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Regular paper

Electronegativity and intrinsic disorder of preeclampsia-related proteins

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Preeclampsia, hemorrhage, and infection are the leading causes of maternal death in underdeveloped countries. Since several proteins associated with preeclampsia are known, we conducted a computational study which evaluated the commonness and potential functionality of intrinsic disorder of these proteins and also made an attempt to characterize their origin. The origin of the preeclampsia-related proteins was assessed with a supervised technique, a Polarity Index Method (PIM), which evaluates the electronegativity of proteins based solely on their sequence. The commonness of intrinsic disorder was evaluated using several disorder predictors from the PONDR family, the charge-hydropathy plot (CH-plot) and cumulative distribution function (CDF) analyses, and using the MobiDB web-based tool, whereas potential functionality of intrinsic disorder was studied with the D2P2 resource and ANCHOR predictor of disorder-based binding sites, and the STRING tool was used to build the interactivity networks of the preeclampsia-related proteins. Peculiarities of the PIM-derived polar profile of the group of preeclampsia-related proteins were then compared with profiles of a group of lipoproteins, antimicrobial peptides, angiogenesis-related proteins, and the intrinsically disordered proteins. Our results showed a high graphical correlation between preeclampsia proteins, lipoproteins, and the angiogenesis proteins. We also showed that many preeclampsia-related proteins contain numerous functional disordered regions. Therefore, these bioinformatics results led us to assume that the preeclampsia proteins are highly associated with the lipoproteins group, and that some preeclampsia-related proteins contain significant amounts of functional disorders.

Key words: preeclampsia, intrinsically disordered proteins, structural proteomics, bioinformatics, antimicrobial peptides, polarity index method, lipoproteins, angiogenesis proteins

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Abbreviations: CH-plot, charge-hydropathy plot; CDF, cumulative distribution function; PIM, Polarity Index Method

Appendix 1. Hits of preeclampsia reviewed proteins.

#	Entry UniprotKB	⚑	Protein expressed as linear sequence of amino acids	PIM (lipoprotein)	PIM (antimicrobial)	PIM (disordered)	Reference
1	Q6ZVD7		MARPVQLAPGSLALVLCRLEAQKAAGAAEEPGGRAVFRAFRRANARCFWNARLARAASRLAFQGWLRRGVLLVRAPPACLQVLRDAWRRRALRPPRGFRIRAVGDVFPVQMNPITQSQFVPLGEVLCCAISDMNTAQIVVTQESLLERLMKHYPGIAIPSEDILYTTLGTLIKERKIYHTGEGYFIVTPQTYFITNTTTQENKRMLPSDESRLMPASMTYLVSMESCAESAQENAAPISHCQSCQCFRDMHTQDVQEAPVAAEVTRKSHRGLGESVSWVQNGAVSVSAEHHICESTKPLPYTRDKEKGKKFGFSLLWRSLSRKEKPKTEHSSFSAQFPPEEWPVRDEDDLDNIPRDVEHEIIKRINPILTVDNLIKHTVLMQKYEEQKKYNSQGTSTDMLTIGHKYPSKEGVKKRQGLSAKPQGQGHSRRDRHKARNQGSEFQPGSIRLEKHPKLPATQPIPRIKSPNEMVGQKPLGEITTVLGSHLIYKKRISNPFQGLSHRGSTISKGHKIQKTSDLKPSQTGPKEKPFQKPRSLDSSRIFDGKAKEPYAEQPNDKMEAESIYINDPTVKPINDDFRGHLFSHPQQSMLQNDGKCCPFMESMLRYEVYGGENEVIPEVLRKSHSHFDKLGETKQTPHSLPSRGASFSDRTPSACRLVDNTIHQFQNLGLLDYPVGVNPLRQAARQDKDSEELLRKGFVQDAETTSLENEQLSNDDQALYQNEVEDDDGACSSLYLEEDDISENDDLRQMLPGHSQYSFTGGSQGNHLGKQKVIERSLTEYNSTMERVESQVLKRNECYKPTGLHATPGESQEPNLSAESCGLNSGAQFGFNYEEEPSVAKCVQASAPADERIFDYYSARKASFEAEVIQDTIGDTGKKPASWSQSPQNQEMRKHFPQKFQLFNTSHMPVLAQDVQYEHSHLEGTENHSMAGDSGIDSPRTQSLGSNNSVILDGLKRRQNFLQNVEGTKSSQPLTSNSLLPLTPVINV	✔	✔	✔	Abel *et al*., 2012.
2	Q6ZVD7-2		MARPVQLAPGSLALVLCRLEAQKAAGAAEEPGGRAVFRAFRRANARCFWNARLARAASRLAFQGWLRRGVLLVRAPPACLQVLRDAWRRRALRPPRGFRIRAVGDVFPVQMNPITQSQFVPLGEVLCCAISDMNTAQIVVTQESLLERLMKHYPGIAIPSEDILYTTLGTLIKERKIYHTGEGYFIVTPQTYFITNTTTQENKRMLPSDESRLMPASMTYLDTESGI	✔	✔	✔	Abel *et al*., 2012.
3	Q6ZVD7-3		MARPVQLAPGSLALVLCRLEAQKAAGAAEEPGGRAVFRAFRRANARCFWNARLARAASRLAFQGWLRRGVLLVRAPPACLQVLRDAWRRRALRPPRGFRIRAVGDVFPVQMNPITQSQFVPLGEVLCCAISDMNTAQIVVTQESLLERLMKHYPGHRVWDLIIQSFWMD	✔	✔	✔	Abel *et al*., 2012.
4	P17948	✔	MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARCDFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKMASTLVVADSRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVYTGEEILQKKEITIRDQEAPYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQQEPGIILGPGSSTLFIERVTEEDEGVYHCKATNQKGSVESSAYLTVQGTSDKSNLELITLTCTCVAATLFWLLLTLFIRKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSVTSSESFASSGFQEDKSLSDVEEEEDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI	✔	✔	✔	Shibuya *et al*., 1990.
5	P17948-2	✔	MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARCDFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKMASTLVVADSRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVYTGEEILQKKEITIRGEHCNKKAVFSRISKFKSTRNDCTTQSNVKH	✔	✔	×	Shibuya *et al*., 1990.
6	P17948-3	✔	MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAG	✔	✔	✔	Shibuya *et al*., 1990.

			QTLHLQCRGEAAHKWSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARCDFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKMASTLVVADSRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVYTGEEILQKKEITIRDQEAPYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQQEPELYTSTSPSSSSSSPLSSSSSSSSSSS				
7	P17948-4	✔	MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARCDFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKLPPANSSFMLPPTSFSSNYFHFLP	✔	✔	✔	Shibuya *et al*., 1990.
8	P17948-5	✔	MKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSVTSSESFASSGFQEDKSLSDVEEEEDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI	✔	✔	✔	Shibuya *et al*., 1990.
9	P17948-6	✔	MTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSVTSSESFASSGFQEDKSLSDVEEEEDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI	✔	✔	✔	Shibuya *et al*., 1990.
10	P17948-7	✔	MEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI	✔	✔	✔	Shibuya *et al*., 1990.
11	P17948-8	✔	MNSDLLVDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI	✔	✔	✔	Shibuya *et al*., 1990.
12	P01019	×	MRKRAPQSEMAPAGVSLRATILCLLAWAGLAAGDRVYIHPFHLVIHNESTCEQLAKANAGKPKDPTFIPAPIQAKTSPVDEKALQDQLVLVAAKLDTEDKLRAAMVGMLANFLGFRIYGMHSELWGVVHGATVLSPTAVFGTLASLYLGALDHTADRLQAILGVPWKDKNCTSRLDAHKVLSALQAVQGLLVAQGRADSQAQLLLSTVVGVFTAPGLHLKQPFVQGLALYTPVVLPRSLDFTELDVAAEKIDRFMQAVTGWKTGCSLMGASVDSTLAFNTYVHFQGKMKGFSLLAEPQEFWVDNSTSVSVPMLSGMGTFQHWSDIQDNFSVTQVPFTESACLLLIQPHYASDLDKVEGLTFQQNSLNWMKKLSPRTIHLTMPQLVLQGSYDLQDLLAQAELPAILHTELNLQKLSNDRIRVGEVLNSIFFELEADEREPTESTQQLNKPEVLEVTLNRPFLFAVYDQSATALHFLGRVANPLSTA	✔	✔	✔	Kageyama et al., 1984.
13	Q9Y5Q5		MKQSPALAPEERCRRAGSPKPVLRADDNNMGNGCSQKLATANLLRFLLLVLIPCICALVLLLVILLSYVGTLQKVYFKSNGSEPLVTDGEIQGSDVILTNTIYNQSTVVSTAHPDQHVPAWTTDASLPGDQSHRNTSACMNITHSQCQMLPYHATLTPLLSVVRNMEMEKFLKFFTYLHRLSCYQHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCEAAKEGCESVLGMVNYSWPDFLRCSQFRNQTESSNVSRICFSPQQENGKQLLCGRGENFLCASGICIPGKLQCNGYNDCDDWSDEAHCNCSENLFHCHTGKCLNYSLVCDGY	×	×	×	Yan *et al*., 1999.

			DDCGDLSDEQNCDCNPTTEHRCGDGRCIAMEWVCDGDHDCVDKSDEVNCSCHSQGLVECRNGQCIPSTFQCDGDEDCKDGSDEENCSVIQTSCQEGDQRCLYNPCLDSCGGSSLCDPNNSLNNCSQCEPITLELCMNLPYNSTSYPNYFGHRTQKEASISWESSLFPALVQTNCYKYLMFFSCTILVPKCDVNTGEHIPPCRALCEHSKERCESVLGIVGLQWPEDTDCSQFPEENSDNQTCLMPDEYVEECSPSHFKCRSGQCVLASRRCDGQADCDDDSDEENCGCKERDLWECPSNKQCLKHTVICDGFPDCPDYMDEKNCSFCQDDELECANHACVSRDLWCDGEADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHHVCADGWQEILSQLACKQMGLGEPSVTKLIQEQEKEPRWLTLHSNWESLNGTTLHELLVNGQSCESRSKISLLCTKQDCGRRPAARMNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGRENAAVWKVVLGINNLDHPSVFMQTRFVKTIILHPRYSRAVVDYDISIVELSEDISETGYVRPVCLPNPEQWLEPDTYCYITGWGHMGNKMPFKLQEGEVRIISLEHCQSYFDMKTITTRMICAGYESGTVDSCMGDSGGPLVCEKPGGRWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVEWIKRQIYIQTFLLN				
14	Q9Y5Q5-2		MGNGCSQKLATANLLRFLLLVLIPCICALVLLLVILLSYVGTLQKVYFKSNGSEPLVTDGEIQGSDVILTNTIYNQSTVVSTAHPDQHVPAWTTDASLPGDQSHRNTSACMNITHSQCQMLPYHATLTPLLSVVRNMEMEKFLKFFTYLHRLSCYQHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCEAAKEGCESVLGMVNYSWPDFLRCSQFRNQTESSNVSRICFSPQQENGKQLLCGRGENFLCASGICIPGKLQCNGYNDCDDWSDEAHCNCSENLFHCHTGKCLNYSLVCDGYDDCGDLSDEQNCDCNPTTEHRCGDGRCIAMEWVCDGDHDCVDKSDEVNCSCHSQGLVECRNGQCIPSTFQCDGDEDCKDGSDEENCSVIQTSCQEGDQRCLYNPCLDSCGGSSLCDPNNSLNNCSQCEPITLELCMNLPYNSTSYPNYFGHRTQKEASISWESSLFPALVQTNCYKYLMFFSCTILVPKCDVNTGEHIPPCRALCEHSKERCESVLGIVGLQWPEDTDCSQFPEENSDNQTCLMPDEYVEECSPSHFKCRSGQCVLASRRCDGQADCDDDSDEENCGCKERDLWECPSNKQCLKHTVICDGFPDCPDYMDEKNCSFCQDDELECANHACVSRDLWCDGEADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHHVCADGWQEILSQLACKQMGLGEPSVTKLIQEQEKEPRWLTLHSNWESLNGTTLHELLVNGQSCESRSKISLLCTKQDCGRRPAARMNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGRENAAVWKVVLGINNLDHPSVFMQTRFVKTIILHPRYSRAVVDYDISIVELSEDISETGYVRPVCLPNPEQWLEPDTYCYITGWGHMGNKMPFKLQEGEVRIISLEHCQSYFDMKTITTRMICAGYESGTVDSCMGDSGGPLVCEKPGGRWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVEWIKRQIYIQTFLLN	✔	✔	✔	Yan *et al*., 1999.
15	P07099		MWLEILLTSVLGFAIYWFISRDKEETLPLEDGWWGPGTRSAAREDDSIRPFKVETSDEEIHDLHQRIDKFRFTPPLEDSCFHYGFNSNYLKKVISYWRNEFDWKKQVEILNRYPHFKTKIEGLDIHFIHVKPPQLPAGHTPKPLLMVHGWPGSFYEFYKIIPLLTDPKNHGLSDEHVFEVICPSIPGYGFSEASSKKGFNSVATARIFYKLMLRLGFQEFYIQGGDWGSLICTNMAQLVPSHVKGLHLNMALVLSNFSTLTLLLGQRFGRFLGLTERDVELLYPVKEKVFYSLMRESGYMHIQCTKPDTVGSALNDSPVGLAAYILEKFSTWTNTEFRYLEDGGLERKFSLDDLLTNVMLYWTTGTIISSQRFYKENLGQGWMTQKHERMKVYVPTGFSAFPFELLHTPEKWVRFKYPKLISYSYMVRGGHFAAFEEPELLAQDIRKFLSVLERQ	×	×	✔	Skoda *et al*., 1998.
16	Q8IVI9		MRDPLTDCPYNKVYKNLKEFSQNGENFCKQVTSVLQQRANLEISYAKGLQKLASKLSKALQNTRKSCVSSAWAWASEGMKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENYYQKNMAGYSTRLKWENTLENCYQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQLSSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGKKGHFPAAYVEELPSNAGNTATKA	✔	✔	✔	Zimmermann *et al*., 2002.
17	Q8IVI9-2		MRDPLTDCPYNKVYKNLKEFSQNGENFCKQVTSVLQQSCVSSAWAWASEGMKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENYYQKNMAGYSTRLKWENTLENCYQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQLSSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGKKGHFPAAYVEELPSNAGNTATKA	✔	✔	✔	Zimmermann *et al*., 2002.
18	Q8IVI9-3		MKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENYYQKNMAGYSTRLKWENTLENCYQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQLSSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGKKGHFPAAYVEELPSNAGNTATKA	×	×	×	Zimmermann *et al*., 2002.
19	Q8IVI9-4		MRDPLTDCPYNKVYKNLKEFSQNGENFCKQVTSVLQQRANLEISYAKGLQKLASKLSKALQNTRKSCVSSAWAWASEGMKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENY	✔	✔	✔	Zimmermann *et al*., 2002.

			YQKNMAGYSTRLKWENTLENCYQVTHSICLYAFWVKRAWGKCVSDLRYQDTFLPGNLPPLWFGYDIVKRLIMRLCSVCLQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQLSSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGKKGHFPAAYVEELPSNAGNTATKA				
20	Q9UHF0		MRIMLLFTAILAFSLAQSFGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKALSQASTDPKESTSPEKRDMHDFFVGLMGKRSVQPDSPTDVNQENVPSFGILKYPPRAE	✔	✔	✔	Sheppard *et al*., 1999.
21	Q9UHF0-2		MRIMLLFTAILAFSLAQSFGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKALSQASTDPKESTSPEKRDMHDFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSSLGTEEQRPL	✔	✔	✔	Sheppard *et al*., 1999.
22	Q9UHF0-3		MRIMLLFTAILAFSLAQSFGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKALSQASTDPKESTSPEKHSPTDVNQENVPSFGILKYPPRAE	✔	✔	✔	Sheppard *et al*., 1999.
23	P30039		MKLPIFIADAFTARAFRGNPAAVCLLENELDEDMHQKIAREMNLSETAFIRKLHPTDNFAQSSCFGLRWFTPASEVPLCGHATLASAAVLFHKIKNMNSTLTFVTLSGELRARRAEDGIVLDLPLYPAHPQDFHEVEDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSFLENLKVNTENLLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSYWSQHLGKKEMHAFQCSHRGGELGISLRPDGRVDIRGGAAVVLEGTLTA	✔	✔	✔	Ota *et al*., 2004.
24	P30039-2		MKLPIFIADAFTARAFRGNPAAVCLLENELDEDMHQKIAREMNLSETAFIRKLHPTDNFAQSSCFGLRWFTPASEVPLCGHATLASAAVLFHKIKNMNSTLTFVTLSGELRARRAEDGIVLDLPLYPAHPQDFHEVEDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSFLENLKVNTENLLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSYWSQHLGKKEMHGRTALYQFLFYLPNSKLVFLLICTIPLKM	✔	✔	✔	Ota *et al*., 2004.

The number of hits of proteins associated with preeclampsia found by polarity index method (PIM) from Uniprot Database (Magrane, 2011), accessed on December 30, 2015. **Lipoprotein**: PIM score using the lipoprotein group fingerprint. **Antimicrobial**: PIM score using antimicrobial peptide group fingerprint. **Disordered**: PIM score using intrinsically disordered protein group fingerprint. (✔): Protein accepted by PIM. (✕): Protein not accepted by PIM. **⚑:** Angiogenesis factor. (✔) Protein associated with angiogenesis. (✕) Protein associated with angiogenesis inhibitor.

Electronegativity and intrinsic disorder of preeclampsia-related proteins

Appendix 2

Carlos Polanco* Jorge Alberto Castañón-González, Vladimir N. Uversky, Thomas Buhse,

and Juan José Calva Mercado

Table 1. Human preeclampsia-related proteins analyzed in this study and their major intrinsic disorder characteristics

Protein ID	Length	DisEMBL -465	DisEMBL -HL	ESpritz -NMR	ESpritz-XRay	IUPred-long	IUPred-short	JRONN	PONDR VSL2b	PONDR VLXT	PONDR VL3	PONDR FIT	**Mean**	AIBs
Q9UHF0	121	31.40	47.93	63.63	85.12	45.45	53.72	73.55	74.38	56.20	72.73	60.33	**60.40**	4
Q9UHF0-2	*135*	*38.89*	*39.26*	*74.07*	*91.11*	*59.26*	*58.52*	*74.81*	*81.48*	*53.33*	*75.56*	*69.63*	***65.08***	*3*
Q9UHF0-3	*103*	*31.07*	*41.75*	*57.28*	*100.00*	*32.72*	*45.63*	*66.99*	*75.73*	*56.31*	*97.69*	*63.11*	***60.75***	*2*
Q6ZVD7	989	21.23	43.58	56.62	32.36	49.95	40.24	61.58	67.64	42.97	61.13	37.92	**46.84**	20
Q6ZVD7-2	*227*	*3.96*	*37.00*	*19.82*	*23.78*	*4.41*	*12.33*	*17.62*	*26.43*	*37.89*	*23.35*	*22.03*	***20.78***	*0*
Q6ZVD7-3	*169*	*5.33*	*30.77*	*11.24*	*15.97*	*2.96*	*0.00*	*7.10*	*18.93*	*34.32*	*19.53*	*15.38*	***14.68***	*0*
Q8IVI9	506	21.74	40.32	52.96	35.96	15.81	11.26	48.62	60.47	28.26	54.94	34.78	**36.83**	4

Q8IVI9-2	*478*	*15.69*	*36.82*	*57.74*	*38.49*	*16.74*	*11.92*	*43.72*	*60.25*	*26.78*	*45.81*	*37.03*	***35.54***	*4*
Q8IVI9-3	*428*	*17.52*	*44.86*	*67.75*	*44.49*	*20.33*	*13.32*	*48.60*	*64.49*	*30.84*	*63.08*	*41.36*	***41.51***	*4*
Q8IVI9-4	*563*	*15.81*	*30.91*	*48.31*	*32.85*	*12.97*	*10.12*	*41.38*	*53.11*	*25.40*	*48.13*	*30.55*	***31.78***	*4*
Q96L47	144	27.78	21.53	53.47	19.44	20.83	21.53	54.17	51.39	29.86	24.31	46.53	**33.71**	0
Q9Y5Q5	1,042	5.18	5.85	33.97	9.98	1.92	4.89	22.55	41.55	15.64	35.60	9.88	**17.00**	0
Q9Y5Q5-2	*1,013*	*3.16*	*3.55*	*31.09*	*10.16*	*0.49*	*2.86*	*21.72*	*40.08*	*14.12*	*33.56*	*8.19*	***15.26***	*0*
P17948	1,338	6.80	39.06	13.30	5.98	2.54	5.46	19.28	24.59	19.81	12.41	7.70	**14.26**	1
P17948-2	*687*	*3.64*	*26.49*	*11.06*	*8.30*	*2.62*	*2.47*	*19.51*	*21.25*	*14.26*	*10.63*	*6.40*	***11.51***	*1*
P17948-3	*733*	*5.18*	*37.79*	*16.50*	*13.23*	*6.68*	*5.87*	*20.05*	*22.24*	*18.42*	*10.78*	*8.73*	***15.04***	*1*
P17948-4	*541*	*1.85*	*30.31*	*15.89*	*8.32*	*2.03*	*2.59*	*26.43*	*26.62*	*16.08*	*8.13*	*7.58*	***13.26***	*1*
P17948-5	*556*	*12.05*	*42.09*	*51.97*	*21.58*	*3.78*	*12.05*	*25.54*	*36.69*	*26.08*	*27.52*	*15.29*	***24.97***	*0*
P17948-6	*463*	*12.74*	*39.96*	*51.83*	*23.54*	*4.54*	*13.82*	*28.94*	*37.80*	*22.89*	*26.57*	*16.63*	***25.39***	*0*
P17948-7	*343*	*3.50*	*37.61*	*42.85*	*10.49*	*0.00*	*2.91*	*20.70*	*32.94*	*17.20*	*16.03*	*7.58*	***17.44***	*0*
P17948-8	*361*	*3.60*	*35.73*	*43.76*	*11.91*	*0.00*	*3.60*	*19.94*	*31.58*	*16.62*	*15.24*	*7.48*	***17.22***	*0*
P01019	485	8.45	12.16	9.69	7.42	5.77	7.22	14.85	13.81	10.52	7.63	7.22	**9.52**	0
P07099	455	2.86	19.56	7.69	2.42	0.88	3.08	10.11	12.32	7.69	2.42	3.74	**6.62**	0
P30039	288	1.74	16.67	11.11	3.82	0.36	2.08	5.21	7.29	7.29	0.00	4.86	**5.49**	0
P30039-2	*280*	*0.00*	*8.57*	*10.00*	*2.86*	*0.36*	*0.36*	*5.36*	*7.14*	*7.14*	*0.00*	*5.36*	***4.29***	*0*

Data for the alternatively spliced isoforms of preeclampsia-related proteins are indicated by the *Italic* font, whereas the mean disorder contents (percent of predicted disordered residues) calculated by averaging the outputs of 11 predictors are shown by the **bold** font.

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E
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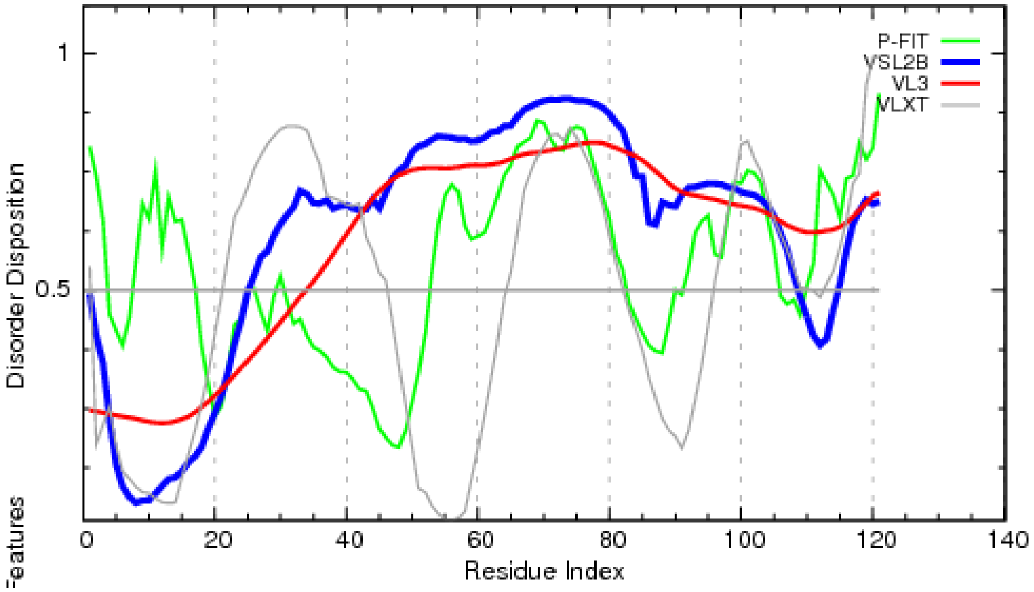

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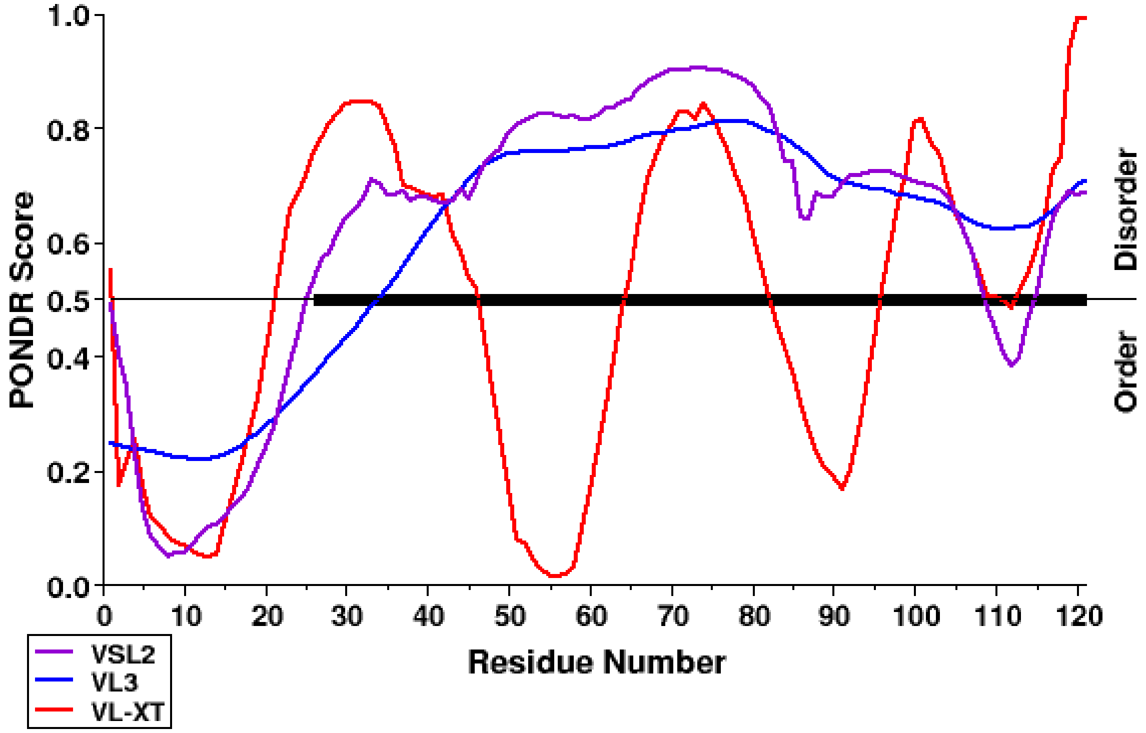

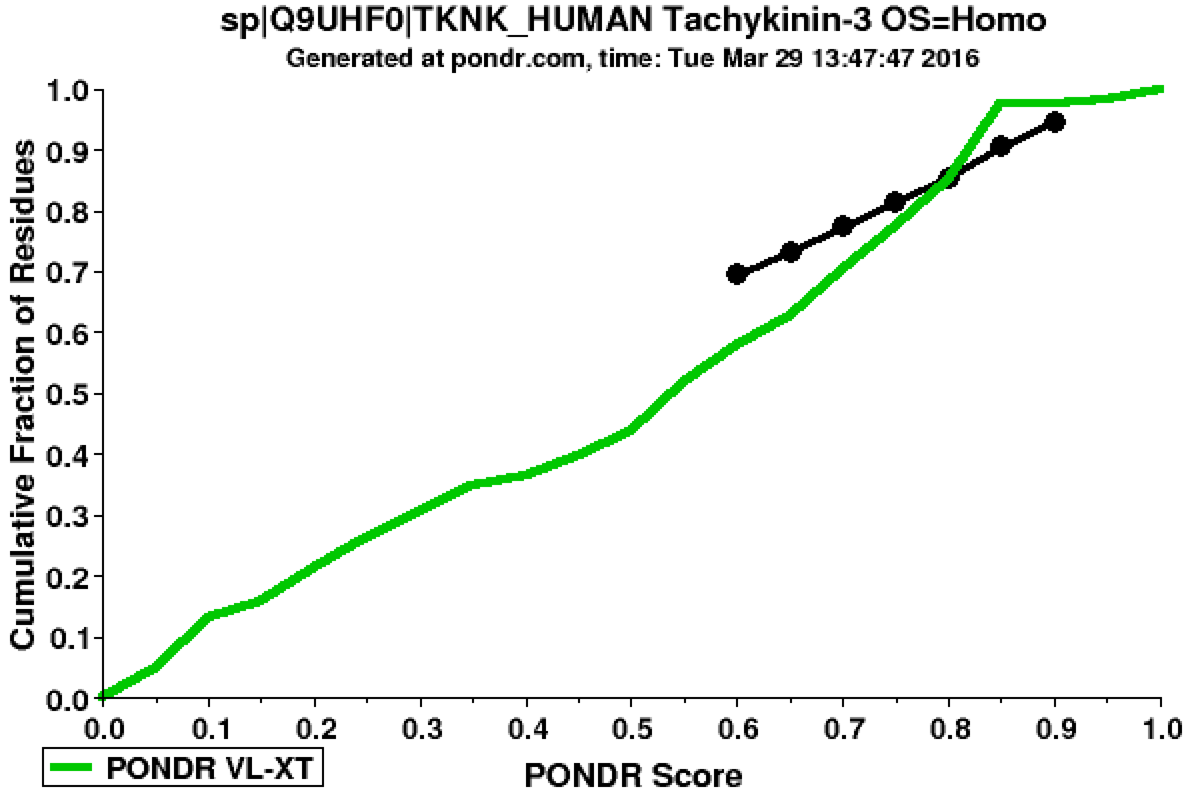
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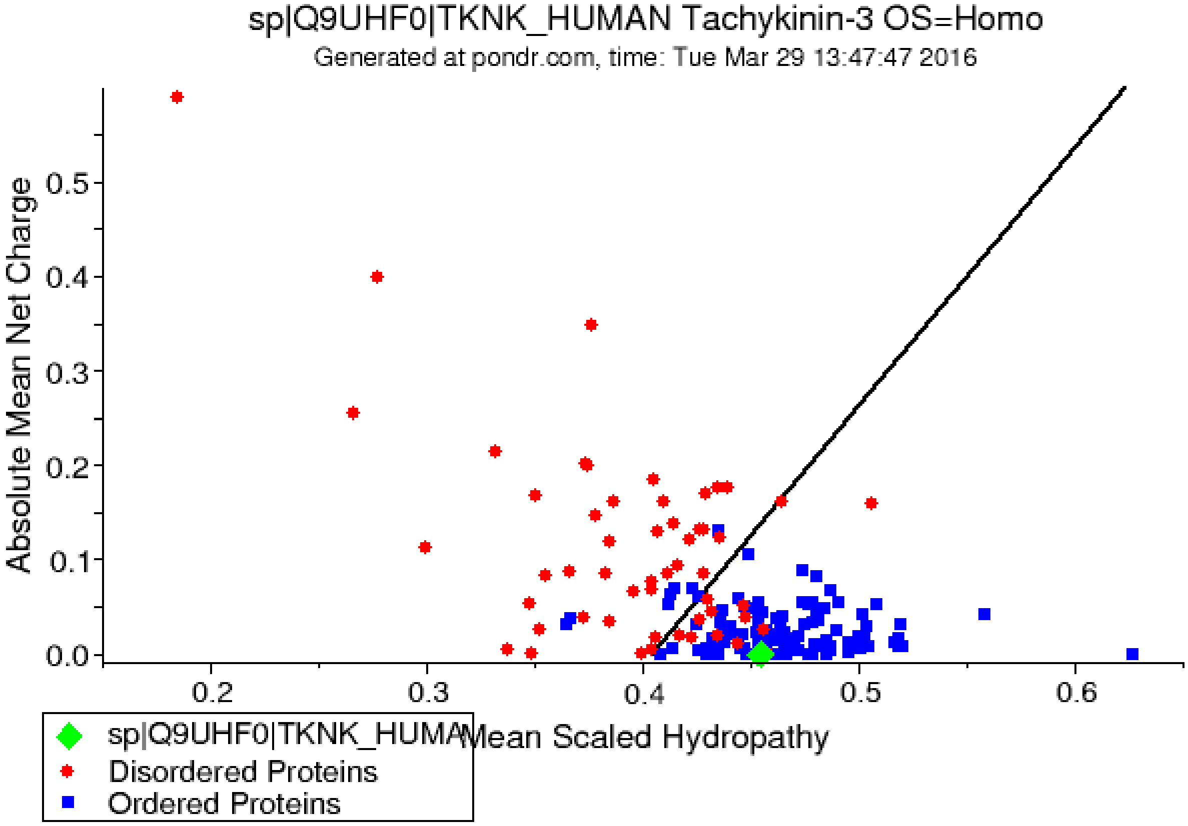
PONDR VL-XT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0.5
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Mean Scaled Hydropathy
sp|Q9UHF0|TKNK_HUMAN
Disordered Proteins
Ordered Proteins

```
========================VLXT NNP STATISTICS================================
Predicted residues: 121                       Number Disordered Regions: 4
Number residues disordered: 68        Longest Disordered Region: 25
Overall percent disordered: 56.20     Average Prediction Score: 0.4911
Predicted disorder segment [22]-[46]  Average Strength= 0.7186
Predicted disorder segment [65]-[82]  Average Strength= 0.7209
Predicted disorder segment [96]-[110] Average Strength= 0.6510
Predicted disorder segment [113]-[121]Average Strength= 0.7425

=========================VL3 NNP STATISTICS================================
Predicted residues: 121                       Number Disordered Regions: 1
Number residues disordered: 88        Longest Disordered Region: 88
Overall percent disordered: 72.73     Average Prediction Score: 0.5986
Predicted disorder segment [34]-[121] Average Strength= 0.7124

========================VSL2 NNP STATISTICS================================
Predicted residues: 121                       Number Disordered Regions: 2
Number residues disordered: 90        Longest Disordered Region: 83
Overall percent disordered: 74.38     Average Prediction Score: 0.6163
Predicted disorder segment [26]-[108] Average Strength= 0.7505
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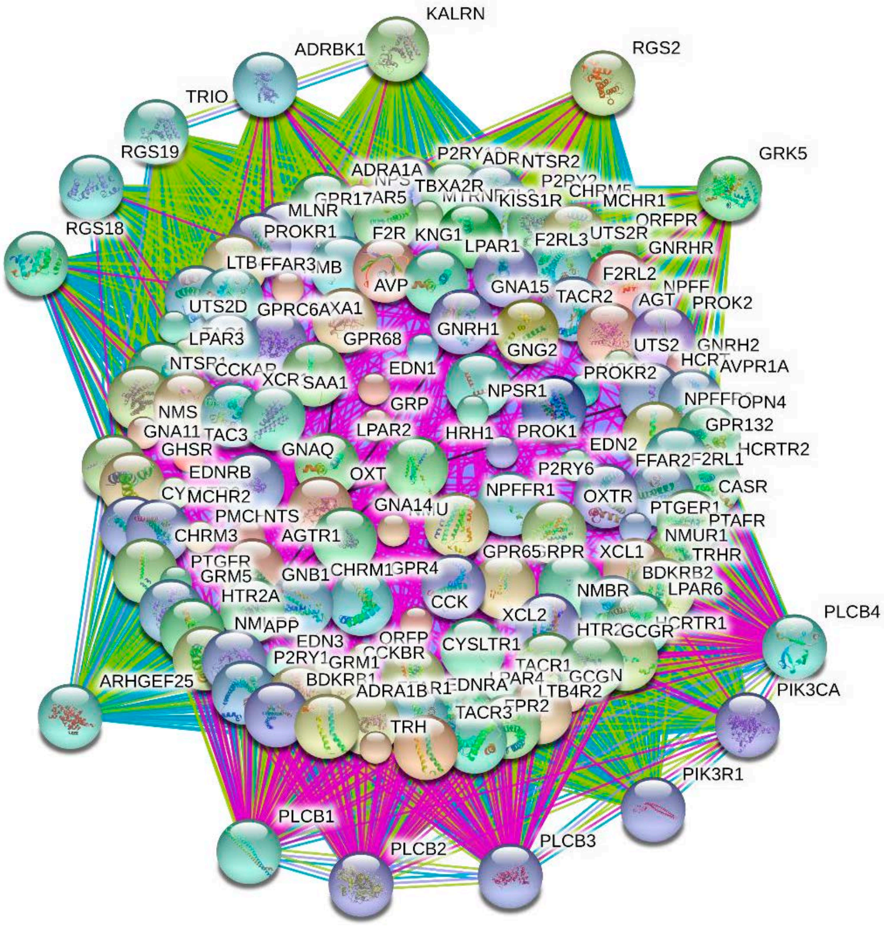

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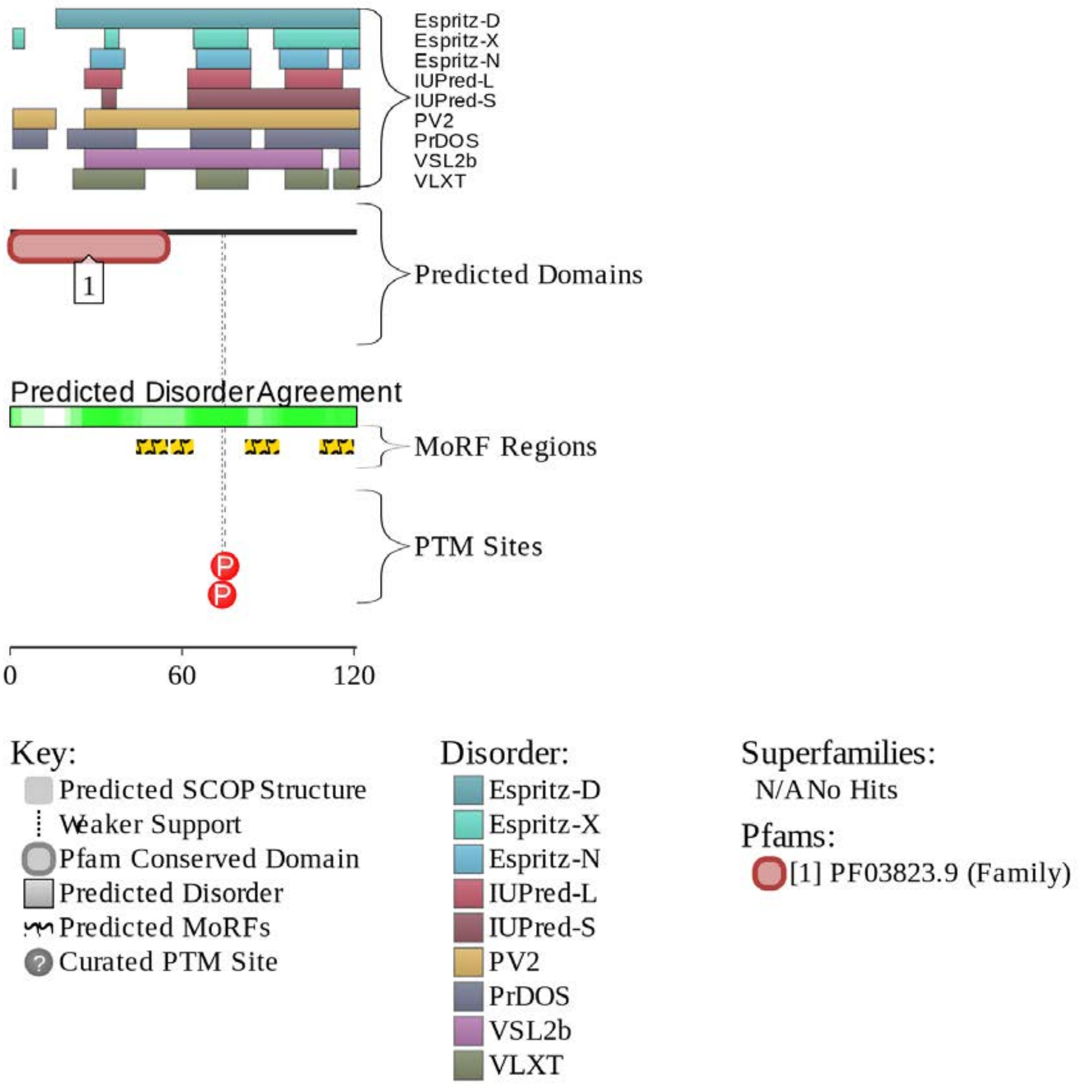

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2	56	63	8
3	82	93	12
4	108	119	12

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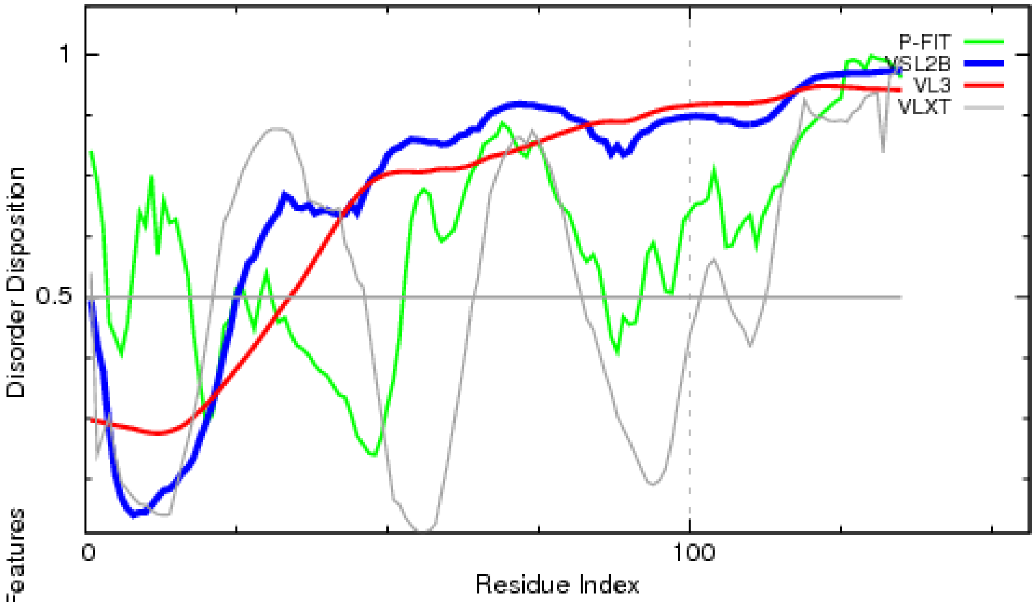

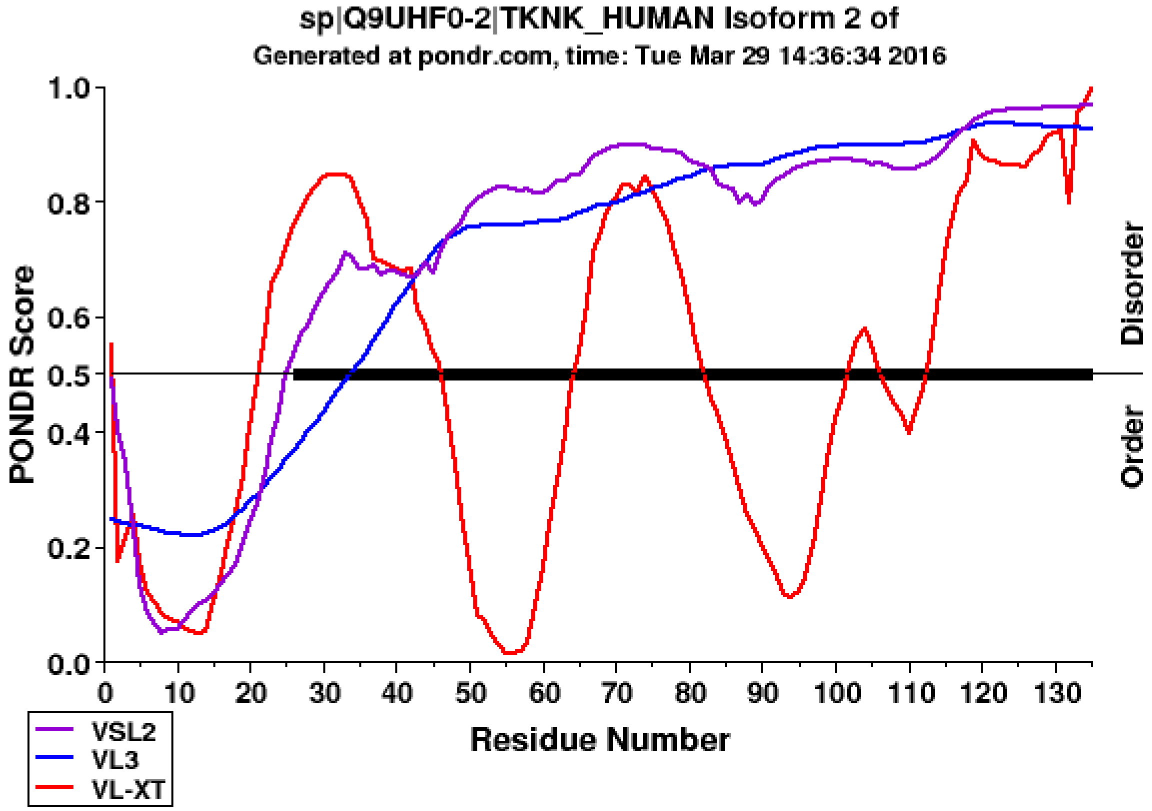

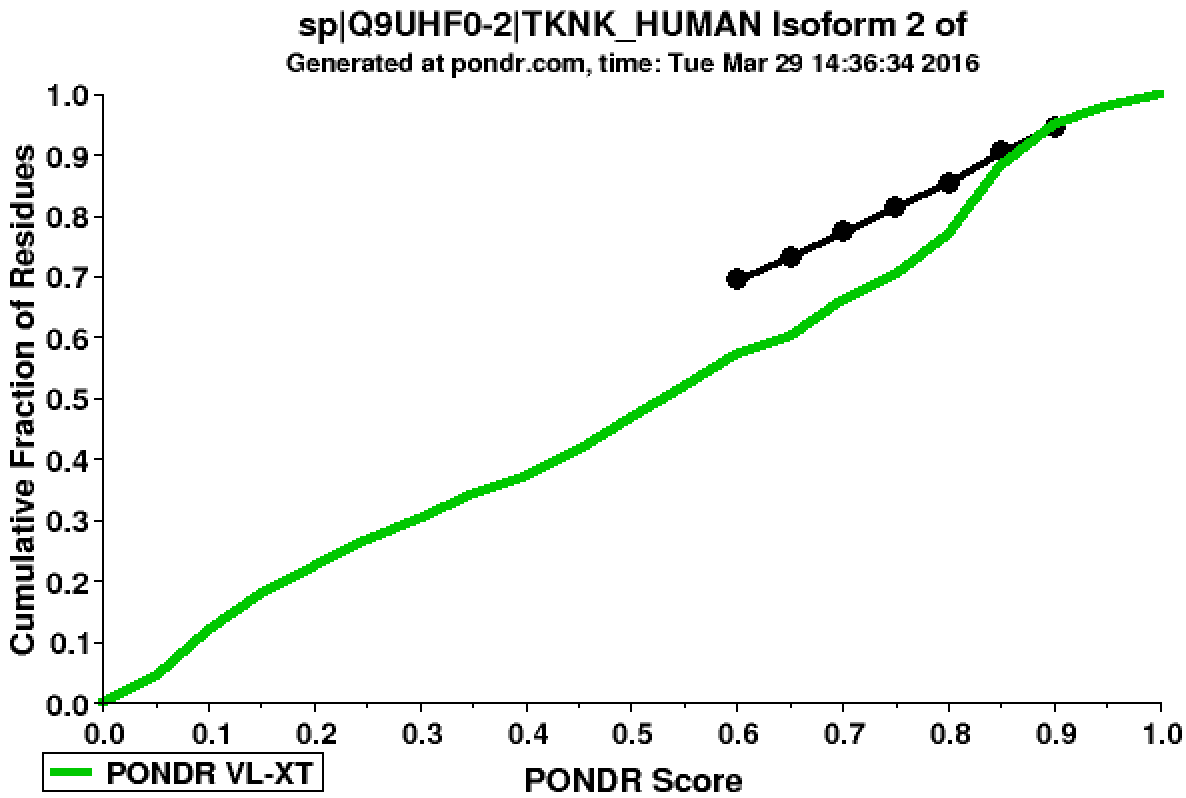
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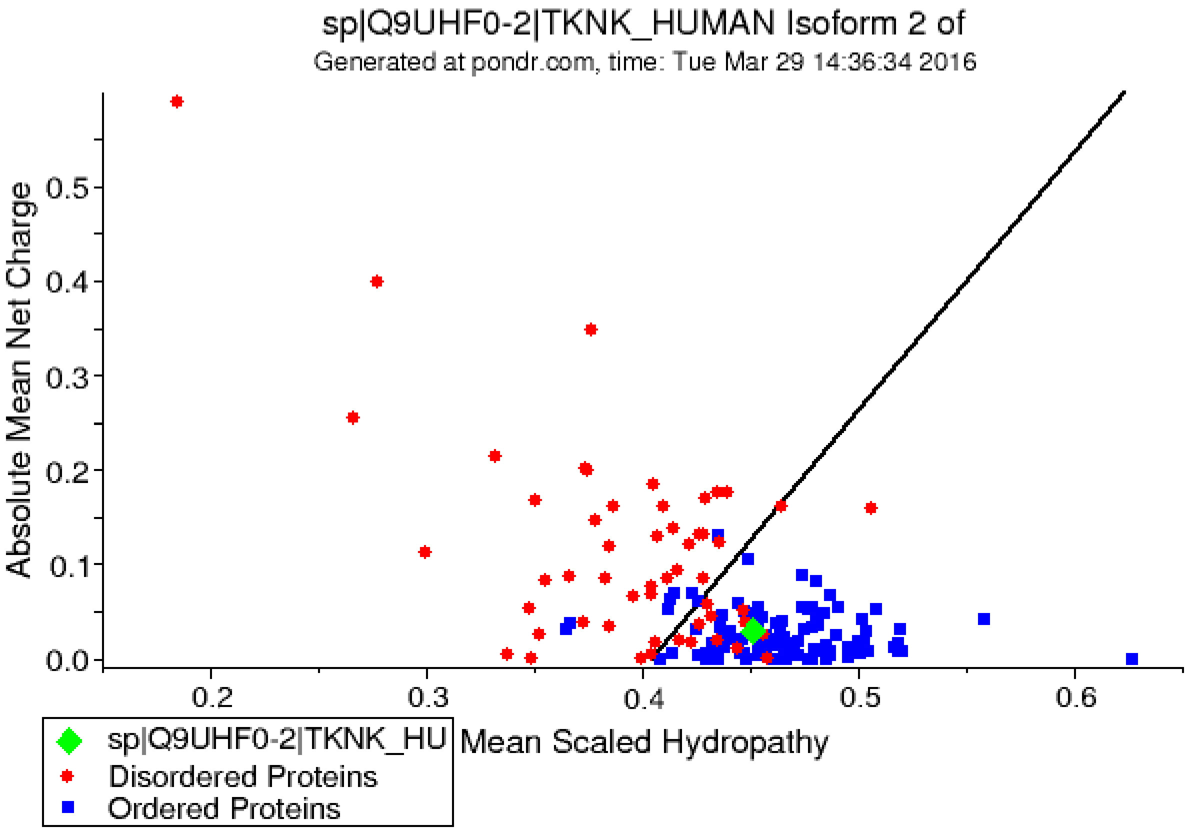
PONDR Score
PONDR VL-XT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Mean Scaled Hydropathy
sp|Q9UHF0-2|TKNK_HU
Disordered Proteins
Ordered Proteins

```
========================VLXT NNP STATISTICS================================
Predicted residues: 135                       Number Disordered Regions: 4
Number residues disordered: 72        Longest Disordered Region: 25
Overall percent disordered: 53.33     Average Prediction Score: 0.5047
Predicted disorder segment [22]-[46]  Average Strength= 0.7186
Predicted disorder segment [65]-[82]  Average Strength= 0.7209
Predicted disorder segment [102]-[106]Average Strength= 0.5423
Predicted disorder segment [113]-[135]Average Strength= 0.8469

=========================VL3 NNP STATISTICS================================
Predicted residues: 135                       Number Disordered Regions: 1
Number residues disordered: 102               Longest Disordered Region: 102
Overall percent disordered: 75.56     Average Prediction Score: 0.6956
Predicted disorder segment [34]-[135] Average Strength= 0.8251

=========================VSL2 NNP STATISTICS================================
Predicted residues: 135                       Number Disordered Regions: 1
Number residues disordered: 110               Longest Disordered Region: 110
Overall percent disordered: 81.48     Average Prediction Score: 0.7164
Predicted disorder segment [26]-[135] Average Strength= 0.8317
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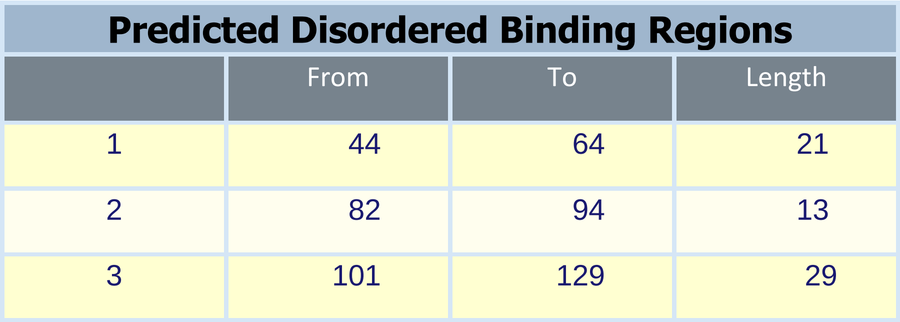
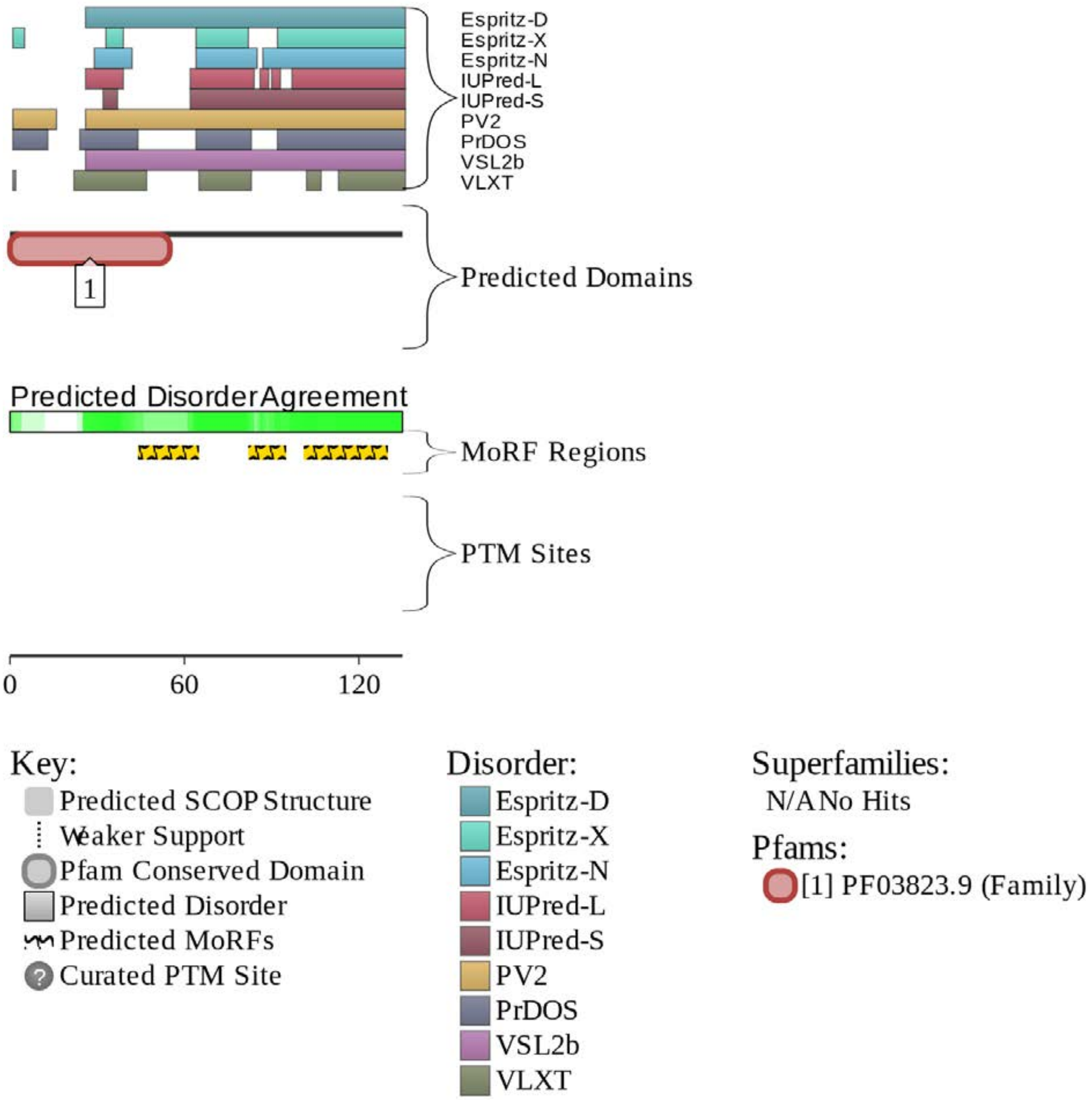


Predicted Disordered Binding Regions

	From	To	Length
1	44	64	21
2	82	94	13
3	101	129	29

ENSP00000408131, ENSP00000377445, ENSP00000350236



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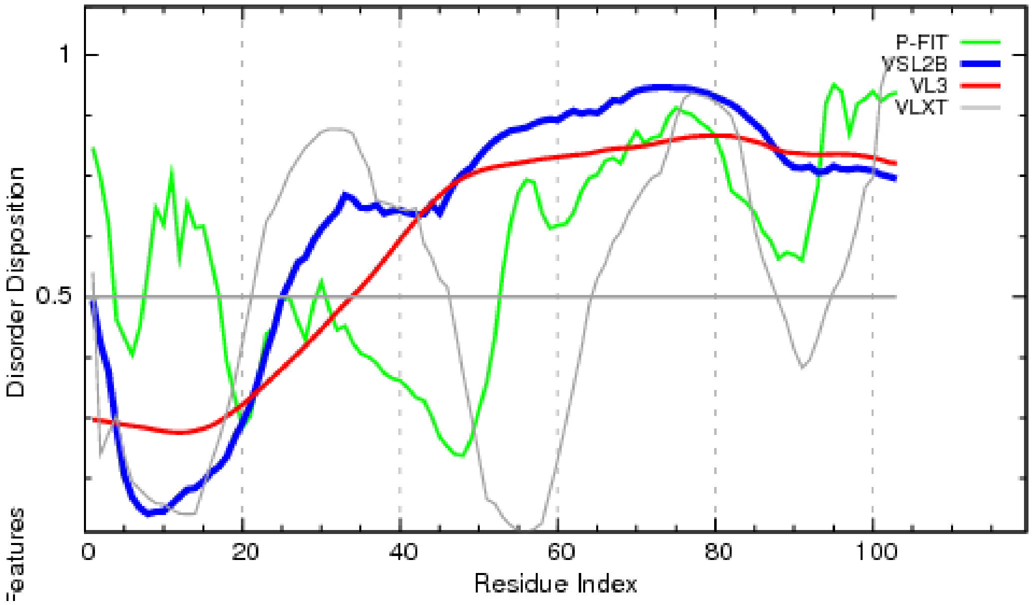

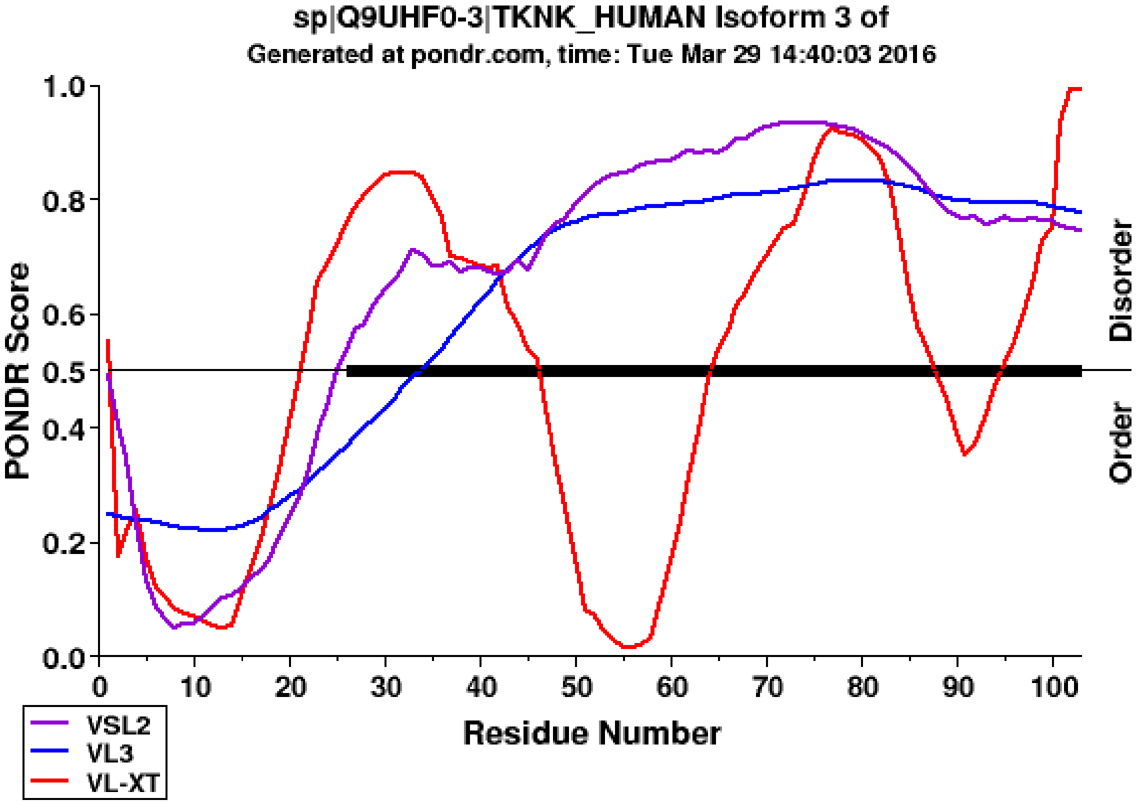
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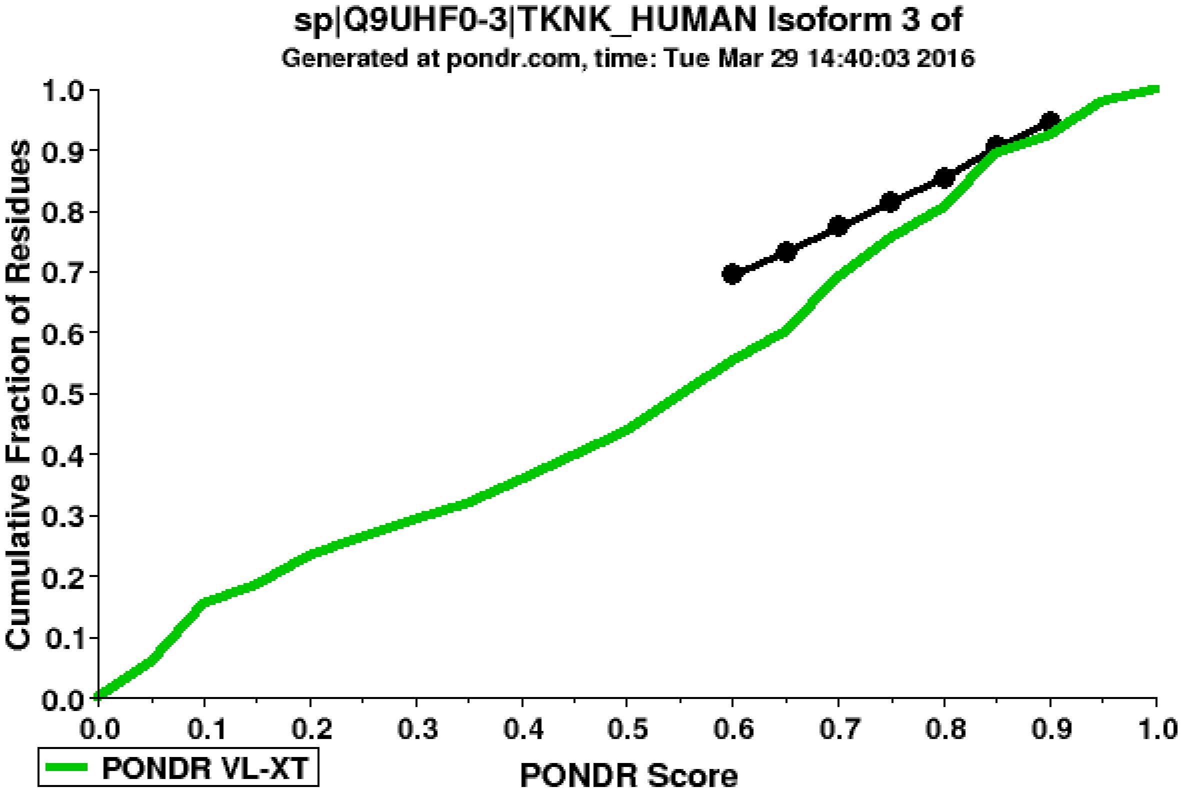
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Cumulative Fraction of Residues
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0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
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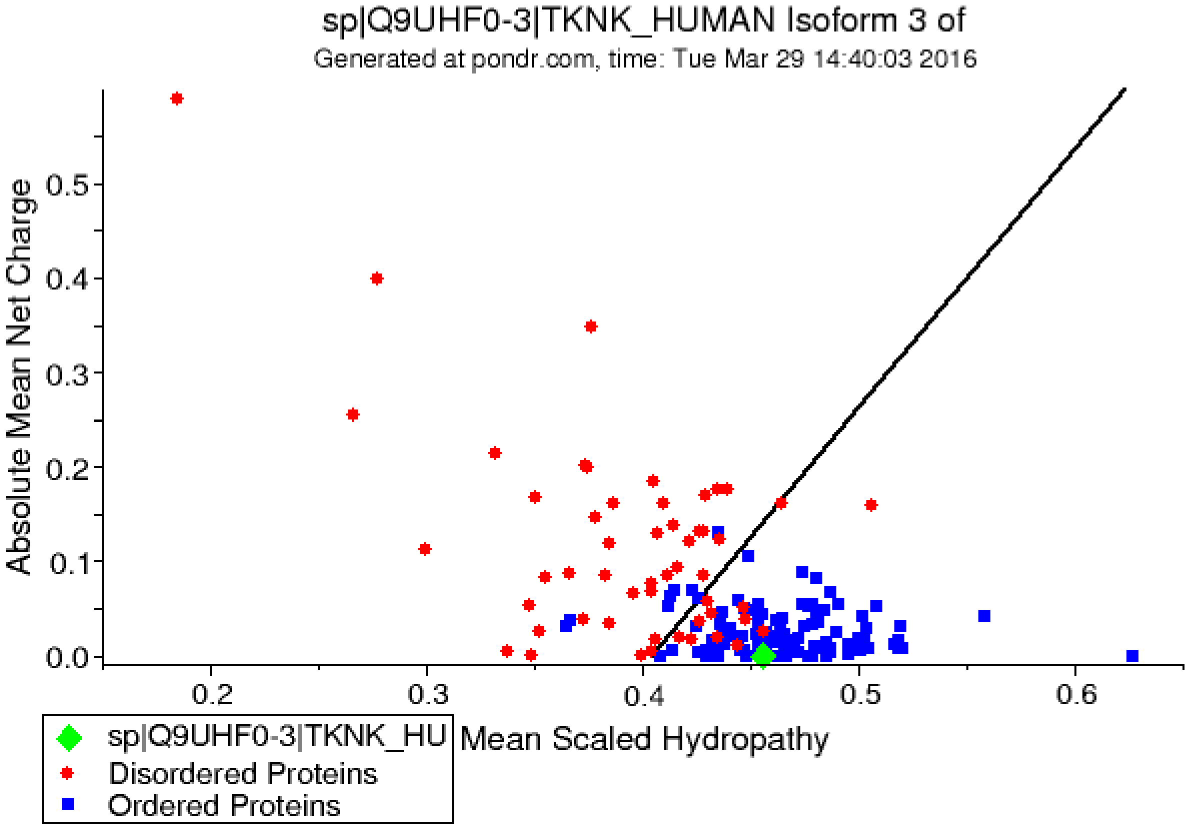
0.5
0.6
0.7
0.8
0.9
1.0
PONDR VL-XT
PONDR Score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0.2
0.3
0.4
0.5
0.6
Mean Scaled Hydropathy
sp|Q9UHF0-3|TKNK_HU
Disordered Proteins
Ordered Proteins

```
========================VLXT NNP STATISTICS================================
Predicted residues: 103                              Number Disordered Regions: 3
Number residues disordered: 58        Longest Disordered Region: 25
Overall percent disordered: 56.31     Average Prediction Score: 0.5054
Predicted disorder segment [22]-[46]  Average Strength= 0.7186
Predicted disorder segment [65]-[87]  Average Strength= 0.7512
Predicted disorder segment [95]-[103] Average Strength= 0.7425

=========================VL3 NNP STATISTICS================================
Predicted residues: 103                              Number Disordered Regions: 1
Number residues disordered: 70        Longest Disordered Region: 70
Overall percent disordered: 67.96     Average Prediction Score: 0.6139
Predicted disorder segment [34]-[103] Average Strength= 0.7641

========================VSL2 NNP STATISTICS================================
Predicted residues: 103                              Number Disordered Regions: 1
Number residues disordered: 78        Longest Disordered Region: 78
Overall percent disordered: 75.73     Average Prediction Score: 0.6519
Predicted disorder segment [26]-[103] Average Strength= 0.7938
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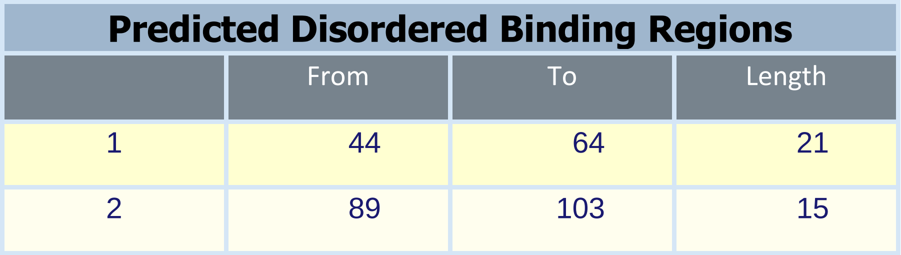

Predicted Disordered Binding Regions

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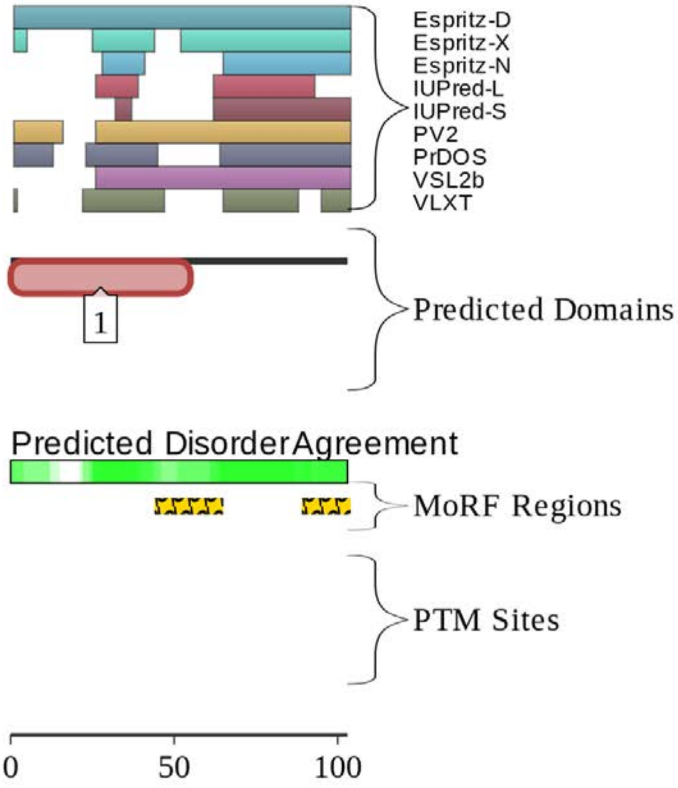
ENSP00000416292, ENSP00000408208, ENSP00000368721



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- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:
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- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:
N/A No Hits

Pfams:
[1] PF03823.9 (Family)

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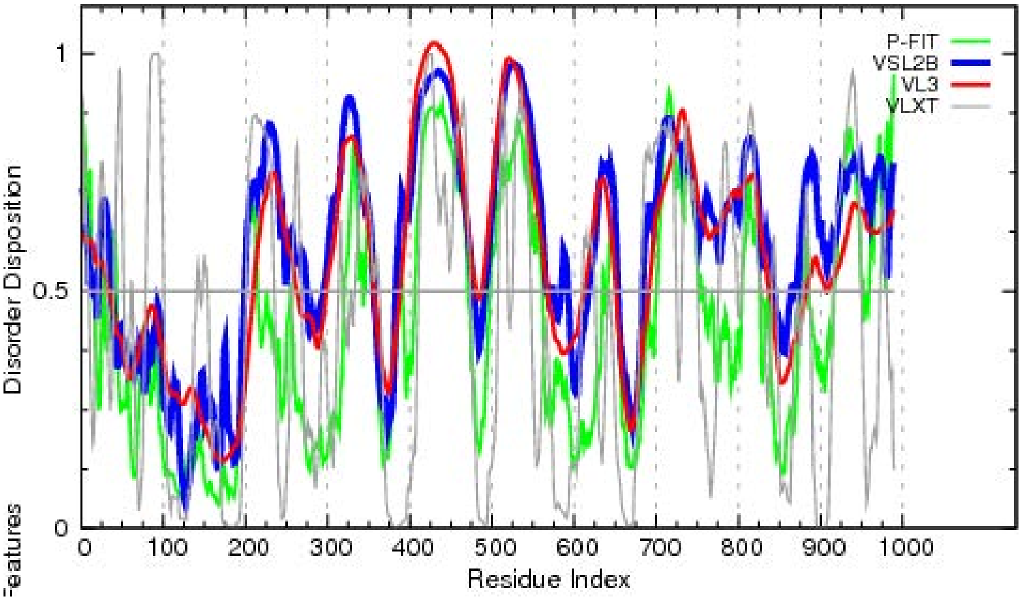

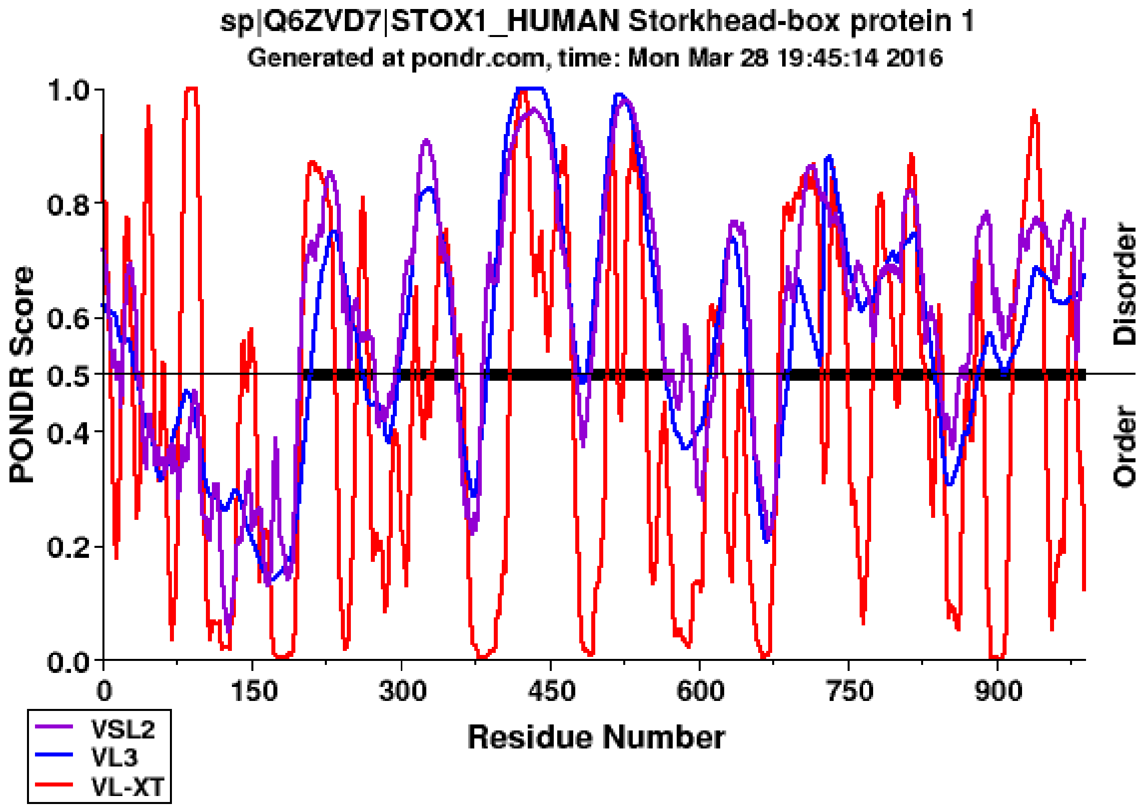
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Generated at pondr.com, time: Mon Mar 28 19:45:14 2016
PONDR Score
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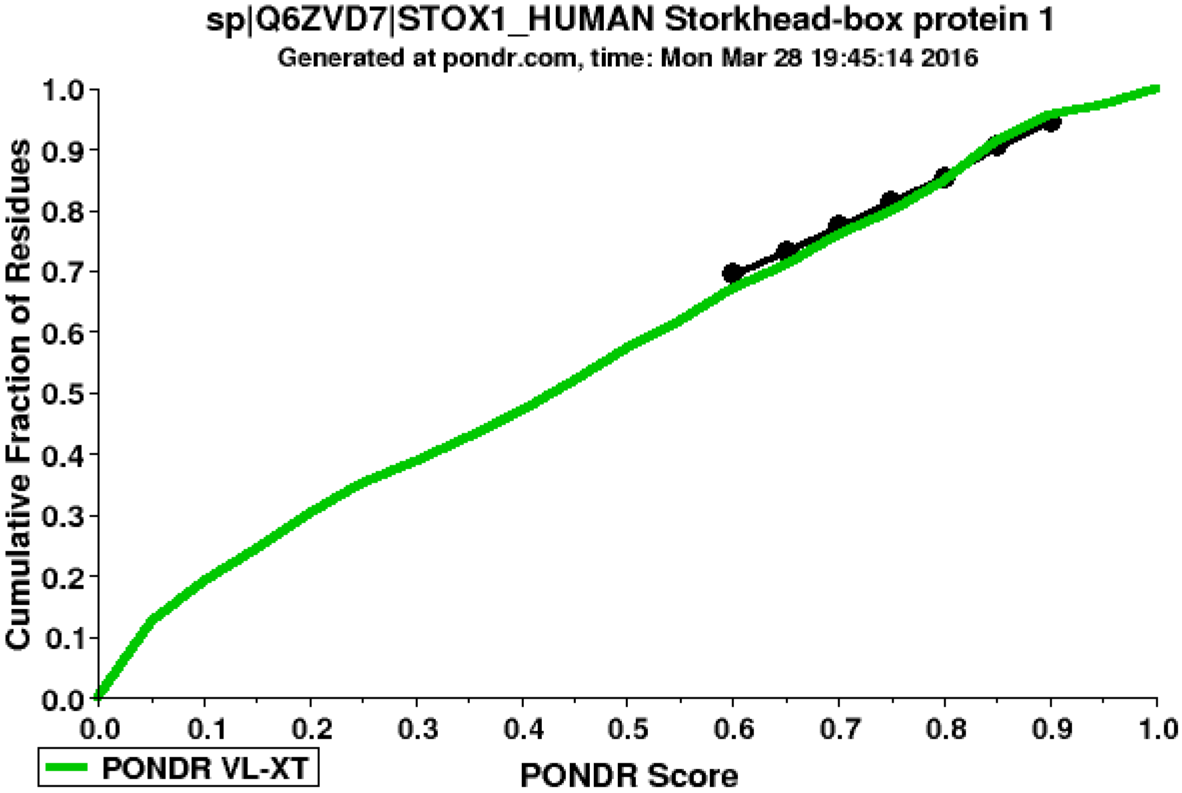
0.8
0.6
0.5
0.4
0.2
0.0
0
150
300
450
600
750
900
Residue Number
Disorder
Order
VSL2
VL3
VL-XT


sp|Q6ZVD7|STOX1_HUMAN Storkhead-box protein 1
Generated at pondr.com, time: Mon Mar 28 19:45:14 2016
Cumulative Fraction of Residues
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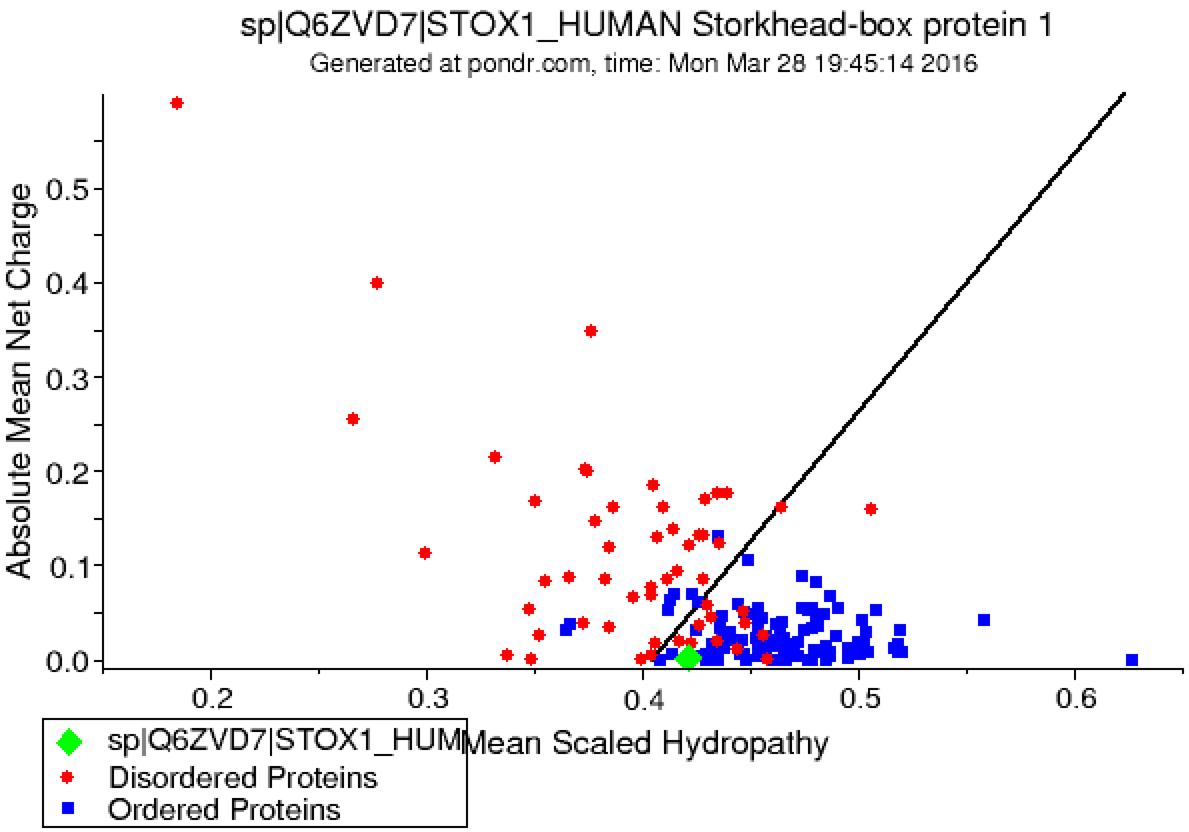
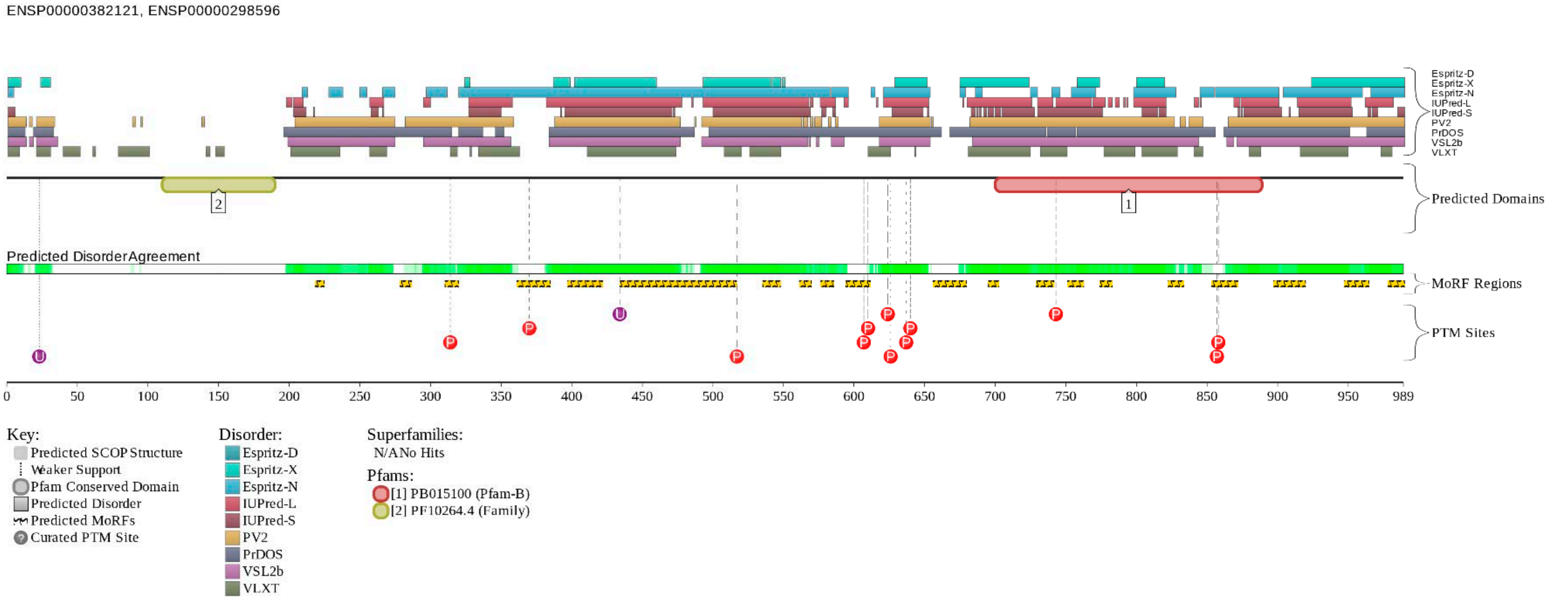
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT

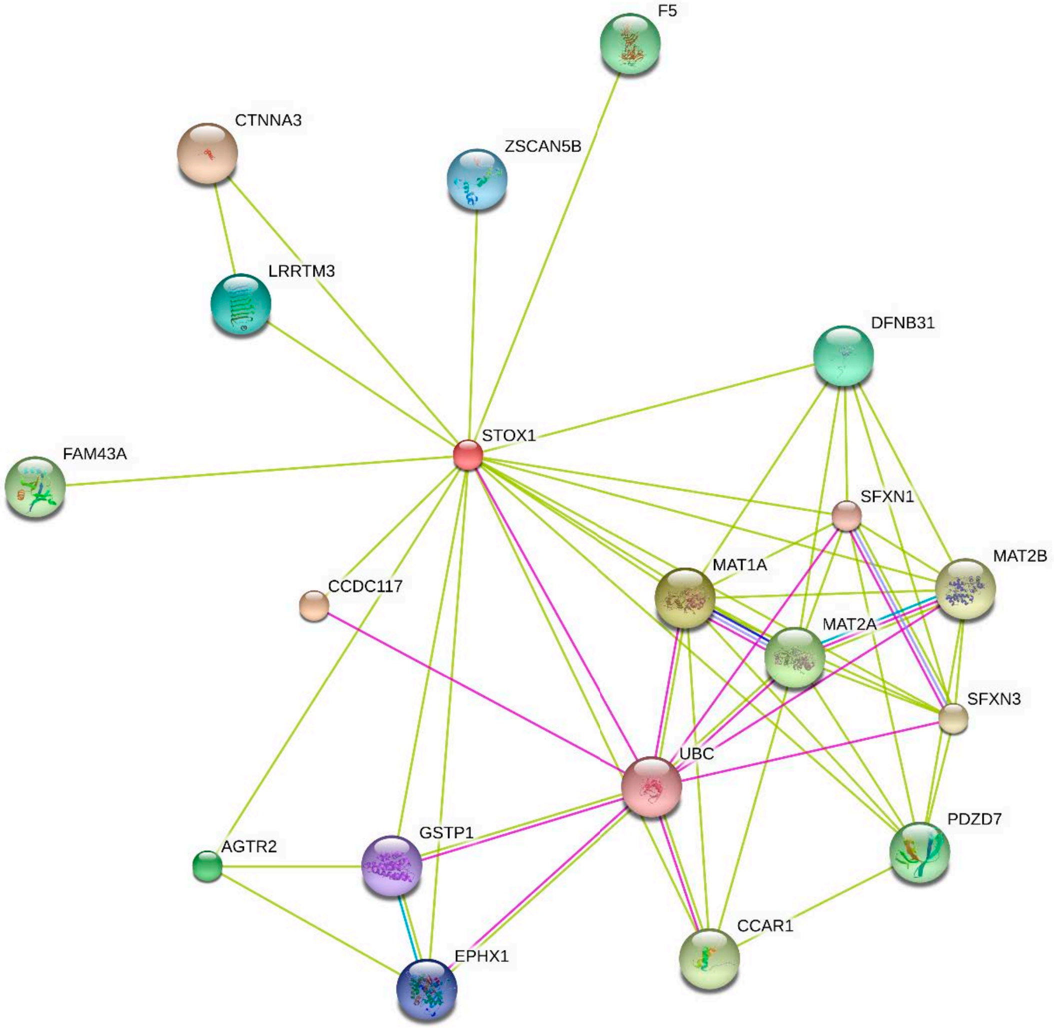


```
=======================VLXT NNP STATISTICS==============================
Predicted residues: 989                      Number Disordered Regions: 25
Number residues disordered: 425              Longest Disordered Region: 63
Overall percent disordered: 42.97     Average Prediction Score: 0.4333
Predicted disorder segment [1]-[8]    Average Strength= 0.6936
Predicted disorder segment [21]-[30]  Average Strength= 0.6799
Predicted disorder segment [40]-[51]  Average Strength= 0.7656
Predicted disorder segment [61]-[62]  Average Strength= 0.5173
Predicted disorder segment [79]-[100] Average Strength= 0.8839
Predicted disorder segment [141]-[143]Average Strength= 0.5462
Predicted disorder segment [148]-[153]Average Strength= 0.5508
Predicted disorder segment [201]-[235]Average Strength= 0.7895
Predicted disorder segment [257]-[268]Average Strength= 0.6718
Predicted disorder segment [314]-[318]Average Strength= 0.5804
Predicted disorder segment [328]-[328]Average Strength= 0.5022
Predicted disorder segment [334]-[362]Average Strength= 0.6395
Predicted disorder segment [411]-[473]Average Strength= 0.7803
Predicted disorder segment [508]-[519]Average Strength= 0.7495
Predicted disorder segment [526]-[547]Average Strength= 0.7932
Predicted disorder segment [610]-[625]Average Strength= 0.5842
Predicted disorder segment [643]-[643]Average Strength= 0.5047
Predicted disorder segment [681]-[724]Average Strength= 0.7780
Predicted disorder segment [732]-[750]Average Strength= 0.7081
Predicted disorder segment [777]-[798]Average Strength= 0.6887
Predicted disorder segment [804]-[828]Average Strength= 0.7060
Predicted disorder segment [841]-[846]Average Strength= 0.5619
Predicted disorder segment [880]-[887]Average Strength= 0.6230
Predicted disorder segment [916]-[949]Average Strength= 0.7803
Predicted disorder segment [973]-[980]Average Strength= 0.6185
```

```
========================VL3 NNP STATISTICS=================================
Predicted residues: 989                           Number Disordered Regions: 9
Number residues disordered: 605                   Longest Disordered Region: 146
Overall percent disordered: 61.17        Average Prediction Score: 0.5619
Predicted disorder segment [1]-[33]      Average Strength= 0.5750
Predicted disorder segment [210]-[262]Average Strength= 0.6447
Predicted disorder segment [299]-[356]Average Strength= 0.7034
Predicted disorder segment [389]-[480]Average Strength= 0.8444
Predicted disorder segment [488]-[567]Average Strength= 0.7902
Predicted disorder segment [613]-[650]Average Strength= 0.6428
Predicted disorder segment [692]-[837]Average Strength= 0.6719
Predicted disorder segment [883]-[906]Average Strength= 0.5376
Predicted disorder segment [909]-[989]Average Strength= 0.6194

=======================VSL2 NNP STATISTICS=================================
Predicted residues: 989                           Number Disordered Regions: 14
Number residues disordered: 669                   Longest Disordered Region: 160
Overall percent disordered: 67.64        Average Prediction Score: 0.5942
Predicted disorder segment [1]-[13]      Average Strength= 0.6147
Predicted disorder segment [16]-[18]     Average Strength= 0.5073
Predicted disorder segment [21]-[35]     Average Strength= 0.6320
Predicted disorder segment [199]-[274]Average Strength= 0.6760
Predicted disorder segment [295]-[356]Average Strength= 0.7321
Predicted disorder segment [384]-[476]Average Strength= 0.8129
Predicted disorder segment [492]-[566]Average Strength= 0.8155
Predicted disorder segment [568]-[568]Average Strength= 0.5036
Predicted disorder segment [573]-[574]Average Strength= 0.5065
Predicted disorder segment [584]-[592]Average Strength= 0.5454
Predicted disorder segment [618]-[653]Average Strength= 0.6754
Predicted disorder segment [684]-[843]Average Strength= 0.7035
Predicted disorder segment [864]-[868]Average Strength= 0.5050
Predicted disorder segment [871]-[989]Average Strength= 0.6919
```

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ZSCAN5B
LRRTM3
DFNB31
STOX1
FAM43A
SFXN1
MAT1A
MAT2B
CCDC117
MAT2A
SFXN3
UBC
PDZD7
AGTR2
GSTP1
CCAR1
EPHX1

Predicted Disordered Binding Regions

	From	To	Length
1	218	224	7
2	278	286	9
3	310	319	10
4	361	384	24
5	397	421	25
6	434	516	83
7	535	547	13
8	561	569	9
9	576	585	10
10	594	611	18
11	656	679	24
12	695	702	8
13	729	741	13
14	751	762	12
15	774	782	9
16	822	833	12
17	853	871	19
18	897	919	23
19	947	964	18
20	978	989	12

>sp|Q6ZVD7-2|STOX1_HUMAN Isoform B of Storkhead-box protein 1 OS=Homo sapiens GN=STOX1
MARPVQLAPGSLALVLCRLEAQKAAGAAEEPGGRAVFRAFRRANARCFWNARLARAASRL
AFQGWLRRGVLLVRAPPACLQVLRDAWRRRALRPPRGFRIRAVGDVFPVQMNPITQSQFV
PLGEVLCCAISDMNTAQIVVTQESLLERLMKHYPGIAIPSEDILYTTLGTLIKERKIYHT
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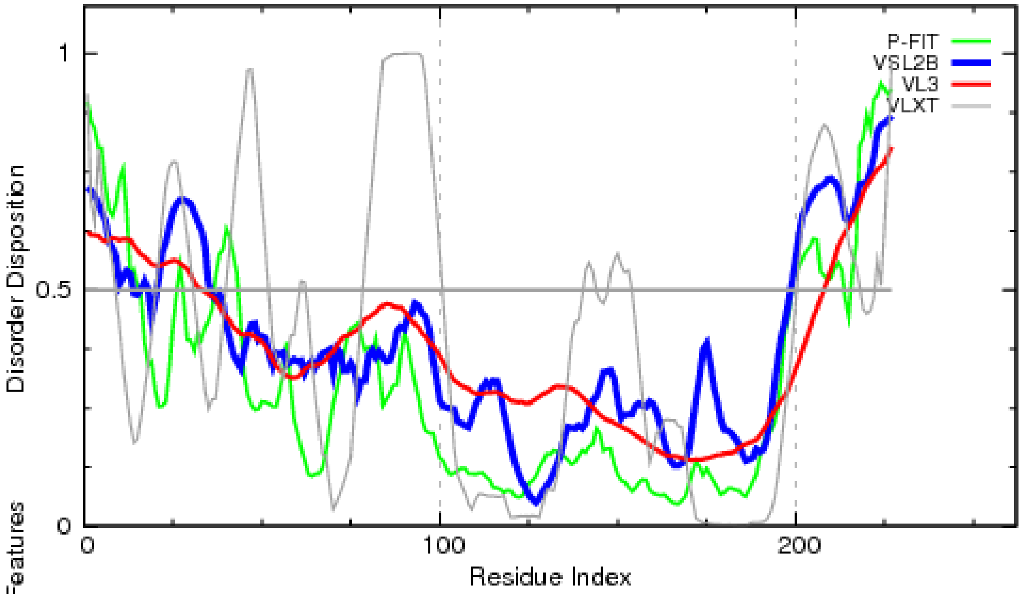

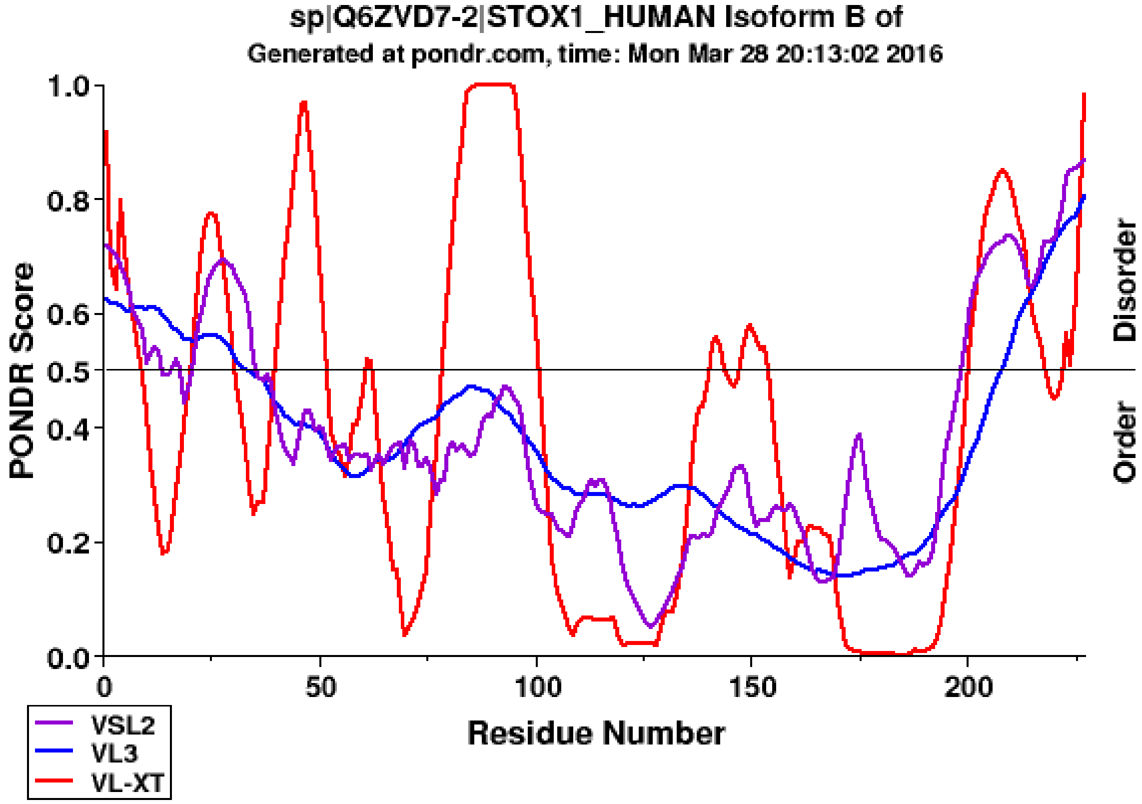

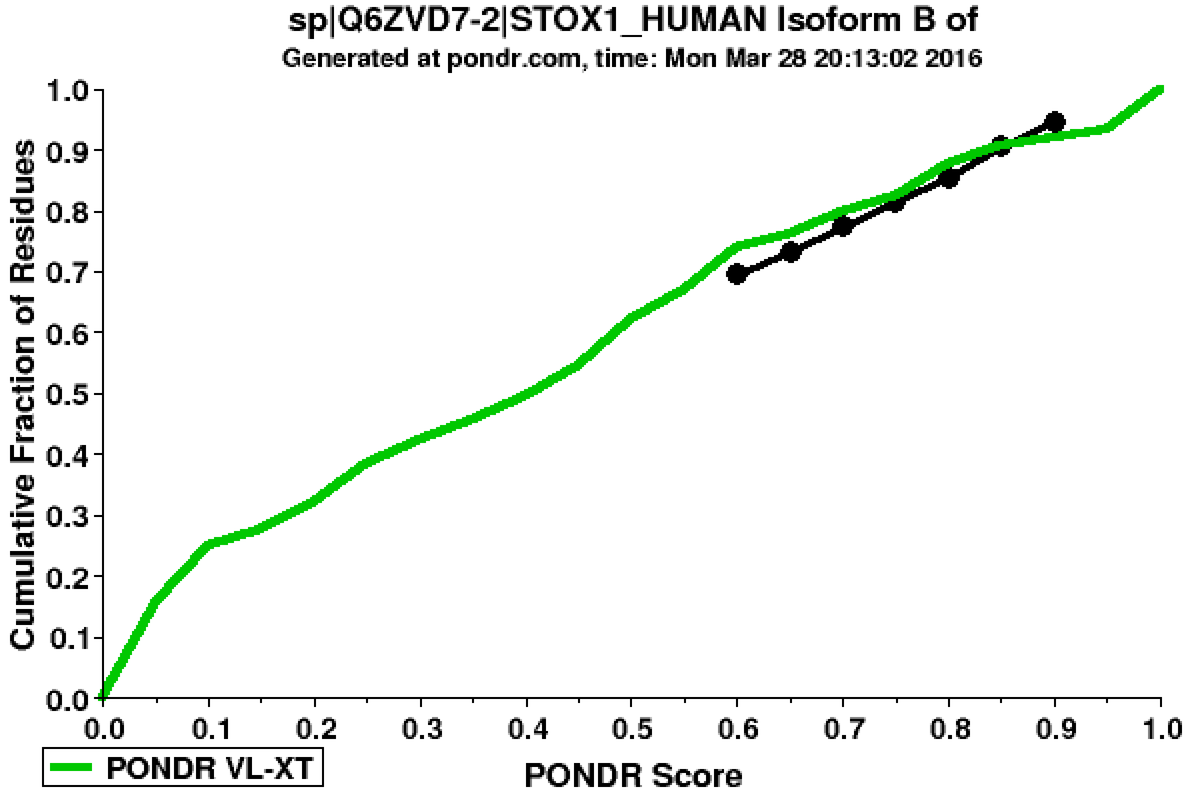

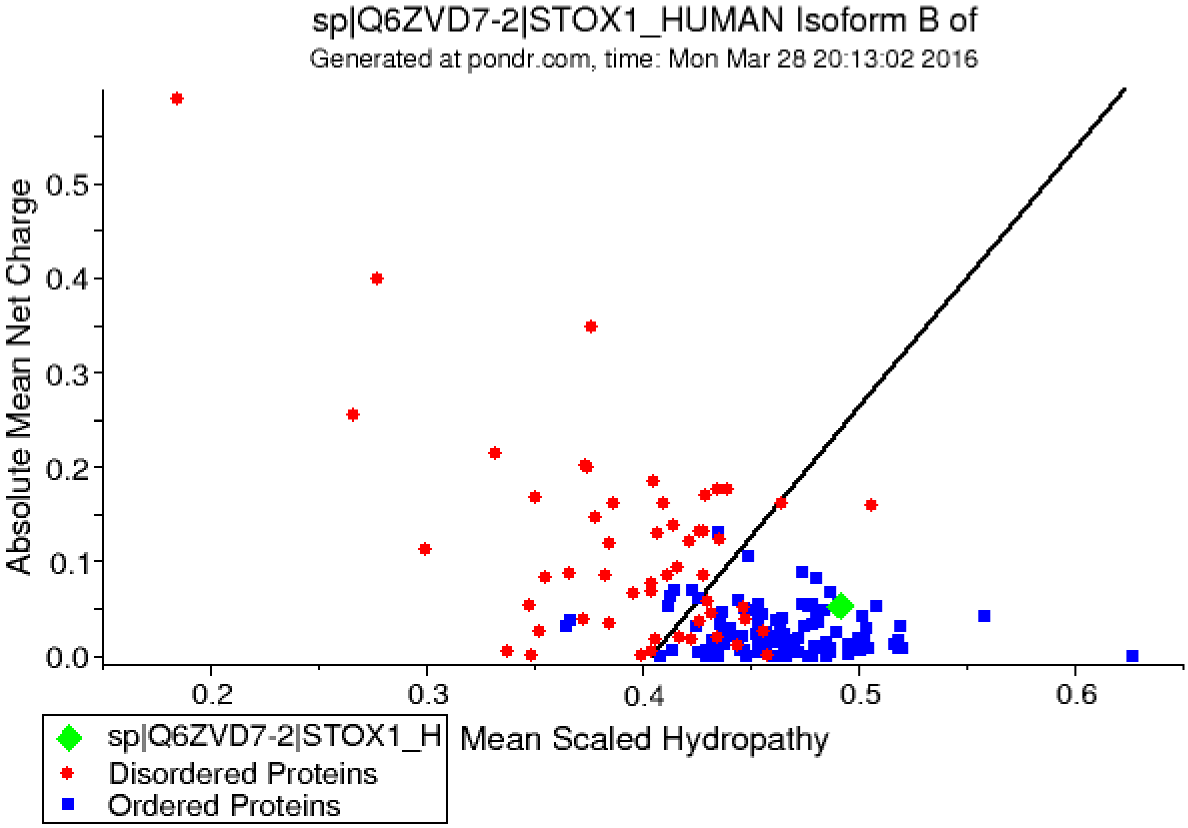

```
======================VLXT NNP STATISTICS===============================
Predicted residues: 227                          Number Disordered Regions: 9
Number residues disordered: 86           Longest Disordered Region: 22
```

```
Overall percent disordered: 37.89     Average Prediction Score: 0.4058
Predicted disorder segment [1]-[8]    Average Strength= 0.6936
Predicted disorder segment [21]-[30]  Average Strength= 0.6799
Predicted disorder segment [40]-[51]  Average Strength= 0.7656
Predicted disorder segment [61]-[62]  Average Strength= 0.5173
Predicted disorder segment [79]-[100] Average Strength= 0.8839
Predicted disorder segment [141]-[143]Average Strength= 0.5462
Predicted disorder segment [148]-[153]Average Strength= 0.5508
Predicted disorder segment [201]-[218]Average Strength= 0.7110
Predicted disorder segment [223]-[227]Average Strength= 0.6947

========================VL3 NNP STATISTICS================================
Predicted residues: 227                      Number Disordered Regions: 2
Number residues disordered: 53        Longest Disordered Region: 33
Overall percent disordered: 23.35     Average Prediction Score: 0.3758
Predicted disorder segment [1]-[33]   Average Strength= 0.5751
Predicted disorder segment [208]-[227]Average Strength= 0.6687

=======================VSL2 NNP STATISTICS================================
Predicted residues: 227                      Number Disordered Regions: 4
Number residues disordered: 60        Longest Disordered Region: 29
Overall percent disordered: 26.43     Average Prediction Score: 0.3872
Predicted disorder segment [1]-[13]   Average Strength= 0.6147
Predicted disorder segment [16]-[18]  Average Strength= 0.5073
Predicted disorder segment [21]-[35]  Average Strength= 0.6320
Predicted disorder segment [199]-[227]Average Strength= 0.7170
```

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AFQGWLRRGVLLVRAPPACLQVLRDAWRRRALRPPRGFRIRAVGDVFPVQMNPITQSQFV
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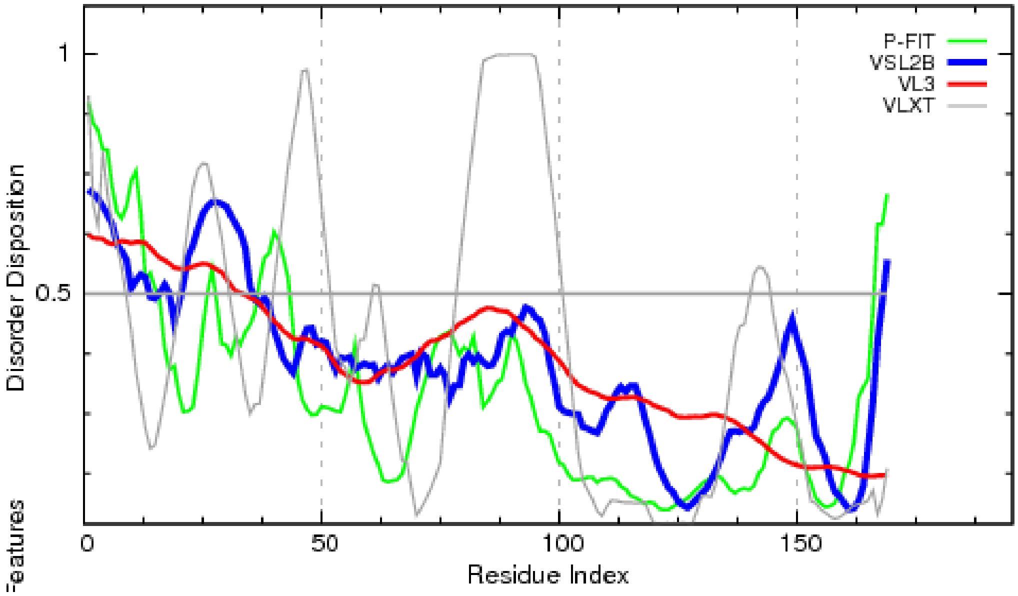

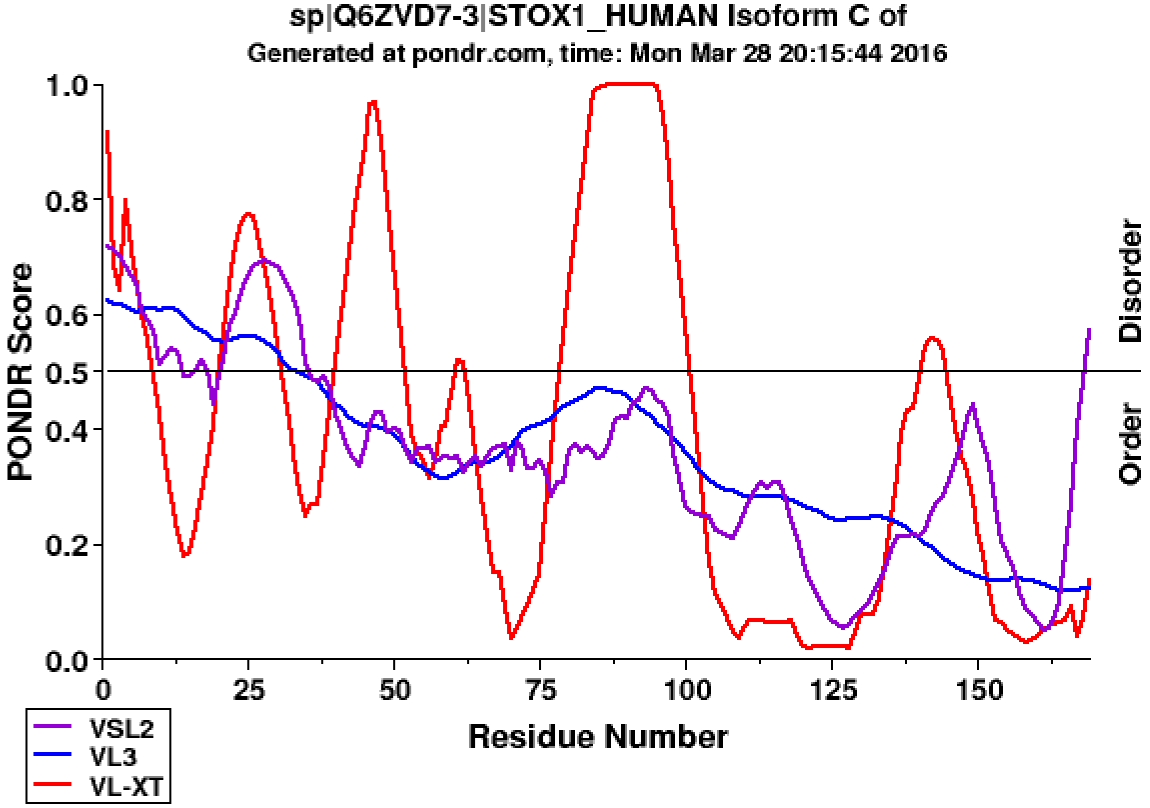

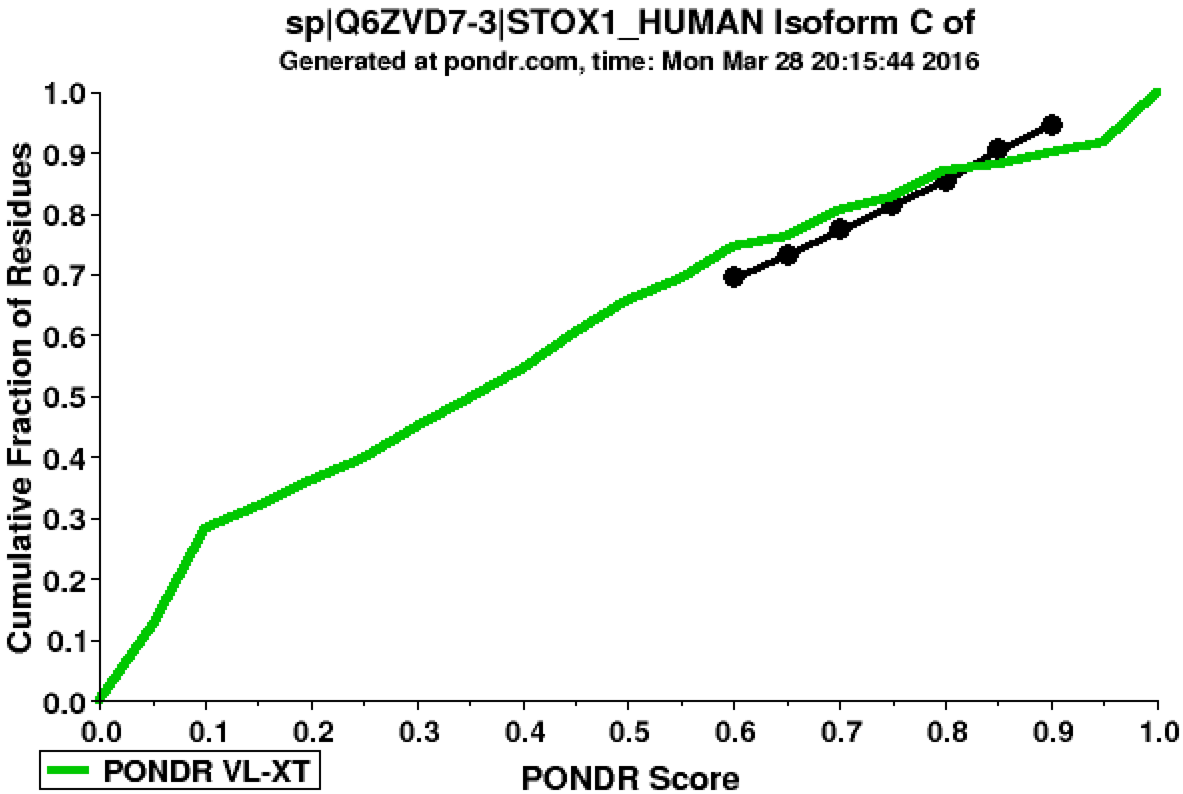

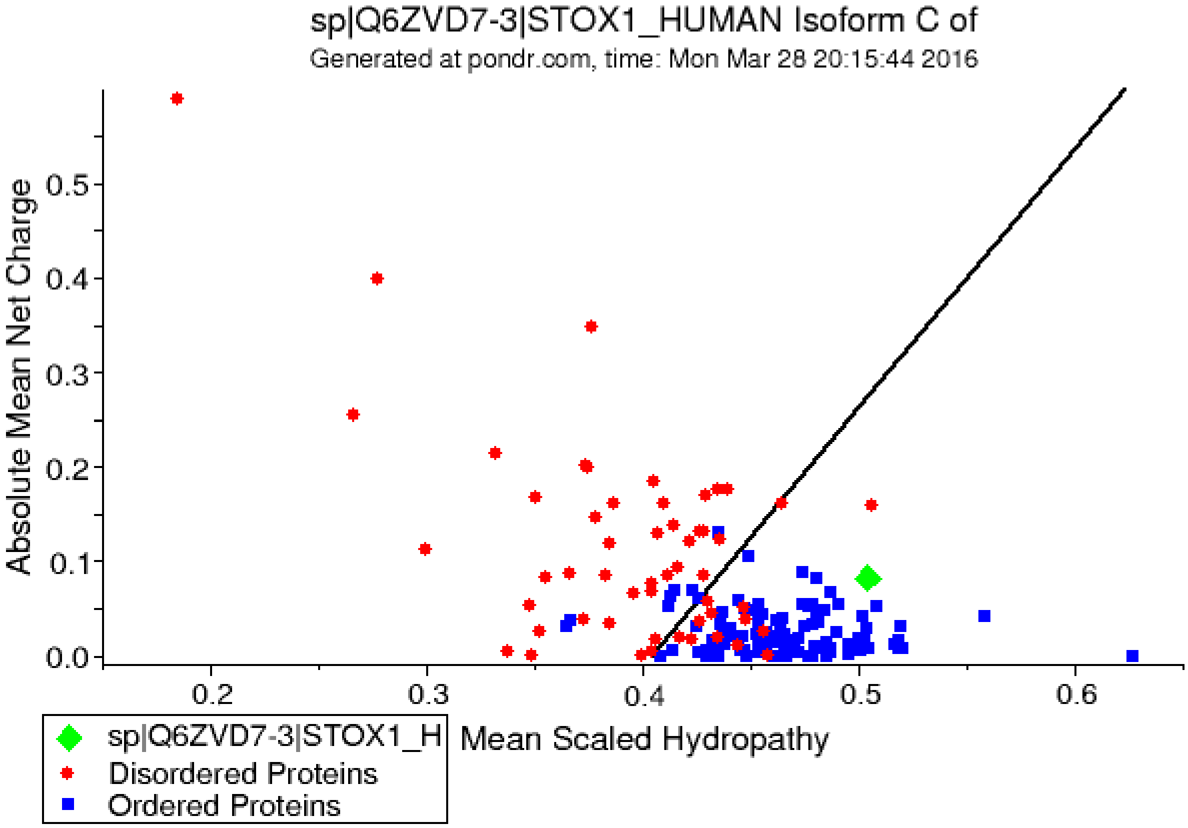

```
======================VLXT NNP STATISTICS===============================
Predicted residues: 169                           Number Disordered Regions: 6
Number residues disordered: 58            Longest Disordered Region: 22
```

```
Overall percent disordered: 34.32     Average Prediction Score: 0.3942
Predicted disorder segment [1]-[8]    Average Strength= 0.6936
Predicted disorder segment [21]-[30]  Average Strength= 0.6799
Predicted disorder segment [40]-[51]  Average Strength= 0.7656
Predicted disorder segment [61]-[62]  Average Strength= 0.5173
Predicted disorder segment [79]-[100] Average Strength= 0.8839
Predicted disorder segment [141]-[144]Average Strength= 0.5461

========================VL3 NNP STATISTICS=================================
Predicted residues: 169                       Number Disordered Regions: 1
Number residues disordered: 33        Longest Disordered Region: 33
Overall percent disordered: 19.53     Average Prediction Score: 0.3599
Predicted disorder segment [1]-[33]   Average Strength= 0.5751

=======================VSL2 NNP STATISTICS=================================
Predicted residues: 169                       Number Disordered Regions: 4
Number residues disordered: 32        Longest Disordered Region: 15
Overall percent disordered: 18.93     Average Prediction Score: 0.3575
Predicted disorder segment [1]-[13]   Average Strength= 0.6147
Predicted disorder segment [16]-[18]  Average Strength= 0.5073
Predicted disorder segment [21]-[35]  Average Strength= 0.6320
Predicted disorder segment [169]-[169]Average Strength= 0.5707
```

```
>sp|Q8IVI9|NOSTN_HUMAN Nostrin OS=Homo sapiens GN=NOSTRIN PE=1 SV=2
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QNTRKSCVSSAWAWASEGMKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVE
KTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKL
EKEDENYYQKNMAGYSTRLKWENTLENCYQSILELEKERIQLLCNNLNQYSQHISLFGQT
LTTCHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKS
LLKPKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLE
ANSYKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASS
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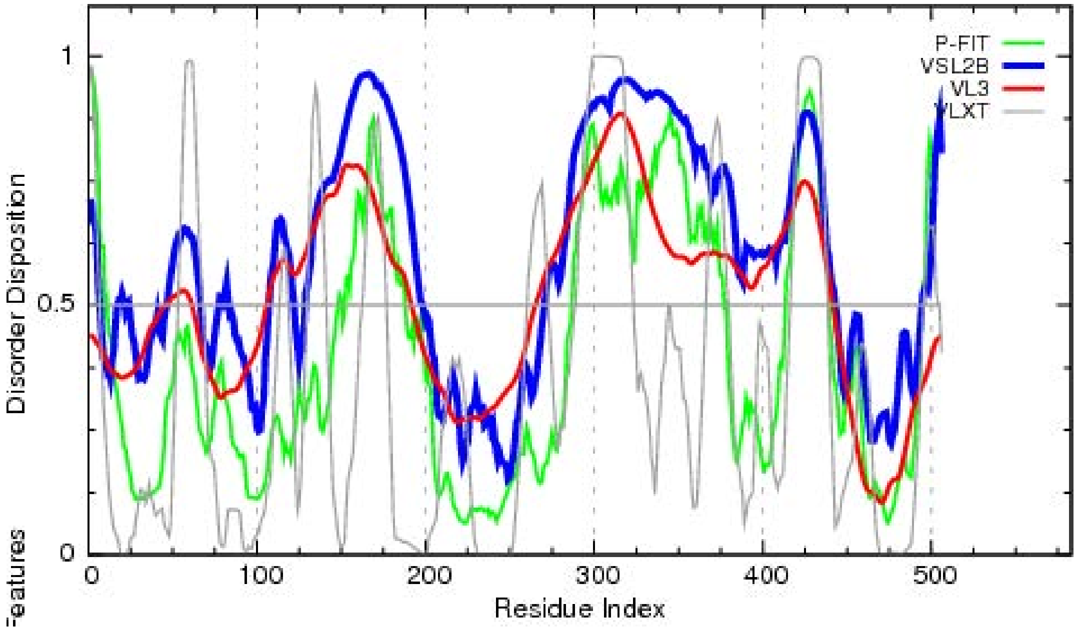
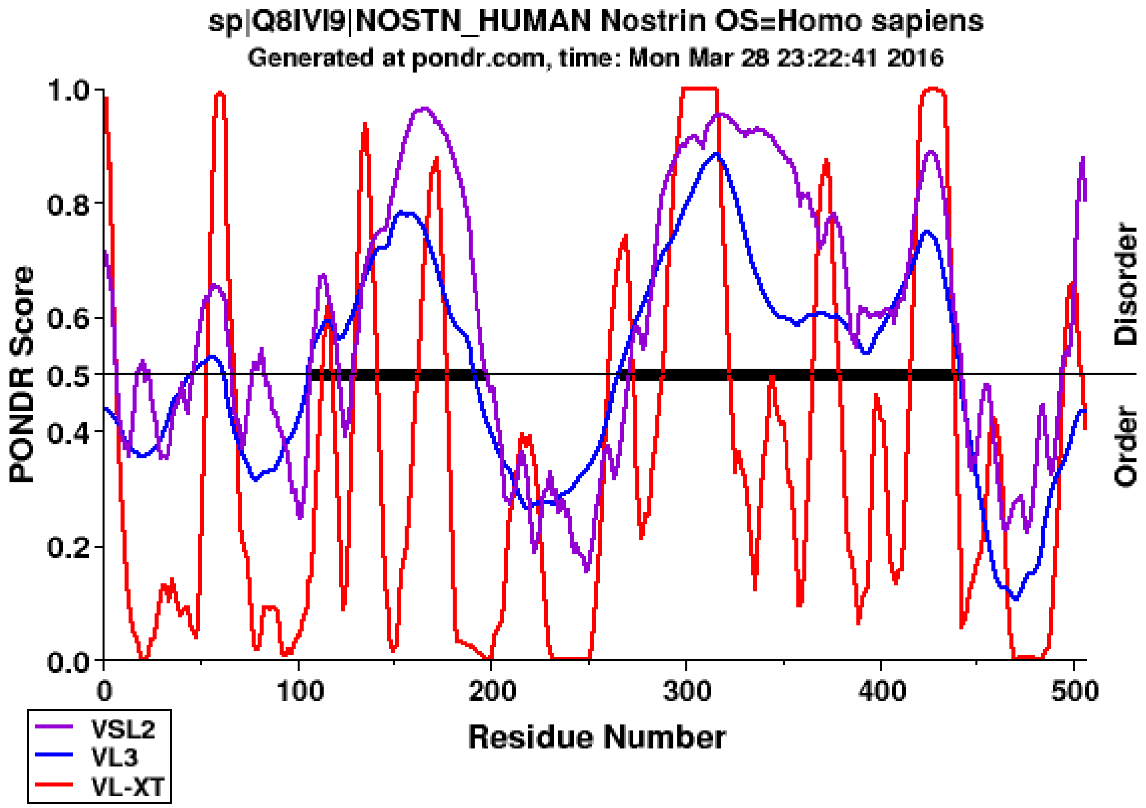
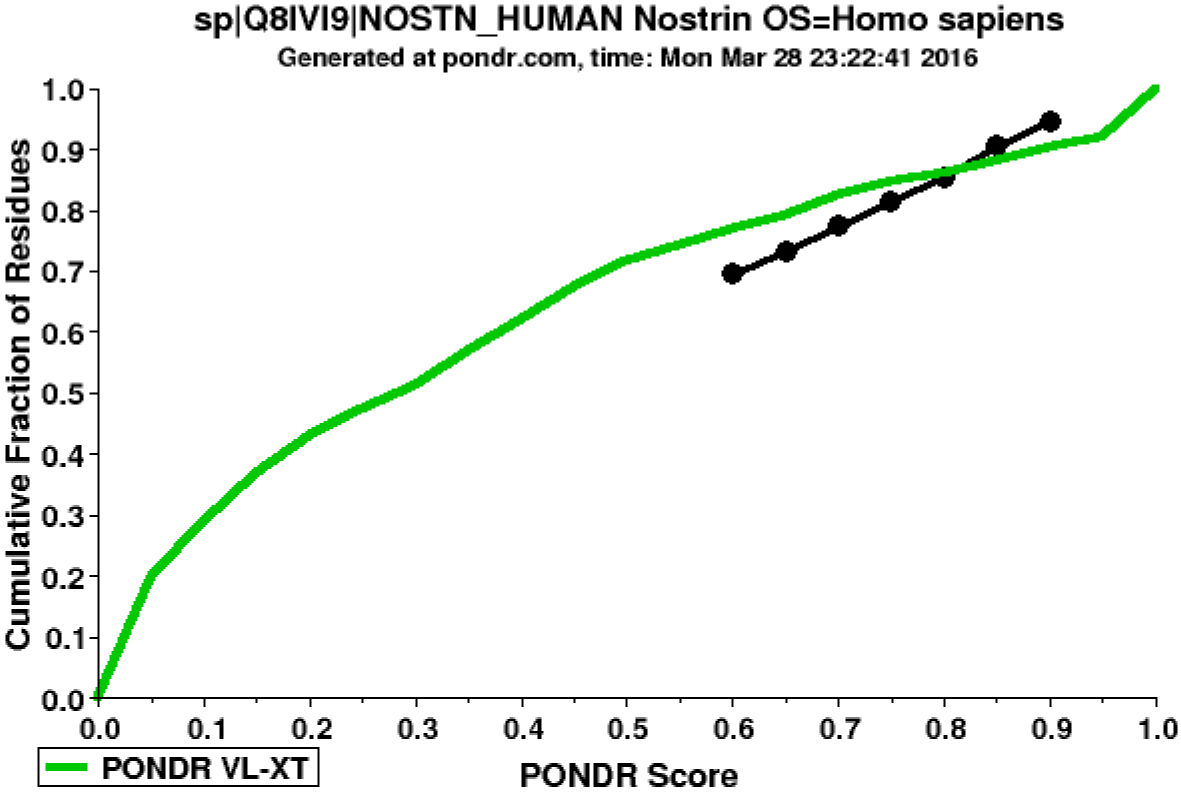
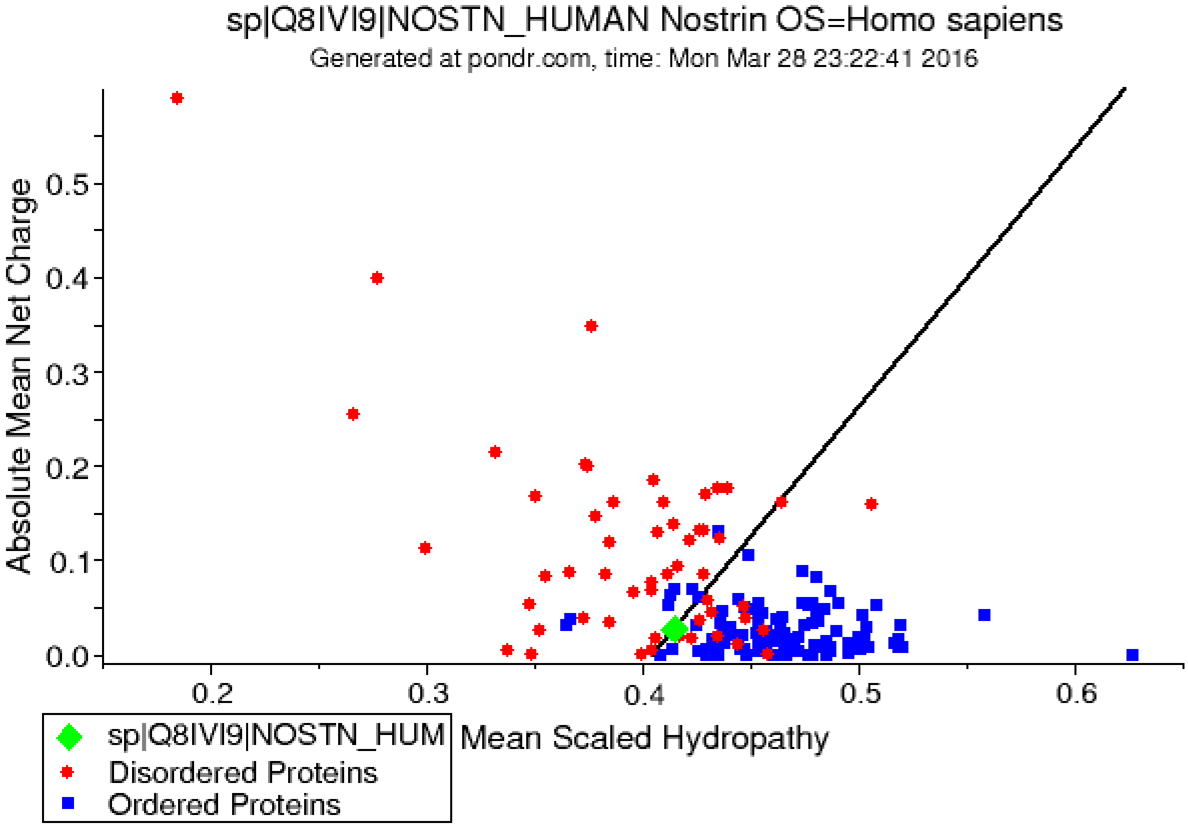


Predicted Disordered Binding Regions

	From	To	Length
1	354	371	18
2	400	413	14
3	439	449	11
4	475	480	6


sp|Q8IVI9|NOSTN_HUMAN Nostrin OS=Homo sapiens
Generated at pondr.com, time: Mon Mar 28 23:22:41 2016
PONDR Score
1.0
0.8
0.6
0.5
0.4
0.2
0.0
0
100
200
300
400
500
Residue Number
Disorder
Order
VSL2
VL3
VL-XT

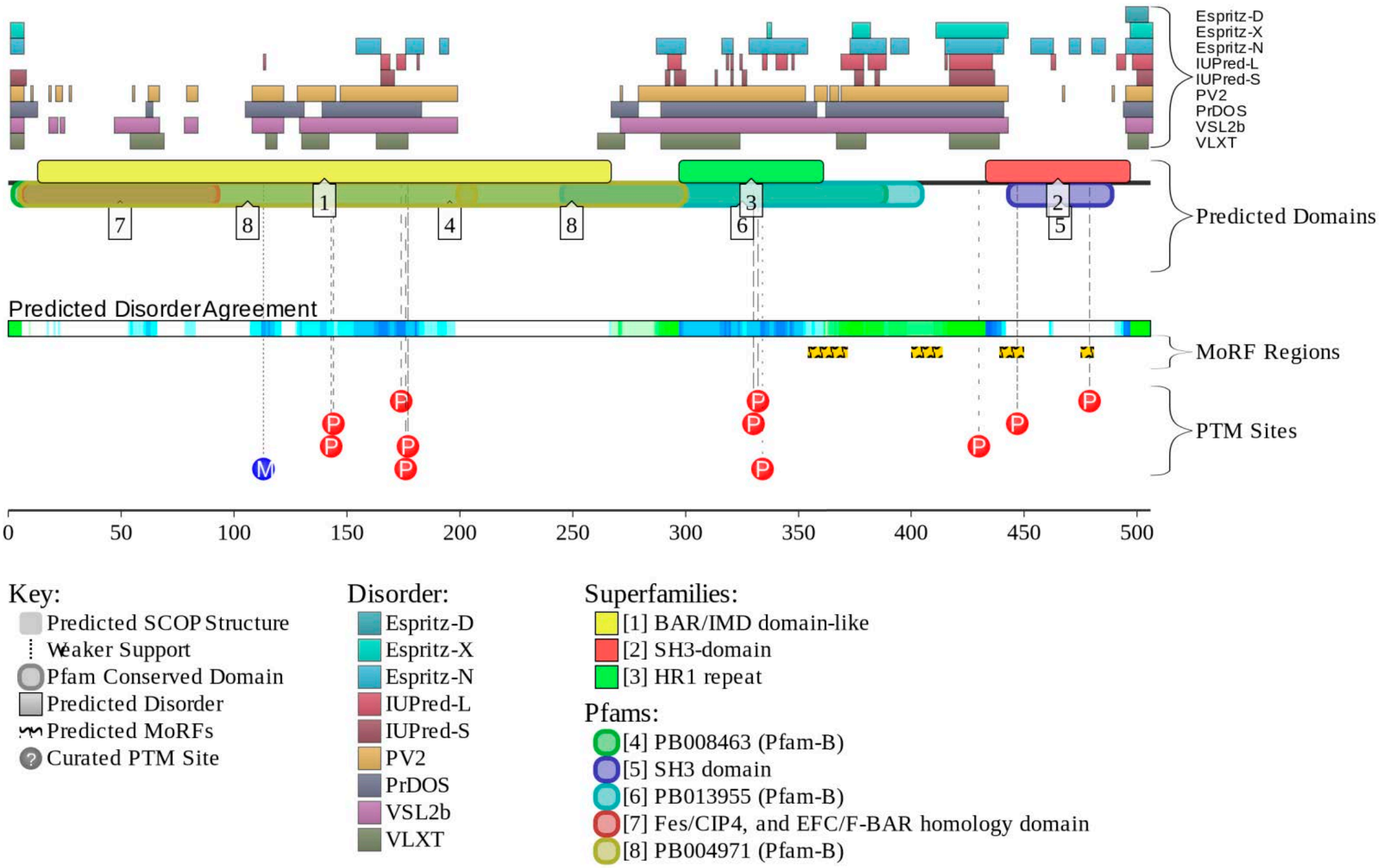

sp|Q8IVI9|NOSTN_HUMAN Nostrin OS=Homo sapiens
Generated at pondr.com, time: Mon Mar 28 23:22:41 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT

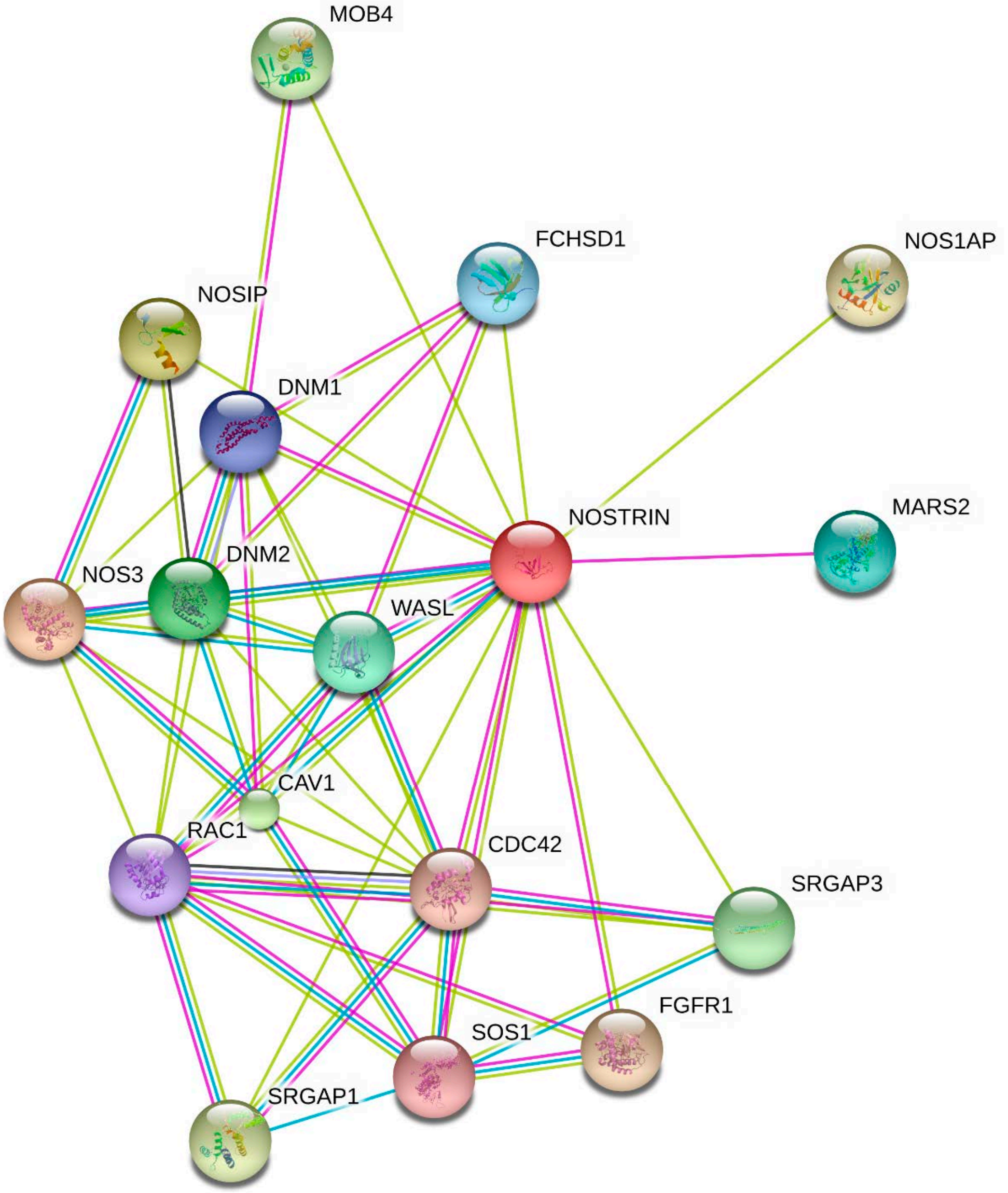


```
========================VLXT NNP STATISTICS================================
Predicted residues: 506                       Number Disordered Regions: 10
Number residues disordered: 143               Longest Disordered Region: 35
Overall percent disordered: 28.26     Average Prediction Score: 0.3538
Predicted disorder segment [1]-[6]    Average Strength= 0.8140
Predicted disorder segment [54]-[68]  Average Strength= 0.8015
Predicted disorder segment [114]-[118]Average Strength= 0.5809
Predicted disorder segment [130]-[141]Average Strength= 0.7541
Predicted disorder segment [163]-[176]Average Strength= 0.7369
Predicted disorder segment [261]-[272]Average Strength= 0.6603
Predicted disorder segment [289]-[323]Average Strength= 0.8849
Predicted disorder segment [367]-[379]Average Strength= 0.7344
Predicted disorder segment [417]-[438]Average Strength= 0.8901
Predicted disorder segment [496]-[504]Average Strength= 0.6027

========================VL3 NNP STATISTICS================================
Predicted residues: 506                       Number Disordered Regions: 3
Number residues disordered: 278               Longest Disordered Region: 176
Overall percent disordered: 54.94     Average Prediction Score: 0.5115
Predicted disorder segment [46]-[61]  Average Strength= 0.5182
Predicted disorder segment [106]-[191]Average Strength= 0.6524
Predicted disorder segment [266]-[441]Average Strength= 0.6661

=======================VSL2 NNP STATISTICS================================
Predicted residues: 506                       Number Disordered Regions: 9
Number residues disordered: 306               Longest Disordered Region: 172
Overall percent disordered: 60.47     Average Prediction Score: 0.5927
Predicted disorder segment [1]-[6]    Average Strength= 0.6523
Predicted disorder segment [18]-[21]  Average Strength= 0.5126
Predicted disorder segment [23]-[24]  Average Strength= 0.5030
Predicted disorder segment [47]-[66]  Average Strength= 0.6069
```

```
Predicted disorder segment [78]-[83]   Average Strength= 0.5211
Predicted disorder segment [108]-[121]Average Strength= 0.6143
Predicted disorder segment [129]-[198]Average Strength= 0.7992
Predicted disorder segment [271]-[442]Average Strength= 0.7788
Predicted disorder segment [495]-[506]Average Strength= 0.6783
```

ENSP00000318921




MOB4
FCHSD1
NOS1AP
NOSIP
DNM1
NOSTRIN
MARS2
DNM2
NOS3
WASL
CAV1
RAC1
CDC42
SRGAP3
FGFR1
SOS1
SRGAP1

```
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LGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKKKLMVSTKKHE
ALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENYYQKNMAGYSTRLKWENTLENC
YQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIEKDIQAVMEET
AILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASKDKEGLERMLK
TYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQPSHPCSNSIF
RWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQLSSRLCKALYS
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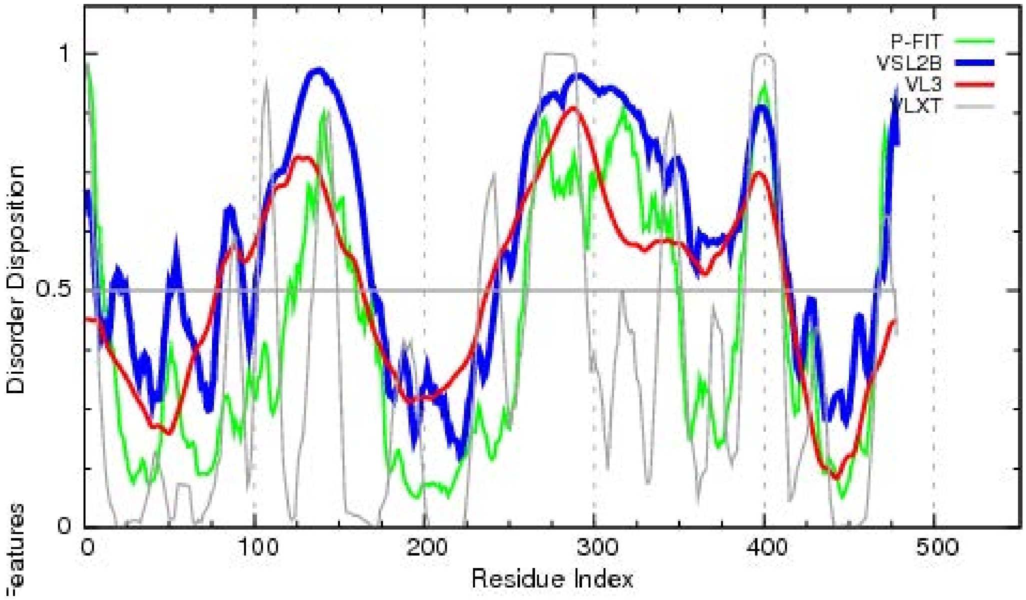
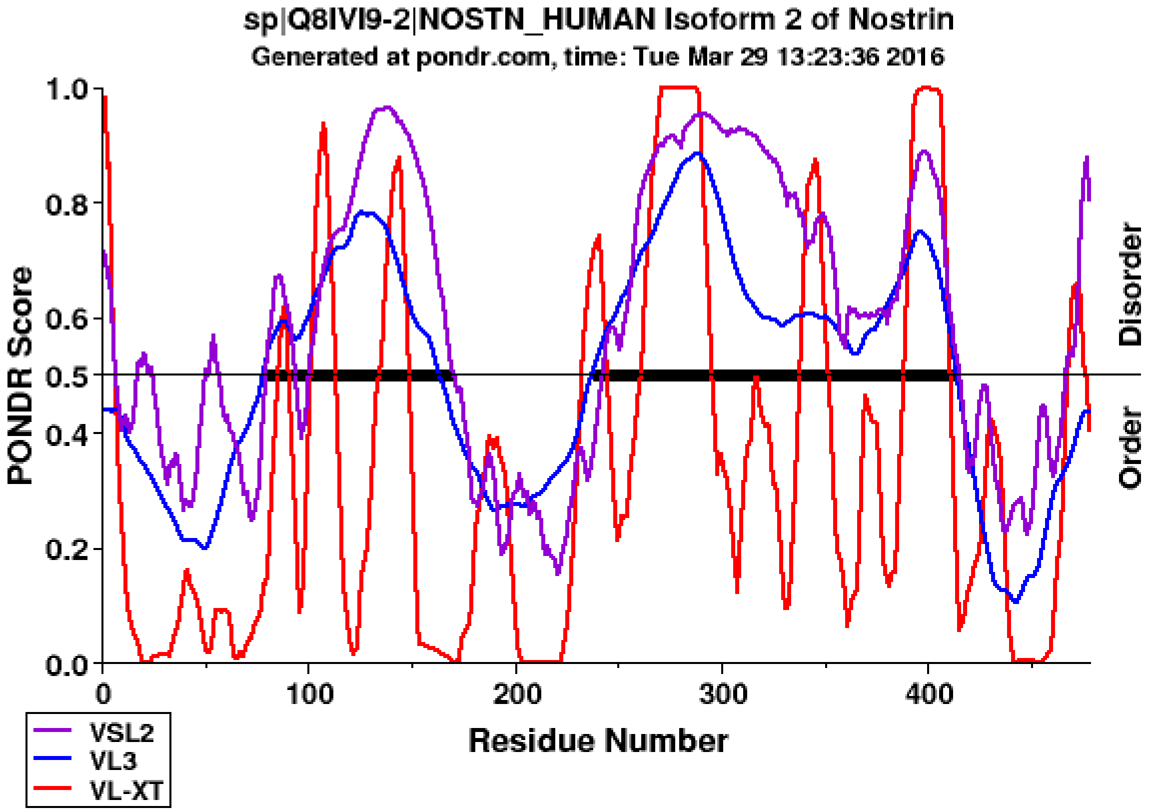
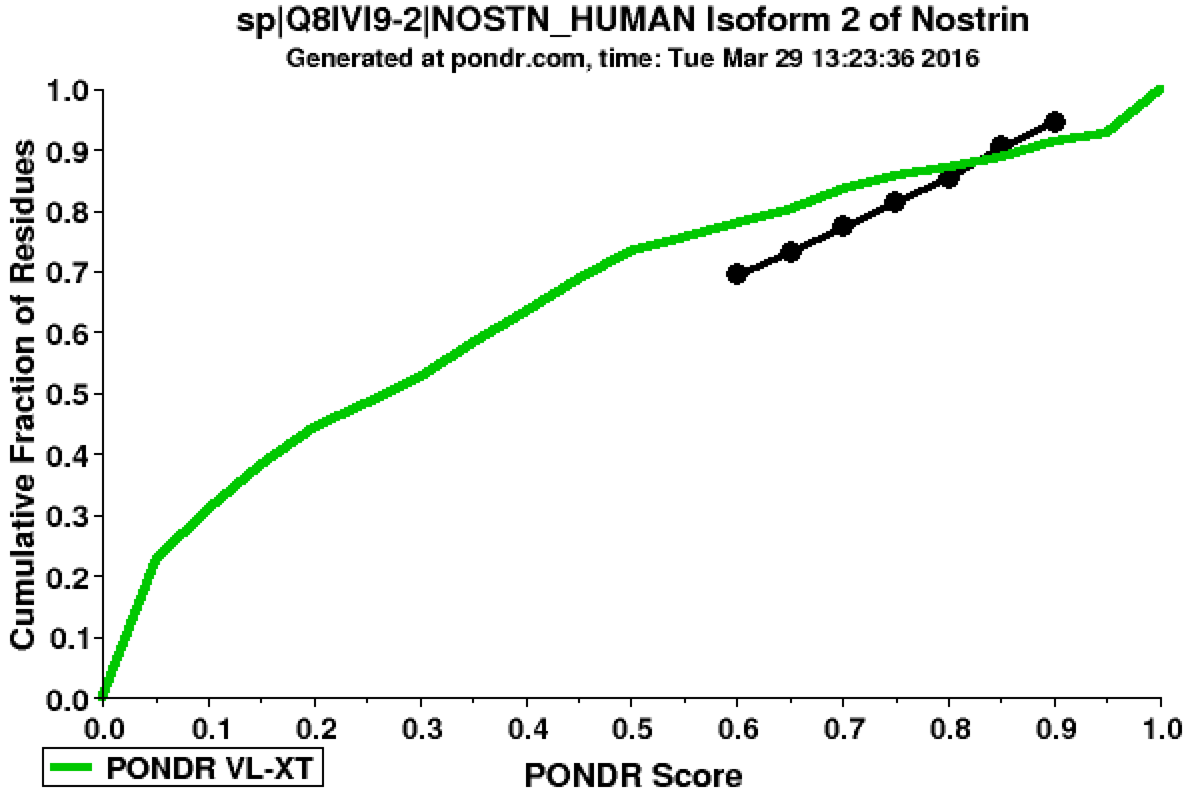
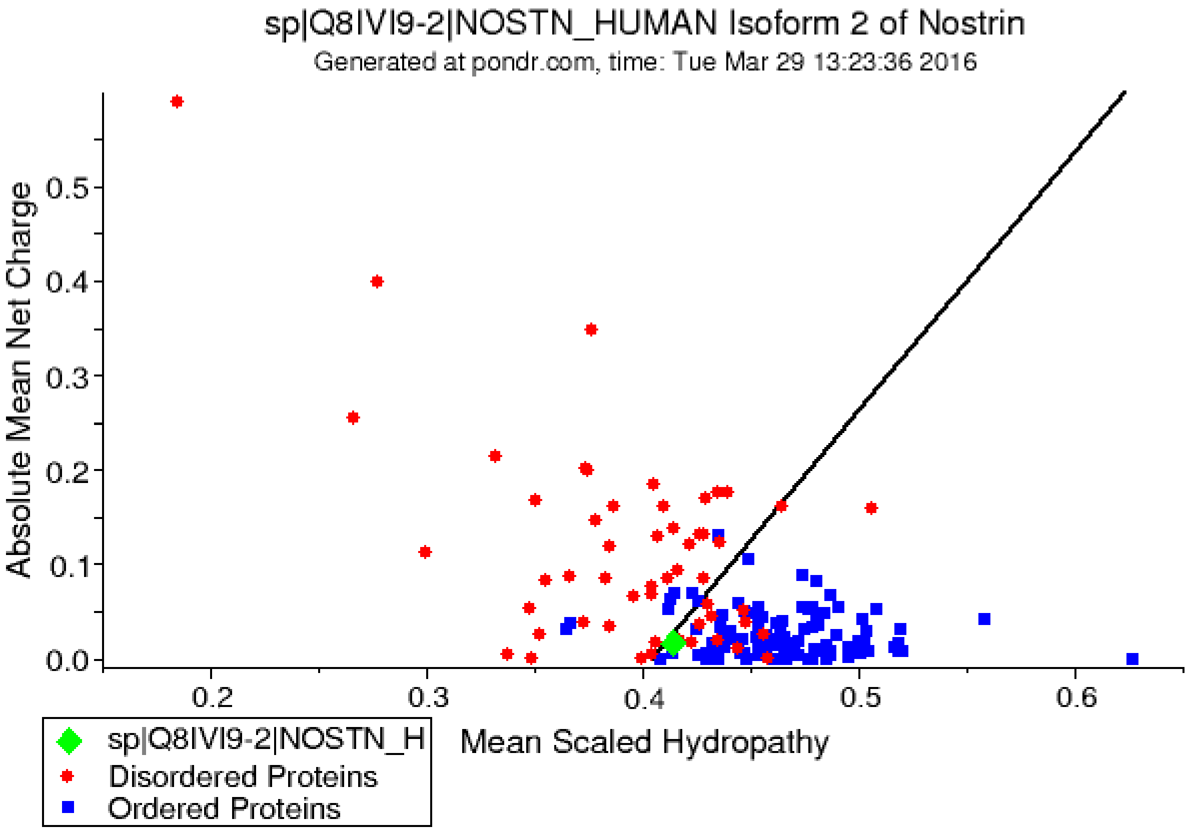






sp|Q8IVI9-2|NOSTN_HUMAN Isoform 2 of Nostrin

Generated at pondr.com, time: Tue Mar 29 13:23:36 2016



sp|Q8IVI9-2|NOSTN_HUMAN Isoform 2 of Nostrin

Generated at pondr.com, time: Tue Mar 29 13:23:36 2016

```
=======================VLXT NNP STATISTICS=================================
Predicted residues: 478                        Number Disordered Regions: 9
Number residues disordered: 128                Longest Disordered Region: 35
Overall percent disordered: 26.78     Average Prediction Score: 0.3416
Predicted disorder segment [1]-[6]    Average Strength= 0.8140
Predicted disorder segment [86]-[90]  Average Strength= 0.5809
Predicted disorder segment [102]-[113]Average Strength= 0.7541
Predicted disorder segment [135]-[148]Average Strength= 0.7369
Predicted disorder segment [233]-[244]Average Strength= 0.6603
Predicted disorder segment [261]-[295]Average Strength= 0.8849
Predicted disorder segment [339]-[351]Average Strength= 0.7344
Predicted disorder segment [389]-[410]Average Strength= 0.8901
Predicted disorder segment [468]-[476]Average Strength= 0.6027

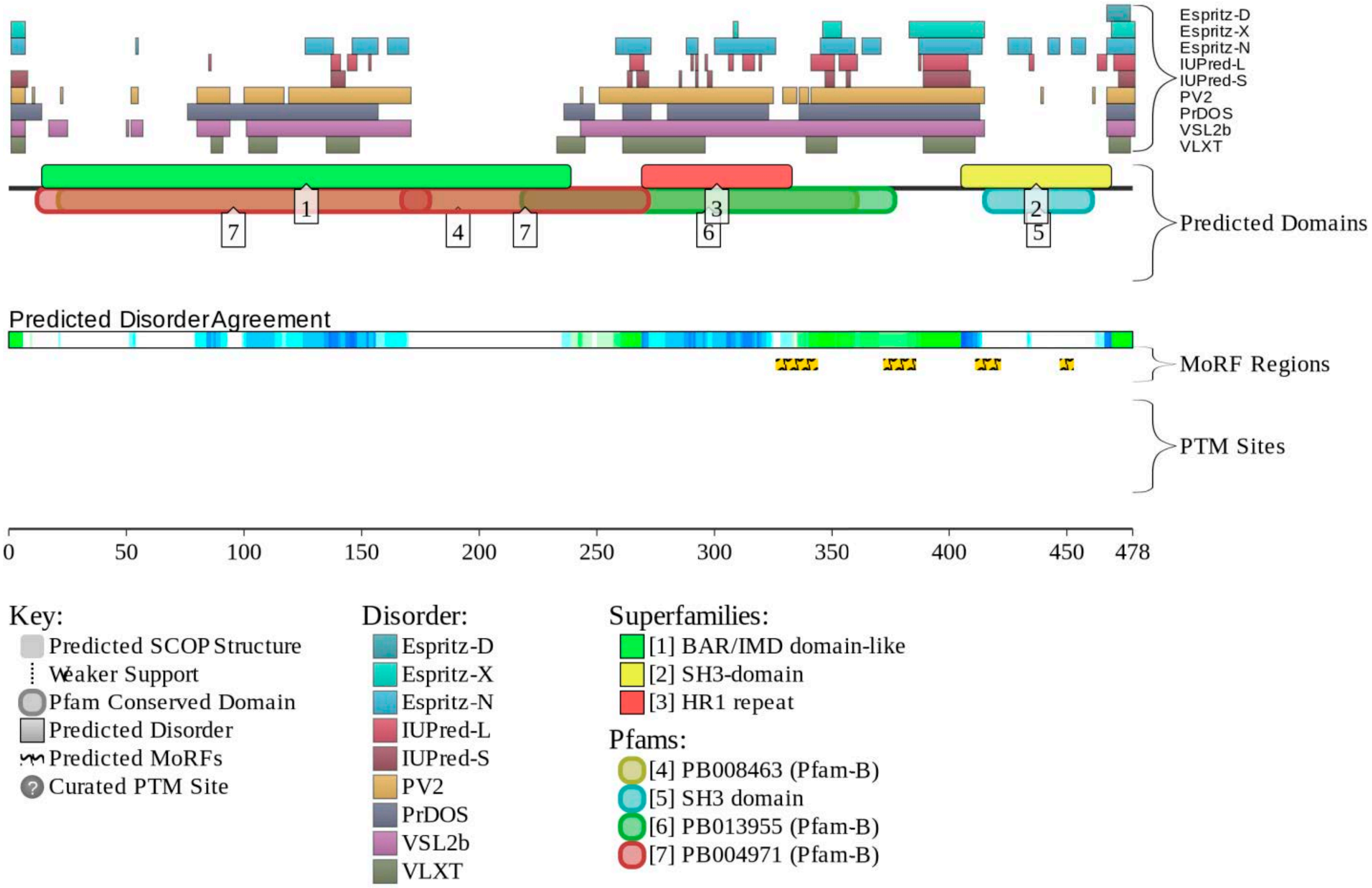
=========================VL3 NNP STATISTICS================================
Predicted residues: 478                        Number Disordered Regions: 2
Number residues disordered: 262                Longest Disordered Region: 176
Overall percent disordered: 54.81     Average Prediction Score: 0.5032
Predicted disorder segment [78]-[163] Average Strength= 0.6524
Predicted disorder segment [238]-[413]Average Strength= 0.6661

========================VSL2 NNP STATISTICS================================
Predicted residues: 478                        Number Disordered Regions: 8
Number residues disordered: 288                Longest Disordered Region: 172
Overall percent disordered: 60.25     Average Prediction Score: 0.5919
Predicted disorder segment [1]-[6]    Average Strength= 0.6549
Predicted disorder segment [17]-[24]  Average Strength= 0.5177
Predicted disorder segment [50]-[50]  Average Strength= 0.5094
Predicted disorder segment [52]-[56]  Average Strength= 0.5312
Predicted disorder segment [80]-[93]  Average Strength= 0.6143
Predicted disorder segment [101]-[170]Average Strength= 0.7992
Predicted disorder segment [243]-[414]Average Strength= 0.7788
Predicted disorder segment [467]-[478]Average Strength= 0.6783
```

Predicted Disordered Binding Regions

	From	To	Length
1	326	343	18
2	372	385	14
3	411	421	11
4	447	452	6

ENSP00000401316, ENSP00000380392



```
>sp|Q8IVI9-3|NOSTN_HUMAN Isoform 3 of Nostrin OS=Homo sapiens GN=NOSTRIN
MKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKK
KLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENYYQKNMAGYSTR
LKWENTLENCYQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIE
KDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASK
DKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQ
PSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQL
SSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGKKGHFPAAYVEELPSN
AGNTATKA
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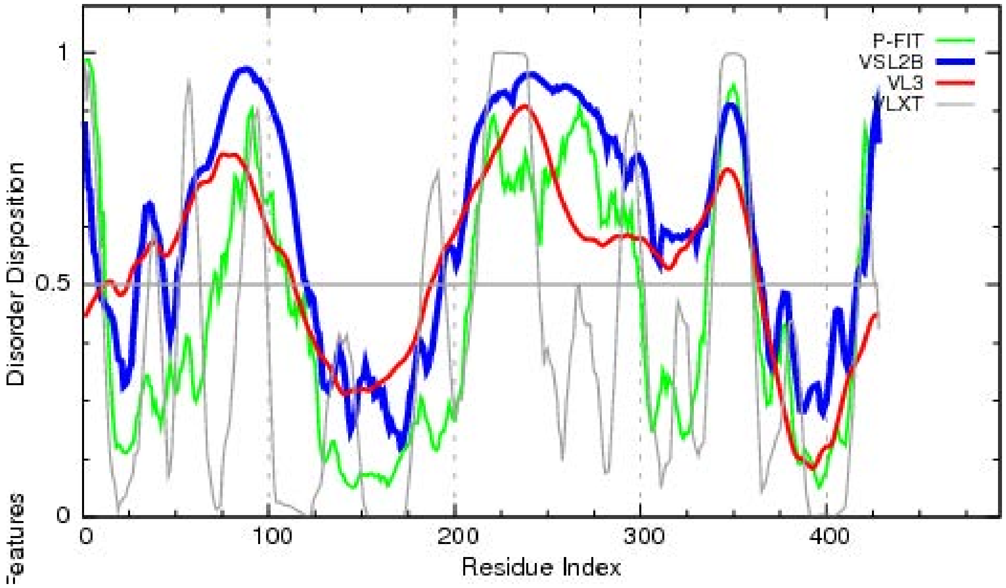
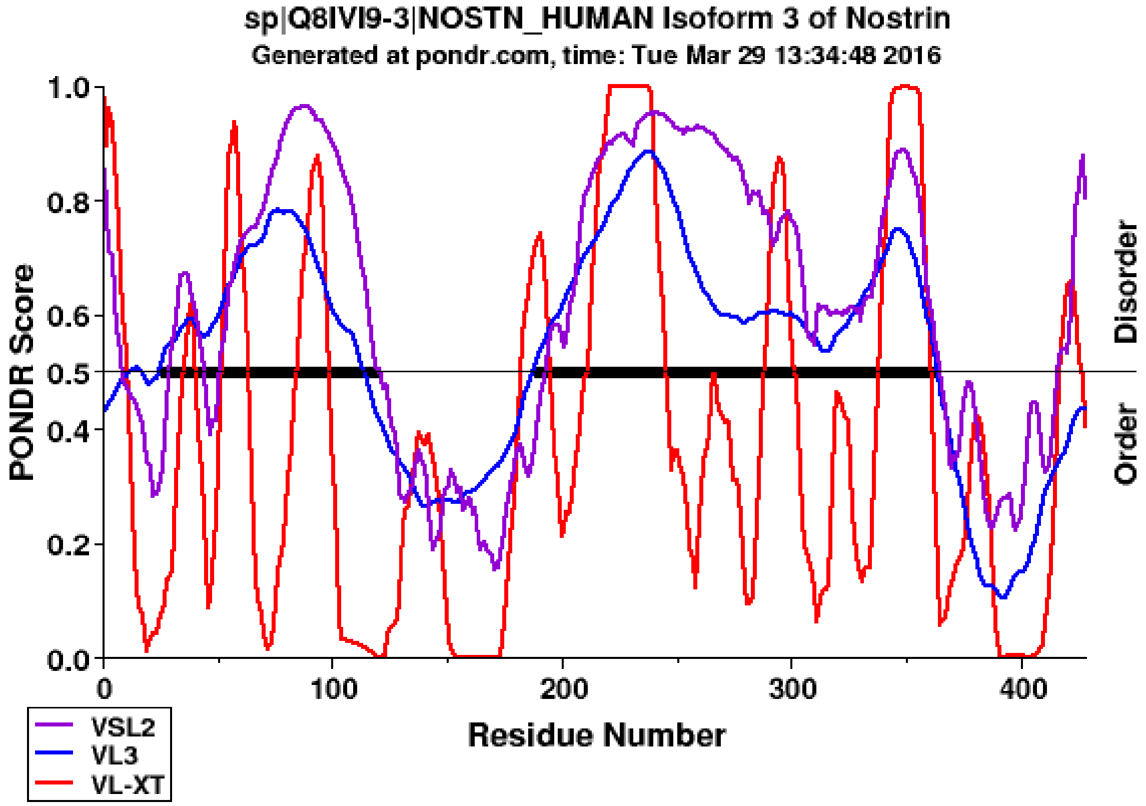
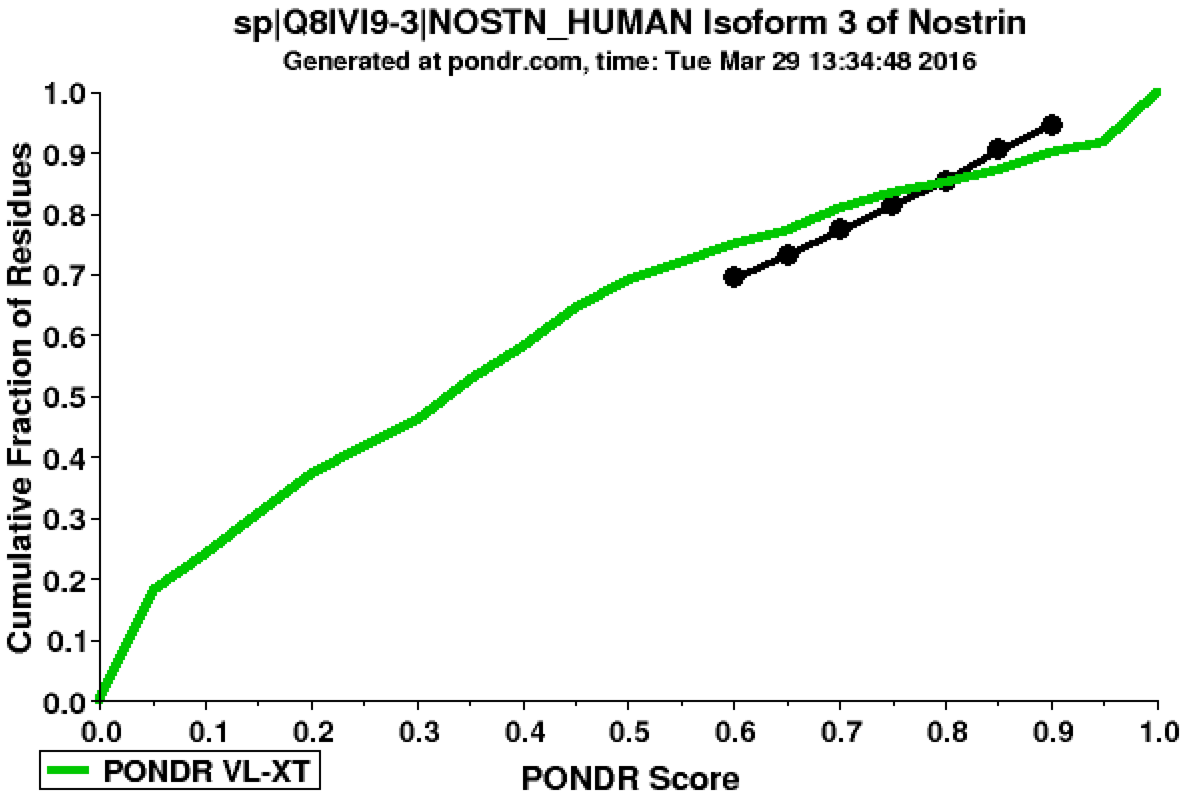
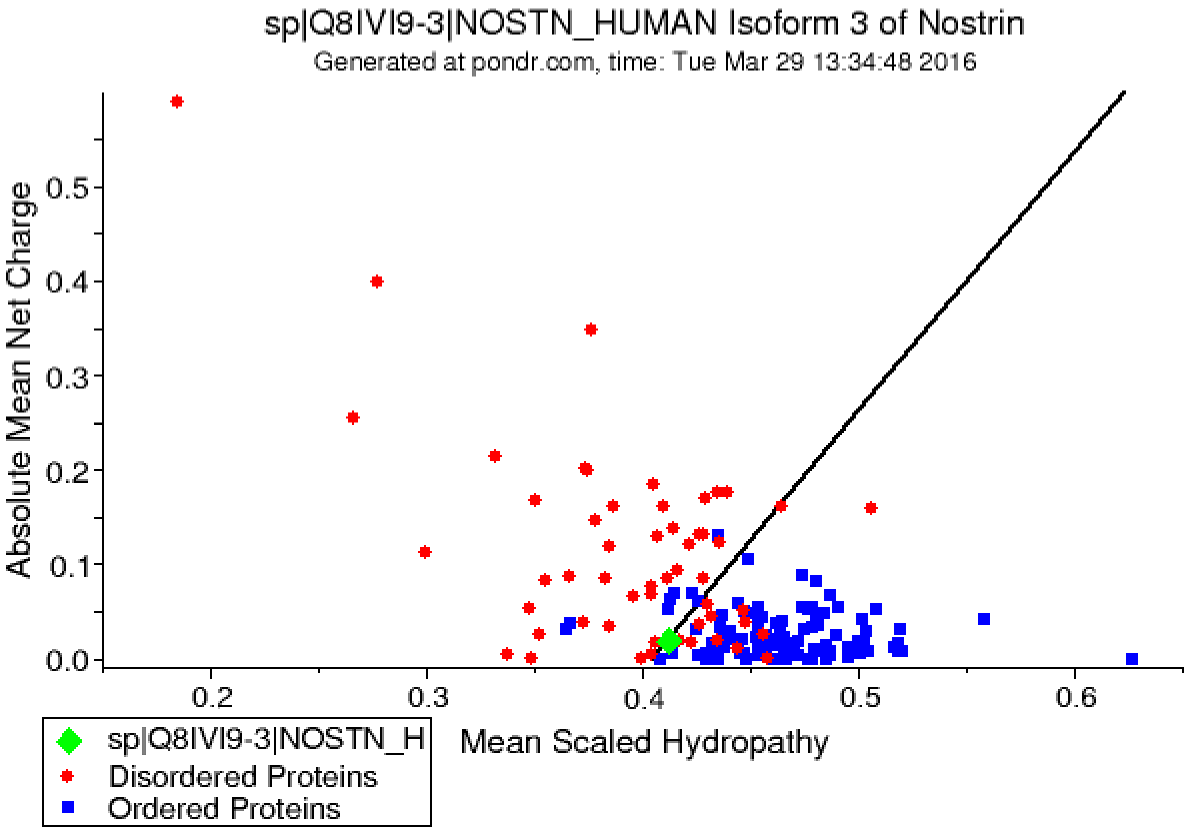





sp|Q8IVI9-3|NOSTN_HUMAN Isoform 3 of Nostrin
Generated at pondr.com, time: Tue Mar 29 13:34:48 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT

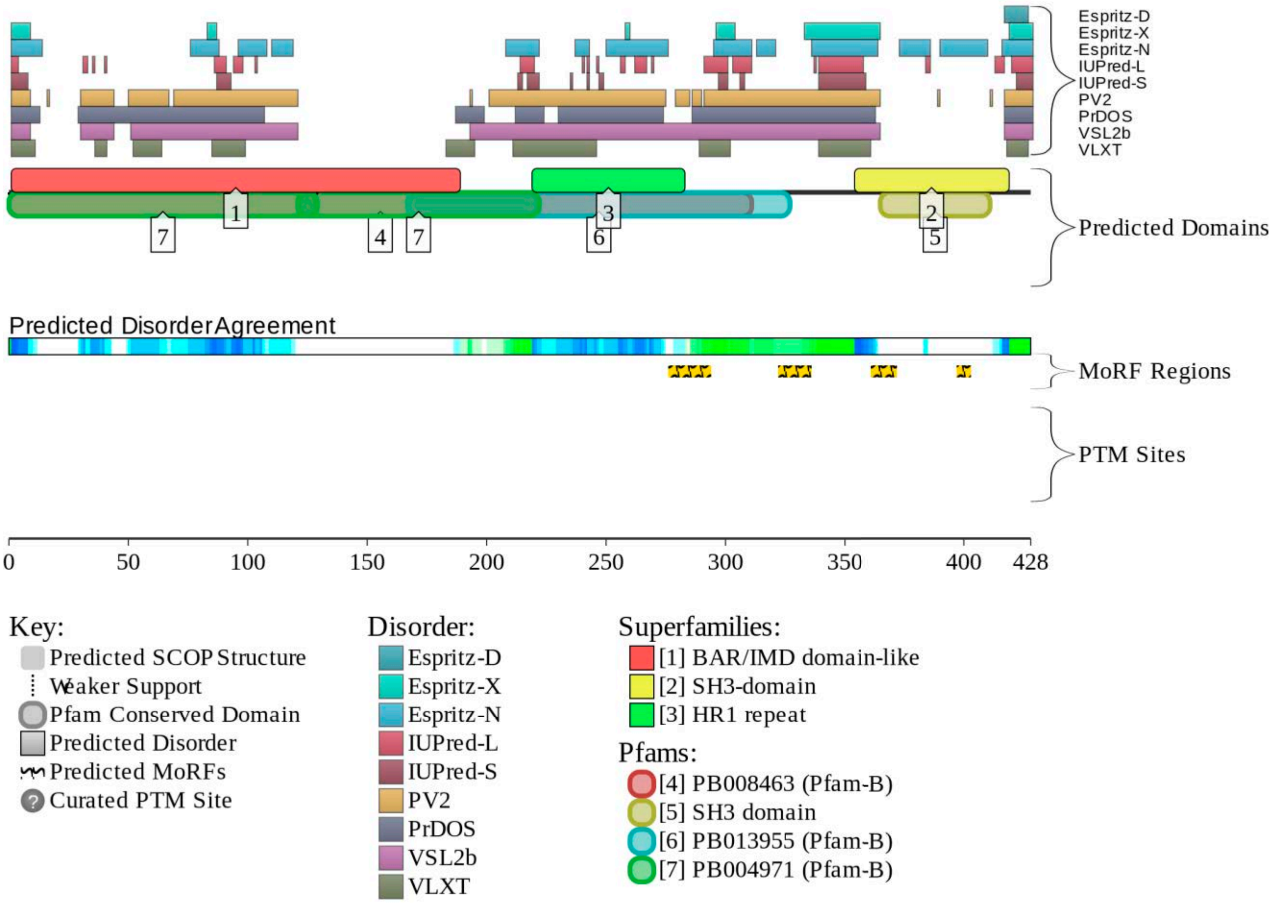

sp|Q8IVI9-3|NOSTN_HUMAN Isoform 3 of Nostrin
Generated at pondr.com, time: Tue Mar 29 13:34:48 2016
Absolute Mean Net Charge
0.5
0.4
0.3
0.2
0.1
0.0
0.2
0.3
0.4
0.5
0.6
Mean Scaled Hydropathy
sp|Q8IVI9-3|NOSTN_H
Disordered Proteins
Ordered Proteins

```
=========================VLXT NNP STATISTICS=================================
Predicted residues: 428                       Number Disordered Regions: 9
Number residues disordered: 132               Longest Disordered Region: 35
Overall percent disordered: 30.84      Average Prediction Score: 0.3814
Predicted disorder segment [1]-[10]    Average Strength= 0.7998
Predicted disorder segment [36]-[40]   Average Strength= 0.5809
Predicted disorder segment [52]-[63]   Average Strength= 0.7541
Predicted disorder segment [85]-[98]   Average Strength= 0.7369
Predicted disorder segment [183]-[194]Average Strength= 0.6603
Predicted disorder segment [211]-[245]Average Strength= 0.8849
Predicted disorder segment [289]-[301]Average Strength= 0.7344
Predicted disorder segment [339]-[360]Average Strength= 0.8901
Predicted disorder segment [418]-[426]Average Strength= 0.6027

=========================VL3 NNP STATISTICS=================================
Predicted residues: 428                       Number Disordered Regions: 3
Number residues disordered: 270               Longest Disordered Region: 176
Overall percent disordered: 63.08      Average Prediction Score: 0.5344
Predicted disorder segment [12]-[16]   Average Strength= 0.5047
Predicted disorder segment [25]-[113]  Average Strength= 0.6490
Predicted disorder segment [188]-[363]Average Strength= 0.6661

========================VSL2 NNP STATISTICS=================================
Predicted residues: 428                       Number Disordered Regions: 5
Number residues disordered: 276               Longest Disordered Region: 172
Overall percent disordered: 64.49      Average Prediction Score: 0.6151
Predicted disorder segment [1]-[8]     Average Strength= 0.6663
Predicted disorder segment [30]-[43]   Average Strength= 0.6141
Predicted disorder segment [51]-[120]  Average Strength= 0.7992
Predicted disorder segment [193]-[364]Average Strength= 0.7788
Predicted disorder segment [417]-[428]Average Strength= 0.6783
```

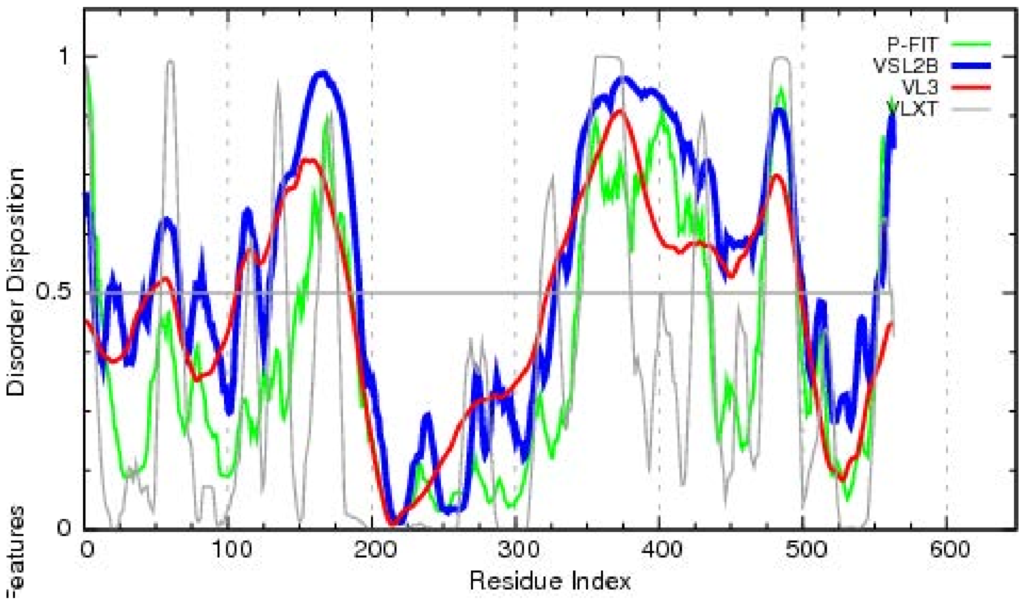
Predicted Disordered Binding Regions

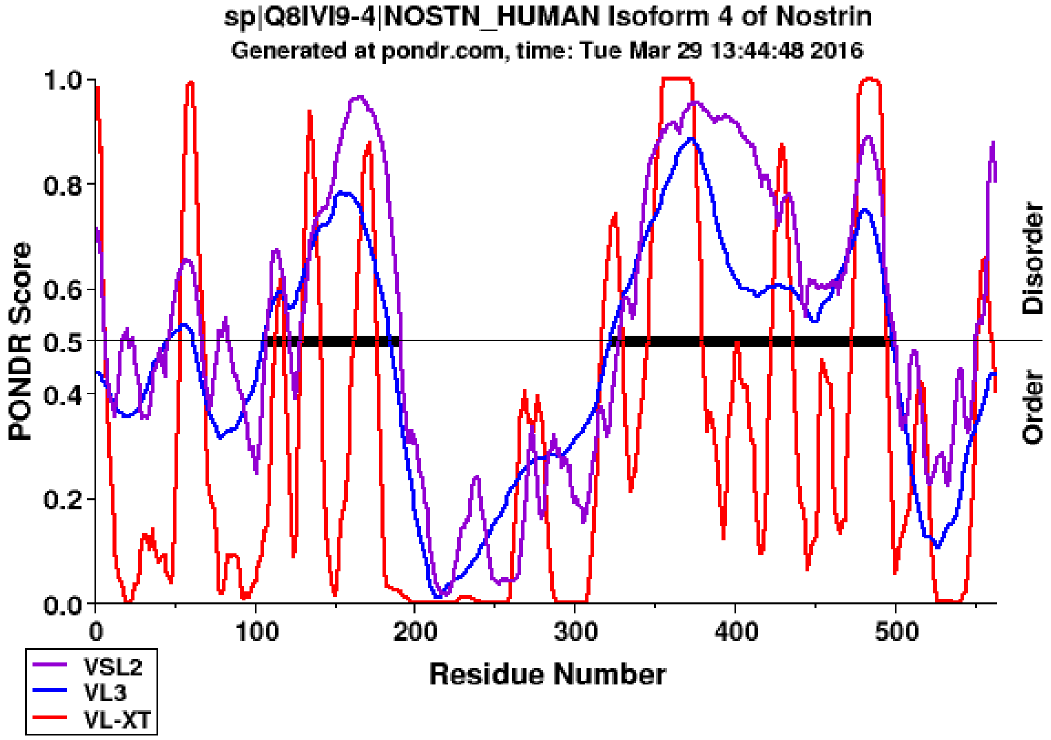
	From	To	Length
1	276	293	18
2	322	335	14
3	361	371	11
4	397	402	6

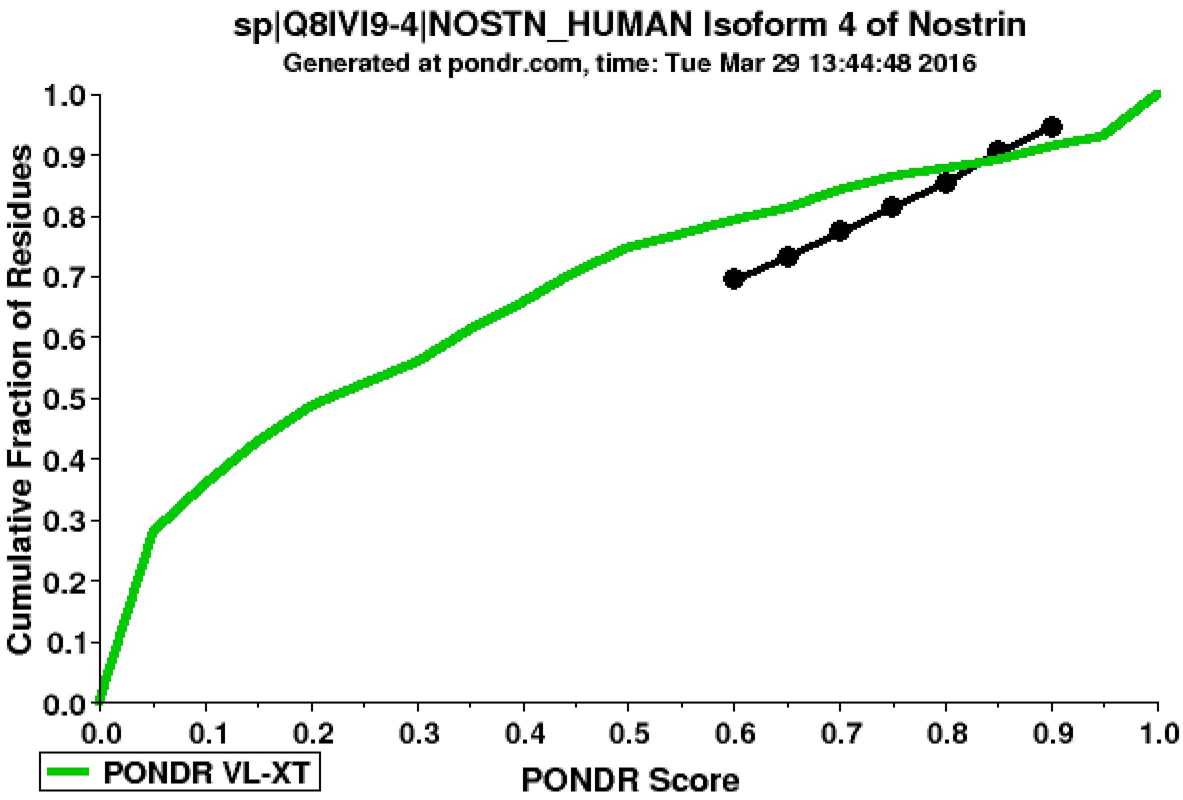
ENSP00000404413, ENSP00000380390

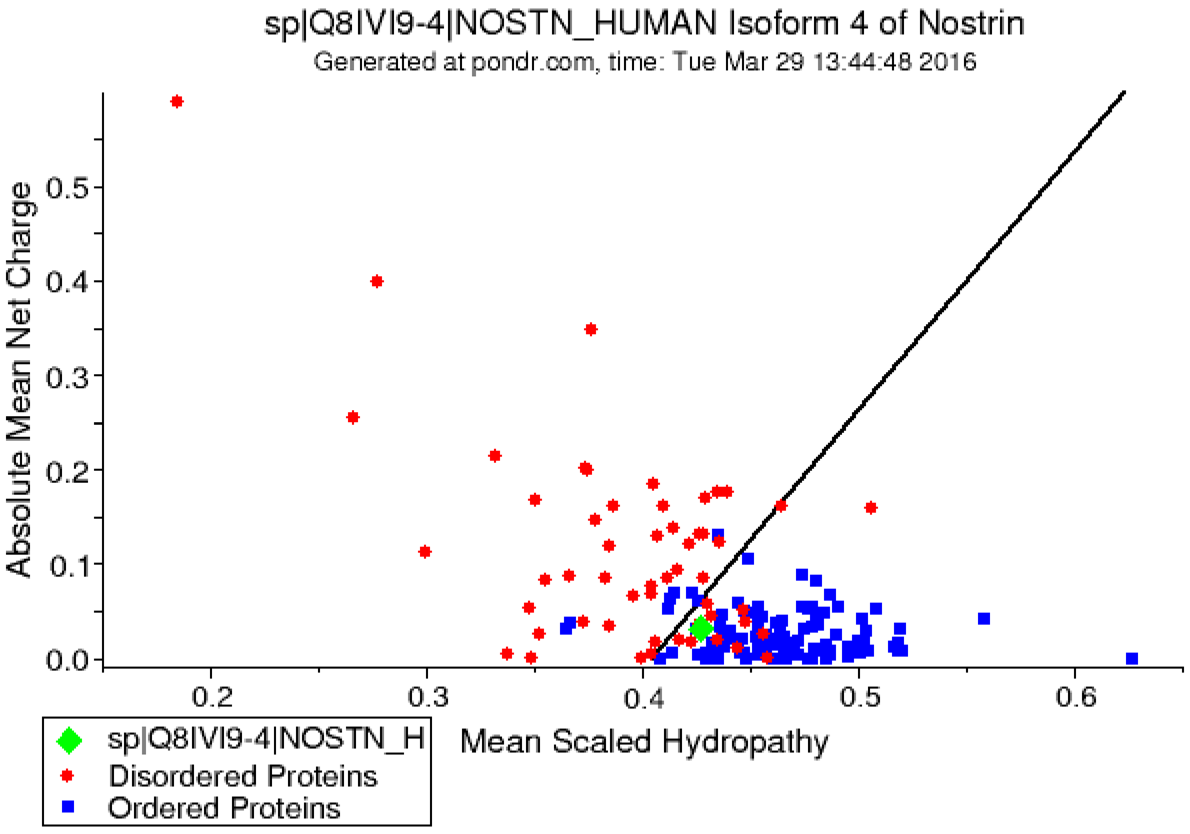


```
>sp|Q8IVI9-4|NOSTN_HUMAN Isoform 4 of Nostrin OS=Homo sapiens GN=NOSTRIN
MRDPLTDCPYNKVYKNLKEFSQNGENFCKQVTSVLQQRANLEISYAKGLQKLASKLSKAL
QNTRKSCVSSAWAWASEGMKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVE
KTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKL
EKEDENYYQKNMAGYSTRLKWENTLENCYQVTHSICLYAFWVKRAWGKCVSDLRYQDTFL
PGNLPPLWFGYDIVKRLIMRLCSVCLQSILELEKERIQLLCNNLNQYSQHISLFGQTLTT
CHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLK
PKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANS
YKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQ
SNPGSSTPAPGAAQLSSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGK
KGHFPAAYVEELPSNAGNTATKA
```

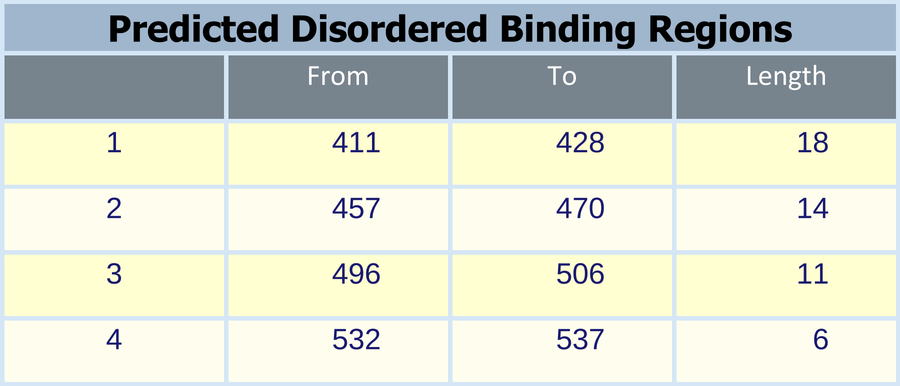





sp|Q8IVI9-4|NOSTN_HUMAN Isoform 4 of Nostrin
Generated at pondr.com, time: Tue Mar 29 13:44:48 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT


sp|Q8IVI9-4|NOSTN_HUMAN Isoform 4 of Nostrin
Generated at pondr.com, time: Tue Mar 29 13:44:48 2016
Absolute Mean Net Charge
0.5
0.4
0.3
0.2
0.1
0.0
0.2
0.3
0.4
0.5
0.6
Mean Scaled Hydropathy
sp|Q8IVI9-4|NOSTN_H
Disordered Proteins
Ordered Proteins

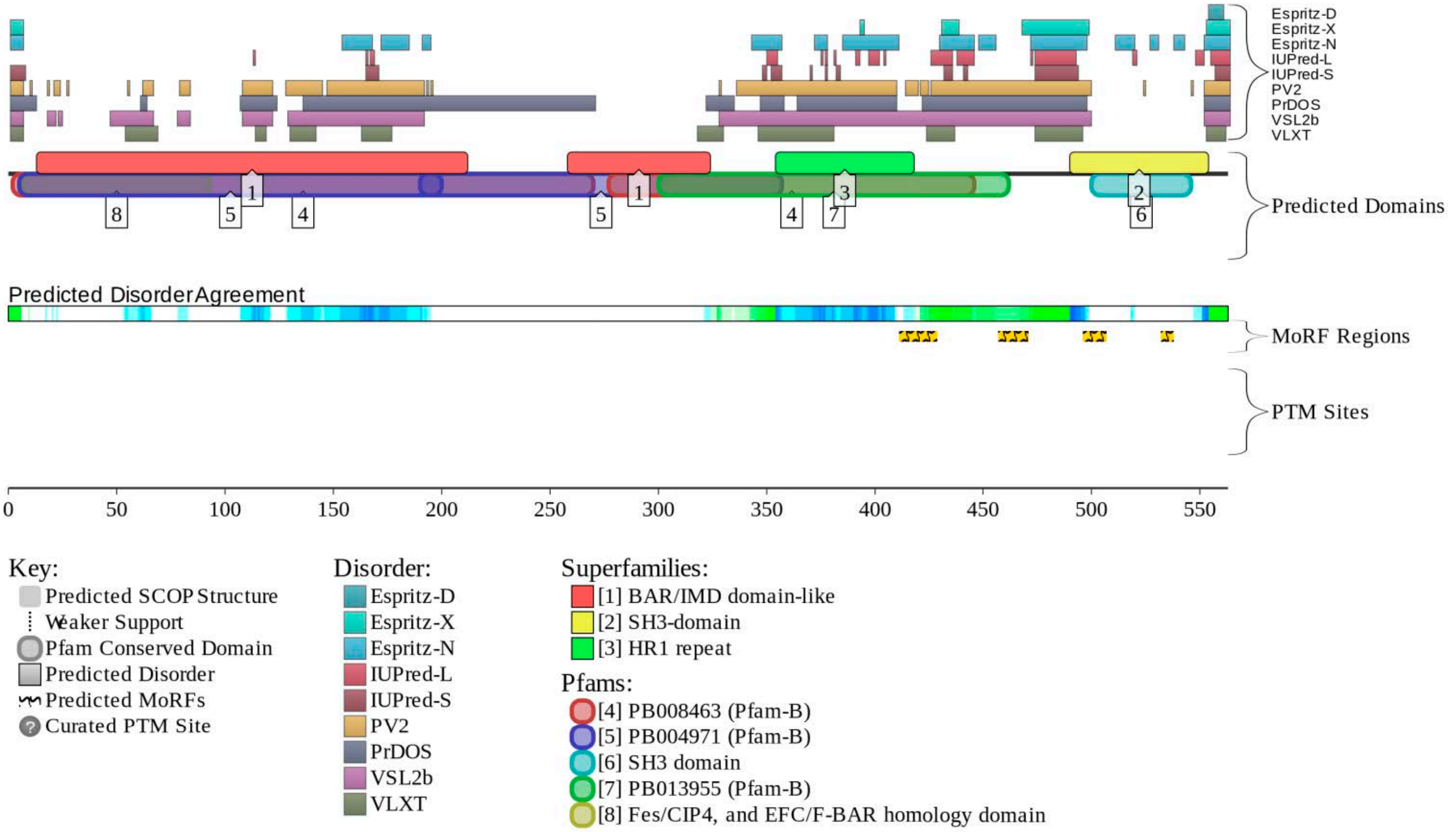
```
=========================VLXT NNP STATISTICS=================================
Predicted residues: 563                       Number Disordered Regions: 10
Number residues disordered: 143               Longest Disordered Region: 35
Overall percent disordered: 25.40     Average Prediction Score: 0.3195
Predicted disorder segment [1]-[6]    Average Strength= 0.8140
Predicted disorder segment [54]-[68]  Average Strength= 0.8015
Predicted disorder segment [114]-[118]Average Strength= 0.5809
Predicted disorder segment [130]-[141]Average Strength= 0.7541
Predicted disorder segment [163]-[176]Average Strength= 0.7369
Predicted disorder segment [318]-[329]Average Strength= 0.6603
Predicted disorder segment [346]-[380]Average Strength= 0.8849
Predicted disorder segment [424]-[436]Average Strength= 0.7344
Predicted disorder segment [474]-[495]Average Strength= 0.8901
Predicted disorder segment [553]-[561]Average Strength= 0.6027

=========================VL3 NNP STATISTICS=================================
Predicted residues: 563                       Number Disordered Regions: 3
Number residues disordered: 271               Longest Disordered Region: 176
Overall percent disordered: 48.13     Average Prediction Score: 0.4613
Predicted disorder segment [46]-[61]  Average Strength= 0.5182
Predicted disorder segment [106]-[184]Average Strength= 0.6599
Predicted disorder segment [323]-[498]Average Strength= 0.6661

=========================VSL2 NNP STATISTICS=================================
Predicted residues: 563                       Number Disordered Regions: 9
Number residues disordered: 299               Longest Disordered Region: 172
Overall percent disordered: 53.11     Average Prediction Score: 0.5325
Predicted disorder segment [1]-[6]    Average Strength= 0.6523
Predicted disorder segment [18]-[21]  Average Strength= 0.5126
Predicted disorder segment [23]-[24]  Average Strength= 0.5030
Predicted disorder segment [47]-[66]  Average Strength= 0.6069
Predicted disorder segment [78]-[83]  Average Strength= 0.5211
Predicted disorder segment [108]-[121]Average Strength= 0.6143
Predicted disorder segment [129]-[191]Average Strength= 0.8089
Predicted disorder segment [328]-[499]Average Strength= 0.7788
Predicted disorder segment [552]-[563]Average Strength= 0.6783
```



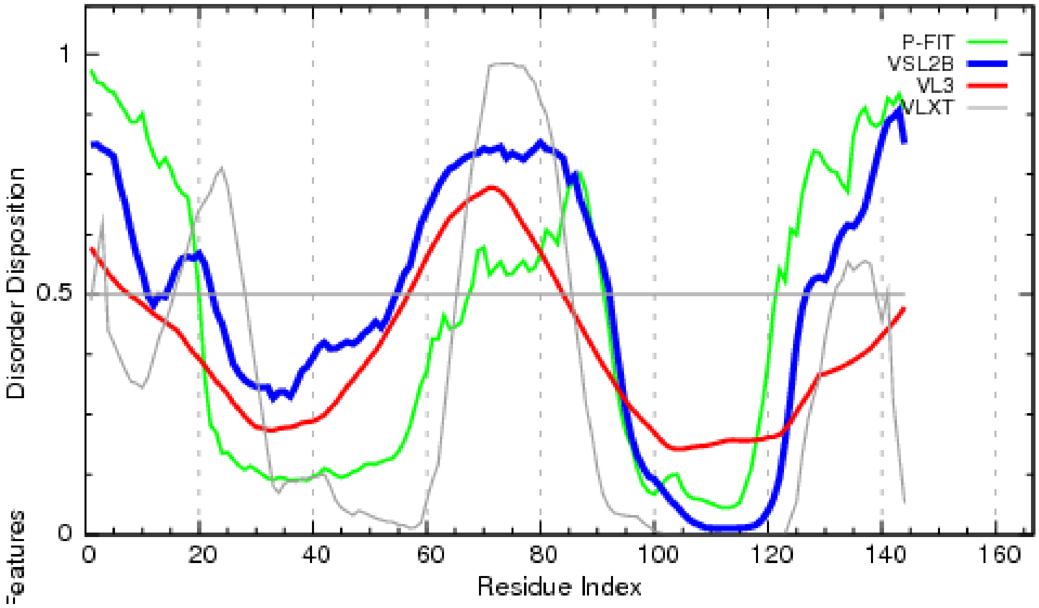
Predicted Disordered Binding Regions

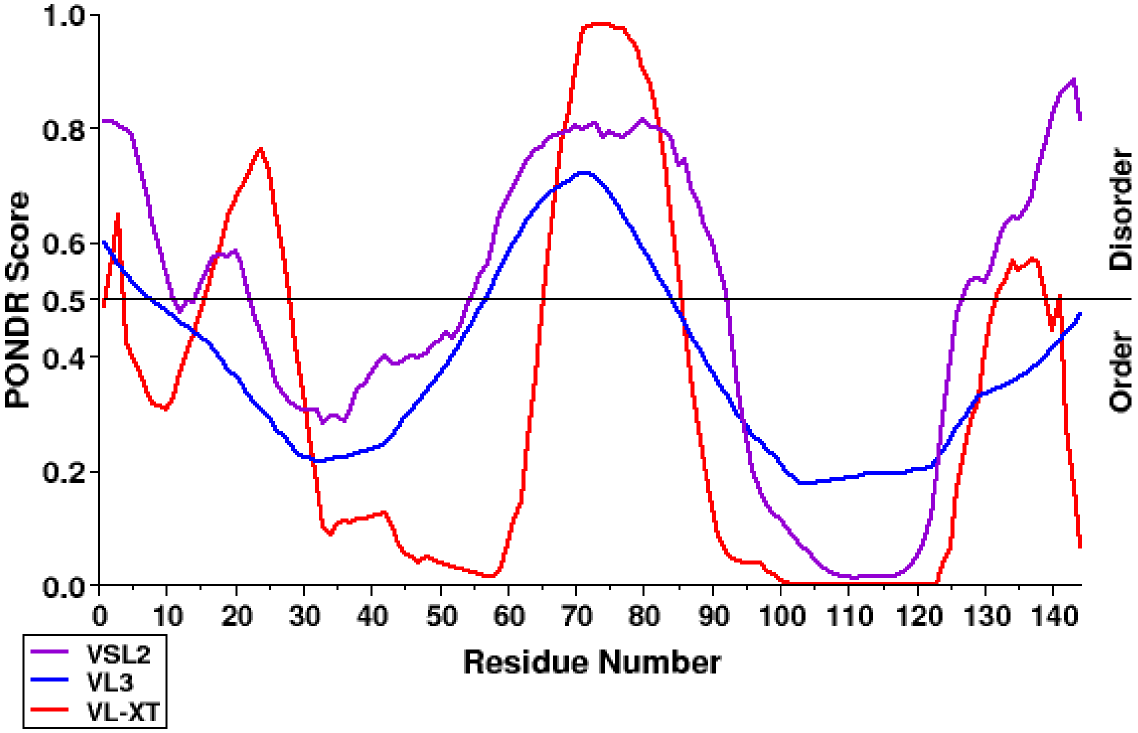
	From	To	Length
1	411	428	18
2	457	470	14
3	496	506	11
4	532	537	6

ENSP00000402140, ENSP00000394051

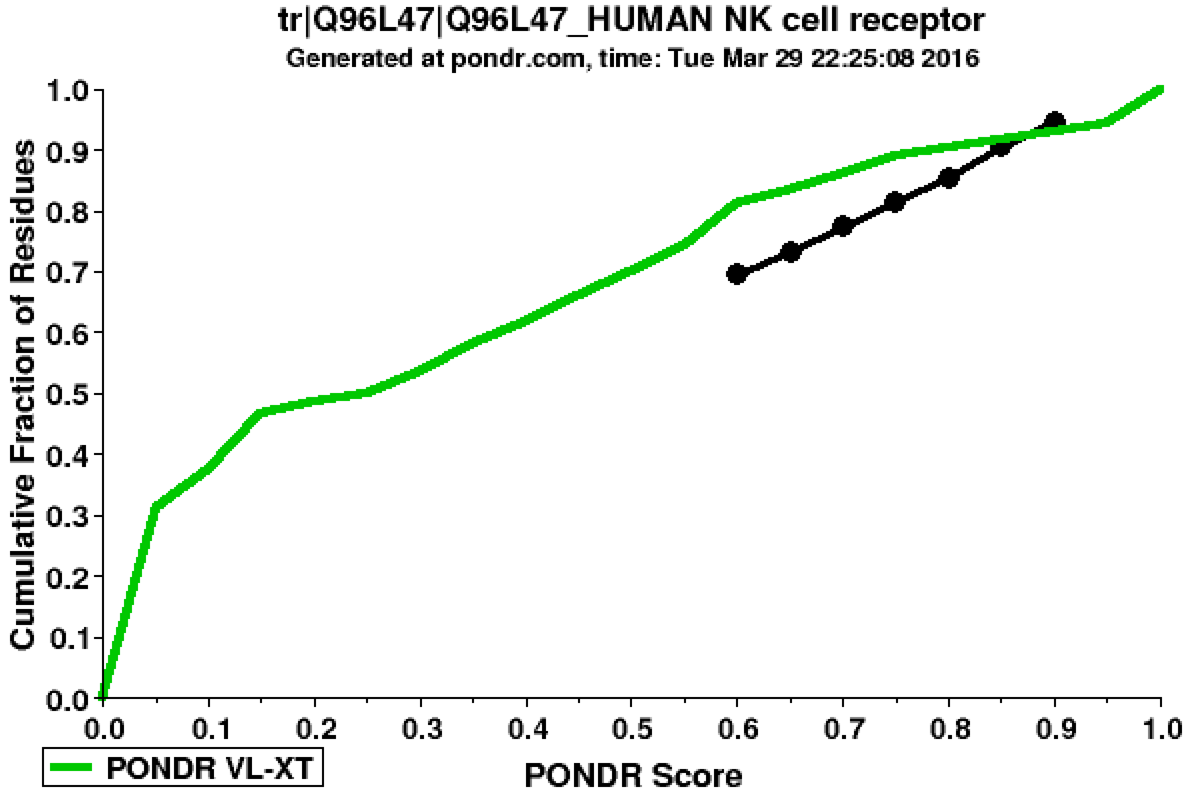


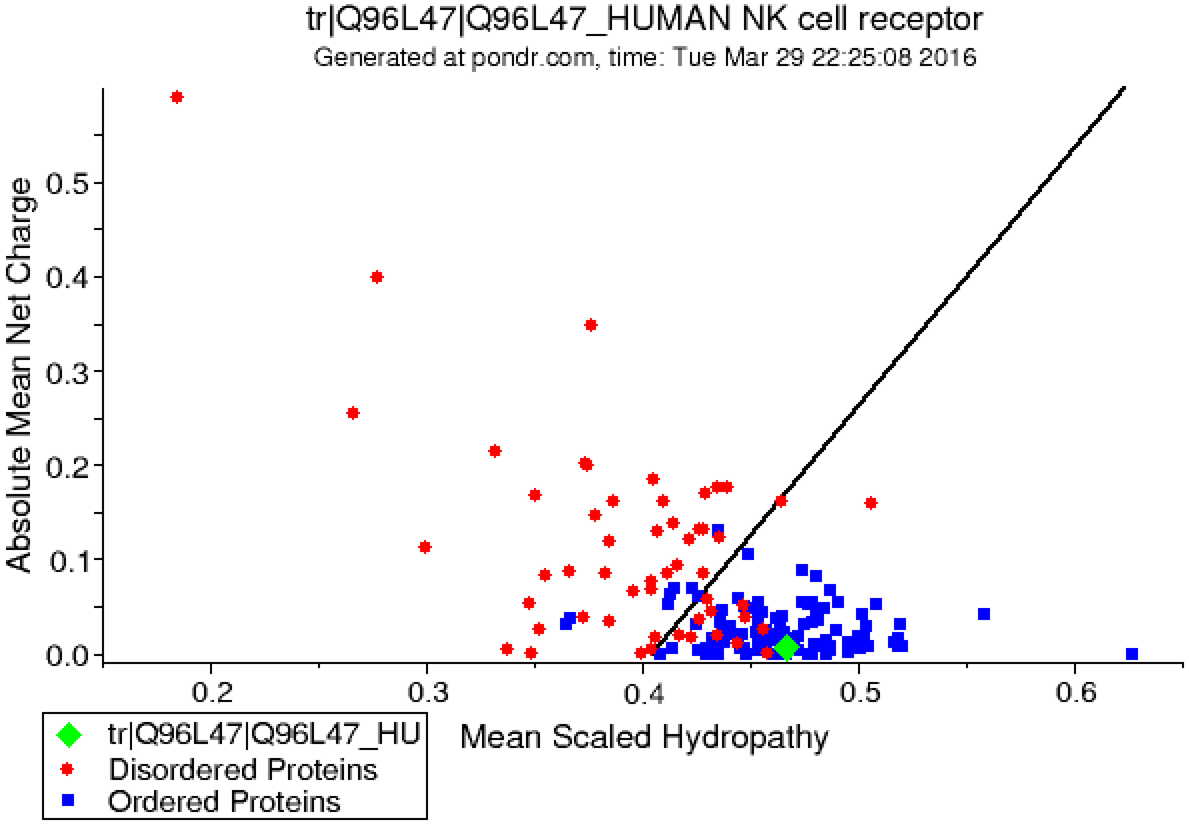
```
>tr|Q96L47|Q96L47_HUMAN NK cell receptor (Fragment) OS=Homo sapiens
GN=KIR2DL4 PE=2 SV=1
LSCSSQSSFDIYHLSREGEAHELRLPAVPSINGTFQADFPLGPATHGETYRCFGSFHGSP
YEWSDPSDPLPVSVTGNPSSSWPSPTEPSFKTGIARHLHAVIRYSVAIILFTILPFFLLH
RWCSKKKNAAVMNQEPAGHRTVNR
```




tr|Q96L47|Q96L47_HUMAN NK cell receptor

Generated at pondr.com, time: Tue Mar 29 22:25:08 2016


tr|Q96L47|Q96L47_HUMAN NK cell receptor
Generated at pondr.com, time: Tue Mar 29 22:25:08 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT


tr|Q96L47|Q96L47_HUMAN NK cell receptor
Generated at pondr.com, time: Tue Mar 29 22:25:08 2016
Absolute Mean Net Charge
0.5
0.4
0.3
0.2
0.1
0.0
0.2
0.3
0.4
0.5
0.6
Mean Scaled Hydropathy
tr|Q96L47|Q96L47_HU
Disordered Proteins
Ordered Proteins

```
=======================VLXT NNP STATISTICS================================
Predicted residues: 144                      Number Disordered Regions: 5
Number residues disordered: 43       Longest Disordered Region: 20
Overall percent disordered: 29.86     Average Prediction Score: 0.3173
Predicted disorder segment [2]-[3]    Average Strength= 0.6094
Predicted disorder segment [16]-[28]  Average Strength= 0.6449
Predicted disorder segment [66]-[85]  Average Strength= 0.8521
Predicted disorder segment [132]-[138]Average Strength= 0.5511
Predicted disorder segment [141]-[141]Average Strength= 0.5052

========================VL3 NNP STATISTICS================================
Predicted residues: 144                      Number Disordered Regions: 2
Number residues disordered: 35       Longest Disordered Region: 28
Overall percent disordered: 24.31     Average Prediction Score: 0.3833
Predicted disorder segment [1]-[7]    Average Strength= 0.5479
Predicted disorder segment [57]-[84]  Average Strength= 0.6310

=======================VSL2 NNP STATISTICS================================
Predicted residues: 144                      Number Disordered Regions: 4
Number residues disordered: 74       Longest Disordered Region: 38
Overall percent disordered: 51.39     Average Prediction Score: 0.4811
Predicted disorder segment [1]-[10]   Average Strength= 0.7188
Predicted disorder segment [15]-[22]  Average Strength= 0.5587
Predicted disorder segment [55]-[92]  Average Strength= 0.7231
Predicted disorder segment [127]-[144]Average Strength= 0.6820
```

```
>sp|Q9Y5Q5|CORIN_HUMAN Atrial natriuretic peptide-converting enzyme
OS=Homo sapiens GN=CORIN PE=1 SV=2
MKQSPALAPEERCRRAGSPKPVLRADDNNMGNGCSQKLATANLLRFLLLVLIPCICALVL
LLVILLSYVGTLQKVYFKSNGSEPLVTDGEIQGSDVILTNTIYNQSTVVSTAHPDQHVPA
WTTDASLPGDQSHRNTSACMNITHSQCQMLPYHATLTPLLSVVRNMEMEKFLKFFTYLHR
LSCYQHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCEAAKEGCESVLGMVNYSWPDFLRC
SQFRNQTESSNVSRICFSPQQENGKQLLCGRGENFLCASGICIPGKLQCNGYNDCDDWSD
EAHCNCSENLFHCHTGKCLNYSLVCDGYDDCGDLSDEQNCDCNPTTEHRCGDGRCIAMEW
VCDGDHDCVDKSDEVNCSCHSQGLVECRNGQCIPSTFQCDGDEDCKDGSDEENCSVIQTS
CQEGDQRCLYNPCLDSCGGSSLCDPNNSLNNCSQCEPITLELCMNLPYNSTSYPNYFGHR
TQKEASISWESSLFPALVQTNCYKYLMFFSCTILVPKCDVNTGEHIPPCRALCEHSKERC
ESVLGIVGLQWPEDTDCSQFPEENSDNQTCLMPDEYVEECSPSHFKCRSGQCVLASRRCD
GQADCDDDSDEENCGCKERDLWECPSNKQCLKHTVICDGFPDCPDYMDEKNCSFCQDDEL
ECANHACVSRDLWCDGEADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHHVCADGWQE
ILSQLACKQMGLGEPSVTKLIQEQEKEPRWLTLHSNWESLNGTTLHELLVNGQSCESRSK
ISLLCTKQDCGRRPAARMNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLT
VAHCFEGRENAAVWKVVLGINNLDHPSVFMQTRFVKTIILHPRYSRAVVDYDISIVELSE
DISETGYVRPVCLPNPEQWLEPDTYCYITGWGHMGNKMPFKLQEGEVRIISLEHCQSYFD
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SNVSYFVEWIKRQIYIQTFLLN
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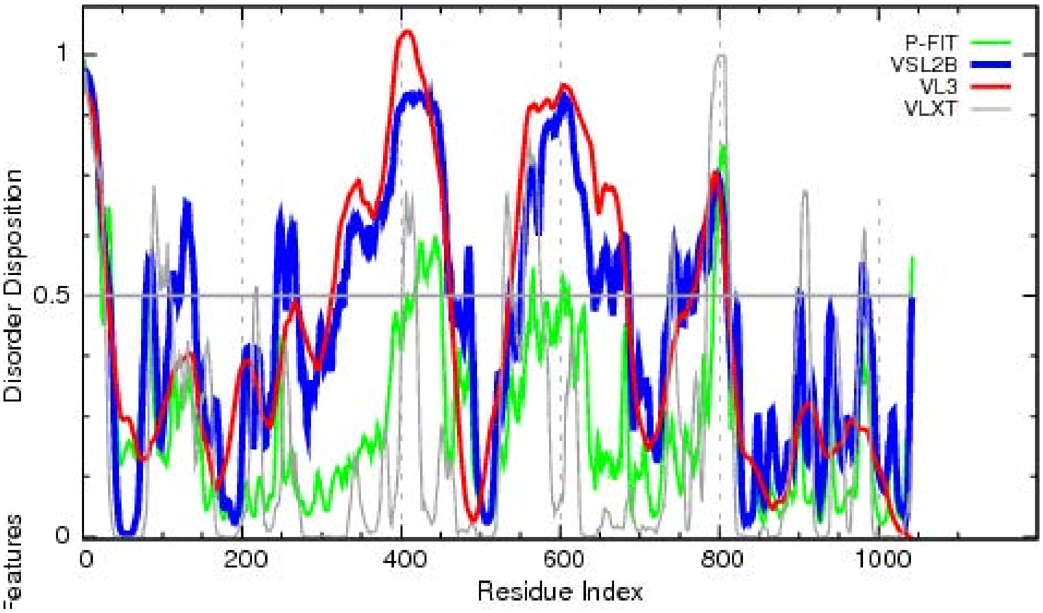

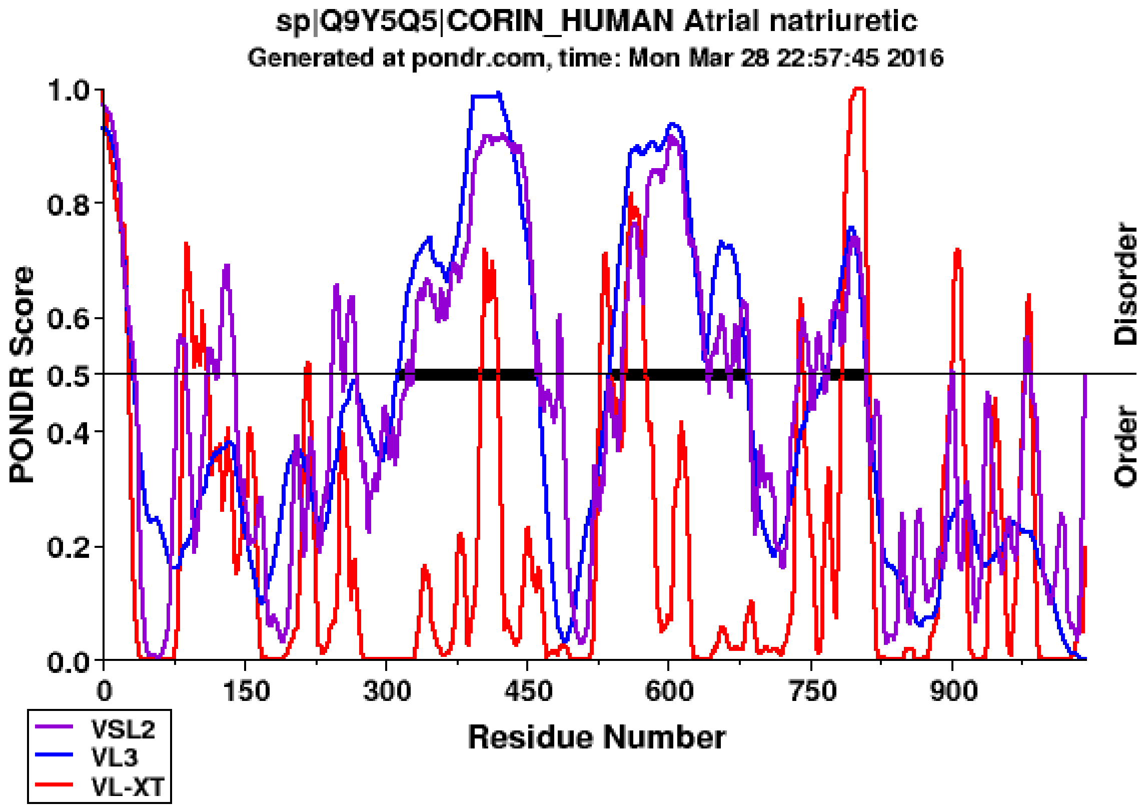
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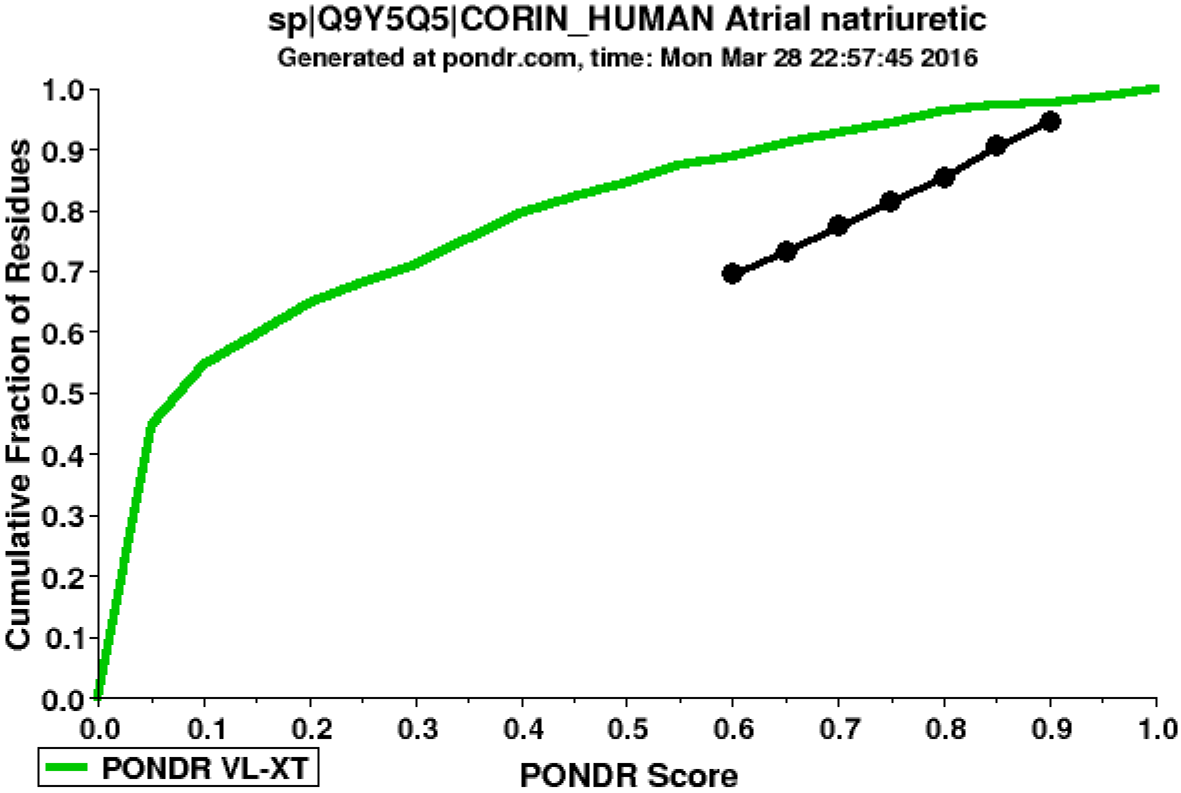
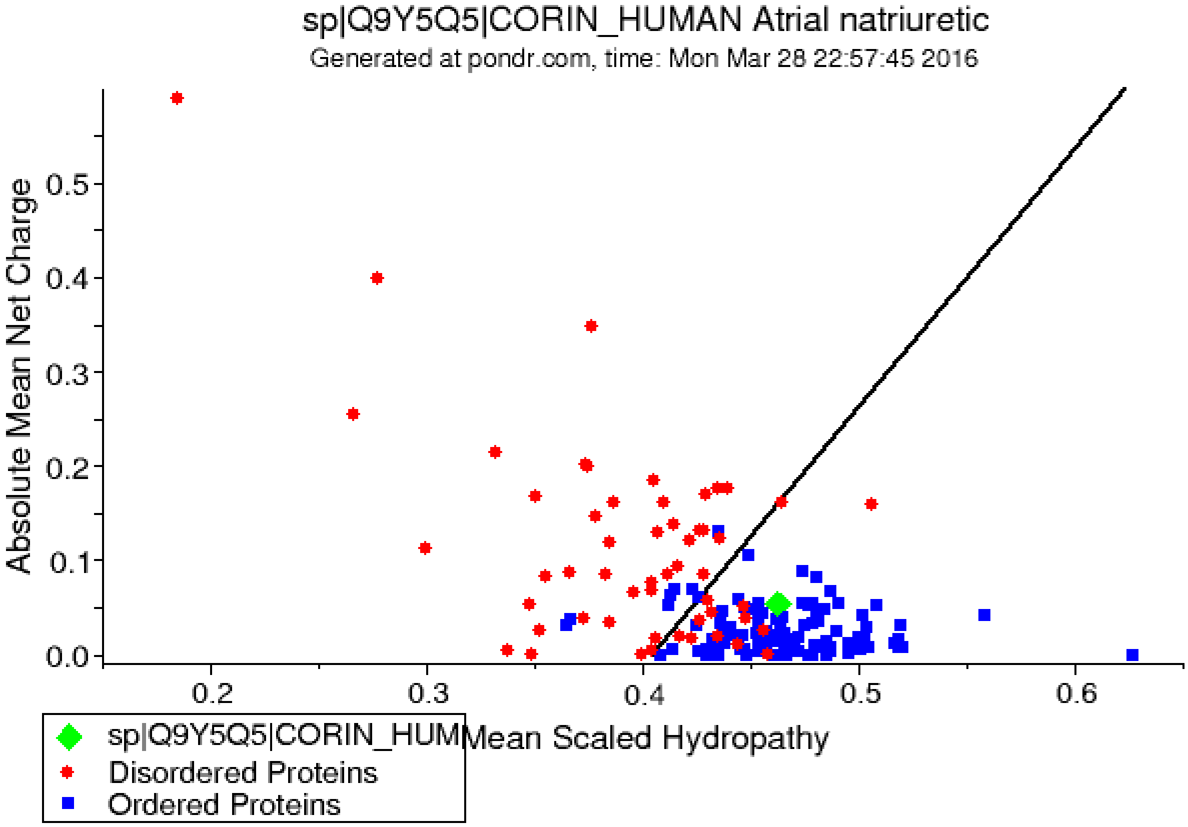
Generated at pondr.com, time: Mon Mar 28 22:57:45 2016
PONDR Score
1.0
0.8
0.6
0.5
0.4
0.2
0.0
0
150
300
450
600
750
900
Residue Number
Disorder
Order
VSL2
VL3
VL-XT


sp|Q9Y5Q5|CORIN_HUMAN Atrial natriuretic
Generated at pondr.com, time: Mon Mar 28 22:57:45 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT

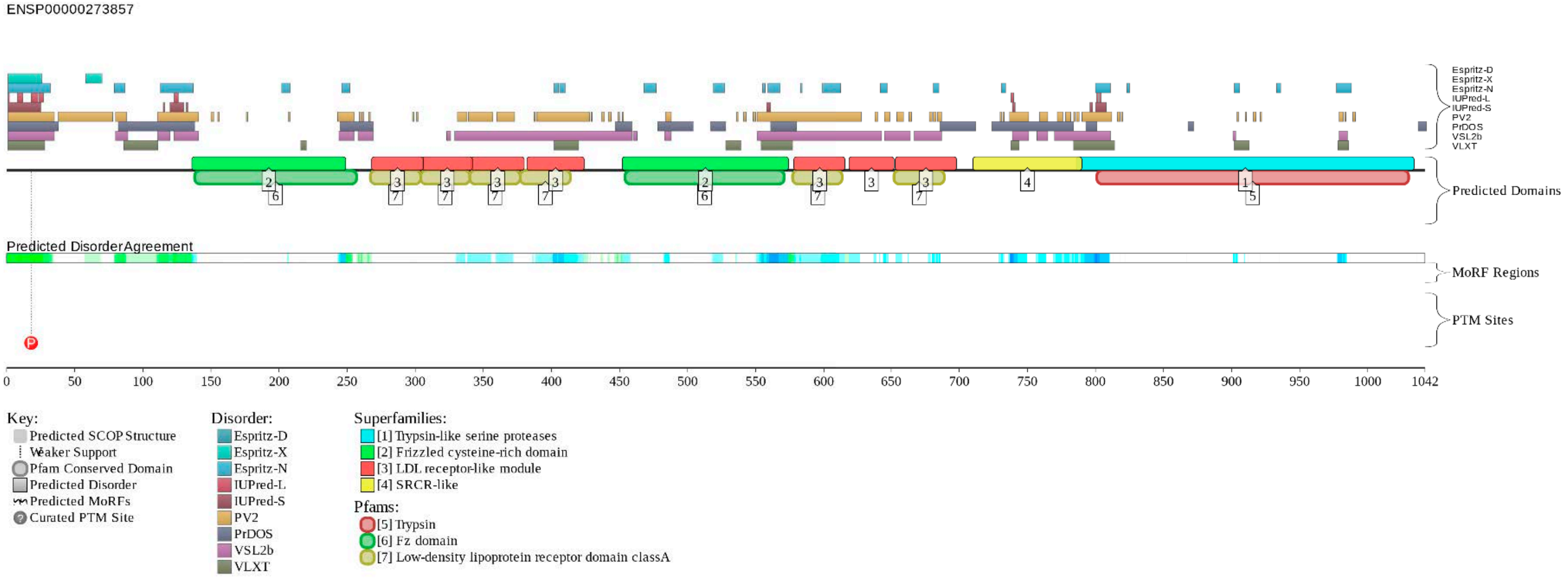


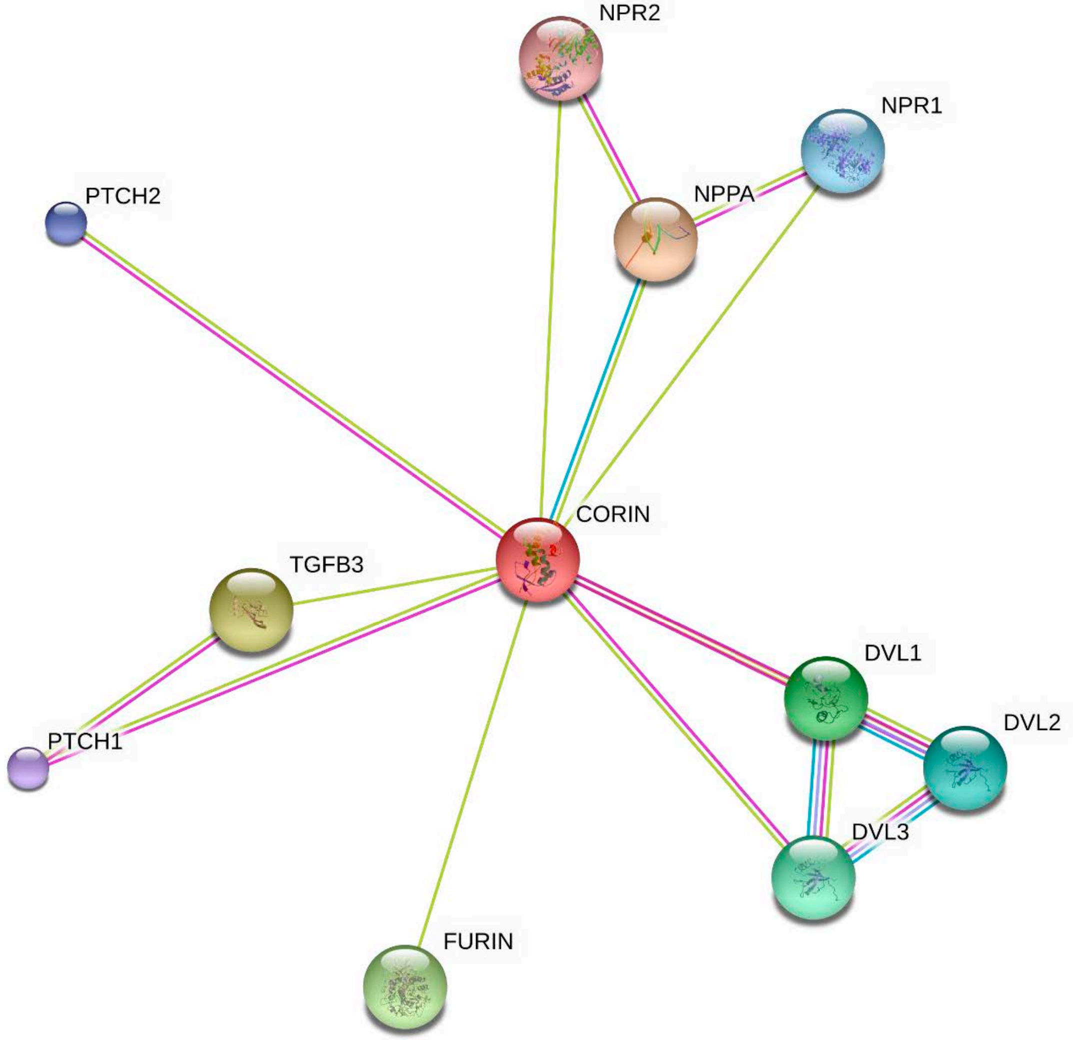
```
========================VLXT NNP STATISTICS================================
Predicted residues: 1042                      Number Disordered Regions: 10
Number residues disordered: 163               Longest Disordered Region: 30
Overall percent disordered: 15.64     Average Prediction Score: 0.2049
Predicted disorder segment [1]-[27]   Average Strength= 0.8110
Predicted disorder segment [86]-[110] Average Strength= 0.5816
Predicted disorder segment [216]-[219]Average Strength= 0.5134
Predicted disorder segment [402]-[419]Average Strength= 0.6391
Predicted disorder segment [528]-[538]Average Strength= 0.6265
Predicted disorder segment [554]-[576]Average Strength= 0.7156
Predicted disorder segment [738]-[743]Average Strength= 0.5789
Predicted disorder segment [784]-[813]Average Strength= 0.8767
Predicted disorder segment [902]-[912]Average Strength= 0.6699
Predicted disorder segment [978]-[985]Average Strength= 0.5767

========================VL3 NNP STATISTICS================================
Predicted residues: 1042                      Number Disordered Regions: 4
Number residues disordered: 371               Longest Disordered Region: 149
Overall percent disordered: 35.60     Average Prediction Score: 0.4311
Predicted disorder segment [1]-[31]   Average Strength= 0.7898
Predicted disorder segment [313]-[461]Average Strength= 0.7894
Predicted disorder segment [537]-[683]Average Strength= 0.7668
Predicted disorder segment [766]-[809]Average Strength= 0.6393

========================VSL2 NNP STATISTICS================================
Predicted residues: 1042                      Number Disordered Regions: 18
Number residues disordered: 433               Longest Disordered Region: 130
Overall percent disordered: 41.55     Average Prediction Score: 0.4379
Predicted disorder segment [1]-[34]   Average Strength= 0.7843
Predicted disorder segment [80]-[88]  Average Strength= 0.5513
Predicted disorder segment [111]-[119]Average Strength= 0.5295
```

```
Predicted disorder segment [123]-[140]Average Strength= 0.6123
Predicted disorder segment [244]-[254]Average Strength= 0.5990
Predicted disorder segment [258]-[268]Average Strength= 0.5912
Predicted disorder segment [323]-[325]Average Strength= 0.5188
Predicted disorder segment [329]-[458]Average Strength= 0.7642
Predicted disorder segment [460]-[462]Average Strength= 0.5380
Predicted disorder segment [483]-[487]Average Strength= 0.5698
Predicted disorder segment [551]-[642]Average Strength= 0.7603
Predicted disorder segment [645]-[663]Average Strength= 0.5546
Predicted disorder segment [667]-[686]Average Strength= 0.5702
Predicted disorder segment [739]-[750]Average Strength= 0.5525
Predicted disorder segment [757]-[764]Average Strength= 0.5463
Predicted disorder segment [770]-[810]Average Strength= 0.6353
Predicted disorder segment [901]-[902]Average Strength= 0.5036
Predicted disorder segment [979]-[984]Average Strength= 0.5369
```




NPR2
NPR1
PTCH2
NPPA
CORIN
TGFB3
DVL1
DVL2
PTCH1
DVL3
FURIN

```
>sp|Q9Y5Q5-2|CORIN_HUMAN Isoform 2 of Atrial natriuretic peptide-
converting enzyme OS=Homo sapiens GN=CORIN
MGNGCSQKLATANLLRFLLLVLIPCICALVLLLVILLSYVGTLQKVYFKSNGSEPLVTDG
EIQGSDVILTNTIYNQSTVVSTAHPDQHVPAWTTDASLPGDQSHRNTSACMNITHSQCQM
LPYHATLTPLLSVVRNMEMEKFLKFFTYLHRLSCYQHIMLFGCTLAFPECIIDGDDSHGL
LPCRSFCEAAKEGCESVLGMVNYSWPDFLRCSQFRNQTESSNVSRICFSPQQENGKQLLC
GRGENFLCASGICIPGKLQCNGYNDCDDWSDEAHCNCSENLFHCHTGKCLNYSLVCDGYD
DCGDLSDEQNCDCNPTTEHRCGDGRCIAMEWVCDGDHDCVDKSDEVNCSCHSQGLVECRN
GQCIPSTFQCDGDEDCKDGSDEENCSVIQTSCQEGDQRCLYNPCLDSCGGSSLCDPNNSL
NNCSQCEPITLELCMNLPYNSTSYPNYFGHRTQKEASISWESSLFPALVQTNCYKYLMFF
SCTILVPKCDVNTGEHIPPCRALCEHSKERCESVLGIVGLQWPEDTDCSQFPEENSDNQT
CLMPDEYVEECSPSHFKCRSGQCVLASRRCDGQADCDDDSDEENCGCKERDLWECPSNKQ
CLKHTVICDGFPDCPDYMDEKNCSFCQDDELECANHACVSRDLWCDGEADCSDSSDEWDC
VTLSINVNSSSFLMVHRAATEHHVCADGWQEILSQLACKQMGLGEPSVTKLIQEQEKEPR
WLTLHSNWESLNGTTLHELLVNGQSCESRSKISLLCTKQDCGRRPAARMNKRILGGRTSR
PGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGRENAAVWKVVLGINNLDHPSVF
MQTRFVKTIILHPRYSRAVVDYDISIVELSEDISETGYVRPVCLPNPEQWLEPDTYCYIT
GWGHMGNKMPFKLQEGEVRIISLEHCQSYFDMKTITTRMICAGYESGTVDSCMGDSGGPL
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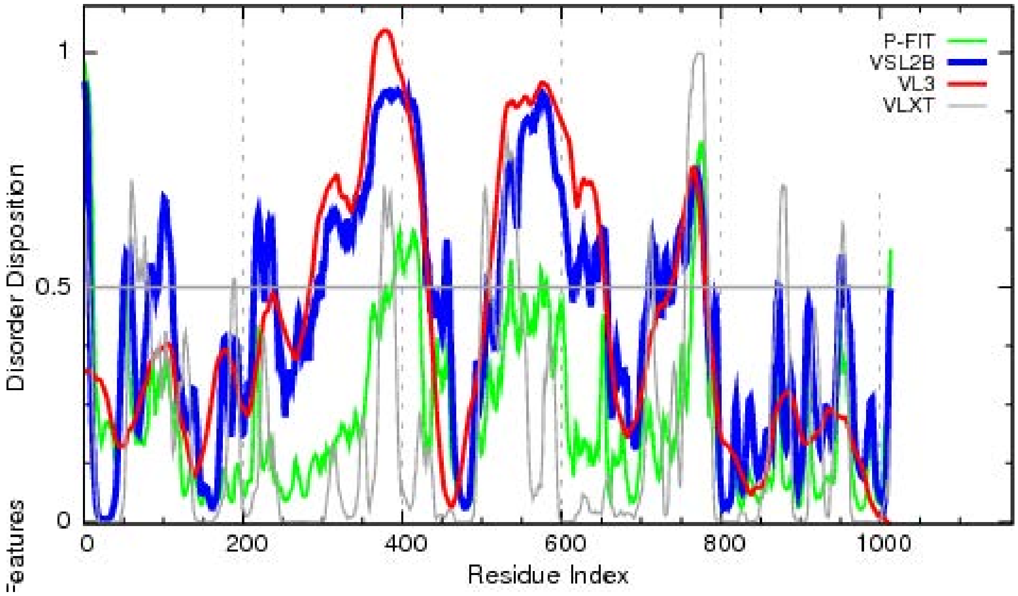

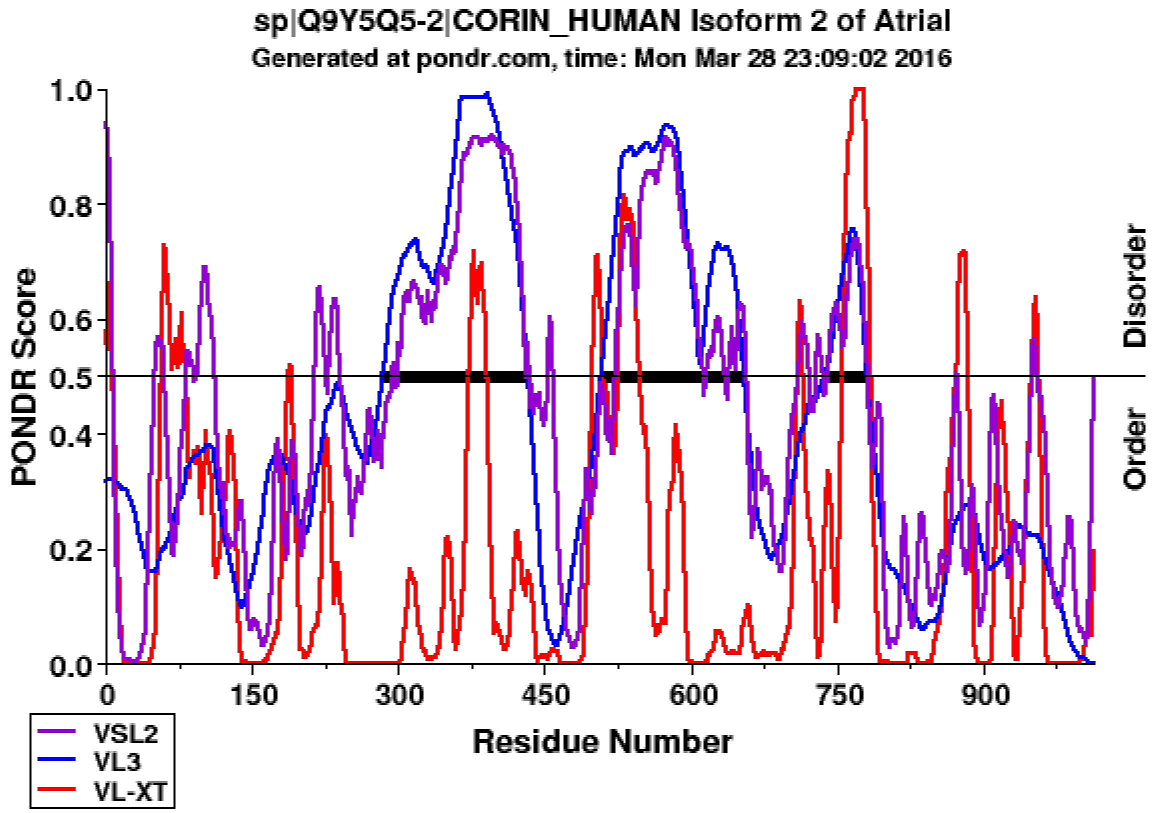
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PONDR Score
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0.5
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750
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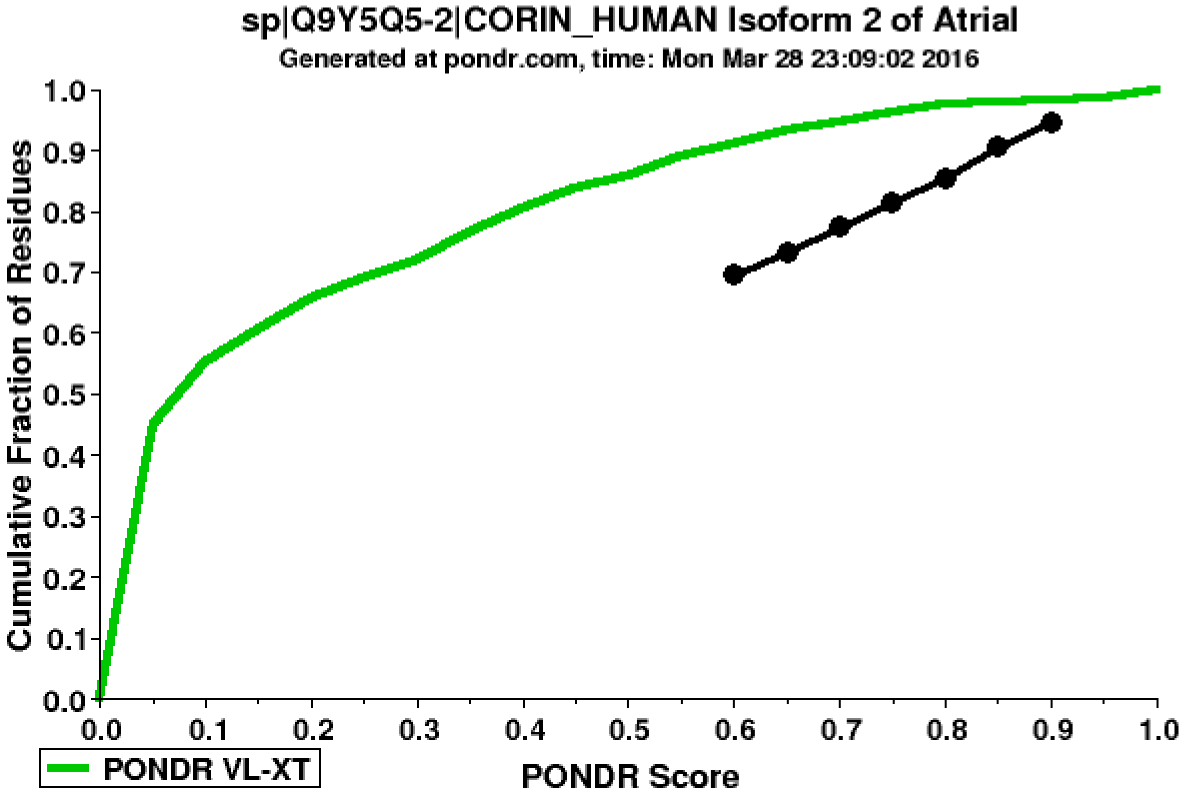
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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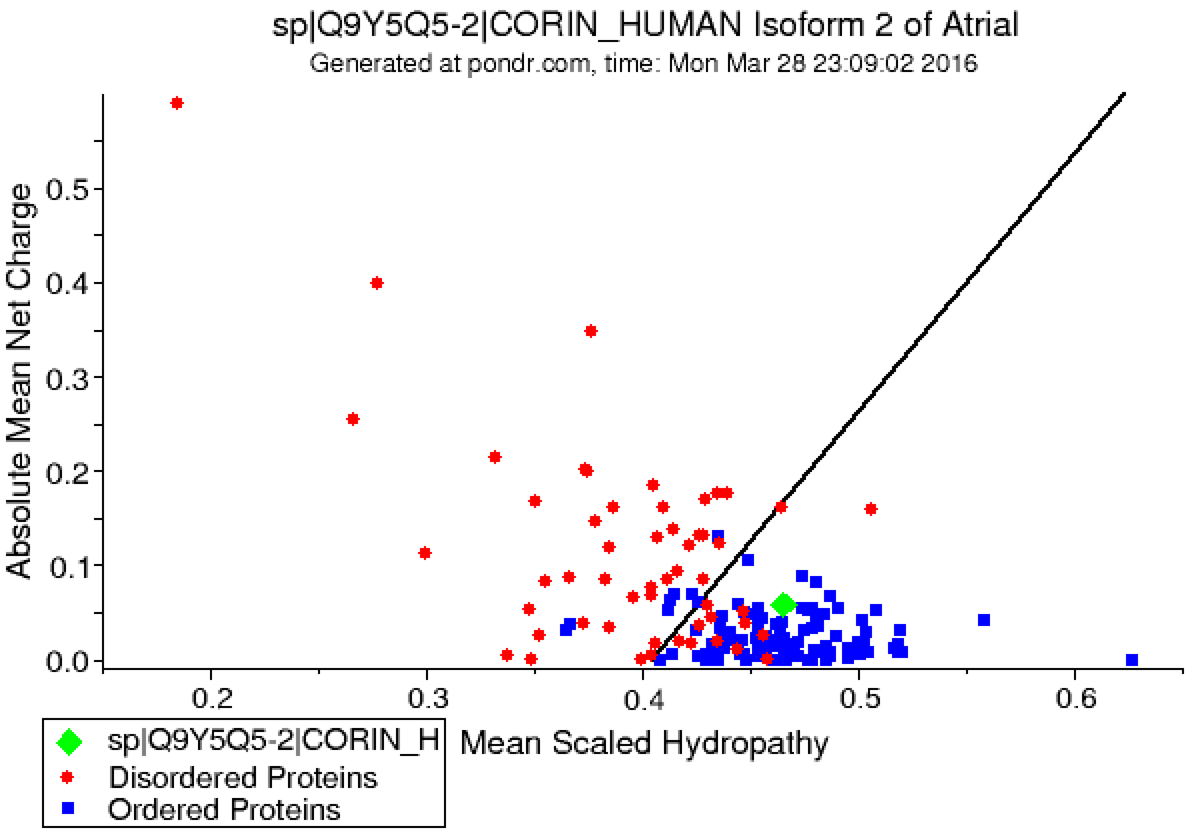
PONDR Score
PONDR VL-XT



```
========================VLXT NNP STATISTICS================================
Predicted residues: 1013                     Number Disordered Regions: 10
Number residues disordered: 143              Longest Disordered Region: 30
Overall percent disordered: 14.12      Average Prediction Score: 0.1933
Predicted disorder segment [1]-[7]     Average Strength= 0.5680
Predicted disorder segment [57]-[81]   Average Strength= 0.5816
Predicted disorder segment [187]-[190] Average Strength= 0.5134
Predicted disorder segment [373]-[390] Average Strength= 0.6391
Predicted disorder segment [499]-[509] Average Strength= 0.6265
Predicted disorder segment [525]-[547] Average Strength= 0.7156
Predicted disorder segment [709]-[714] Average Strength= 0.5789
Predicted disorder segment [755]-[784] Average Strength= 0.8767
Predicted disorder segment [873]-[883] Average Strength= 0.6699
Predicted disorder segment [949]-[956] Average Strength= 0.5767

========================VL3 NNP STATISTICS=================================
Predicted residues: 1013                     Number Disordered Regions: 3
Number residues disordered: 340              Longest Disordered Region: 149
Overall percent disordered: 33.56      Average Prediction Score: 0.4196
Predicted disorder segment [284]-[432] Average Strength= 0.7894
Predicted disorder segment [508]-[654] Average Strength= 0.7668
Predicted disorder segment [737]-[780] Average Strength= 0.6393

========================VSL2 NNP STATISTICS================================
Predicted residues: 1013                     Number Disordered Regions: 18
Number residues disordered: 406              Longest Disordered Region: 130
Overall percent disordered: 40.08      Average Prediction Score: 0.4288
Predicted disorder segment [1]-[7]     Average Strength= 0.8079
Predicted disorder segment [51]-[59]   Average Strength= 0.5513
Predicted disorder segment [82]-[90]   Average Strength= 0.5295
Predicted disorder segment [94]-[111]  Average Strength= 0.6123
```

```
Predicted disorder segment [215]-[225]Average Strength= 0.5990
Predicted disorder segment [229]-[239]Average Strength= 0.5912
Predicted disorder segment [294]-[296]Average Strength= 0.5188
Predicted disorder segment [300]-[429]Average Strength= 0.7642
Predicted disorder segment [431]-[433]Average Strength= 0.5380
Predicted disorder segment [454]-[458]Average Strength= 0.5698
Predicted disorder segment [522]-[613]Average Strength= 0.7603
Predicted disorder segment [616]-[634]Average Strength= 0.5546
Predicted disorder segment [638]-[657]Average Strength= 0.5702
Predicted disorder segment [710]-[721]Average Strength= 0.5525
Predicted disorder segment [728]-[735]Average Strength= 0.5463
Predicted disorder segment [741]-[781]Average Strength= 0.6353
Predicted disorder segment [872]-[873]Average Strength= 0.5036
Predicted disorder segment [950]-[955]Average Strength= 0.5369
```

```
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WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDK
MQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVK
AFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTA
TLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARC
DFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKMASTLVVADSRISGIYICIASNK
VGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTM
HYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVYTGEEILQKKEITIRDQEA
PYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQQEPGIILGPGSSTLFIER
VTEEDEGVYHCKATNQKGSVESSAYLTVQGTSDKSNLELITLTCTCVAATLFWLLLTLFI
RKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGK
VVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKILTHIGHHLNVVNLLGACTK
QGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSV
TSSESFASSGFQEDKSLSDVEEEEDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIH
RDLAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKS
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PKERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISA
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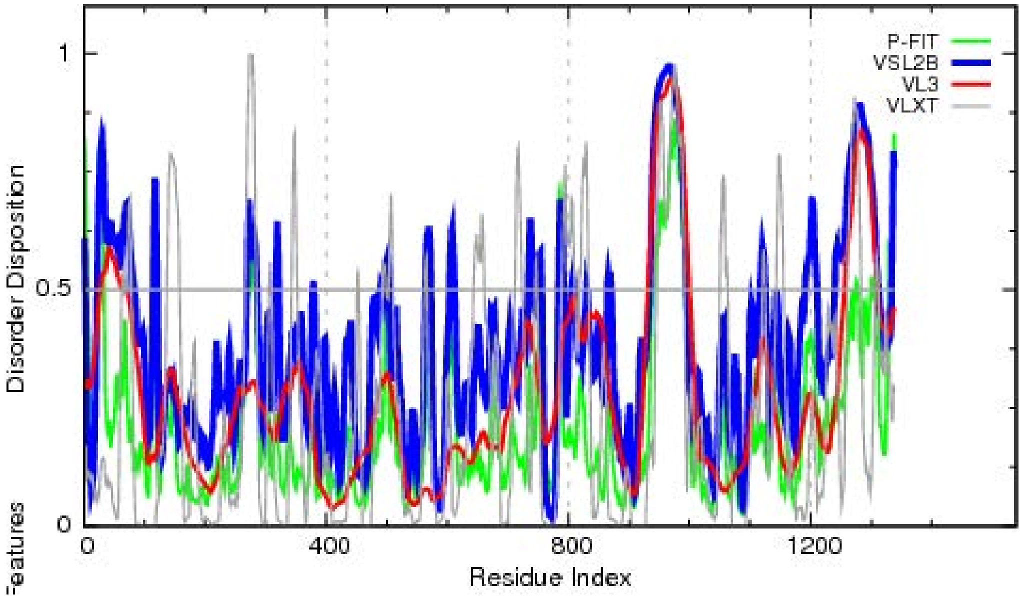

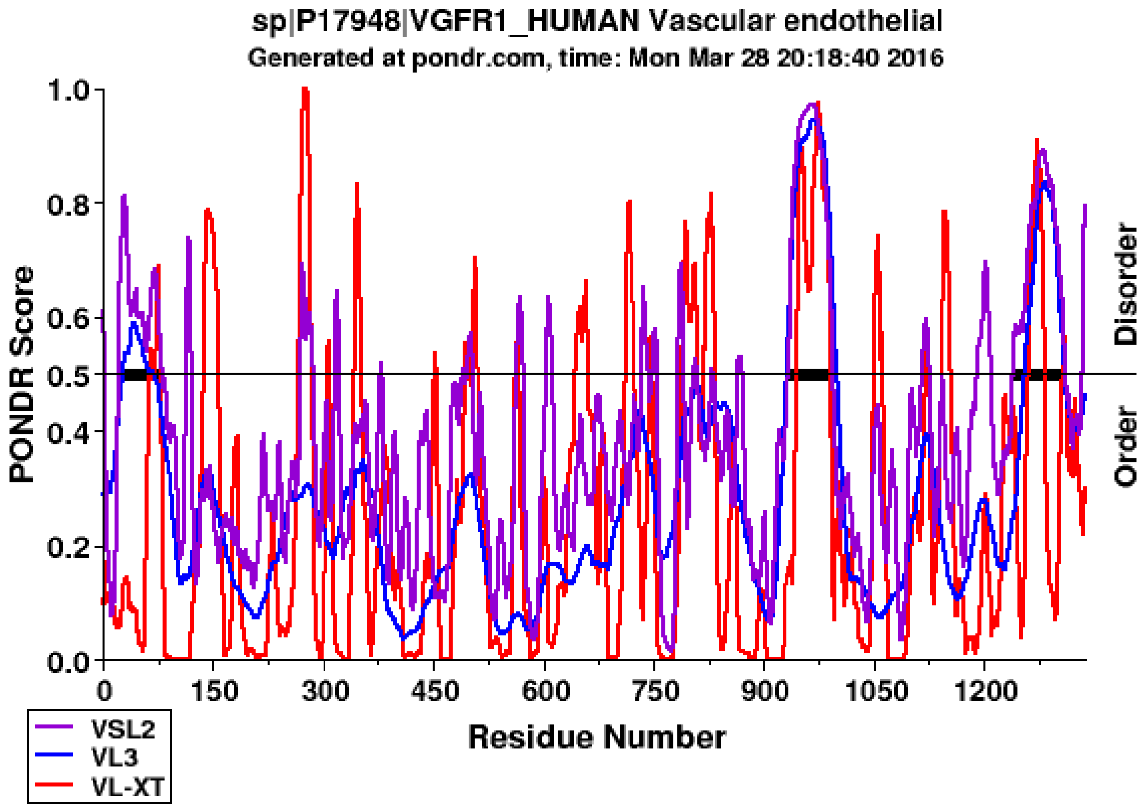
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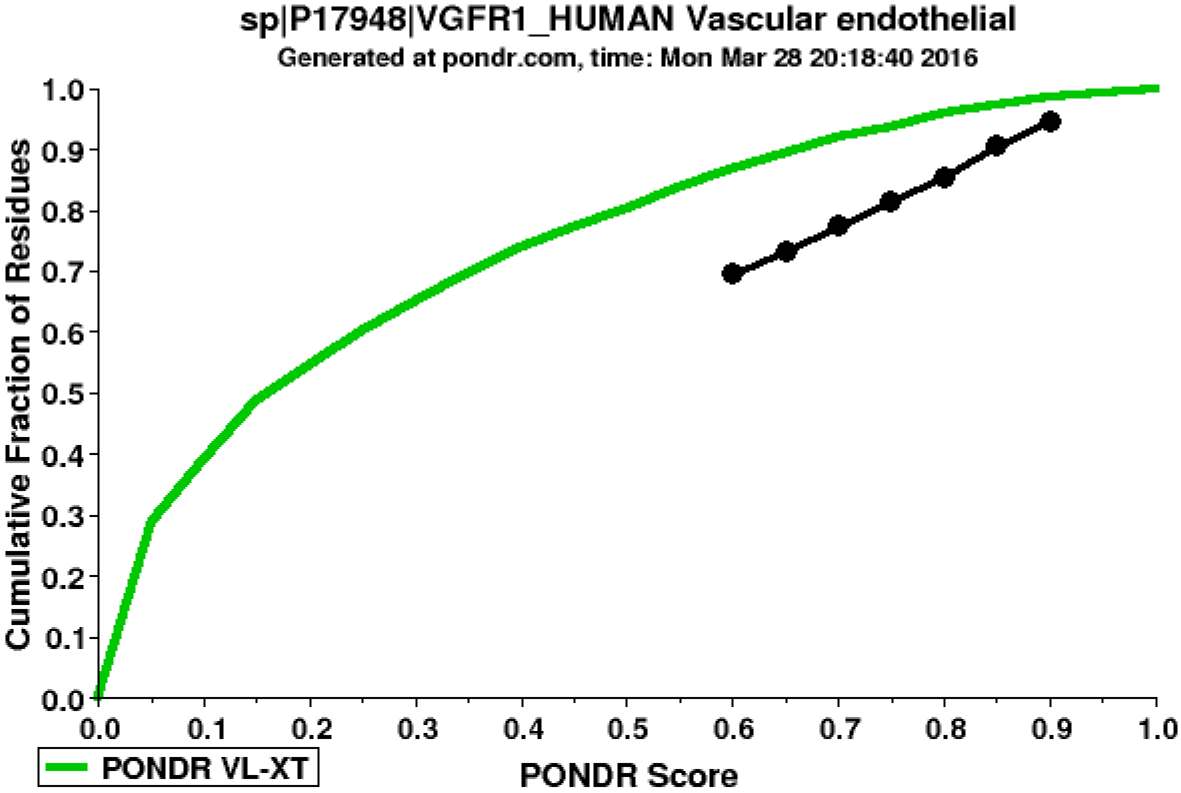
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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Cumulative Fraction of Residues
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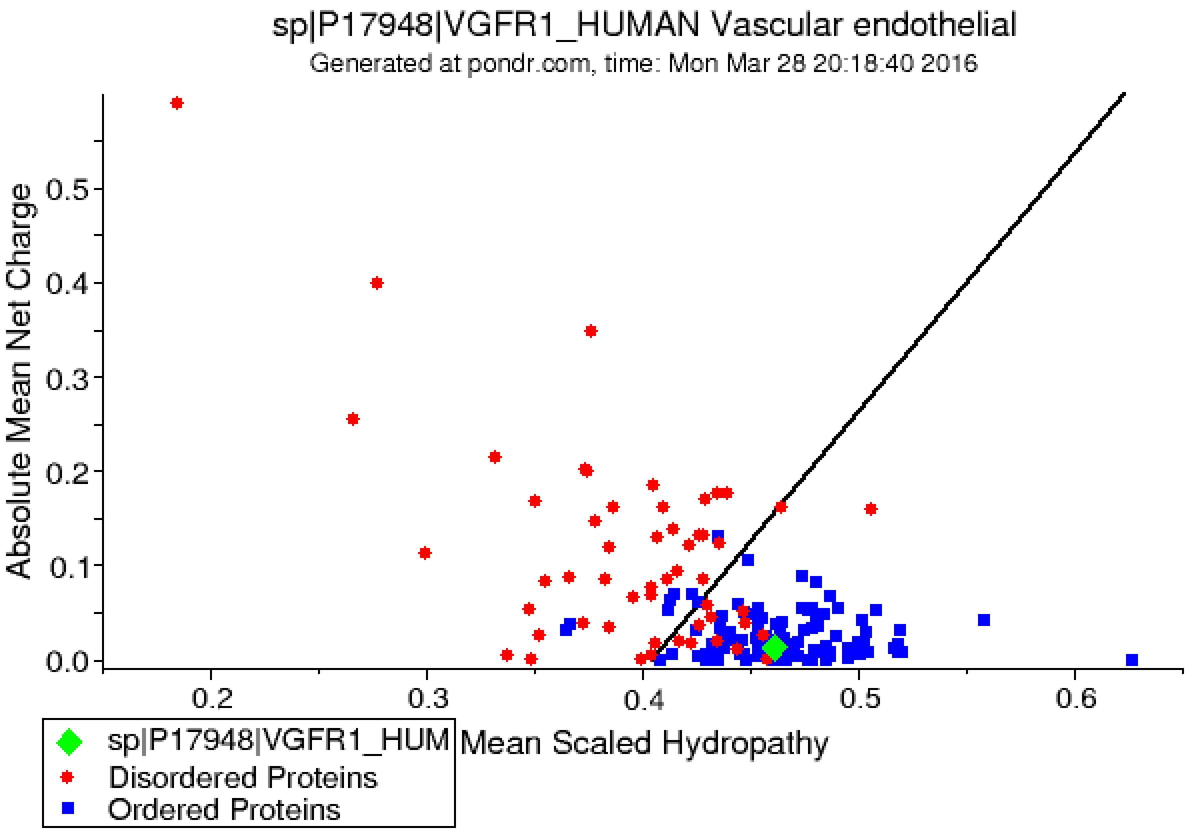
PONDR Score
PONDR VL-XT



```
========================VLXT NNP STATISTICS================================
Predicted residues: 1338                       Number Disordered Regions: 21
Number residues disordered: 265                Longest Disordered Region: 46
Overall percent disordered: 19.81      Average Prediction Score: 0.2548
Predicted disorder segment [63]-[67]   Average Strength= 0.5253
Predicted disorder segment [70]-[78]   Average Strength= 0.5990
Predicted disorder segment [137]-[157]Average Strength= 0.7081
Predicted disorder segment [266]-[284]Average Strength= 0.8337
Predicted disorder segment [306]-[309]Average Strength= 0.5323
Predicted disorder segment [343]-[352]Average Strength= 0.6979
Predicted disorder segment [451]-[453]Average Strength= 0.5333
Predicted disorder segment [493]-[498]Average Strength= 0.5394
Predicted disorder segment [503]-[510]Average Strength= 0.6131
Predicted disorder segment [563]-[567]Average Strength= 0.5417
Predicted disorder segment [644]-[660]Average Strength= 0.5876
Predicted disorder segment [711]-[723]Average Strength= 0.6820
Predicted disorder segment [745]-[747]Average Strength= 0.5448
Predicted disorder segment [789]-[810]Average Strength= 0.6340
Predicted disorder segment [818]-[833]Average Strength= 0.6881
Predicted disorder segment [946]-[991]Average Strength= 0.7961
Predicted disorder segment [1051]-[1062]       Average Strength= 0.6313
Predicted disorder segment [1121]-[1124]       Average Strength= 0.5638
Predicted disorder segment [1143]-[1155]       Average Strength= 0.6823
Predicted disorder segment [1261]-[1283]       Average Strength= 0.7577
Predicted disorder segment [1307]-[1312]       Average Strength= 0.5398

========================VL3 NNP STATISTICS================================
Predicted residues: 1338                       Number Disordered Regions: 3
Number residues disordered: 166                Longest Disordered Region: 68
Overall percent disordered: 12.41      Average Prediction Score: 0.2848
Predicted disorder segment [27]-[69]   Average Strength= 0.5398
```

```
Predicted disorder segment [932]-[999]Average Strength= 0.8242
Predicted disorder segment [1256]-[1310]      Average Strength= 0.7098

========================VSL2 NNP STATISTICS================================
Predicted residues: 1338                      Number Disordered Regions: 22
Number residues disordered: 329               Longest Disordered Region: 72
Overall percent disordered: 24.59      Average Prediction Score: 0.3823
Predicted disorder segment [1]-[2]     Average Strength= 0.5727
Predicted disorder segment [22]-[79]   Average Strength= 0.6396
Predicted disorder segment [114]-[121]Average Strength= 0.6256
Predicted disorder segment [269]-[285]Average Strength= 0.5983
Predicted disorder segment [317]-[322]Average Strength= 0.5797
Predicted disorder segment [379]-[380]Average Strength= 0.5123
Predicted disorder segment [490]-[492]Average Strength= 0.5073
Predicted disorder segment [495]-[495]Average Strength= 0.5002
Predicted disorder segment [497]-[503]Average Strength= 0.5475
Predicted disorder segment [564]-[572]Average Strength= 0.5935
Predicted disorder segment [604]-[612]Average Strength= 0.5762
Predicted disorder segment [734]-[743]Average Strength= 0.5718
Predicted disorder segment [749]-[755]Average Strength= 0.5582
Predicted disorder segment [784]-[791]Average Strength= 0.6245
Predicted disorder segment [805]-[810]Average Strength= 0.5140
Predicted disorder segment [830]-[830]Average Strength= 0.5077
Predicted disorder segment [865]-[870]Average Strength= 0.5224
Predicted disorder segment [934]-[994]Average Strength= 0.8569
Predicted disorder segment [1116]-[1126]      Average Strength= 0.5531
Predicted disorder segment [1191]-[1210]      Average Strength= 0.5929
Predicted disorder segment [1240]-[1311]      Average Strength= 0.7271
Predicted disorder segment [1334]-[1338]      Average Strength= 0.6908
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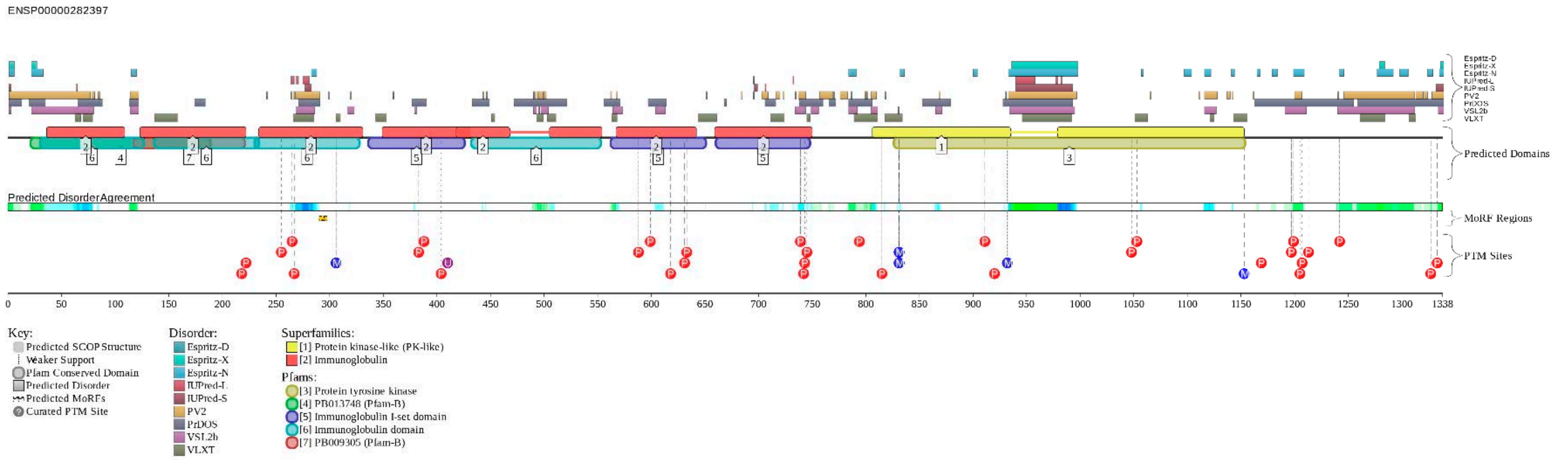

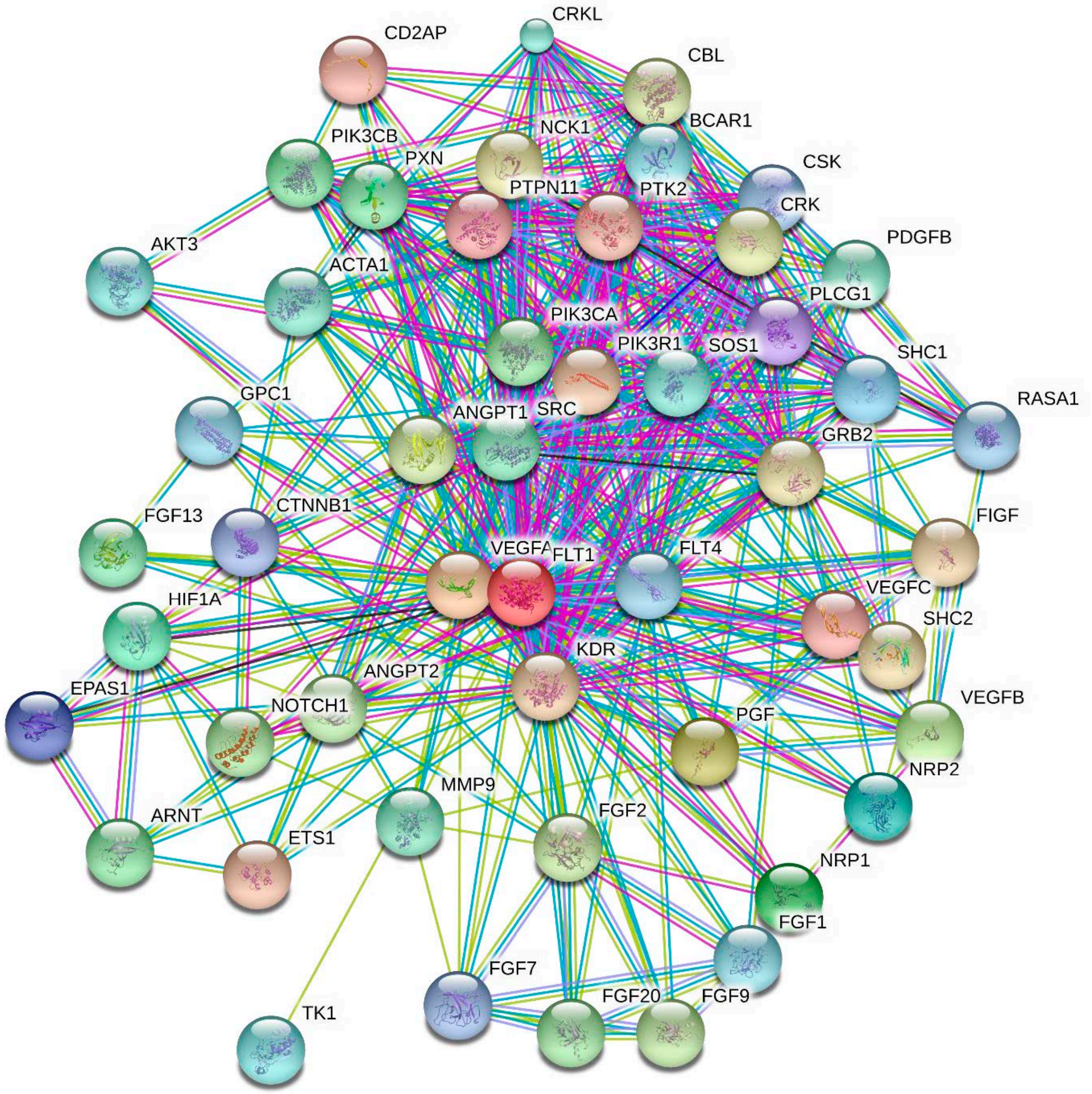

Predicted Disordered Binding Regions			
	From	To	Length
1	290	297	8

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receptor 1 OS=Homo sapiens GN=FLT1
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WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDK
MQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVK
AFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTA
TLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARC
DFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKMASTLVVADSRISGIYICIASNK
VGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTM
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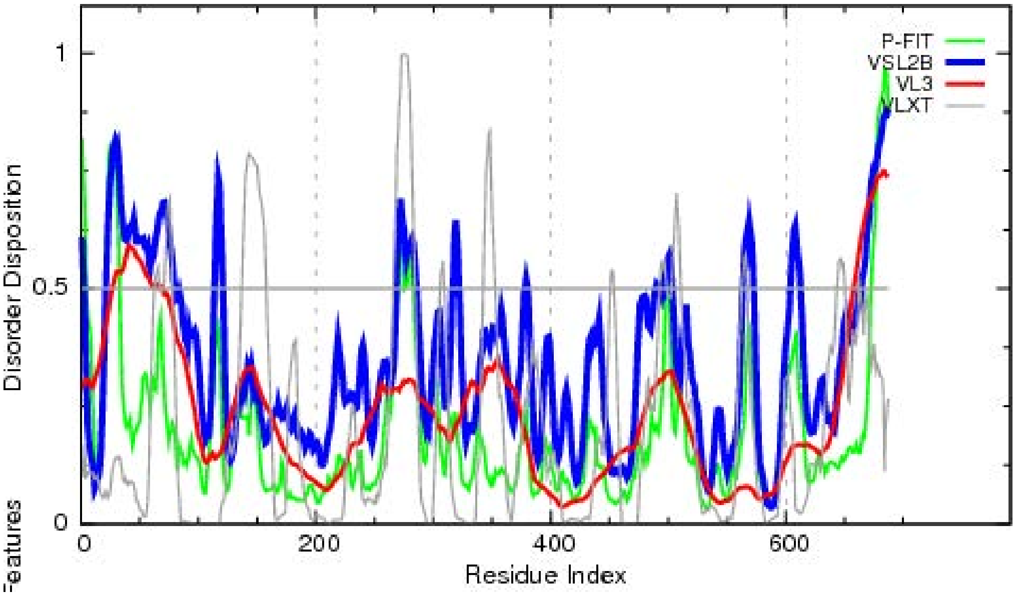
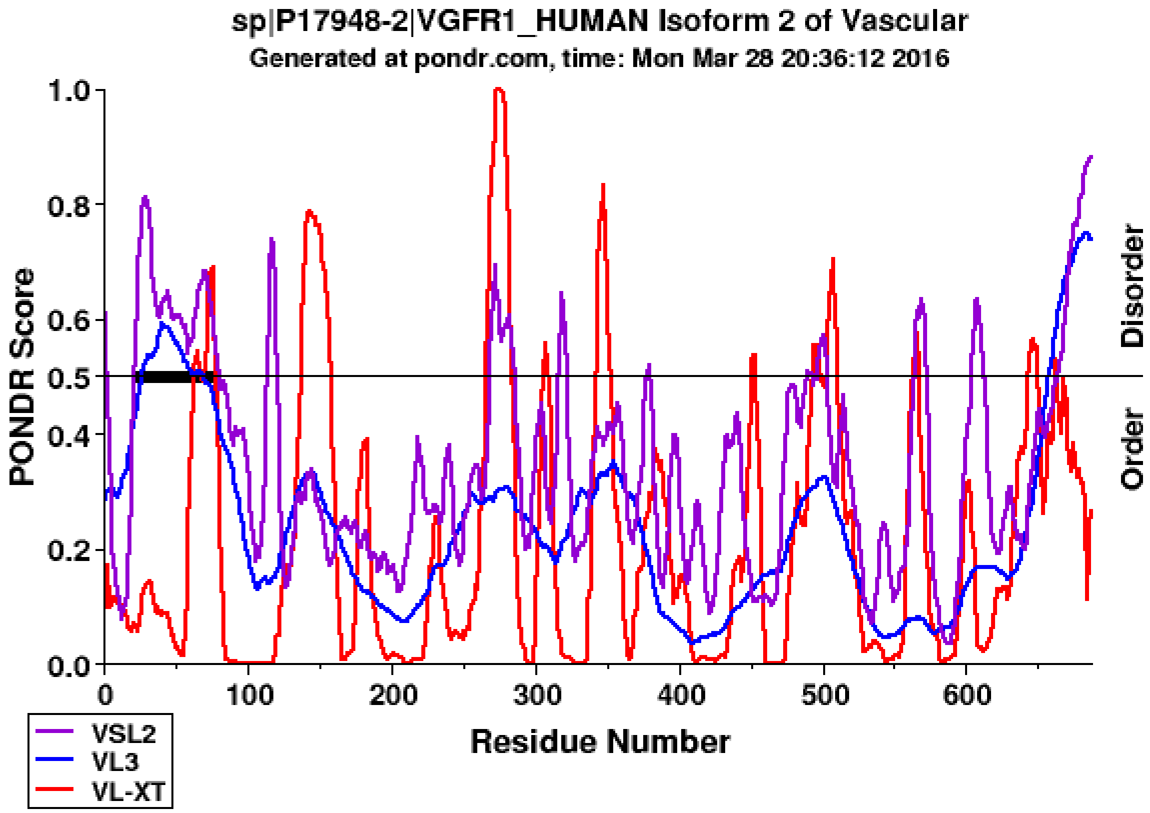


Predicted Disordered Binding Regions

	From	To	Length
1	290	297	8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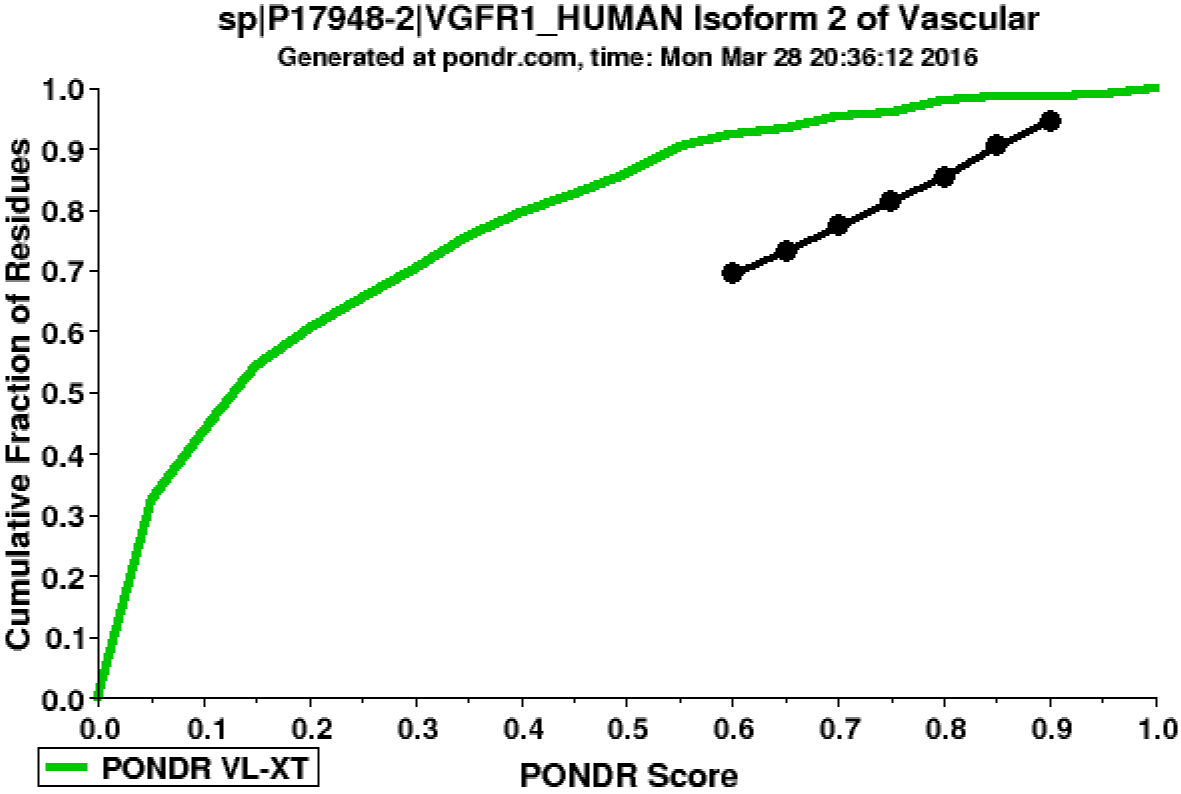
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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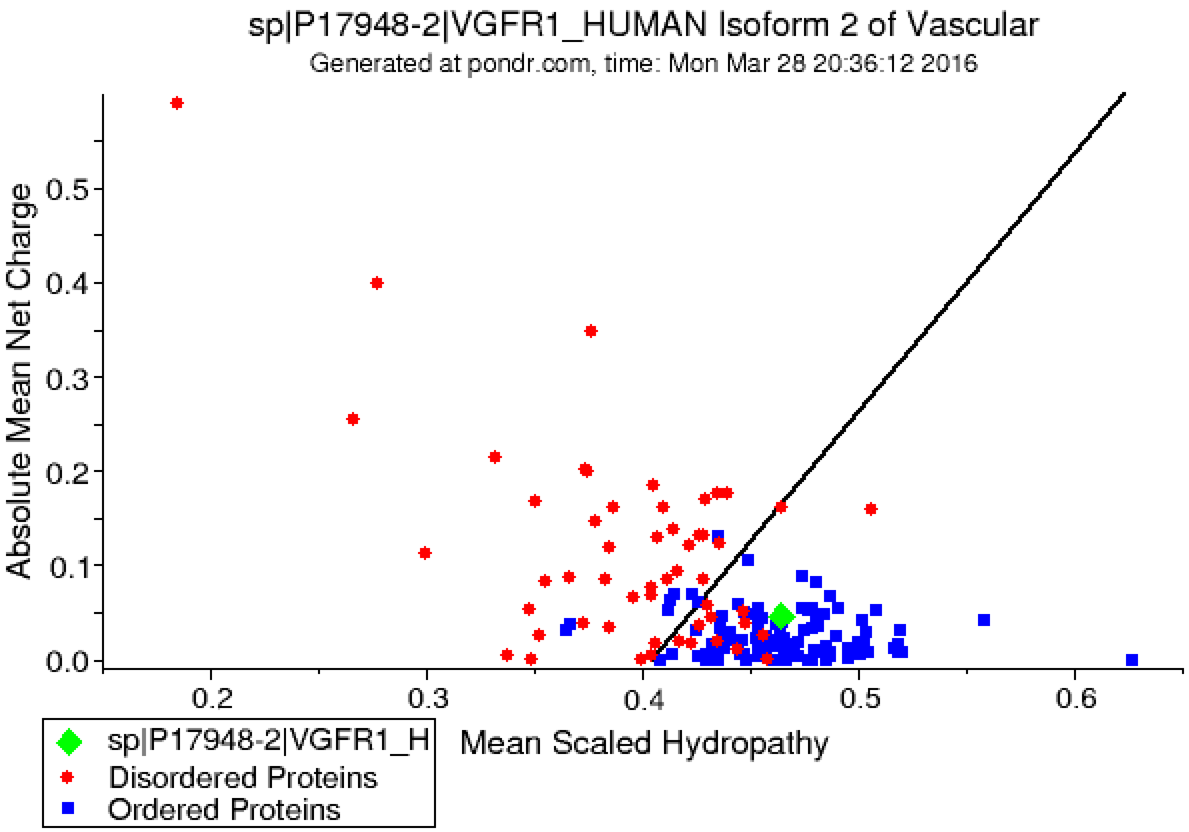
PONDR Score
PONDR VL-XT



```
========================VLXT NNP STATISTICS=================================
Predicted residues: 687                        Number Disordered Regions: 12
Number residues disordered: 98         Longest Disordered Region: 21
Overall percent disordered: 14.26      Average Prediction Score: 0.2156
Predicted disorder segment [63]-[67]   Average Strength= 0.5253
Predicted disorder segment [70]-[78]   Average Strength= 0.5990
Predicted disorder segment [137]-[157]Average Strength= 0.7081
Predicted disorder segment [266]-[284]Average Strength= 0.8337
Predicted disorder segment [306]-[309]Average Strength= 0.5323
Predicted disorder segment [343]-[352]Average Strength= 0.6979
Predicted disorder segment [451]-[453]Average Strength= 0.5333
Predicted disorder segment [493]-[498]Average Strength= 0.5394
Predicted disorder segment [503]-[510]Average Strength= 0.6131
Predicted disorder segment [563]-[567]Average Strength= 0.5417
Predicted disorder segment [644]-[650]Average Strength= 0.5456
Predicted disorder segment [662]-[662]Average Strength= 0.5290

========================VL3 NNP STATISTICS=================================
Predicted residues: 687                        Number Disordered Regions: 2
Number residues disordered: 73         Longest Disordered Region: 43
Overall percent disordered: 10.63      Average Prediction Score: 0.2409
Predicted disorder segment [27]-[69]   Average Strength= 0.5400
Predicted disorder segment [658]-[687]Average Strength= 0.6713

========================VSL2 NNP STATISTICS=================================
Predicted residues: 687                        Number Disordered Regions: 13
Number residues disordered: 146                Longest Disordered Region: 58
Overall percent disordered: 21.25      Average Prediction Score: 0.3472
Predicted disorder segment [1]-[2]     Average Strength= 0.5727
Predicted disorder segment [22]-[79]   Average Strength= 0.6396
Predicted disorder segment [114]-[121]Average Strength= 0.6256
```

```
Predicted disorder segment [269]-[285]Average Strength= 0.5983
Predicted disorder segment [317]-[322]Average Strength= 0.5797
Predicted disorder segment [379]-[380]Average Strength= 0.5123
Predicted disorder segment [490]-[492]Average Strength= 0.5073
Predicted disorder segment [495]-[495]Average Strength= 0.5002
Predicted disorder segment [497]-[503]Average Strength= 0.5475
Predicted disorder segment [564]-[572]Average Strength= 0.5935
Predicted disorder segment [604]-[612]Average Strength= 0.5762
Predicted disorder segment [663]-[663]Average Strength= 0.5015
Predicted disorder segment [665]-[687]Average Strength= 0.7367
```

```
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MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK
WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
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MQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVK
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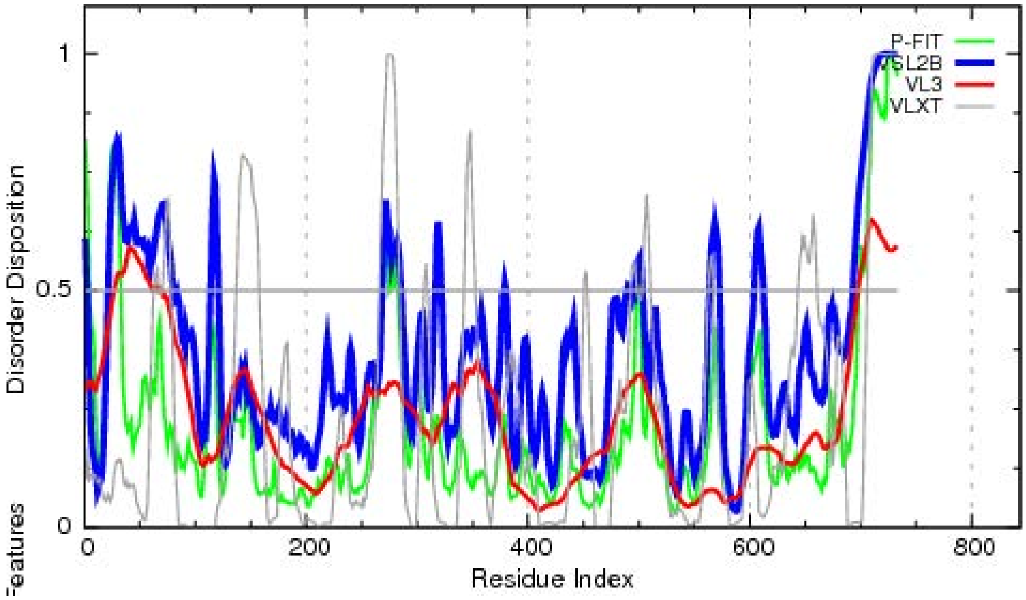

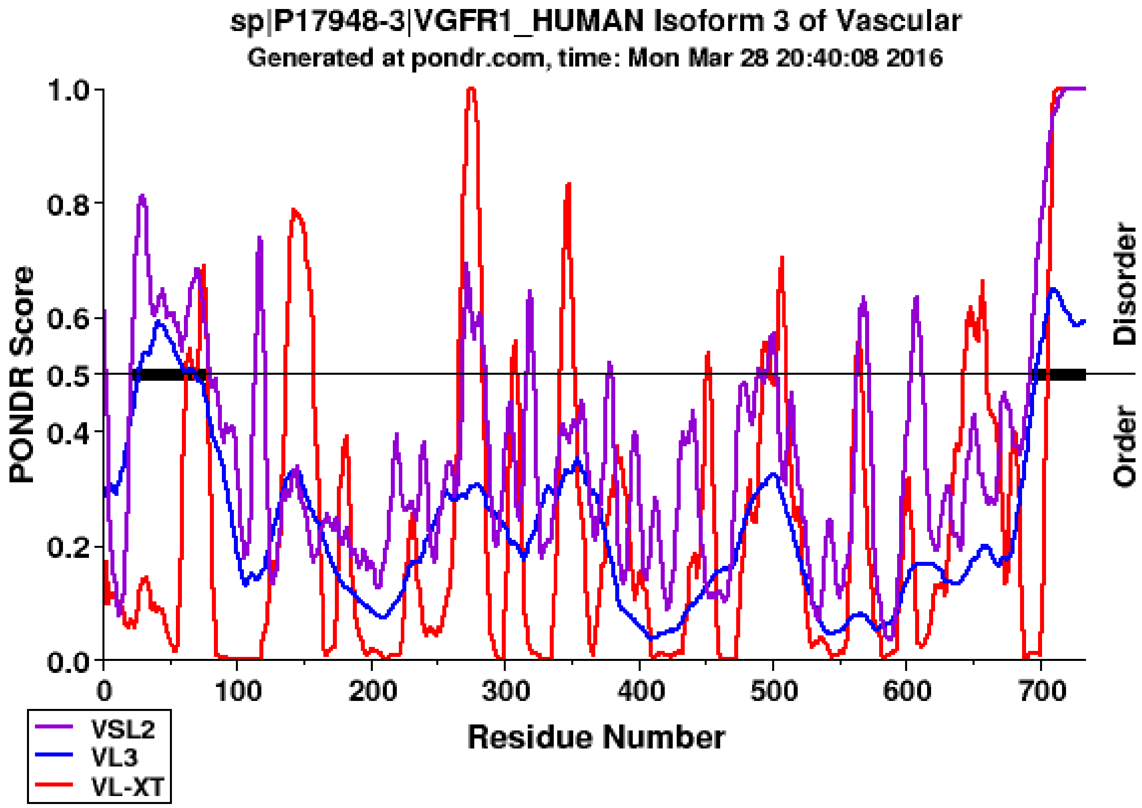
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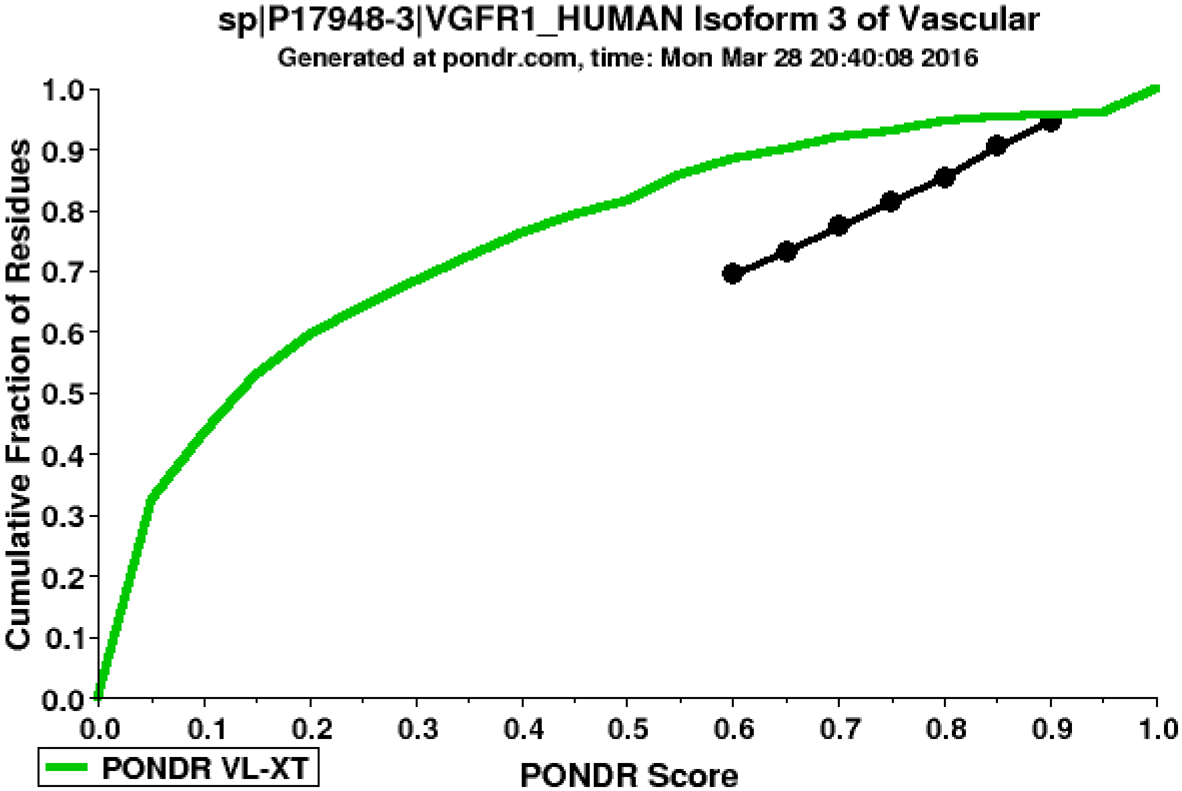
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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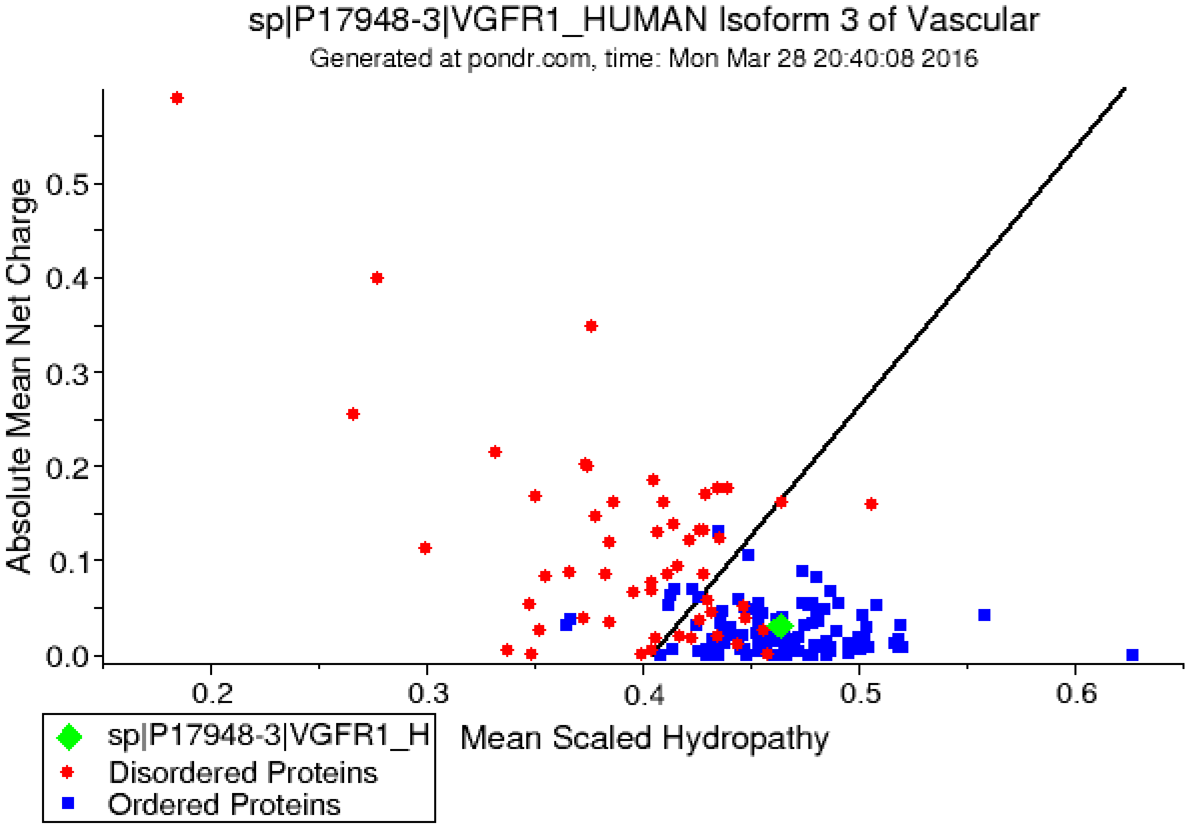

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========================VLXT NNP STATISTICS================================
Predicted residues: 733                       Number Disordered Regions: 12
Number residues disordered: 135               Longest Disordered Region: 28
Overall percent disordered: 18.42     Average Prediction Score: 0.2419
Predicted disorder segment [63]-[67]  Average Strength= 0.5253
Predicted disorder segment [70]-[78]  Average Strength= 0.5990
Predicted disorder segment [137]-[157]Average Strength= 0.7081
Predicted disorder segment [266]-[284]Average Strength= 0.8337
Predicted disorder segment [306]-[309]Average Strength= 0.5323
Predicted disorder segment [343]-[352]Average Strength= 0.6979
Predicted disorder segment [451]-[453]Average Strength= 0.5333
Predicted disorder segment [493]-[498]Average Strength= 0.5394
Predicted disorder segment [503]-[510]Average Strength= 0.6131
Predicted disorder segment [563]-[567]Average Strength= 0.5417
Predicted disorder segment [644]-[660]Average Strength= 0.5876
Predicted disorder segment [706]-[733]Average Strength= 0.9514

========================VL3 NNP STATISTICS================================
Predicted residues: 733                       Number Disordered Regions: 2
Number residues disordered: 79        Longest Disordered Region: 43
Overall percent disordered: 10.78     Average Prediction Score: 0.2368
Predicted disorder segment [27]-[69]  Average Strength= 0.5400
Predicted disorder segment [698]-[733]Average Strength= 0.5987

========================VSL2 NNP STATISTICS================================
Predicted residues: 733                       Number Disordered Regions: 12
Number residues disordered: 163               Longest Disordered Region: 58
Overall percent disordered: 22.24     Average Prediction Score: 0.3647
Predicted disorder segment [1]-[2]    Average Strength= 0.5727
Predicted disorder segment [22]-[79]  Average Strength= 0.6396
Predicted disorder segment [114]-[121]Average Strength= 0.6256
Predicted disorder segment [269]-[285]Average Strength= 0.5983
```
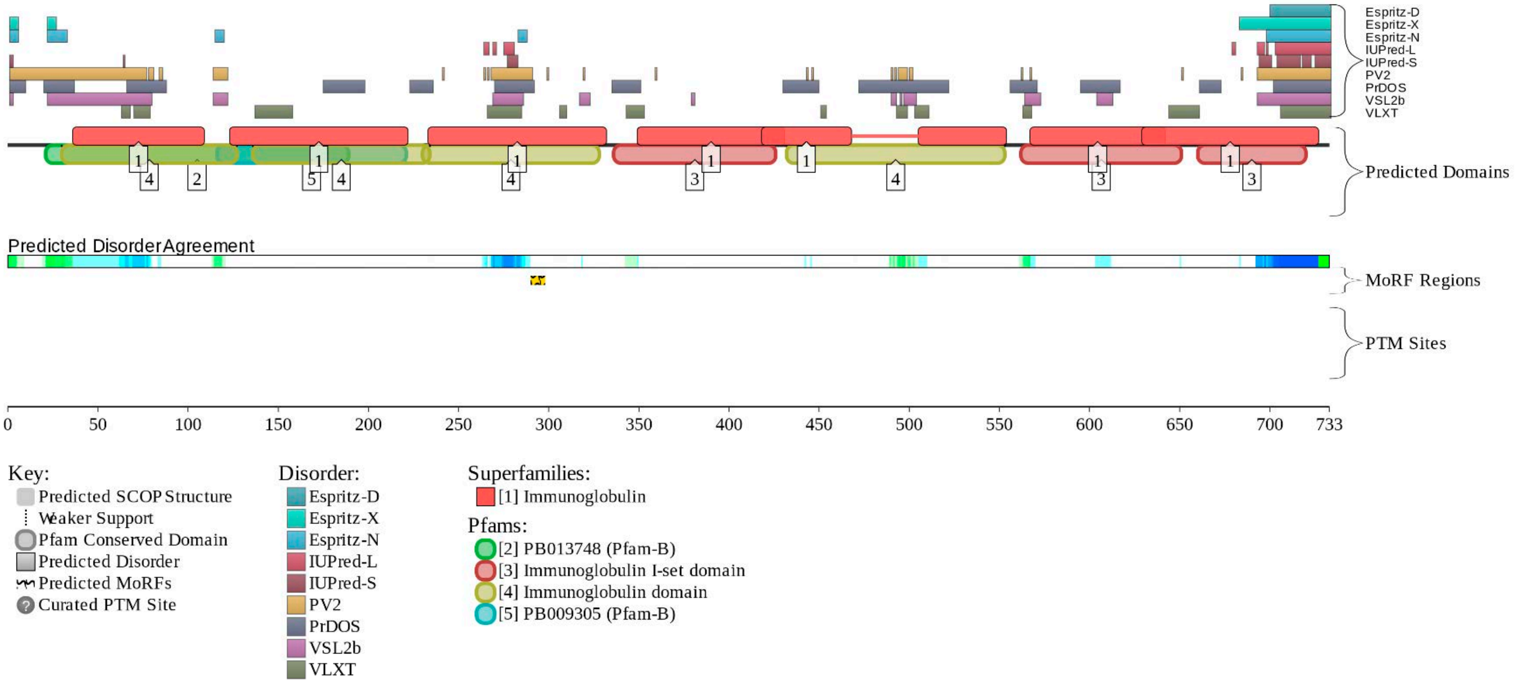

```
Predicted disorder segment [317]-[322]Average Strength= 0.5797
Predicted disorder segment [379]-[380]Average Strength= 0.5123
Predicted disorder segment [490]-[492]Average Strength= 0.5073
Predicted disorder segment [495]-[495]Average Strength= 0.5002
Predicted disorder segment [497]-[503]Average Strength= 0.5475
Predicted disorder segment [564]-[572]Average Strength= 0.5935
Predicted disorder segment [604]-[612]Average Strength= 0.5762
Predicted disorder segment [693]-[733]Average Strength= 0.8889
```

ENSP00000437631



Predicted Disordered Binding Regions

	From	To	Length
1	290	297	8

```
>sp|P17948-4|VGFR1_HUMAN Isoform 4 of Vascular endothelial growth factor
receptor 1 OS=Homo sapiens GN=FLT1
MVSYWDTGVLLCALLSCLLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK
WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDK
MQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVK
AFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTA
TLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARC
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P
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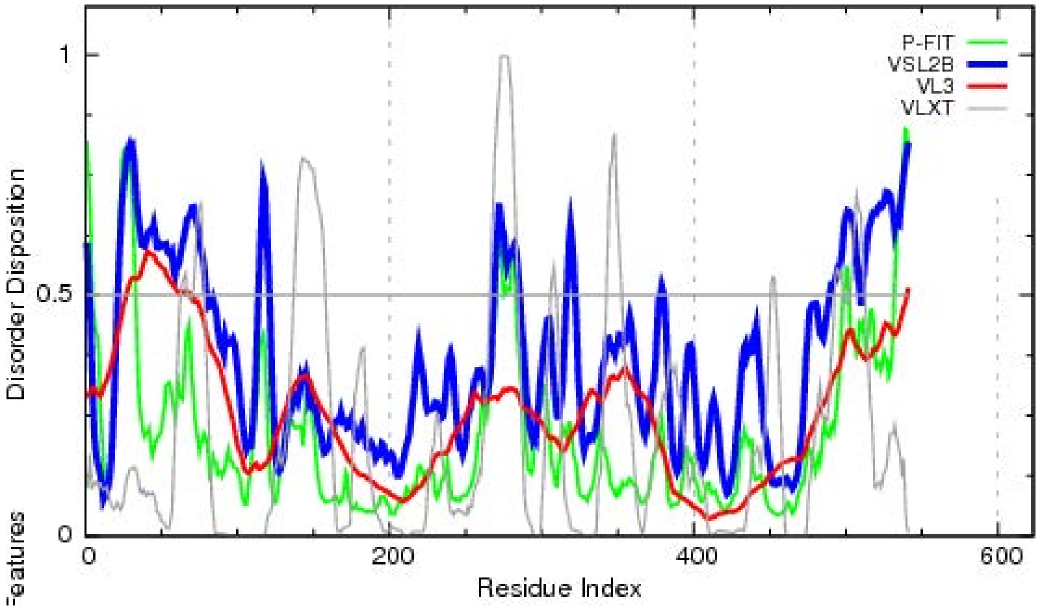
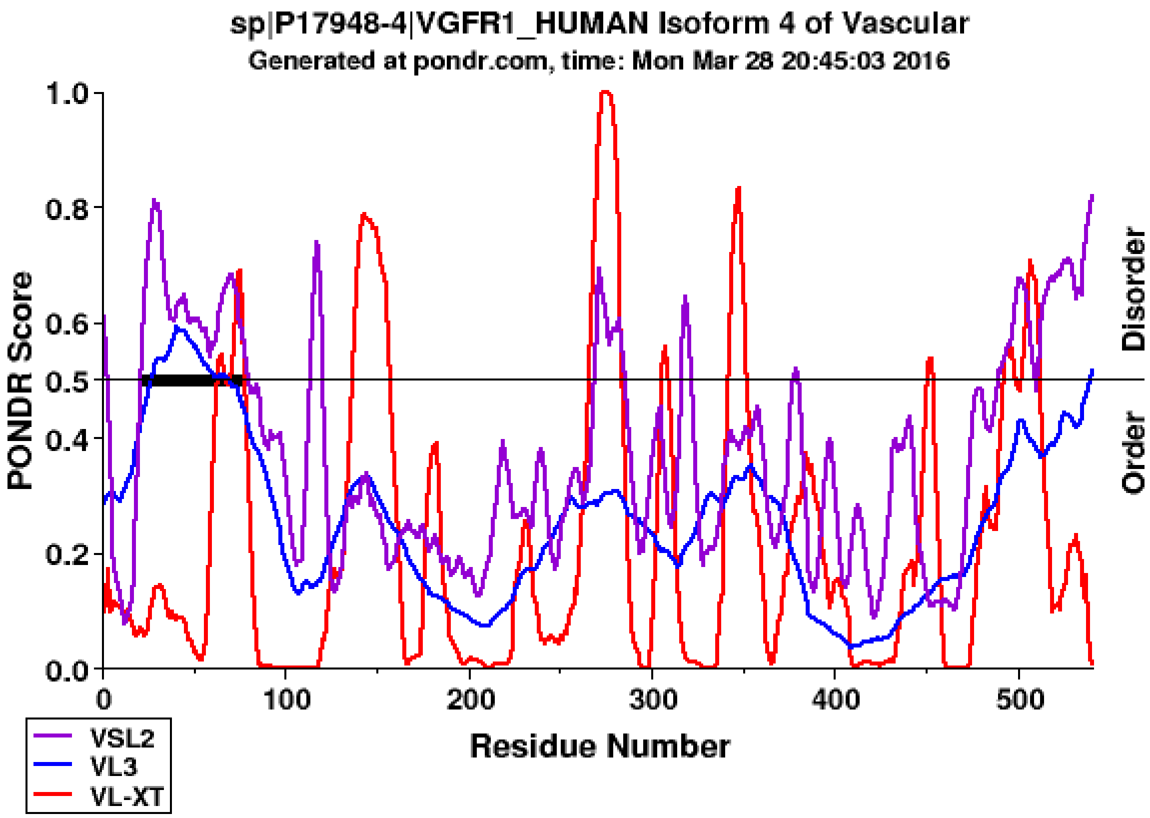
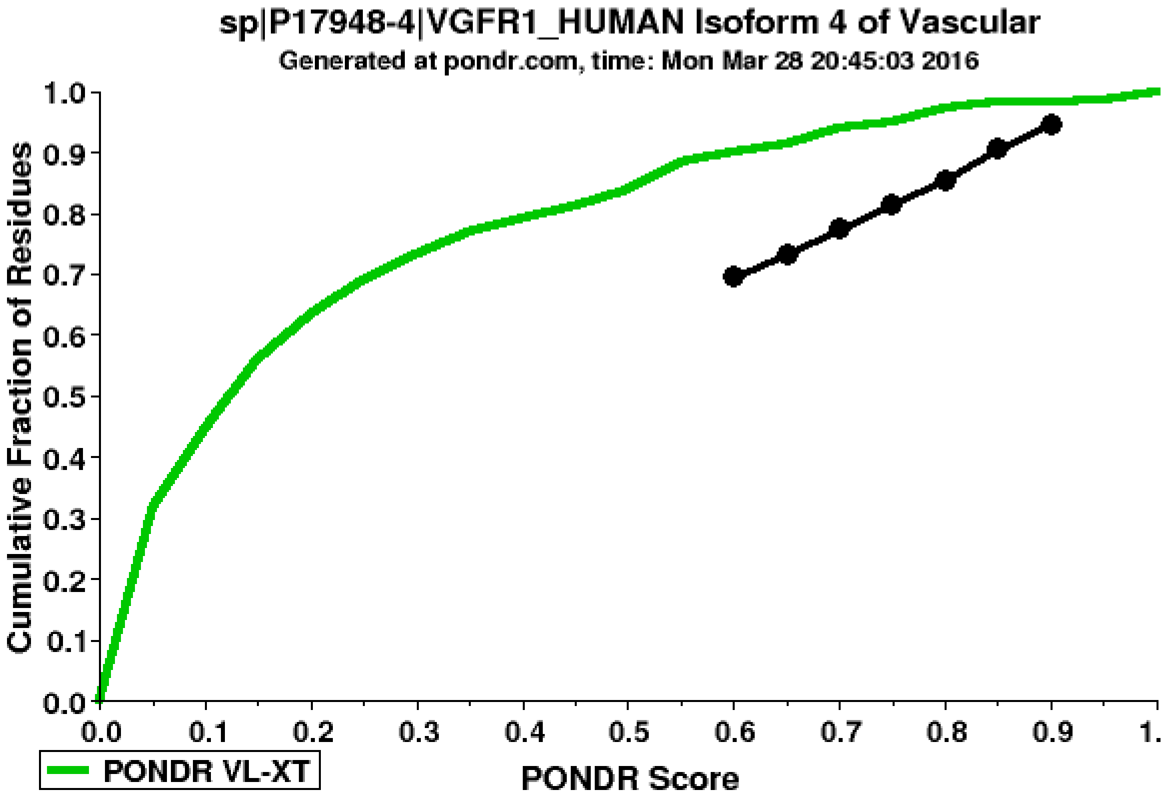
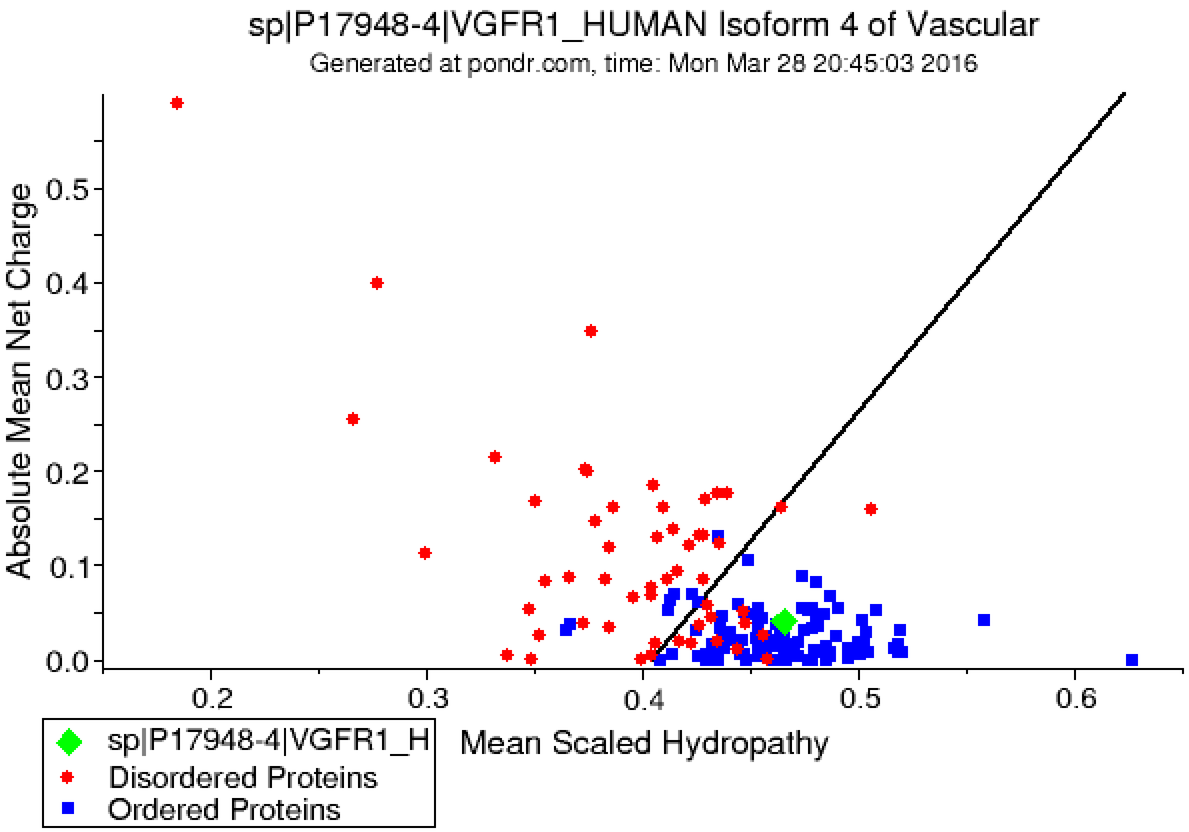



sp|P17948-4|VGFR1_HUMAN Isoform 4 of Vascular
Generated at pondr.com, time: Mon Mar 28 20:45:03 2016
PONDR Score
1.0
0.8
0.6
0.5
0.4
0.2
0.0
0
100
200
300
400
500
Residue Number
Disorder
Order
VSL2
VL3
VL-XT


sp|P17948-4|VGFR1_HUMAN Isoform 4 of Vascular
Generated at pondr.com, time: Mon Mar 28 20:45:03 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT


sp|P17948-4|VGFR1_HUMAN Isoform 4 of Vascular

Generated at pondr.com, time: Mon Mar 28 20:45:03 2016

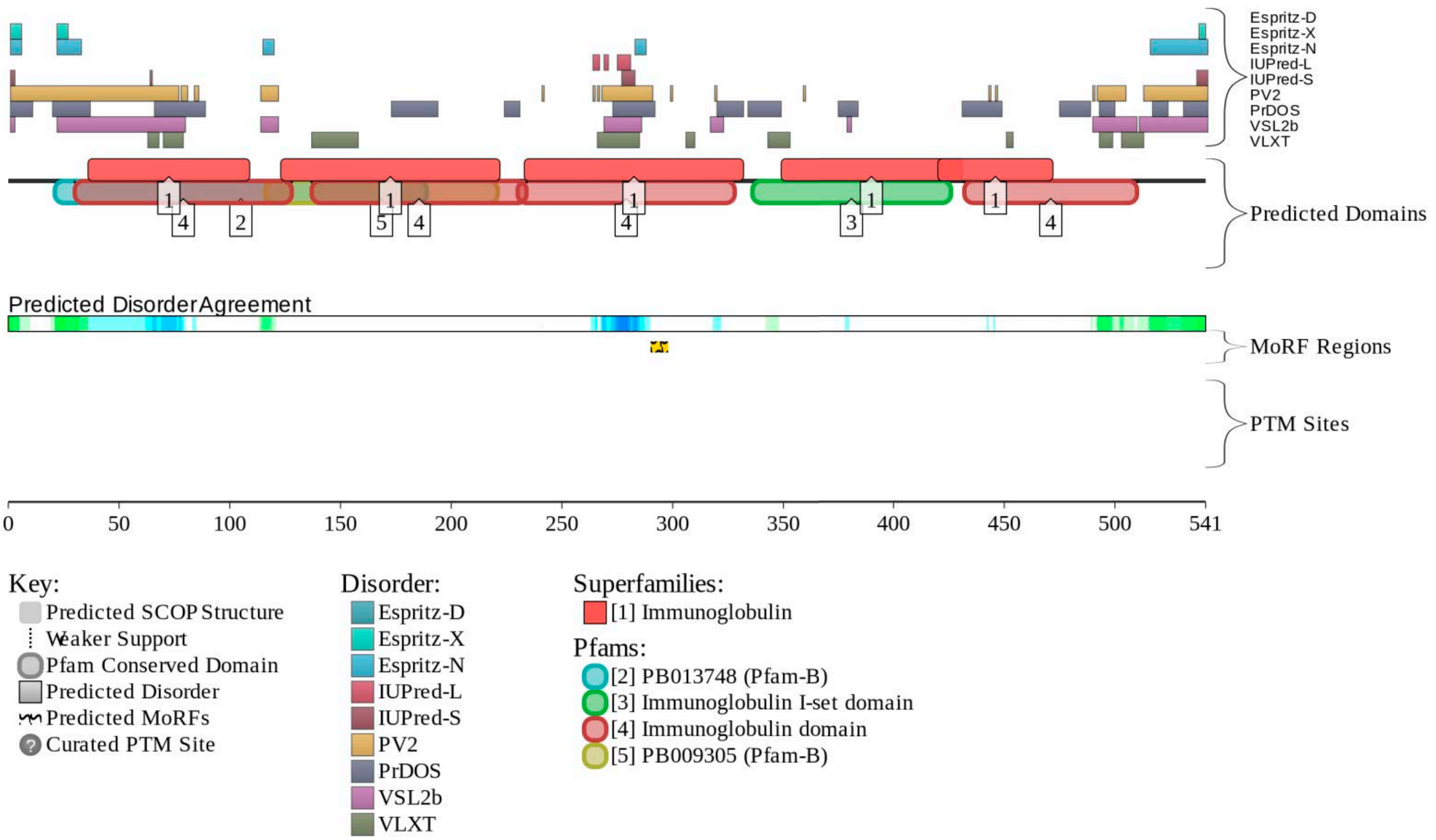
```
=======================VLXT NNP STATISTICS================================
Predicted residues: 541                          Number Disordered Regions: 9
Number residues disordered: 87           Longest Disordered Region: 21
Overall percent disordered: 16.08        Average Prediction Score: 0.2154
Predicted disorder segment [63]-[67]     Average Strength= 0.5253
Predicted disorder segment [70]-[78]     Average Strength= 0.5990
Predicted disorder segment [137]-[157]Average Strength= 0.7081
Predicted disorder segment [266]-[284]Average Strength= 0.8337
Predicted disorder segment [306]-[309]Average Strength= 0.5323
Predicted disorder segment [343]-[352]Average Strength= 0.6979
Predicted disorder segment [451]-[453]Average Strength= 0.5333
Predicted disorder segment [493]-[498]Average Strength= 0.5394
Predicted disorder segment [503]-[512]Average Strength= 0.6209

========================VL3 NNP STATISTICS================================
Predicted residues: 541                          Number Disordered Regions: 2
Number residues disordered: 44           Longest Disordered Region: 43
Overall percent disordered: 8.13         Average Prediction Score: 0.2571
Predicted disorder segment [27]-[69]     Average Strength= 0.5400
Predicted disorder segment [541]-[541]Average Strength= 0.5168

=======================VSL2 NNP STATISTICS================================
Predicted residues: 541                          Number Disordered Regions: 8
Number residues disordered: 144                  Longest Disordered Region: 58
Overall percent disordered: 26.62        Average Prediction Score: 0.3704
Predicted disorder segment [1]-[2]       Average Strength= 0.5727
Predicted disorder segment [22]-[79]     Average Strength= 0.6396
Predicted disorder segment [114]-[121]Average Strength= 0.6256
Predicted disorder segment [269]-[285]Average Strength= 0.5983
Predicted disorder segment [317]-[322]Average Strength= 0.5797
Predicted disorder segment [379]-[380]Average Strength= 0.5123
```

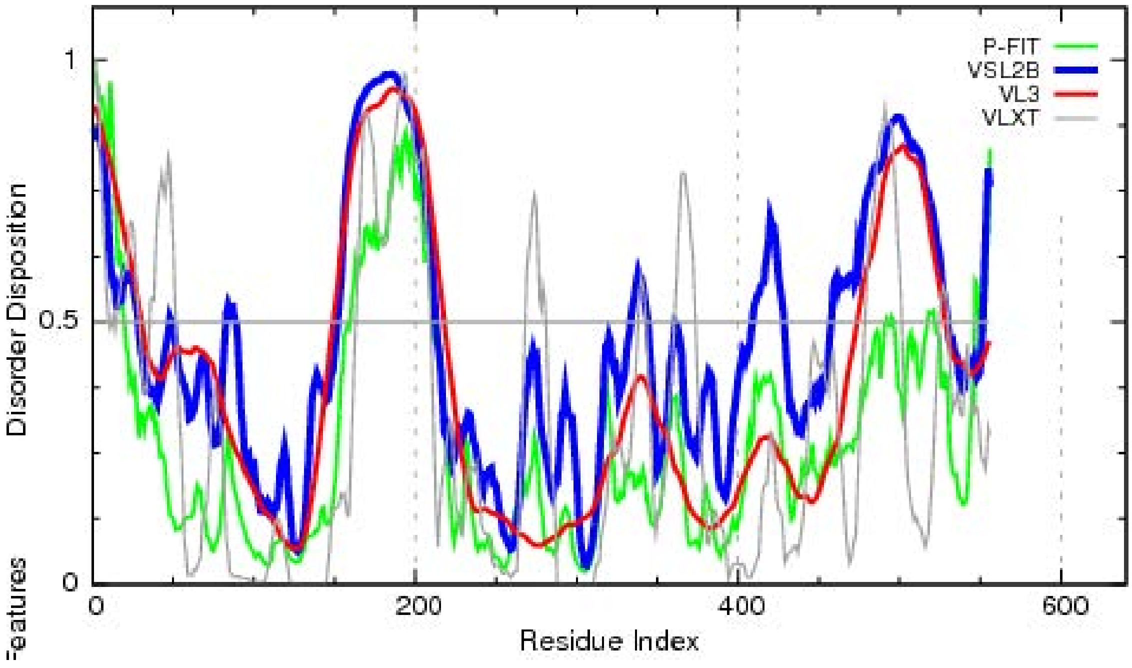
```
Predicted disorder segment [490]-[509]Average Strength= 0.5922
Predicted disorder segment [511]-[541]Average Strength= 0.6787
```

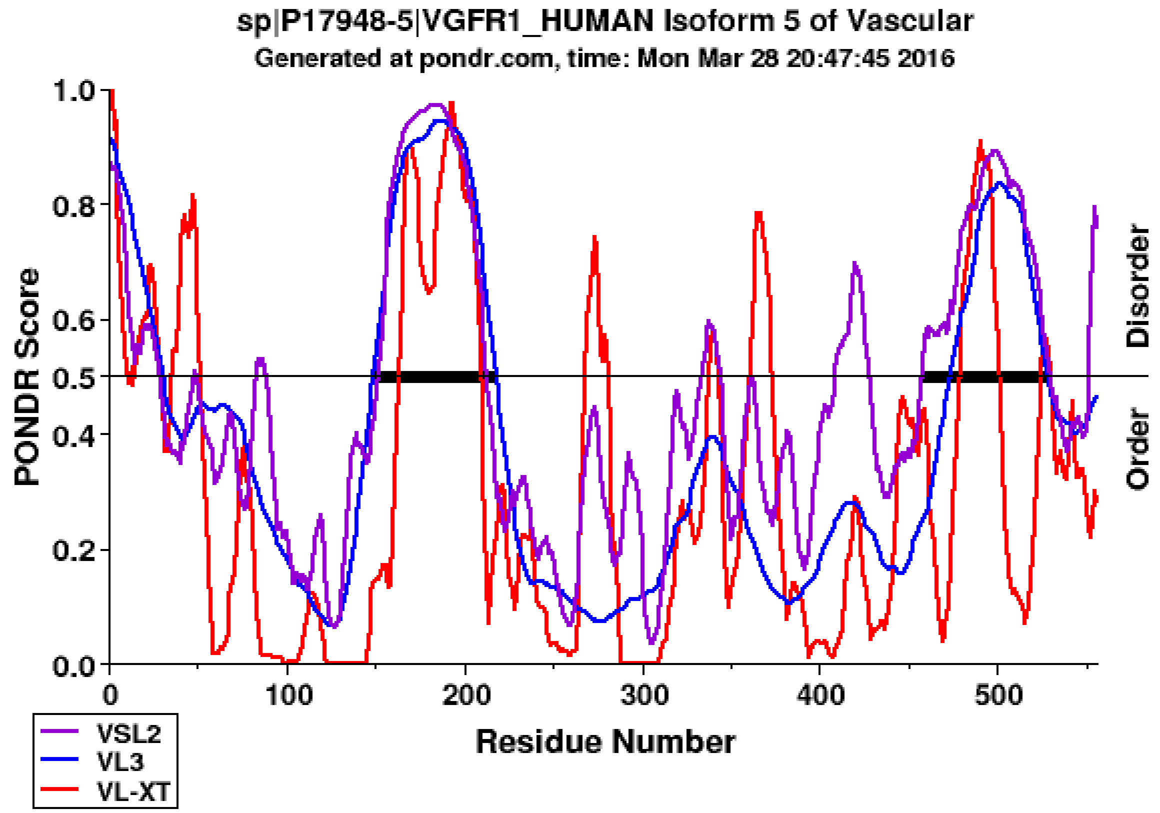
ENSP00000442630

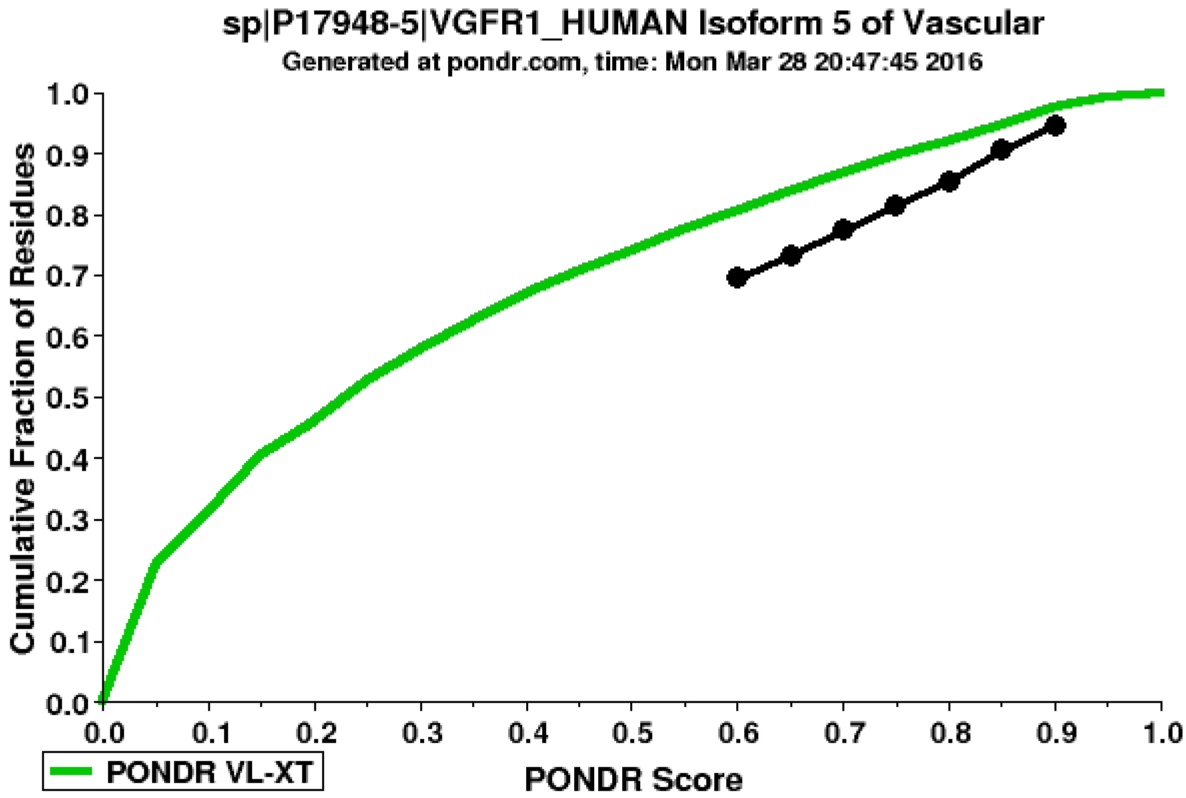


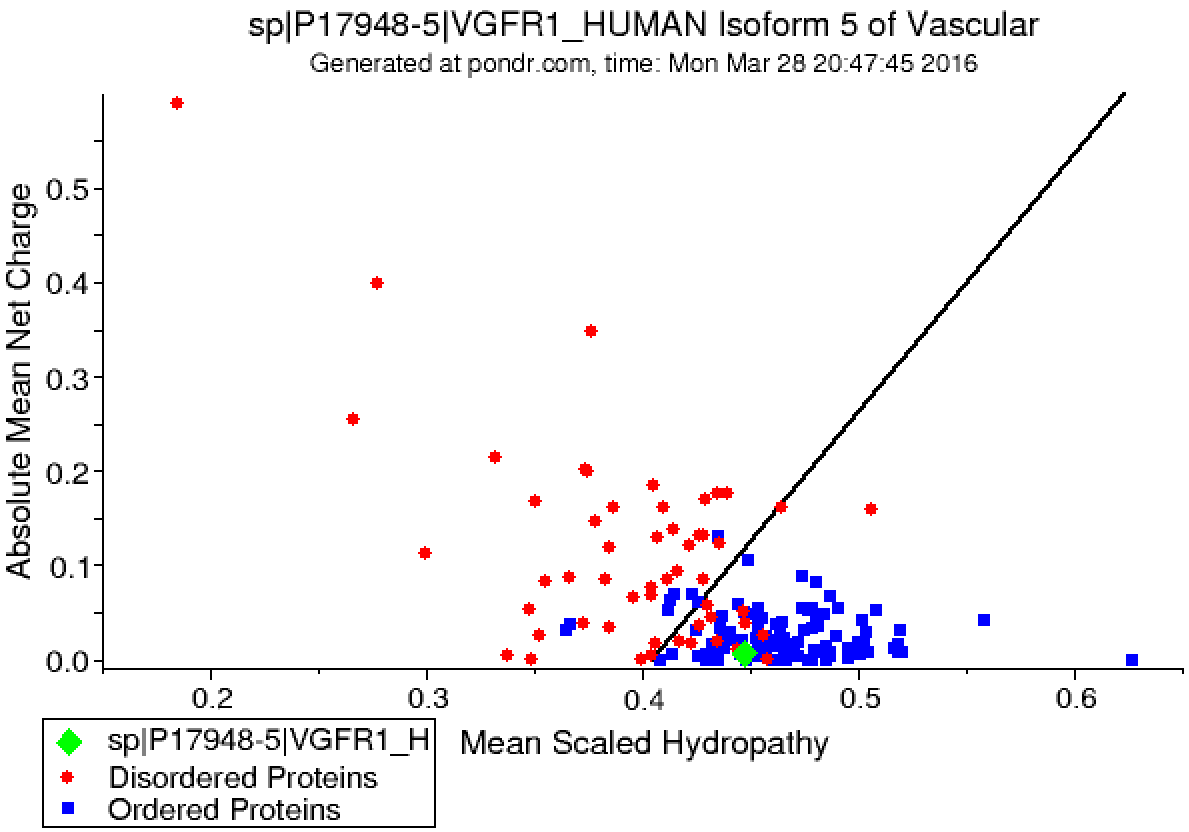
Predicted Disordered Binding Regions			
	From	To	Length
1	290	297	8

```
>sp|P17948-5|VGFR1_HUMAN Isoform 5 of Vascular endothelial growth factor
receptor 1 OS=Homo sapiens GN=FLT1
MKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVV
QASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKILTHIGHHLNVVNLLGACTKQG
GPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSVTS
SESFASSGFQEDKSLSDVEEEEDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRD
LAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDV
WSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPK
ERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPK
FNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTD
SKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCS
PPPDYNSVVLYSTPPI
```




sp|P17948-5|VGFR1_HUMAN Isoform 5 of Vascular
Generated at pondr.com, time: Mon Mar 28 20:47:45 2016
PONDR Score
1.0
0.8
0.6
0.5
0.4
0.2
0.0
0
100
200
300
400
500
Residue Number
Disorder
Order
VSL2
VL3
VL-XT


sp|P17948-5|VGFR1_HUMAN Isoform 5 of Vascular
Generated at pondr.com, time: Mon Mar 28 20:47:45 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT



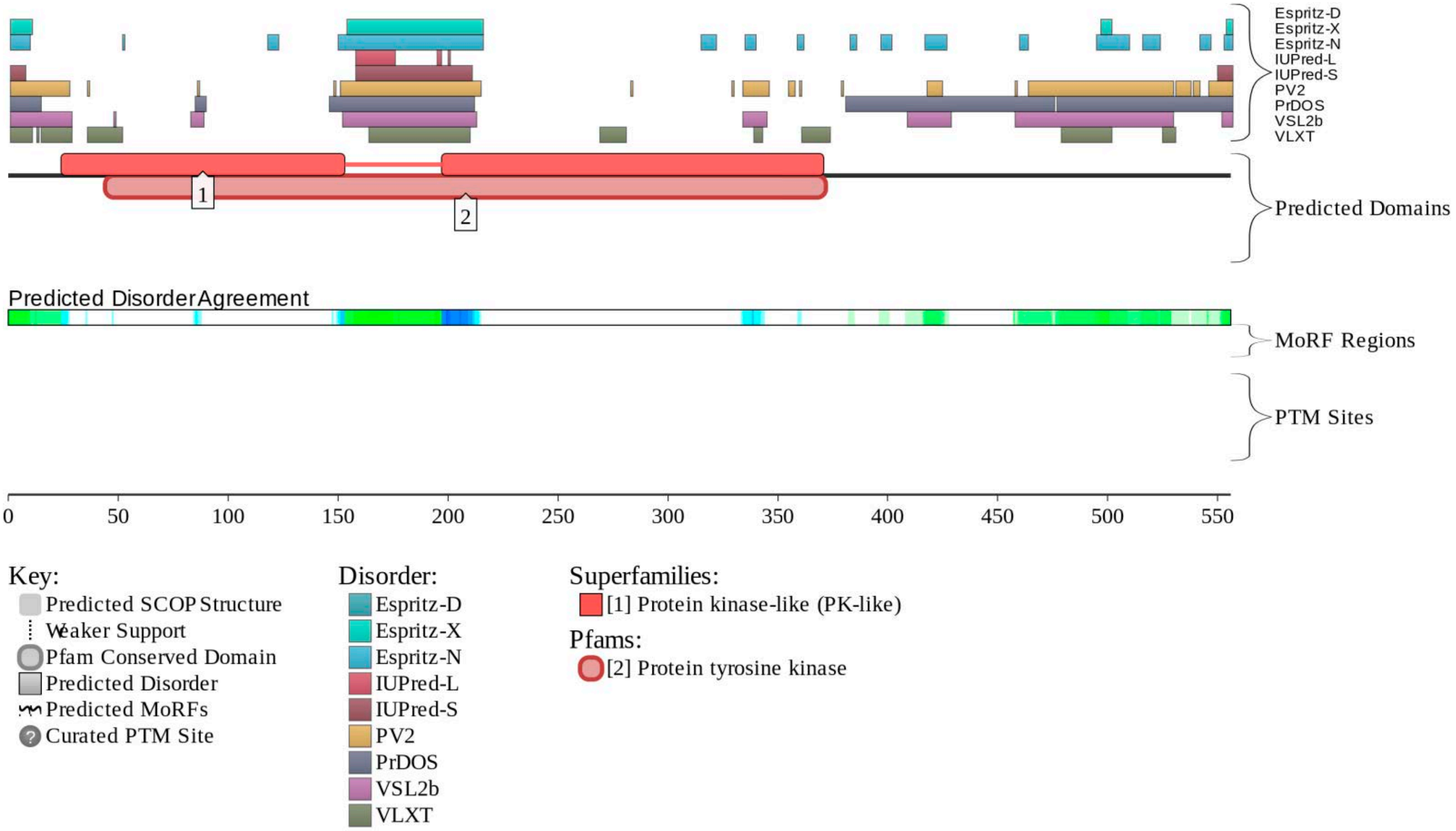
```
=======================VLXT NNP STATISTICS================================
Predicted residues: 556                       Number Disordered Regions: 10
Number residues disordered: 145               Longest Disordered Region: 46
Overall percent disordered: 26.08     Average Prediction Score: 0.3103
Predicted disorder segment [1]-[10]   Average Strength= 0.7736
Predicted disorder segment [13]-[13]  Average Strength= 0.5153
Predicted disorder segment [15]-[28]  Average Strength= 0.6018
Predicted disorder segment [36]-[51]  Average Strength= 0.6881
Predicted disorder segment [164]-[209]Average Strength= 0.7961
Predicted disorder segment [269]-[280]Average Strength= 0.6313
Predicted disorder segment [339]-[342]Average Strength= 0.5638
Predicted disorder segment [361]-[373]Average Strength= 0.6823
Predicted disorder segment [479]-[501]Average Strength= 0.7577
Predicted disorder segment [525]-[530]Average Strength= 0.5398

=======================VL3 NNP STATISTICS================================
Predicted residues: 556                       Number Disordered Regions: 3
Number residues disordered: 153               Longest Disordered Region: 68
Overall percent disordered: 27.52     Average Prediction Score: 0.3884
Predicted disorder segment [1]-[30]   Average Strength= 0.7285
Predicted disorder segment [150]-[217]Average Strength= 0.8242
Predicted disorder segment [474]-[528]Average Strength= 0.7098

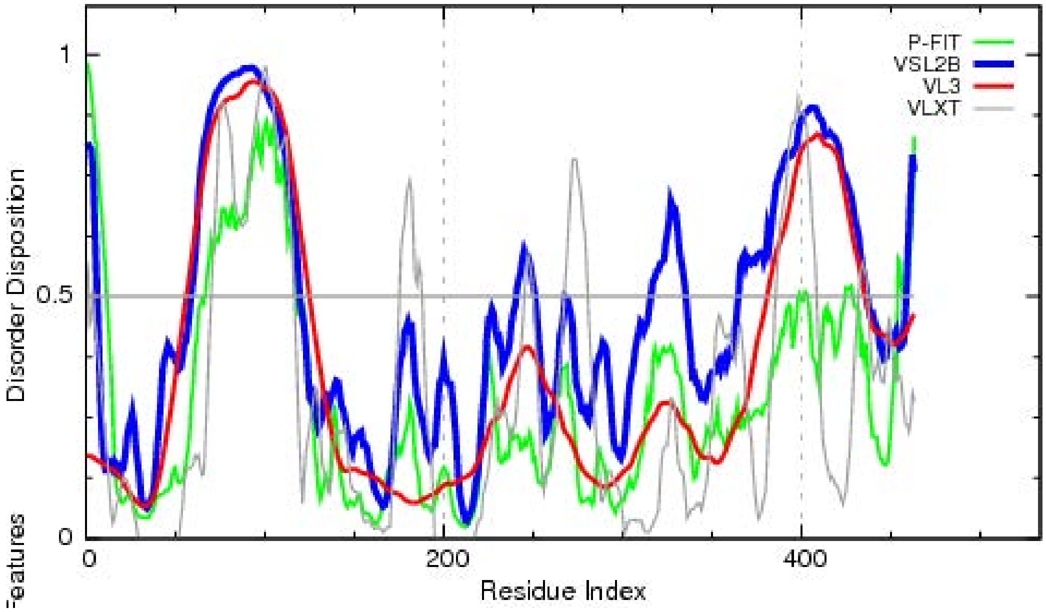
=======================VSL2 NNP STATISTICS================================
Predicted residues: 556                       Number Disordered Regions: 8
Number residues disordered: 204               Longest Disordered Region: 72
Overall percent disordered: 36.69     Average Prediction Score: 0.4615
Predicted disorder segment [1]-[28]   Average Strength= 0.6531
Predicted disorder segment [48]-[48]  Average Strength= 0.5077
Predicted disorder segment [83]-[88]  Average Strength= 0.5224
Predicted disorder segment [152]-[212]Average Strength= 0.8569
```

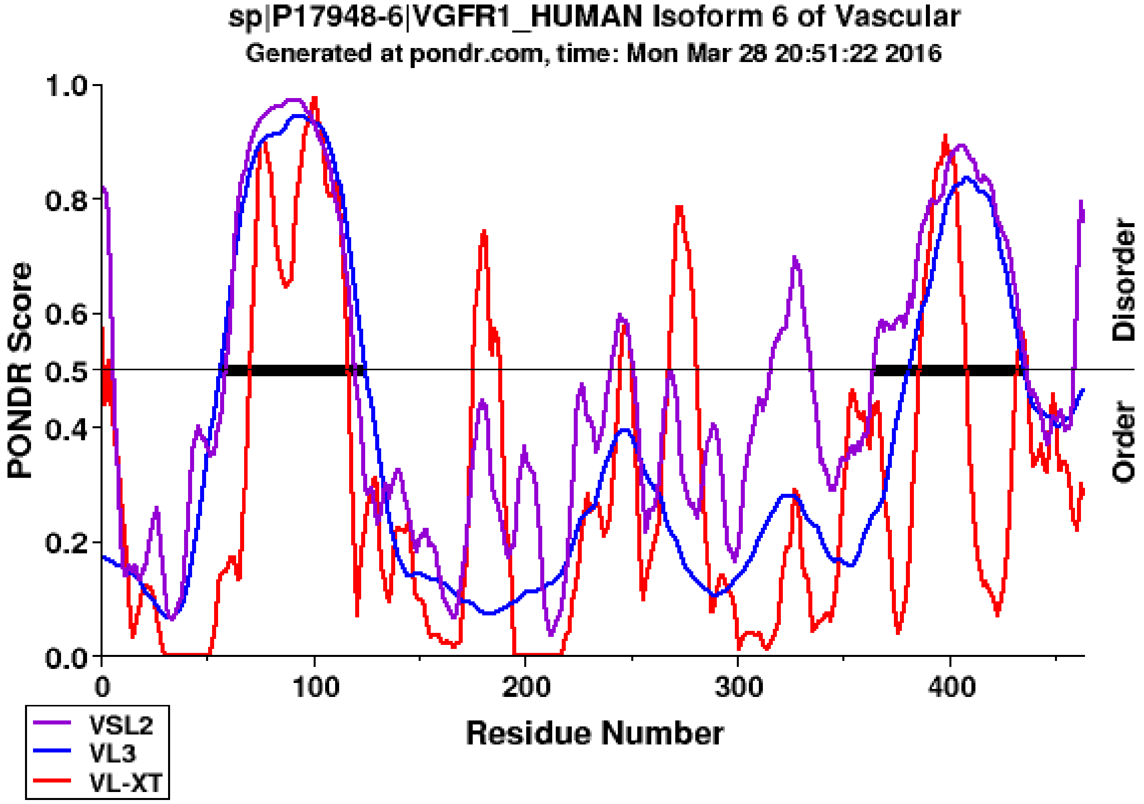
```
Predicted disorder segment [334]-[344]Average Strength= 0.5531
Predicted disorder segment [409]-[428]Average Strength= 0.5929
Predicted disorder segment [458]-[529]Average Strength= 0.7271
Predicted disorder segment [552]-[556]Average Strength= 0.6908
```

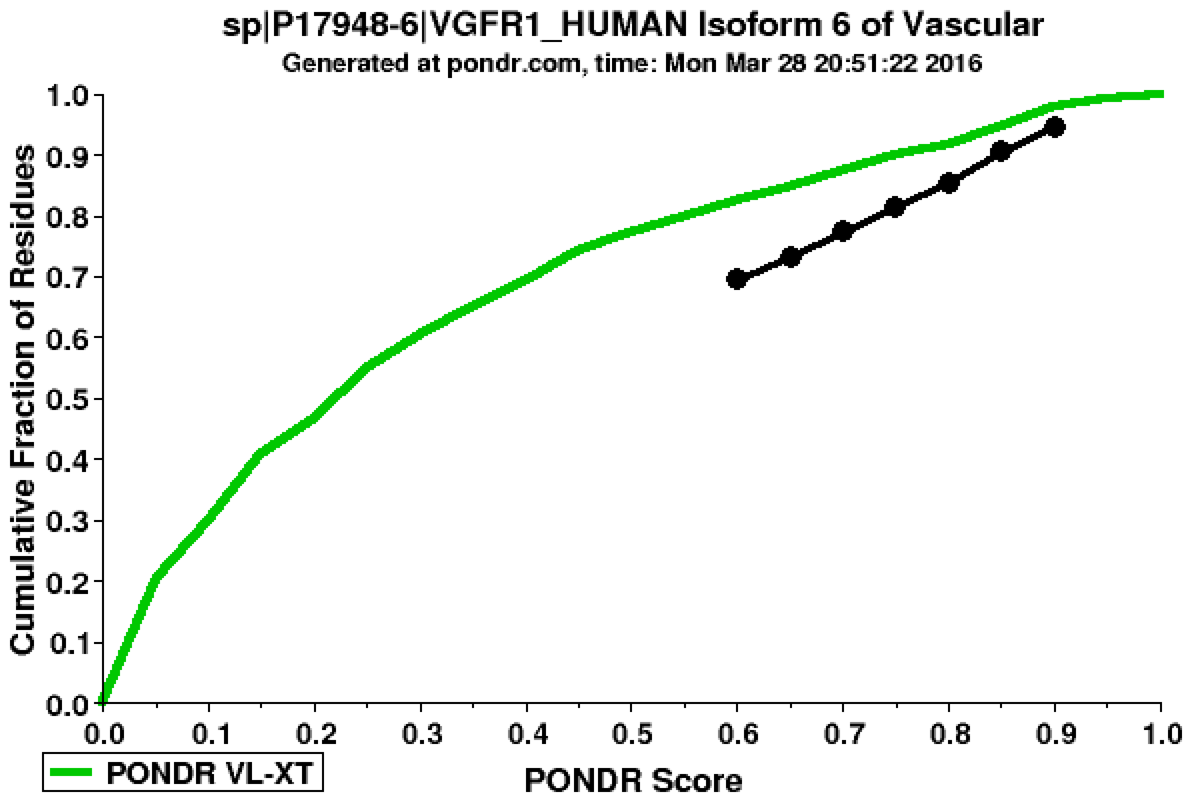
ENSP00000443311

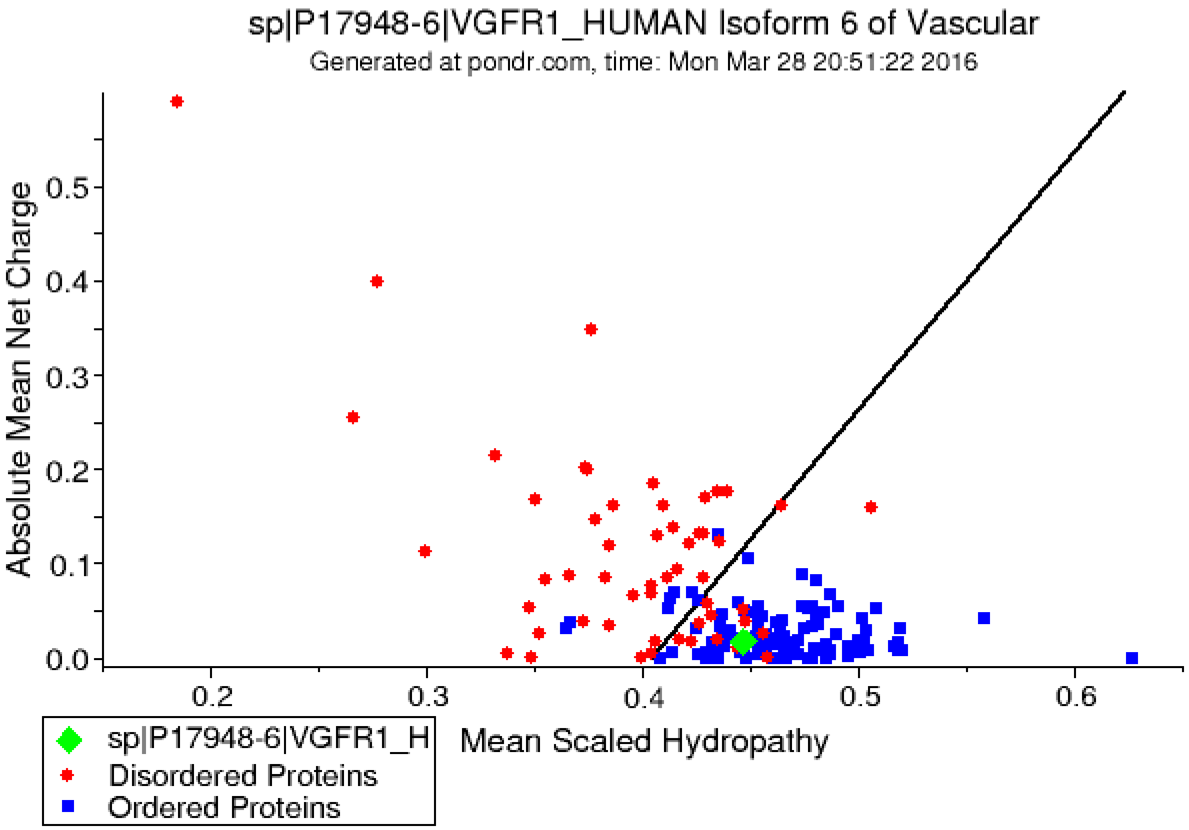


```
>sp|P17948-6|VGFR1_HUMAN Isoform 6 of Vascular endothelial growth factor
receptor 1 OS=Homo sapiens GN=FLT1
MTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAA
LHMEPKKEKMEPGLEQGKKPRLDSVTSSESFASSGFQEDKSLSDVEEEEDSDGFYKEPIT
MEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVR
KGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLRE
GMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQQDGKDYIPINAI
LTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNA
TSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTSKSKESGLSDVSRPSFCHS
SCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI
```









```
=======================VLXT NNP STATISTICS================================
Predicted residues: 463                      Number Disordered Regions: 7
Number residues disordered: 106              Longest Disordered Region: 46
Overall percent disordered: 22.89      Average Prediction Score: 0.3001
```

```
Predicted disorder segment [4]-[4]    Average Strength= 0.5163
Predicted disorder segment [71]-[116] Average Strength= 0.7961
Predicted disorder segment [176]-[187]Average Strength= 0.6313
Predicted disorder segment [246]-[249]Average Strength= 0.5638
Predicted disorder segment [268]-[280]Average Strength= 0.6823
Predicted disorder segment [386]-[408]Average Strength= 0.7577
Predicted disorder segment [432]-[437]Average Strength= 0.5398

========================VL3 NNP STATISTICS================================
Predicted residues: 463                       Number Disordered Regions: 2
Number residues disordered: 123               Longest Disordered Region: 68
Overall percent disordered: 26.57     Average Prediction Score: 0.3651
Predicted disorder segment [57]-[124] Average Strength= 0.8242
Predicted disorder segment [381]-[435]Average Strength= 0.7098

=======================VSL2 NNP STATISTICS================================
Predicted residues: 463                       Number Disordered Regions: 6
Number residues disordered: 175               Longest Disordered Region: 72
Overall percent disordered: 37.80     Average Prediction Score: 0.4656
Predicted disorder segment [1]-[6]    Average Strength= 0.7285
Predicted disorder segment [59]-[119] Average Strength= 0.8569
Predicted disorder segment [241]-[251]Average Strength= 0.5531
Predicted disorder segment [316]-[335]Average Strength= 0.5929
Predicted disorder segment [365]-[436]Average Strength= 0.7271
Predicted disorder segment [459]-[463]Average Strength= 0.6908
```

>sp|P17948-7|VGFR1_HUMAN Isoform 7 of Vascular endothelial growth factor receptor 1 OS=Homo sapiens GN=FLT1
MEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVR
KGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLRE
GMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQQDGKDYIPINAI
LTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNA
TSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTSKSKESGLSDVSRPSFCHS
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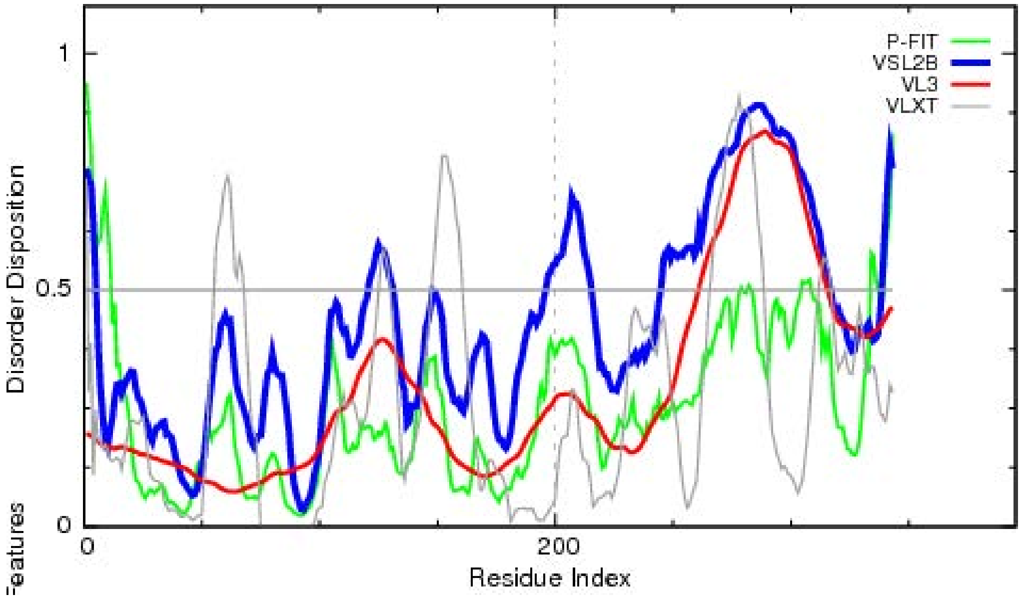
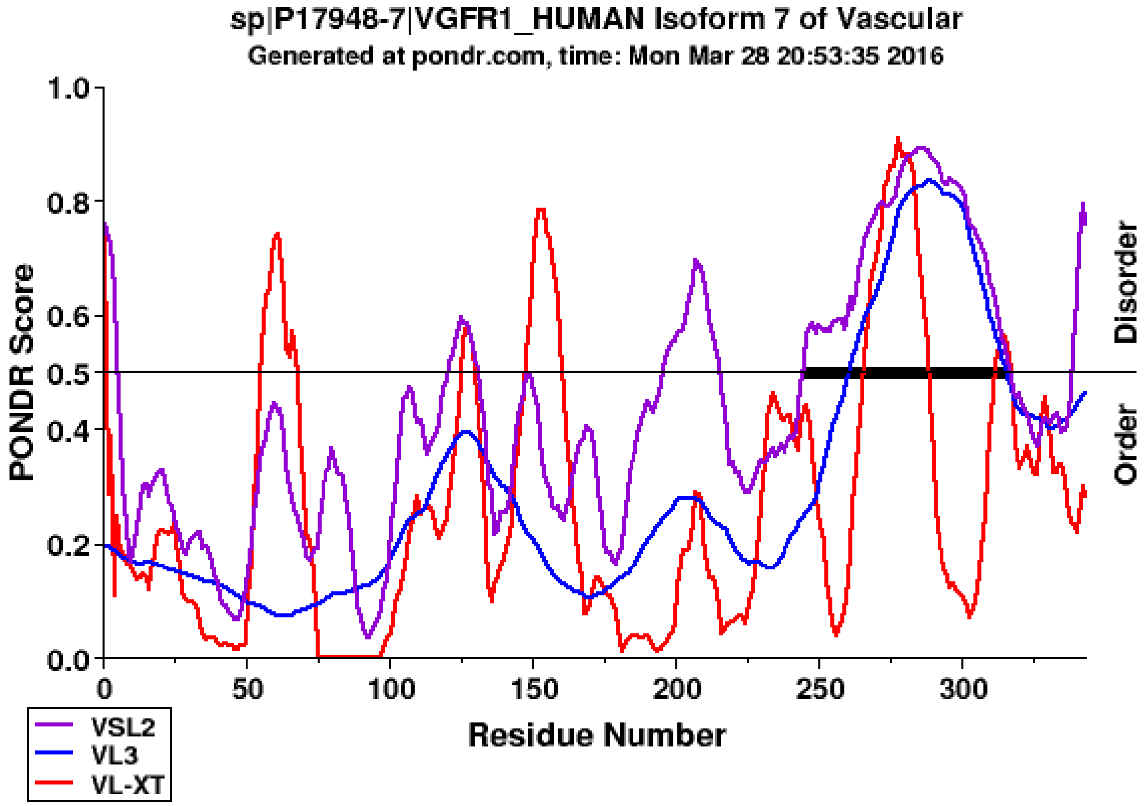
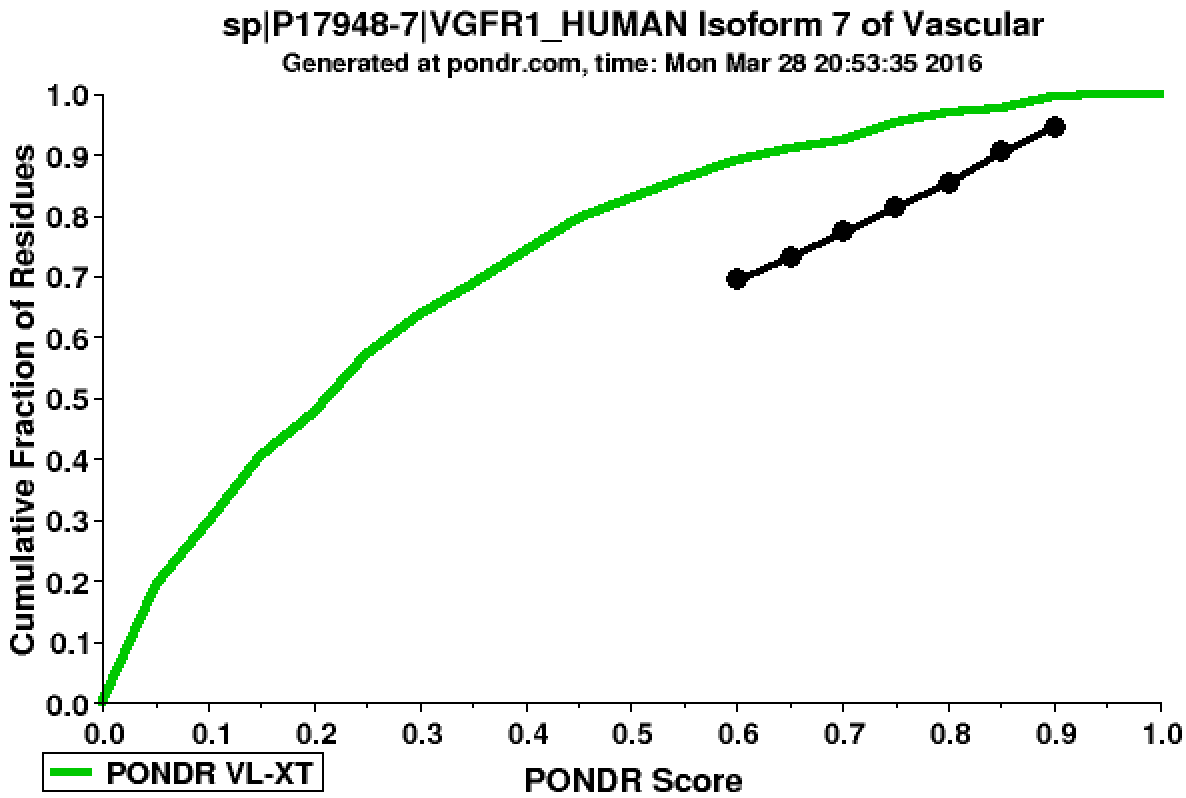
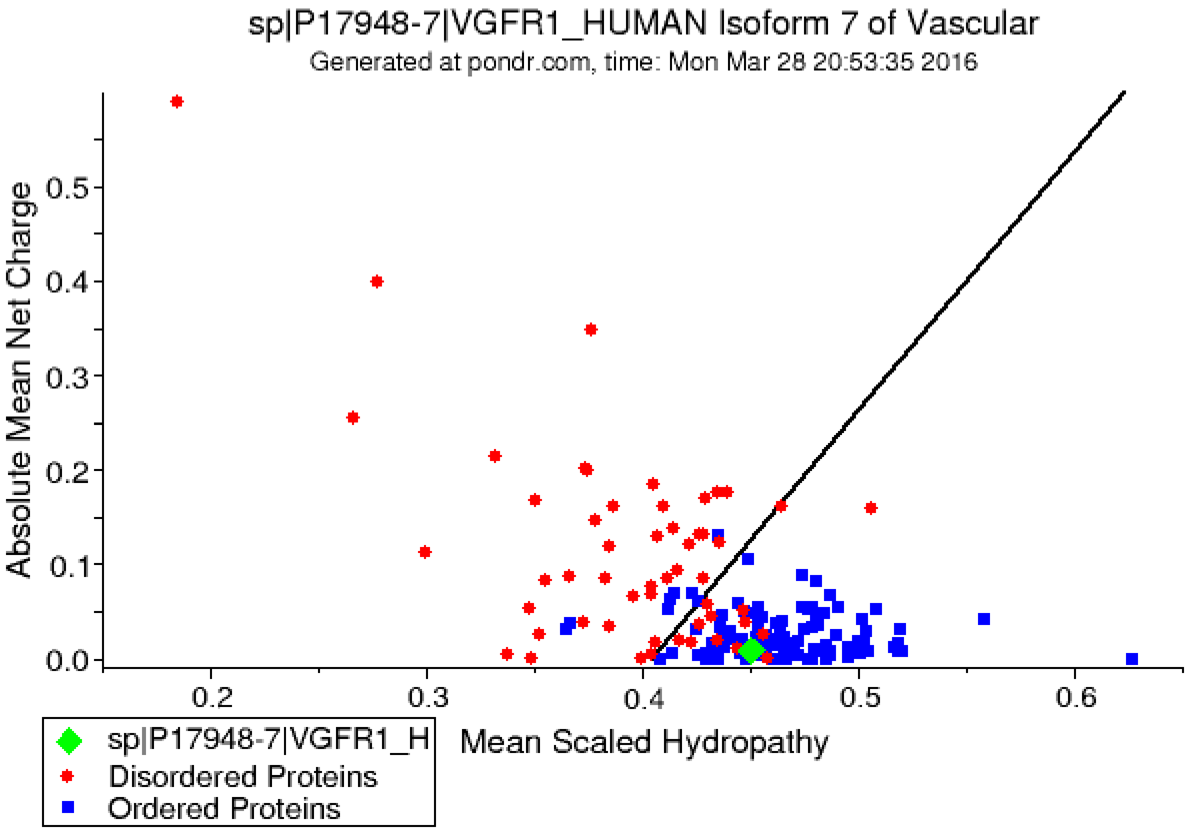








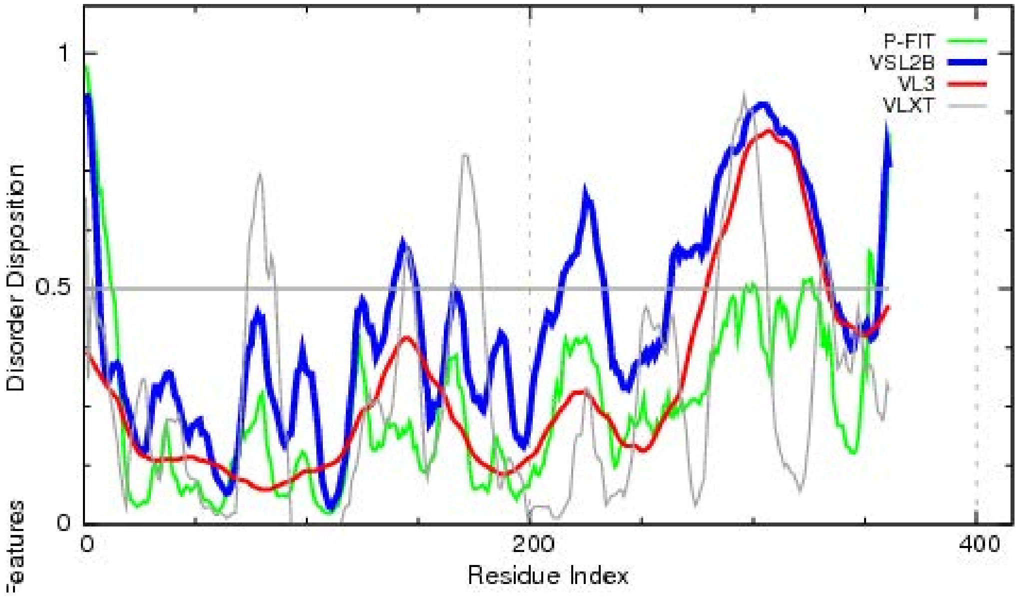
```
======================VLXT NNP STATISTICS===============================
Predicted residues: 343                       Number Disordered Regions: 5
Number residues disordered: 59          Longest Disordered Region: 23
```

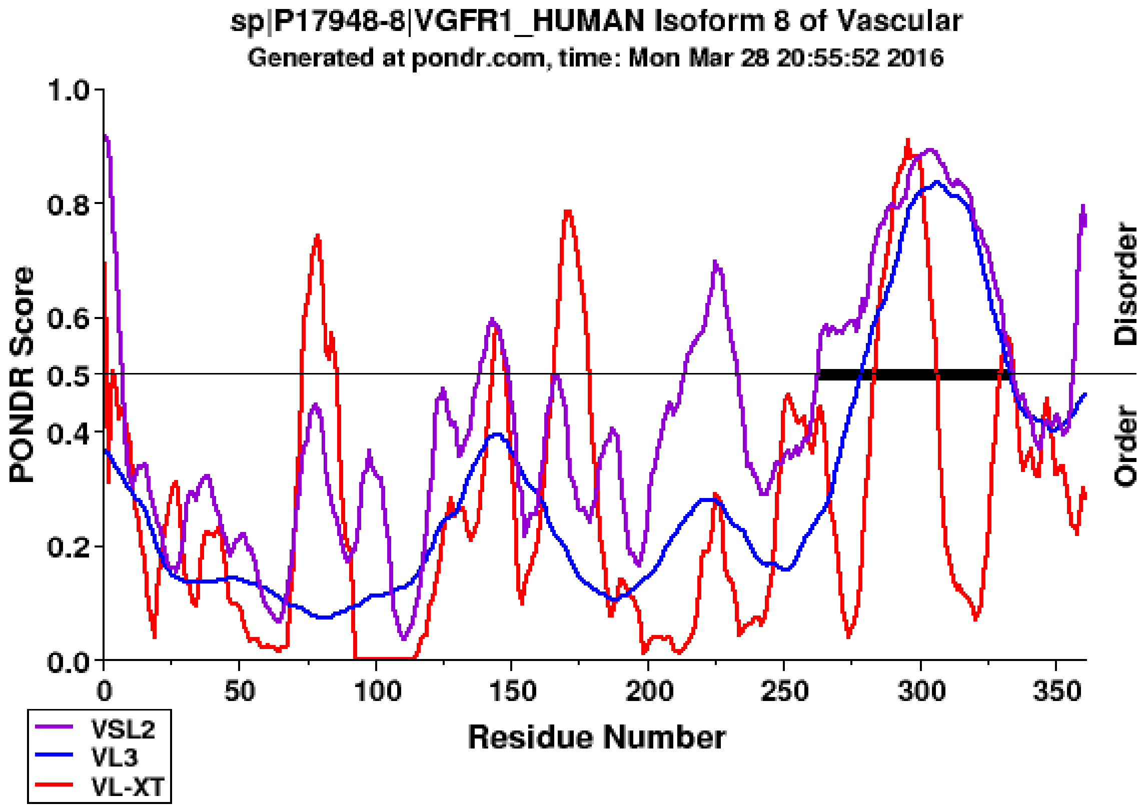
```
Overall percent disordered: 17.20     Average Prediction Score: 0.2696
Predicted disorder segment [56]-[67]  Average Strength= 0.6313
Predicted disorder segment [126]-[129]Average Strength= 0.5638
Predicted disorder segment [148]-[160]Average Strength= 0.6823
Predicted disorder segment [266]-[288]Average Strength= 0.7577
Predicted disorder segment [312]-[317]Average Strength= 0.5398

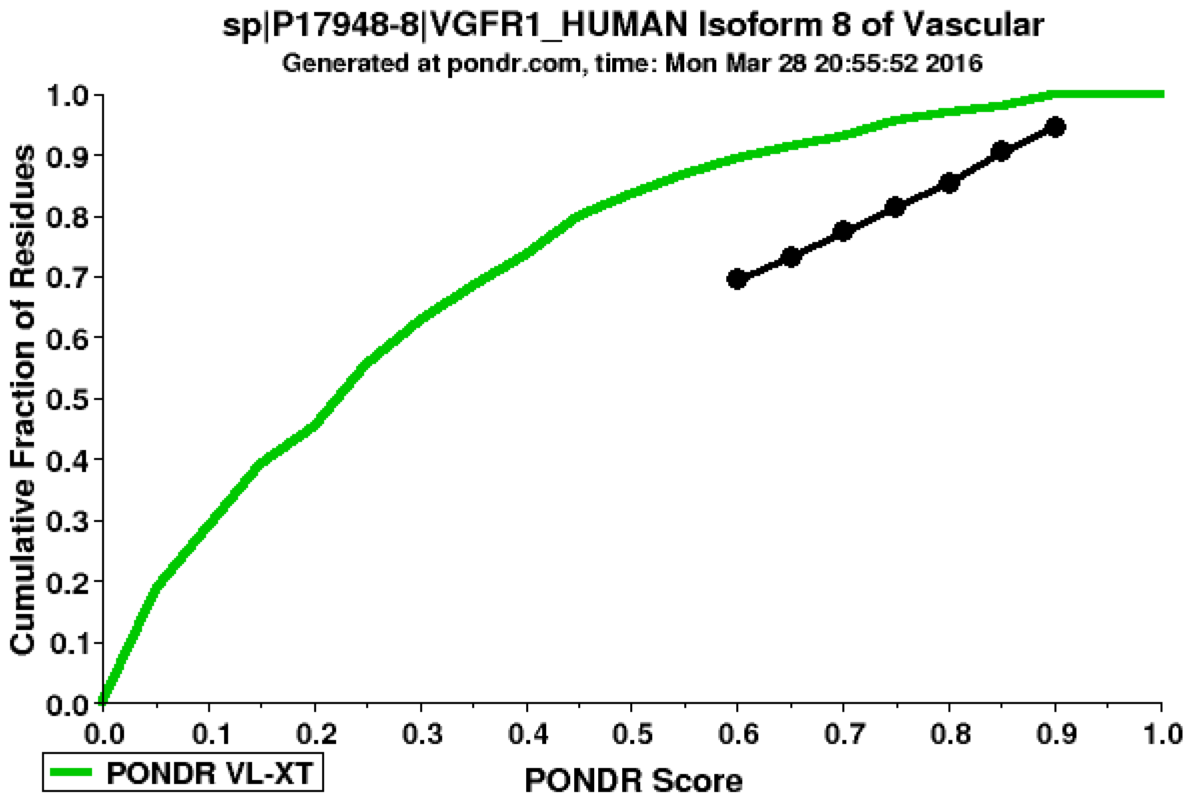
=======================VL3 NNP STATISTICS================================
Predicted residues: 343                      Number Disordered Regions: 1
Number residues disordered: 55        Longest Disordered Region: 55
Overall percent disordered: 16.03     Average Prediction Score: 0.2968
Predicted disorder segment [261]-[315]Average Strength= 0.7098

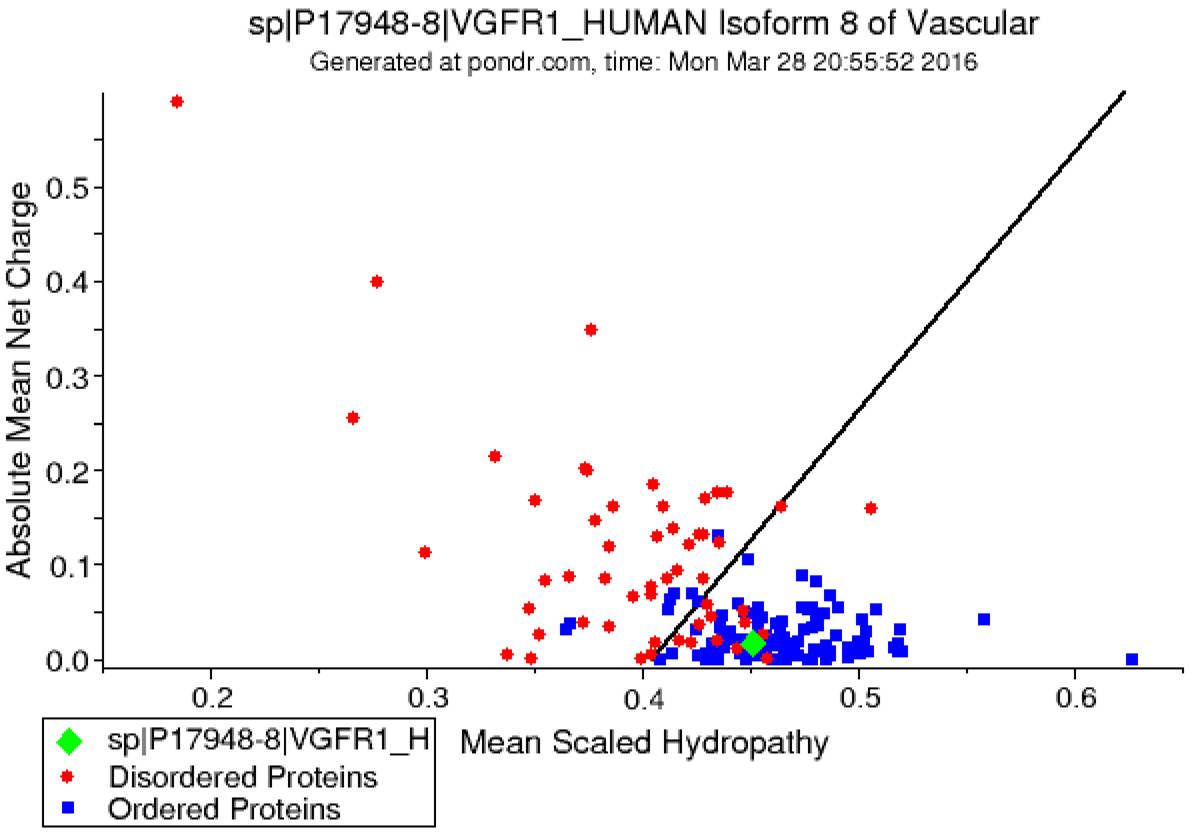
======================VSL2 NNP STATISTICS================================
Predicted residues: 343                      Number Disordered Regions: 5
Number residues disordered: 113              Longest Disordered Region: 72
Overall percent disordered: 32.94     Average Prediction Score: 0.4304
Predicted disorder segment [1]-[5]    Average Strength= 0.6783
Predicted disorder segment [121]-[131]Average Strength= 0.5531
Predicted disorder segment [196]-[215]Average Strength= 0.5929
Predicted disorder segment [245]-[316]Average Strength= 0.7271
Predicted disorder segment [339]-[343]Average Strength= 0.6908
```

```
>sp|P17948-8|VGFR1_HUMAN Isoform 8 of Vascular endothelial growth factor
receptor 1 OS=Homo sapiens GN=FLT1
MNSDLLVDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVK
ICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGG
SPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDL
LQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAF
KFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTDSKPKASLKIDLRVTS
KSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPP
I
```









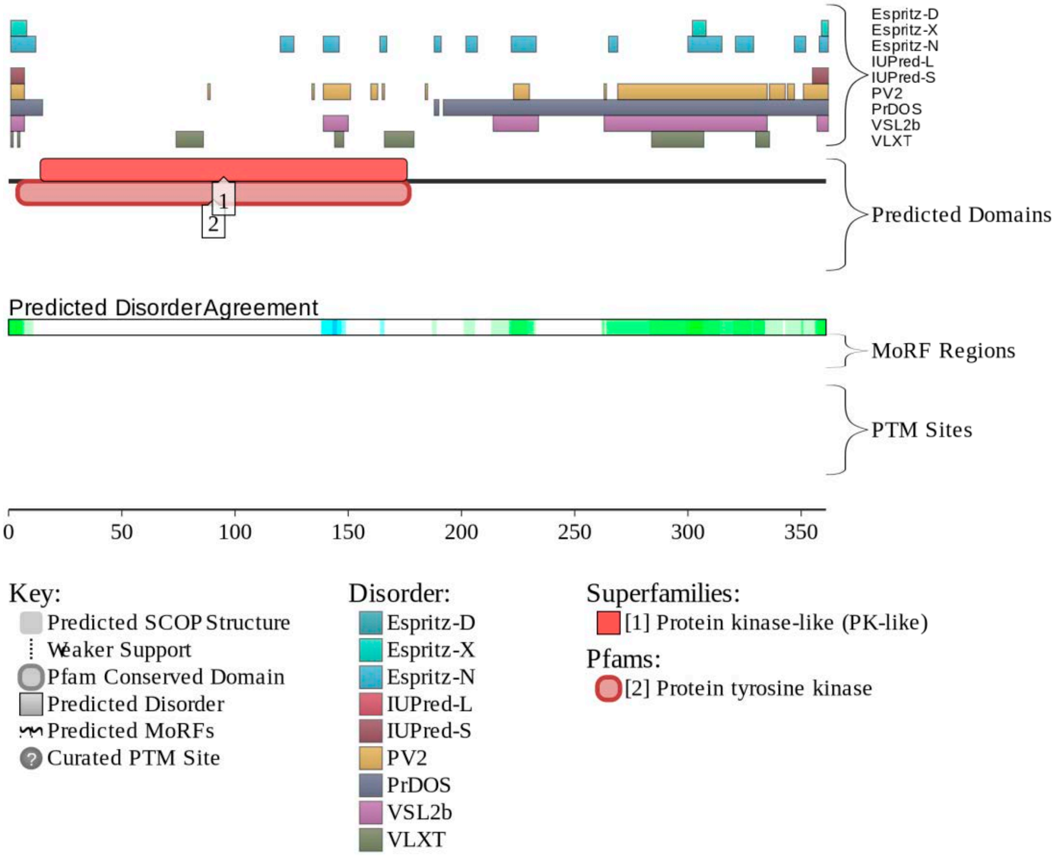
```
======================VLXT NNP STATISTICS===============================
Predicted residues: 361                         Number Disordered Regions: 6
Number residues disordered: 60          Longest Disordered Region: 23
```

```
Overall percent disordered: 16.62     Average Prediction Score: 0.2713
Predicted disorder segment [4]-[4]    Average Strength= 0.5068
Predicted disorder segment [74]-[85]  Average Strength= 0.6313
Predicted disorder segment [144]-[147]Average Strength= 0.5638
Predicted disorder segment [166]-[178]Average Strength= 0.6823
Predicted disorder segment [284]-[306]Average Strength= 0.7577
Predicted disorder segment [330]-[335]Average Strength= 0.5398

=======================VL3 NNP STATISTICS================================
Predicted residues: 361                        Number Disordered Regions: 1
Number residues disordered: 55        Longest Disordered Region: 55
Overall percent disordered: 15.24     Average Prediction Score: 0.2955
Predicted disorder segment [279]-[333]Average Strength= 0.7098

======================VSL2 NNP STATISTICS================================
Predicted residues: 361                        Number Disordered Regions: 5
Number residues disordered: 114                Longest Disordered Region: 72
Overall percent disordered: 31.58     Average Prediction Score: 0.4256
Predicted disorder segment [1]-[6]    Average Strength= 0.7881
Predicted disorder segment [139]-[149]Average Strength= 0.5531
Predicted disorder segment [214]-[233]Average Strength= 0.5929
Predicted disorder segment [263]-[334]Average Strength= 0.7271
Predicted disorder segment [357]-[361]Average Strength= 0.6908
```

ENSP00000437841



```
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KPKDPTFIPAPIQAKTSPVDEKALQDQLVLVAAKLDTEDKLRAAMVGMLANFLGFRIYGM
HSELWGVVHGATVLSPTAVFGTLASLYLGALDHTADRLQAILGVPWKDKNCTSRLDAHKV
LSALQAVQGLLVAQGRADSQAQLLLSTVVGVFTAPGLHLKQPFVQGLALYTPVVLPRSLD
FTELDVAAEKIDRFMQAVTGWKTGCSLMGASVDSTLAFNTYVHFQGKMKGFSLLAEPQEF
WVDNSTSVSVPMLSGMGTFQHWSDIQDNFSVTQVPFTESACLLLIQPHYASDLDKVEGLT
FQQNSLNWMKKLSPRTIHLTMPQLVLQGSYDLQDLLAQAELPAILHTELNLQKLSNDRIR
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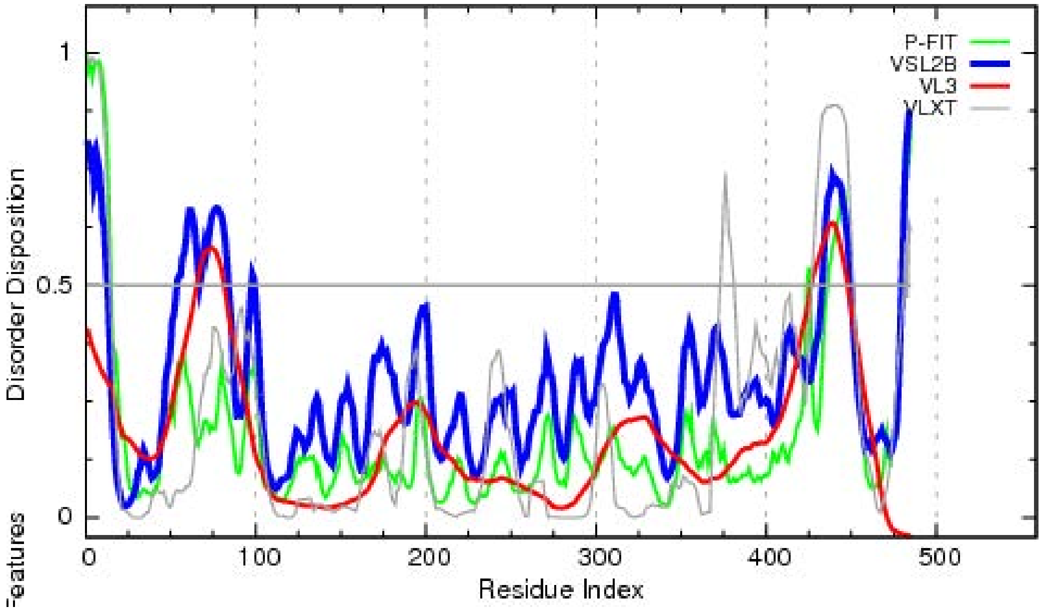
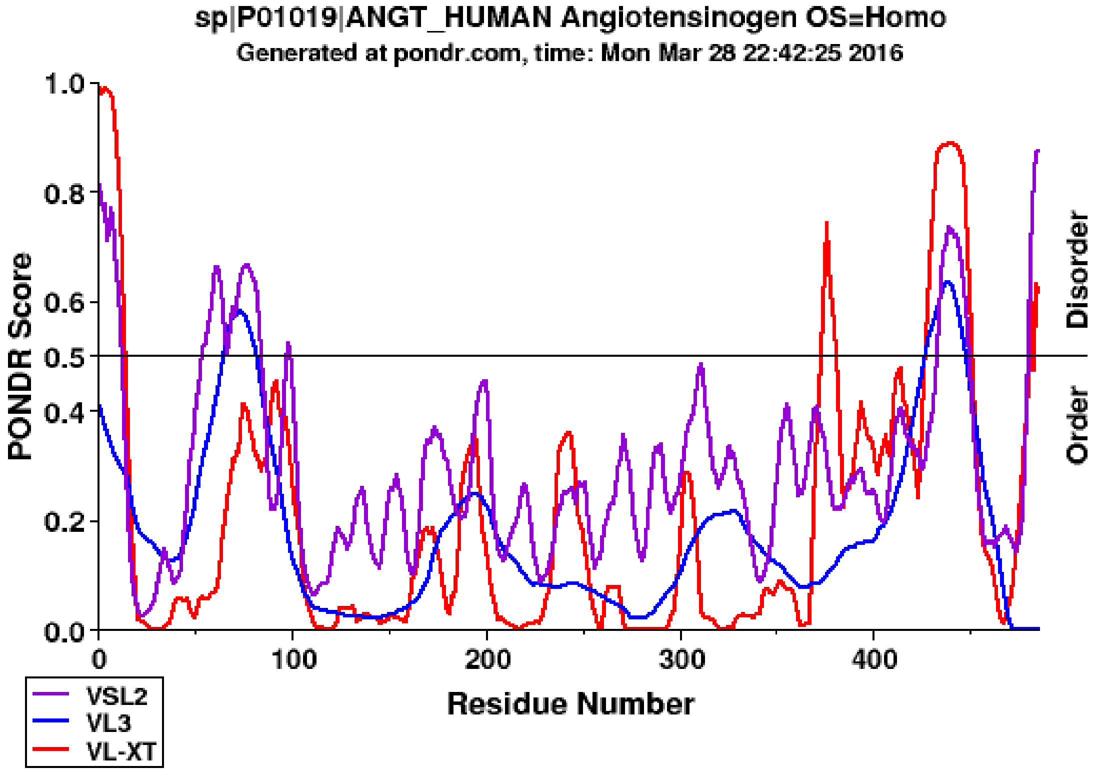
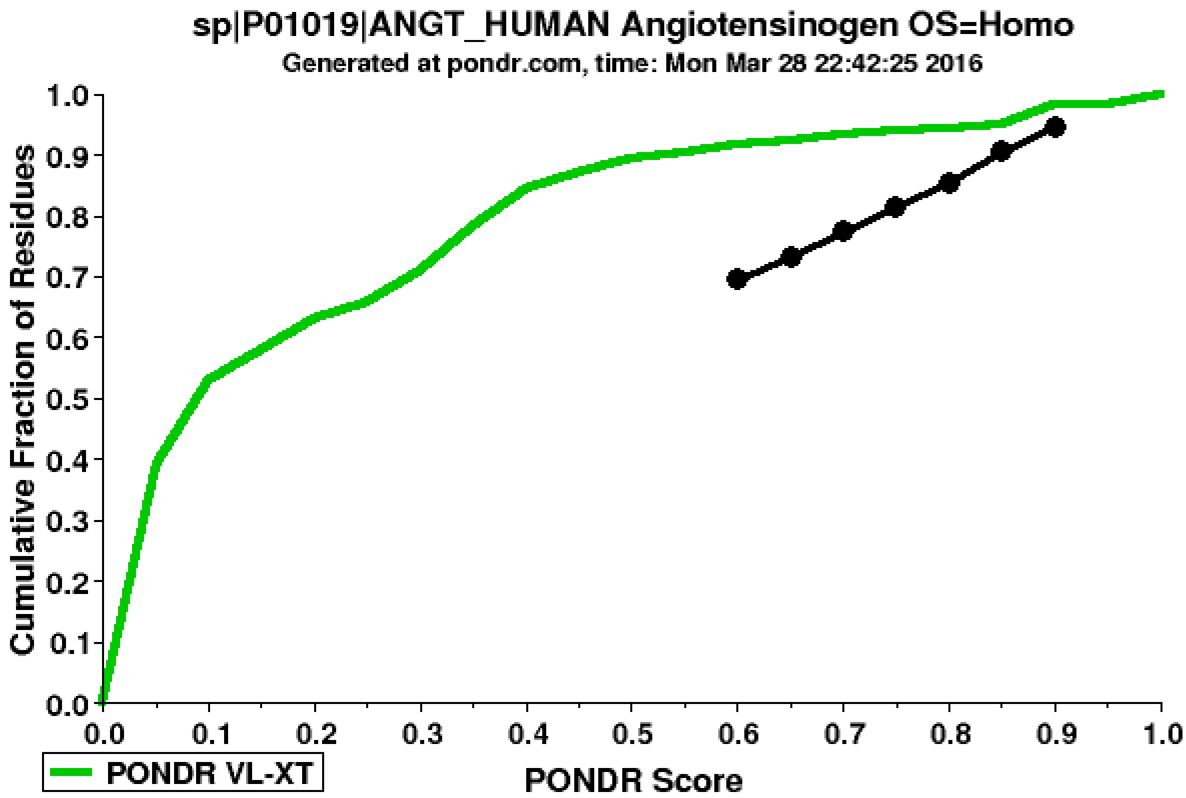
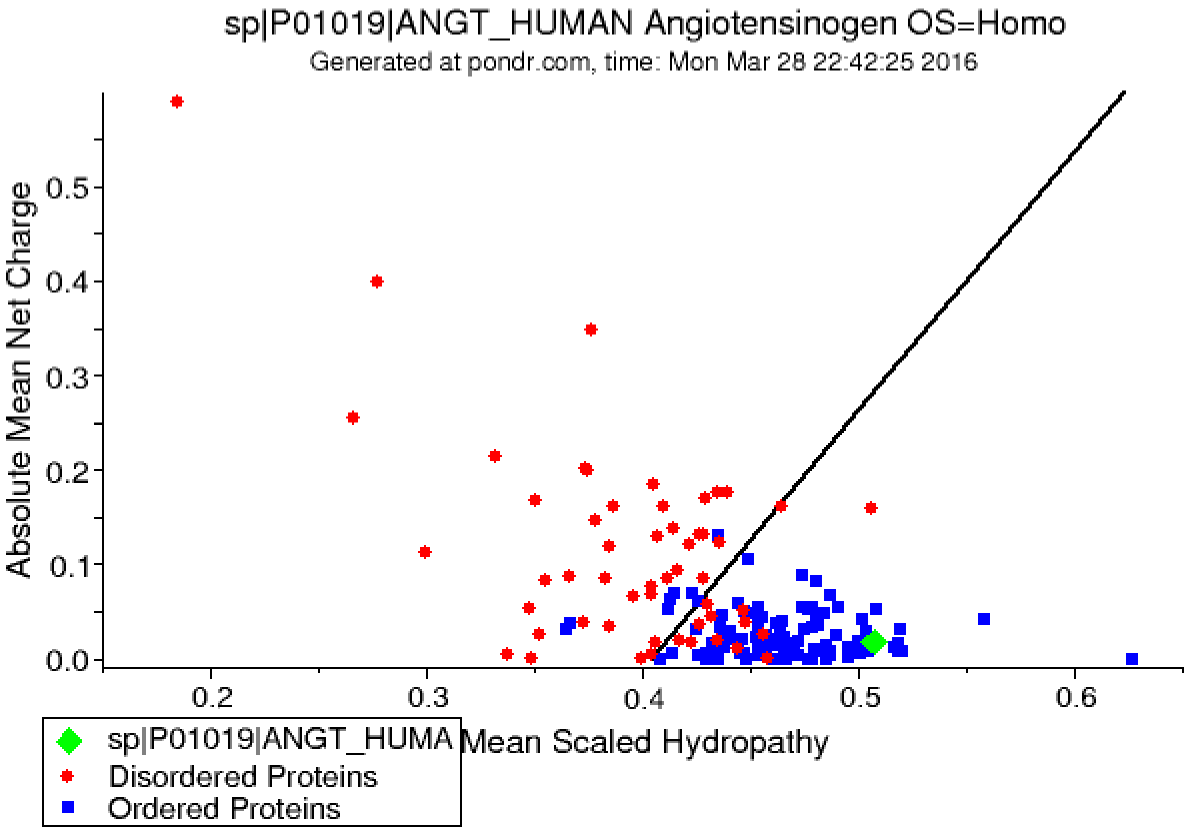
PLSTA
```









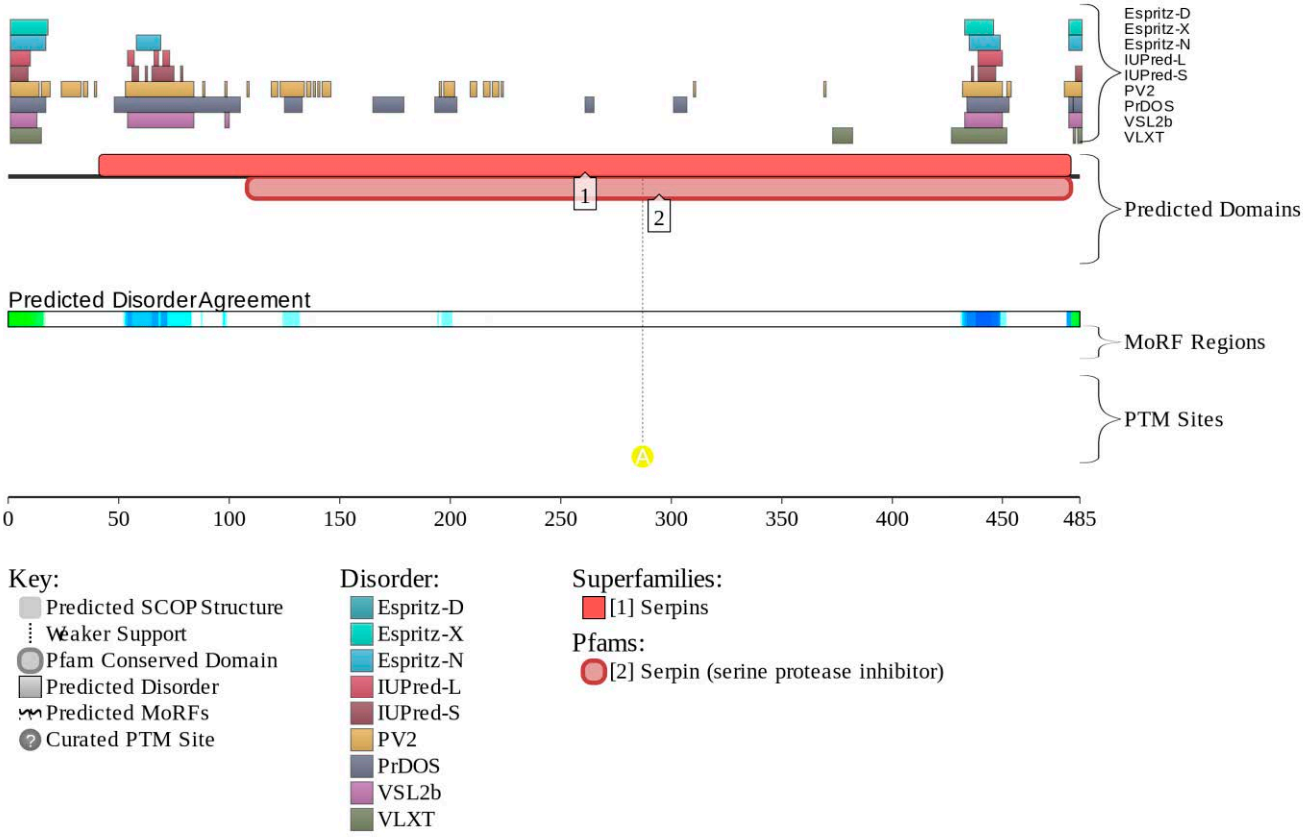
```
======================VLXT NNP STATISTICS===============================
Predicted residues: 485                              Number Disordered Regions: 5
Number residues disordered: 51            Longest Disordered Region: 25
```

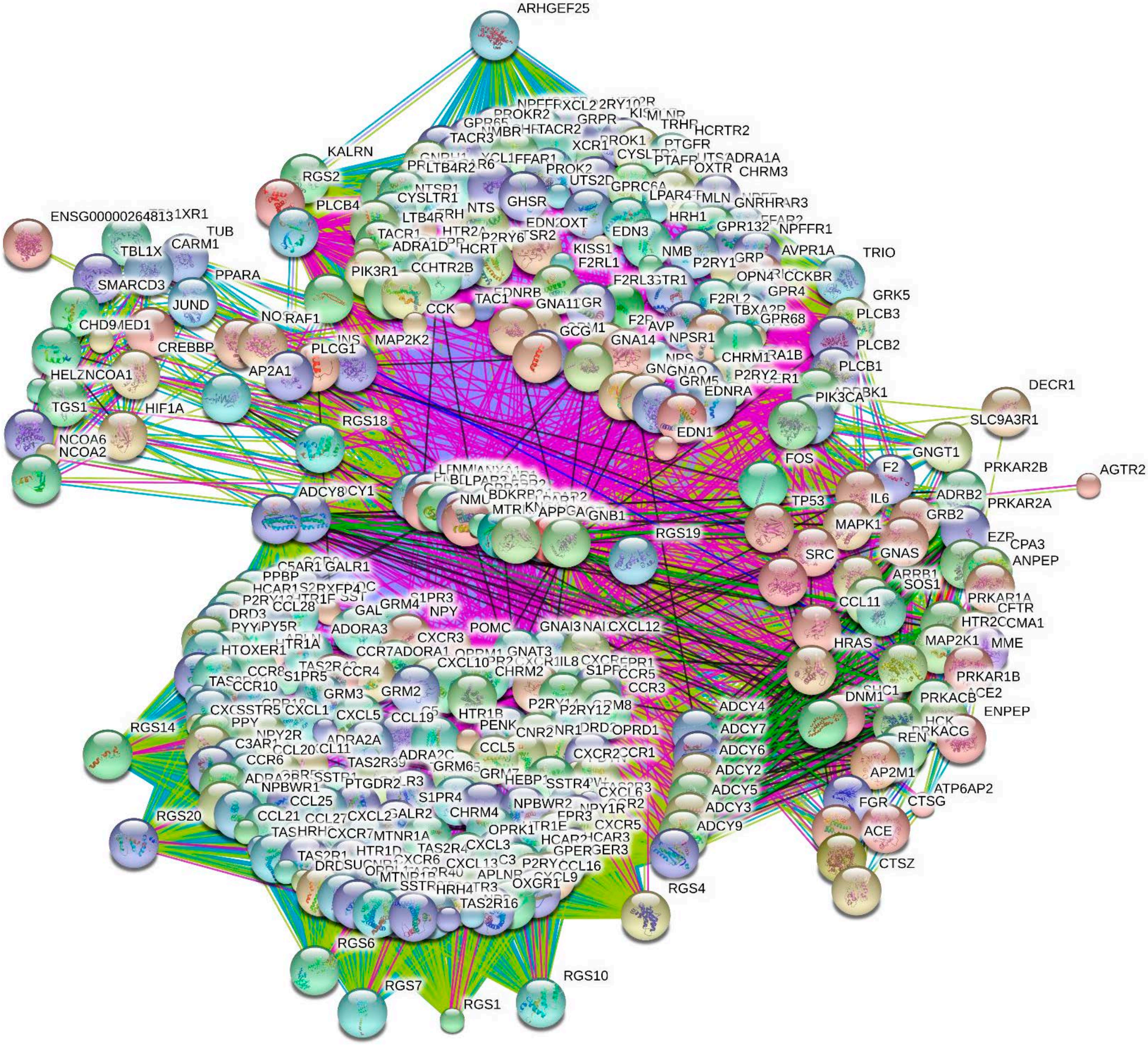
```
Overall percent disordered: 10.52     Average Prediction Score: 0.2024
Predicted disorder segment [1]-[14]   Average Strength= 0.8920
Predicted disorder segment [373]-[381]Average Strength= 0.6030
Predicted disorder segment [427]-[451]Average Strength= 0.7946
Predicted disorder segment [482]-[482]Average Strength= 0.5948
Predicted disorder segment [484]-[485]Average Strength= 0.6231

========================VL3 NNP STATISTICS=================================
Predicted residues: 485                       Number Disordered Regions: 2
Number residues disordered: 37        Longest Disordered Region: 21
Overall percent disordered: 7.63      Average Prediction Score: 0.1821
Predicted disorder segment [66]-[81]  Average Strength= 0.5565
Predicted disorder segment [427]-[447]Average Strength= 0.5822

=======================VSL2 NNP STATISTICS=================================
Predicted residues: 485                       Number Disordered Regions: 5
Number residues disordered: 67        Longest Disordered Region: 30
Overall percent disordered: 13.81     Average Prediction Score: 0.2970
Predicted disorder segment [1]-[12]   Average Strength= 0.7180
Predicted disorder segment [54]-[83]  Average Strength= 0.5988
Predicted disorder segment [98]-[99]  Average Strength= 0.5176
Predicted disorder segment [433]-[449]Average Strength= 0.6616
Predicted disorder segment [480]-[485]Average Strength= 0.7573
```

ENSP00000355627

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PROKR2
GRPR
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TRHR
HCRTR2
GPR65
NMBR
TACR2
TACR3
XCR1
PROK1
PTGFR
ADRA1A
KALRN
CHRM3
RGS2
LTB4R2
R6
FFAR1
PROK2
CYSLTR2
PTAFR
OXTR
UTS2D
GPRC6A
NTSR1
CYSLTR1
LPAR4
MLN
GNRHR
PLCB4
LTB4R
NTS
GHSR
HRH1
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XR1
TUB
TACR1
HTR2A
EDN2
OXT
EDN3
GPR132
NPFFR1
TBL1X
CARM1
P2RY6
SR2
KISS1
AVPR1A
TRIO
ADRA1D
HCRT
NMB
P2RY1
GRP
F2RL1
SMARCD3
PPARA
PIK3R1
CCHTR2B
F2RL3
STR1
OPN4
CCKBR
JUND
EDNRB
GPR4
GRK5
TAC1
GNA11
GR
F2RL2
CCK
TBXA2R
NO
RAF1
GPR68
PLCB3
CHD9
MED1
F2R
AVP
GCG
M1
MAP2K2
CREBBP
NPSR1
INS
GNA14
PLCB2
PLCG1
NPS
CHRM1
RA1B
HELZ
NCOA1
AP2A1
GNAO
PLCB1
P2RY2
GRM5
R1
TGS1
HIF1A
EDNRA
PIK3CA
RBK1
DECR1
RGS18
EDN1
SLC9A3R1
NCOA6
FOS
NCOA2
GNGT1
F2
PRKAR2B
AGTR2
LPAR2
ADCY8
CY1
BDKRB
NMU
TP53
IL6
ADRB2
PRKAR2A
MTR
APP
GNB1
RGS19
MAPK1
GRB2
EZP
CPA3
SRC
GNAS
ANPEP
C5AR1
GALR1
PPBP
HCAR1
RXFP4
ARRB1
SOS1
P2RY13
HTR1F
SST
S1PR3
GRM4
GAL
NPY
CCL11
PRKAR1A
CFTR
DRD3
CCL28
PYY
PY5R
ADORA3
CXCR3
HTR2C
CMA1
POMC
GNAI3
NAI
CXCL12
HTOXER1
HTR1A
CCR7
ADORA1
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GNAT3
MAP2K1
MME
HRAS
CCR8
TAS2R
S1PR5
CCR4
CXCL10
CHRM2
IL8
S1PR
CCR5
PRKAR1B
CCR10
GRM3
GRM2
CCR3
DNM1
PRKACB
ACE2
CXCL1
SSTR5
CXCL5
CCL19
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GRM8
ADCY4
HTR1B
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RGS14
PPY
PENK
CNR2
NR1
DRD
OPRD1
ADCY7
HCK
NPY2R
ADRA2A
PRKACG
C3AR1
CCL20
CL11
CCL5
CXCR2
CCR1
ADCY6
REN
CCR6
TAS2R39
ADRA2C
GRM6
ADRA2B
SSTR1
PTGDR2
R3
GRM7
HEBP1
SSTR4
ADCY2
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AP2M1
ADCY5
CCL25
S1PR4
CHRM4
NPBWR2
NPY1R
CXCL6
ATP6AP2
RGS20
CCL21
CCL27
CXCL2
GALR2
ADCY3
FGR
CTSG
TAS
HRH
CXCR7
MTNR1A
TR1E
FPR3
CXCR5
ADCY9
OPRK1
HCAR2
HCAR3
ACE
TAS2R1
HTR1D
TAS2R4
CXCL3
GPER
GER3
CXCR6
CXCL13
C3
CTSZ
DRD
SUCNR1
P2RY
CCL16
MTNR1B
R40
APLNR
OXGR1
L9
RGS4
SSTR
HRH4
TR3
TAS2R16
RGS6
RGS10
RGS7
RGS1

```
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SV=1
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HDLHQRIDKFRFTPPLEDSCFHYGFNSNYLKKVISYWRNEFDWKKQVEILNRYPHFKTKI
EGLDIHFIHVKPPQLPAGHTPKPLLMVHGWPGSFYEFYKIIPLLTDPKNHGLSDEHVFEV
ICPSIPGYGFSEASSKKGFNSVATARIFYKLMLRLGFQEFYIQGGDWGSLICTNMAQLVP
SHVKGLHLNMALVLSNFSTLTLLLGQRFGRFLGLTERDVELLYPVKEKVFYSLMRESGYM
HIQCTKPDTVGSALNDSPVGLAAYILEKFSTWTNTEFRYLEDGGLERKFSLDDLLTNVML
YWTTGTIISSQRFYKENLGQGWMTQKHERMKVYVPTGFSAFPFELLHTPEKWVRFKYPKL
ISYSYMVRGGHFAAFEEPELLAQDIRKFLSVLERQ
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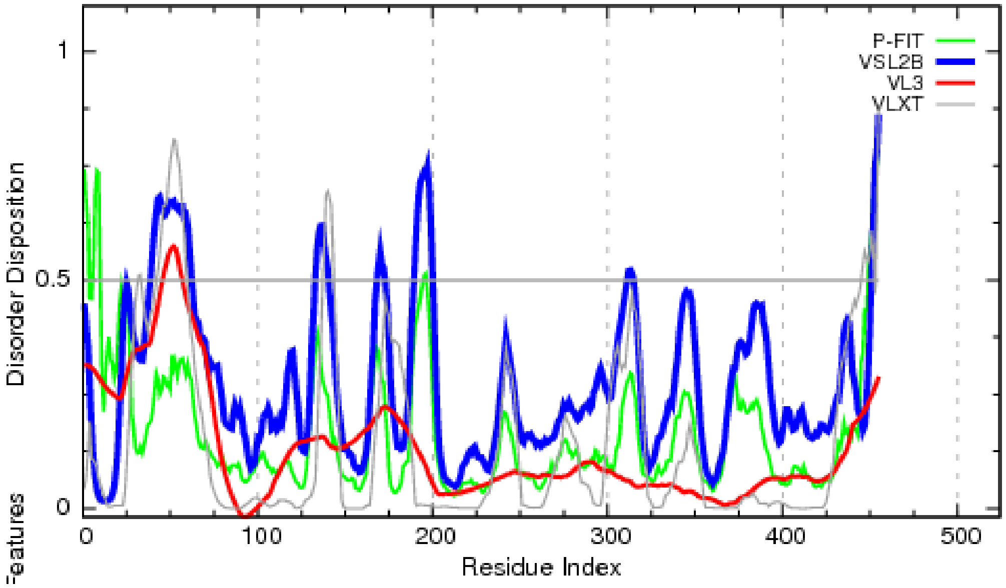

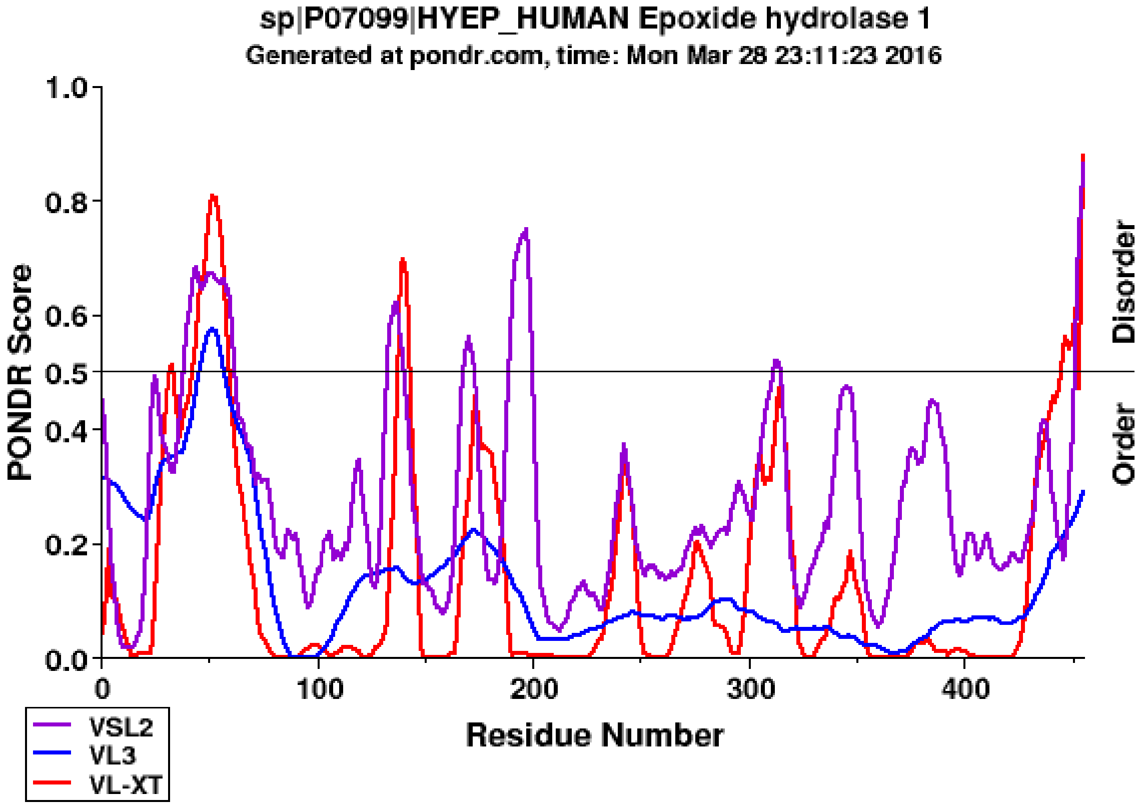

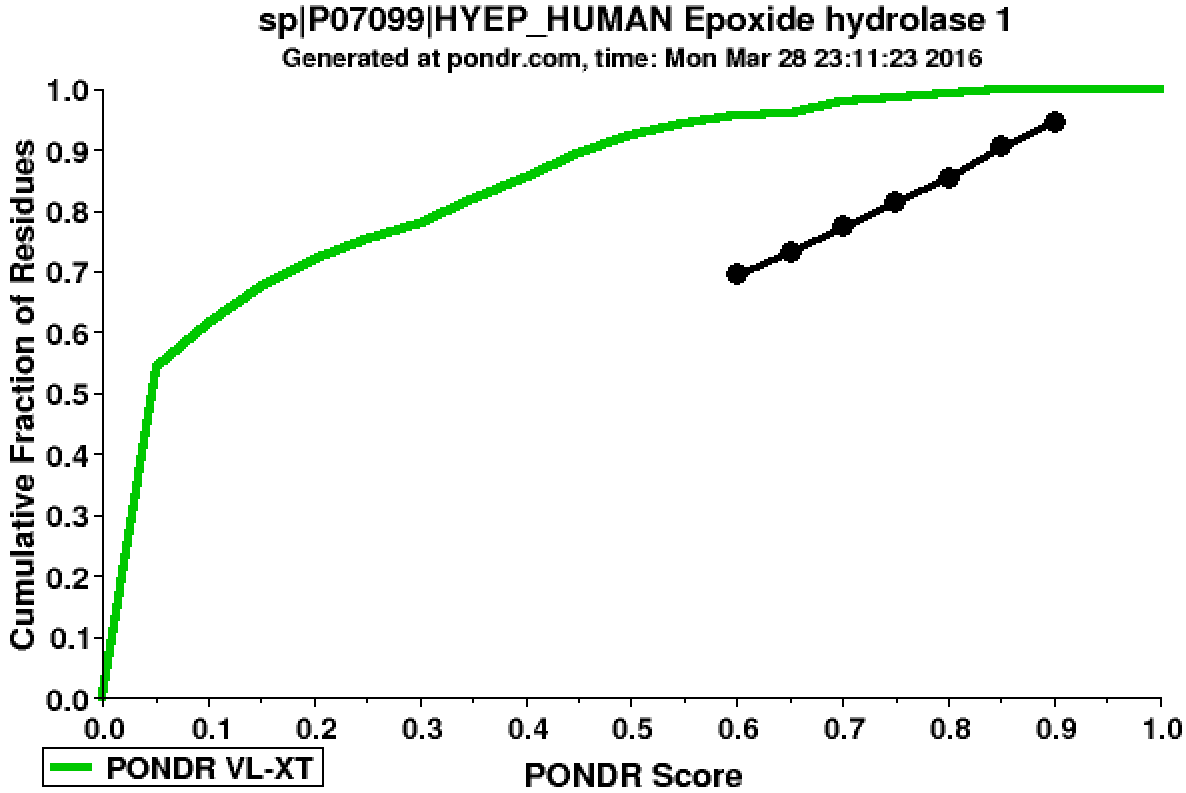

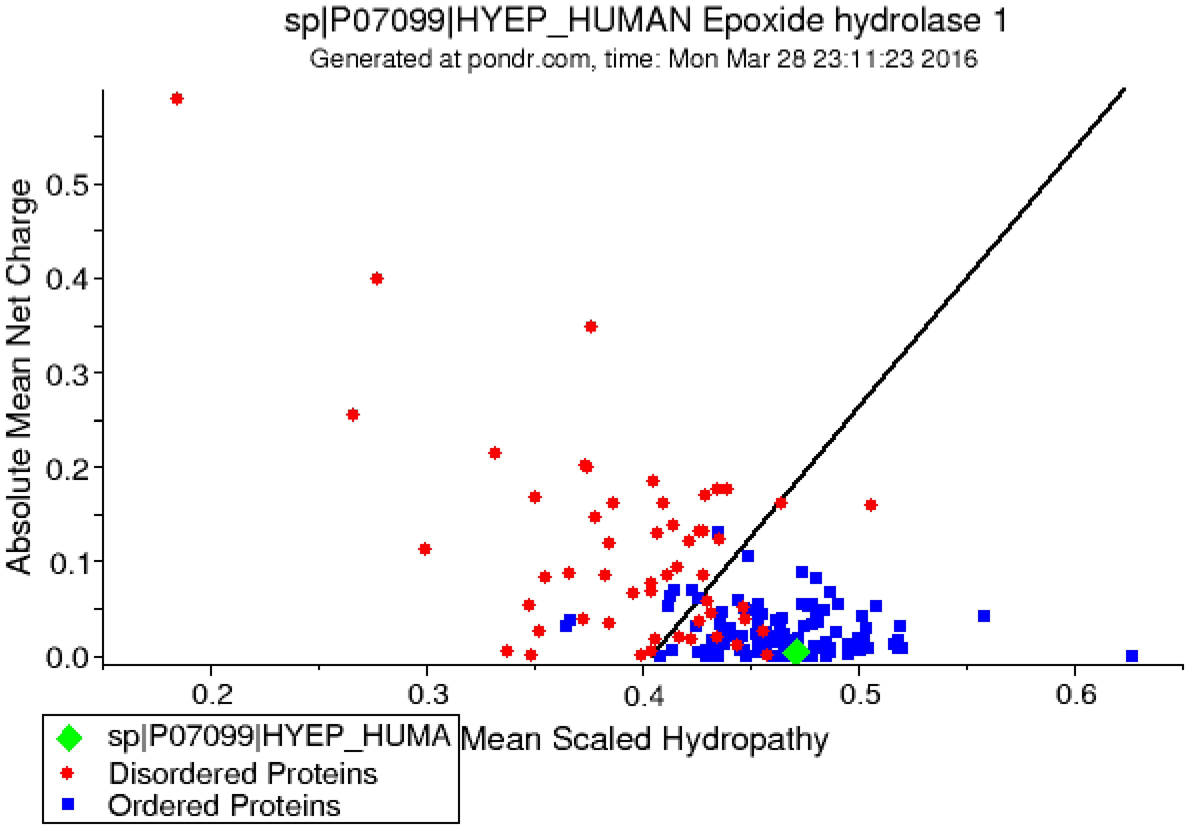

```
======================VLXT NNP STATISTICS===============================
Predicted residues: 455                        Number Disordered Regions: 5
Number residues disordered: 35         Longest Disordered Region: 18
```

```
Overall percent disordered: 7.69      Average Prediction Score: 0.1461
Predicted disorder segment [32]-[33]  Average Strength= 0.5110
Predicted disorder segment [42]-[59]  Average Strength= 0.6712
Predicted disorder segment [138]-[143]Average Strength= 0.6445
Predicted disorder segment [446]-[452]Average Strength= 0.5569
Predicted disorder segment [454]-[455]Average Strength= 0.7860

========================VL3 NNP STATISTICS================================
Predicted residues: 455                       Number Disordered Regions: 1
Number residues disordered: 11        Longest Disordered Region: 11
Overall percent disordered: 2.42      Average Prediction Score: 0.1315
Predicted disorder segment [46]-[56]  Average Strength= 0.5465

=======================VSL2 NNP STATISTICS================================
Predicted residues: 455                       Number Disordered Regions: 6
Number residues disordered: 56        Longest Disordered Region: 24
Overall percent disordered: 12.31     Average Prediction Score: 0.2772
Predicted disorder segment [39]-[62]  Average Strength= 0.6362
Predicted disorder segment [133]-[140]Average Strength= 0.5729
Predicted disorder segment [169]-[172]Average Strength= 0.5392
Predicted disorder segment [190]-[200]Average Strength= 0.6707
Predicted disorder segment [312]-[315]Average Strength= 0.5133
Predicted disorder segment [451]-[455]Average Strength= 0.7157
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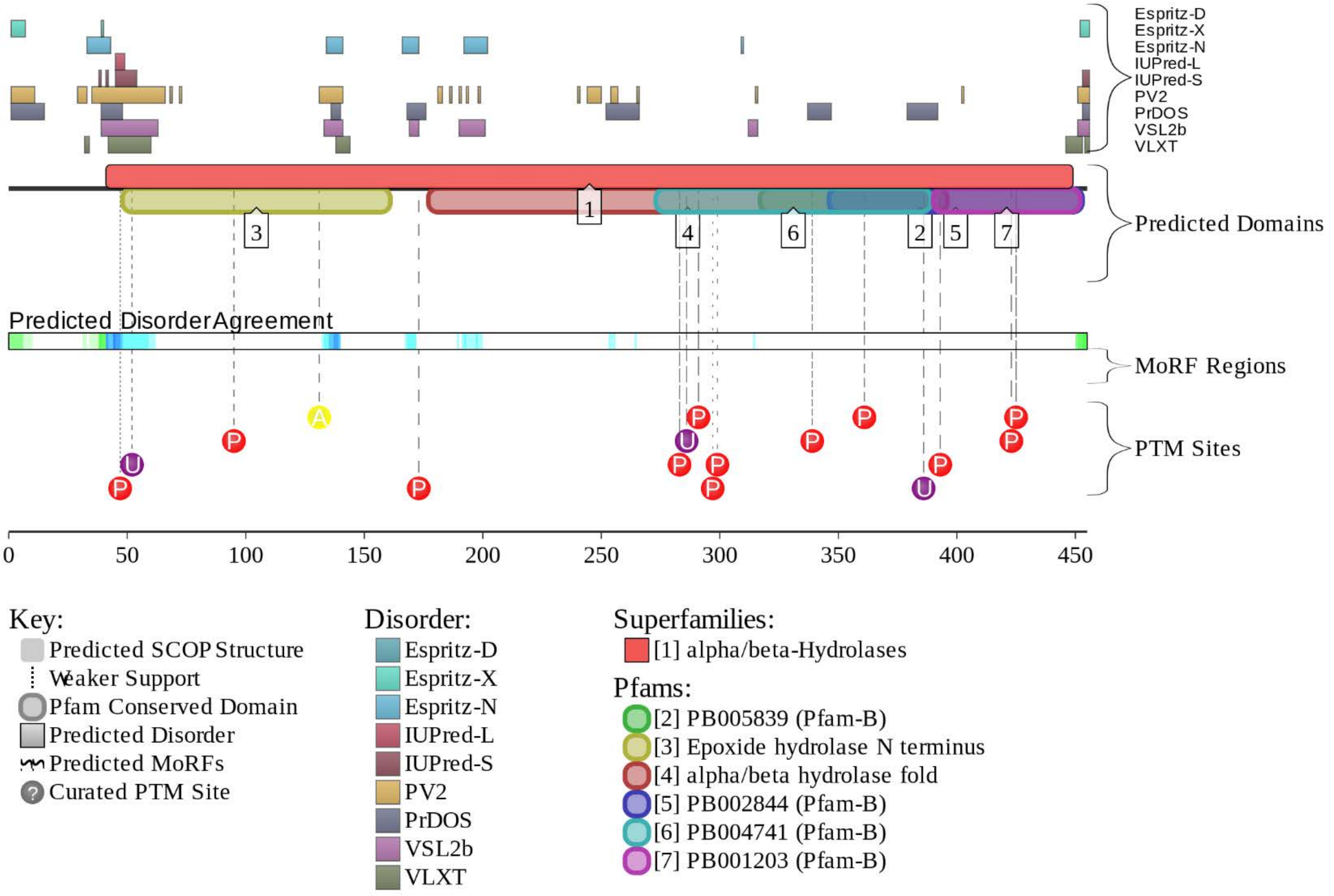
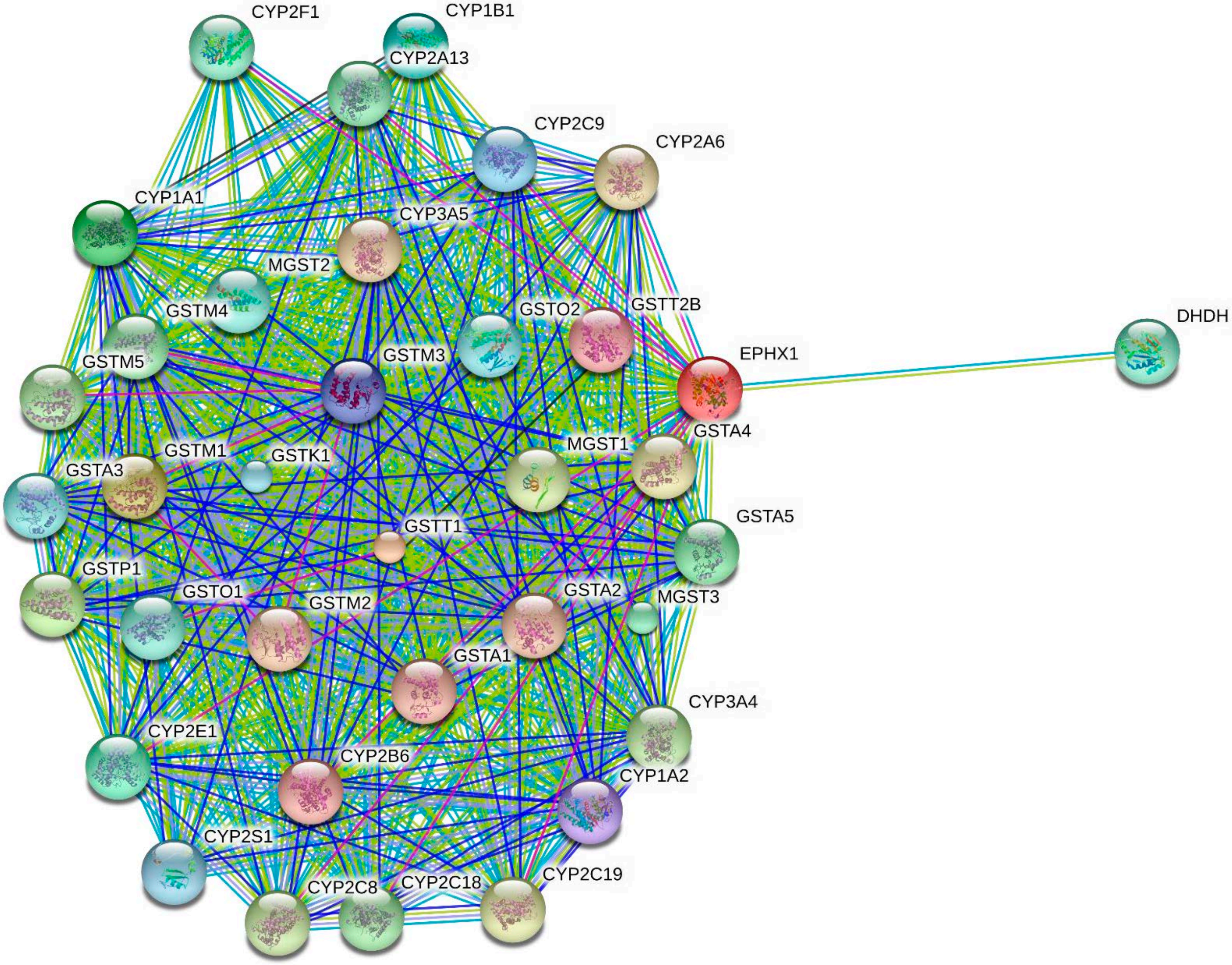
ENSP00000355802, ENSP00000272167

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CYP2A13
CYP2C9
CYP2A6
CYP1A1
CYP3A5
MGST2
GSTM4
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GSTT2B
DHDH
EPHX1
GSTM5
GSTM3
GSTA4
GSTM1
GSTK1
MGST1
GSTA3
GSTA5
GSTT1
GSTP1
GSTO1
GSTM2
GSTA2
MGST3
GSTA1
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CYP2E1
CYP2B6
CYP1A2
CYP2S1
CYP2C8
CYP2C18
CYP2C19

```
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QSSCFGLRWFTPASEVPLCGHATLASAAVLFHKIKNMNSTLTFVTLSGELRARRAEDGIV
LDLPLYPAHPQDFHEVEDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSFLENLKVN
TENLLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSY
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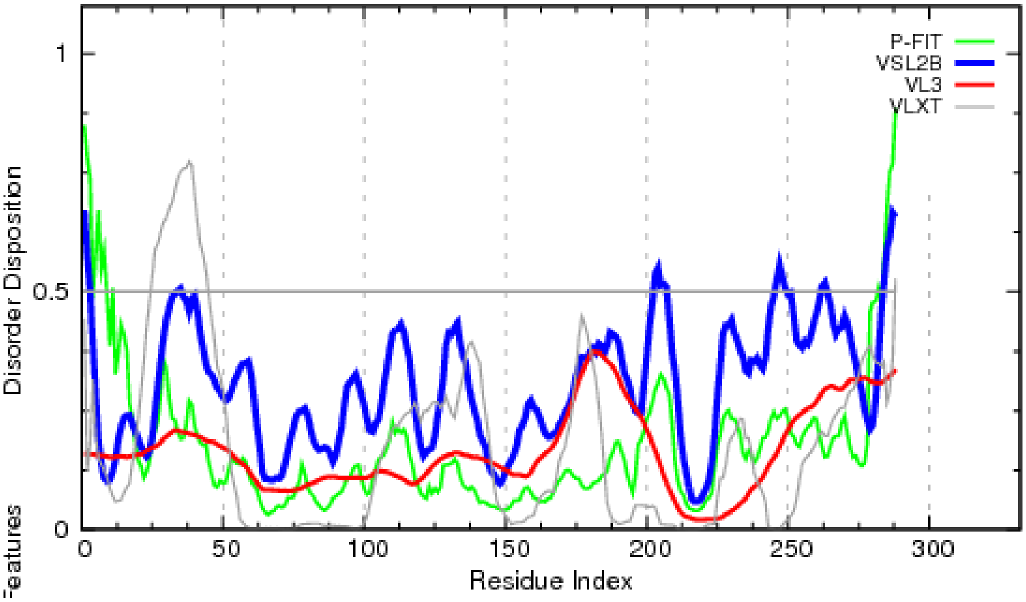

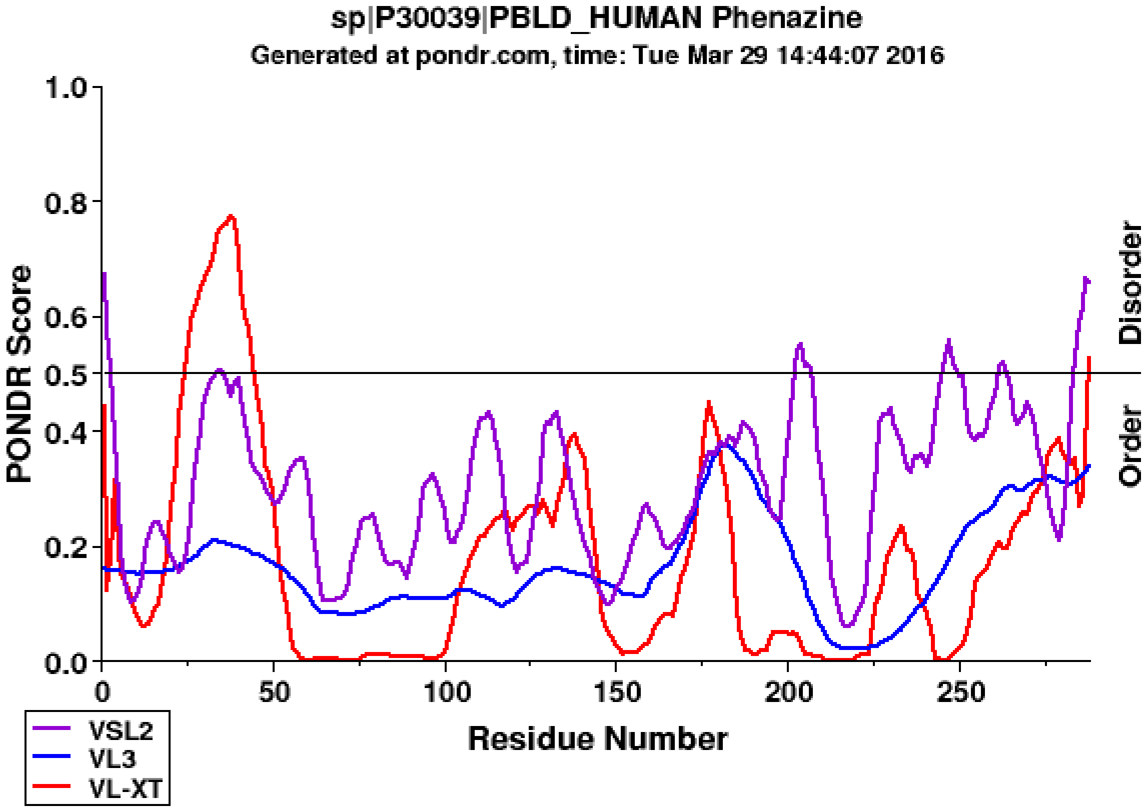

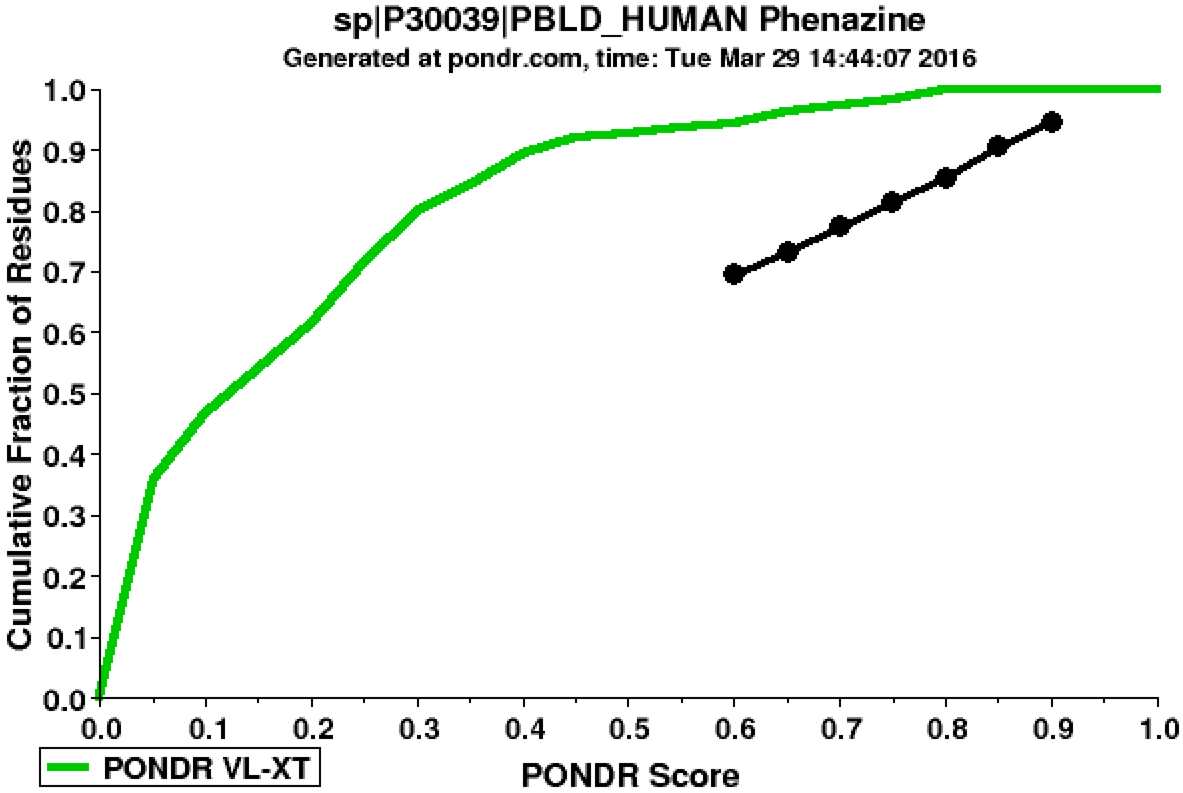
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Generated at pondr.com, time: Tue Mar 29 14:44:07 2016
Cumulative Fraction of Residues
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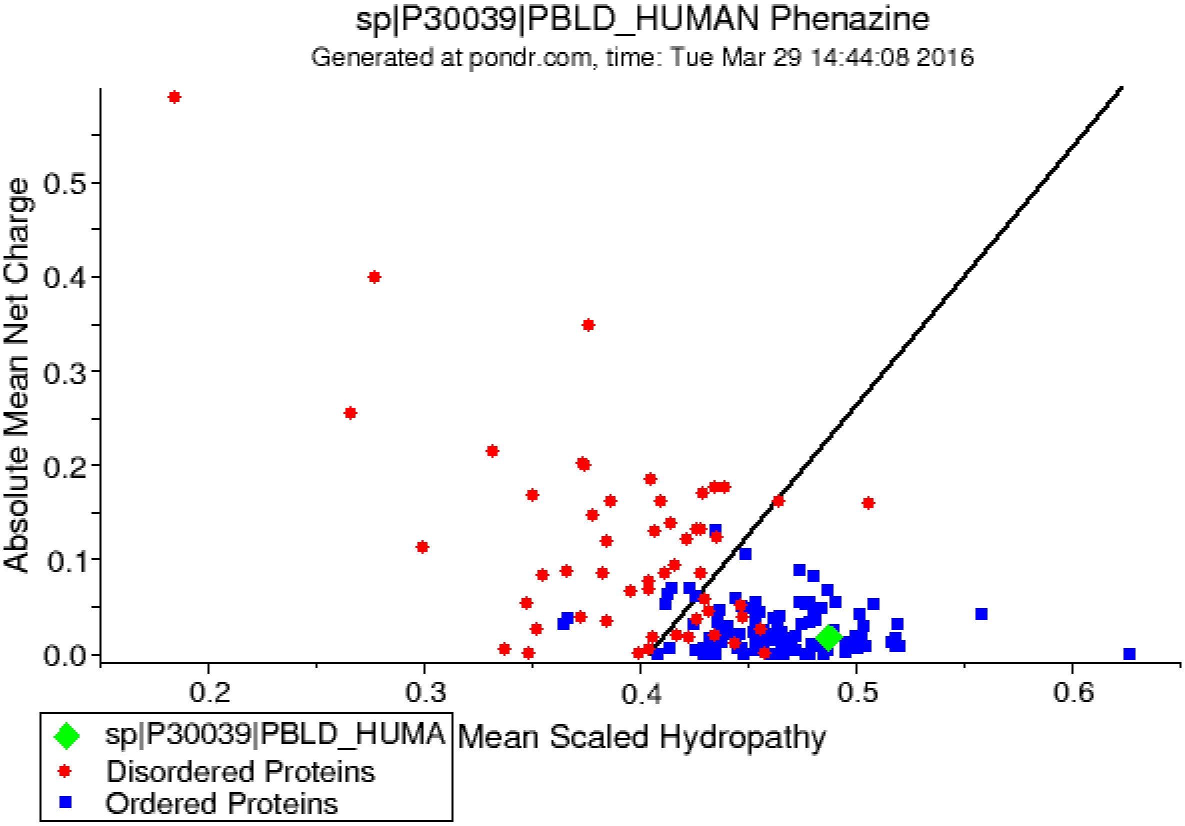
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR VL-XT
PONDR Score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Generated at pondr.com, time: Tue Mar 29 14:44:08 2016
Absolute Mean Net Charge
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0.4
0.3
0.2
0.1
0.0
0.2
0.3
0.4
0.5
0.6
Mean Scaled Hydropathy
sp|P30039|PBLD_HUMA
Disordered Proteins
Ordered Proteins

```
========================VLXT NNP STATISTICS================================
Predicted residues: 288                      Number Disordered Regions: 2
Number residues disordered: 21        Longest Disordered Region: 20
Overall percent disordered: 7.29      Average Prediction Score: 0.1771
Predicted disorder segment [25]-[44]  Average Strength= 0.6671
Predicted disorder segment [288]-[288]Average Strength= 0.5271

=========================VL3 NNP STATISTICS================================
Predicted residues: 288                      Number Disordered Regions: 0
Number residues disordered: 0         Longest Disordered Region: 0
Overall percent disordered: 0.00      Average Prediction Score: 0.1663

========================VSL2 NNP STATISTICS================================
Predicted residues: 288                      Number Disordered Regions: 6
Number residues disordered: 21        Longest Disordered Region: 5
Overall percent disordered: 7.29      Average Prediction Score: 0.3056
Predicted disorder segment [1]-[3]    Average Strength= 0.5842
Predicted disorder segment [34]-[35]  Average Strength= 0.5038
Predicted disorder segment [203]-[207]Average Strength= 0.5255
Predicted disorder segment [246]-[249]Average Strength= 0.5304
Predicted disorder segment [262]-[263]Average Strength= 0.5149
Predicted disorder segment [284]-[288]Average Strength= 0.6104
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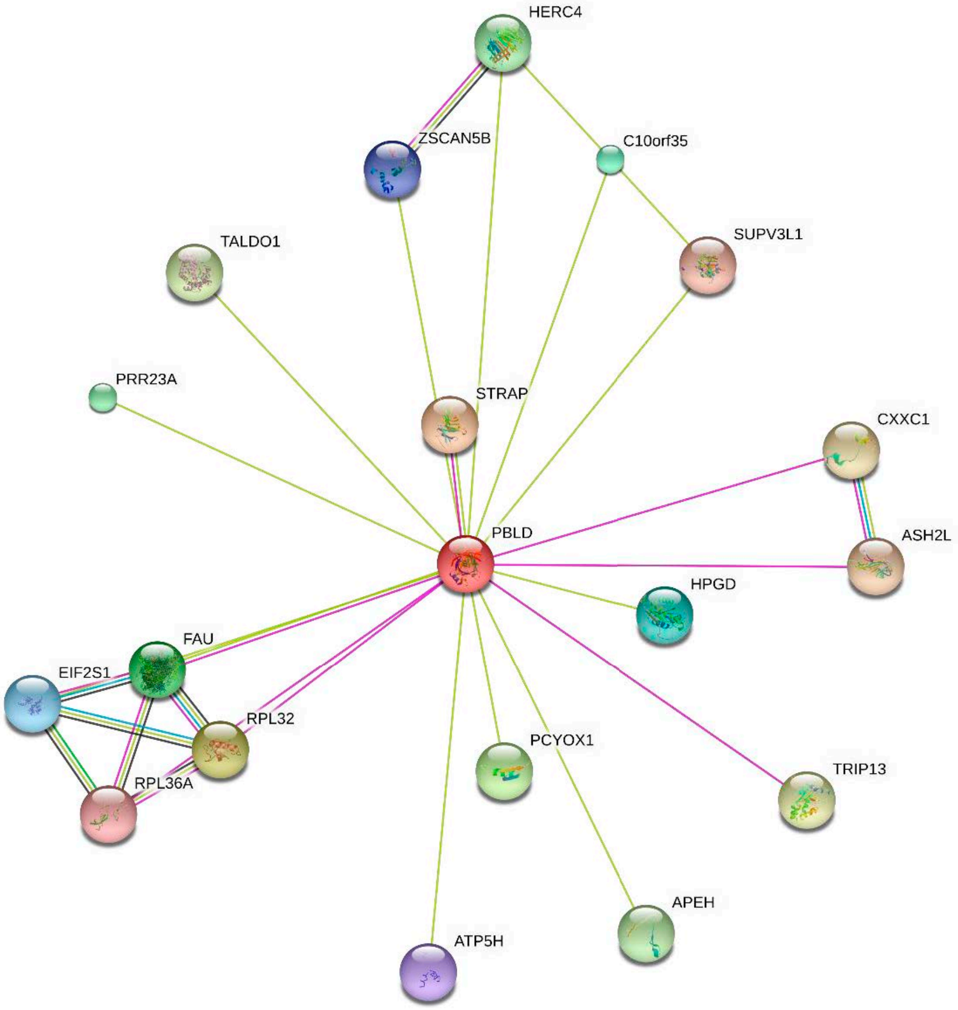
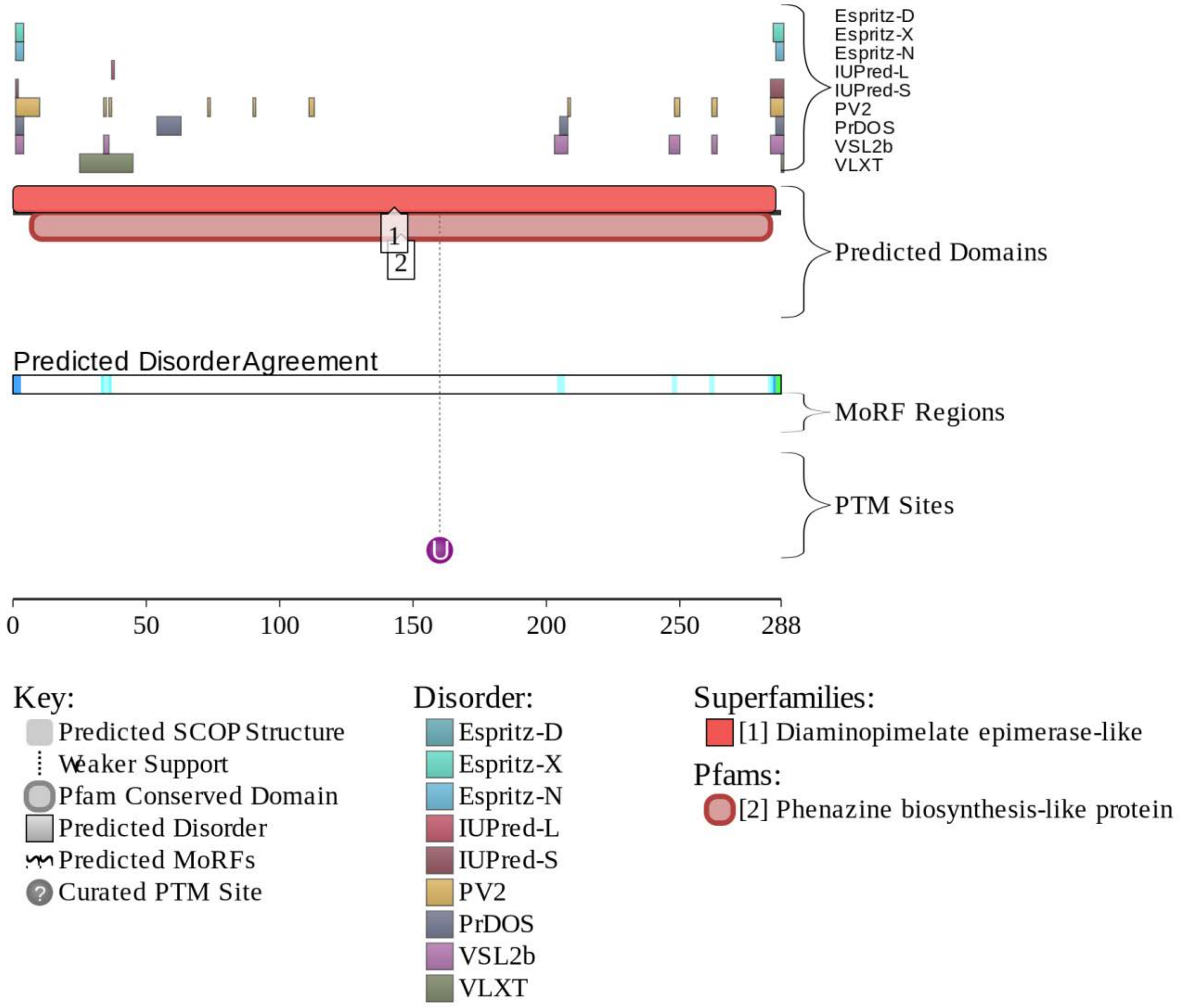


ENSP00000351619, ENSP00000308466



```
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containing protein OS=Homo sapiens GN=PBLD
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QSSCFGLRWFTPASEVPLCGHATLASAAVLFHKIKNMNSTLTFVTLSGELRARRAEDGIV
LDLPLYPAHPQDFHEVEDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSFLENLKVN
TENLLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSY
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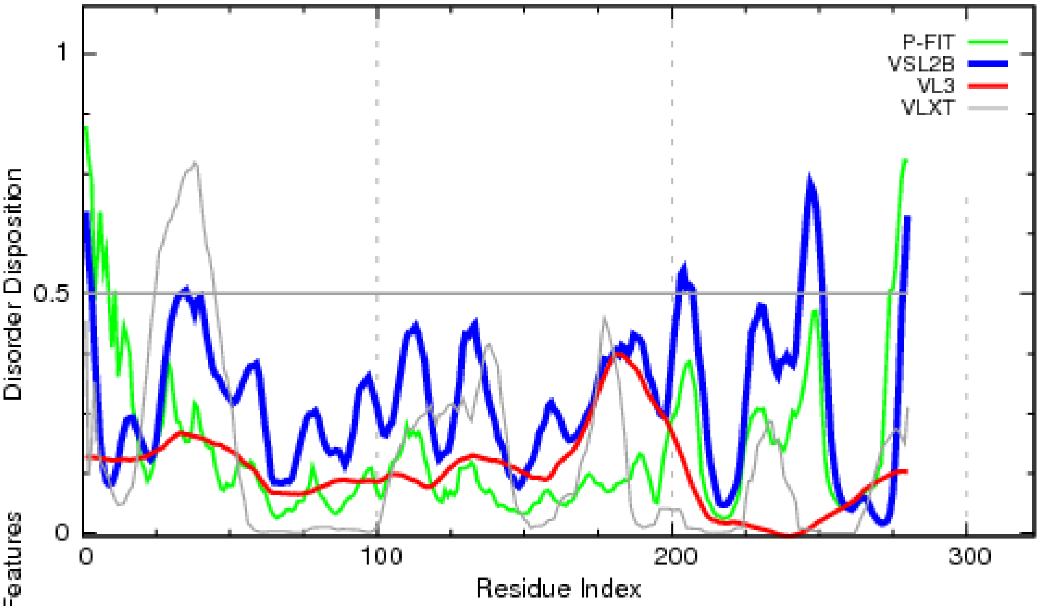

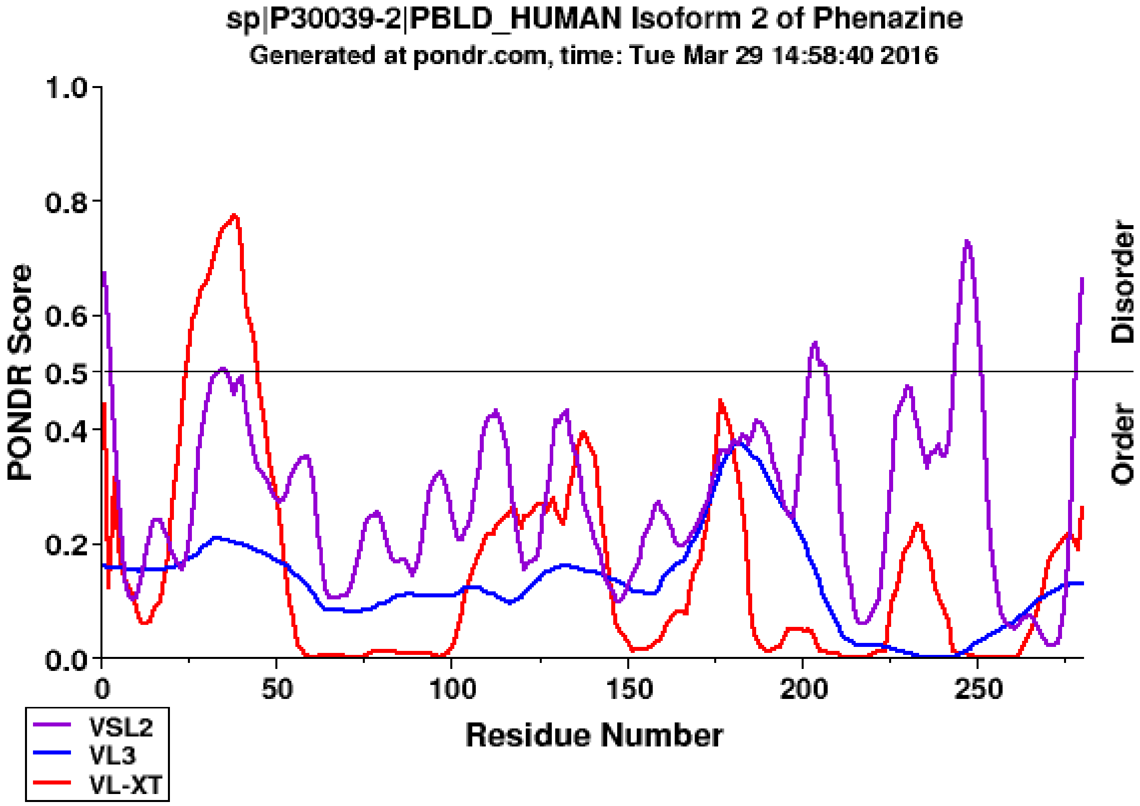

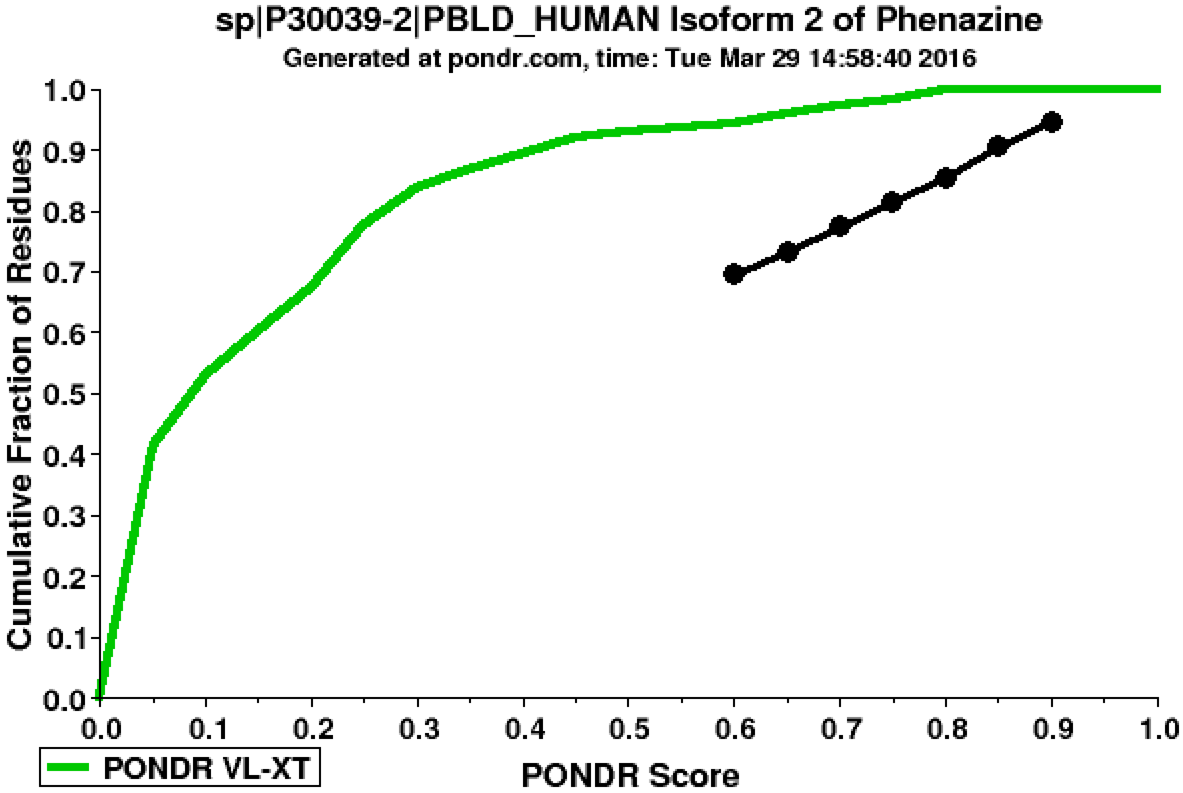
sp|P30039-2|PBLD_HUMAN Isoform 2 of Phenazine
Generated at pondr.com, time: Tue Mar 29 14:58:40 2016
Cumulative Fraction of Residues
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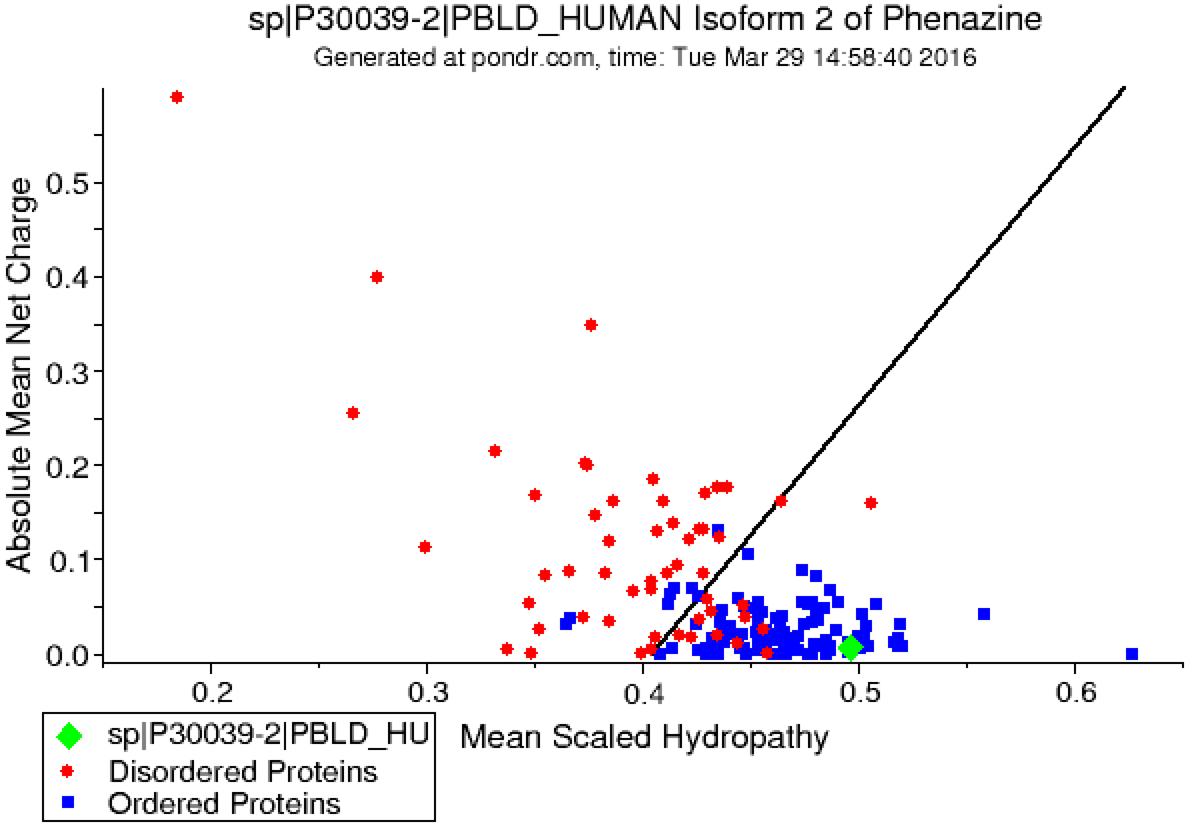
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR VL-XT
PONDR Score


sp|P30039-2|PBLD_HUMAN Isoform 2 of Phenazine
Generated at pondr.com, time: Tue Mar 29 14:58:40 2016
Absolute Mean Net Charge
0.5
0.4
0.3
0.2
0.1
0.0
0.2
0.3
0.4
0.5
0.6
Mean Scaled Hydropathy
sp|P30039-2|PBLD_HU
Disordered Proteins
Ordered Proteins

```
=========================VLXT NNP STATISTICS================================
Predicted residues: 280                        Number Disordered Regions: 1
Number residues disordered: 20         Longest Disordered Region: 20
Overall percent disordered: 7.14       Average Prediction Score: 0.1572
Predicted disorder segment [25]-[44]   Average Strength= 0.6671

==========================VL3 NNP STATISTICS================================
Predicted residues: 280                        Number Disordered Regions: 0
Number residues disordered: 0          Longest Disordered Region: 0
Overall percent disordered: 0.00       Average Prediction Score: 0.1324

=========================VSL2 NNP STATISTICS================================
Predicted residues: 280                        Number Disordered Regions: 5
Number residues disordered: 20         Longest Disordered Region: 8
Overall percent disordered: 7.14       Average Prediction Score: 0.2787
Predicted disorder segment [1]-[3]     Average Strength= 0.5842
Predicted disorder segment [34]-[35]   Average Strength= 0.5038
Predicted disorder segment [203]-[207]Average Strength= 0.5255
Predicted disorder segment [244]-[251]Average Strength= 0.6326
Predicted disorder segment [279]-[280]Average Strength= 0.6100
```