance reflects in the severity of thalassemia [2, 4]. Comprehensive studies on the effect of the non-synonymous SNPs in the *AHSP* gene and their impact on the alpha globin-AHSP interaction is needed to device their direct and indirect impact. Wet lab experimental methods to identify the protein-protein interactions are expensive and tedious; it can be unraveled cost effectively by in-silico approaches. In the study we aimed to use various state-of-the-art tools extensively to understand the effect of nsSNPs on the structural and functional impacts to categorize the most deleterious nsSNPs at the AHSP and their pathogenic effect during AHSP-globin interaction.

Materials and methods

Datasets and SNP retrieval

AHSP, HBA1, HBA2, HBB, HBD, KLF1 and *HBQ1* gene sequences were downloaded during December 2015 from NCBI [5, 6]. The protein sequences of the HBA1, HBA2, HBB, HBD, KLF1, HBQ1 and AHSP proteins were retrieved by limiting our search only to human from RCSB Protein Data Bank (PDB ID: 1a00, 1hbb, 2w72, 5bnv, 2l2i.1.A, P09105 and Q9NZD4) [6]. The dbSNPs of *AHSP* gene was retrieved from NCBI. The non-synonymous SNPs (nsSNPs) of *AHSP* gene were screened to identify their damaging effects on AHSP protein.

Table 1. Possible pathogenic non-synonymous substitution mutations in the *ANSP* gene predicted using various state-of-art-tools

S. No.	SNP	Coordinate	Amino Acid change	SIFT score	SIFT prediction	PolyPhen Score	Prediction	FATHMM Coding Score	PANTHER subPSEC	PROVEAN score	PREDICTION (cutoff=-2.5)	SNAP2 Score	Predicted Effect	SNPs&GO Effect	VEST *p*-value
1	rs144861094	31539497	A13P	0.073	TOLERATED	0.028	BENIGN	0.06082	-2.43754	-2.04	Neutral	-43	Neutral	Neutral	0.2587
2	rs201919859	31539509	E17K	0.054	TOLERATED	0.936	PROBABLY DAMAGING	0.76085	-2.48368	-3.47	Deleterious	50	Effect	Disease	0.0043
3	rs372264195	31539994	H97Q	0.113	TOLERATED	0	UNKNOWN	0.1351	-1.15018	-1.92	Neutral	12	Effect	Neutral	0.5607
4	rs147251409	31539897	K65M	0.032	DELETERIOUS	0.329	POSSIBLY DAMAGING	0.03781	-3.40556	-4.07	Deleterious	30	Effect	Neutral	0.3437
5	rs140200160	31539522	L21P*	0	DELETERIOUS	0.999	PROBABLY DAMAGING	0.8301	-4.87126	-6.24	Deleterious	83	Effect	Disease	0.0061
6	rs10920	31539837	M45K	0.008	DELETERIOUS	0.001	BENIGN	0.8711	-3.16676	-3.72	Deleterious	73	Effect	Disease	0.0229
7	rs75782426	31539927	N75I	0.05	TOLERATED	0.902	PROBABLY DAMAGING	0.05718	-2.70452	-6.02	Deleterious	6	Effect	Neutral	0.3279
8	rs36018996	31540001	P100T	0	DELETERIOUS	0	UNKNOWN	0.15999	-2.99152	-4.03	Deleterious	76	Effect	Neutral	0.5319
9	rs147349976	31539999	P99L	1	TOLERATED	0	UNKNOWN	0.00783	-0.84752	-0.33	Neutral	25	Effect	Neutral	0.6600
10	rs142369727	31539929	T76A	0.667	TOLERATED	0.001	BENIGN	0.04407	-1.23877	-2.2	Neutral	26	Effect	Neutral	0.8676
11	rs200722385	31539824	V41L	0.154	TOLERATED	0.002	BENIGN	0.46605	-2.61048	-2.46	Neutral	28	Effect	Disease	0.2642
12	rs186590045	31539870	V56G*	0.01	DELETERIOUS	0.932	PROBABLY DAMAGING	0.68878	-3.77106	-5.07	Deleterious	69	Effect	Disease	0.0162
13	rs372200025	31539957	Y85C*	0	DELETERIOUS	1	PROBABLY DAMAGING	0.87283	-5.22604	-8.84	Deleterious	76	Effect	Disease	0.0083

*Highly pathogenic nsSNPs of *ANSP* gene agreed unanimously as deleterious by all the tools. Shaded cells indicate the deleterious nsSNPs predicted by the respective state-of-art-tool. Threshold values: PROVEAN (<-2.5, SIFT (=0), SNAP2 (>50), SNPs&GO (>0.5), PolyPhen (>0.5), FATHMM (>0.6), PANTHER (<-3), VEST (P<0.05).

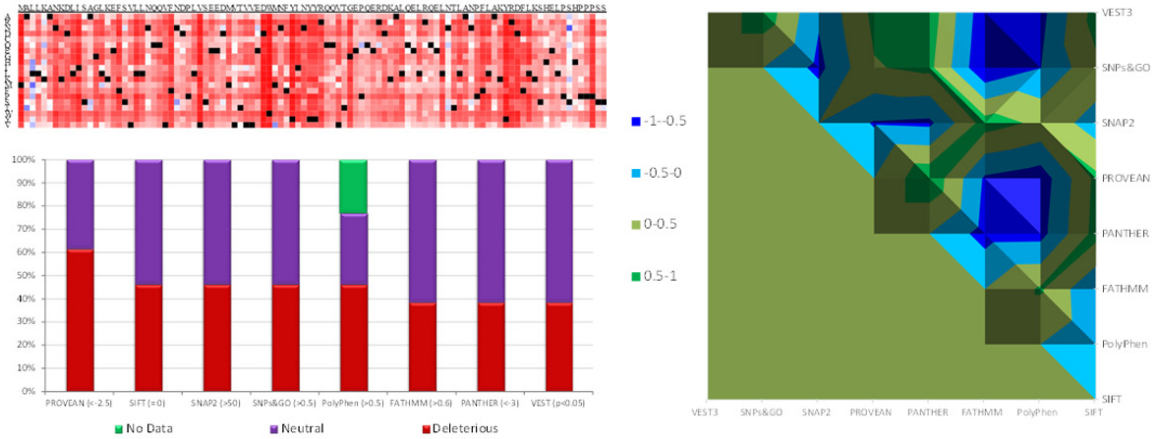

Figure 1. Heatmap of AHSP protein. Top Left: Heatmap of AHSP protein generated using SNAP2. Dark red: Strong signal for high level pathogenicity. Bottom Left: Pathogenicity of nsSNPs in the predicted using various state-of-art-tools. A value in the parenthesis indicates the threshold value for pathogenicity. Right: Surface chart of correlation between the predictions of pathogenicity of nsSNPs in *AHSP* gene by various state-of-art-tools.

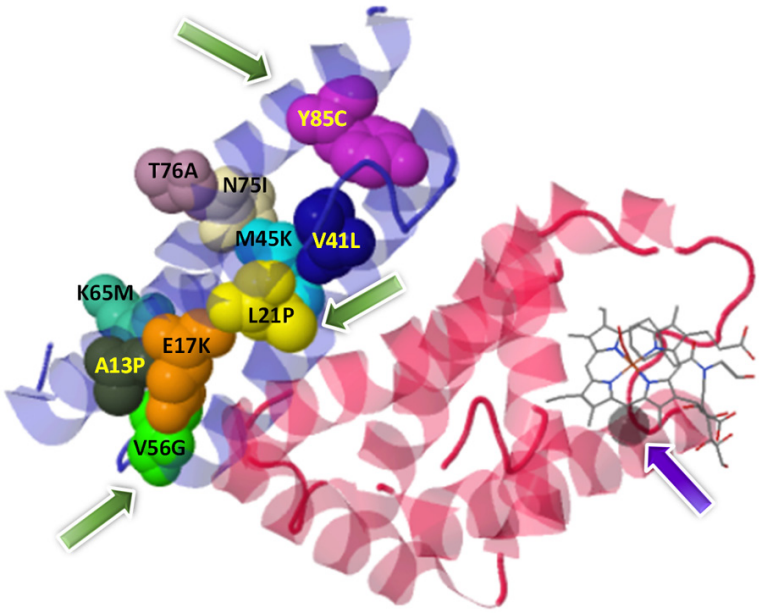

Figure 2. Three-dimensional (3D) protein structure of the α-Hemoglobin stabilizing protein (chain colored blue) complex with hemoglobin alpha chain (chain colored red). Green arrow: Most deleterious substitutions. Violet arrow: Iron (Fe) atom.

Mutation effect prediction

The state-of-art-tools such as SIFT (Sorts intolerant from tolerant) [7], PolyPhen 2.0 (Polymorphism Phenotyping v2) [8], PROVEAN (Protein variation effect analyzer) [9], SNAP2 (Screening for Non-Acceptable Polymorphisms) [10], SNPs&GO (Single nucleotide polymorphisms and Gene Ontology) [11, 12], PANTHER [13], FATHMM (Functional Analysis through Hidden Markov Models) [14] and VEST3 (Variant Effect Scoring Tool) [15] were used to predict the effect of the substitution mutations on the *AHSP* gene. The standard cutoff or the threshold values for PROVEAN (<-2.5, SIFT (=0), SNAP2 (>50), SNPs&GO (>0.5), PolyPhen (>0.5), FATHMM (>0.6), PANTHER (<-3), VEST (P<0.05) were maintained to predict the effect of change in amino acid sequence in the biological function, solvent accessibility, and structure of the ANSP protein [7-15].

Structure modeling and predicting residue positions

The 3D structures (resolution 2.80 Å) of the native and the mutated AHSP chains were designed based on template PDB ID: 1a00 to evaluate the stability of mutant using automated homology modeling tool such as SWISS MODEL [16-18]. The designed AHSP 3D structure was validated using PROCHECK [19]. The Swiss-Pdb Viewer software was used to generate mutated AHSP models using the validated AHSP 3D structure [20]. The native and mutated AHSP 3D models

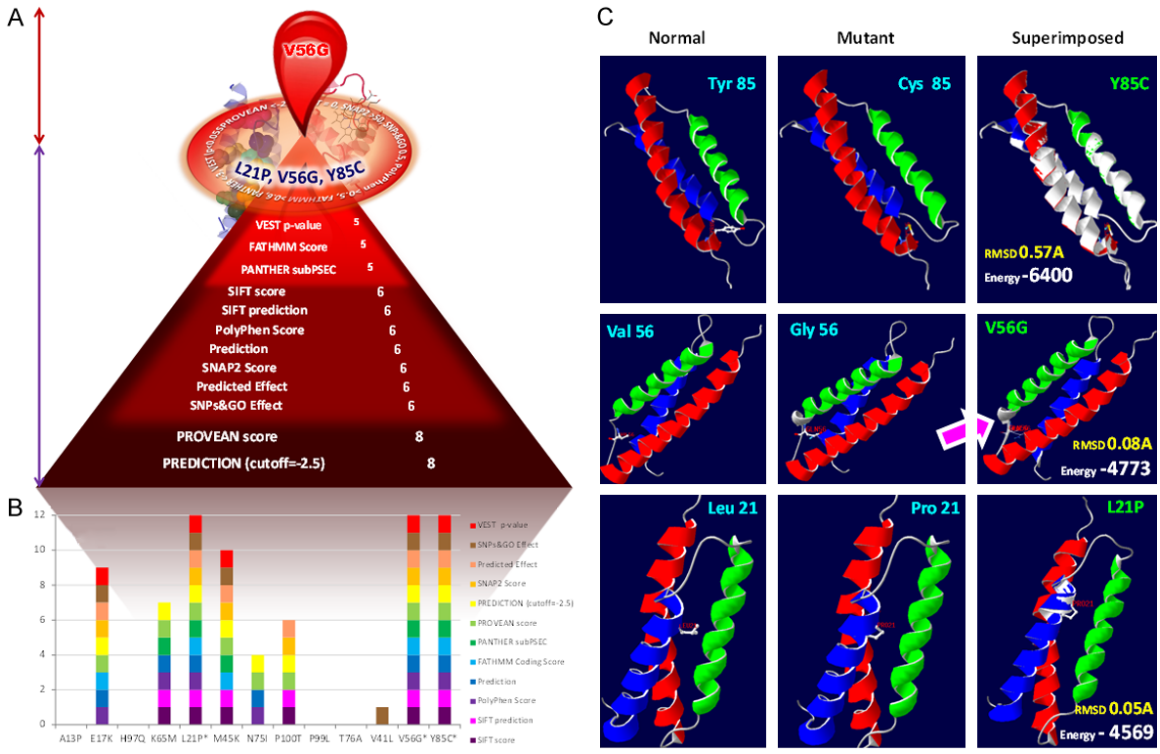

Figure 3. Graphic illustration of the state of art tools applied for the accurate detection of the highly pathogenic ns-SNPs of *AHSP* gene. A: SNPs on the circle: The most deleterious nsSNPs of *ANSP* gene agreed consistently by all the state of art tools. Nut brown colored double headed arrow region: Region holds the substitution highly pathogenic as per the structural and protein-protein interaction analysis. Violet colored double headed arrow region: Number of deleterious SNPs by a particular tool. B: Deleterious effect of each substitution. Number of blocks corresponds to the number of tools agreed as deleterious. C: Superimposed models of AHSP normal and mutant. Arrow locates the extra helix due to the V56G mutation in the *AHSP* gene. Pink arrow indicates the resulted additional helix due to the glycine substitution at the 56th position.

were subjected for energy minimization using the GROMACS program [21]. FASTA format of the AHSP protein sequence were provided to FlexPred to identify the solvent accessibility of AHSP protein to predict conformational switches and residue positions involved in kinetic energy and pathogenic disorders.

Visualize the nsSNPs location

Three-dimensional (3D) crystal structure of AHSP protein corresponding to the ID: 1Y01 was generated using the muPIT interactive [22]. The binding nature of the AHSP protein with Fe (II) alpha-hemoglobin was checked. All the 13 nsSNPs listed in the **Table 1** was given as input to visualize the location of the substitutions at *AHSP*.

AHSP and globin interaction

We applied a comprehensive protein-protein interaction prediction structure and modeling assembly tool named PRISM for modeling the interactions between the AHSP and other proteins [23]. Two different input sets such as the template and the target sets were provided to the PRISM algorithm to obtain interaction predictions between them. HBA1, HBA2, HBB, HBD, KLF1 and HBQ1 proteins were included in the study; selection was based on the reported interaction in STRING 10 [4]. PRISM explores the hot spots of the interface between the target and template by analyzing the geometrical and evolutionary conservation of both the proteins using the 3D structures of the proteins [24].

Statistical analysis

The correlations between the predictions of various bioinformatics tools were carried out using SPSS. Significance between the predictions of various state-of-art-tools was tested using student T-test. Probabilities were main-

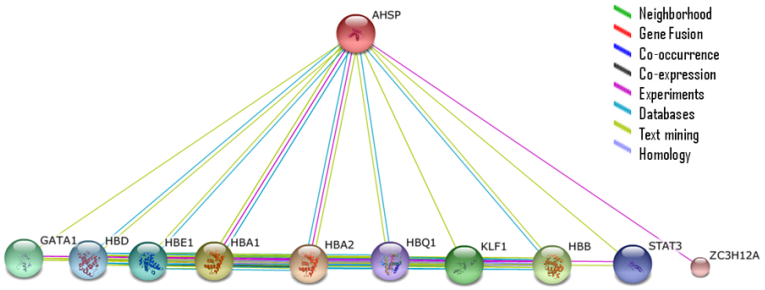

Figure 4. AHSP interacts with other proteins (using STRING 10).

tained at *P<0.0001* for most significant combinations.

Results

A total of 244 SNPs at *AHSP* gene were retrieved from the dbSNP including 53 nsSNPs. All the nsSNPs were subjected for the prediction analysis using various effective state of art bioinformatics tools. The prediction from PROVEAN (<-2.5, SIFT (=0), SNAP2 (>50), SNPs&GO (>0.5), PolyPhen (>0.5), FATHMM (>0.6), PANTHER (<-3), VEST (P<0.05) were found to be highly significant (*P=1.27E-13* of single factor ANOVA test). Heatmap of AHSP protein generated using SNAP2 reveals most of the substitution with dark red corresponding to a strong signal for high level of pathogenicity (**Figure 1**). The correlations between the predictions of the tools were found to be varied (**Figure 1**). Prediction between two state-of-art-tools were significant at *P<0.0001 (student T-test)* for most the combinations (**Figure 1**). All the state-of-the-art tools (PROVEAN <-2.5, SIFT=0, SNAP2 >50, SNPs&GO >0.5, PolyPhen >0.5, FATHMM >0.6, PANTHER <-3, VEST P<0.05) have consistently and significantly agreed the pathogenicity of V56G, L21P and Y85C substitution of the AHS protein (*P=1.27E-13*) (**Table 1**).

Three-dimensional (3D) crystal structure of AHSP protein (ID: 1a00) was generated and its binding site with Fe(II) alpha-hemoglobin was checked using the muPIT interactive (**Figure 2**). Total of 80.39% of amino acids (R=rigid=82) in the AHSP protein are not flexible enough to participate in the processes of interaction as per the output from FlexPred. All the 13 nsSNPs were given as input to visualize the location of the substitutions at AHSP. Identification of location of various nsSNPs using muPIT interactive exposed the position of the V56G, which is near the physical contact site or hot spot between AHSP and HBA1 (**Figure 2**). The nsSNP, V56G exists near the interactive area and was found to be the highly pathogenic (**Figure 3**; **Table 1**). As an extra helix was formed due to the V56G mutation in the *AHSP* gene, it blocks some of the protein to be engaged physically (**Figure 3**). AHSP proteins always act with various type globin proteins (**Figure 4**). It was highly evident from the interaction of AHSP with HBA2 and KLF1 proteins, that the physical contact between AHSP with V56G and HBA2 or KLF1 was found to be completely absent (**Figure 5**). Interface energy and predicted hot spots interface residues of the template with pathogenic substitution at target-template protein complexes are enormously varied when compare with the wild template-wild target protein complex (Supplementary Table 1; **Figure 6**). Leucine at the position 21 is involved in the binding of HBA1 and AHSP. No involvement was observed for valine and tyrosine at position 56 and 85 respectively (Supplementary Table 1). Significant (>100%) variations in binding energies were observed in the interaction between wild HBA1 with mutated *AHSP* gene. Similar significant (>100%) variations were noted among the highly deleterious mutation of HBA1 (G60V and W15R) and wild type AHSP (**Figure 6**).

Discussion

The *AHSP* and the *HBA1* genes are almost similar in size, but there were 201 non-coding synonymous (nsSNPs) retrieved in the *HBA1* genes [25], while in the present study we have retrieved only 53 nsSNPs in the *AHSP* gene it indicates clearly and confirm that the *AHSP* gene is highly conserved during the evolution. As we shown in the previous study [25], the selected tools and their threshold values, PROVEAN (<-2.5), SIFT (=0), SNAP2 (>50), SNPs&GO (>0.5), PolyPhen (>0.5), FATHMM (>0.6), PANTHER (<-3), VEST (P<0.05) are adequate to calculate and predict the deleterious nature of the nsSNPs as they cover the needed attributes such as structural and sequence also the conservation analysis [7-15, 25]. All the state-of-the-art tools were unanimously

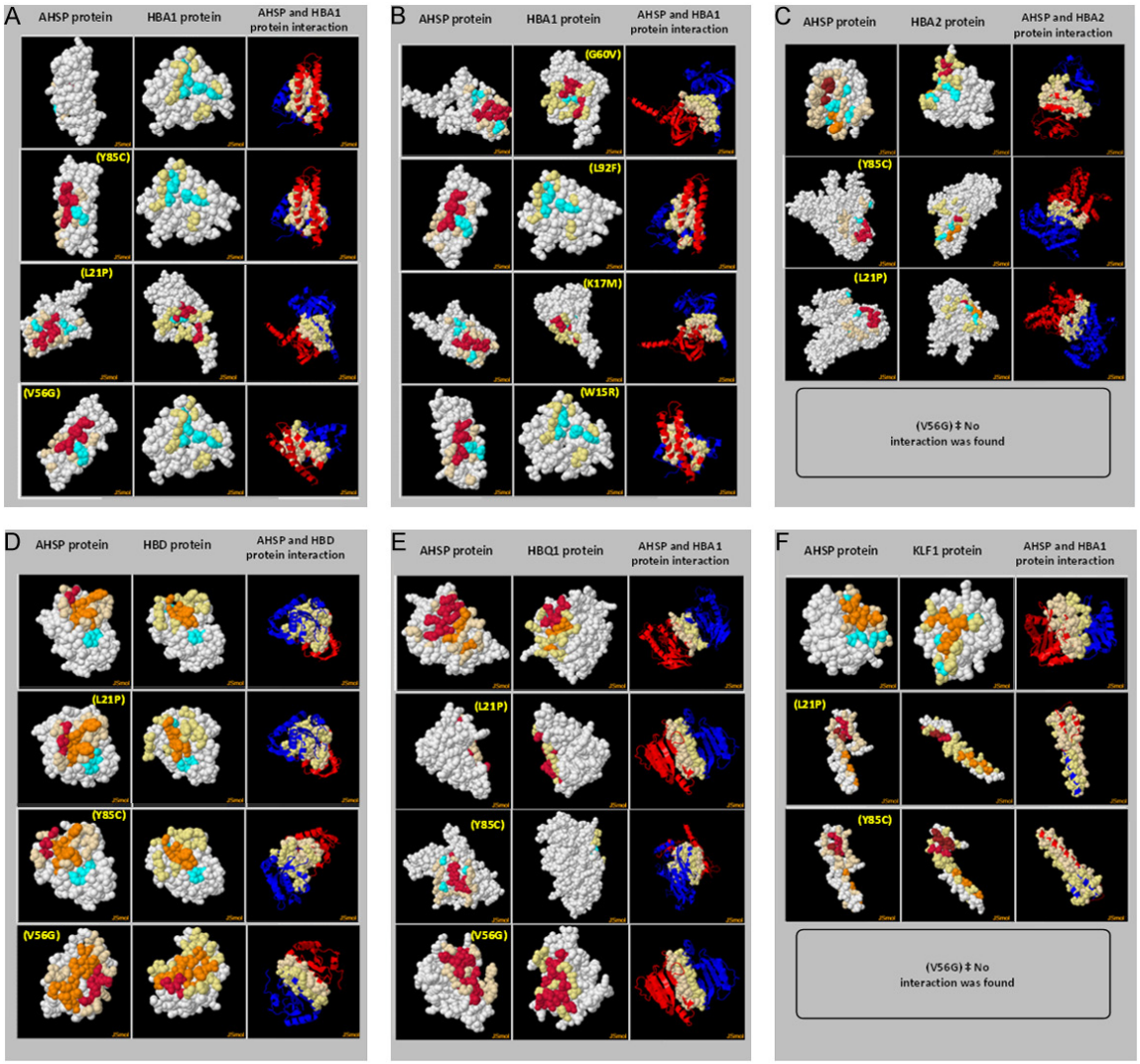

Figure 5. AHSP protein and globin protein interaction. Colum number 1 of each box indicates the template AHSP protein, column 2 denotes the target globin protein and text in parenthesis indicate the amino acid substitution. Column number 3 indicates the complex of the target protein-template protein interaction of the protein in the respective rows. A: Interaction between wild/mutated AHSP and native HBA1. B: Interaction between native AHSP and mutated HBA1. C: Interaction between mutated AHSP and native HBA2. D: Interaction between mutated AHSP and native HBD. E: Interaction between mutated AHSP and native HBQ1. F: Interaction between mutated AHSP and native KLF1.

agreed (P=1.27E-13) the pathogenicity of V56G, L21P and Y85C amino acid substitutions at AHSP based on the calculations such as homology-based analysis, position-specific independent count score, sequence clustering and alignment-based scoring, Hidden Markov Models, Variant Effect Scoring and unfolding Gibbs free energy score [7-15].

A well-known fact is that the free alpha globin chains always unstable, it is stabilized by a chaperone AHSP, and prevents its precipitation, which is toxic to the body [18, 26-28]. Sequence changes in the *HBA1* and *HBA2* genes are more common [29, 30] their effect on the HBA1-AHSP or HBA2-AHSP interaction would disclose the adverse effects. Detailed study on 30 point mutants by Feng *et al*. [18] revealed the adverse effect of three amino acid substitutions (Lys99, His103 and Phe117) in alpha globin chain. Mutations such Hb Constant Spring, Hb Pakse, and cod 117 (GH5) in the alpha globin were reported to be affecting the AHSP-HBA1 interactions significantly [28, 31,

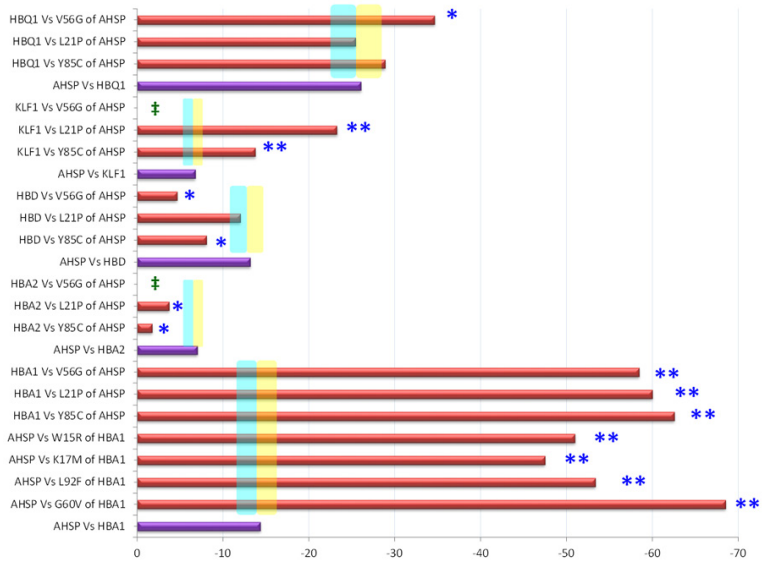

Figure 6. Binding energy of the template-target protein complex. ‡No interaction was found. *Less significantly at 10% varied binding energy compare to the wild type interaction. Shades colored sky blue and yellow indicates +10% and -10% variation compare to the wild type. **More Significant at >100% varied binding energy.

32]. We have taken a comprehensive computational step to identify the interaction difficulties of the most pathogenic HBA1 nsSNP mutations (W15R, K17M, L92F and G60V) [25] with the wild and mutated AHSP proteins. Non-interaction between the AHSP with V56G vs HBA2 and AHSP with V56G vs KLF1 indicates the negative impact of the mutation. V56G was tested in wet lab by Feng *et al.* [18] while L21P and Y85C were not. Here we report the pathogenicity of L21P and Y85C through a collective, comprehensive and computational approach.

The hot regions are tightly packed regions in protein-protein interfaces, have the most prominent cooperative behavioral property to interpret the protein-protein interface and their stability [24, 33-35]. Binding energies were significantly varied upon highly deleterious mutation at *AHSP* and/or *HBA1* gene. A threshold of 10% variation in the binding energy has been set as less significant by Chen *et al.* [36] to identify the very little influence and sensitivity of the binding energy on amino acid substitution. While we have set 100% variation as the threshold to predict the most influential effect of the amino acid substitution on the binding energy, which disclosed the most deleterious effect of the amino acid substitution among the 47.36% of tested combinations (**Figure 6**). Decrease in the binding energy is a prominent value that could justify the pathogenic effect of mutations as described earlier by Thorn and Bogan [37], which was reflected in 47.36% of tested combinations (**Figure 6**). Furthermore, the V56G substitution is not participating directly in the host spot binding region, while it affects the AHSP interaction badly with HBA1 and KLF1 proteins.

The ethical approval was obtained from the University of Dammam (IRB-2014-08-041) for the study to identify the prevalence of mutations at *AHSP* gene in Saudi population. Blood samples were collected from transfusion dependent Saudi beta thalassemia major patients (n=100) and healthy controls (n=100) after getting informed consent. All the samples were subjected for the sequencing of the *AHSP* gene. Interestingly we have identified the most pathogenic mutations AHSP:c.167T>G (V56G) in three (1♂ patient and 2♂ controls) subjects. Furthermore, three other mutations were also identified in the coding regions such as AHSP:c.231G>T (L77L), AHSP:c.45G>T (L15F), and AHSP:c.168G>T (V56V). All these samples were screened for the presence mutation in the *KLF1*, *HBA1*, *HBA2* and *HBB* genes [29, 38, 39]. Subjects with the *AHSP* gene mutation were found to be free from *KLF1* gene mutations, hence we couldn't confirm the predictions. We have also identified the co-inheritance of AHSP:c.167T>G (V56G) and $-\alpha_2^{3.7}/\alpha_1\alpha_2$. Moreover, a large scale study on the subjects with AHSP:c.167T>G (V56G) may give the actual influence of the mutation. At the end of the story we could say that the limitation of the study is that the computational results needs to be taken for the wet lab analysis to confirm the results.

In conclusion we could say that the glycine substitution at the 56th position (V56G) is the most pathogenic. Replacing wet lab by web lab is not completely advisable, but can be considered to reduce the cost and time by selecting best options to proceed to wet lab. Furthermore, the

study endorses the mutated AHSP^{V56G} protein for detailed confirmatory wet lab analysis. We are in the stage of proposing possible ways to confirm the results in wet lab.

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Disclosure of conflict of interest

None.

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References

[1] Mahmoud HM, Shoeib AA, Abd El Ghany SM, Reda MM and Ragab IA. Study of alpha hemoglobin stabilizing protein expression in patients with beta thalassemia and sickle cell anemia and its impact on clinical severity. Blood Cells Mol Dis 2015; 55: 358-362.

[2] Sagar CS, Kumar R, Sharma DC and Kishor P. Alpha hemoglobin stabilizing protein: its causal relationship with the severity of beta thalassemia. Blood Cells Mol Dis 2015; 55: 104-107.

[3] Schrier SL. Pathophysiology of thalassemia. Curr Opin Hematol 2002; 9: 123-126.

[4] Szklarczyk D, Franceschini A, Kuhn M, Simonovic M, Roth A, Minguez P, Doerks T, Stark M, Muller J, Bork P, Jensen LJ and von Mering C. The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. Nucleic Acids Res 2011; 39: D561-568.

[5] Sherry ST, Ward MH, Kholodov M, Baker J, Phan L, Smigielski EM and Sirotkin K. dbSNP: the NCBI database of genetic variation. Nucleic Acids Res 2001; 29: 308-311.

[6] Goodsell DS, Dutta S, Zardecki C, Voigt M, Berman HM and Burley SK. The RCSB PDB "molecule of the month": inspiring a molecular view of biology. PLoS Biol 2015; 13: e1002140.

[7] Kumar P, Henikoff S and Ng PC. Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. Nature Protocols 2009; 4: 1073-1082.

[8] Adzhubei IA, Schmidt S, Peshkin L, Ramensky VE, Gerasimova A, Bork P, Kondrashov AS and Sunyaev SR. A method and server for predicting damaging missense mutations. Nat Methods 2010; 7: 248-249.

[9] Choi Y, Sims GE, Murphy S, Miller JR and Chan AP. Predicting the functional effect of amino acid substitutions and indels. PLoS One 2012; 7: e46688.

[10] Hecht M, Bromberg Y and Rost B. Better prediction of functional effects for sequence variants. BMC Genomics 2015; 16 Suppl 8: S1.

[11] Calabrese R, Capriotti E, Fariselli P, Martelli PL and Casadio R. Functional annotations improve the predictive score of human disease-related mutations in proteins. Hum Mutat 2009; 30: 1237-1244.

[12] Capriotti E, Calabrese R, Fariselli P, Martelli PL, Altman RB and Casadio R. WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation. BMC Genomics 2013; 14 Suppl 3: S6.

[13] Mi H, Muruganujan A and Thomas PD. PANTHER in 2013: modeling the evolution of gene function, and other gene attributes, in the context of phylogenetic trees. Nucleic Acids Res 2013; 41: D377-386.

[14] Shihab HA, Gough J, Cooper DN, Stenson PD, Barker GL, Edwards KJ, Day IN and Gaunt TR. Predicting the functional, molecular, and phenotypic consequences of amino acid substitutions using hidden Markov models. Hum Mutat 2013; 34: 57-65.

[15] Carter H, Douville C, Stenson PD, Cooper DN and Karchin R. Identifying Mendelian disease genes with the variant effect scoring tool. BMC Genomics 2013; 14 Suppl 3: S3.

[16] Kiefer F, Arnold K, Kunzli M, Bordoli L and Schwede T. The SWISS-MODEL Repository and associated resources. Nucleic Acids Res 2009; 37: D387-392.

[17] Berman HM, Westbrook J, Feng Z, Gilliland G, Bhat T, Weissig H, Shindyalov IN and Bourne PE. The protein data bank. Nucleic Acids Res 2000; 28: 235-242.

[18] Feng L, Gell DA, Zhou S, Gu L, Kong Y, Li J, Hu M, Yan N, Lee C, Rich AM, Armstrong RS, Lay PA, Gow AJ, Weiss MJ, Mackay JP and Shi Y. Molecular mechanism of AHSP-mediated stabilization of alpha-hemoglobin. Cell 2004; 119: 629-640.

[19] Laskowski RA, Macarthur MW, Moss DS and Thornton JM. Procheck-a program to check the stereochemical quality of protein structures.

Journal of Applied Crystallography 1993; 26: 283-291.
[20] Guex N and Peitsch MC. SWISS-MODEL and the Swiss-Pdb Viewer: an environment for comparative protein modeling. Electrophoresis 1997; 18: 2714-2723.
[21] Lindahl E, Azuara C, Koehl P and Delarue M. NOMAD-Ref: visualization, deformation and refinement of macromolecular structures based on all-atom normal mode analysis. Nucleic Acids Res 2006; 34: W52-56.
[22] Niknafs N, Kim D, Kim R, Diekhans M, Ryan M, Stenson PD, Cooper DN and Karchin R. MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. Hum Genet 2013; 132: 1235-1243.
[23] Baspinar A, Cukuroglu E, Nussinov R, Keskin O and Gursoy A. PRISM: a web server and repository for prediction of protein-protein interactions and modeling their 3D complexes. Nucleic Acids Res 2014; 42: W285-289.
[24] Tuncbag N, Gursoy A, Nussinov R and Keskin O. Predicting protein-protein interactions on a proteome scale by matching evolutionary and structural similarities at interfaces using PRISM. Nat Protoc 2011; 6: 1341-1354.
[25] AbdulAzeez S and Borgio JF. In-Silico computing of the most deleterious nsSNPs in HBA1 gene. PLoS One 2016; 11: e0147702.
[26] Khafizov K, Ivanov MV, Glazova OV and Kovalenko SP. Computational approaches to study the effects of small genomic variations. J Mol Model 2015; 21: 251.
[27] Feng L, Zhou S, Gu L, Gell DA, Mackay JP, Weiss MJ, Gow AJ and Shi Y. Structure of oxidized alpha-haemoglobin bound to AHSP reveals a protective mechanism for haem. Nature 2005; 435: 697-701.
[28] Lacerra G, Scarano C, Musollino G, Flagiello A, Pucci P and Carestia C. Hb Foggia or alpha 117(GH5)Phe ->Ser: a new alpha 2 globin allele affecting the alpha Hb-AHSP interaction. Haematologica 2008; 93: 141-142.
[29] Borgio JF, AbdulAzeez S, Al-Nafie AN, Naserullah ZA, Al-Jarrash S, Al-Madan MS, Al-Muhanna F, Steinberg MH and Al-Ali AK. A novel HBA2 gene conversion in cis or trans: "alpha12 allele" in a Saudi population. Blood Cells Mol Dis 2014; 53: 199-203.
[30] Borgio JF. Molecular nature of alpha-globin genes in the Saudi population. Saudi Med J 2015; 36: 1271-1276.
[31] Vasseur-Godbillon C, Marden MC, Giordano P, Wajcman H and Baudin-Creuza V. Impaired binding of AHSP to alpha chain variants: Hb groene hart illustrates a mechanism leading to unstable hemoglobins with alpha thalassemic like syndrome. Blood Cells Mol Dis 2006; 37: 173-179.
[32] Turbpaiboon C, Limjindaporn T, Wongwiwat W, U-Pratya Y, Siritanaratkul N, Yenchitsomanus PT, Jitrapakdee S and Wilairat P. Impaired interaction of alpha-haemoglobin-stabilising protein with alpha-globin termination mutant in a yeast two-hybrid system. Br J Haematol 2006; 132: 370-373.
[33] Bogan AA and Thorn KS. Anatomy of hot spots in protein interfaces. J Mol Biol 1998; 280: 1-9.
[34] Cukuroglu E, Gursoy A and Keskin O. Analysis of hot region organization in hub proteins. Ann Biomed Eng 2010; 38: 2068-2078.
[35] Liu T, Whitten ST and Hilser VJ. Functional residues serve a dominant role in mediating the cooperativity of the protein ensemble. Proc Natl Acad Sci U S A 2007; 104: 4347-4352.
[36] Chen DE, Willick DL, Ruckel JB and Floriano WB. Principal component analysis of binding energies for single-point mutants of hT2R16 bound to an agonist correlate with experimental mutant cell response. J Comput Biol 2015; 22: 37-53.
[37] Thorn KS and Bogan AA. ASEdb: a database of alanine mutations and their effects on the free energy of binding in protein interactions. Bioinformatics 2001; 17: 284-285.
[38] Borgio JF, AbdulAzeez S, Naserullah ZA, Al-Jarrash S, Al-Ali RA, Al-Madan MS, Al-Muhanna F, Al-Suliman AM, Al-Nafie A, Steinberg MH and Al-Ali AK. Mutations in the beta-globin gene from a Saudi population: an update. Int J Lab Hematol 2016; 38: e38-40.
[39] Singleton BK, Burton NM, Green C, Brady RL and Anstee DJ. Mutations in EKLF/KLF1 form the molecular basis of the rare blood group In(Lu) phenotype. Blood 2008; 112: 2081-2088.

Supplementary Table 1. Interface energy and predicted hot spots interface residues of the template-target protein complex

Template	Target	Interface Energy	Interface Residues Contacts at Template <--> Target
AHSP	HBA1	-14.34	pdb2_A_ASP_43 <--> pdb1_A_ASP_29
			pdb2_A_VAL_26 <--> pdb1_A_TYR_51
			pdb2_A_VAL_26 <--> pdb1_A_ASN_50
			pdb2_A_GLN_24 <--> pdb1_A_TYR_51
			pdb2_A_GLN_24 <--> pdb1_A_TYR_52
			pdb2_A_ASP_29 <--> pdb1_A_PHE_47
			pdb2_A_ASP_29 <--> pdb1_A_ASN_46
			pdb2_A_ASP_29 <--> pdb1_A_ASP_43
			pdb2_A_GLN_25 <--> pdb1_A_PHE_47
			pdb2_A_GLN_25 <--> pdb1_A_TRP_44
			pdb2_A_PHE_47 <--> pdb1_A_GLN_25
			pdb2_A_PHE_47 <--> pdb1_A_GLN_24
			pdb2_A_TYR_48 <--> pdb1_A_GLN_24
			pdb2_A_PHE_47 <--> pdb1_A_VAL_26
			pdb2_A_TYR_48 <--> pdb1_A_LEU_21
			pdb2_A_VAL_20 <--> pdb1_A_GLU_17
			pdb2_A_ASN_50 <--> pdb1_A_ASP_29
			pdb2_A_GLN_24 <--> pdb1_A_PHE_47
			pdb2_A_GLN_24 <--> pdb1_A_TYR_48
			pdb2_A_VAL_26 <--> pdb1_A_PHE_47
			pdb2_A_PHE_47 <--> pdb1_A_ASP_29
			pdb2_A_TRP_44 <--> pdb1_A_TRP_44
			pdb2_A_TYR_51 <--> pdb1_A_GLN_24
			pdb2_A_ASN_46 <--> pdb1_A_ASP_29
			pdb2_A_TYR_51 <--> pdb1_A_VAL_26
			pdb2_A_ASN_50 <--> pdb1_A_VAL_26
			pdb2_A_ASP_29 <--> pdb1_A_ASN_50
			pdb2_A_LEU_21 <--> pdb1_A_LEU_21
			pdb2_A_PHE_47 <--> pdb1_A_PRO_30
			pdb2_A_GLU_17 <--> pdb1_A_GLN_24
			pdb2_A_GLU_17 <--> pdb1_A_VAL_20
			pdb2_A_TYR_52 <--> pdb1_A_GLN_24
			pdb2_A_LEU_21 <--> pdb1_A_TRP_44
			pdb2_A_GLN_24 <--> pdb1_A_GLU_17
AHSP	G60V of HBA1	-68.52	pdb2_A_LEU_31 <--> pdb1_A_PHE_118
			pdb2_A_LEU_31 <--> pdb1_A_ALA_111
			pdb2_A_LEU_31 <--> pdb1_A_LEU_110
			pdb2_A_GLN_24 <--> pdb1_A_SER_36
			pdb2_A_GLN_24 <--> pdb1_A_LEU_35
			pdb2_A_VAL_26 <--> pdb1_A_ARG_32
			pdb2_A_PHE_47 <--> pdb1_A_THR_39
			pdb2_A_SER_91 <--> pdb1_A_PRO_120
			pdb2_A_ASP_43 <--> pdb1_A_VAL_97
			pdb2_A_LEU_21 <--> pdb1_A_SER_36
			pdb2_A_LEU_21 <--> pdb1_A_PHE_37

AHSP	L92F of HBA1	-53.37	pdb2_A_LYS_90 <--> pdb1_A_PRO_120 pdb2_A_PHE_88 <--> pdb1_A_HIS_123 pdb2_A_LEU_21 <--> pdb1_A_PRO_38 pdb2_A_LEU_31 <--> pdb1_A_LEU_107 pdb2_A_ASP_29 <--> pdb1_A_ALA_112 pdb2_A_PRO_30 <--> pdb1_A_ALA_111 pdb2_A_ASP_29 <--> pdb1_A_ALA_111 pdb2_A_LEU_31 <--> pdb1_A_ASP_127 pdb2_A_LEU_31 <--> pdb1_A_HIS_123 pdb2_A_VAL_32 <--> pdb1_A_HIS_123 pdb2_A_VAL_32 <--> pdb1_A_HIS_104 pdb2_A_VAL_32 <--> pdb1_A_LEU_107 pdb2_A_VAL_32 <--> pdb1_A_ASP_127 pdb2_A_GLN_25 <--> pdb1_A_VAL_108 pdb2_A_GLN_25 <--> pdb1_A_HIS_104 pdb2_A_PHE_47 <--> pdb1_A_PHE_37 pdb2_A_LEU_89 <--> pdb1_A_PRO_120 pdb2_A_SER_33 <--> pdb1_A_HIS_123 pdb2_A_SER_33 <--> pdb1_A_ALA_124 pdb2_A_SER_33 <--> pdb1_A_ASP_127 pdb2_A_ASP_29 <--> pdb1_A_VAL_108 pdb2_A_PRO_30 <--> pdb1_A_HIS_123 pdb2_A_TYR_85 <--> pdb1_A_HIS_123 pdb2_A_PRO_30 <--> pdb1_A_VAL_108 pdb2_A_PRO_30 <--> pdb1_A_LEU_107 pdb2_A_PRO_30 <--> pdb1_A_HIS_104 pdb2_A_GLN_25 <--> pdb1_A_SER_36 pdb2_A_VAL_97 <--> pdb1_A_LEU_31 pdb2_A_VAL_97 <--> pdb1_A_VAL_32 pdb2_A_LYS_128 <--> pdb1_A_GLN_24 pdb2_A_SER_36 <--> pdb1_A_THR_39 pdb2_A_PRO_120 <--> pdb1_A_TYR_51 pdb2_A_ALA_124 <--> pdb1_A_LEU_21 pdb2_A_PRO_120 <--> pdb1_A_TYR_52 pdb2_A_ALA_124 <--> pdb1_A_GLN_24 pdb2_A_PHE_37 <--> pdb1_A_THR_39 pdb2_A_PHE_37 <--> pdb1_A_ASP_36 pdb2_A_PRO_96 <--> pdb1_A_LEU_31 pdb2_A_THR_135 <--> pdb1_A_ASP_29 pdb2_A_ASP_127 <--> pdb1_A_GLN_25 pdb2_A_ALA_121 <--> pdb1_A_GLU_17 pdb2_A_PRO_120 <--> pdb1_A_GLU_17 pdb2_A_PHE_118 <--> pdb1_A_TYR_51 pdb2_A_LEU_107 <--> pdb1_A_TRP_44 pdb2_A_LEU_101 <--> pdb1_A_ASP_36 pdb2_A_LEU_101 <--> pdb1_A_VAL_32 pdb2_A_THR_119 <--> pdb1_A_TYR_51 pdb2_A_PRO_115 <--> pdb1_A_TYR_51 pdb2_A_HIS_104 <--> pdb1_A_TRP_44

			pdb2_A_PRO_120 <--> pdb1_A_TYR_48
			pdb2_A_HIS_104 <--> pdb1_A_VAL_40
			pdb2_A_LYS_100 <--> pdb1_A_PRO_30
			pdb2_A_ASP_127 <--> pdb1_A_LEU_21
			pdb2_A_HIS_104 <--> pdb1_A_ASP_43
			pdb2_A_ALA_111 <--> pdb1_A_PHE_47
			pdb2_A_VAL_108 <--> pdb1_A_ASP_43
			pdb2_A_ASP_127 <--> pdb1_A_TRP_44
			pdb2_A_HIS_123 <--> pdb1_A_TYR_48
			pdb2_A_HIS_123 <--> pdb1_A_LEU_21
			pdb2_A_PHE_118 <--> pdb1_A_PHE_47
			pdb2_A_HIS_123 <--> pdb1_A_TRP_44
			pdb2_A_HIS_123 <--> pdb1_A_PHE_47
AHSP	K17M of HBA1	-47.51	pdb2_A_LEU_31 <--> pdb1_A_PHE_118
			pdb2_A_ASN_50 <--> pdb1_A_THR_39
			pdb2_A_LEU_31 <--> pdb1_A_ALA_111
			pdb2_A_PHE_27 <--> pdb1_A_LEU_3
			pdb2_A_ASN_46 <--> pdb1_A_THR_39
			pdb2_A_ASN_46 <--> pdb1_A_PRO_38
			pdb2_A_ASP_87 <--> pdb1_A_LEU_3
			pdb2_A_LEU_31 <--> pdb1_A_HIS_104
			pdb2_A_ASN_28 <--> pdb1_A_LYS_8
			pdb2_A_ASP_29 <--> pdb1_A_PHE_118
			pdb2_A_LEU_31 <--> pdb1_A_LEU_107
			pdb2_A_ASP_29 <--> pdb1_A_ALA_112
			pdb2_A_PRO_30 <--> pdb1_A_ALA_111
			pdb2_A_ASP_29 <--> pdb1_A_ALA_111
			pdb2_A_LEU_31 <--> pdb1_A_VAL_108
			pdb2_A_ASN_28 <--> pdb1_A_SER_4
			pdb2_A_ASN_28 <--> pdb1_A_ASP_7
			pdb2_A_ASP_29 <--> pdb1_A_PRO_115
			pdb2_A_ASP_29 <--> pdb1_A_VAL_11
			pdb2_A_ASN_28 <--> pdb1_A_VAL_11
			pdb2_A_ASP_43 <--> pdb1_A_PRO_38
			pdb2_A_ASP_43 <--> pdb1_A_SER_36
			pdb2_A_ASP_43 <--> pdb1_A_PHE_37
			pdb2_A_LEU_31 <--> pdb1_A_HIS_123
			pdb2_A_VAL_32 <--> pdb1_A_HIS_123
			pdb2_A_VAL_32 <--> pdb1_A_HIS_104
			pdb2_A_PHE_47 <--> pdb1_A_LEU_35
			pdb2_A_ASN_28 <--> pdb1_A_PRO_120
			pdb2_A_PHE_47 <--> pdb1_A_PRO_38
			pdb2_A_LEU_31 <--> pdb1_A_VAL_11
			pdb2_A_SER_33 <--> pdb1_A_ASP_127
			pdb2_A_PRO_30 <--> pdb1_A_VAL_108
			pdb2_A_ASP_43 <--> pdb1_A_LEU_101
			pdb2_A_PRO_30 <--> pdb1_A_HIS_104
			pdb2_A_ASN_28 <--> pdb1_A_PHE_118
AHSP	W15R of HBA1	-50.98	pdb2_A_VAL_97 <--> pdb1_A_LEU_31

			pdb2_A_VAL_97 <--> pdb1_A_VAL_32
			pdb2_A_LYS_128 <--> pdb1_A_GLN_24
			pdb2_A_SER_36 <--> pdb1_A_THR_39
			pdb2_A_PRO_120 <--> pdb1_A_TYR_51
			pdb2_A_ALA_124 <--> pdb1_A_LEU_21
			pdb2_A_PRO_120 <--> pdb1_A_TYR_52
			pdb2_A_ALA_124 <--> pdb1_A_GLN_24
			pdb2_A_PHE_37 <--> pdb1_A_THR_39
			pdb2_A_LYS_100 <--> pdb1_A_ASP_29
			pdb2_A_PRO_96 <--> pdb1_A_LEU_31
			pdb2_A_ASP_127 <--> pdb1_A_GLN_25
			pdb2_A_ALA_121 <--> pdb1_A_GLU_17
			pdb2_A_PRO_120 <--> pdb1_A_GLY_14
			pdb2_A_PRO_120 <--> pdb1_A_GLU_17
			pdb2_A_PHE_37 <--> pdb1_A_ASP_36
			pdb2_A_LEU_3 <--> pdb1_A_VAL_20
			pdb2_A_PHE_118 <--> pdb1_A_TYR_51
			pdb2_A_LEU_107 <--> pdb1_A_TRP_44
			pdb2_A_LEU_101 <--> pdb1_A_VAL_32
			pdb2_A_THR_119 <--> pdb1_A_TYR_51
			pdb2_A_PHE_37 <--> pdb1_A_VAL_40
			pdb2_A_PRO_115 <--> pdb1_A_TYR_51
			pdb2_A_HIS_104 <--> pdb1_A_TRP_44
			pdb2_A_PRO_120 <--> pdb1_A_TYR_48
			pdb2_A_ASP_127 <--> pdb1_A_GLN_24
			pdb2_A_HIS_104 <--> pdb1_A_VAL_40
			pdb2_A_LYS_100 <--> pdb1_A_PRO_30
			pdb2_A_ASP_127 <--> pdb1_A_LEU_21
			pdb2_A_HIS_104 <--> pdb1_A_ASP_43
			pdb2_A_ALA_111 <--> pdb1_A_PHE_47
			pdb2_A_VAL_108 <--> pdb1_A_ASP_43
			pdb2_A_ASP_127 <--> pdb1_A_TRP_44
			pdb2_A_HIS_123 <--> pdb1_A_TYR_48
			pdb2_A_HIS_123 <--> pdb1_A_LEU_21
			pdb2_A_SER_4 <--> pdb1_A_GLU_17
			pdb2_A_PHE_118 <--> pdb1_A_PHE_47
			pdb2_A_ALA_116 <--> pdb1_A_TYR_51
			pdb2_A_HIS_123 <--> pdb1_A_TRP_44
			pdb2_A_HIS_123 <--> pdb1_A_PHE_47
HBA1	Y85C of AHSP	-62.56	pdb1_A_VAL_97 <--> pdb2_A_LEU_31
			pdb1_A_VAL_97 <--> pdb2_A_VAL_32
			pdb1_A_LYS_128 <--> pdb2_A_GLN_24
			pdb1_A_SER_36 <--> pdb2_A_THR_39
			pdb1_A_PRO_120 <--> pdb2_A_TYR_51
			pdb1_A_ALA_124 <--> pdb2_A_LEU_21
			pdb1_A_PRO_120 <--> pdb2_A_TYR_52
			pdb1_A_ALA_124 <--> pdb2_A_GLN_24
			pdb1_A_PHE_37 <--> pdb2_A_THR_39
			pdb1_A_LYS_100 <--> pdb2_A_ASP_29

			pdb1_A_PRO_96 <--> pdb2_A_LEU_31
			pdb1_A_ASP_127 <--> pdb2_A_GLN_25
			pdb1_A_ALA_121 <--> pdb2_A_GLU_17
			pdb1_A_PRO_120 <--> pdb2_A_GLU_17
			pdb1_A_PHE_37 <--> pdb2_A_ASP_36
			pdb1_A_PHE_118 <--> pdb2_A_TYR_51
			pdb1_A_LEU_107 <--> pdb2_A_TRP_44
			pdb1_A_LEU_101 <--> pdb2_A_ASP_36
			pdb1_A_LEU_101 <--> pdb2_A_VAL_32
			pdb1_A_THR_119 <--> pdb2_A_TYR_51
			pdb1_A_PHE_37 <--> pdb2_A_VAL_40
			pdb1_A_PRO_115 <--> pdb2_A_TYR_51
			pdb1_A_HIS_104 <--> pdb2_A_TRP_44
			pdb1_A_PRO_120 <--> pdb2_A_TYR_48
			pdb1_A_HIS_104 <--> pdb2_A_VAL_40
			pdb1_A_LYS_100 <--> pdb2_A_PRO_30
			pdb1_A_ASP_127 <--> pdb2_A_LEU_21
			pdb1_A_HIS_104 <--> pdb2_A_ASP_43
			pdb1_A_ALA_111 <--> pdb2_A_PHE_47
			pdb1_A_VAL_108 <--> pdb2_A_ASP_43
			pdb1_A_ASP_127 <--> pdb2_A_TRP_44
			pdb1_A_HIS_123 <--> pdb2_A_TYR_48
			pdb1_A_HIS_123 <--> pdb2_A_LEU_21
			pdb1_A_PHE_118 <--> pdb2_A_PHE_47
			pdb1_A_HIS_123 <--> pdb2_A_TRP_44
			pdb1_A_HIS_123 <--> pdb2_A_PHE_47
HBA1	L21P of AHSP	-60.0	pdb2_A_LEU_31 <--> pdb1_A_PHE_118
			pdb2_A_ASP_43 <--> pdb1_A_LEU_101
			pdb2_A_LEU_31 <--> pdb1_A_ALA_111
			pdb2_A_LEU_31 <--> pdb1_A_LEU_110
			pdb2_A_SER_91 <--> pdb1_A_PRO_120
			pdb2_A_TRP_44 <--> pdb1_A_SER_36
			pdb2_A_LYS_90 <--> pdb1_A_PRO_120
			pdb2_A_PRO_21 <--> pdb1_A_SER_36
			pdb2_A_PRO_21 <--> pdb1_A_LEU_35
			pdb2_A_PRO_21 <--> pdb1_A_PRO_38
			pdb2_A_LEU_31 <--> pdb1_A_LEU_107
			pdb2_A_ASP_29 <--> pdb1_A_ALA_112
			pdb2_A_PRO_30 <--> pdb1_A_ALA_111
			pdb2_A_ASP_29 <--> pdb1_A_ALA_111
			pdb2_A_ASP_36 <--> pdb1_A_ASP_127
			pdb2_A_LEU_31 <--> pdb1_A_ASP_127
			pdb2_A_LEU_31 <--> pdb1_A_HIS_123
			pdb2_A_VAL_32 <--> pdb1_A_HIS_123
			pdb2_A_VAL_32 <--> pdb1_A_HIS_104
			pdb2_A_VAL_32 <--> pdb1_A_LEU_107
			pdb2_A_VAL_32 <--> pdb1_A_ASP_127
			pdb2_A_GLN_25 <--> pdb1_A_VAL_108
			pdb2_A_GLN_25 <--> pdb1_A_HIS_104

HBA1	V56G of AHSP	-58.47	pdb2_A_PHE_47 <--> pdb1_A_THR_39 pdb2_A_PHE_47 <--> pdb1_A_PRO_38 pdb2_A_SER_33 <--> pdb1_A_HIS_123 pdb2_A_SER_33 <--> pdb1_A_ALA_124 pdb2_A_SER_33 <--> pdb1_A_ASP_127 pdb2_A_ASP_29 <--> pdb1_A_VAL_108 pdb2_A_PRO_30 <--> pdb1_A_HIS_123 pdb2_A_TYR_85 <--> pdb1_A_HIS_123 pdb2_A_PRO_30 <--> pdb1_A_VAL_108 pdb2_A_PRO_30 <--> pdb1_A_LEU_107 pdb2_A_GLN_25 <--> pdb1_A_SER_36 pdb2_A_LEU_89 <--> pdb1_A_HIS_123 pdb1_A_VAL_97 <--> pdb2_A_LEU_31 pdb1_A_VAL_97 <--> pdb2_A_VAL_32 pdb1_A_LYS_128 <--> pdb2_A_GLN_24 pdb1_A_SER_36 <--> pdb2_A_THR_39 pdb1_A_PRO_120 <--> pdb2_A_TYR_51 pdb1_A_ALA_124 <--> pdb2_A_LEU_21 pdb1_A_PRO_120 <--> pdb2_A_TYR_52 pdb1_A_ALA_124 <--> pdb2_A_GLN_24 pdb1_A_PHE_37 <--> pdb2_A_THR_39 pdb1_A_PHE_37 <--> pdb2_A_ASP_36 pdb1_A_PRO_96 <--> pdb2_A_LEU_31 pdb1_A_THR_135 <--> pdb2_A_ASP_29 pdb1_A_ASP_127 <--> pdb2_A_GLN_25 pdb1_A_ALA_121 <--> pdb2_A_GLU_17 pdb1_A_PRO_120 <--> pdb2_A_GLU_17 pdb1_A_PHE_118 <--> pdb2_A_TYR_51 pdb1_A_LEU_107 <--> pdb2_A_TRP_44 pdb1_A_LEU_101 <--> pdb2_A_ASP_36 pdb1_A_LEU_101 <--> pdb2_A_VAL_32 pdb1_A_THR_119 <--> pdb2_A_TYR_51 pdb1_A_PRO_115 <--> pdb2_A_TYR_51 pdb1_A_HIS_104 <--> pdb2_A_TRP_44 pdb1_A_PRO_120 <--> pdb2_A_TYR_48 pdb1_A_HIS_104 <--> pdb2_A_VAL_40 pdb1_A_LYS_100 <--> pdb2_A_PRO_30 pdb1_A_ASP_127 <--> pdb2_A_LEU_21 pdb1_A_HIS_104 <--> pdb2_A_ASP_43 pdb1_A_ALA_111 <--> pdb2_A_PHE_47 pdb1_A_VAL_108 <--> pdb2_A_ASP_43 pdb1_A_ASP_127 <--> pdb2_A_TRP_44 pdb1_A_HIS_123 <--> pdb2_A_LEU_21 pdb1_A_PHE_118 <--> pdb2_A_PHE_47 pdb1_A_HIS_123 <--> pdb2_A_TRP_44 pdb1_A_HIS_123 <--> pdb2_A_PHE_47
AHSP	HBA2	-7.05	pdb1_A_HIS_112 <--> pdb2_B_THR_8 pdb1_A_PRO_114 <--> pdb2_B_LYS_11 pdb1_A_GLU_116 <--> pdb2_B_LYS_7

			pdb1_B_LYS_120 <--> pdb2_B_THR_8
			pdb1_A_HIS_20 <--> pdb2_B_PRO_4
			pdb1_B_HIS_116 <--> pdb2_B_ALA_71
			pdb1_B_GLU_121 <--> pdb2_B_GLY_15
			pdb1_B_LYS_120 <--> pdb2_B_LYS_11
			pdb1_A_HIS_112 <--> pdb2_B_LYS_7
			pdb1_B_GLY_119 <--> pdb2_B_LYS_11
			pdb1_A_TYR_24 <--> pdb2_B_PRO_4
			pdb1_A_PRO_114 <--> pdb2_B_HIS_72
			pdb1_A_PRO_114 <--> pdb2_B_VAL_73
			pdb1_A_PRO_114 <--> pdb2_B_ALA_71
			pdb1_B_HIS_117 <--> pdb2_B_ALA_71
			pdb1_B_GLU_121 <--> pdb2_B_LYS_11
			pdb1_A_ALA_115 <--> pdb2_B_ASP_75
			pdb1_B_LYS_120 <--> pdb2_B_ALA_12
			pdb1_A_ALA_115 <--> pdb2_B_VAL_73
			pdb1_B_PHE_118 <--> pdb2_B_LYS_11
HBA2	Y85C of AHSP	-1.77	pdb1_A_PRO_5 <--> pdb2_A_GLN_68
			pdb1_B_PRO_52 <--> pdb2_A_ASN_50
			pdb1_A_ALA_121 <--> pdb2_A_ASN_50
			pdb1_A_ASN_10 <--> pdb2_A_ASN_46
			pdb1_A_THR_9 <--> pdb2_A_ARG_71
			pdb1_B_THR_51 <--> pdb2_A_TYR_51
			pdb1_A_LYS_17 <--> pdb2_A_GLU_35
			pdb1_C_SER_344 <--> pdb2_A_PRO_60
			pdb1_A_SER_4 <--> pdb2_A_ARG_53
			pdb1_A_PRO_5 <--> pdb2_A_ASP_64
			pdb1_A_THR_119 <--> pdb2_A_ASP_43
			pdb1_A_ALA_121 <--> pdb2_A_ASN_46
			pdb1_B_SER_50 <--> pdb2_A_GLN_54
			pdb1_B_ASP_53 <--> pdb2_A_PHE_47
			pdb1_A_ALA_6 <--> pdb2_A_ARG_53
			pdb1_B_THR_51 <--> pdb2_A_ASN_50
			pdb1_A_ALA_6 <--> pdb2_A_ILE_49
			pdb1_A_GLU_117 <--> pdb2_A_THR_39
			pdb1_A_ALA_116 <--> pdb2_A_THR_39
HBA2	L21P of AHSP	-3.74	pdb1_B_THR_51 <--> pdb2_A_TYR_51
			pdb1_B_THR_51 <--> pdb2_A_ASN_50
			pdb1_A_ALA_13 <--> pdb2_A_GLU_42
			pdb1_A_SER_4 <--> pdb2_A_ARG_53
			pdb1_A_THR_119 <--> pdb2_A_ASP_43
			pdb1_B_SER_50 <--> pdb2_A_GLN_54
			pdb1_B_PRO_52 <--> pdb2_A_ASN_50
			pdb1_A_THR_9 <--> pdb2_A_ARG_71
			pdb1_A_LYS_17 <--> pdb2_A_GLU_35
			pdb1_A_ALA_6 <--> pdb2_A_ARG_53
			pdb1_C_SER_344 <--> pdb2_A_PRO_60
			pdb1_A_ALA_116 <--> pdb2_A_ASP_43
			pdb1_A_ALA_121 <--> pdb2_A_ASN_50

			pdb1_A_ALA_116 <--> pdb2_A_THR_39
			pdb1_A_PRO_5 <--> pdb2_A_GLN_68
			pdb1_A_PRO_5 <--> pdb2_A_ASP_64
			pdb1_B_ASP_53 <--> pdb2_A_PHE_47
			pdb1_A_ASN_10 <--> pdb2_A_ASN_46
			pdb1_A_VAL_122 <--> pdb2_A_ASN_46
			pdb1_A_ALA_121 <--> pdb2_A_ASN_46
			pdb1_A_ALA_6 <--> pdb2_A_ILE_49
			pdb1_A_GLU_117 <--> pdb2_A_THR_39
HBA2	V56G of AHSP	‡	
AHSP	HBD	-13.21	pdb2_B_VAL_60 <--> pdb1_A_ASN_46
			pdb2_B_VAL_57 <--> pdb1_A_ASP_43
			pdb2_A_GLN_76 <--> pdb1_A_GLN_54
			pdb2_B_GLY_56 <--> pdb1_A_ASP_43
			pdb2_B_GLU_53 <--> pdb1_A_TRP_44
			pdb2_A_ILE_74 <--> pdb1_A_GLN_54
			pdb2_B_SER_47 <--> pdb1_A_ASP_29
			pdb2_B_LEU_49 <--> pdb1_A_GLN_25
			pdb2_B_GLY_48 <--> pdb1_A_ASP_29
			pdb2_A_MET_120 <--> pdb1_A_LEU_31
			pdb2_A_MET_120 <--> pdb1_A_PRO_30
			pdb2_B_LEU_49 <--> pdb1_A_ASP_29
			pdb2_B_VAL_60 <--> pdb1_A_ASP_43
			pdb2_A_LYS_122 <--> pdb1_A_ASP_36
			pdb2_A_LYS_122 <--> pdb1_A_LEU_31
			pdb2_A_LYS_122 <--> pdb1_A_SER_33
			pdb2_A_LYS_122 <--> pdb1_A_VAL_32
			pdb2_A_PRO_121 <--> pdb1_A_VAL_32
			pdb2_A_ASP_77 <--> pdb1_A_GLN_54
			pdb2_A_PRO_121 <--> pdb1_A_PRO_30
			pdb2_A_ASP_77 <--> pdb1_A_ASN_50
			pdb2_A_ASP_77 <--> pdb1_A_ARG_53
			pdb2_B_LEU_49 <--> pdb1_A_PRO_30
			pdb2_B_LYS_59 <--> pdb1_A_PHE_47
			pdb2_C_ASP_68 <--> pdb1_A_ASP_29
			pdb2_A_GLU_73 <--> pdb1_A_TYR_51
			pdb2_A_GLU_73 <--> pdb1_A_GLN_54
			pdb2_A_MET_120 <--> pdb1_A_ASP_29
			pdb2_A_GLN_125 <--> pdb1_A_ASP_36
			pdb2_B_GLU_63 <--> pdb1_A_ASN_50
			pdb2_B_GLU_52 <--> pdb1_A_TRP_44
			pdb2_B_GLU_52 <--> pdb1_A_LEU_21
			pdb2_B_GLU_52 <--> pdb1_A_GLN_25
			pdb2_A_GLN_125 <--> pdb1_A_THR_39
			pdb2_A_PRO_121 <--> pdb1_A_VAL_40
			pdb2_A_ASP_77 <--> pdb1_A_ARG_63
			pdb2_A_ARG_116 <--> pdb1_A_LEU_31
HBD	Y85C of AHSP	-8.09	pdb1_B_VAL_60 <--> pdb2_A_ASN_46
			pdb1_A_GLN_125 <--> pdb2_A_VAL_40

			pdb1_A_GLN_125 <--> pdb2_A_THR_39
			pdb1_B_LYS_59 <--> pdb2_A_PHE_47
			pdb1_B_LEU_49 <--> pdb2_A_VAL_26
			pdb1_B_LEU_49 <--> pdb2_A_ASP_29
			pdb1_A_ARG_134 <--> pdb2_A_ASP_43
			pdb1_B_VAL_60 <--> pdb2_A_ASP_43
			pdb1_A_LYS_122 <--> pdb2_A_ASP_36
			pdb1_A_LYS_122 <--> pdb2_A_LEU_31
			pdb1_A_LYS_122 <--> pdb2_A_PRO_30
			pdb1_A_LYS_122 <--> pdb2_A_SER_33
			pdb1_A_LYS_122 <--> pdb2_A_VAL_32
			pdb1_A_ASP_77 <--> pdb2_A_GLN_54
			pdb1_A_ASP_77 <--> pdb2_A_ASN_50
			pdb1_A_ASP_77 <--> pdb2_A_ARG_53
			pdb1_A_ARG_129 <--> pdb2_A_ASP_36
			pdb1_A_ARG_129 <--> pdb2_A_GLU_35
			pdb1_A_GLU_73 <--> pdb2_A_GLN_54
			pdb1_A_ARG_128 <--> pdb2_A_ASP_43
			pdb1_A_MET_120 <--> pdb2_A_ASP_29
			pdb1_A_GLN_125 <--> pdb2_A_ASP_36
			pdb1_B_GLU_63 <--> pdb2_A_ASN_50
			pdb1_B_GLU_52 <--> pdb2_A_LEU_21
			pdb1_B_GLU_52 <--> pdb2_A_GLN_24
			pdb1_A_ARG_116 <--> pdb2_A_LEU_31
HBD	L21P of AHSP	-12.05	pdb1_A_GLN_125 <--> pdb2_A_ASP_36
			pdb1_B_LYS_59 <--> pdb2_A_ASN_50
			pdb1_A_ARG_129 <--> pdb2_A_ASP_36
			pdb1_B_GLU_63 <--> pdb2_A_ARG_53
			pdb1_B_LEU_49 <--> pdb2_A_GLN_25
			pdb1_A_ARG_129 <--> pdb2_A_GLU_35
			pdb1_B_GLU_52 <--> pdb2_A_PHE_47
			pdb1_B_LEU_49 <--> pdb2_A_GLN_24
			pdb1_B_GLN_27 <--> pdb2_A_GLN_54
			pdb1_A_GLN_125 <--> pdb2_A_THR_39
			pdb1_A_GLU_73 <--> pdb2_A_ARG_53
			pdb1_A_LYS_122 <--> pdb2_A_ASP_36
			pdb1_B_VAL_60 <--> pdb2_A_ASN_46
			pdb1_A_GLU_73 <--> pdb2_A_GLN_54
			pdb1_A_GLN_125 <--> pdb2_A_VAL_40
			pdb1_A_GLN_76 <--> pdb2_A_ARG_63
			pdb1_B_GLU_53 <--> pdb2_A_ASP_43
			pdb1_D_LYS_115 <--> pdb2_A_LEU_31
			pdb1_B_GLY_56 <--> pdb2_A_ASP_43
			pdb1_A_ASP_77 <--> pdb2_A_ARG_53
HBD	V56G of AHSP	-4.66	pdb2_A_LEU_67 <--> pdb1_D_ASP_77
			pdb2_A_ASP_43 <--> pdb1_D_ARG_69
			pdb2_A_GLN_54 <--> pdb1_D_GLN_76
			pdb2_A_GLN_54 <--> pdb1_D_ASP_77
			pdb2_A_GLU_42 <--> pdb1_E_GLY_28

AHSP	KLF1	-6.79	pdb2_A_ARG_71 <--> pdb1_D_LEU_70 pdb2_A_GLN_72 <--> pdb1_E_GLN_27 pdb2_A_ASN_50 <--> pdb1_D_GLU_73 pdb2_A_GLU_42 <--> pdb1_E_GLN_27 pdb2_A_ASN_50 <--> pdb1_D_GLN_76 pdb2_A_ARG_53 <--> pdb1_D_ASP_77 pdb2_A_ARG_53 <--> pdb1_D_GLN_76 pdb2_A_ASN_46 <--> pdb1_D_GLU_73 pdb2_A_ARG_53 <--> pdb1_D_GLU_73 pdb2_A_PRO_60 <--> pdb1_E_ARG_67 pdb2_A_ASN_46 <--> pdb1_E_ILE_26 pdb2_A_ARG_71 <--> pdb1_E_ILE_26 pdb2_A_ARG_71 <--> pdb1_E_GLN_27 pdb2_A_GLN_54 <--> pdb1_D_THR_80 pdb2_A_ASP_64 <--> pdb1_E_GLU_63 pdb2_A_ASP_64 <--> pdb1_E_ARG_67 pdb2_A_ARG_63 <--> pdb1_D_PHE_78 pdb2_A_ASN_75 <--> pdb1_E_GLN_27 pdb2_A_THR_39 <--> pdb1_F_LEU_87 pdb2_A_ARG_63 <--> pdb1_D_ASP_77 pdb2_A_GLN_61 <--> pdb1_A_SER_23 pdb2_A_ARG_71 <--> pdb1_A_HIS_38 pdb2_A_ASN_46 <--> pdb1_A_VAL_37 pdb2_A_GLU_34 <--> pdb1_A_GLU_10 pdb2_A_GLN_68 <--> pdb1_A_SER_43 pdb2_A_ASN_46 <--> pdb1_A_THR_39 pdb2_A_GLN_72 <--> pdb1_A_THR_44 pdb2_A_GLN_72 <--> pdb1_A_LYS_65 pdb2_A_GLU_35 <--> pdb1_A_LYS_11 pdb2_A_GLU_35 <--> pdb1_A_GLU_10 pdb2_A_GLU_42 <--> pdb1_A_PHE_9 pdb2_A_ASN_79 <--> pdb1_A_PRO_84 pdb2_A_ASN_79 <--> pdb1_A_GLN_85 pdb2_A_ASN_79 <--> pdb1_A_ARG_86 pdb2_A_VAL_38 <--> pdb1_A_GLU_10 pdb2_A_GLN_68 <--> pdb1_A_PRO_24 pdb2_A_THR_39 <--> pdb1_A_VAL_12 pdb2_A_THR_39 <--> pdb1_A_GLU_10 pdb2_A_ASP_43 <--> pdb1_A_LYS_36 pdb2_A_THR_39 <--> pdb1_A_LYS_36 pdb2_A_GLU_42 <--> pdb1_A_HIS_38 pdb2_A_VAL_38 <--> pdb1_A_PHE_9 pdb2_A_GLN_68 <--> pdb1_A_VAL_41 pdb2_A_GLN_68 <--> pdb1_A_THR_44 pdb2_A_ASP_64 <--> pdb1_A_PRO_24 pdb2_A_ASP_64 <--> pdb1_A_SER_23 pdb2_A_ASN_75 <--> pdb1_A_GLN_85 pdb2_A_ASN_75 <--> pdb1_A_HIS_87 pdb2_A_THR_76 <--> pdb1_A_GLN_85

			pdb2_A_ARG_71 <--> pdb1_A_HIS_87
KLF1	Y85C of AHSP	-13.77	pdb1_A_PRO_24 <--> pdb2_A_LEU_77
			pdb1_A_THR_39 <--> pdb2_A_ASN_23
			pdb1_A_GLU_20 <--> pdb2_A_PHE_81
			pdb1_A_ASN_19 <--> pdb2_A_LEU_22
			pdb1_A_ASN_19 <--> pdb2_A_GLN_25
			pdb1_A_ASN_19 <--> pdb2_A_VAL_26
			pdb1_A_ASN_19 <--> pdb2_A_PHE_27
			pdb1_A_ASN_19 <--> pdb2_A_ASN_28
			pdb1_A_THR_28 <--> pdb2_A_VAL_26
			pdb1_A_GLU_20 <--> pdb2_A_MET_37
			pdb1_A_VAL_41 <--> pdb2_A_ASN_23
			pdb1_A_VAL_41 <--> pdb2_A_LEU_22
			pdb1_A_VAL_22 <--> pdb2_A_LEU_22
			pdb1_A_VAL_22 <--> pdb2_A_LEU_21
			pdb1_A_SER_23 <--> pdb2_A_PHE_81
			pdb1_A_VAL_22 <--> pdb2_A_TRP_44
			pdb1_A_GLU_26 <--> pdb2_A_LEU_22
			pdb1_A_GLU_26 <--> pdb2_A_ASN_23
			pdb1_A_ALA_25 <--> pdb2_A_PHE_81
			pdb1_A_VAL_22 <--> pdb2_A_PHE_81
			pdb1_A_PRO_24 <--> pdb2_A_LEU_22
			pdb1_A_ILE_107 <--> pdb2_A_LYS_84
			pdb1_A_GLN_106 <--> pdb2_A_LYS_84
			pdb1_A_ARG_110 <--> pdb2_A_LYS_84
			pdb1_A_SER_23 <--> pdb2_A_PHE_18
			pdb1_A_ASP_21 <--> pdb2_A_PHE_27
			pdb1_A_ASP_21 <--> pdb2_A_ASN_28
			pdb1_A_VAL_22 <--> pdb2_A_PHE_18
			pdb1_A_ASP_21 <--> pdb2_A_TRP_44
			pdb1_A_SER_23 <--> pdb2_A_ALA_78
			pdb1_A_ASP_21 <--> pdb2_A_VAL_41
			pdb1_A_ASP_21 <--> pdb2_A_VAL_40
			pdb1_A_PRO_24 <--> pdb2_A_PHE_18
			pdb1_A_SER_23 <--> pdb2_A_LEU_77
			pdb1_A_GLU_20 <--> pdb2_A_ASN_28
KLF1	L21P of AHSP	-23.27	pdb2_A_ASP_43 <--> pdb1_A_ASP_29
			pdb2_A_VAL_26 <--> pdb1_A_TYR_51
			pdb2_A_VAL_26 <--> pdb1_A_ASN_50
			pdb2_A_GLN_24 <--> pdb1_A_TYR_51
			pdb2_A_GLN_24 <--> pdb1_A_TYR_52
			pdb2_A_ASP_29 <--> pdb1_A_PHE_47
			pdb2_A_ASP_29 <--> pdb1_A_ASN_46
			pdb2_A_ASP_29 <--> pdb1_A_ASP_43
			pdb2_A_GLN_25 <--> pdb1_A_PHE_47
			pdb2_A_GLN_25 <--> pdb1_A_TRP_44
			pdb2_A_PHE_47 <--> pdb1_A_GLN_25
			pdb2_A_PHE_47 <--> pdb1_A_GLN_24
			pdb2_A_TYR_48 <--> pdb1_A_GLN_24

			pdb2_A_PHE_47 <--> pdb1_A_VAL_26
			pdb2_A_TYR_48 <--> pdb1_A_LEU_21
			pdb2_A_VAL_20 <--> pdb1_A_GLU_17
			pdb2_A_ASN_50 <--> pdb1_A_ASP_29
			pdb2_A_GLN_24 <--> pdb1_A_PHE_47
			pdb2_A_GLN_24 <--> pdb1_A_TYR_48
			pdb2_A_VAL_26 <--> pdb1_A_PHE_47
			pdb2_A_PHE_47 <--> pdb1_A_ASP_29
			pdb2_A_TRP_44 <--> pdb1_A_TRP_44
			pdb2_A_TYR_51 <--> pdb1_A_GLN_24
			pdb2_A_ASN_46 <--> pdb1_A_ASP_29
			pdb2_A_TYR_51 <--> pdb1_A_VAL_26
			pdb2_A_ASN_50 <--> pdb1_A_VAL_26
			pdb2_A_ASP_29 <--> pdb1_A_ASN_50
			pdb2_A_LEU_21 <--> pdb1_A_LEU_21
			pdb2_A_PHE_47 <--> pdb1_A_PRO_30
			pdb2_A_GLU_17 <--> pdb1_A_GLN_24
			pdb2_A_GLU_17 <--> pdb1_A_VAL_20
			pdb2_A_TYR_52 <--> pdb1_A_GLN_24
			pdb2_A_LEU_21 <--> pdb1_A_TRP_44
			pdb2_A_GLN_24 <--> pdb1_A_GLU_17
KLF1	V56G of AHSP	‡	
AHSP	HBQ1	-26.08	pdb1_A_PRO_80 <--> pdb2_A_ALA_36
			pdb1_A_PRO_80 <--> pdb2_A_THR_33
			pdb1_A_PRO_80 <--> pdb2_A_ARG_32
			pdb1_A_THR_76 <--> pdb2_A_ARG_112
			pdb1_A_PHE_81 <--> pdb2_A_ALA_36
			pdb1_A_ASN_79 <--> pdb2_A_VAL_108
			pdb1_A_PRO_80 <--> pdb2_A_CYS_105
			pdb1_A_PRO_80 <--> pdb2_A_LEU_101
			pdb1_A_THR_76 <--> pdb2_A_ARG_32
			pdb1_A_ASP_87 <--> pdb2_A_GLN_100
			pdb1_A_SER_19 <--> pdb2_A_LYS_41
			pdb1_A_LYS_84 <--> pdb2_A_ALA_97
			pdb1_A_SER_12 <--> pdb2_A_PRO_51
			pdb1_A_LYS_16 <--> pdb2_A_SER_50
			pdb1_A_LYS_16 <--> pdb2_A_PRO_51
			pdb1_A_LEU_77 <--> pdb2_A_ALA_36
			pdb1_A_LEU_77 <--> pdb2_A_LEU_35
			pdb1_A_ALA_83 <--> pdb2_A_HIS_104
			pdb1_A_LYS_84 <--> pdb2_A_PHE_37
			pdb1_A_SER_19 <--> pdb2_A_LEU_35
			pdb1_A_LEU_15 <--> pdb2_A_PRO_51
			pdb1_A_LEU_22 <--> pdb2_A_PRO_38
			pdb1_A_ASN_23 <--> pdb2_A_PRO_38
			pdb1_A_LYS_84 <--> pdb2_A_LEU_101
			pdb1_A_LEU_22 <--> pdb2_A_LEU_35
			pdb1_A_LEU_22 <--> pdb2_A_ALA_36
			pdb1_A_LEU_15 <--> pdb2_A_LEU_35

HBQ1	Y85C of AHSP	-28.89	pdb2_A_GLN_54 <--> pdb1_A_ARG_112 pdb2_A_GLN_54 <--> pdb1_A_ALA_111 pdb2_A_GLU_59 <--> pdb1_A_LEU_101 pdb2_A_GLN_54 <--> pdb1_A_ARG_32 pdb2_A_ARG_53 <--> pdb1_A_VAL_108 pdb2_A_ASN_46 <--> pdb1_A_PRO_120 pdb2_A_ASN_50 <--> pdb1_A_PHE_118 pdb2_A_THR_57 <--> pdb1_A_HIS_104 pdb2_A_ARG_53 <--> pdb1_A_PHE_118 pdb2_A_ARG_53 <--> pdb1_A_ALA_111 pdb2_A_GLY_58 <--> pdb1_A_HIS_104 pdb2_A_THR_57 <--> pdb1_A_ALA_36 pdb2_A_PRO_60 <--> pdb1_A_GLN_100 pdb2_A_GLN_54 <--> pdb1_A_VAL_108 pdb2_A_ASN_50 <--> pdb1_A_ALA_111 pdb2_A_GLN_55 <--> pdb1_A_VAL_108 pdb2_A_GLU_59 <--> pdb1_A_PHE_37 pdb2_A_ARG_53 <--> pdb1_A_GLN_123 pdb2_A_ARG_53 <--> pdb1_A_PRO_120 pdb2_A_ARG_63 <--> pdb1_A_HIS_104 pdb2_A_VAL_56 <--> pdb1_A_VAL_108 pdb2_A_VAL_56 <--> pdb1_A_HIS_104 pdb2_A_ARG_63 <--> pdb1_A_GLN_123 pdb2_A_ASN_50 <--> pdb1_A_PRO_115
HBQ1	L21P of AHSP	-25.45	pdb1_A_HIS_104 <--> pdb2_A_LYS_16 pdb1_A_PRO_120 <--> pdb2_A_ALA_6 pdb1_A_PRO_120 <--> pdb2_A_GLN_55 pdb1_A_PRO_120 <--> pdb2_A_VAL_56 pdb1_A_PRO_120 <--> pdb2_A_LEU_10 pdb1_A_ALA_111 <--> pdb2_A_GLU_17 pdb1_A_VAL_108 <--> pdb2_A_GLU_17 pdb1_A_VAL_108 <--> pdb2_A_LYS_16 pdb1_A_GLN_123 <--> pdb2_A_LEU_10 pdb1_A_PHE_118 <--> pdb2_A_ALA_13 pdb1_A_PHE_118 <--> pdb2_A_GLN_55 pdb1_A_GLN_123 <--> pdb2_A_ALA_13 pdb1_A_CYS_105 <--> pdb2_A_VAL_20 pdb1_A_SER_119 <--> pdb2_A_GLN_55 pdb1_A_ALA_36 <--> pdb2_A_VAL_20 pdb1_A_ALA_36 <--> pdb2_A_ASN_23 pdb1_A_ALA_36 <--> pdb2_A_GLN_24 pdb1_A_PRO_115 <--> pdb2_A_TYR_51 pdb1_A_LEU_35 <--> pdb2_A_GLN_24 pdb1_A_PRO_115 <--> pdb2_A_GLN_55 pdb1_A_PHE_37 <--> pdb2_A_VAL_20 pdb1_A_PHE_37 <--> pdb2_A_ASN_23 pdb1_A_ARG_32 <--> pdb2_A_GLN_24 pdb1_A_VAL_108 <--> pdb2_A_VAL_20 pdb1_A_ALA_124 <--> pdb2_A_ASP_9

HBQ1	V56G of AHSP	-34.64	pdb1_A_PRO_120 <--> pdb2_A_ASP_9
			pdb1_A_PRO_120 <--> pdb2_A_ASN_7
			pdb1_A_PRO_120 <--> pdb2_A_ALA_6
			pdb1_A_PRO_120 <--> pdb2_A_GLN_55
			pdb1_A_GLN_123 <--> pdb2_A_GLU_17
			pdb1_A_PRO_120 <--> pdb2_A_LEU_10
			pdb1_A_ALA_111 <--> pdb2_A_GLU_17
			pdb1_A_SER_119 <--> pdb2_A_LEU_10
			pdb1_A_VAL_108 <--> pdb2_A_GLU_17
			pdb1_A_VAL_108 <--> pdb2_A_LYS_16
			pdb1_A_PHE_118 <--> pdb2_A_LEU_10
			pdb1_A_GLN_123 <--> pdb2_A_ALA_13
			pdb1_A_CYS_105 <--> pdb2_A_VAL_20
			pdb1_A_ALA_36 <--> pdb2_A_ASN_23
			pdb1_A_ALA_36 <--> pdb2_A_GLN_24
			pdb1_A_LEU_35 <--> pdb2_A_VAL_26
			pdb1_A_LEU_35 <--> pdb2_A_GLN_24
			pdb1_A_PRO_115 <--> pdb2_A_GLN_55
			pdb1_A_HIS_104 <--> pdb2_A_VAL_20
			pdb1_A_PHE_37 <--> pdb2_A_ASN_23
			pdb1_A_ARG_32 <--> pdb2_A_GLN_24
			pdb1_A_ARG_32 <--> pdb2_A_VAL_20
			pdb1_A_LEU_107 <--> pdb2_A_GLU_17
			pdb1_A_VAL_108 <--> pdb2_A_VAL_20
			pdb1_A_ALA_124 <--> pdb2_A_ASP_9
			pdb1_A_ASP_127 <--> pdb2_A_LYS_16

‡No interaction was found.