Appendix 2

Electronegativity and intrinsic disorder of preeclampsia-related proteins

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3. Department of Molecular Medicine and USF Health Byrd Alzheimer's Research Institute, Morsani College of Medicine, University of South Florida, 12901 Bruce B. Downs Blvd. MDC07 Tampa, FL 33647, USA.
4. Laboratory of Structural Dynamics, Stability and Folding of Proteins, Institute of Cytology, Russian Academy of Sciences, St. Petersburg, Russia.
5. Centro de Investigaciones Químicas, Universidad Autónoma del Estado de Morelos. Av. Universidad No. 1001, C.P. 62209 Chamilpa, Cuernavaca, Morelos, México.
6. Department of Infectious Diseases, Instituto Nacional de Ciencias Médicas y Nutrición "Salvador Zubirán", Av. Vasco de Quiroga 15, C.P. 14080 México City, México.

>sp|Q9UHF0|TKNK_HUMAN Tachykinin-3 OS=Homo sapiens GN=TAC3 PE=1 SV=1
MRIMLLFTAILAFSLAQSFGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGL
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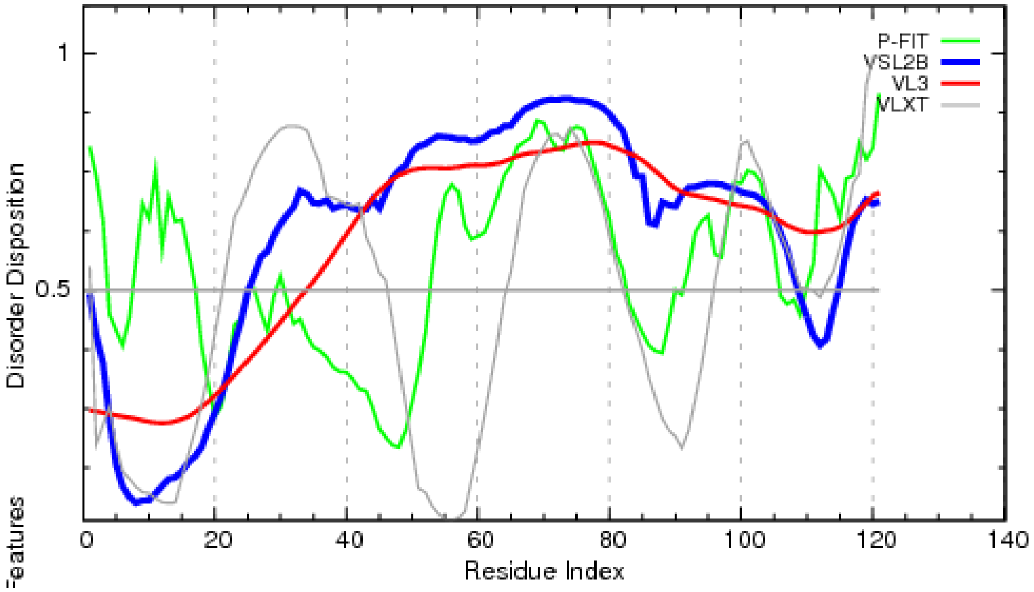

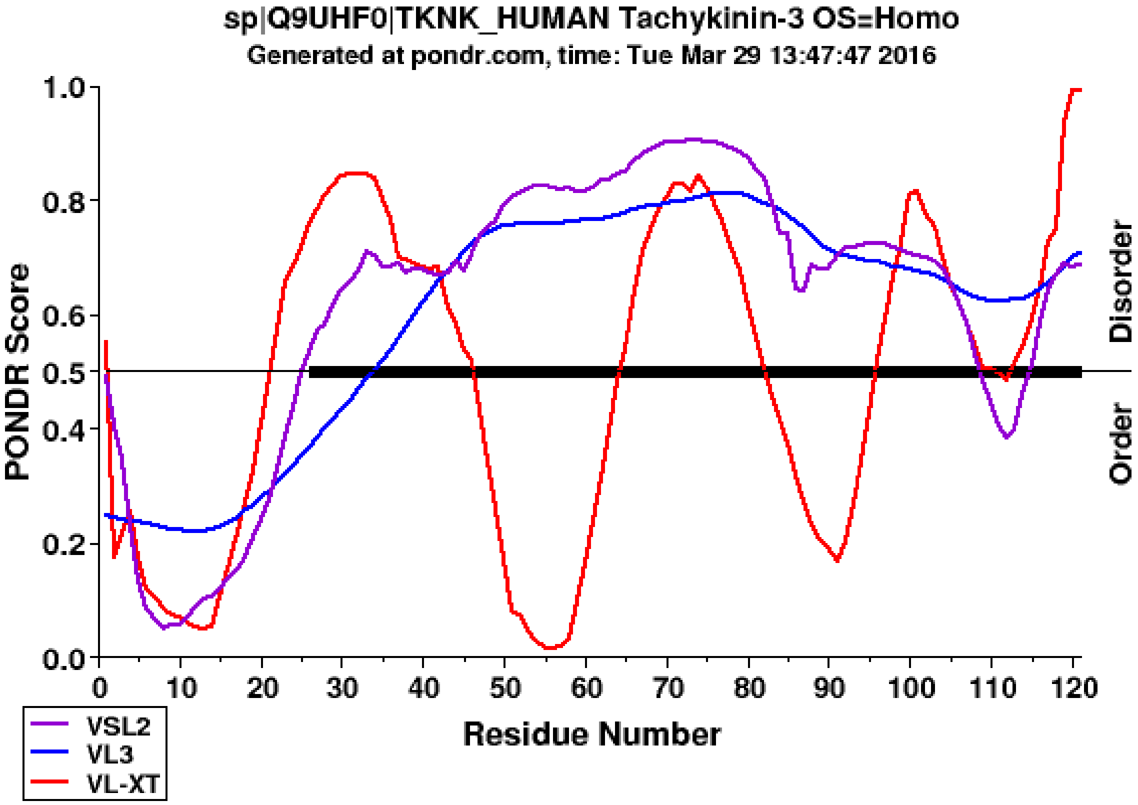

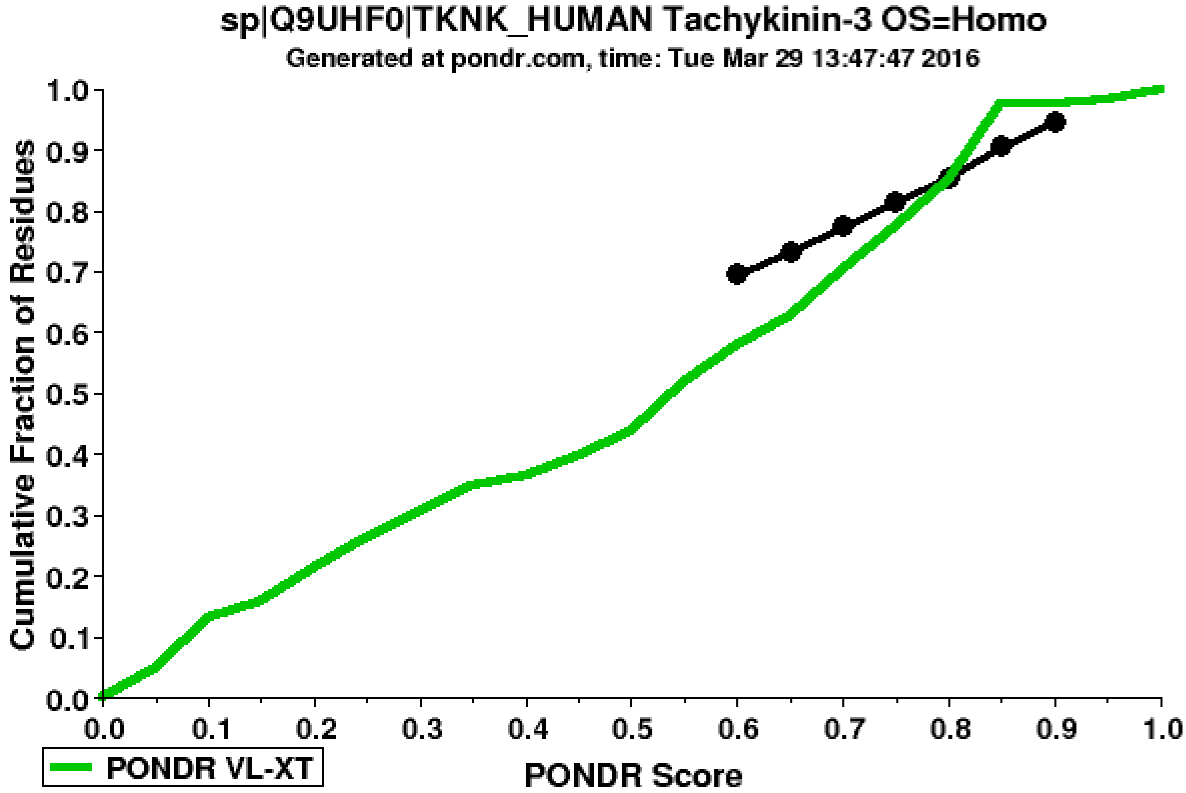

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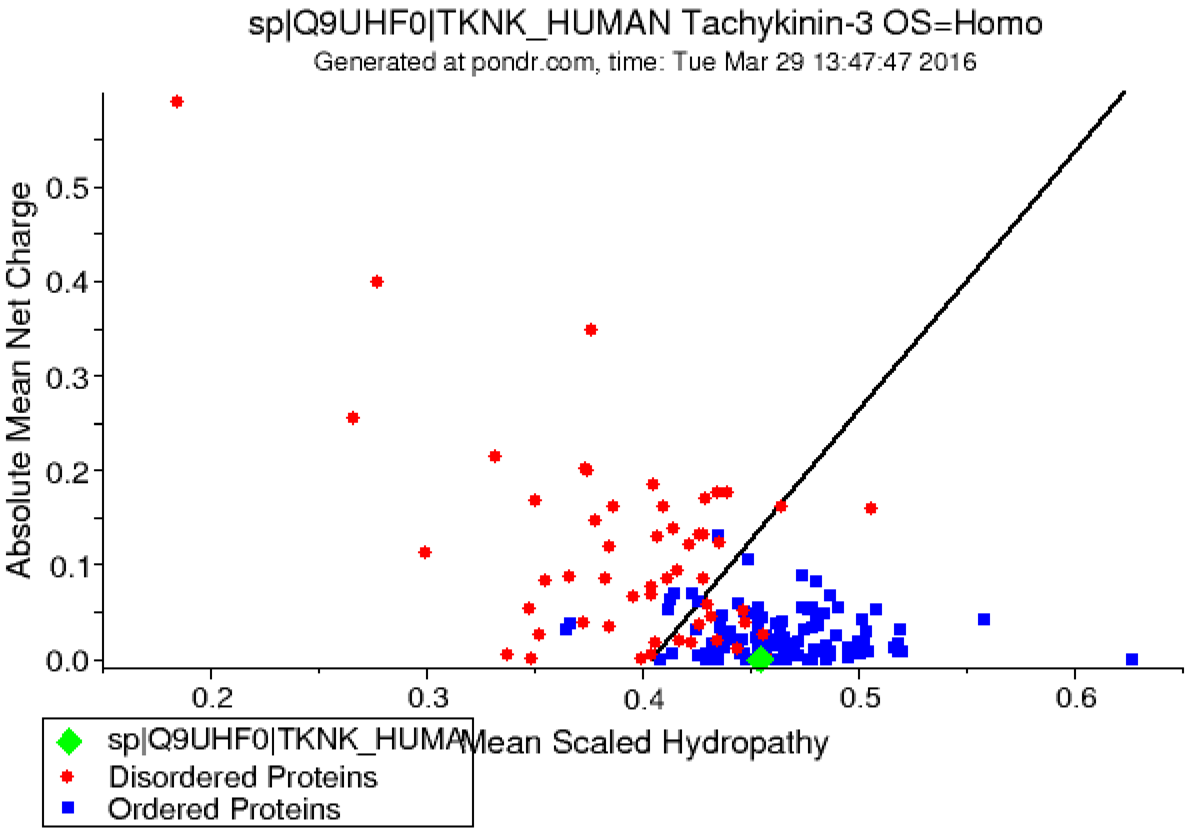

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Generated at pondr.com, time: Tue Mar 29 13:47:47 2016

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========================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
Predicted disorder segment [115]-[121]Average Strength= 0.6380
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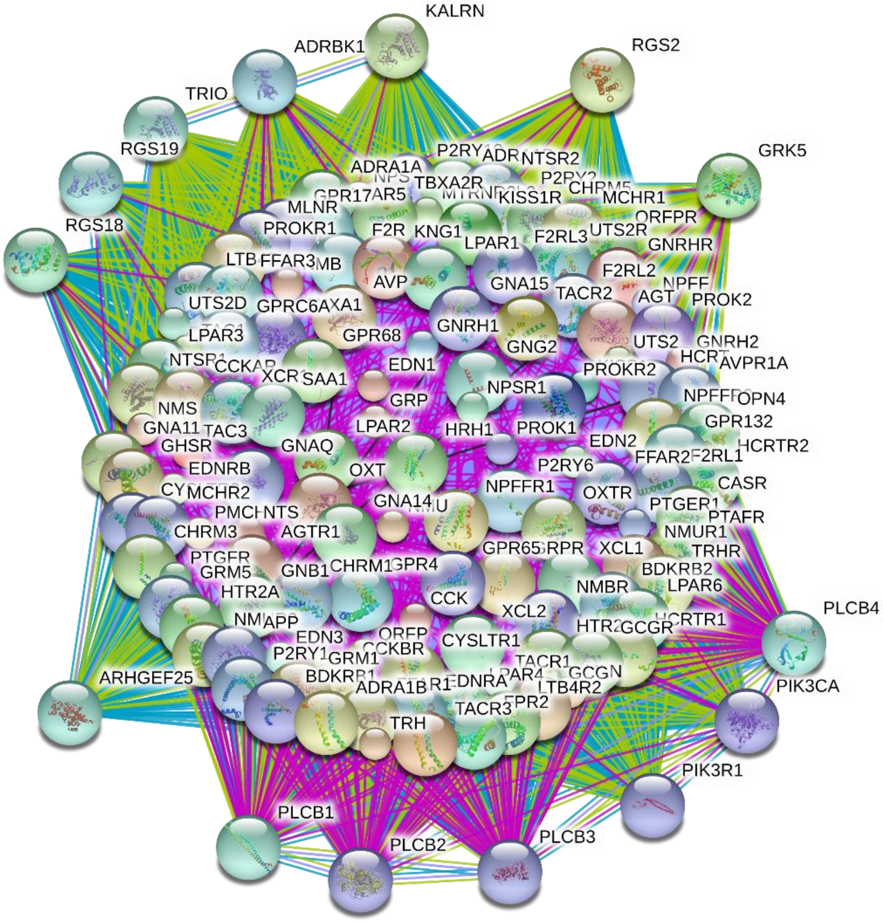

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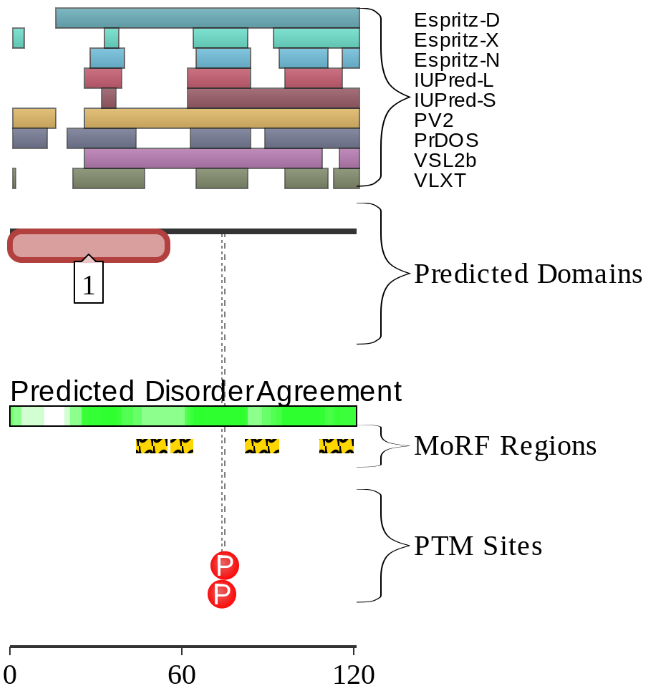

Key:
▢ Predicted SCOP Structure
⋮ Weaker Support
◯ Pfam Conserved Domain
▢ Predicted Disorder
〰 Predicted MoRFs
? Curated PTM Site

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

Superfamilies:
N/A No Hits

Pfams:
◯ [1] PF03823.9 (Family)

Predicted Disordered Binding Regions			
	From	To	Length
1	44	54	11
2	56	63	8
3	82	93	12
4	108	119	12

```
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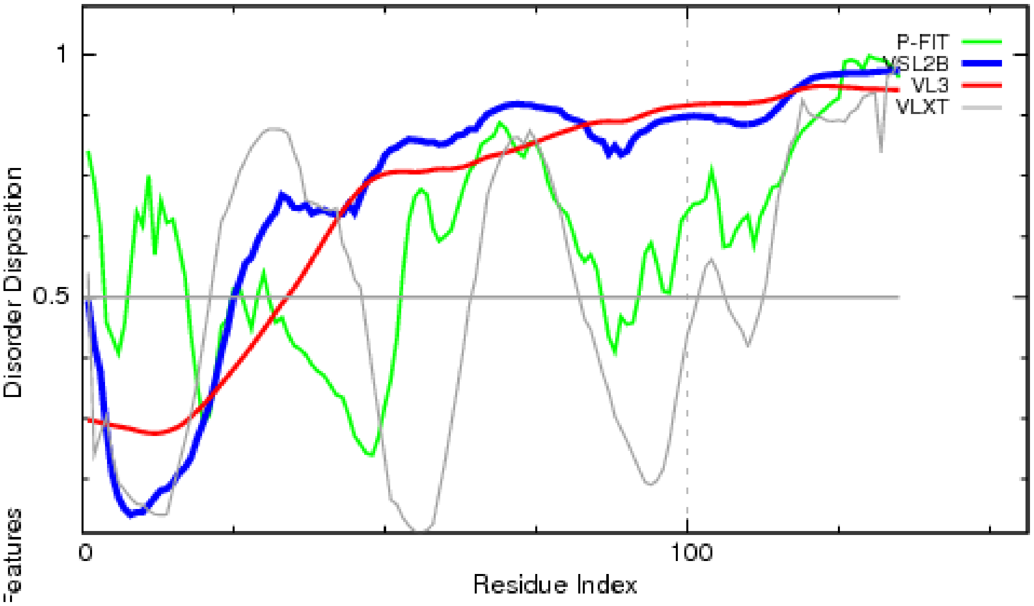

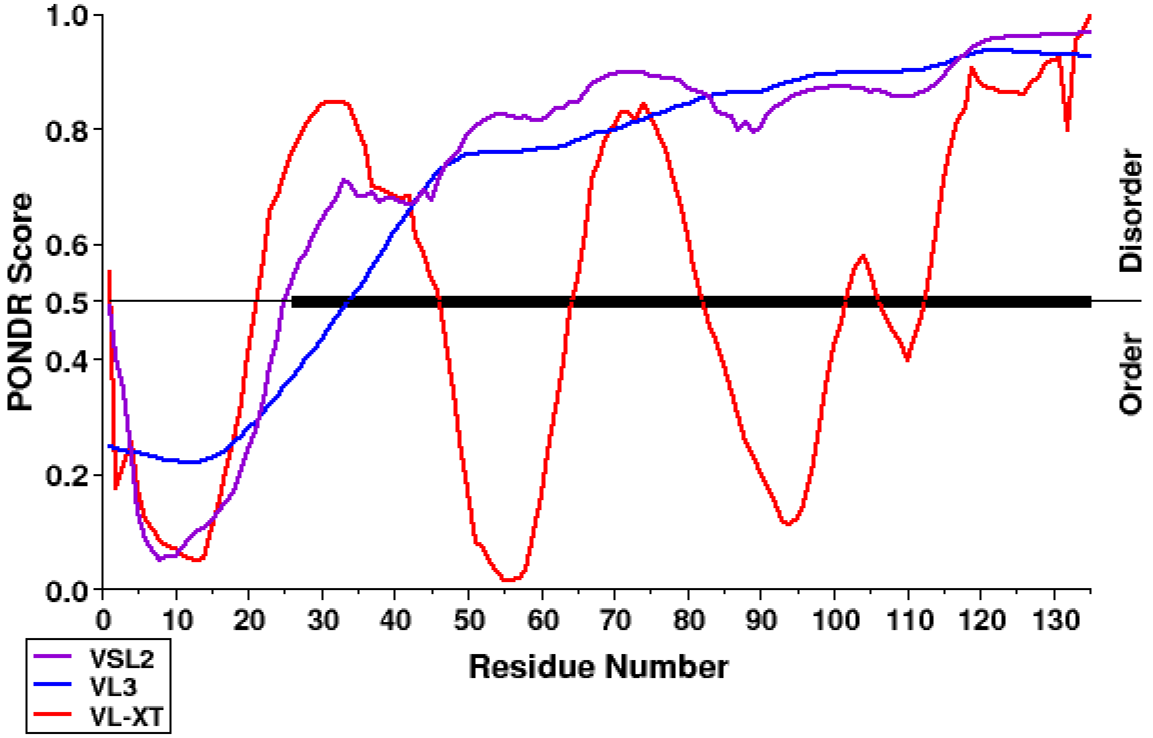
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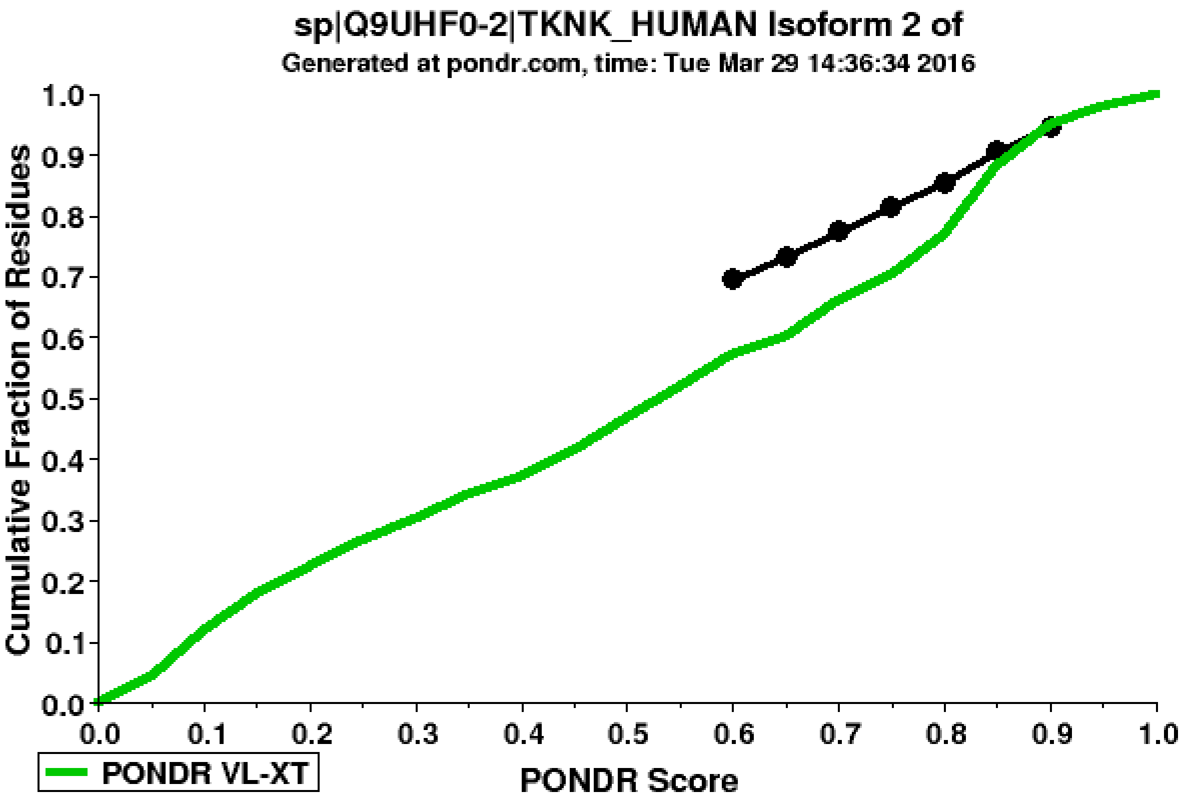
Generated at pondr.com, time: Tue Mar 29 14:36:34 2016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Generated at pondr.com, time: Tue Mar 29 14:36:34 2016
Cumulative Fraction of Residues
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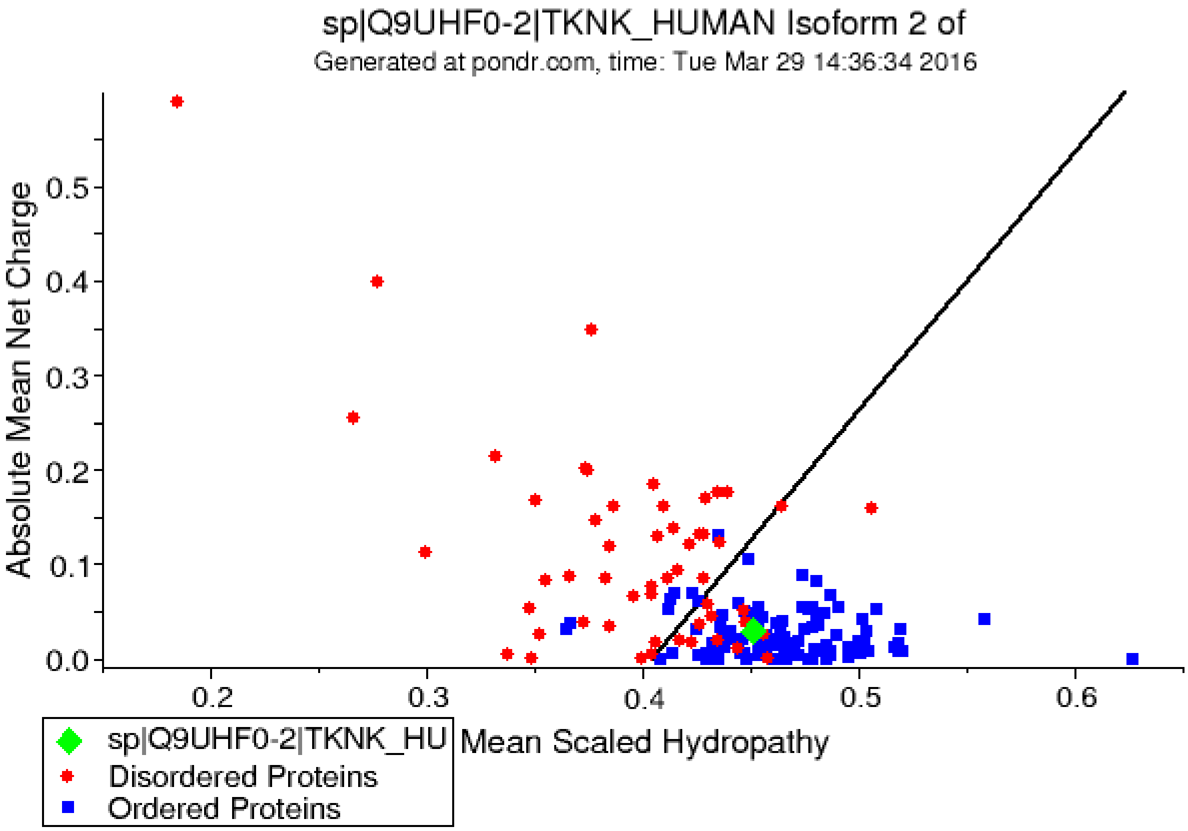
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT


sp|Q9UHF0-2|TKNK_HUMAN Isoform 2 of
Generated at pondr.com, time: Tue Mar 29 14:36:34 2016
Absolute Mean Net Charge
0.0
0.1
0.2
0.3
0.4
0.5
0.2
0.3
0.4
0.5
0.6
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

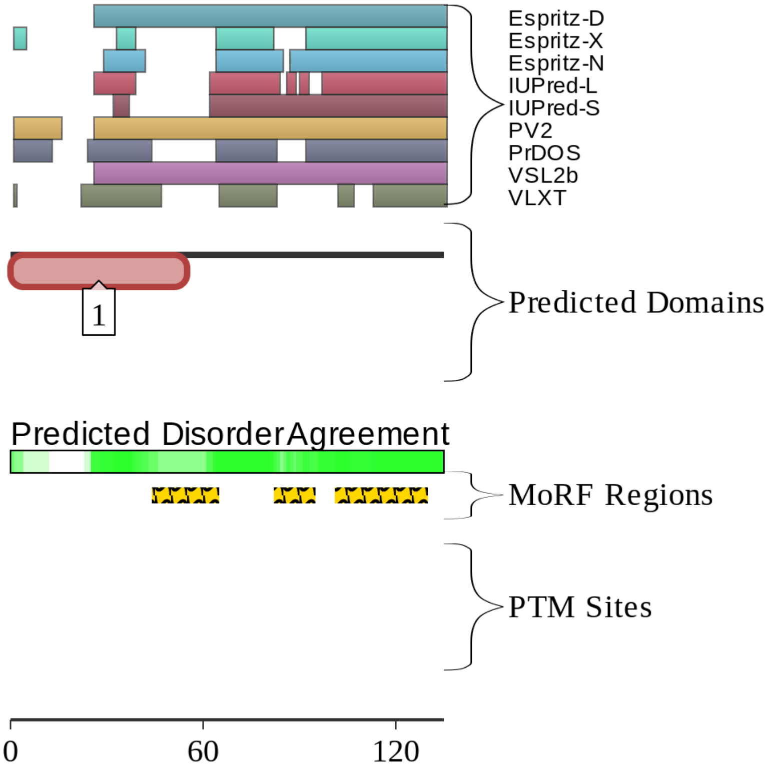
=========================VL3 NNP STATISTICS================================
Predicted residues: 135                       Number Disordered Regions: 1
Number residues disordered: 102               Longest Disordered Region: 102
Overall percent disordered: 75.56     Average Prediction Score: 0.6956
Predicted 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
```

Predicted Disordered Binding Regions

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

ENSP00000408131, ENSP00000377445, ENSP00000350236



Key:
- ■ Predicted SCOP Structure
- ⋮ Weaker Support
- ▢ Pfam Conserved Domain
- ■ Predicted Disorder
- 〰 Predicted MoRFs
- ? Curated PTM Site

Disorder:
- ■ Espritz-D
- ■ 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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MRIMLLFTAILAFSLAQSFGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGL
LKALSQASTDPKESTSPEKHSPTDVNQENVPSFGILKYPPRAE
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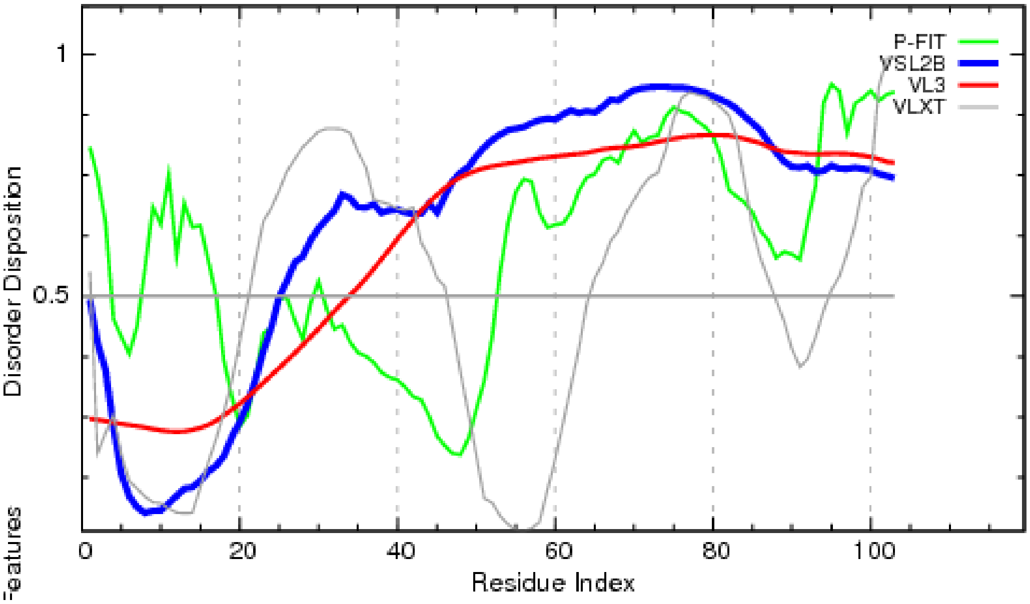

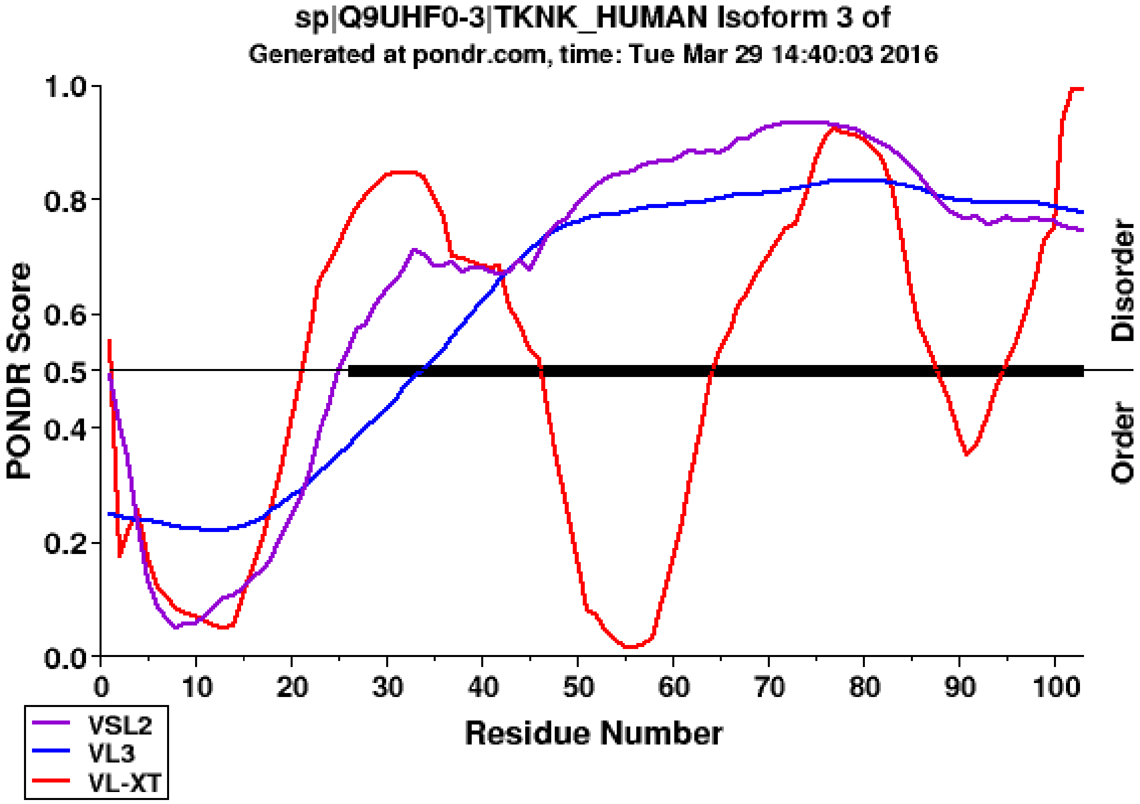

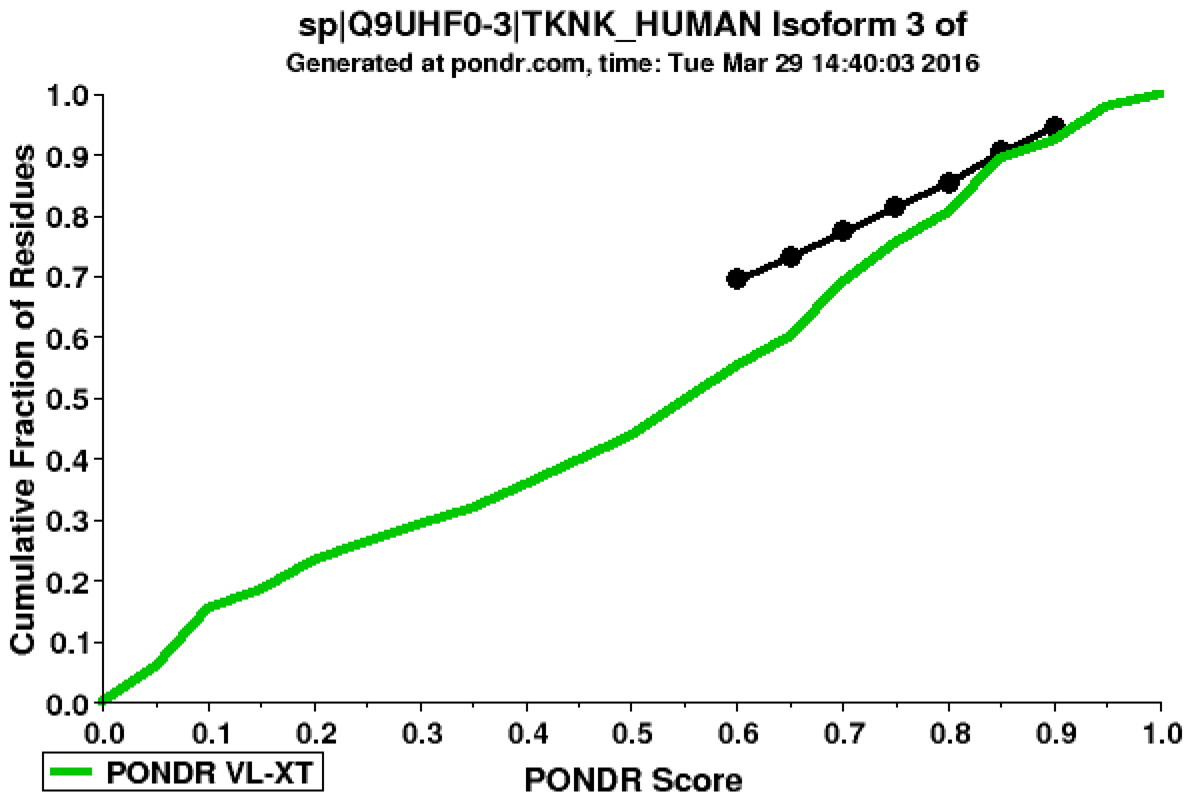
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Generated at pondr.com, time: Tue Mar 29 14:40:03 2016
Cumulative Fraction of Residues
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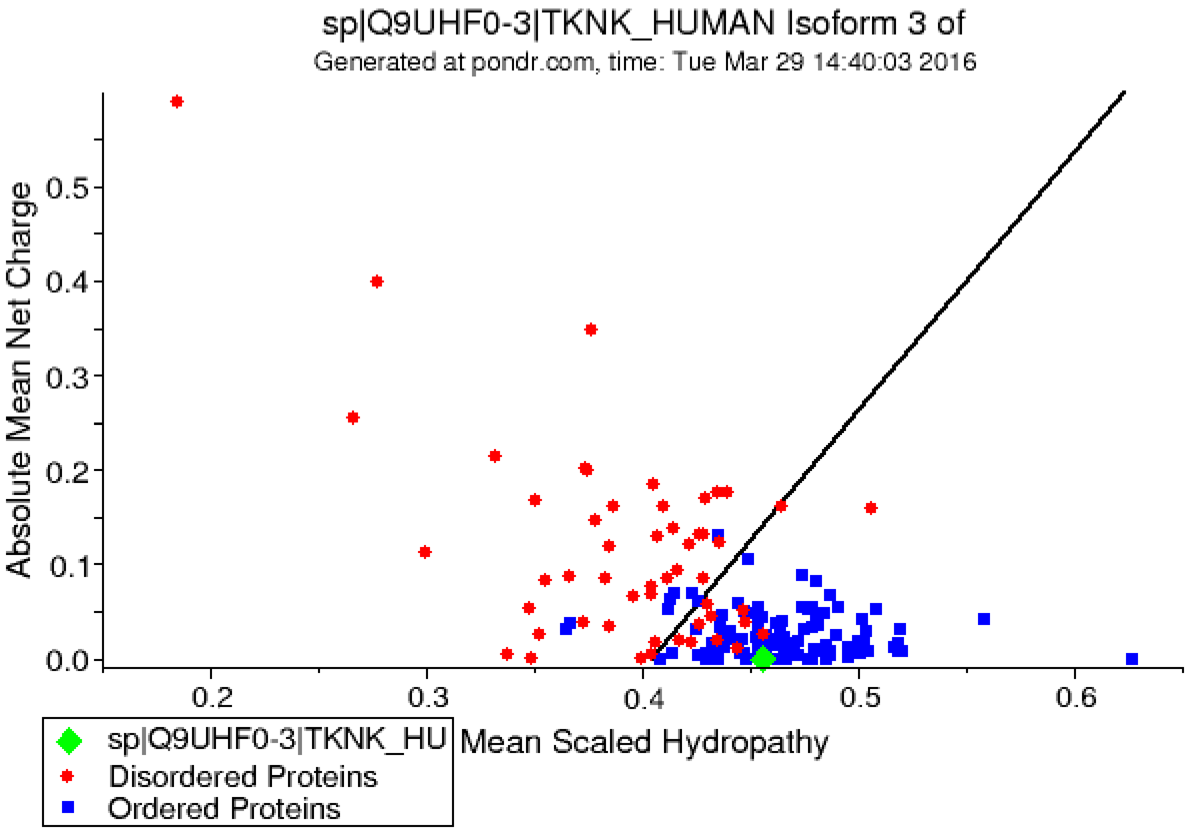
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR VL-XT
PONDR Score


sp|Q9UHF0-3|TKNK_HUMAN Isoform 3 of
Generated at pondr.com, time: Tue Mar 29 14:40:03 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|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

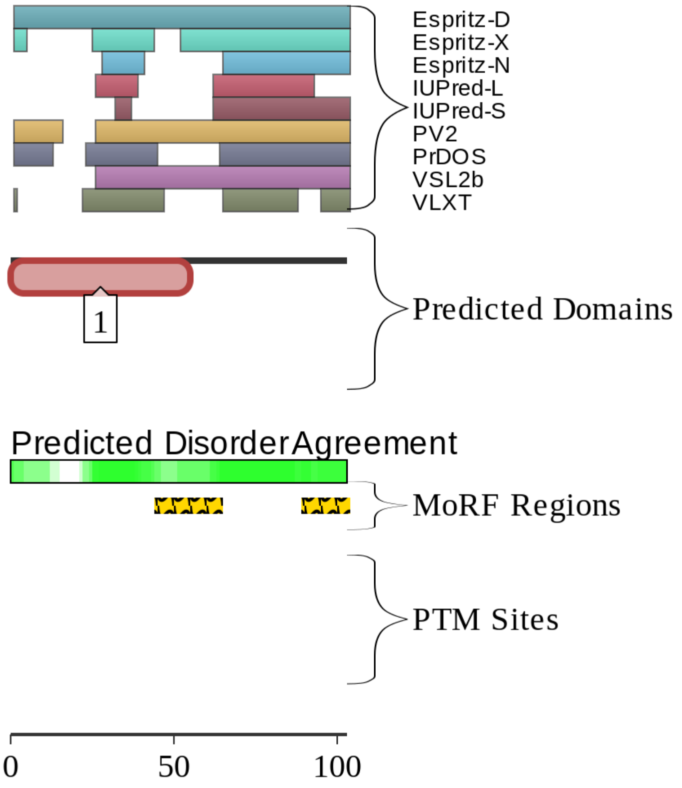
=========================VL3 NNP STATISTICS================================
Predicted residues: 103                       Number Disordered Regions: 1
Number residues disordered: 70        Longest Disordered Region: 70
Overall percent disordered: 67.96     Average Prediction Score: 0.6139
Predicted disorder 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
```

Predicted Disordered Binding Regions

	From	To	Length
1	44	64	21
2	89	103	15

ENSP00000416292, ENSP00000408208, ENSP00000368721



Key:

- ▨ Predicted SCOP Structure
- ⋮ Weaker Support
- ▢ Pfam Conserved Domain
- ▨ Predicted Disorder
- ∿ Predicted MoRFs
- ? Curated PTM Site

Disorder:

- ▨ Espritz-D
- ▨ 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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CQSCQCFRDMHTQDVQEAPVAAEVTRKSHRGLGESVSWVQNGAVSVSAEHHICESTKPLP
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EYNSTMERVESQVLKRNECYKPTGLHATPGESQEPNLSAESCGLNSGAQFGFNYEEEPSV
AKCVQASAPADERIFDYYSARKASFEAEVIQDTIGDTGKKPASWSQSPQNQEMRKHFPQK
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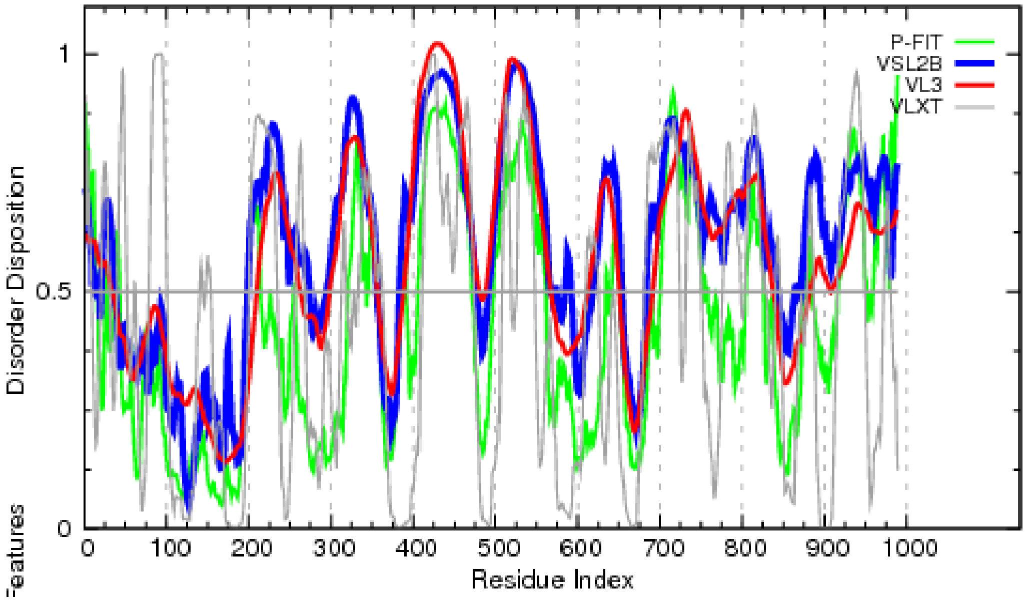

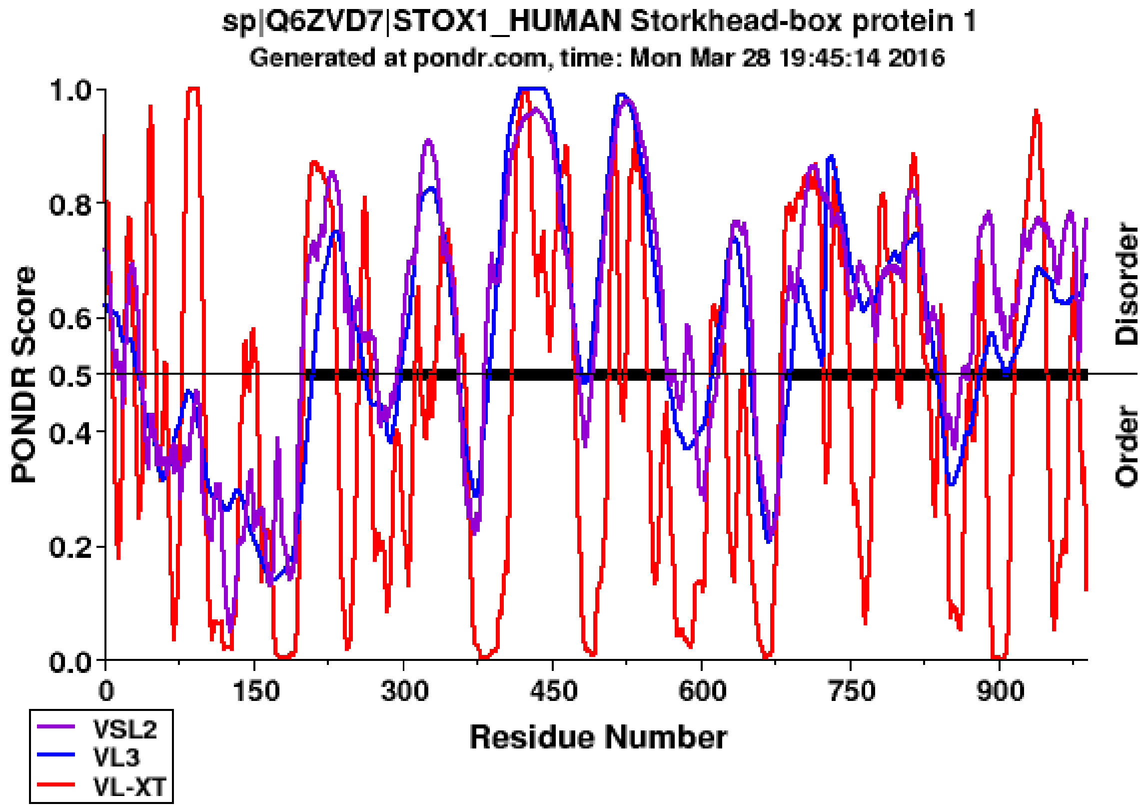
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PONDR Score
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0.6
0.5
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300
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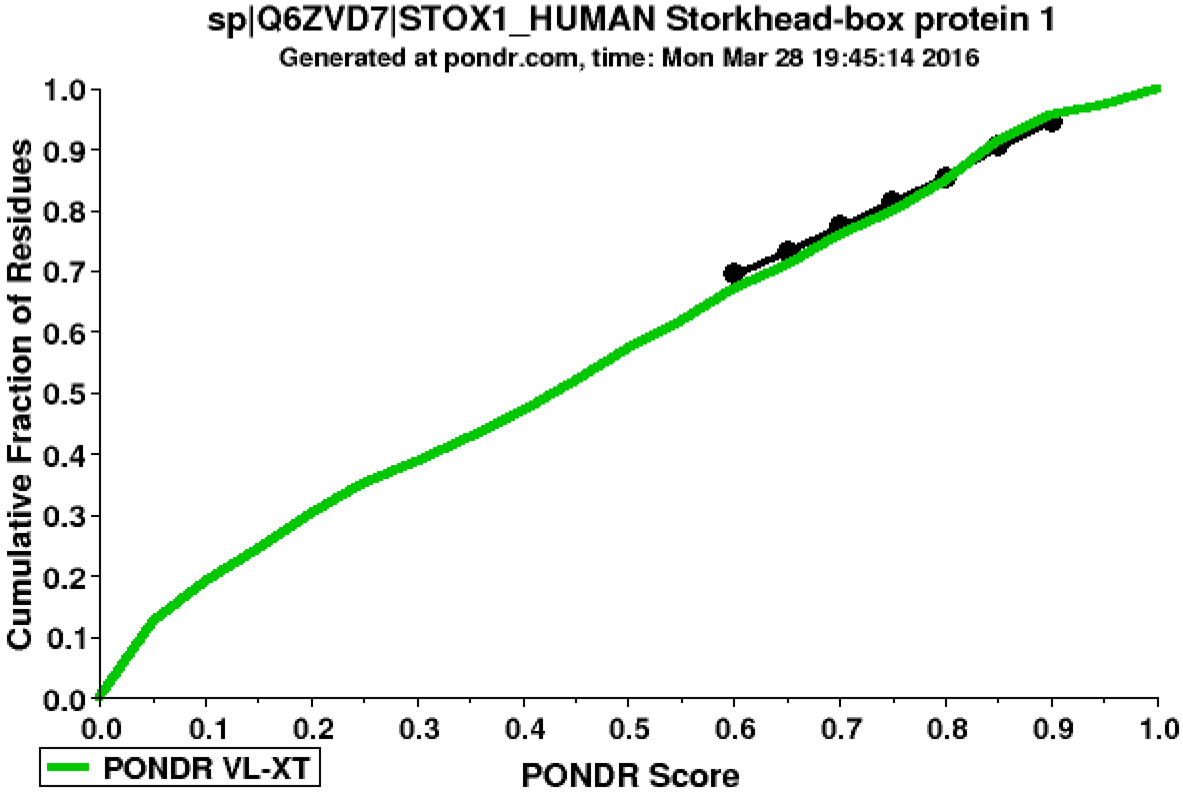
600
750
900
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
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0.9
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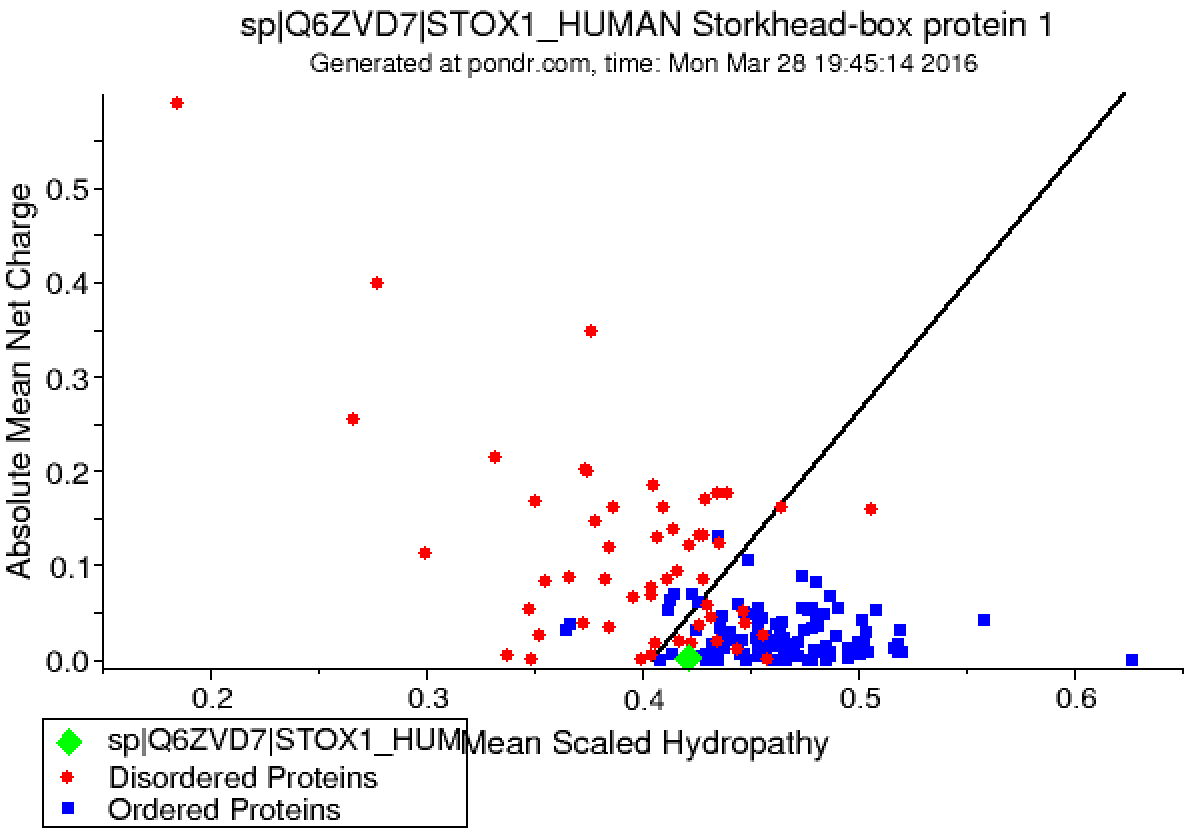
PONDR Score
PONDR VL-XT



```
=======================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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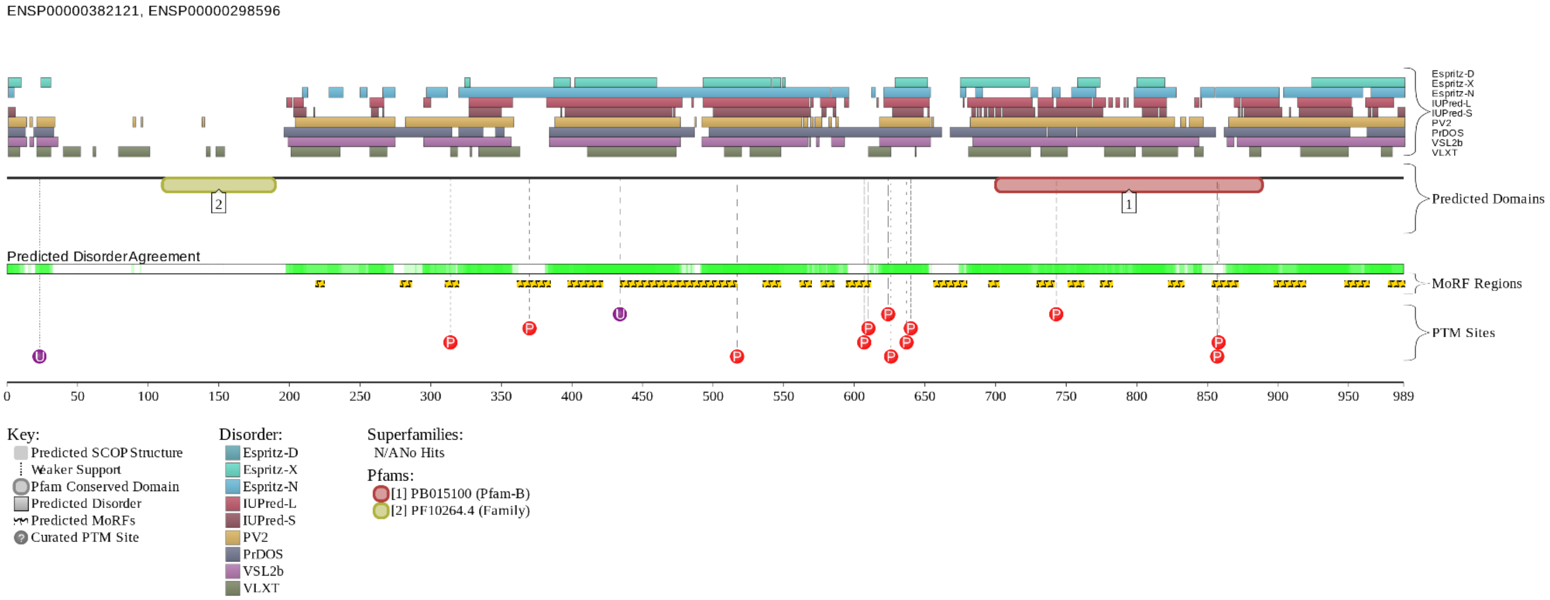

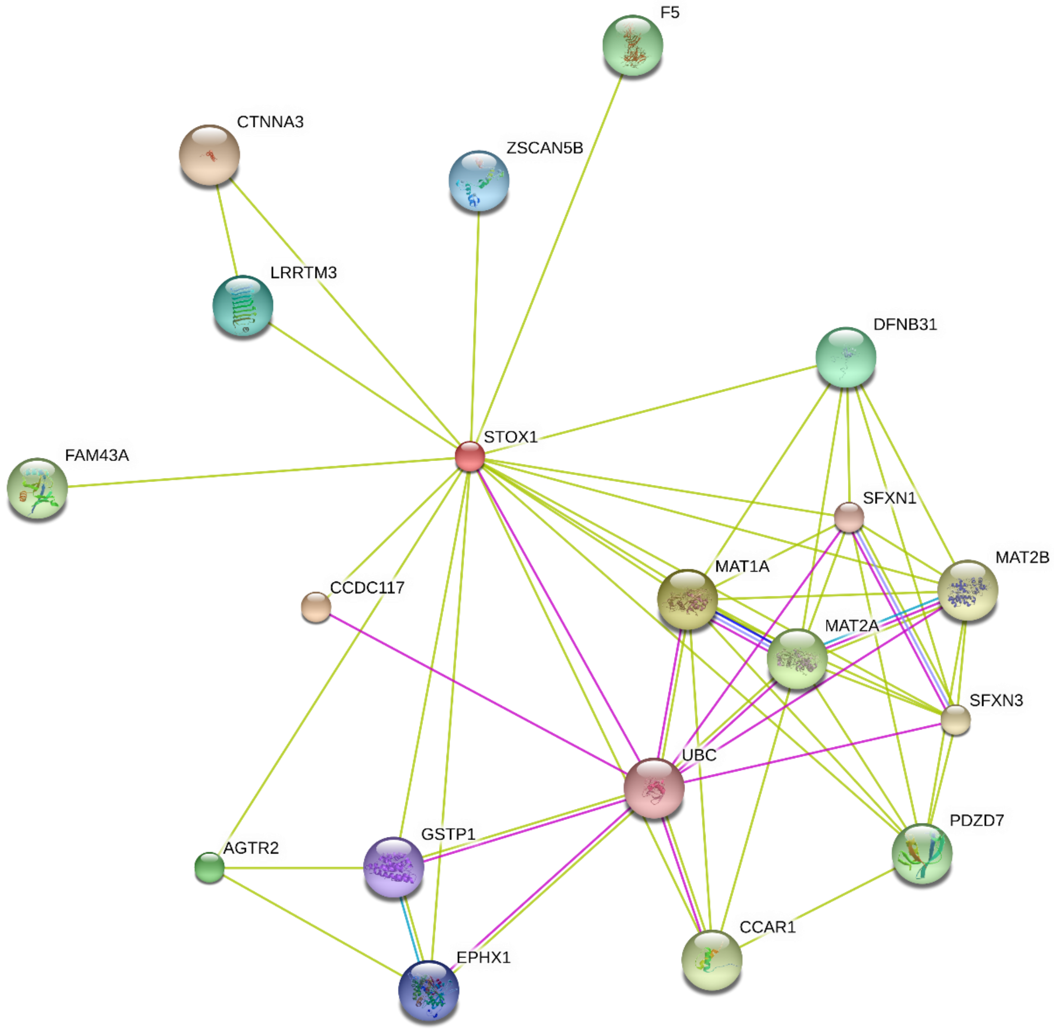
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MAT2A
SFXN3
UBC
PDZD7
AGTR2
GSTP1
CCAR1
EPHX1

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

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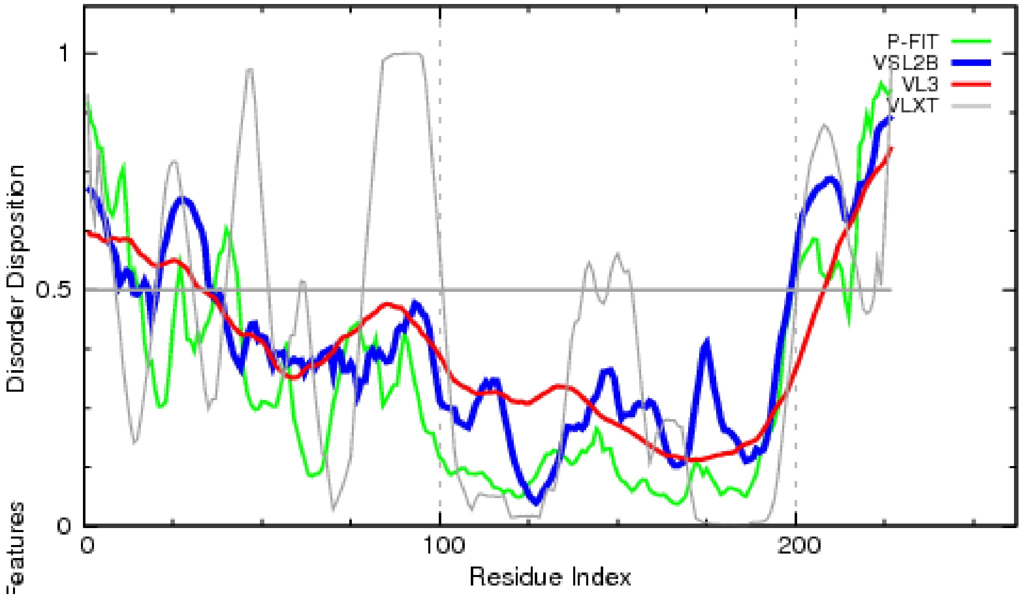
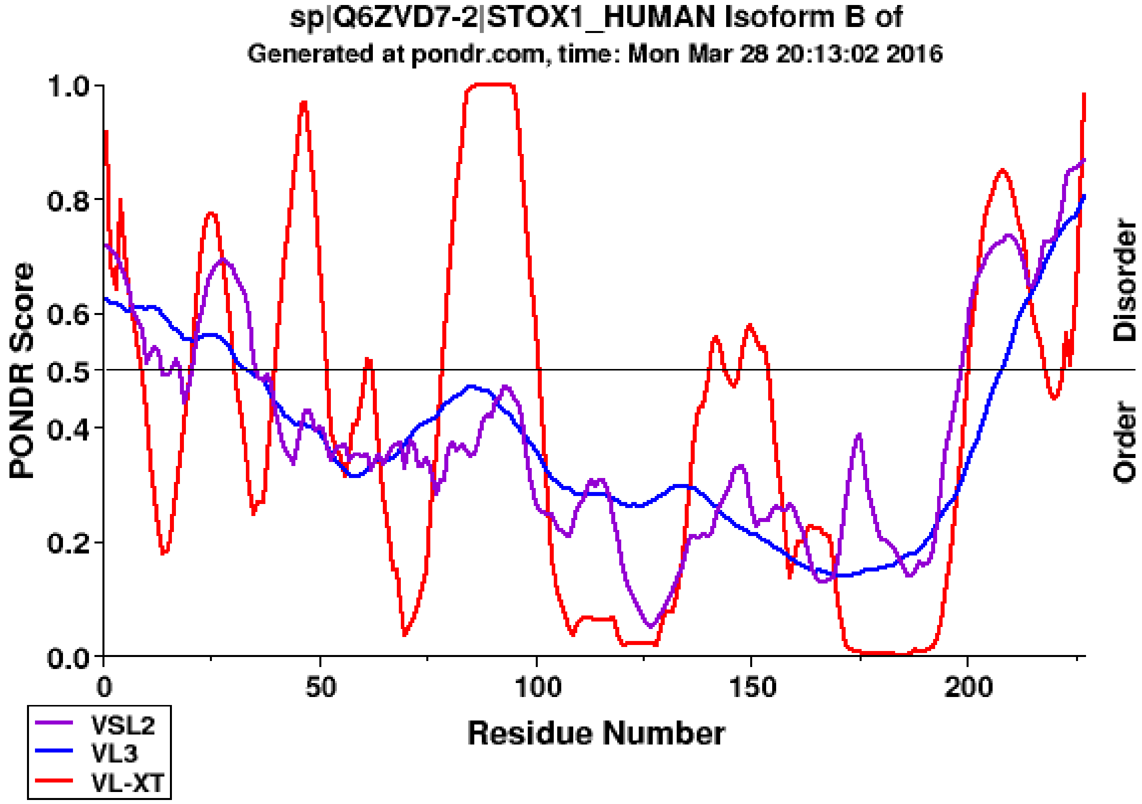
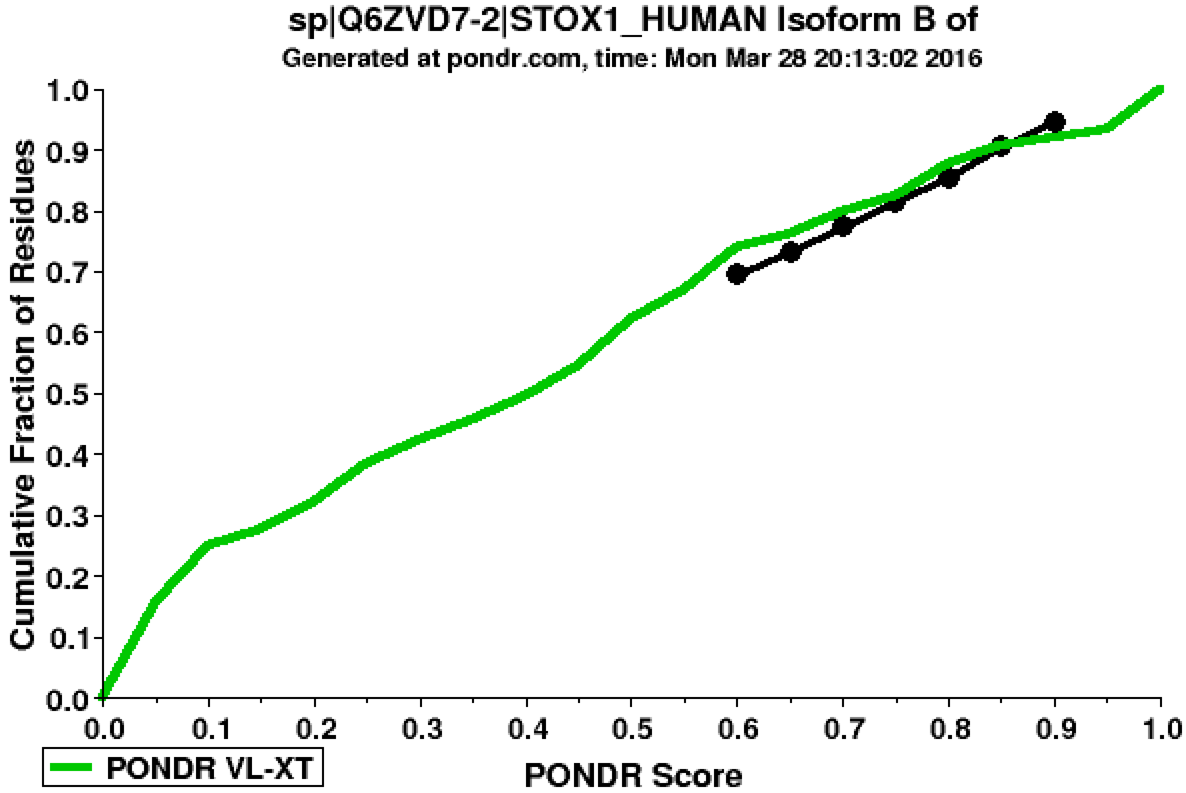
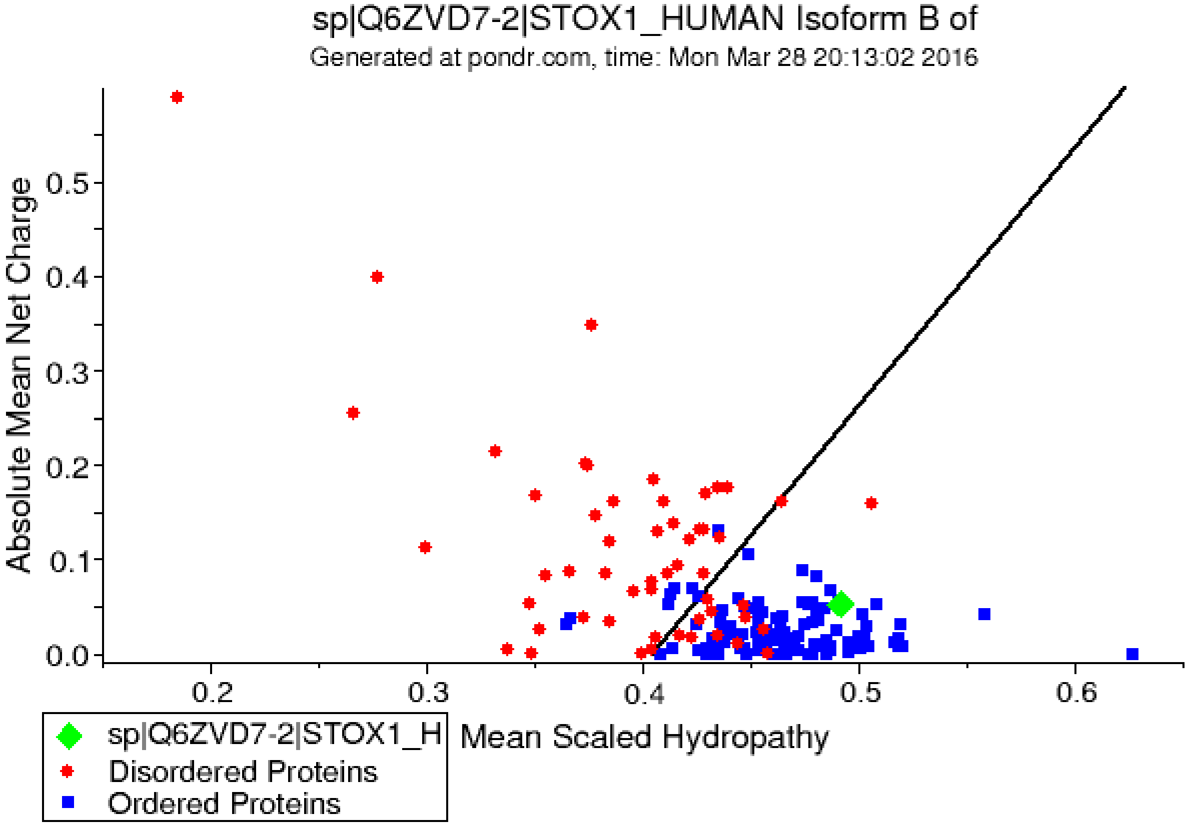



sp|Q6ZVD7-2|STOX1_HUMAN Isoform B of

Generated at pondr.com, time: Mon Mar 28 20:13:02 2016





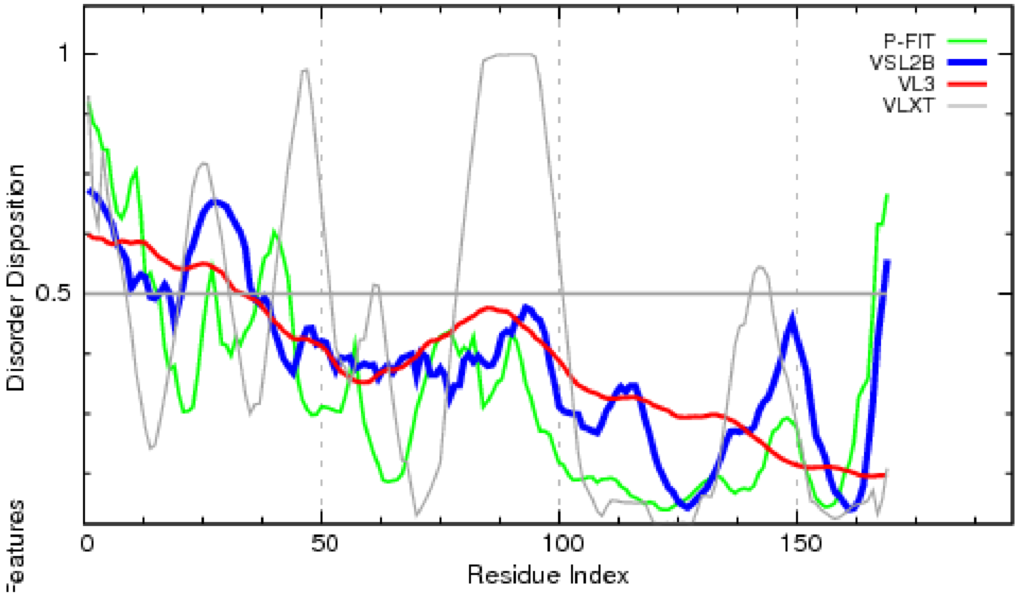
```
======================VLXT NNP STATISTICS===============================
Predicted residues: 227                           Number Disordered Regions: 9
Number residues disordered: 86            Longest Disordered Region: 22
```

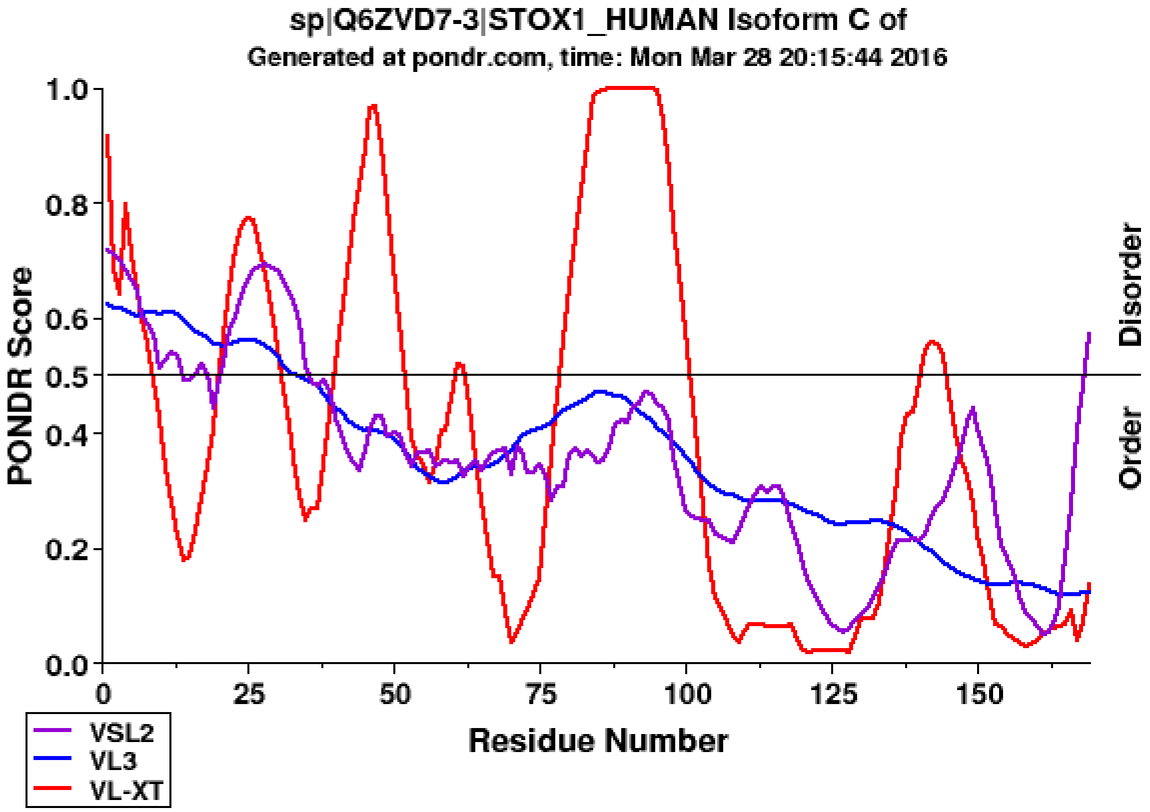
```
Overall percent disordered: 37.89     Average Prediction Score: 0.4058
Predicted disorder segment [1]-[8]    Average Strength= 0.6936
Predicted disorder segment [21]-[30]  Average Strength= 0.6799
Predicted disorder segment [40]-[51]  Average Strength= 0.7656
Predicted disorder segment [61]-[62]  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

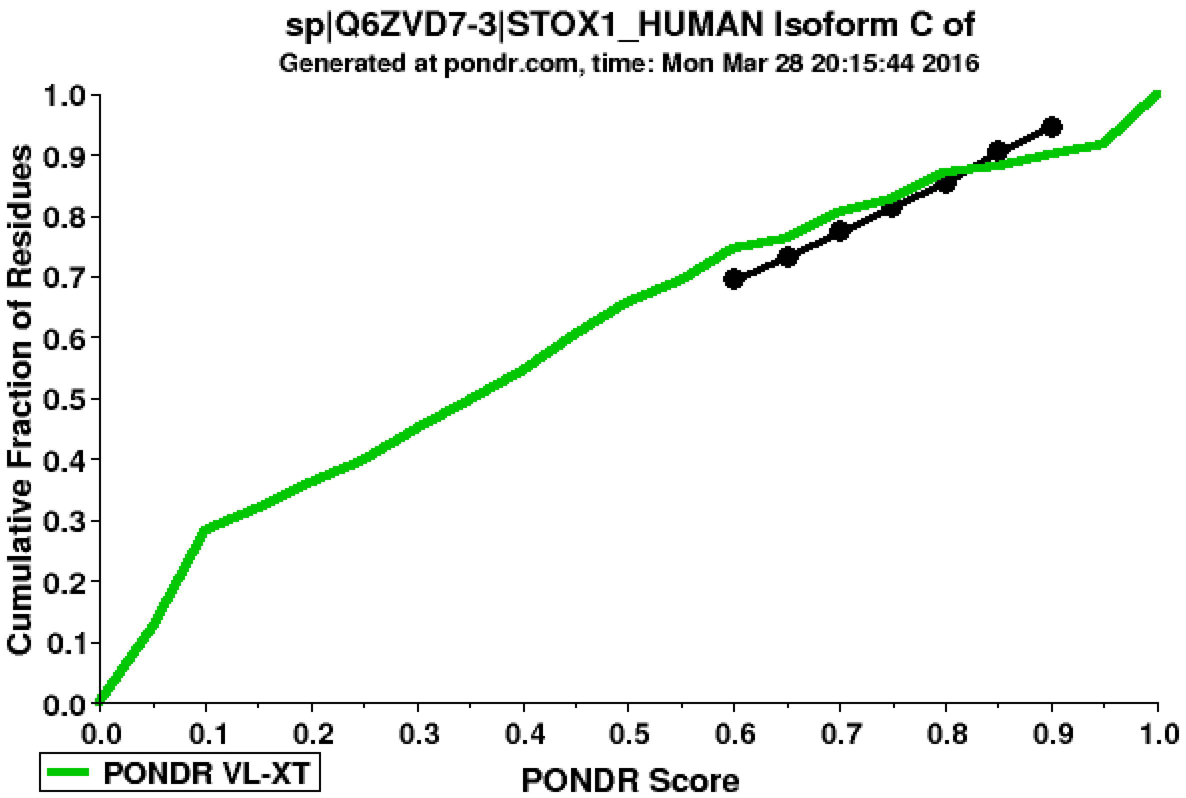
=======================VL3 NNP STATISTICS=================================
Predicted residues: 227                      Number Disordered Regions: 2
Number residues disordered: 53        Longest Disordered Region: 33
Overall percent disordered: 23.35     Average Prediction Score: 0.3758
Predicted disorder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

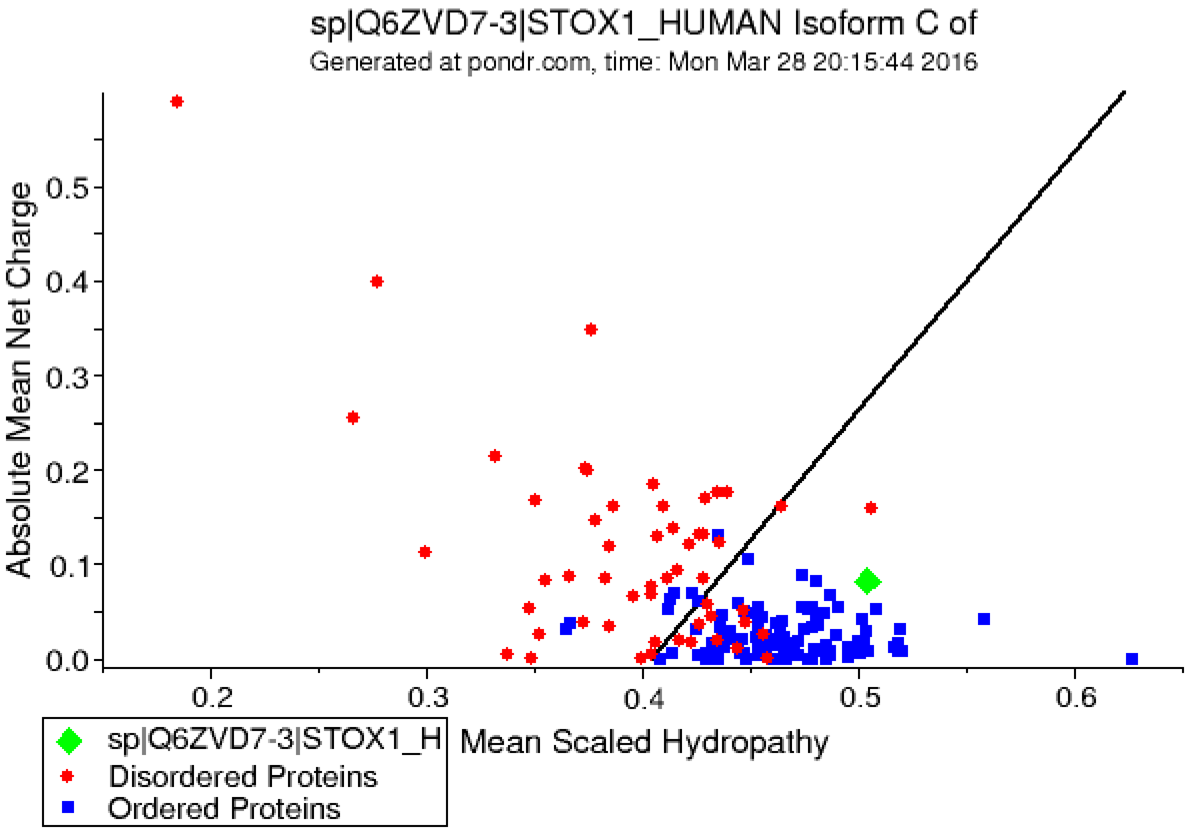
======================VSL2 NNP STATISTICS=================================
Predicted residues: 227                      Number Disordered Regions: 4
Number residues disordered: 60        Longest Disordered Region: 29
Overall percent disordered: 26.43     Average Prediction Score: 0.3872
Predicted disorder 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
```

>sp|Q6ZVD7-3|STOX1_HUMAN Isoform C of Storkhead-box protein 1 OS=Homo sapiens GN=STOX1
MARPVQLAPGSLALVLCRLEAQKAAGAAEEPGGRAVFRAFRRANARCFWNARLARAASRL
AFQGWLRRGVLLVRAPPACLQVLRDAWRRRALRPPRGFRIRAVGDVFPVQMNPITQSQFV
PLGEVLCCAISDMNTAQIVVTQESLLERLMKHYPGHRVWDLIIQSFWMD









```
======================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
MRDPLTDCPYNKVYKNLKEFSQNGENFCKQVTSVLQQRANLEISYAKGLQKLASKLSKAL
QNTRKSCVSSAWAWASEGMKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVE
KTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKL
EKEDENYYQKNMAGYSTRLKWENTLENCYQSILELEKERIQLLCNNLNQYSQHISLFGQT
LTTCHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKS
LLKPKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLE
ANSYKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASS
GGQSNPGSSTPAPGAAQLSSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSL
NGKKGHFPAAYVEELPSNAGNTATKA
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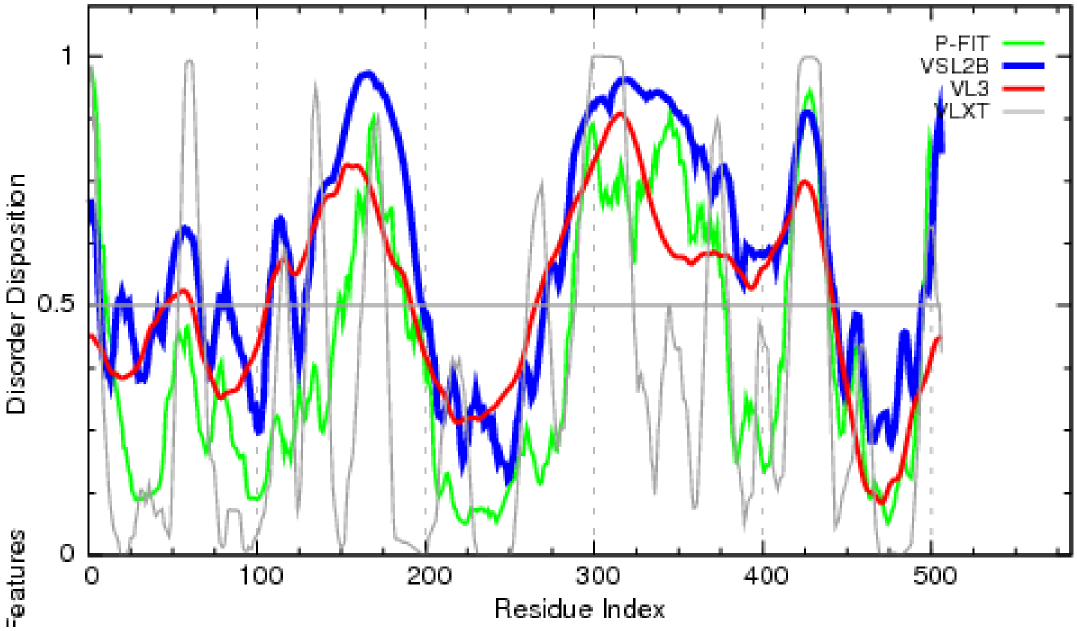
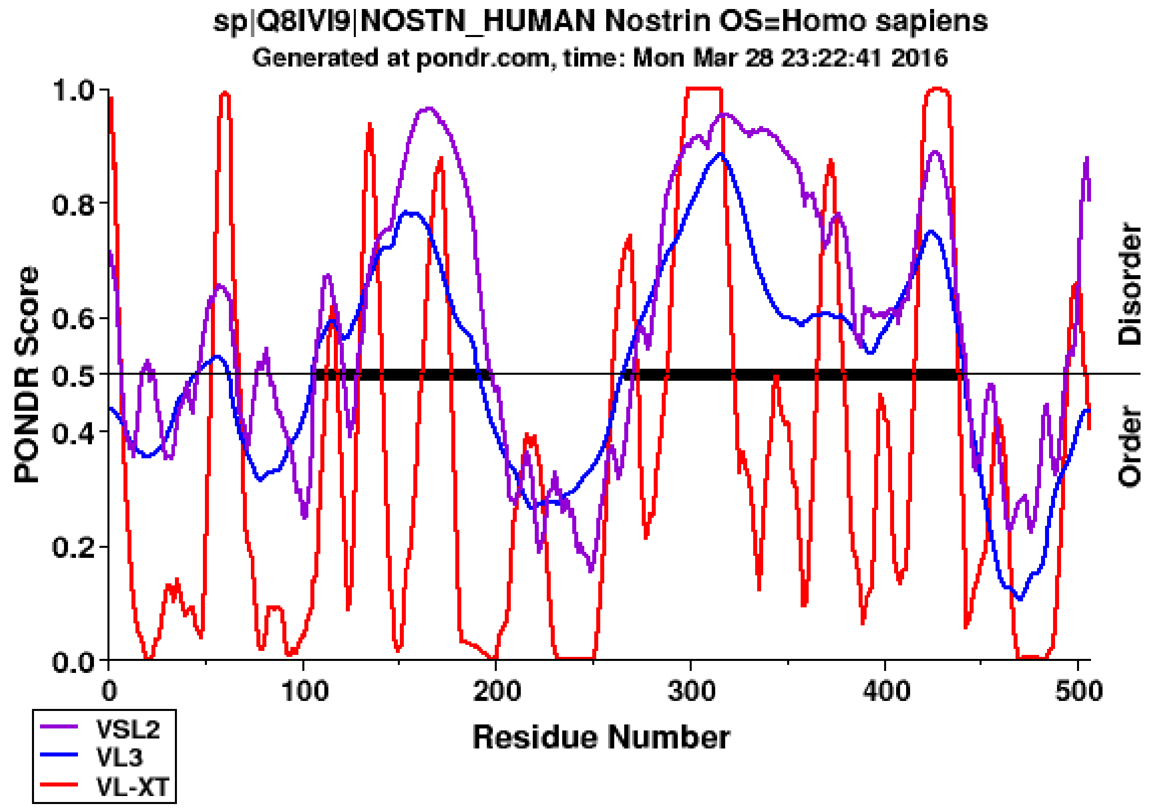
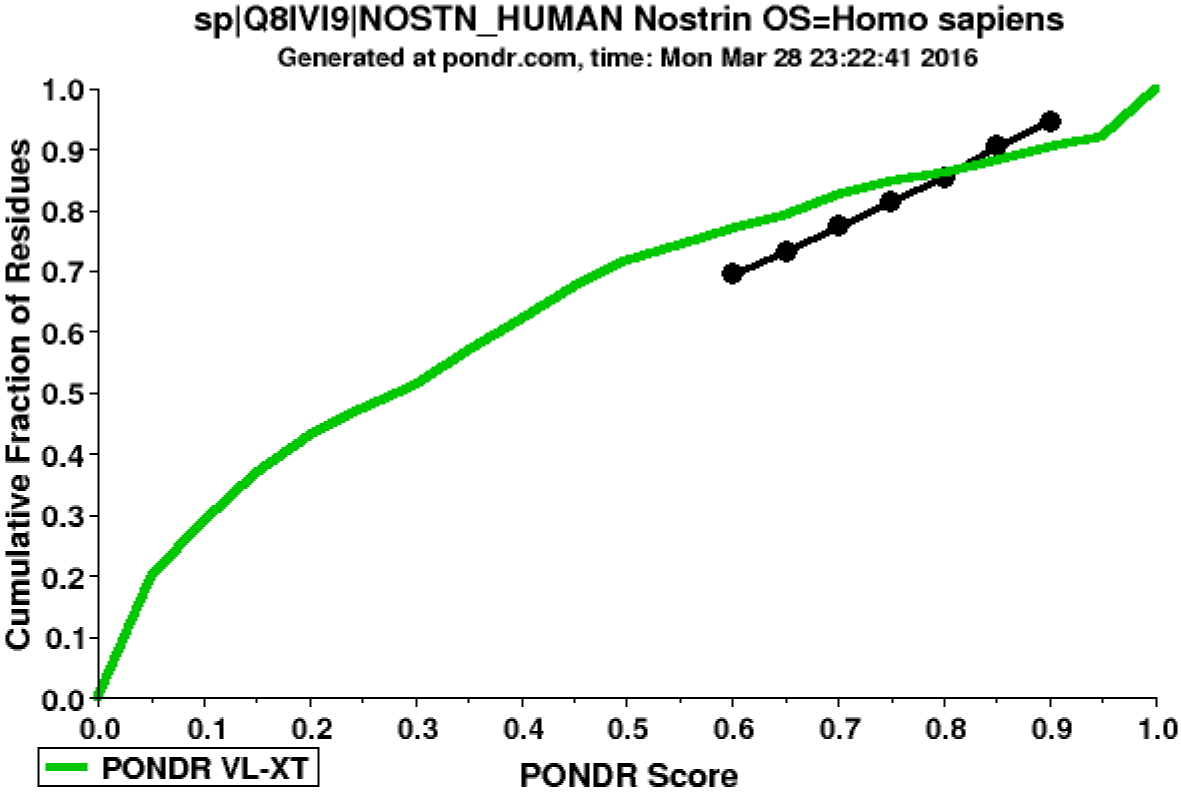
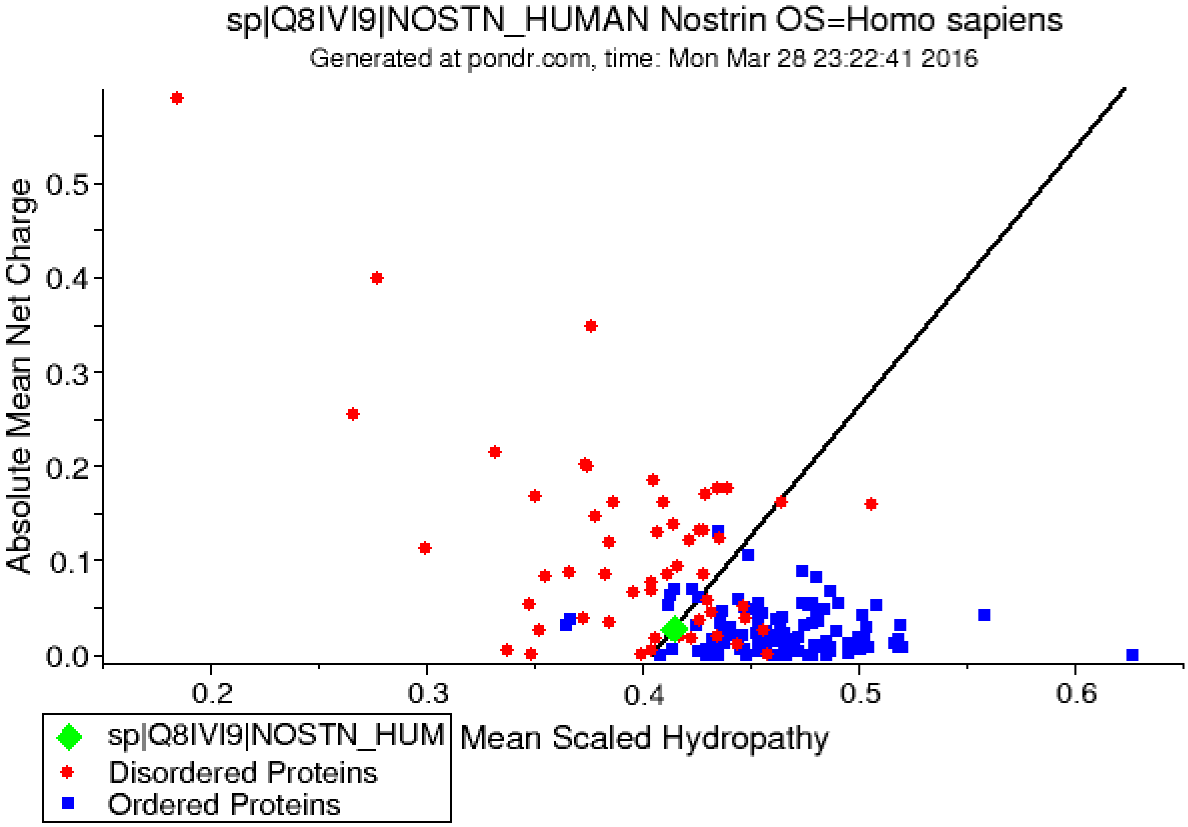


Predicted Disordered Binding Regions

	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



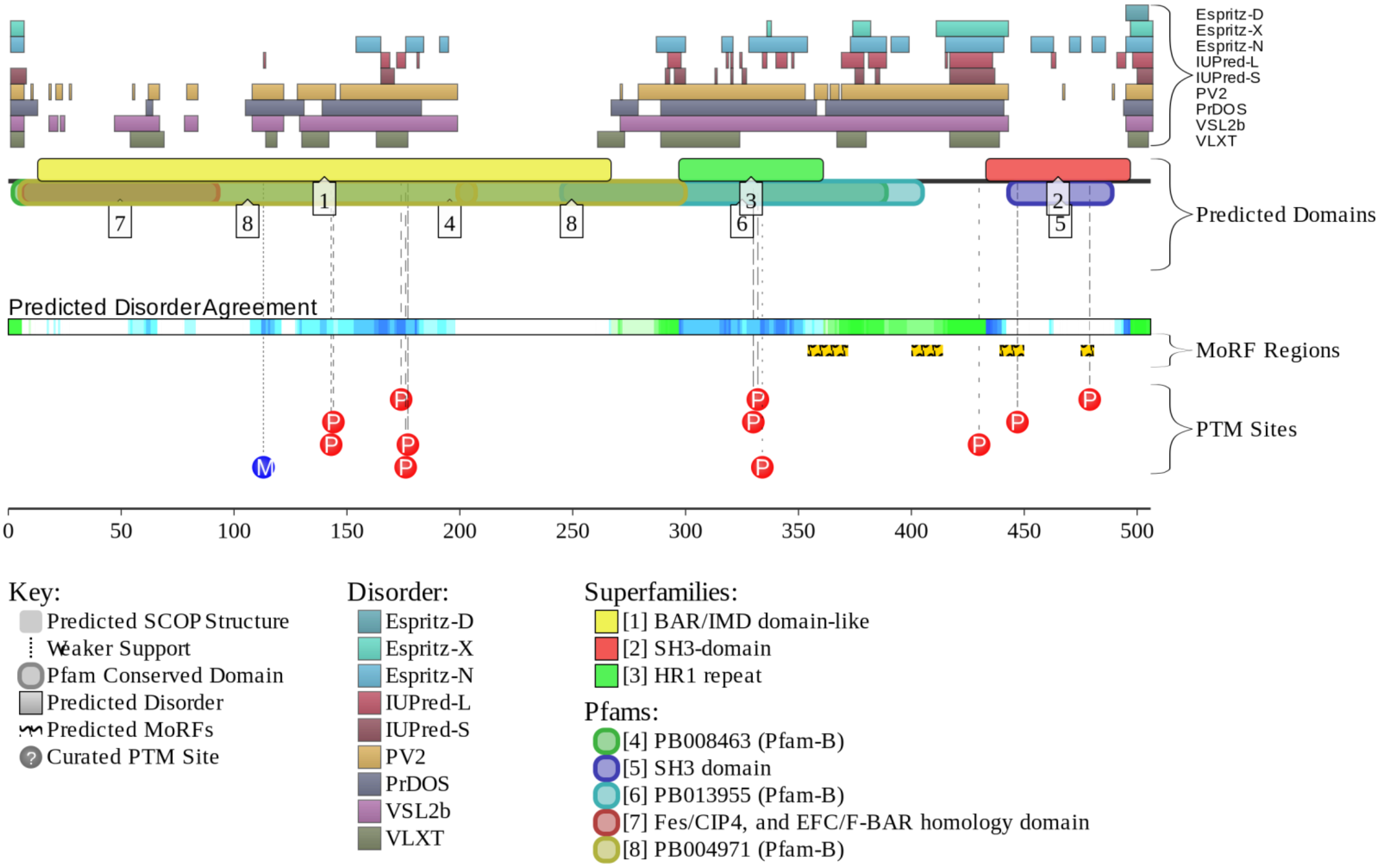
```
=======================VLXT NNP STATISTICS================================
Predicted residues: 506                      Number Disordered Regions: 10
Number residues disordered: 143              Longest Disordered Region: 35
Overall percent disordered: 28.26      Average Prediction Score: 0.3538
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

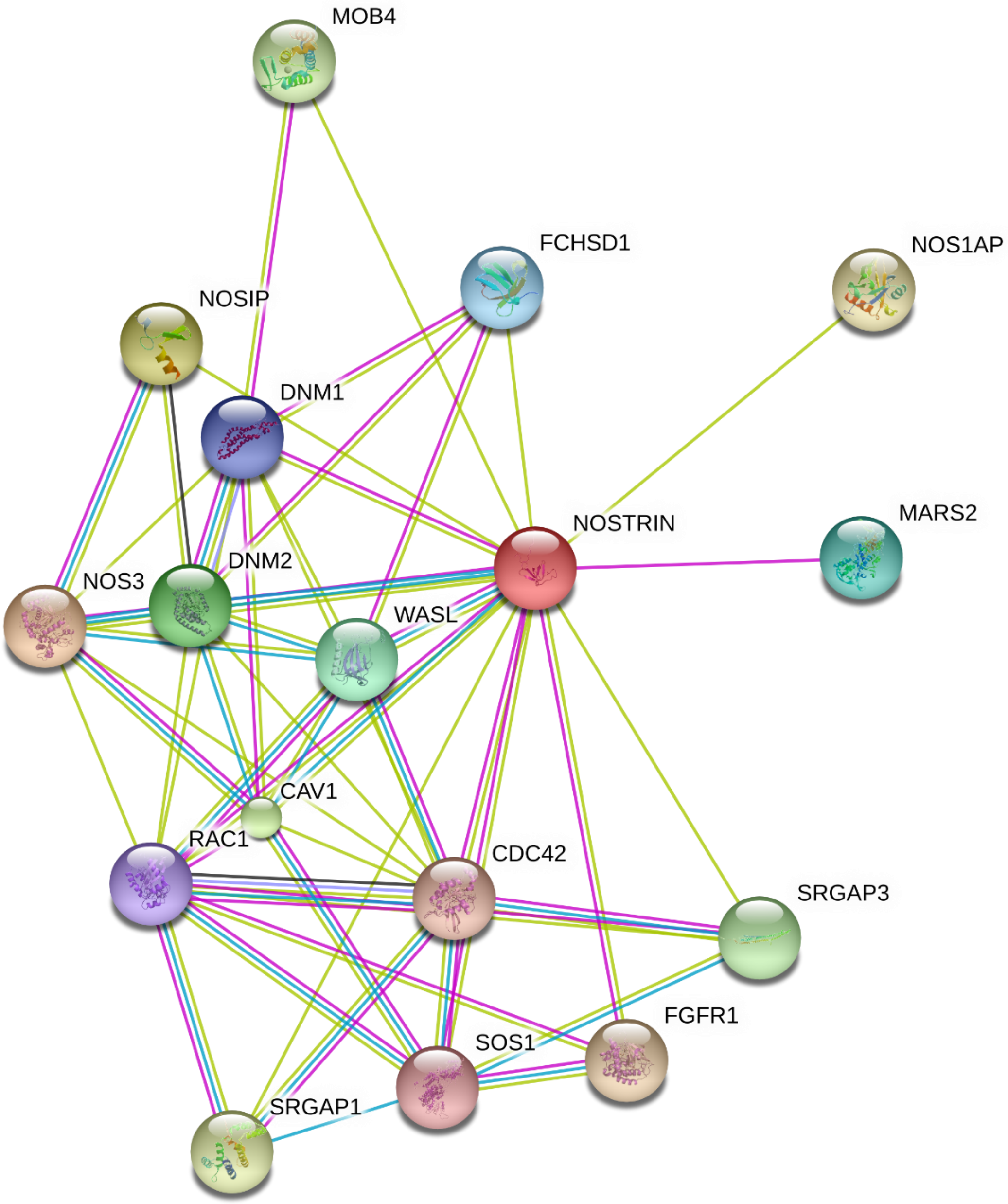
=======================VL3 NNP STATISTICS================================
Predicted residues: 506                      Number Disordered Regions: 3
Number residues disordered: 278              Longest Disordered Region: 176
Overall percent disordered: 54.94      Average Prediction Score: 0.5115
Predicted 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

```
>sp|Q8IVI9-2|NOSTN_HUMAN Isoform 2 of Nostrin OS=Homo sapiens GN=NOSTRIN
MRDPLTDCPYNKVYKNLKEFSQNGENFCKQVTSVLQQSCVSSAWAWASEGMKSTADLHQK
LGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKKKLMVSTKKHE
ALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENYYQKNMAGYSTRLKWENTLENC
YQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIEKDIQAVMEET
AILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASKDKEGLERMLK
TYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQPSHPCSNSIF
RWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQLSSRLCKALYS
FQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGKKGHFPAAYVEELPSNAGNTATKA
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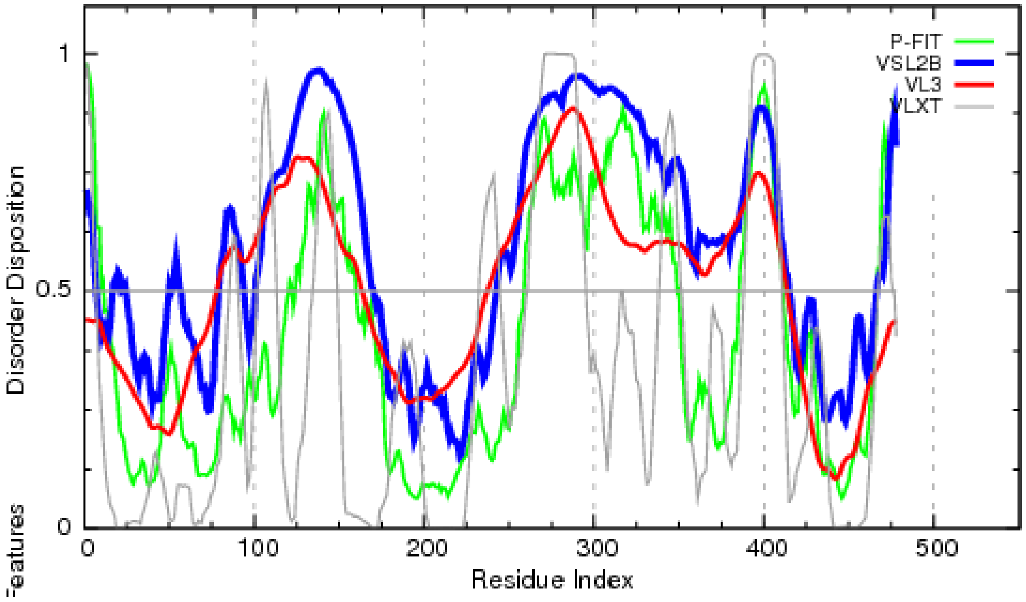
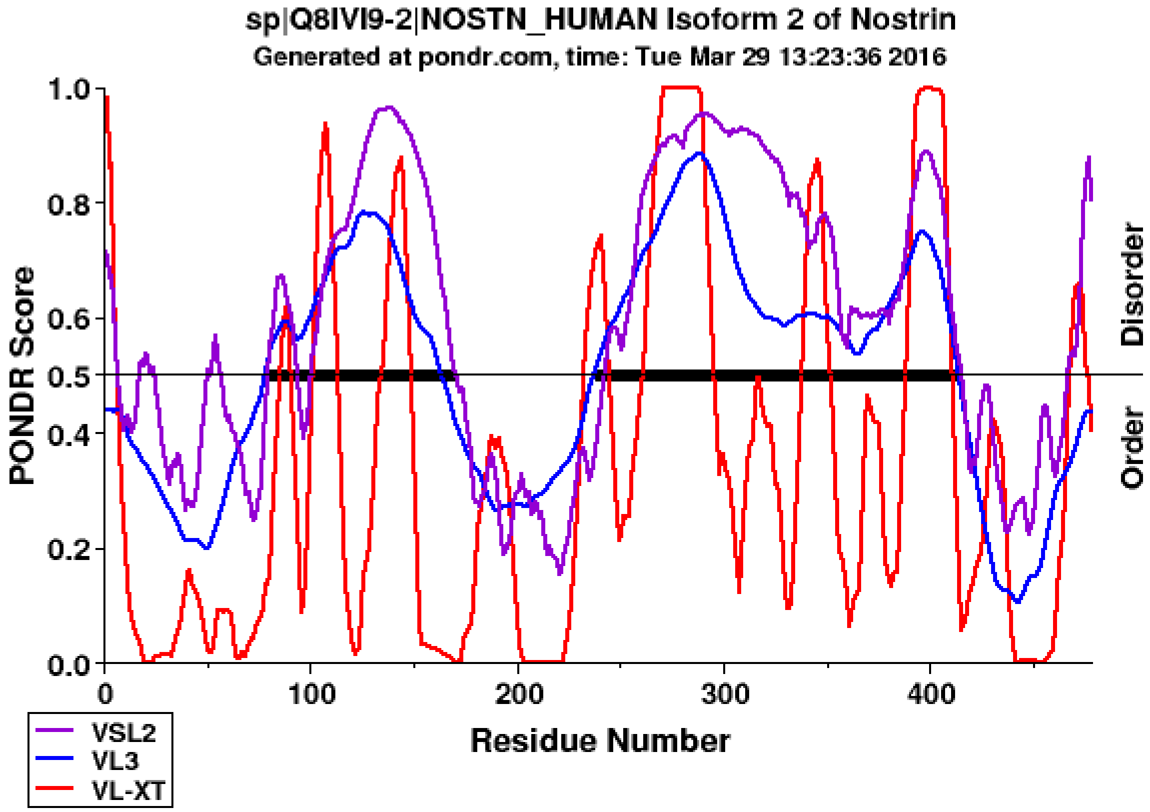
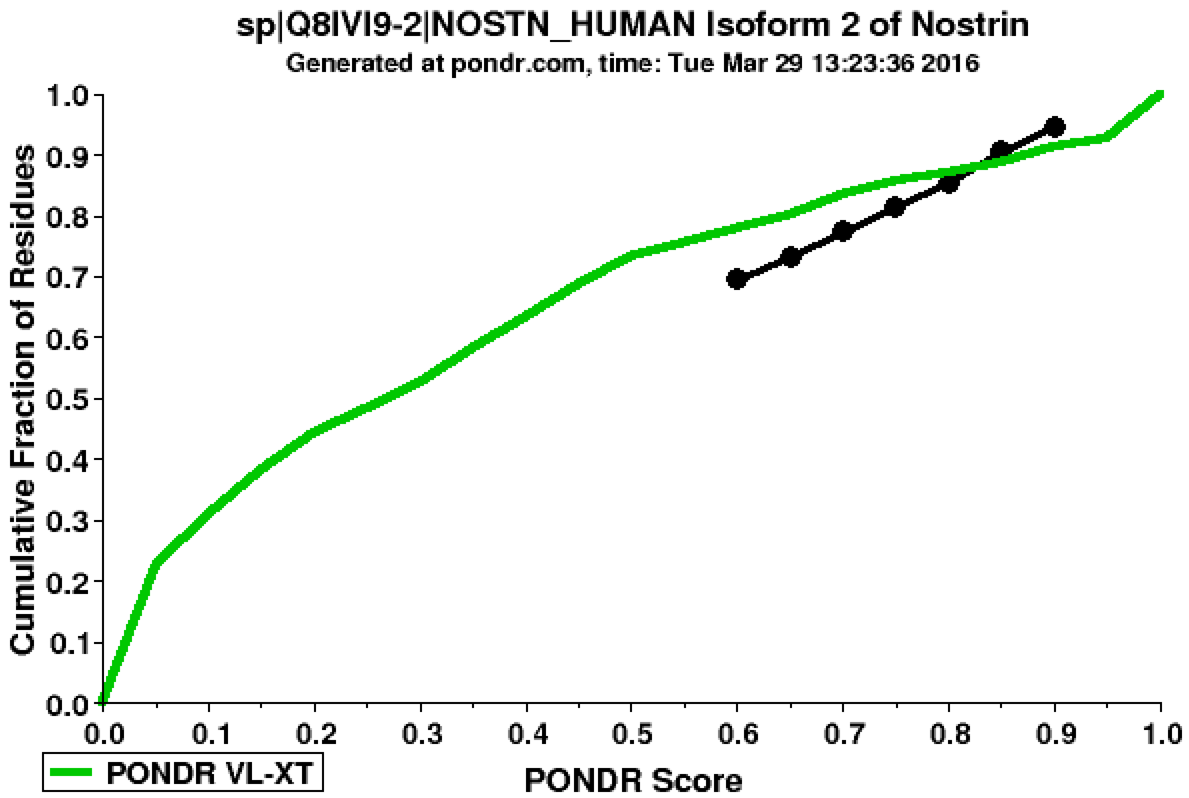
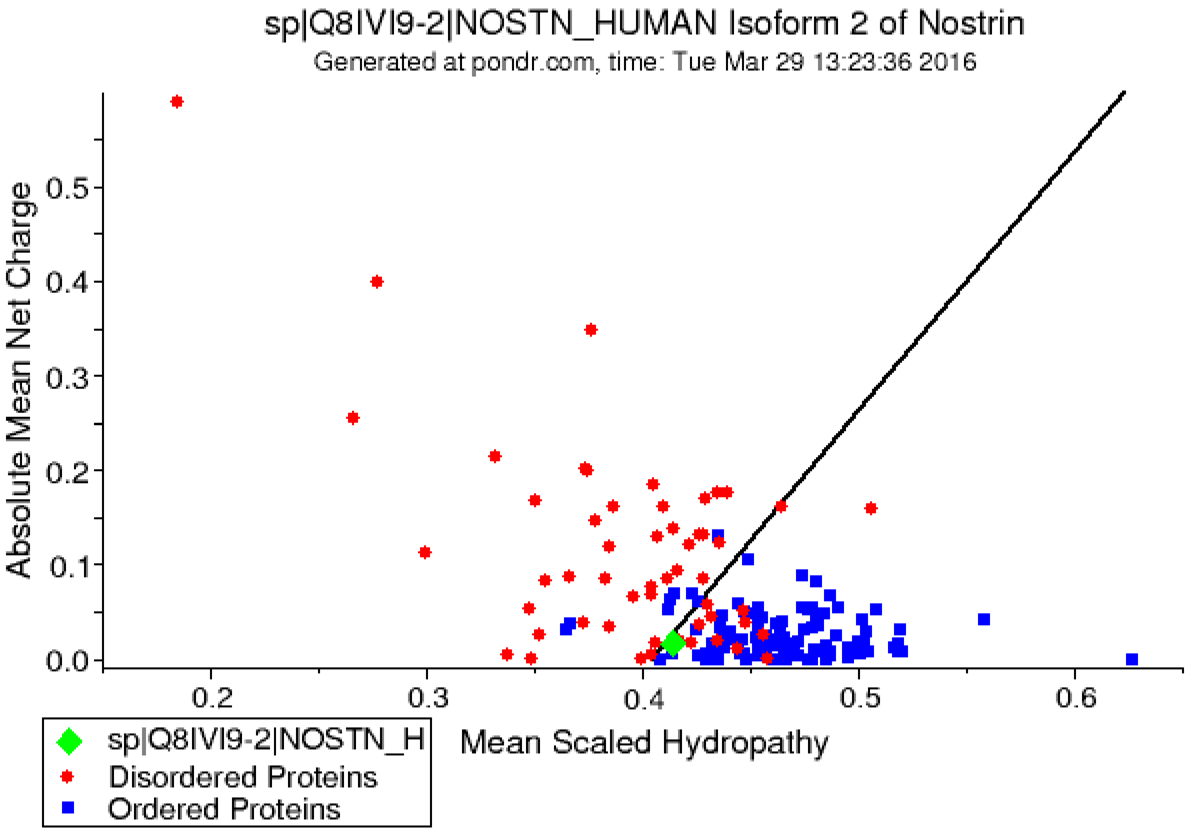






sp|Q8IVI9-2|NOSTN_HUMAN Isoform 2 of Nostrin

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



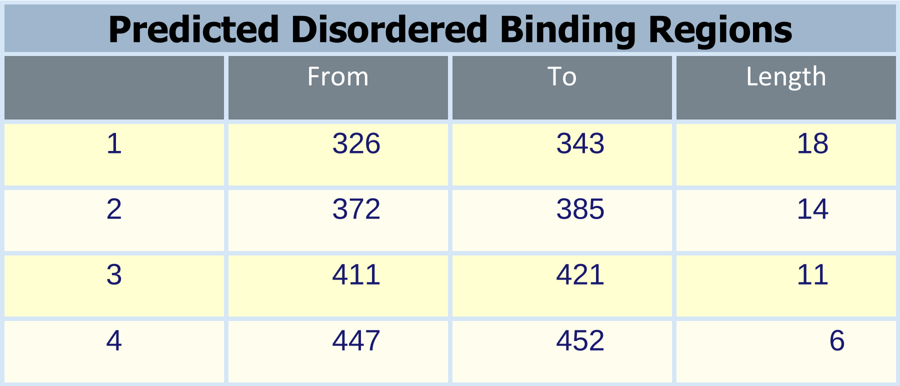
sp|Q8IVI9-2|NOSTN_HUMAN Isoform 2 of Nostrin

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

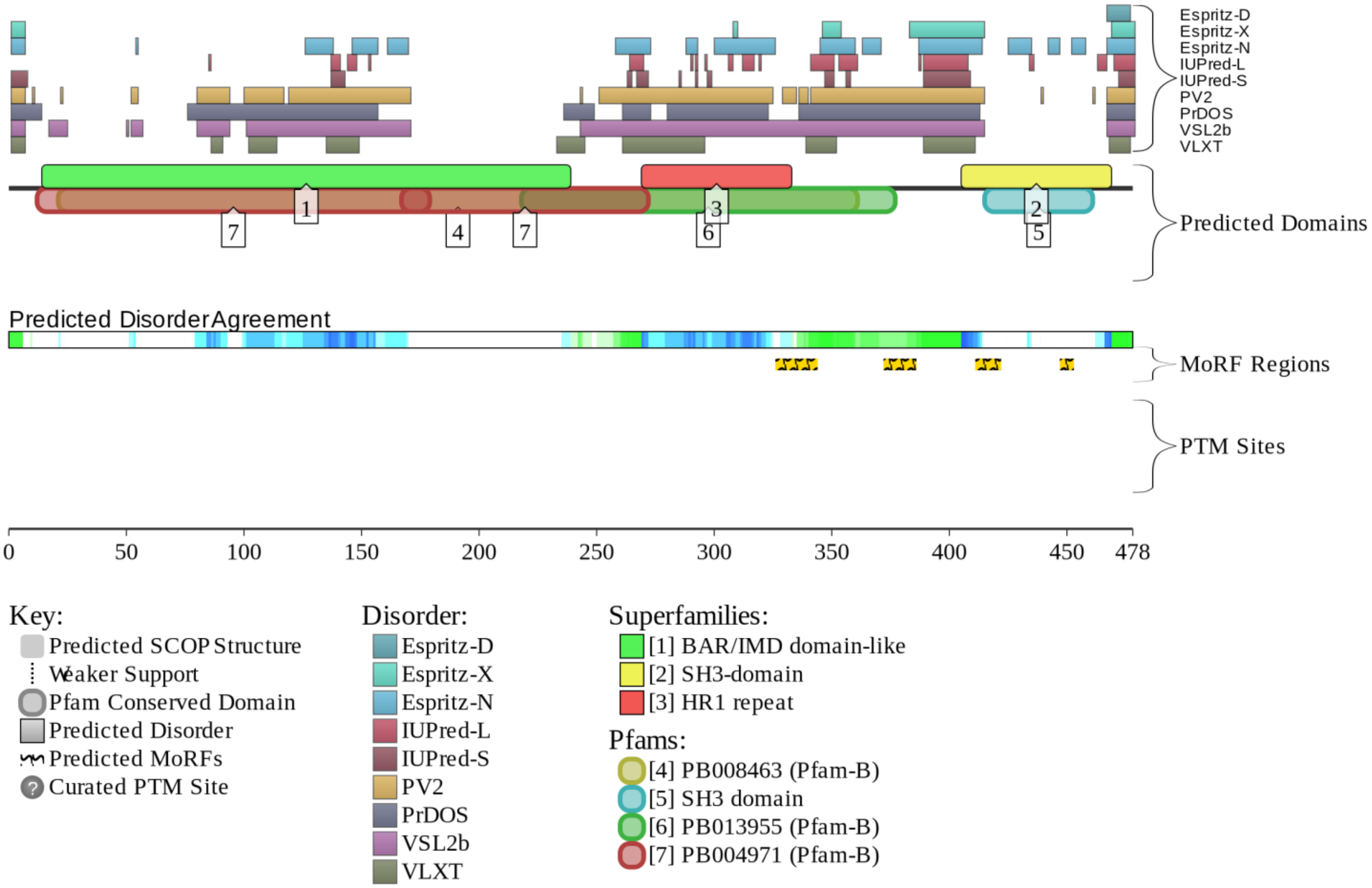
=======================VSL2 NNP STATISTICS================================
Predicted residues: 478                      Number Disordered Regions: 8
Number residues disordered: 288              Longest Disordered Region: 172
Overall percent disordered: 60.25     Average Prediction Score: 0.5919
Predicted 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



```
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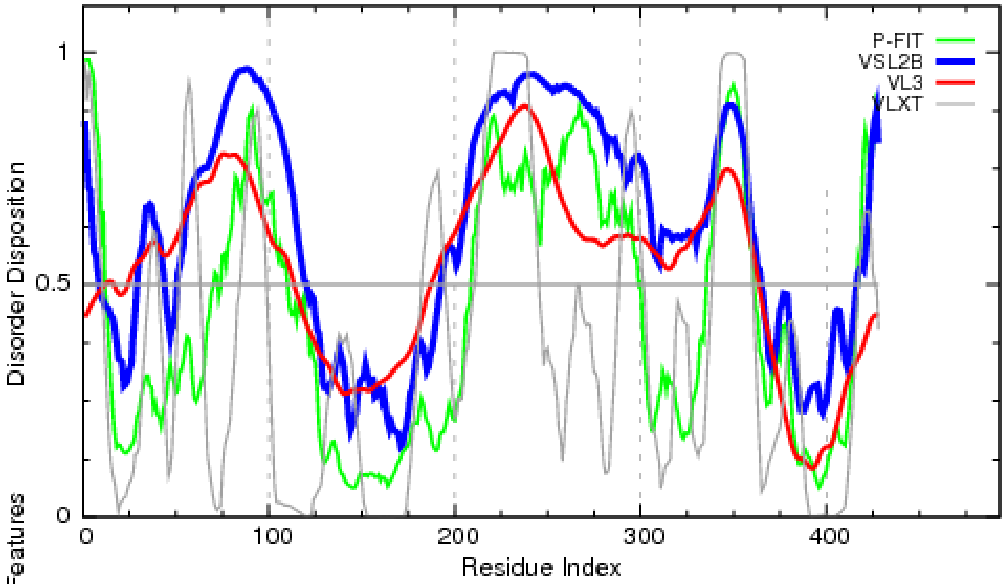
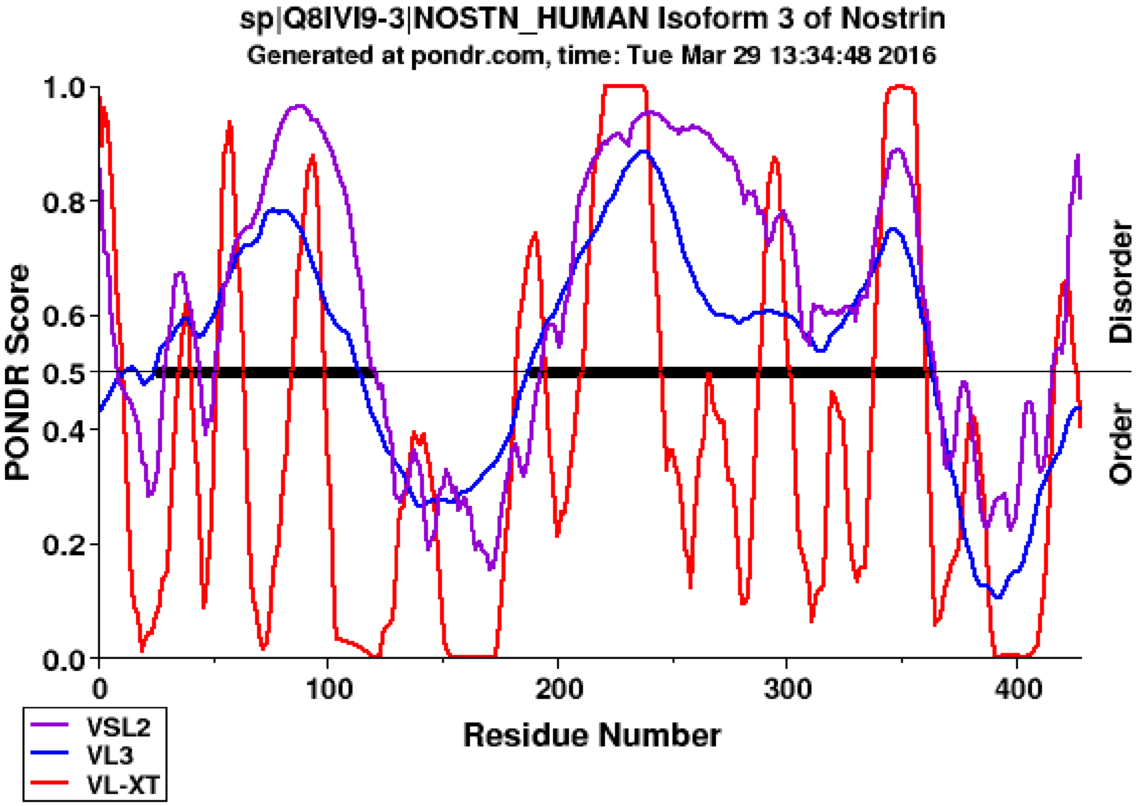
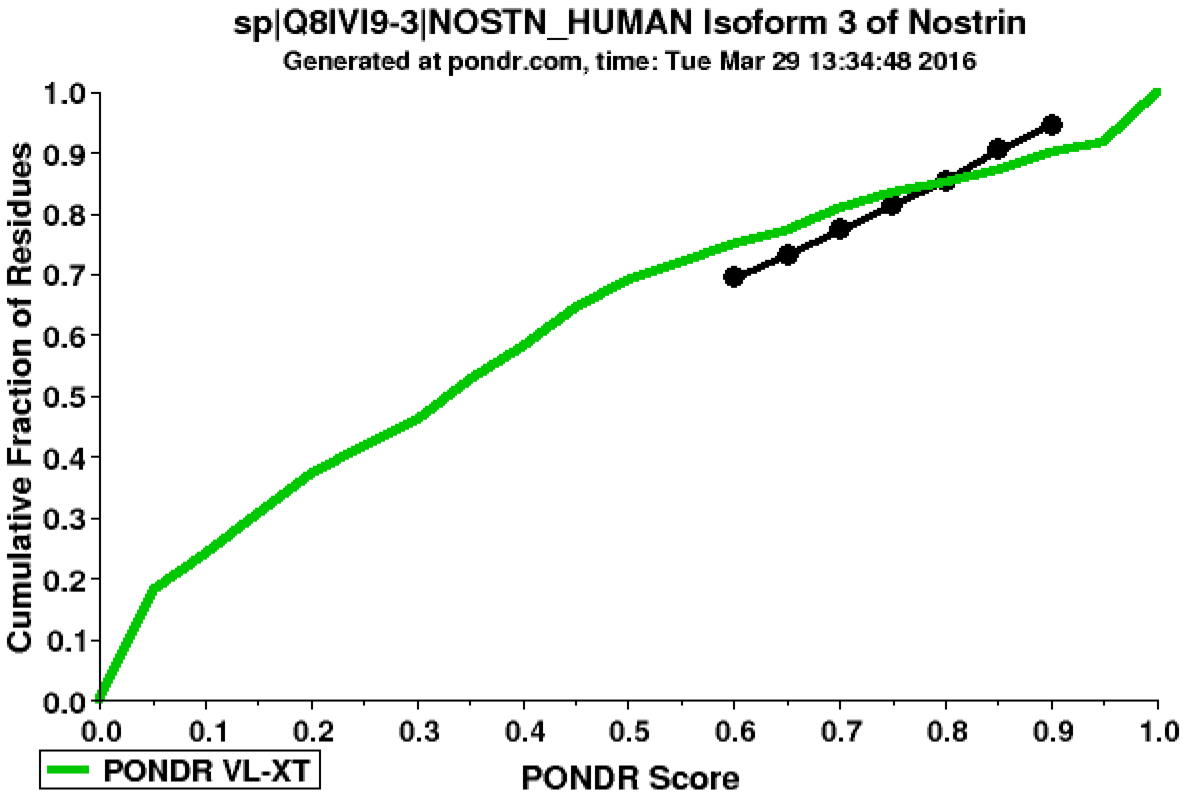
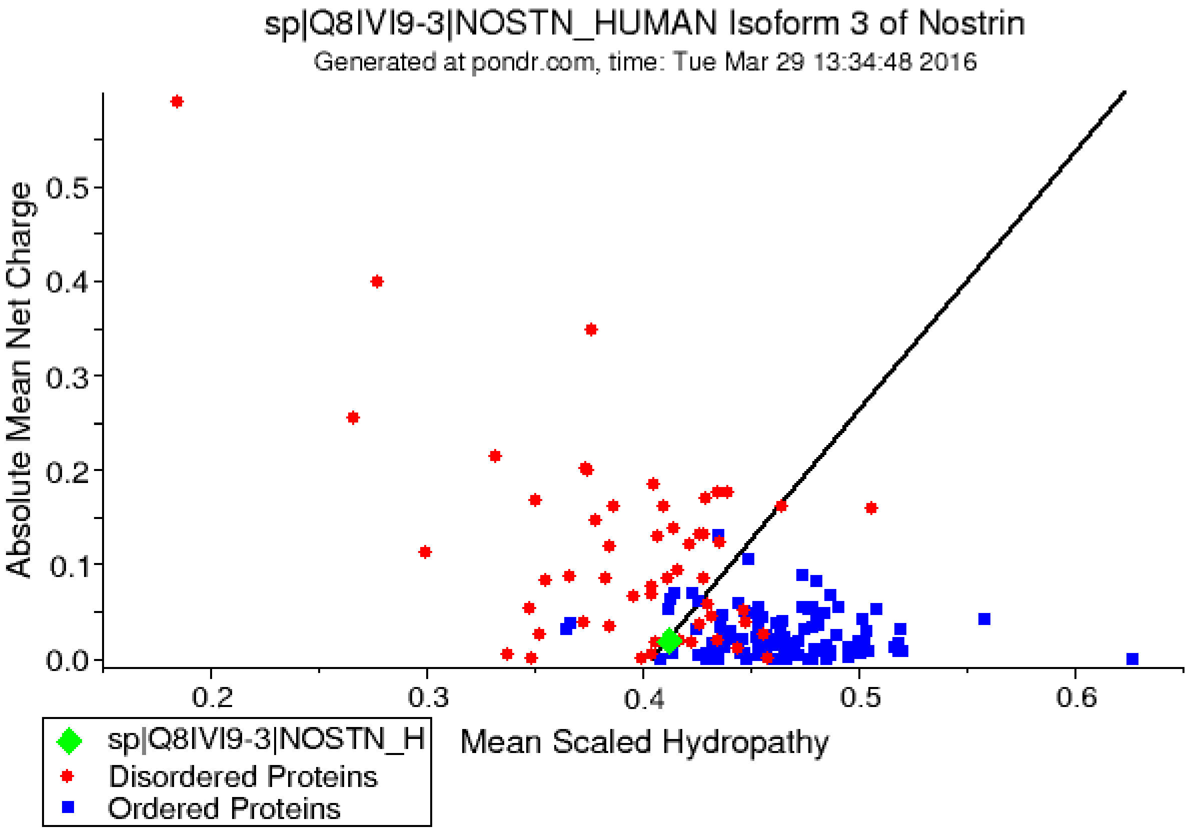
MKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVEKTANLVISNWNQQIKAKK
KLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKLEKEDENYYQKNMAGYSTR
LKWENTLENCYQSILELEKERIQLLCNNLNQYSQHISLFGQTLTTCHTQIHCAISKIDIE
KDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLKPKLLRLQRDIEKASK
DKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANSYKLSSMLAELEQRPQ
PSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQSNPGSSTPAPGAAQL
SSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGKKGHFPAAYVEELPSN
AGNTATKA
```





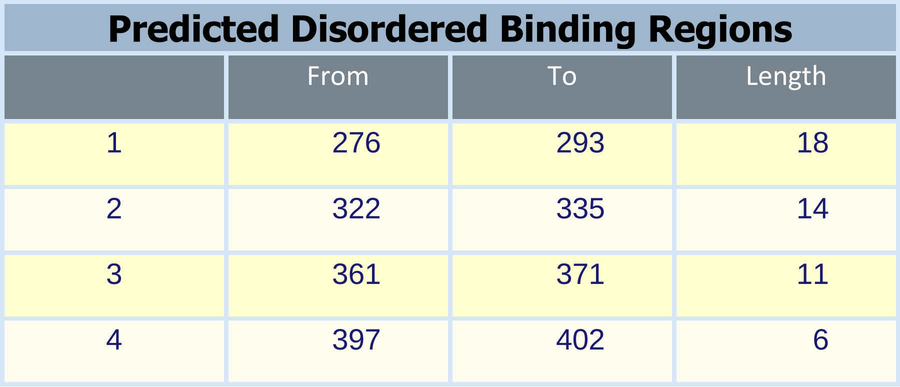

sp|Q8IVI9-3|NOSTN_HUMAN Isoform 3 of Nostrin
Generated at pondr.com, time: Tue Mar 29 13:34:48 2016
Cumulative Fraction of Residues
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT


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
0.0
0.1
0.2
0.3
0.4
0.5
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

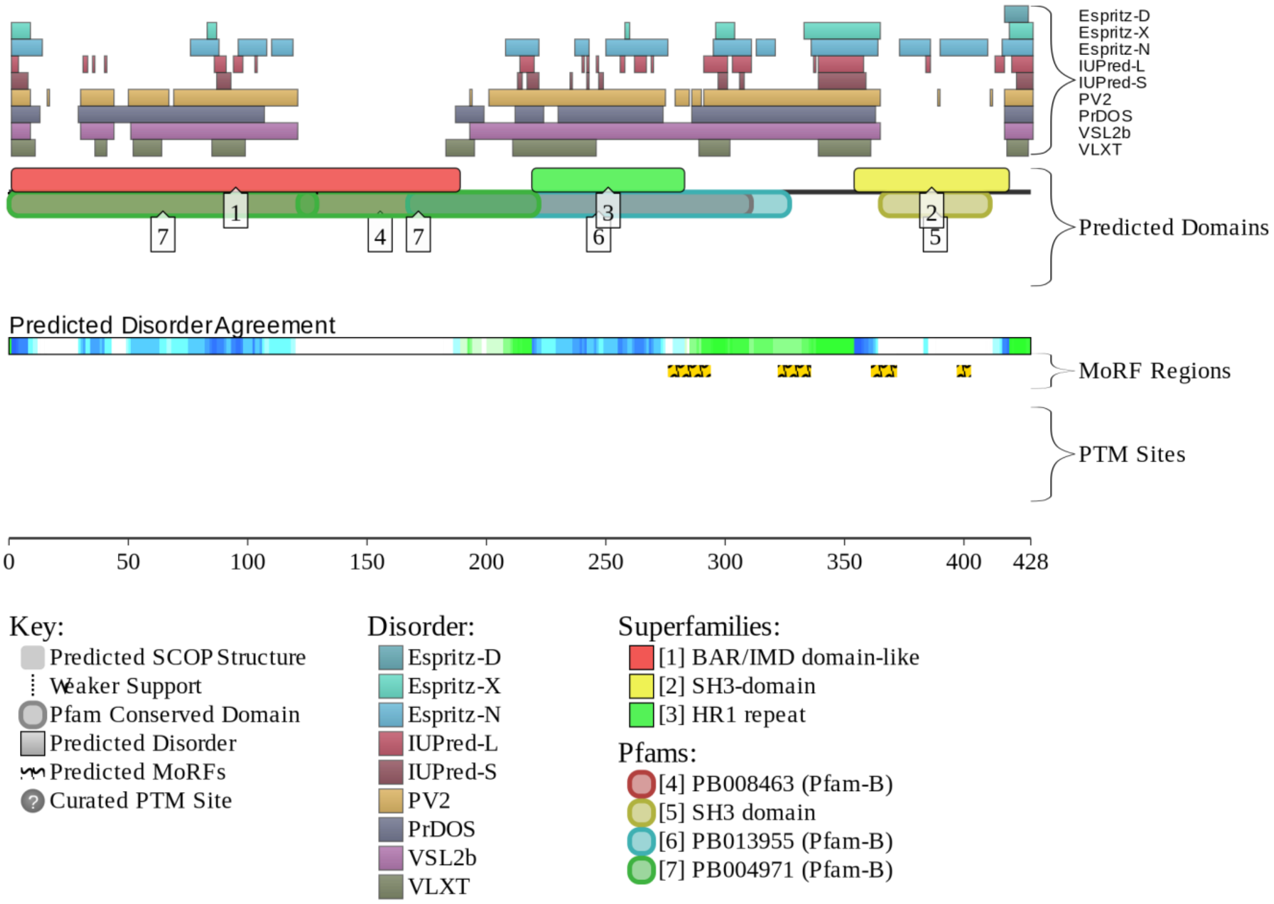
========================VSL2 NNP STATISTICS=================================
Predicted residues: 428                       Number Disordered Regions: 5
Number residues disordered: 276               Longest Disordered Region: 172
Overall percent disordered: 64.49     Average Prediction Score: 0.6151
Predicted 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



```
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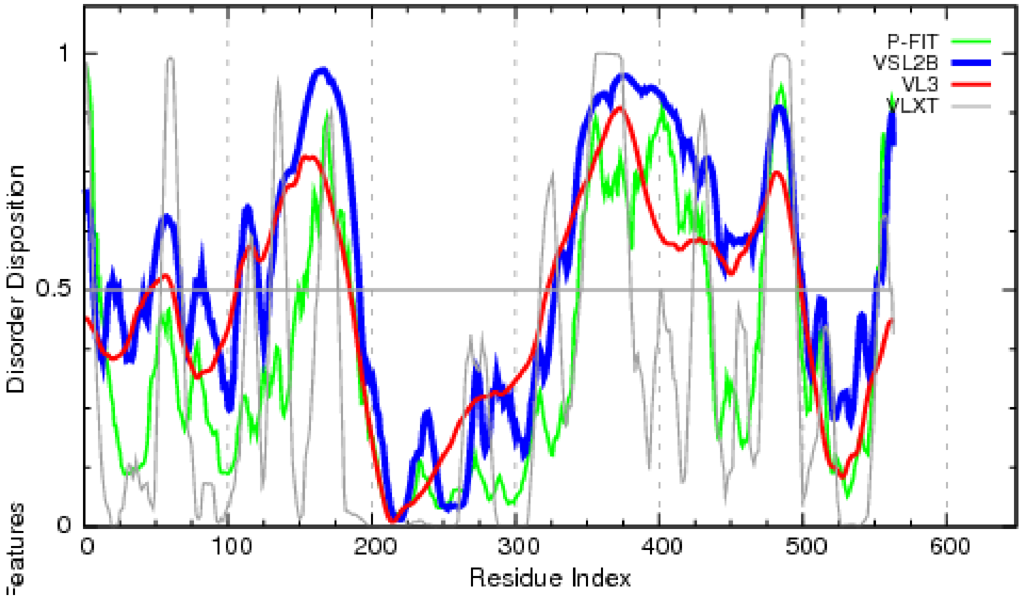
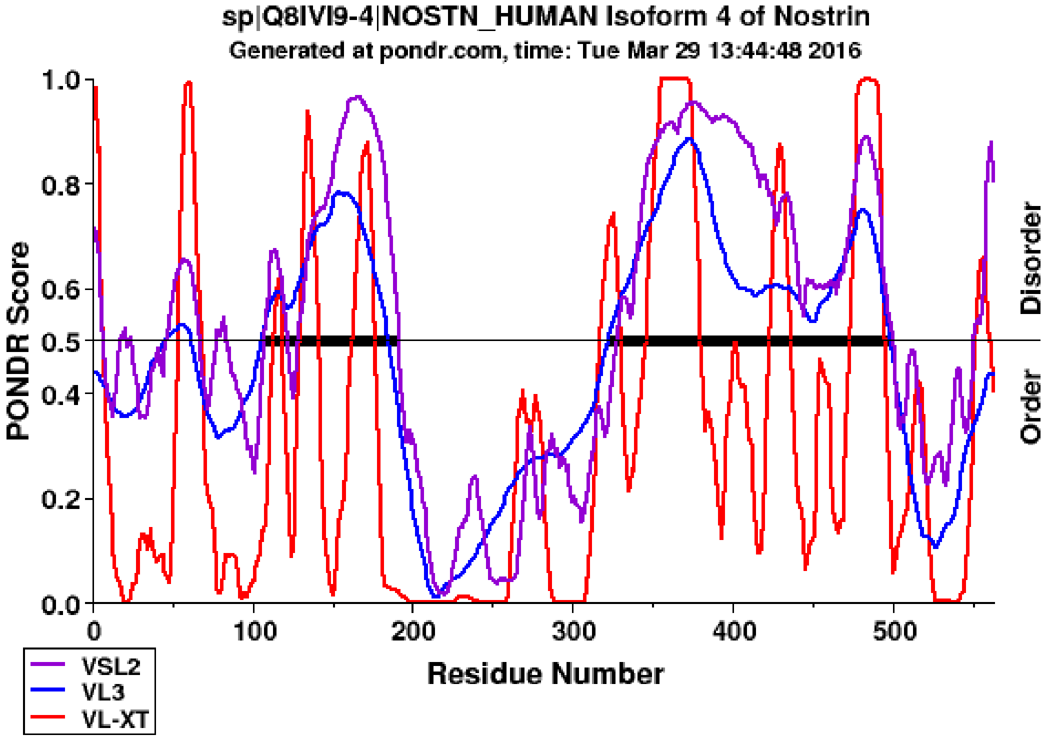
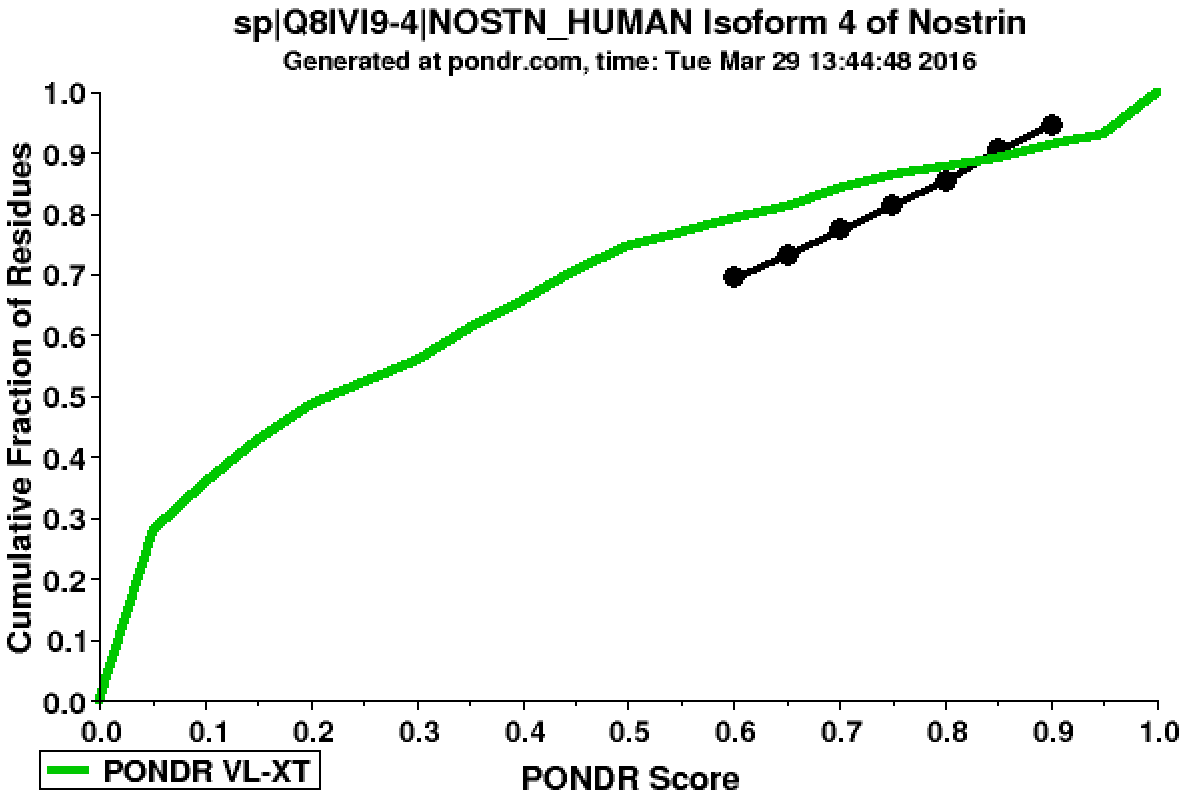
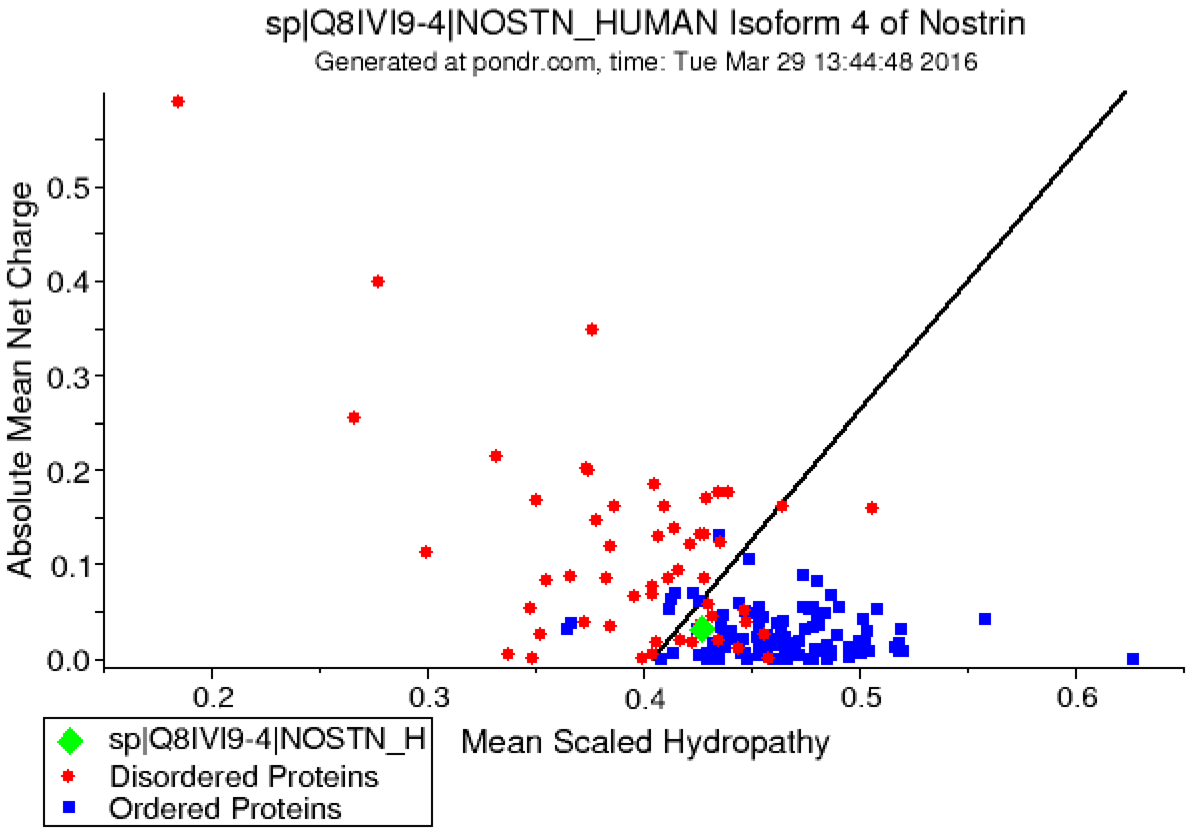
QNTRKSCVSSAWAWASEGMKSTADLHQKLGKAIELEAIKPTYQVLNVQEKKRKSLDNEVE
KTANLVISNWNQQIKAKKKLMVSTKKHEALFQLVESSKQSMTEKEKRKLLNKLTKSTEKL
EKEDENYYQKNMAGYSTRLKWENTLENCYQVTHSICLYAFWVKRAWGKCVSDLRYQDTFL
PGNLPPLWFGYDIVKRLIMRLCSVCLQSILELEKERIQLLCNNLNQYSQHISLFGQTLTT
CHTQIHCAISKIDIEKDIQAVMEETAILSTENKSEFLLTDYFEEDPNSAMDKERRKSLLK
PKLLRLQRDIEKASKDKEGLERMLKTYSSTSSFSDAKSQKDTAALMDENNLKLDLLEANS
YKLSSMLAELEQRPQPSHPCSNSIFRWREKEHTHSYVKISRPFLMKRLENIVSKASSGGQ
SNPGSSTPAPGAAQLSSRLCKALYSFQARQDDELNLEKGDIVIIHEKKEGGWWFGSLNGK
KGHFPAAYVEELPSNAGNTATKA
```





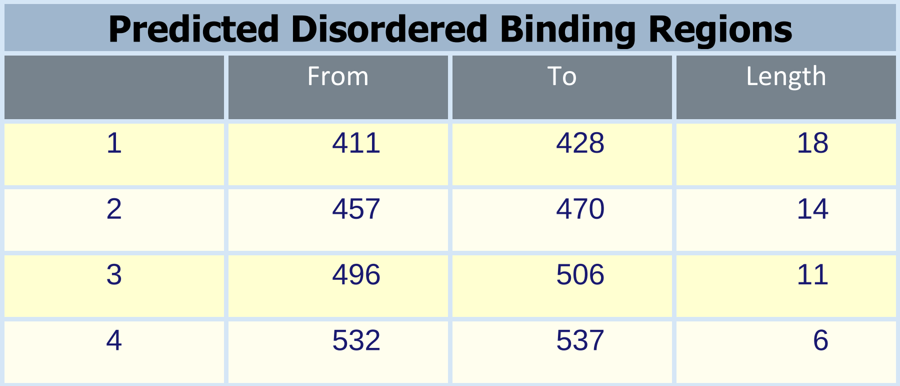

sp|Q8IVI9-4|NOSTN_HUMAN Isoform 4 of Nostrin
Generated at pondr.com, time: Tue Mar 29 13:44:48 2016
Cumulative Fraction of Residues
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT


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
0.0
0.1
0.2
0.3
0.4
0.5
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

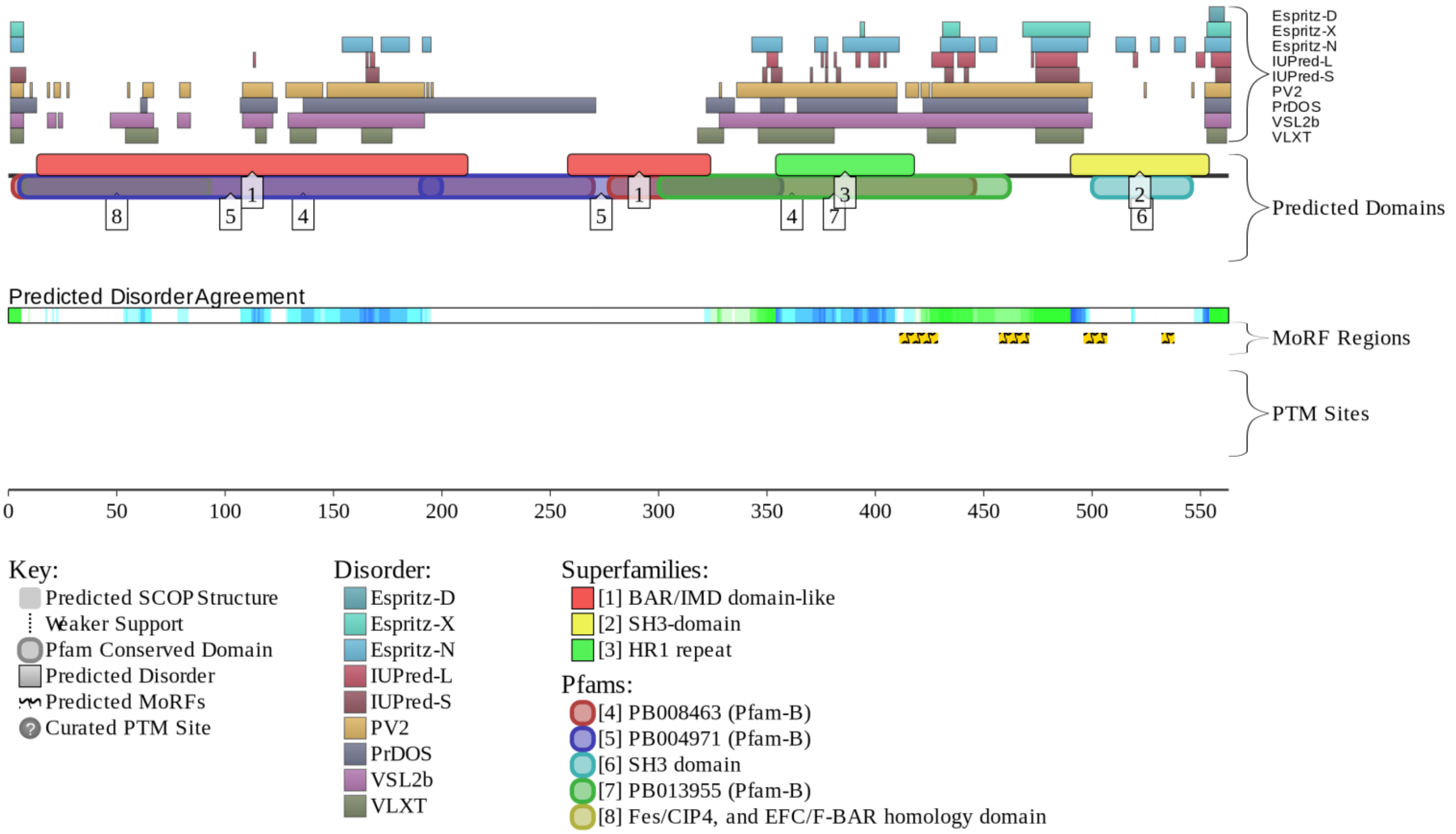
=========================VSL2 NNP STATISTICS==================================
Predicted residues: 563                      Number Disordered Regions: 9
Number residues disordered: 299              Longest Disordered Region: 172
Overall percent disordered: 53.11     Average Prediction Score: 0.5325
Predicted 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



```
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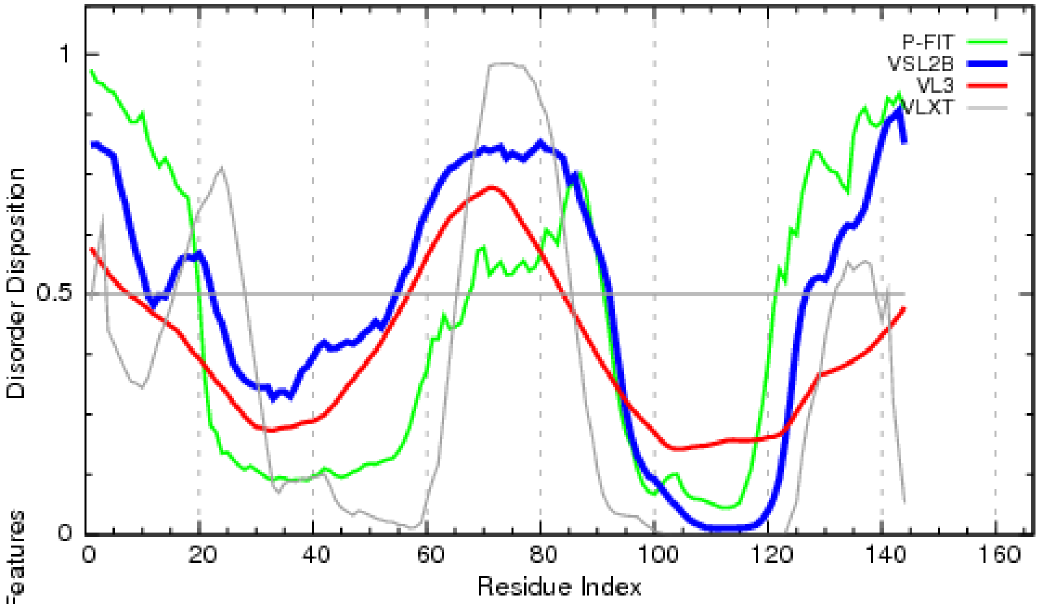
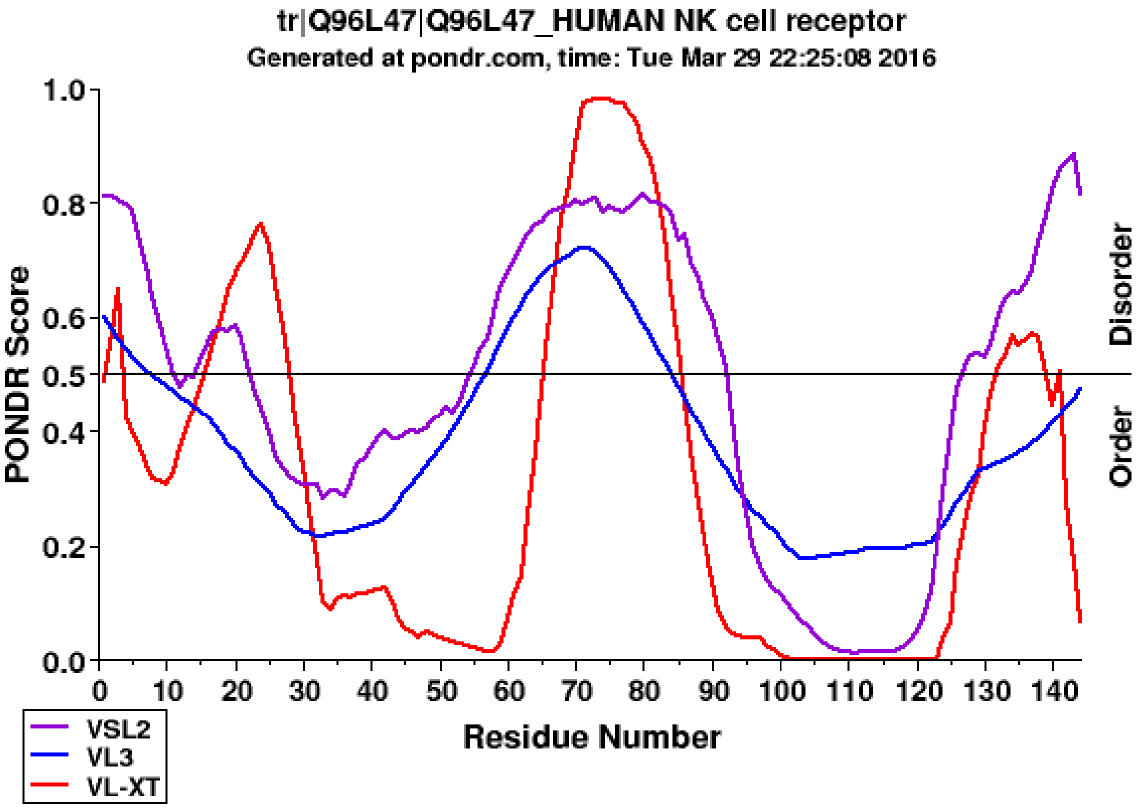
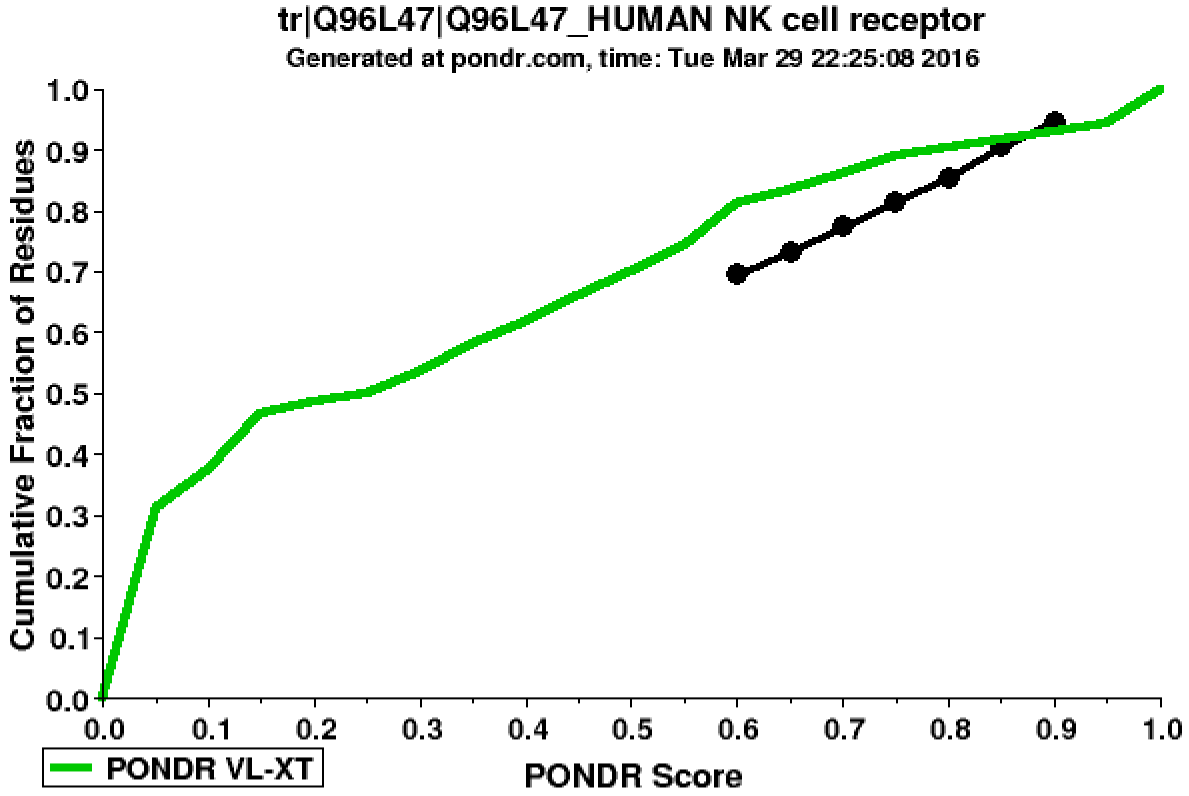
GN=KIR2DL4 PE=2 SV=1
LSCSSQSSFDIYHLSREGEAHELRLPAVPSINGTFQADFPLGPATHGETYRCFGSFHGSP
YEWSDPSDPLPVSVTGNPSSSWPSPTEPSFKTGIARHLHAVIRYSVAIILFTILPFFLLH
RWCSKKKNAAVMNQEPAGHRTVNR
```






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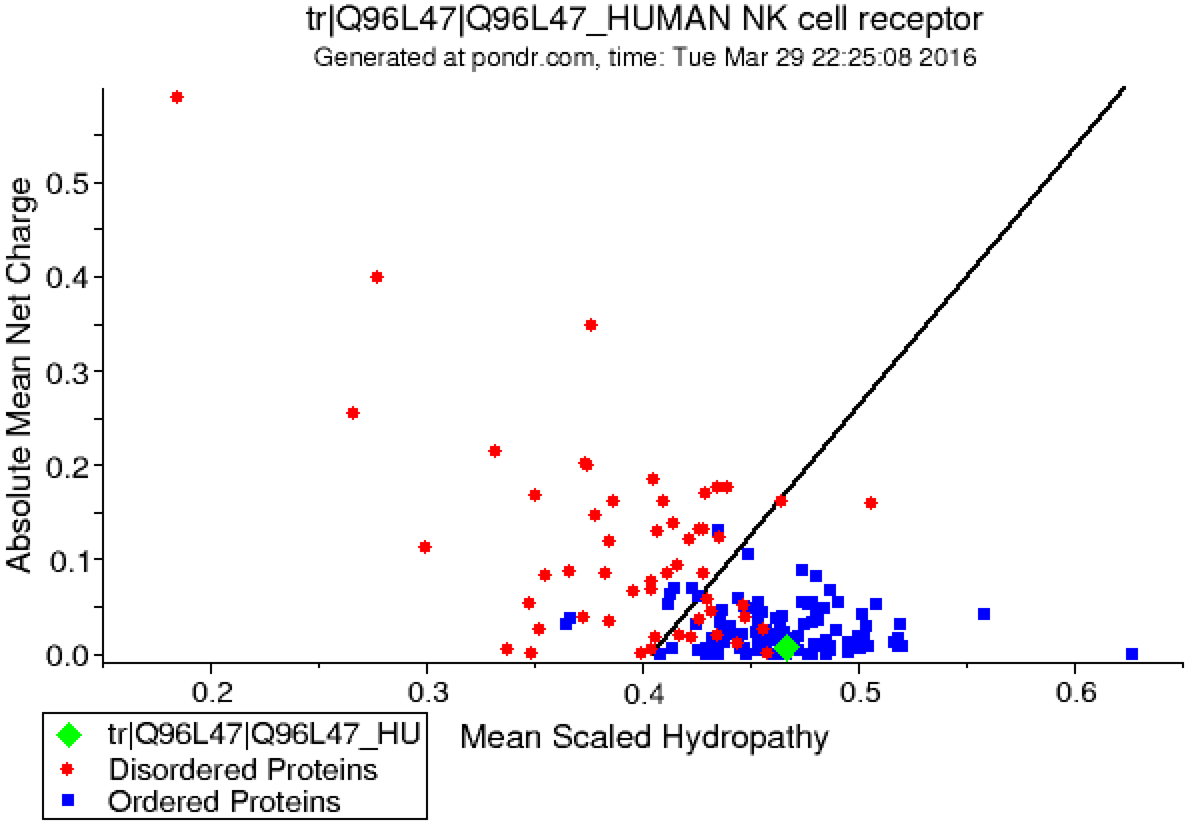
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR VL-XT
PONDR Score


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
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LLVILLSYVGTLQKVYFKSNGSEPLVTDGEIQGSDVILTNTIYNQSTVVSTAHPDQHVPA
WTTDASLPGDQSHRNTSACMNITHSQCQMLPYHATLTPLLSVVRNMEMEKFLKFFTYLHR
LSCYQHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCEAAKEGCESVLGMVNYSWPDFLRC
SQFRNQTESSNVSRICFSPQQENGKQLLCGRGENFLCASGICIPGKLQCNGYNDCDDWSD
EAHCNCSENLFHCHTGKCLNYSLVCDGYDDCGDLSDEQNCDCNPTTEHRCGDGRCIAMEW
VCDGDHDCVDKSDEVNCSCHSQGLVECRNGQCIPSTFQCDGDEDCKDGSDEENCSVIQTS
CQEGDQRCLYNPCLDSCGGSSLCDPNNSLNNCSQCEPITLELCMNLPYNSTSYPNYFGHR
TQKEASISWESSLFPALVQTNCYKYLMFFSCTILVPKCDVNTGEHIPPCRALCEHSKERC
ESVLGIVGLQWPEDTDCSQFPEENSDNQTCLMPDEYVEECSPSHFKCRSGQCVLASRRCD
GQADCDDDSDEENCGCKERDLWECPSNKQCLKHTVICDGFPDCPDYMDEKNCSFCQDDEL
ECANHACVSRDLWCDGEADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHHVCADGWQE
ILSQLACKQMGLGEPSVTKLIQEQEKEPRWLTLHSNWESLNGTTLHELLVNGQSCESRSK
ISLLCTKQDCGRRPAARMNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLT
VAHCFEGRENAAVWKVVLGINNLDHPSVFMQTRFVKTIILHPRYSRAVVDYDISIVELSE
DISETGYVRPVCLPNPEQWLEPDTYCYITGWGHMGNKMPFKLQEGEVRIISLEHCQSYFD
MKTITTRMICAGYESGTVDSCMGDSGGPLVCEKPGGRWTLFGLTSWGSVCFSKVLGPGVY
SNVSYFVEWIKRQIYIQTFLLN
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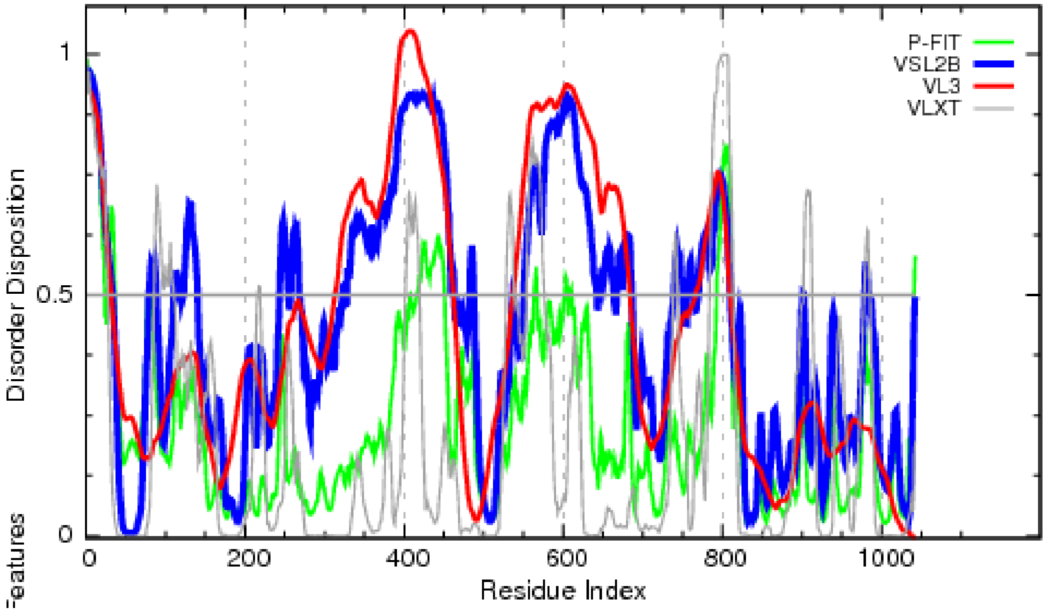

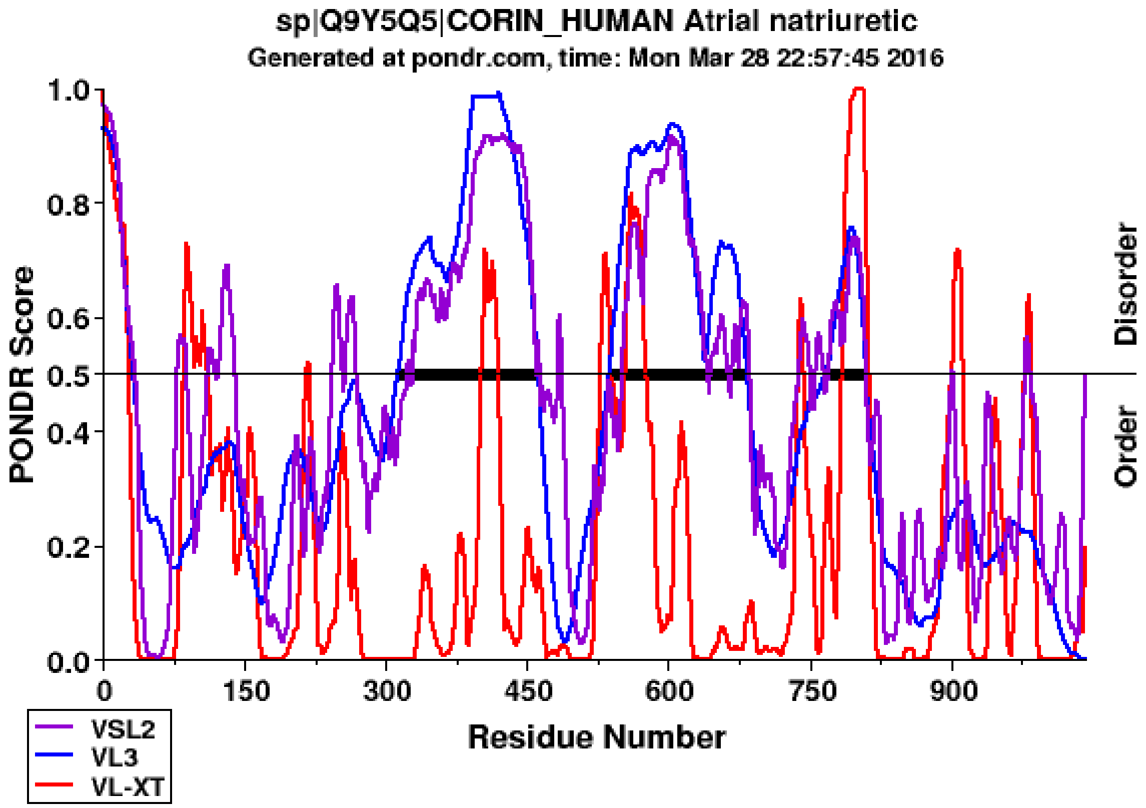

sp|Q9Y5Q5|CORIN_HUMAN Atrial natriuretic
Generated at pondr.com, time: Mon Mar 28 22:57:45 2016
PONDR Score
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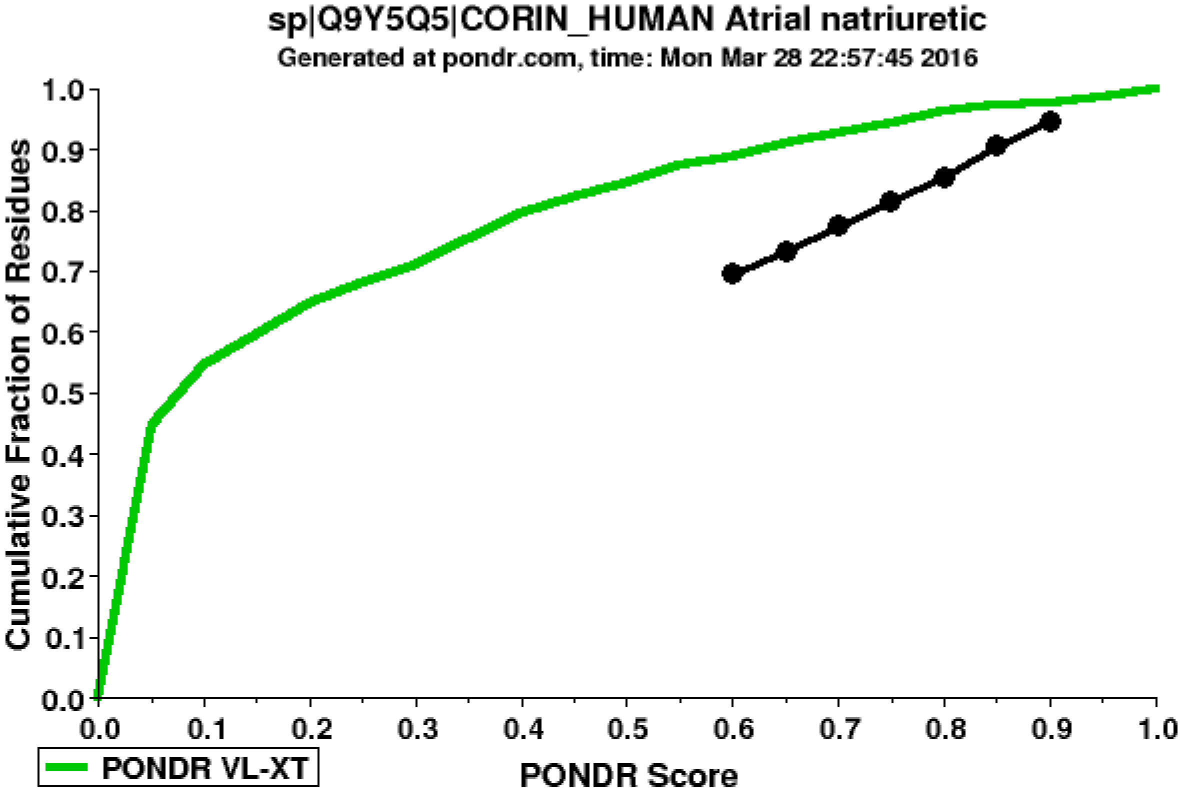
0.8
0.6
0.5
0.4
0.2
0.0
0
150
300
450
600
750
900
Residue Number
Disorder
Order
VSL2
VL3
VL-XT



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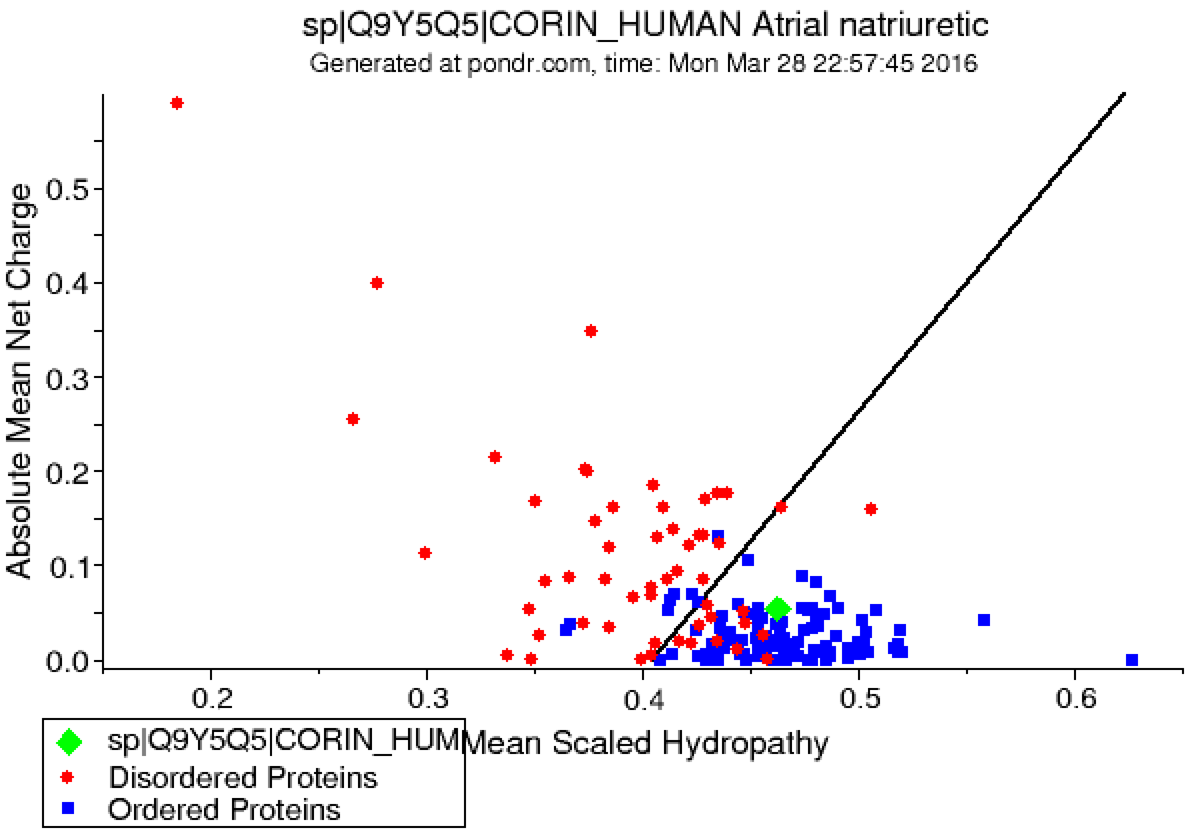
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT



```
========================VLXT NNP STATISTICS================================
Predicted residues: 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
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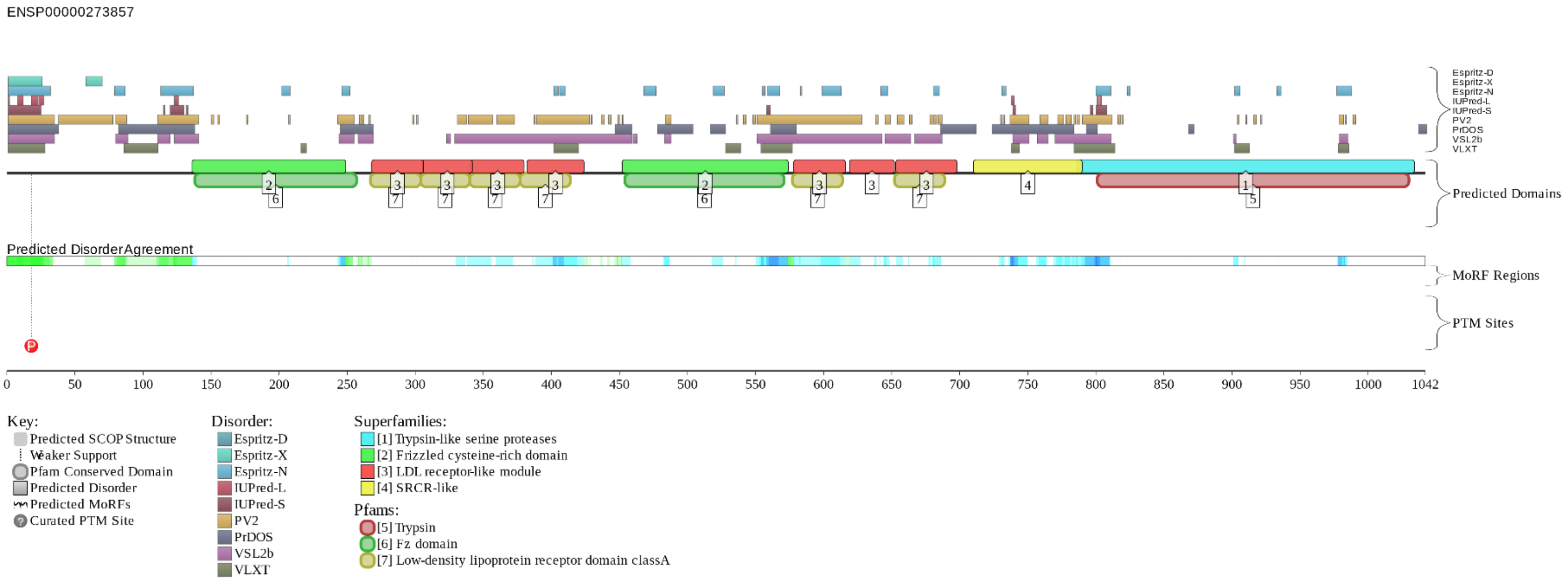

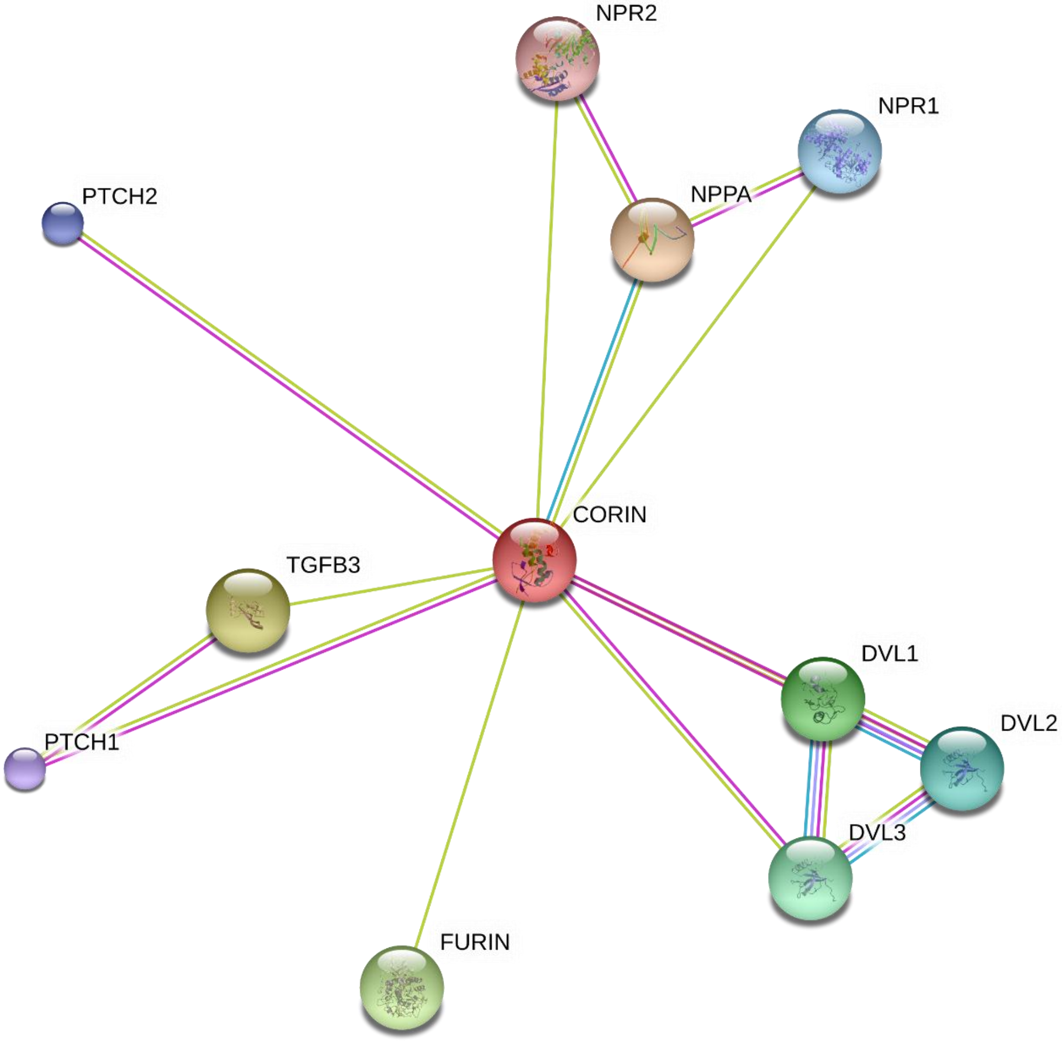
NPR2
NPR1
PTCH2
NPPA
CORIN
TGFB3
DVL1
DVL2
PTCH1
DVL3
FURIN

```
>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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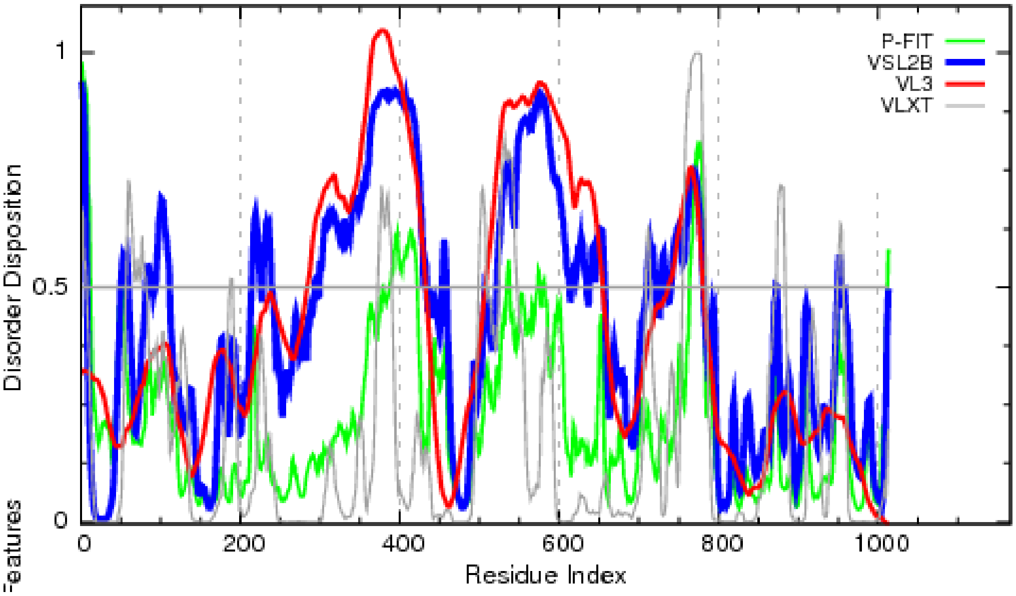

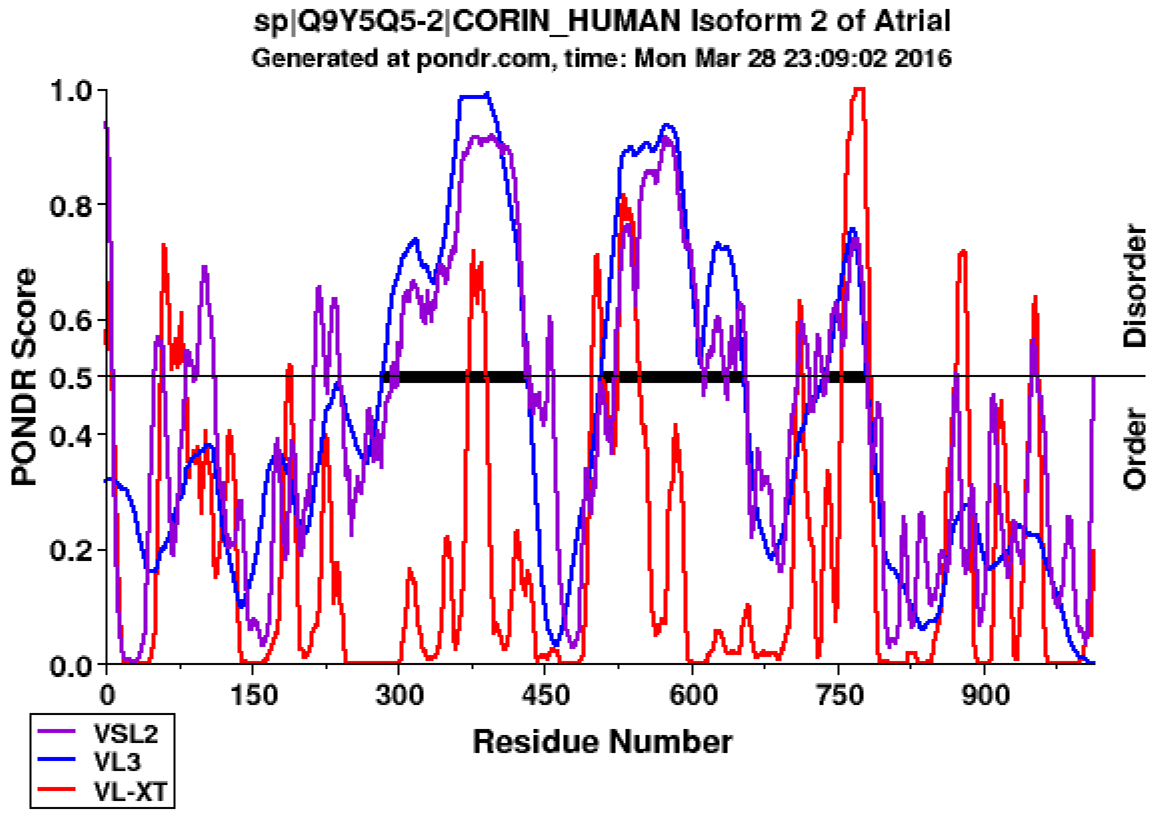

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Generated at pondr.com, time: Mon Mar 28 23:09:02 2016
PONDR Score
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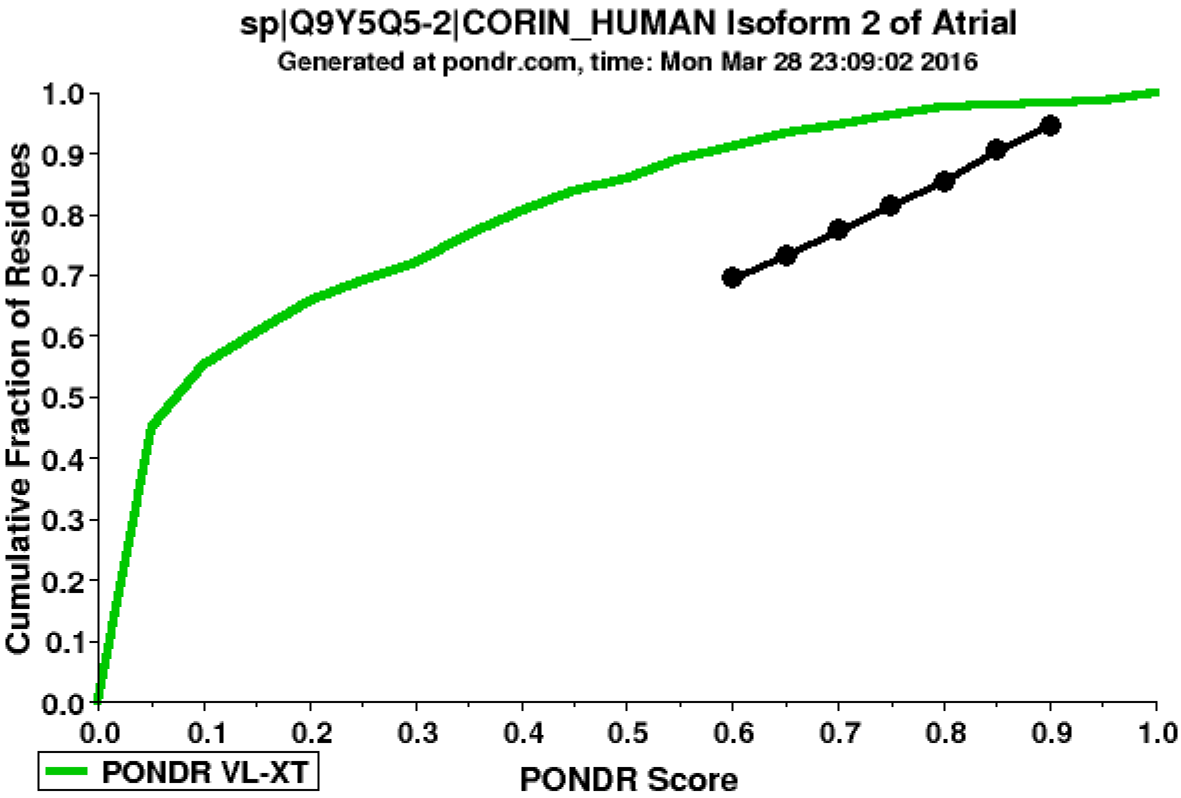
0.8
0.6
0.5
0.4
0.2
0.0
0
150
300
450
600
750
900
Residue Number
Disorder
Order
VSL2
VL3
VL-XT



sp|Q9Y5Q5-2|CORIN_HUMAN Isoform 2 of Atrial
Generated at pondr.com, time: Mon Mar 28 23:09:02 2016
Cumulative Fraction of Residues
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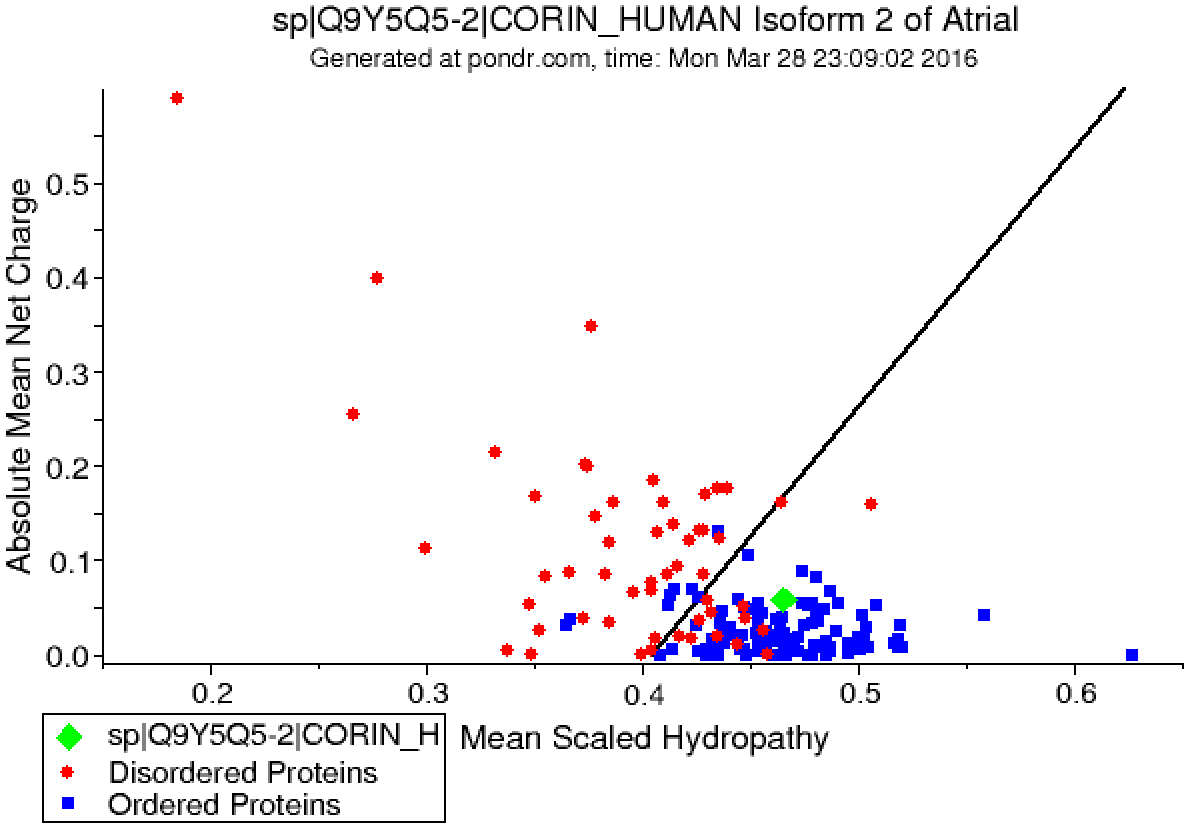
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR Score
PONDR VL-XT



```
========================VLXT NNP STATISTICS================================
Predicted residues: 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
```

```
>sp|P17948|VGFR1_HUMAN Vascular endothelial growth factor receptor 1
OS=Homo sapiens GN=FLT1 PE=1 SV=2
MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK
WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDK
MQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVK
AFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTA
TLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARC
DFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKMASTLVVADSRISGIYICIASNK
VGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTM
HYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVYTGEEILQKKEITIRDQEA
PYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQQEPGIILGPGSSTLFIER
VTEEDEGVYHCKATNQKGSVESSAYLTVQGTSDKSNLELITLTCTCVAATLFWLLLTLFI
RKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGK
VVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKILTHIGHHLNVVNLLGACTK
QGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSV
TSSESFASSGFQEDKSLSDVEEEEDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIH
RDLAARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKS
DVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRD
PKERPRFAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISA
PKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTW
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CSPPPDYNSVVLYSTPPI
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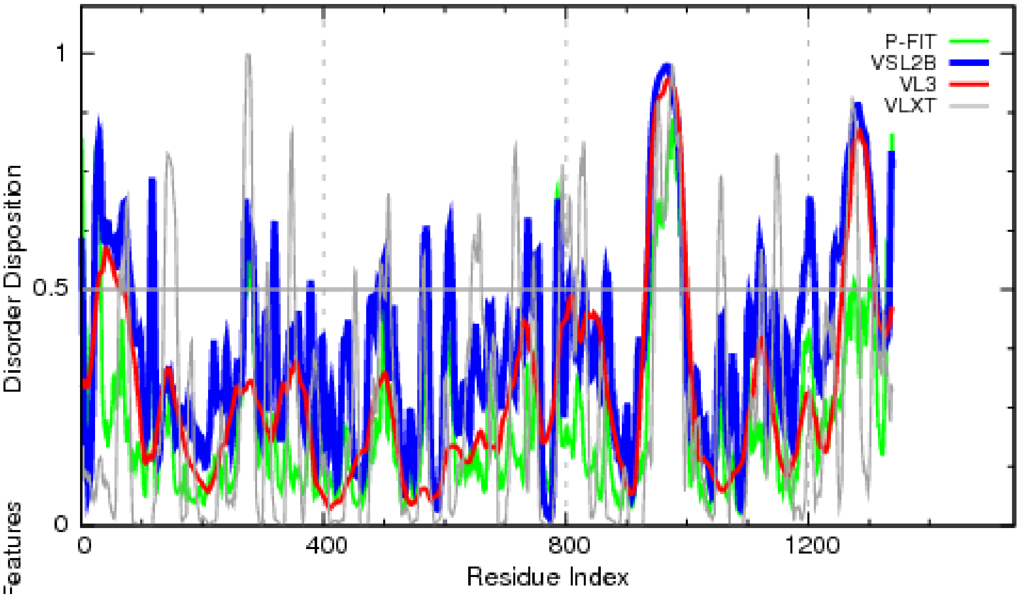

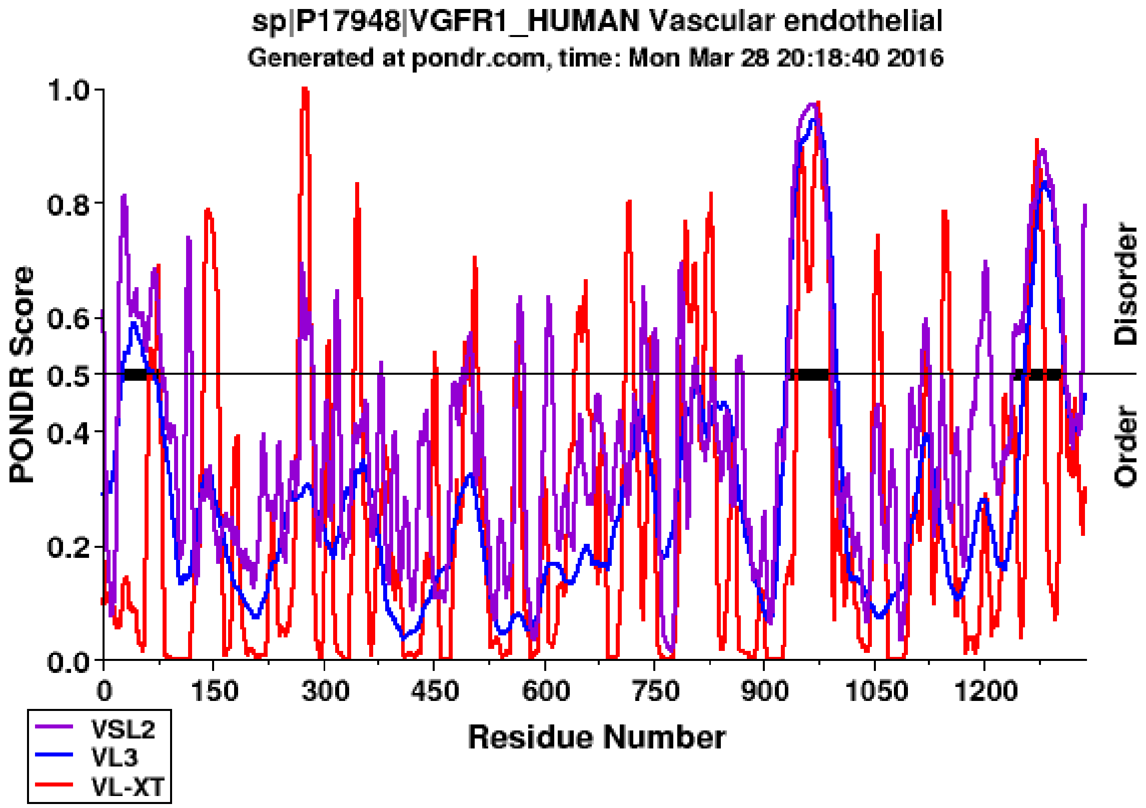
sp|P17948|VGFR1_HUMAN Vascular endothelial
Generated at pondr.com, time: Mon Mar 28 20:18:40 2016
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0.5
0.4
0.2
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750
900
1050
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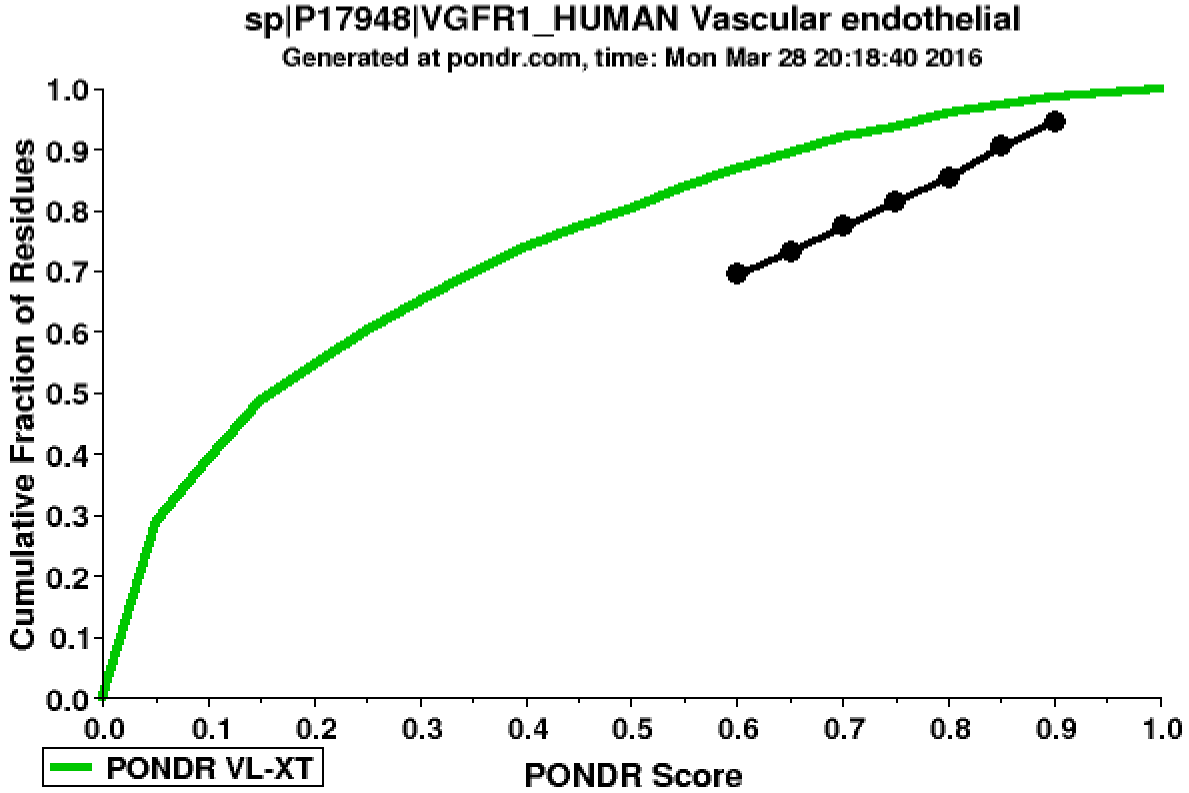
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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Generated at pondr.com, time: Mon Mar 28 20:18:40 2016
Cumulative Fraction of Residues
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0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
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0.6
0.7
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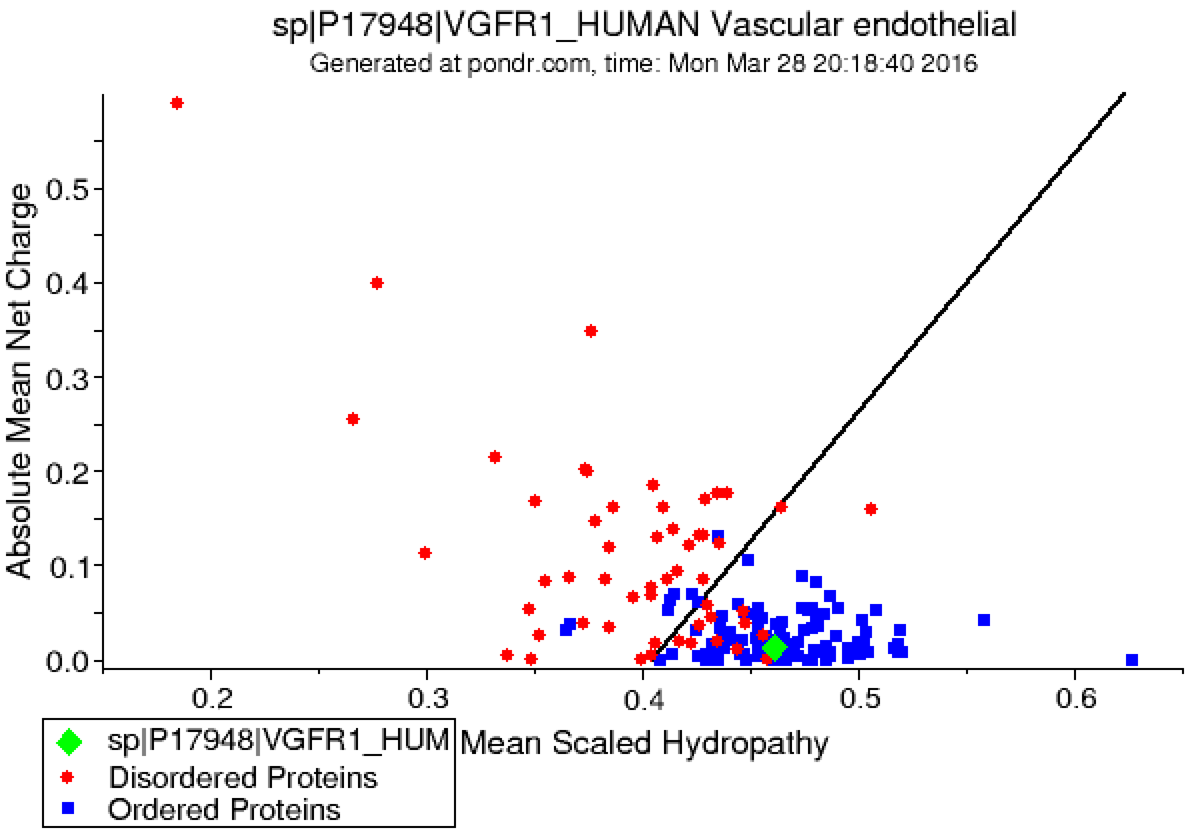
0.9
1.0
PONDR Score
PONDR VL-XT

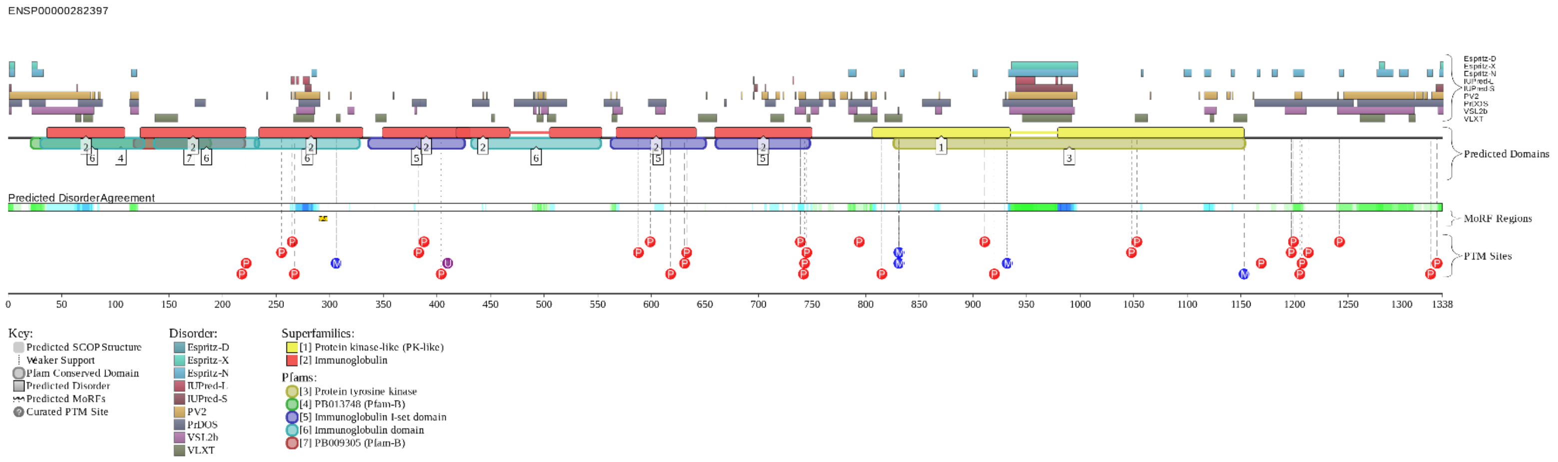


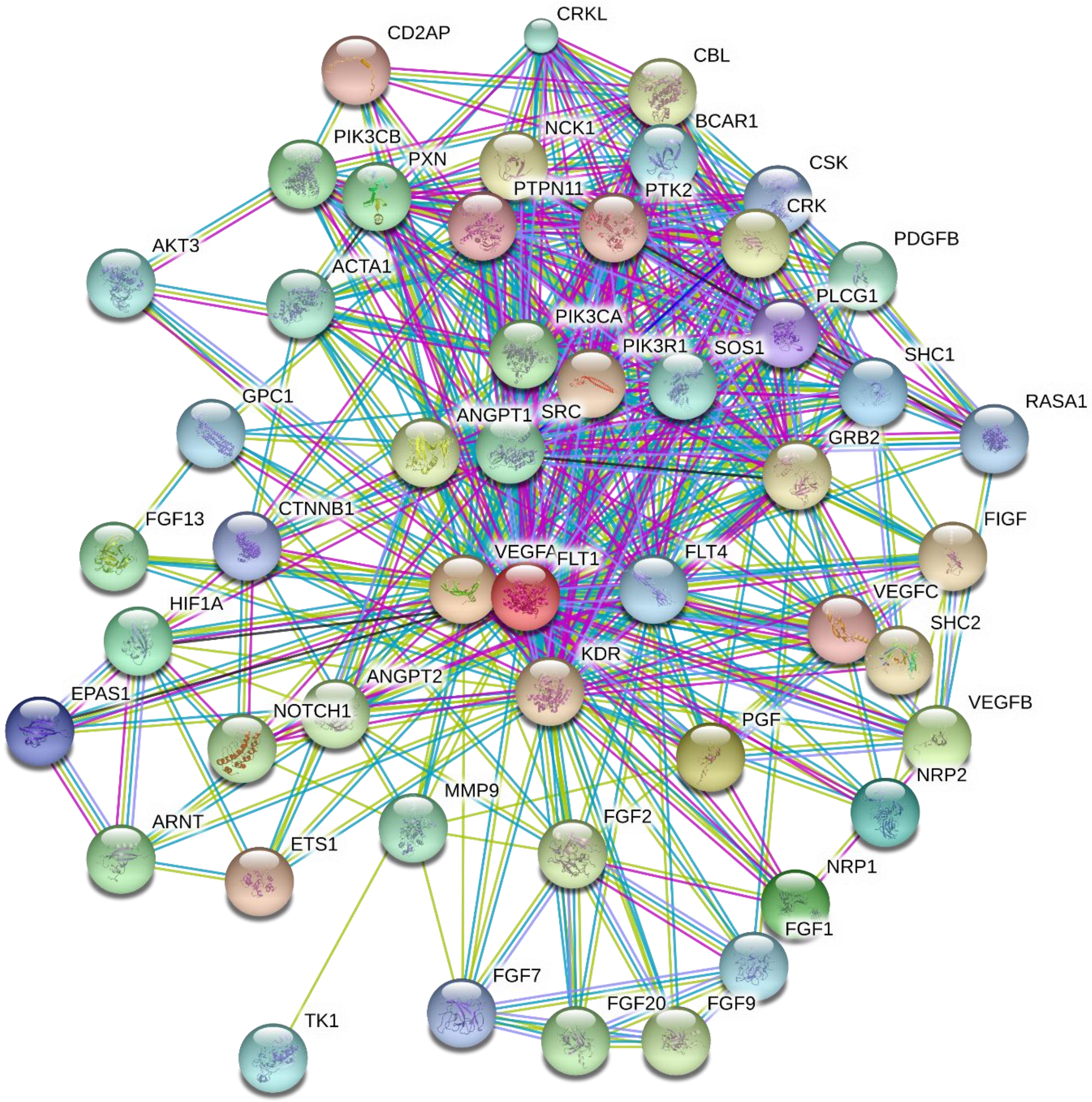
```
========================VLXT NNP STATISTICS================================
Predicted residues: 1338                       Number Disordered Regions: 21
Number residues disordered: 265                Longest Disordered Region: 46
Overall percent disordered: 19.81      Average Prediction Score: 0.2548
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
```





Predicted Disordered Binding Regions

	From	To	Length
1	290	297	8

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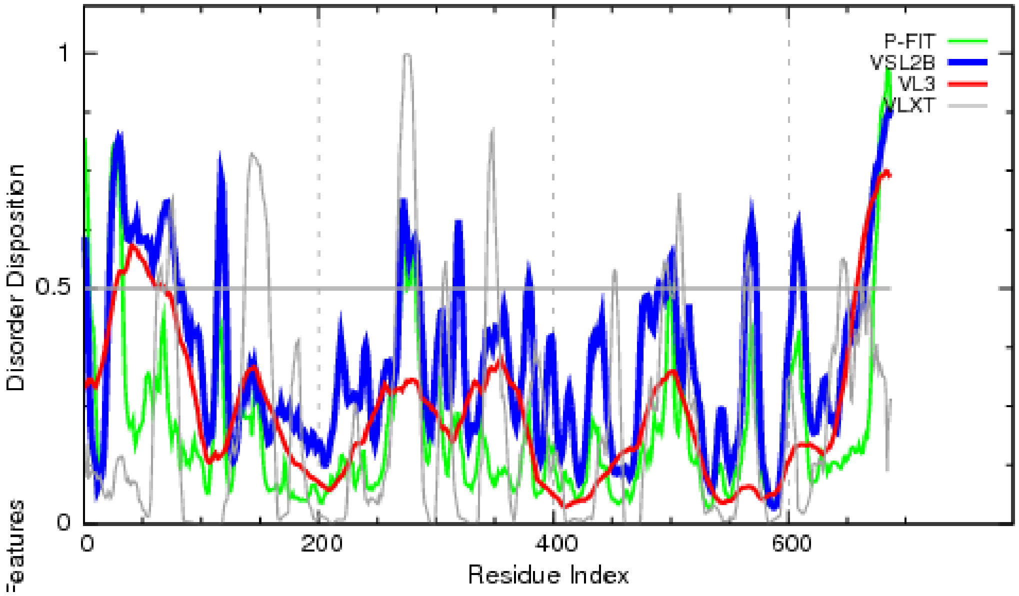
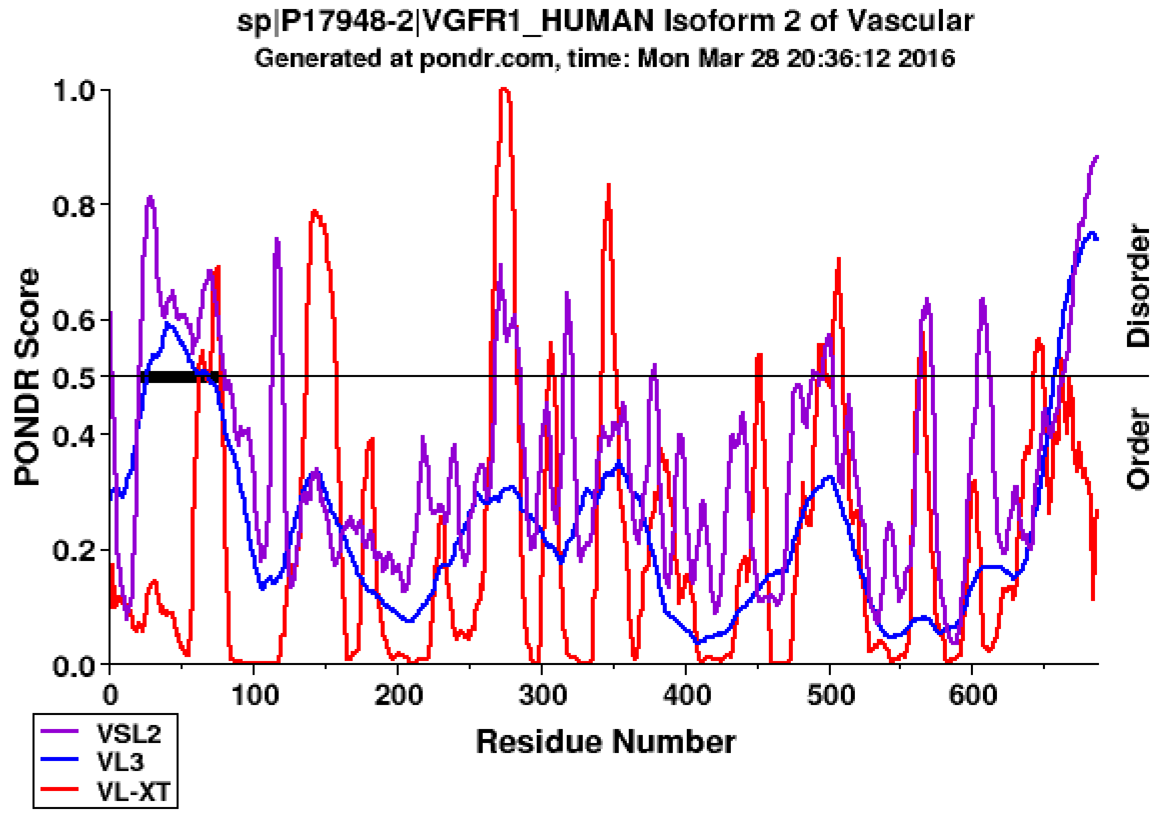


Predicted Disordered Binding Regions			
	From	To	Length
1	290	297	8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Generated at pondr.com, time: Mon Mar 28 20:36:12 2016
PONDR Score
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0.6
0.5
0.4
0.2
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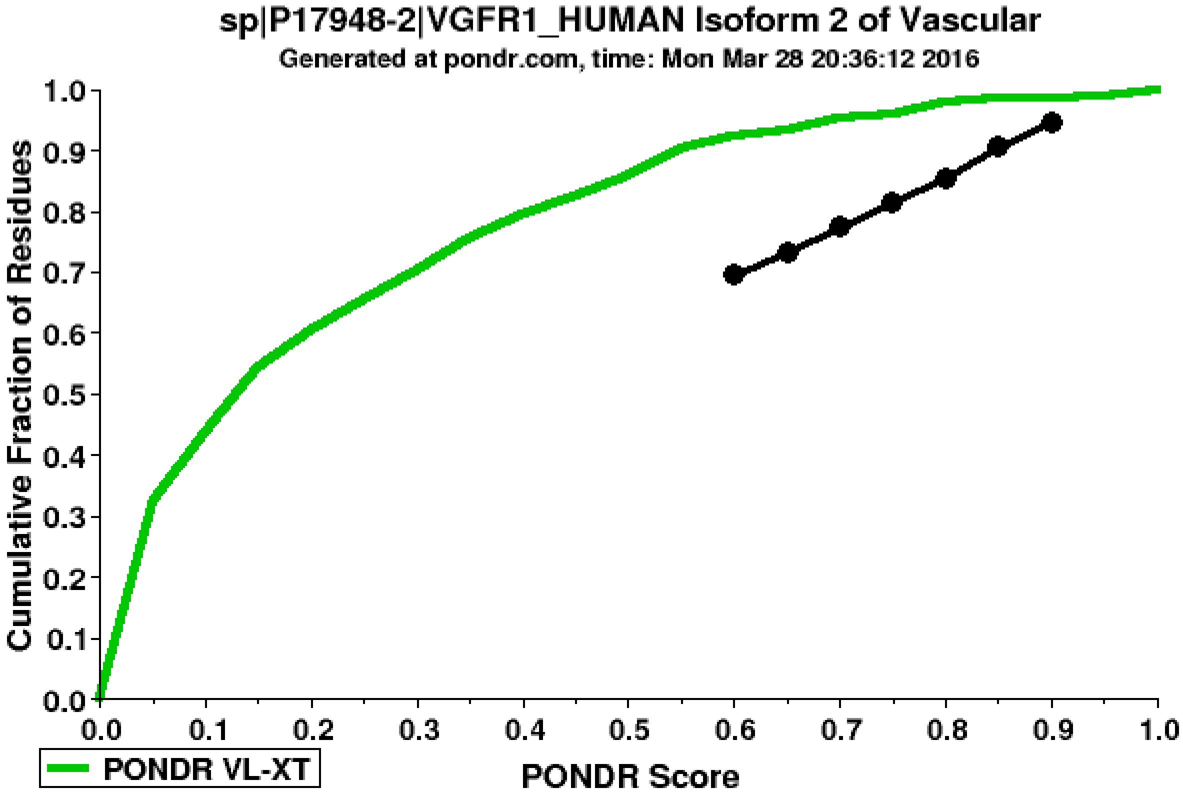
0
100
200
300
400
500
600
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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Generated at pondr.com, time: Mon Mar 28 20:36:12 2016
Cumulative Fraction of Residues
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0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
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0.5
0.6
0.7
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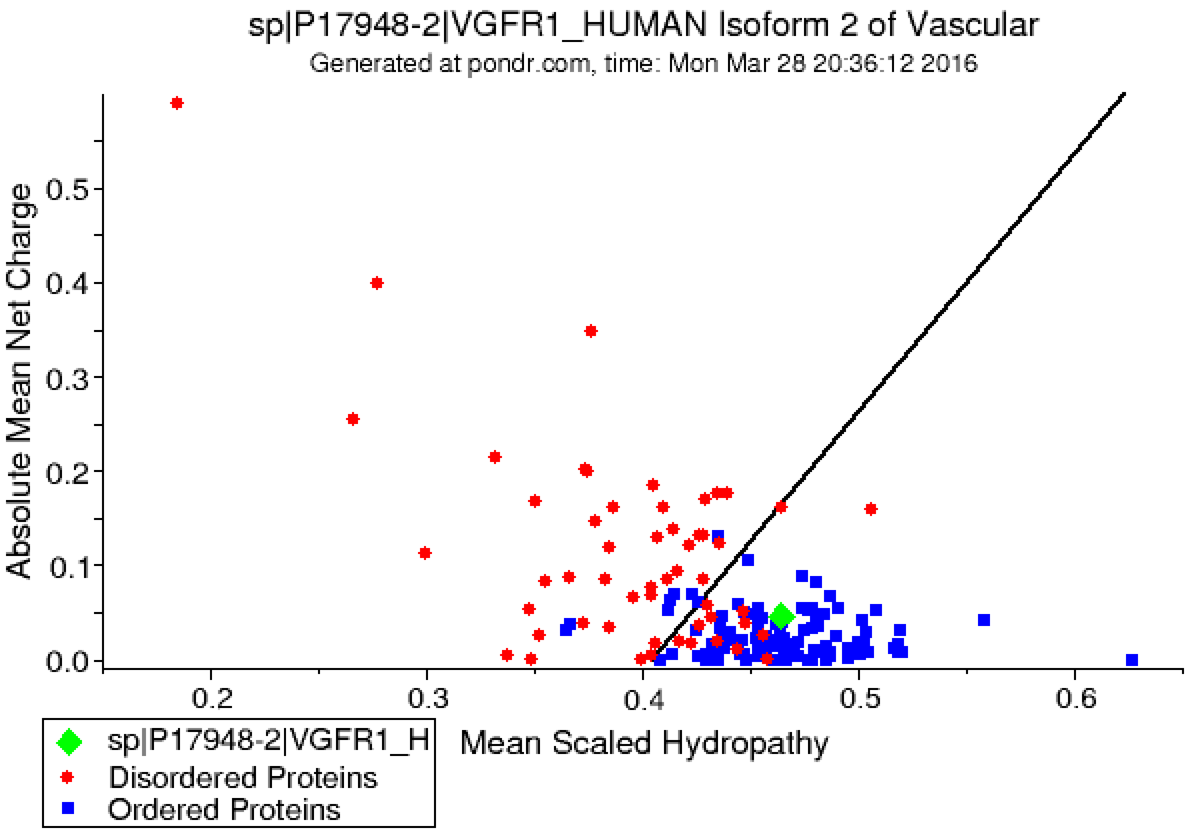
0.9
1.0
PONDR Score
PONDR VL-XT



```
========================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
```

```
>sp|P17948-3|VGFR1_HUMAN Isoform 3 of Vascular endothelial growth factor
receptor 1 OS=Homo sapiens GN=FLT1
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WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDK
MQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVK
AFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTA
TLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARC
DFCSNNEESFILDADSNMGNRIESITQRMAIIEGKNKMASTLVVADSRISGIYICIASNK
VGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTM
HYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVYTGEEILQKKEITIRDQEA
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LSSSSSSSSSSSS
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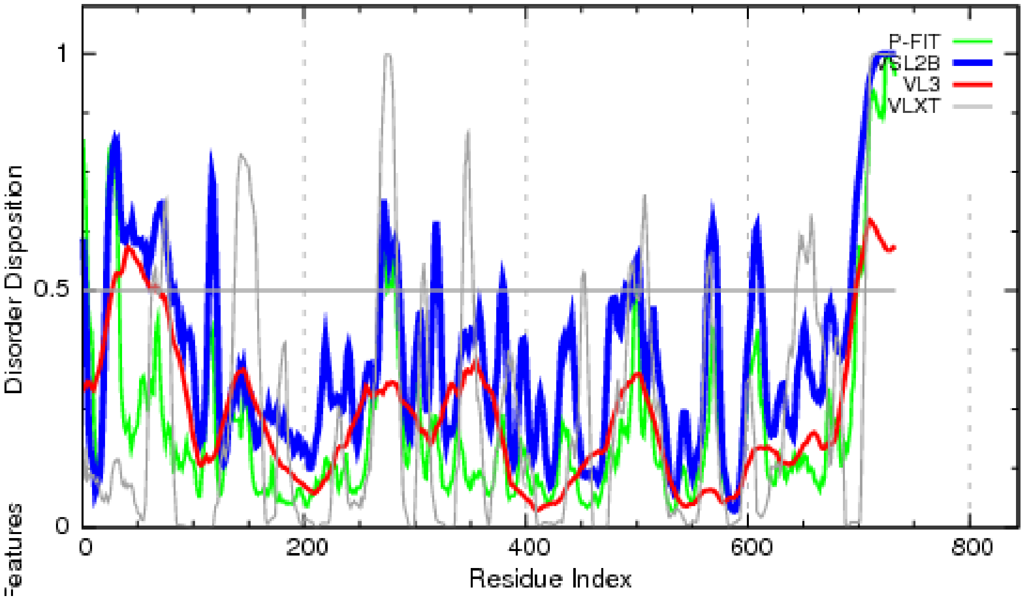

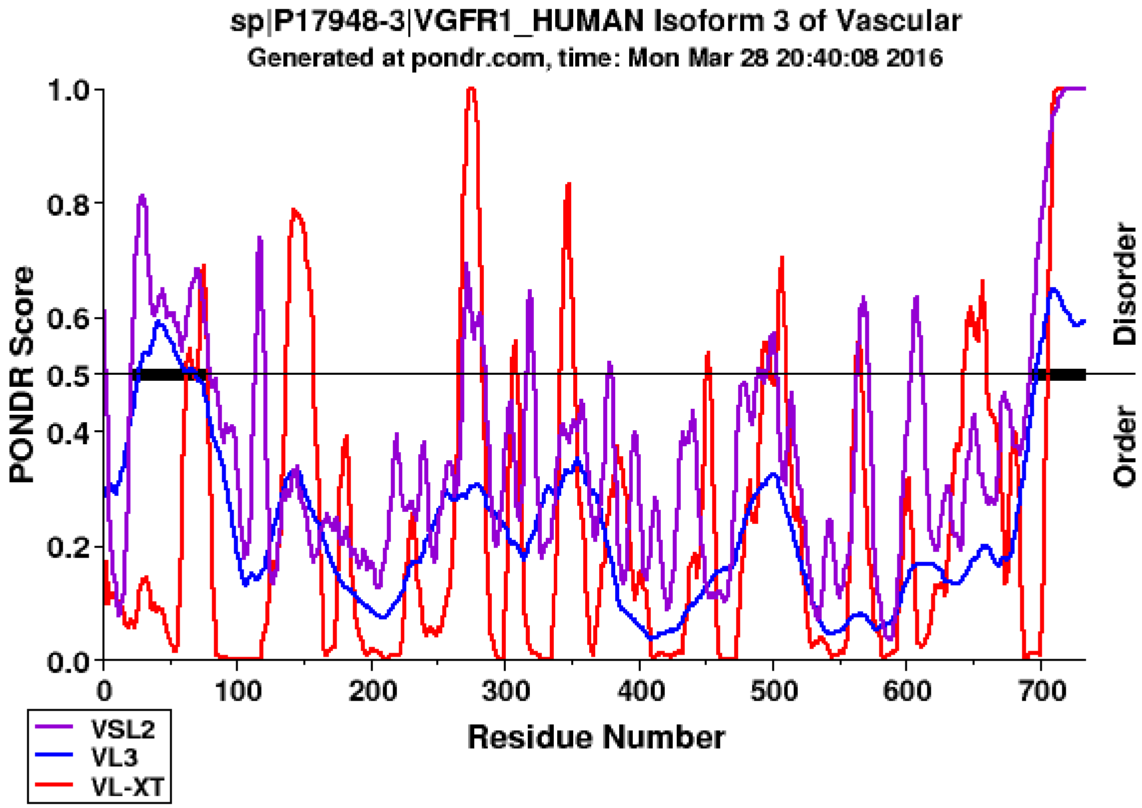
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PONDR Score
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0.6
0.5
0.4
0.2
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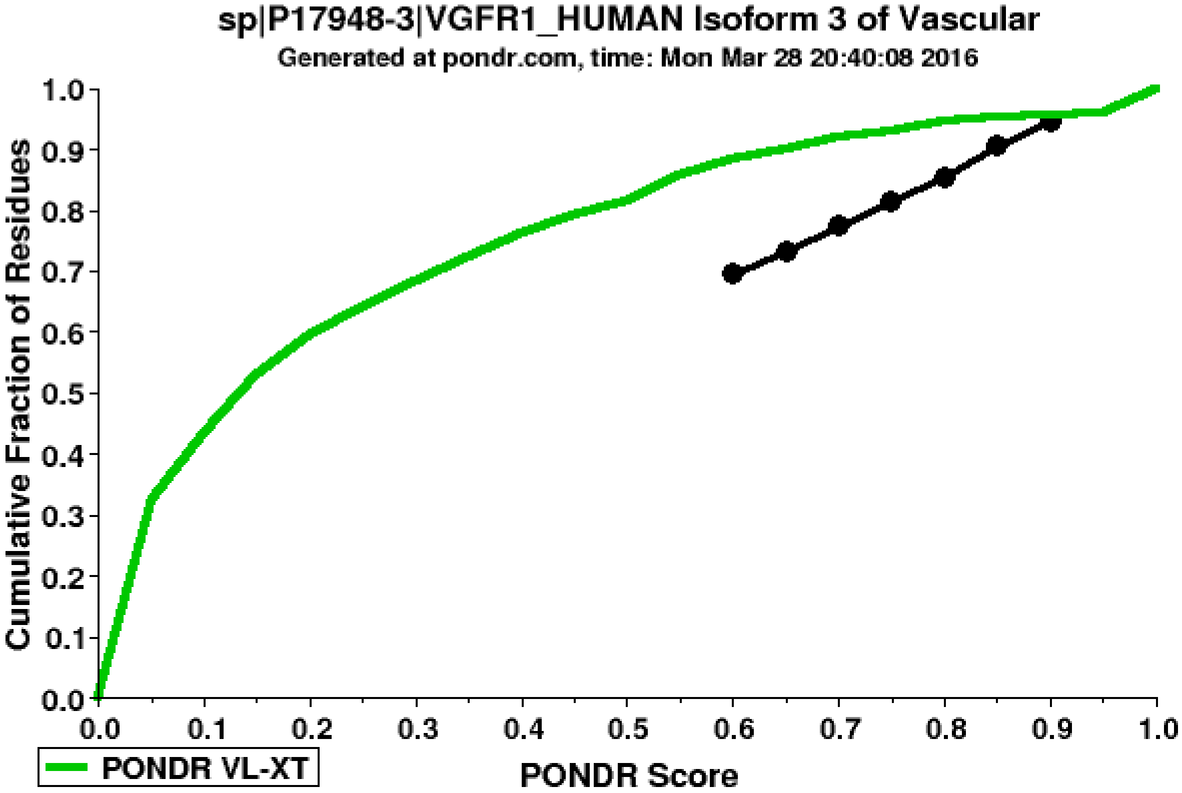
100
200
300
400
500
600
700
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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Generated at pondr.com, time: Mon Mar 28 20:40:08 2016
Cumulative Fraction of Residues
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0.9
0.8
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0.4
0.3
0.2
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0.0
0.1
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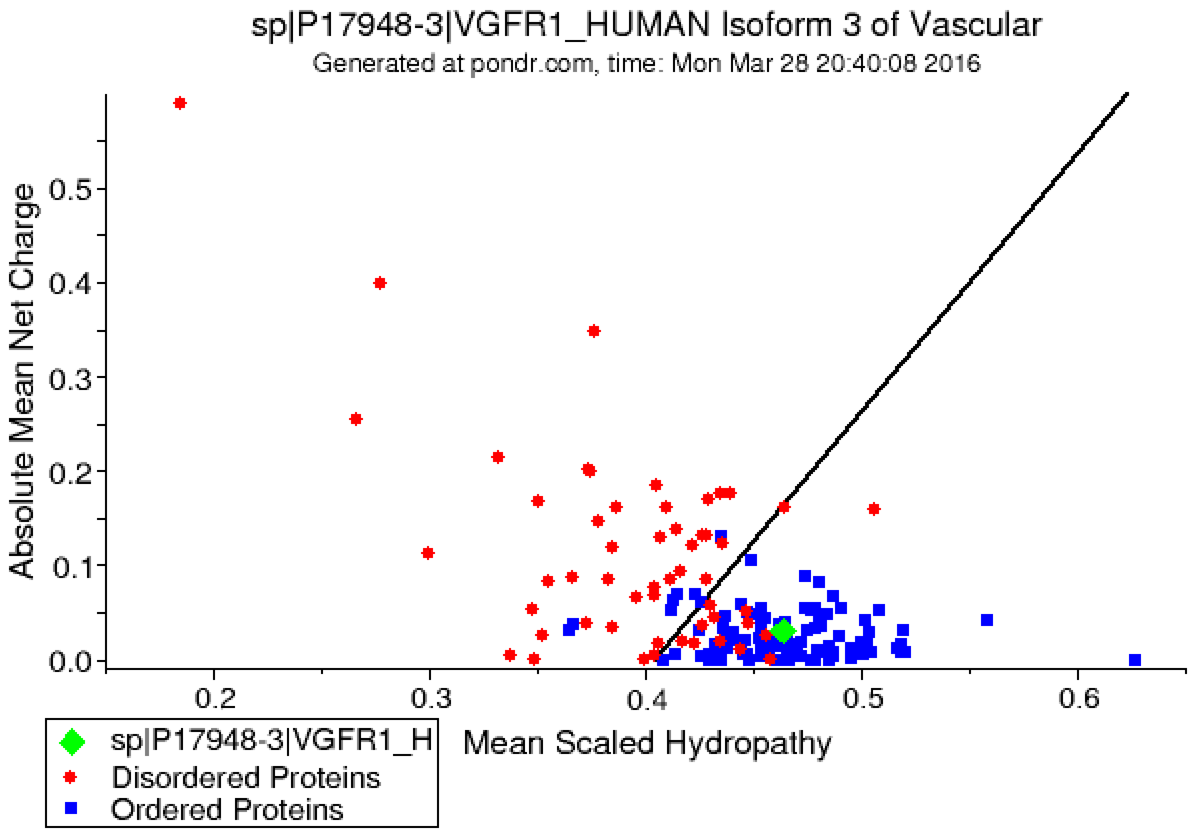
PONDR Score
PONDR VL-XT



```
========================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
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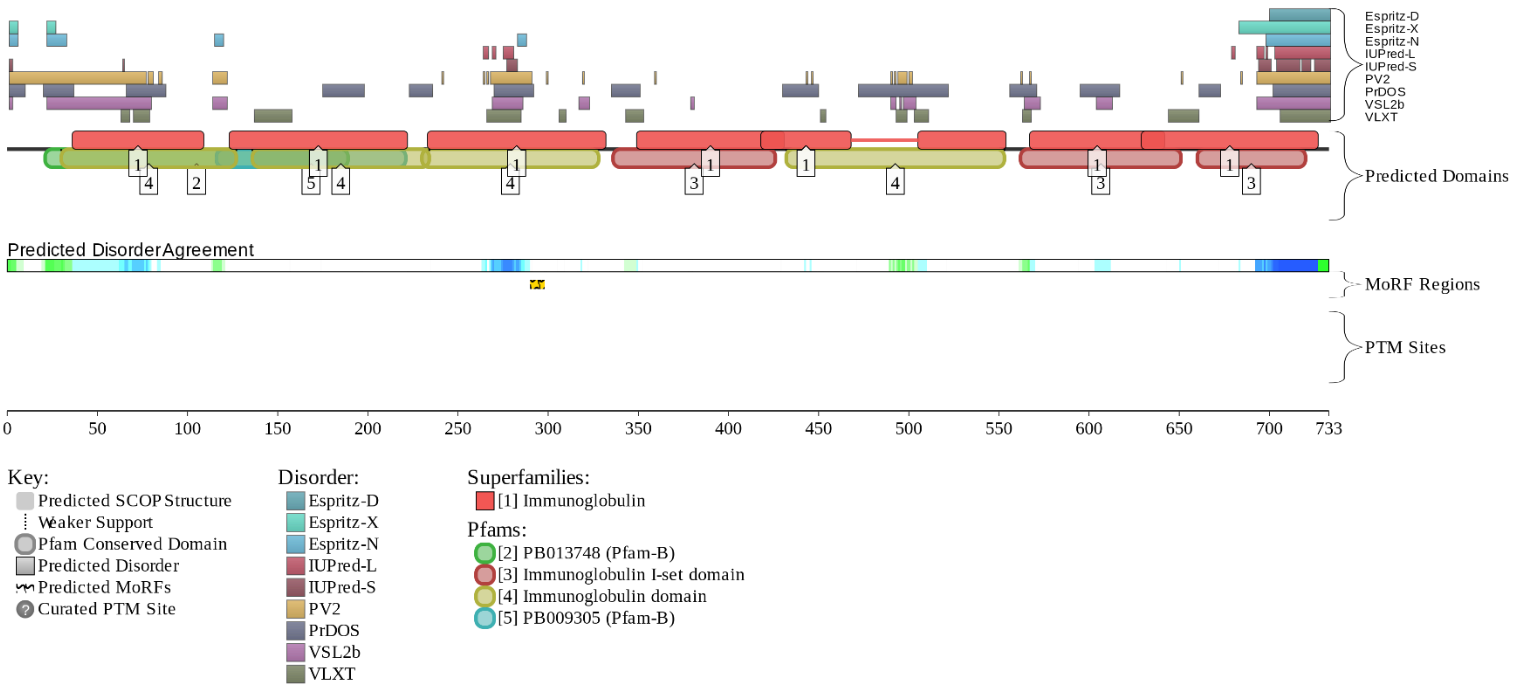
ENSP00000437631



Predicted Disordered Binding Regions

	From	To	Length
1	290	297	8

```
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MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK
WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDK
MQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVK
AFPSPEVVWLKDGLPATEKSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSNVFKNLTA
TLIVNVKPQIYEKAVSSFPDPALYPLGSRQILTCTAYGIPQPTIKWFWHPCNHNHSEARC
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P
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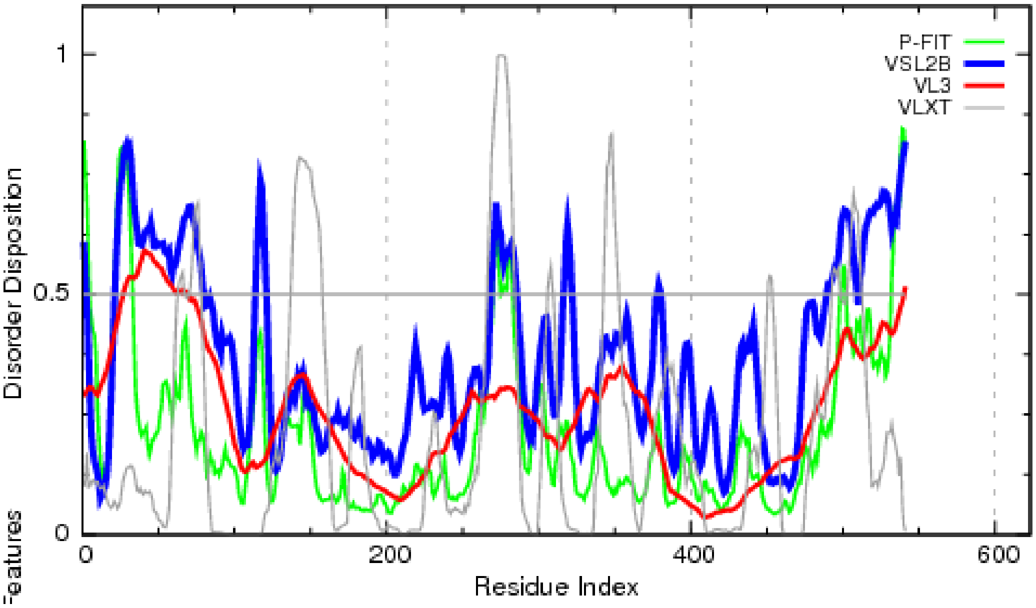

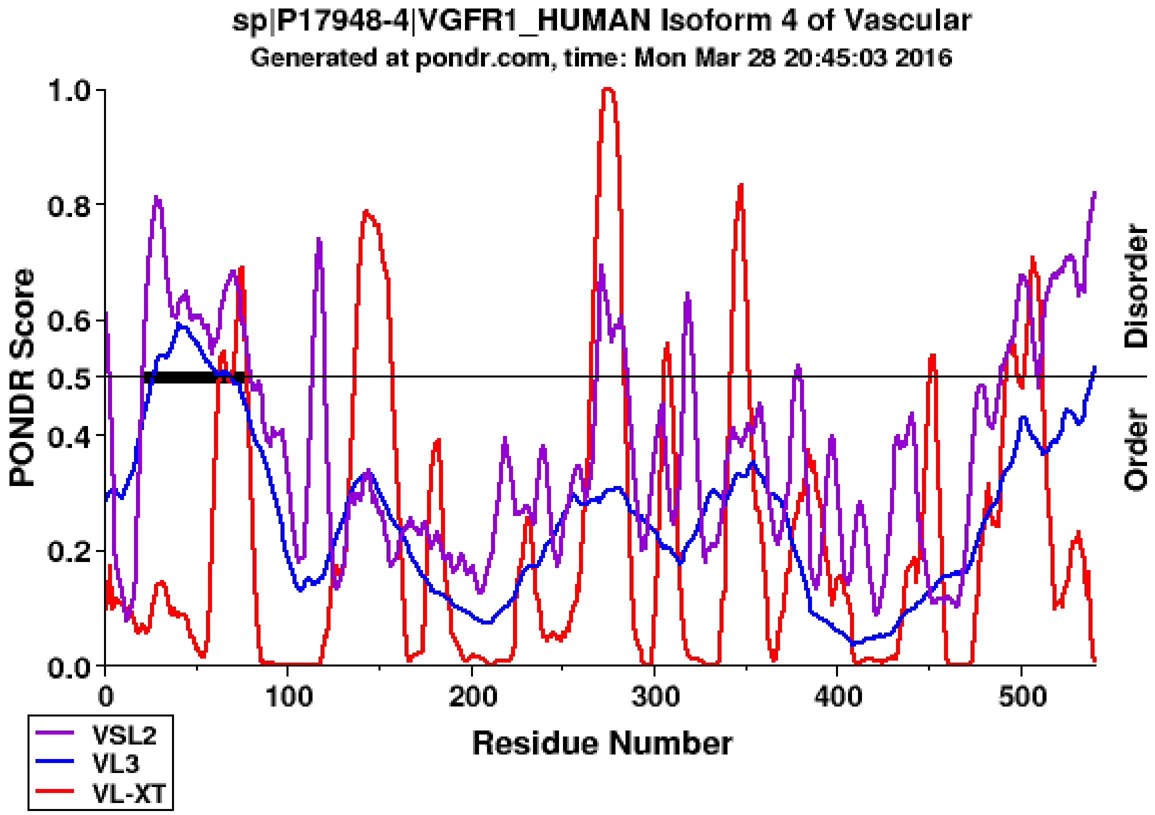
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0.5
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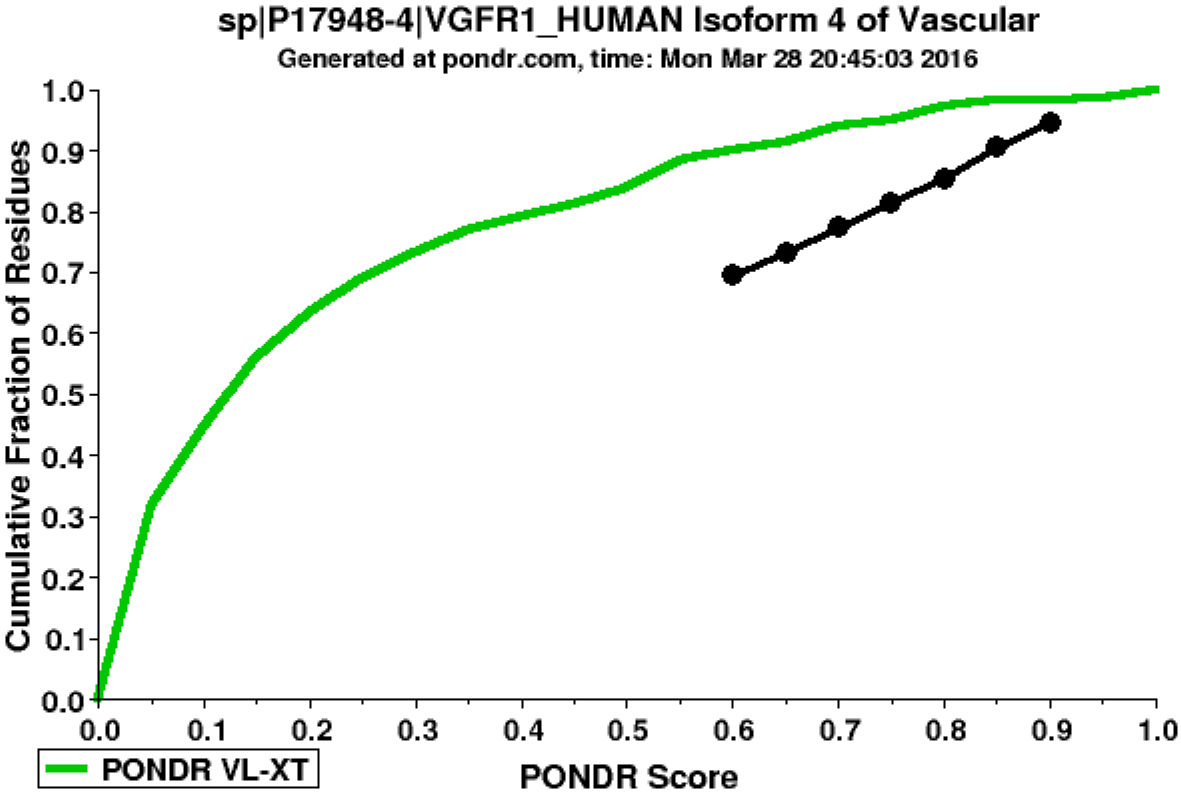
0
100
200
300
400
500
Residue Number
Disorder
Order
VSL2
VL3
VL-XT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Generated at pondr.com, time: Mon Mar 28 20:45:03 2016
Cumulative Fraction of Residues
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0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
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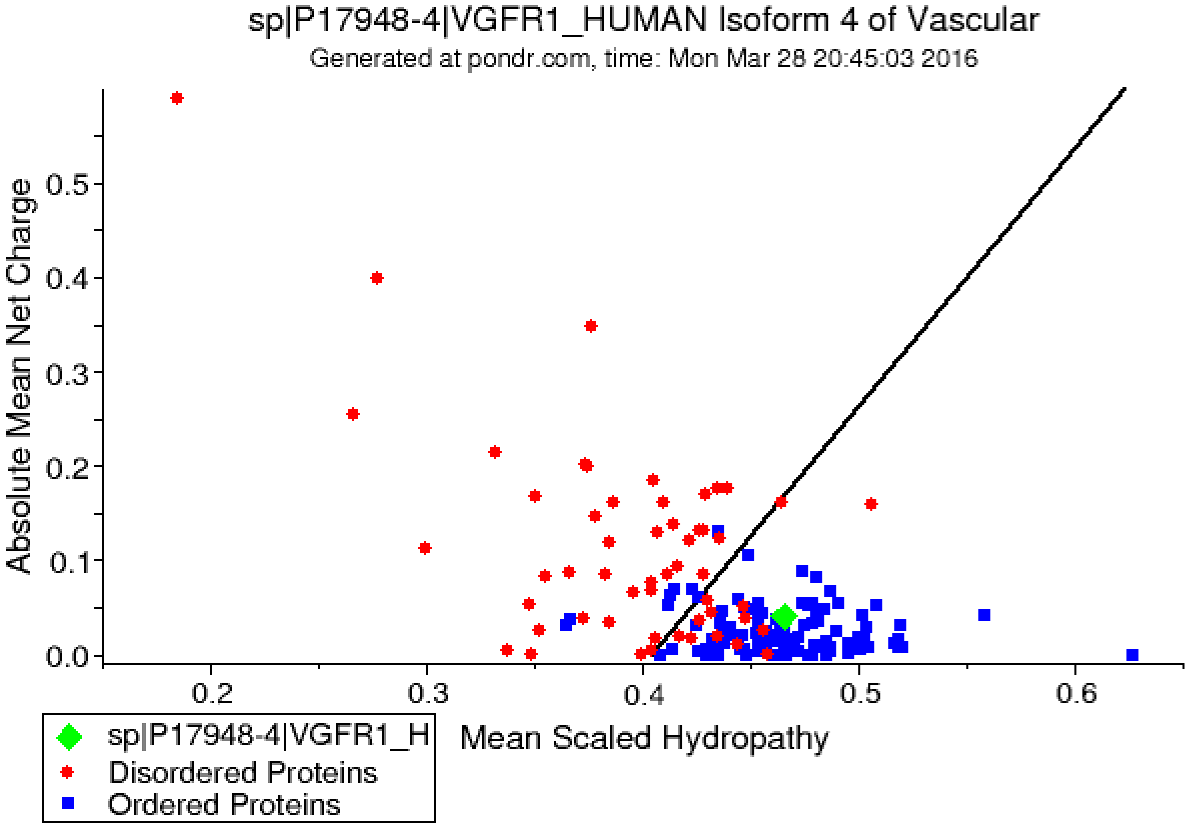
0.9
1.0
PONDR Score
PONDR VL-XT



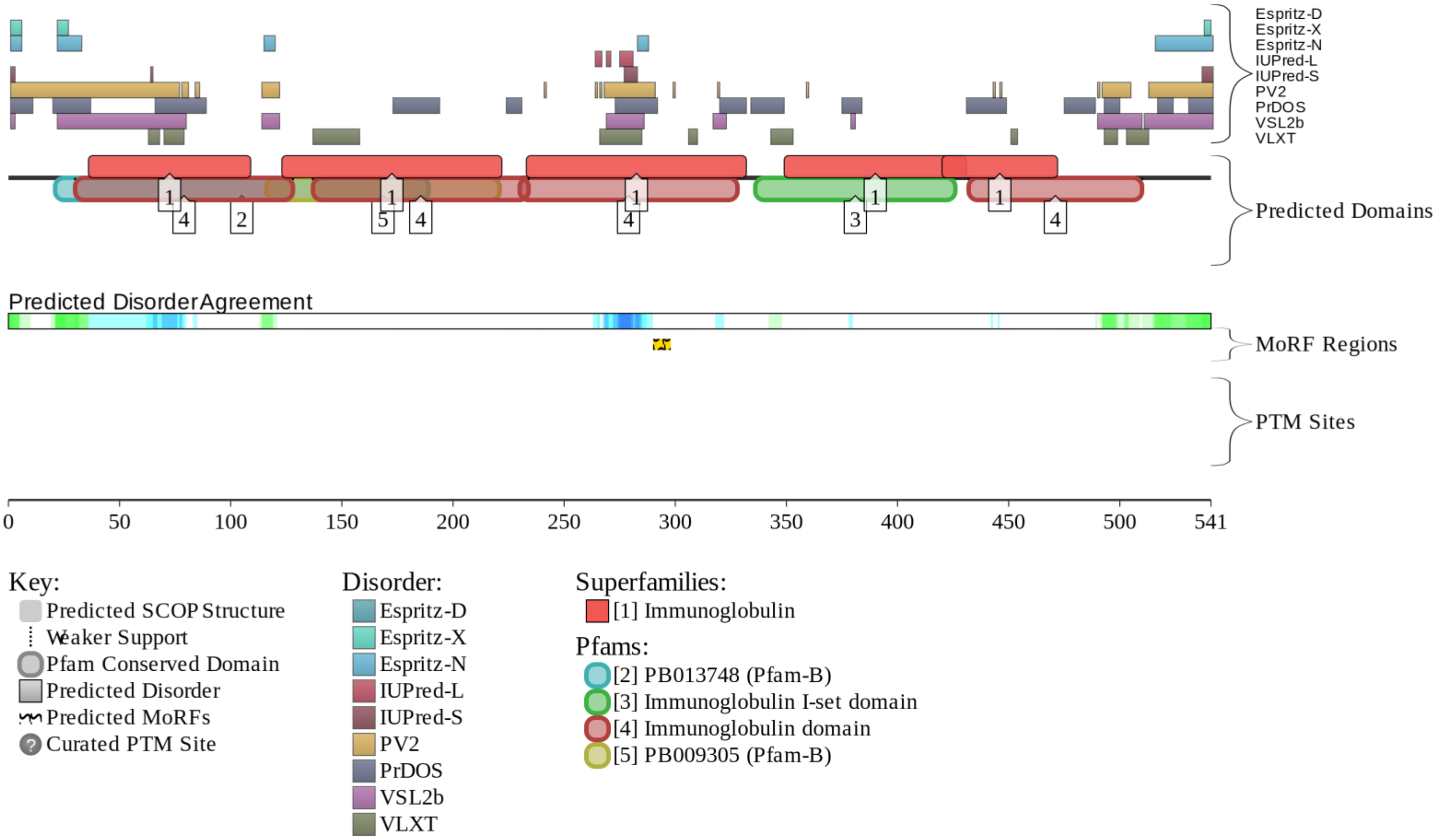
```
=======================VLXT NNP STATISTICS=================================
Predicted residues: 541                        Number Disordered Regions: 9
Number residues disordered: 87         Longest Disordered Region: 21
Overall percent disordered: 16.08      Average Prediction Score: 0.2154
Predicted 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
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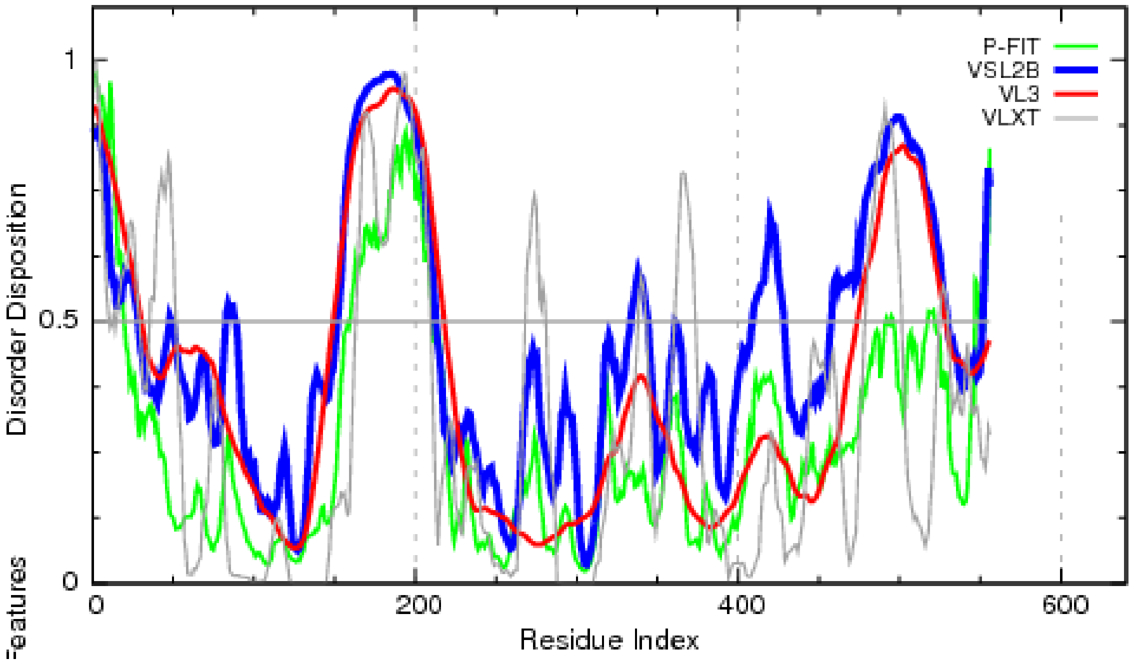
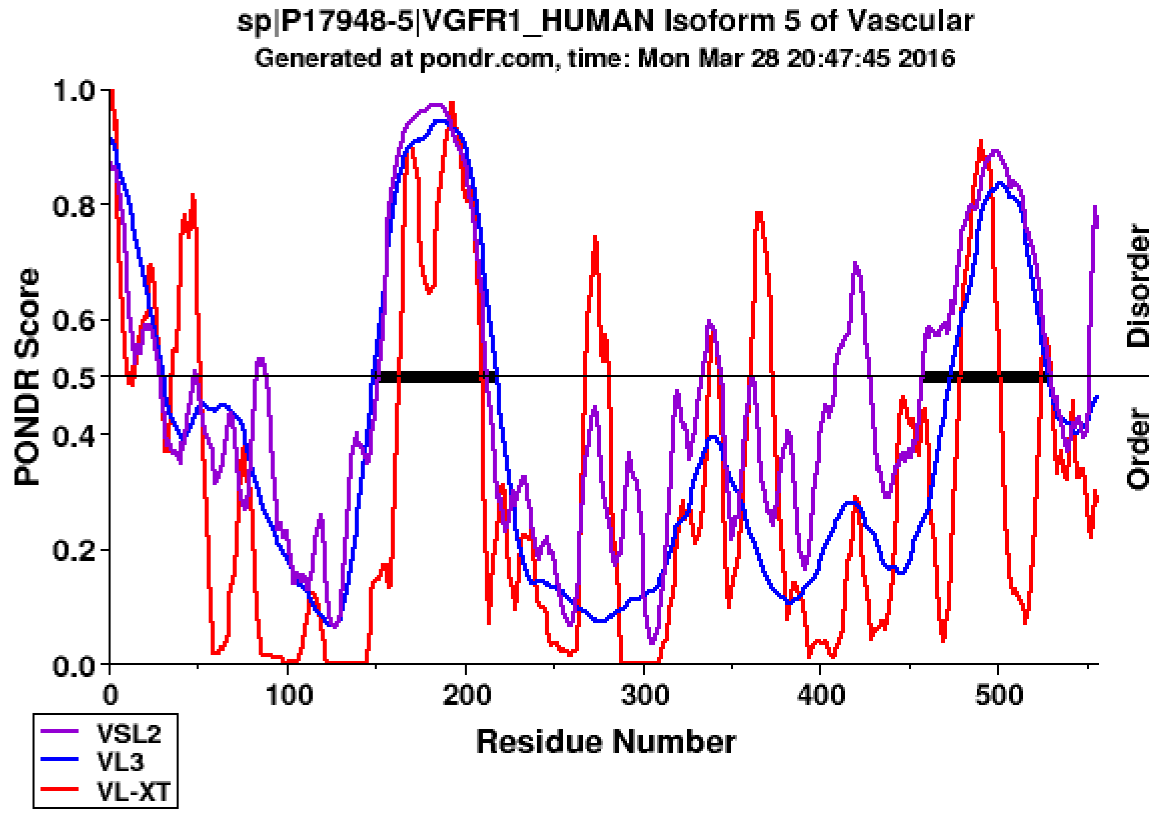
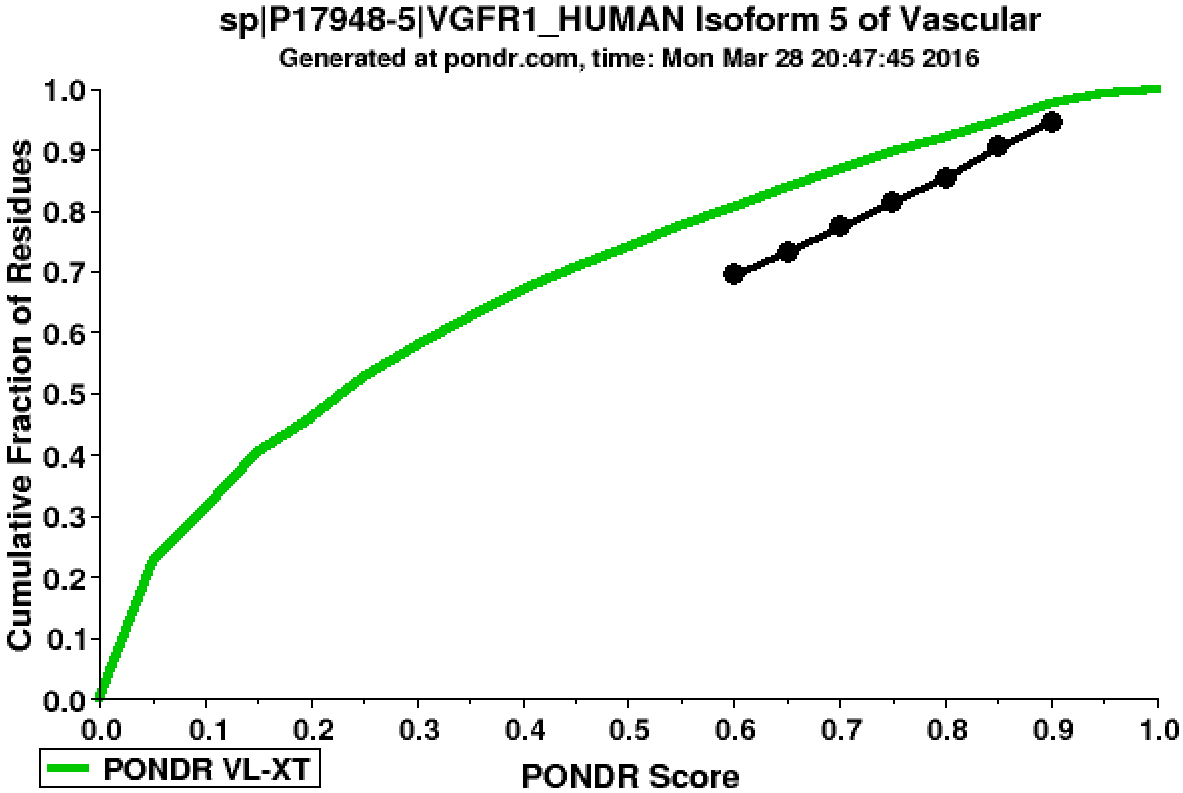
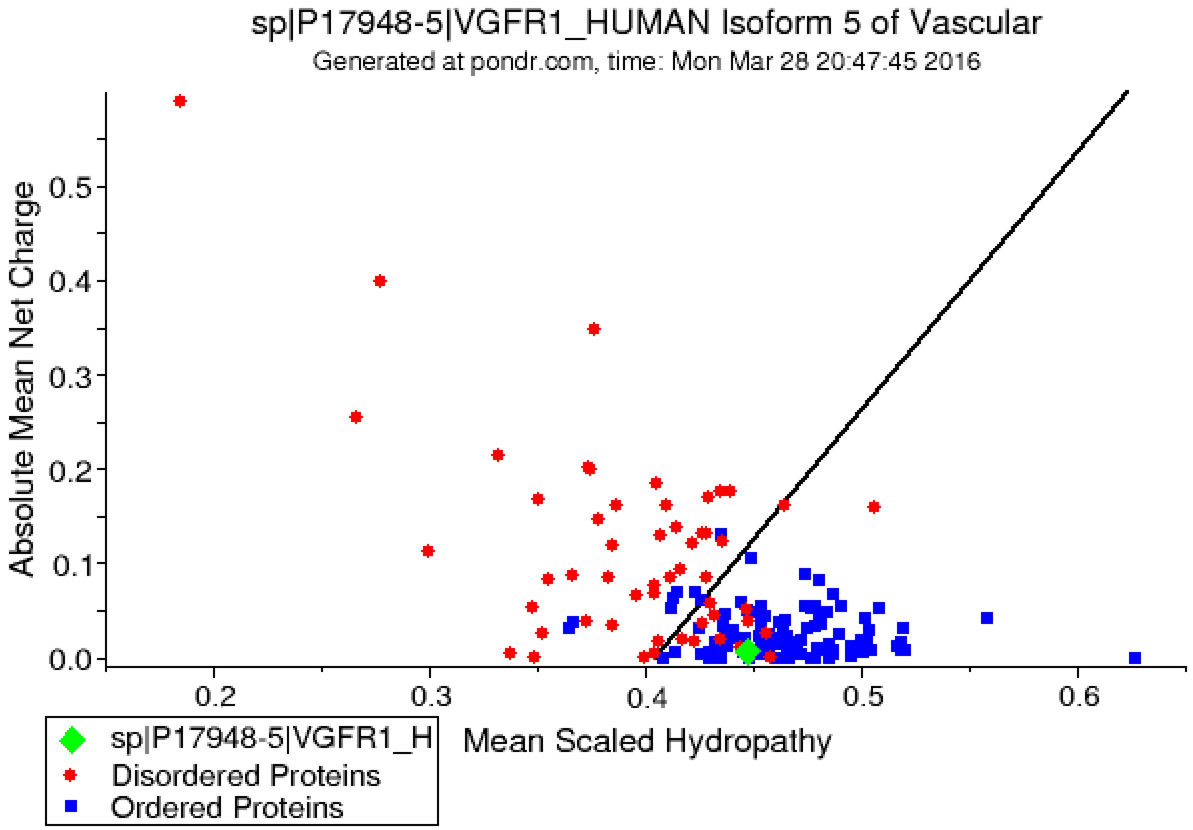



sp|P17948-5|VGFR1_HUMAN Isoform 5 of Vascular
Generated at pondr.com, time: Mon Mar 28 20:47:45 2016
PONDR Score
1.0
0.8
0.6
0.5
0.4
0.2
0.0
0
100
200
300
400
500
Residue Number
Disorder
Order
VSL2
VL3
VL-XT


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



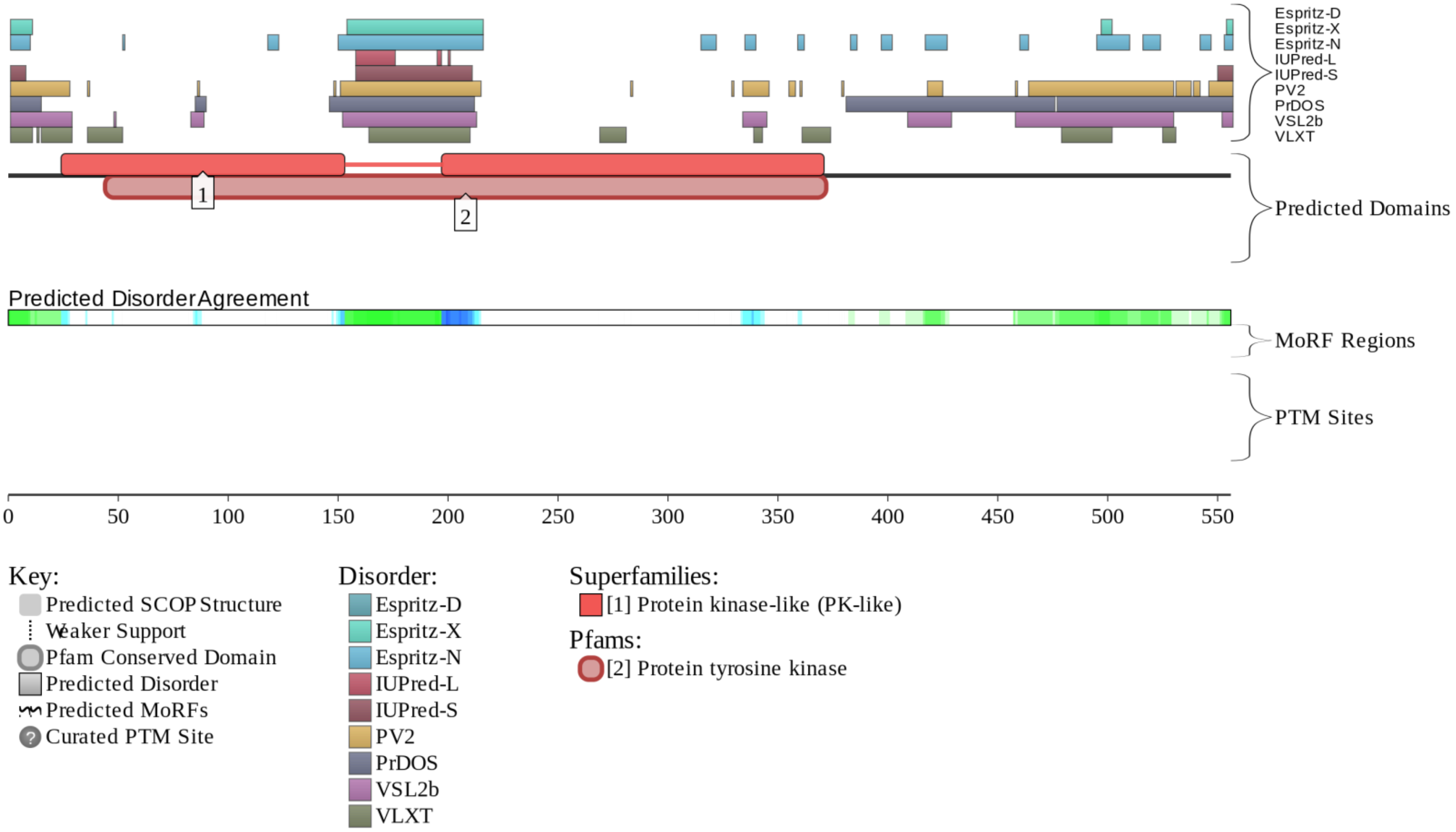
```
========================VLXT NNP STATISTICS================================
Predicted residues: 556                        Number Disordered Regions: 10
Number residues disordered: 145                Longest Disordered Region: 46
Overall percent disordered: 26.08      Average Prediction Score: 0.3103
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

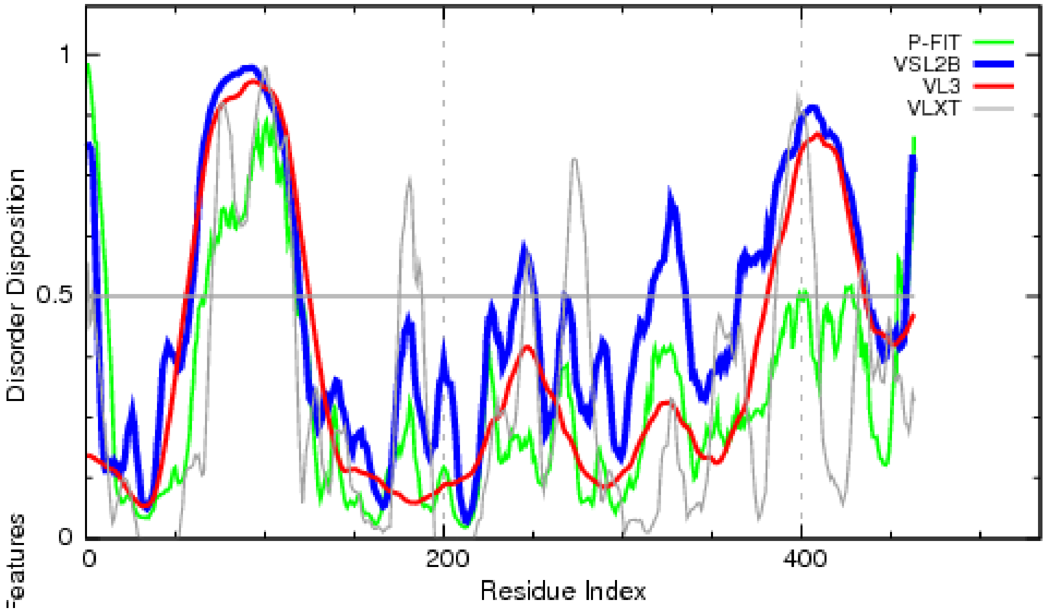
=======================VSL2 NNP STATISTICS================================
Predicted residues: 556                        Number Disordered Regions: 8
Number residues disordered: 204                Longest Disordered Region: 72
Overall percent disordered: 36.69      Average Prediction Score: 0.4615
Predicted 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
```

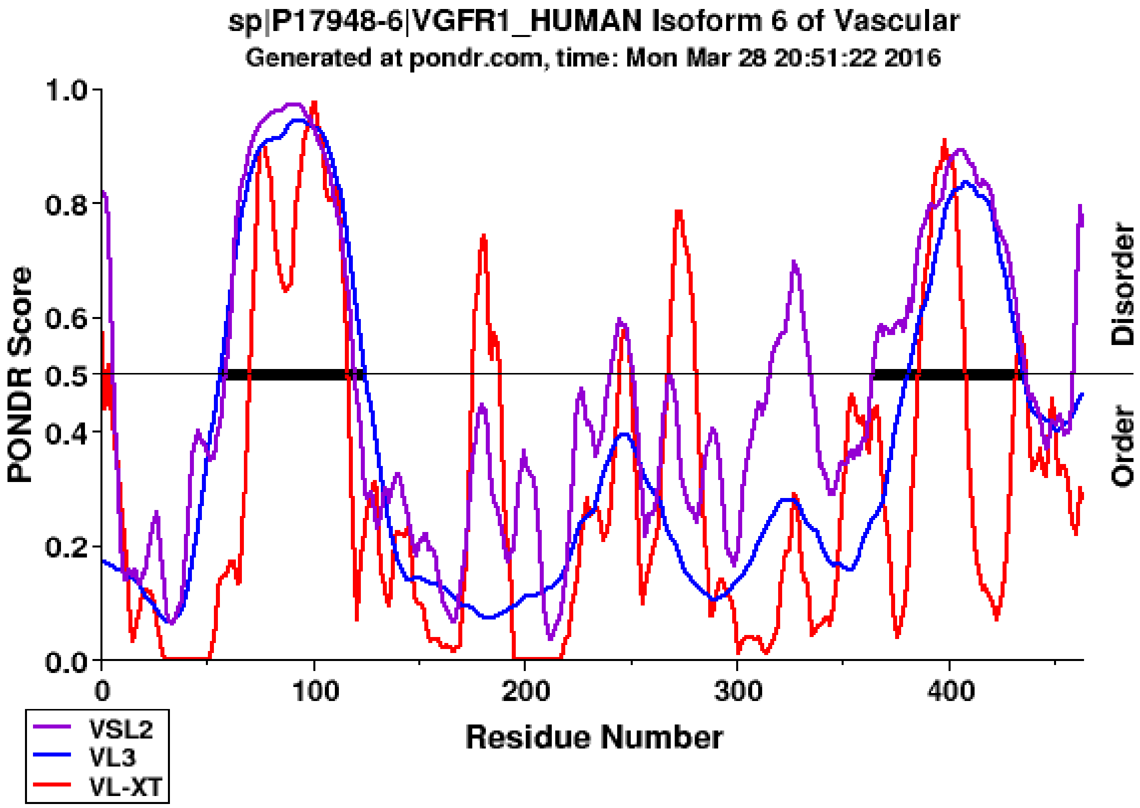
```
Predicted disorder segment [334]-[344]Average Strength= 0.5531
Predicted disorder segment [409]-[428]Average Strength= 0.5929
Predicted disorder segment [458]-[529]Average Strength= 0.7271
Predicted disorder segment [552]-[556]Average Strength= 0.6908
```

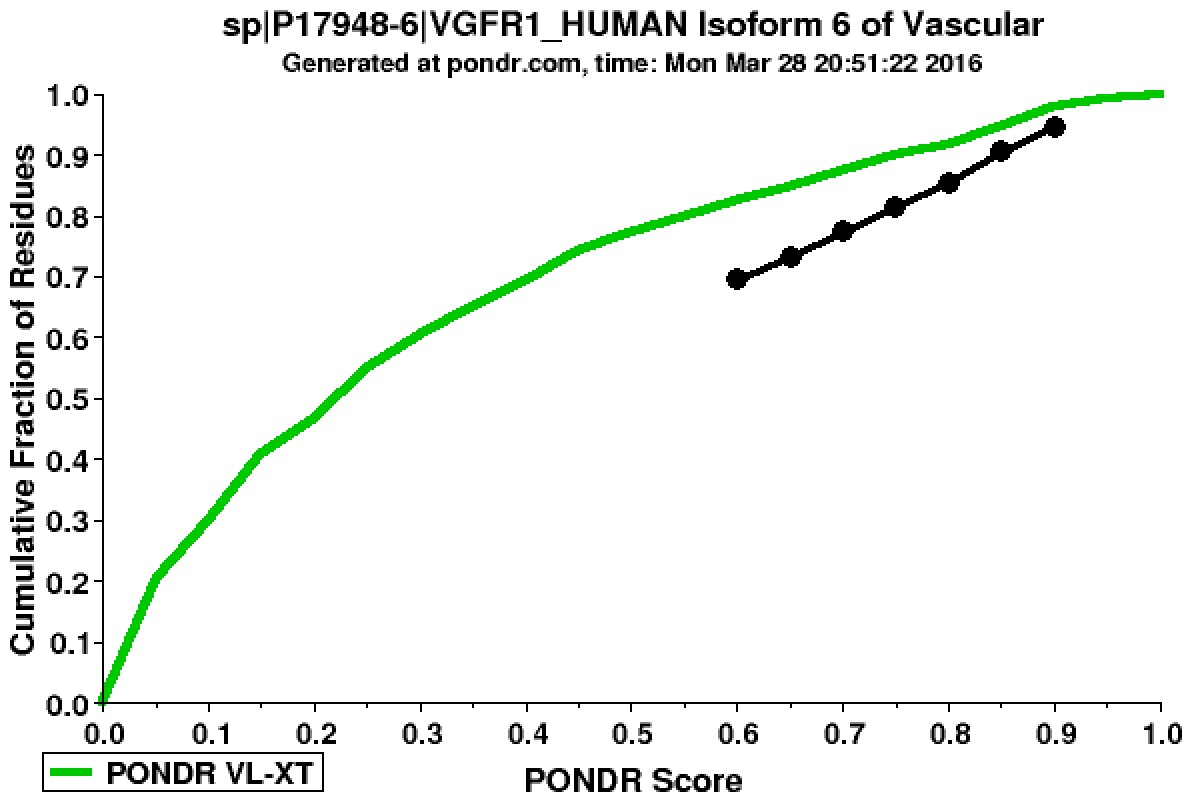
ENSP00000443311

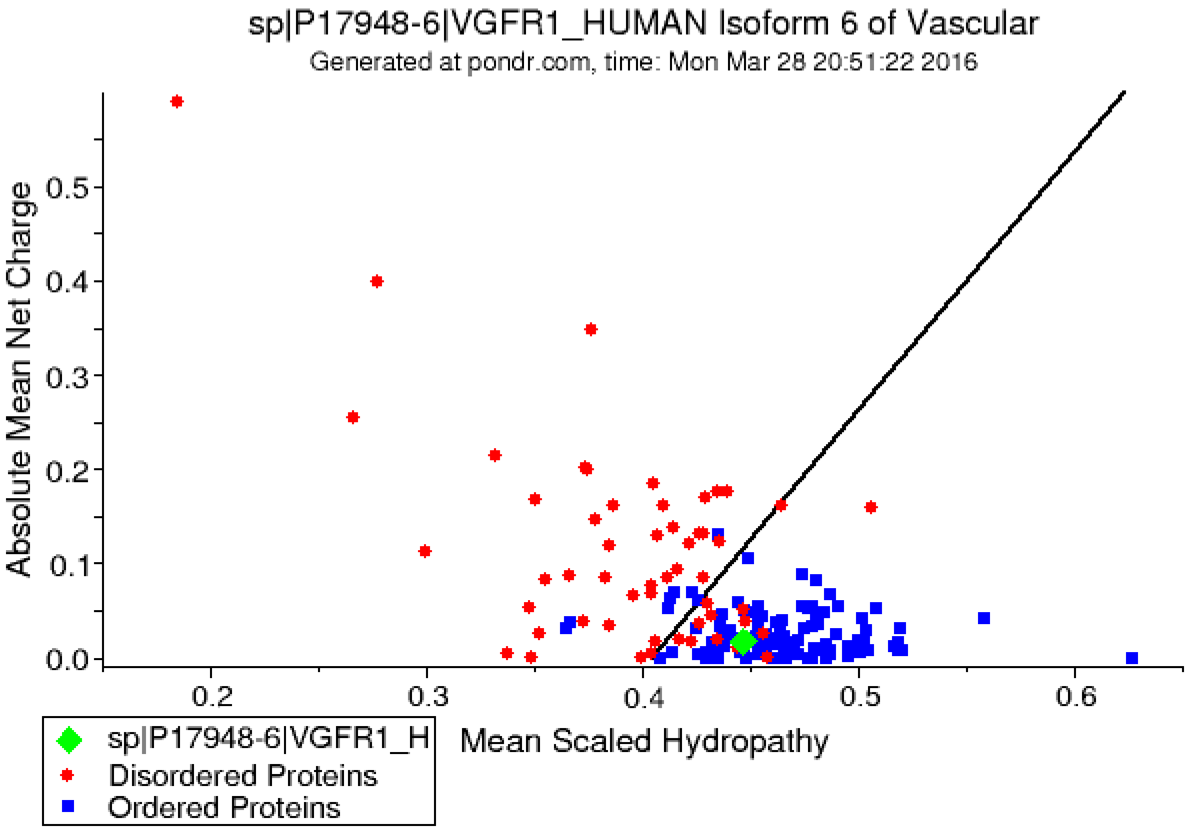


```
>sp|P17948-6|VGFR1_HUMAN Isoform 6 of Vascular endothelial growth factor
receptor 1 OS=Homo sapiens GN=FLT1
MTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAA
LHMEPKKEKMEPGLEQGKKPRLDSVTSSESFASSGFQEDKSLSDVEEEEDSDGFYKEPIT
MEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVR
KGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLRE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









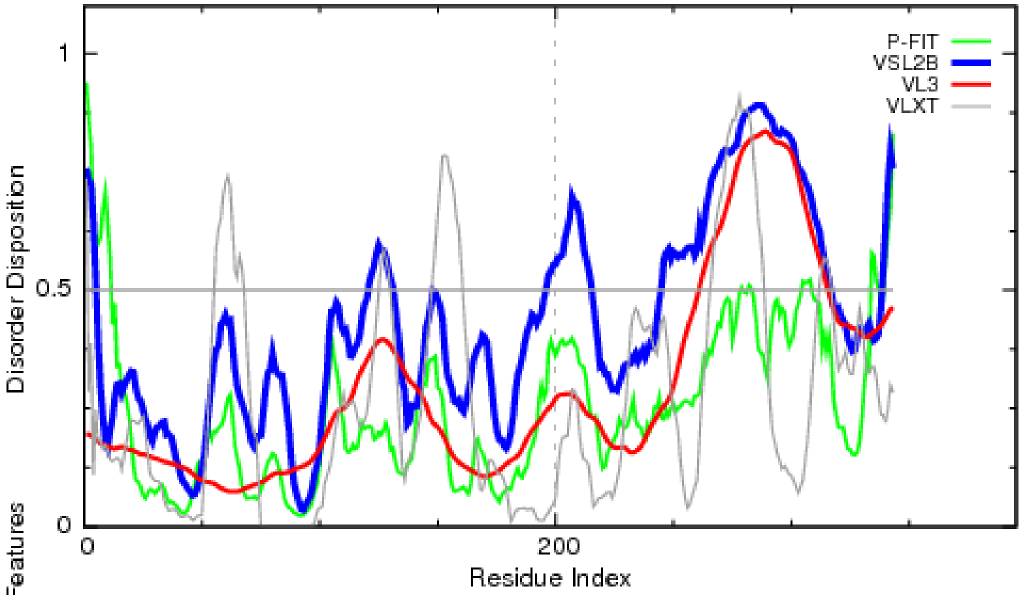
```
======================VLXT NNP STATISTICS================================
Predicted residues: 463                      Number Disordered Regions: 7
Number residues disordered: 106              Longest Disordered Region: 46
Overall percent disordered: 22.89      Average Prediction Score: 0.3001
```

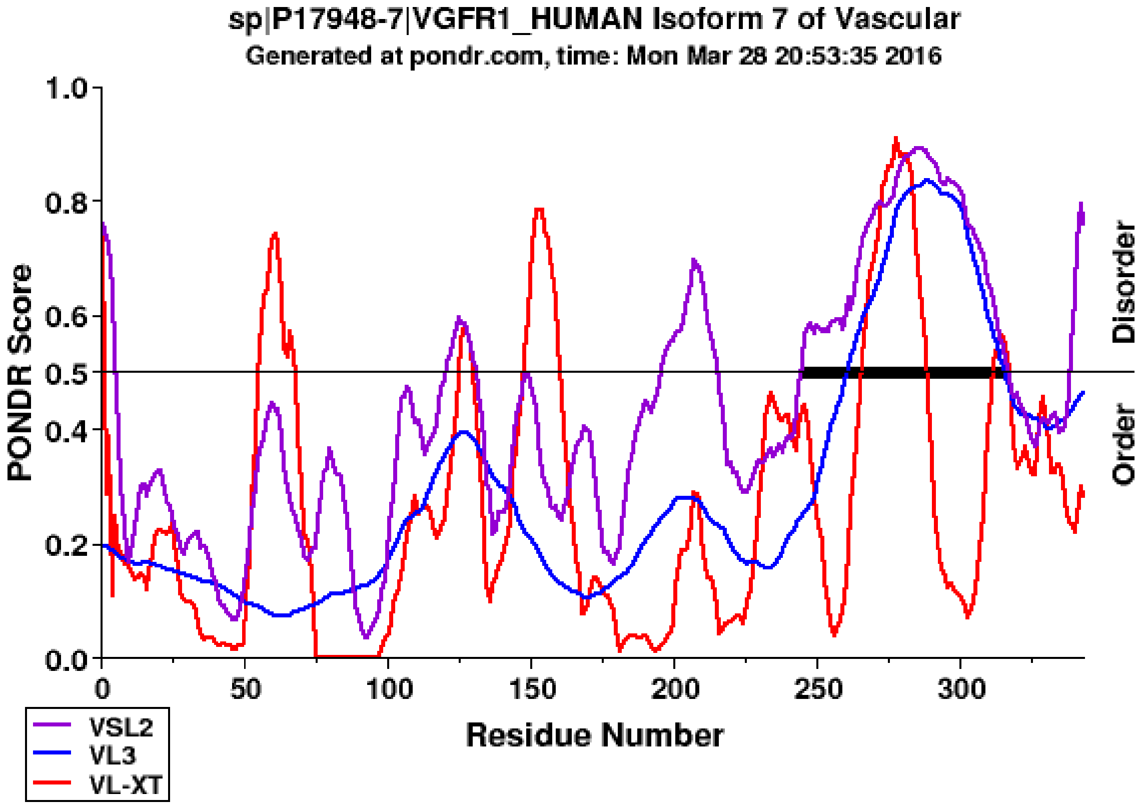
```
Predicted disorder segment [4]-[4]    Average Strength= 0.5163
Predicted disorder segment [71]-[116] Average Strength= 0.7961
Predicted disorder segment [176]-[187]Average Strength= 0.6313
Predicted disorder segment [246]-[249]Average Strength= 0.5638
Predicted disorder segment [268]-[280]Average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

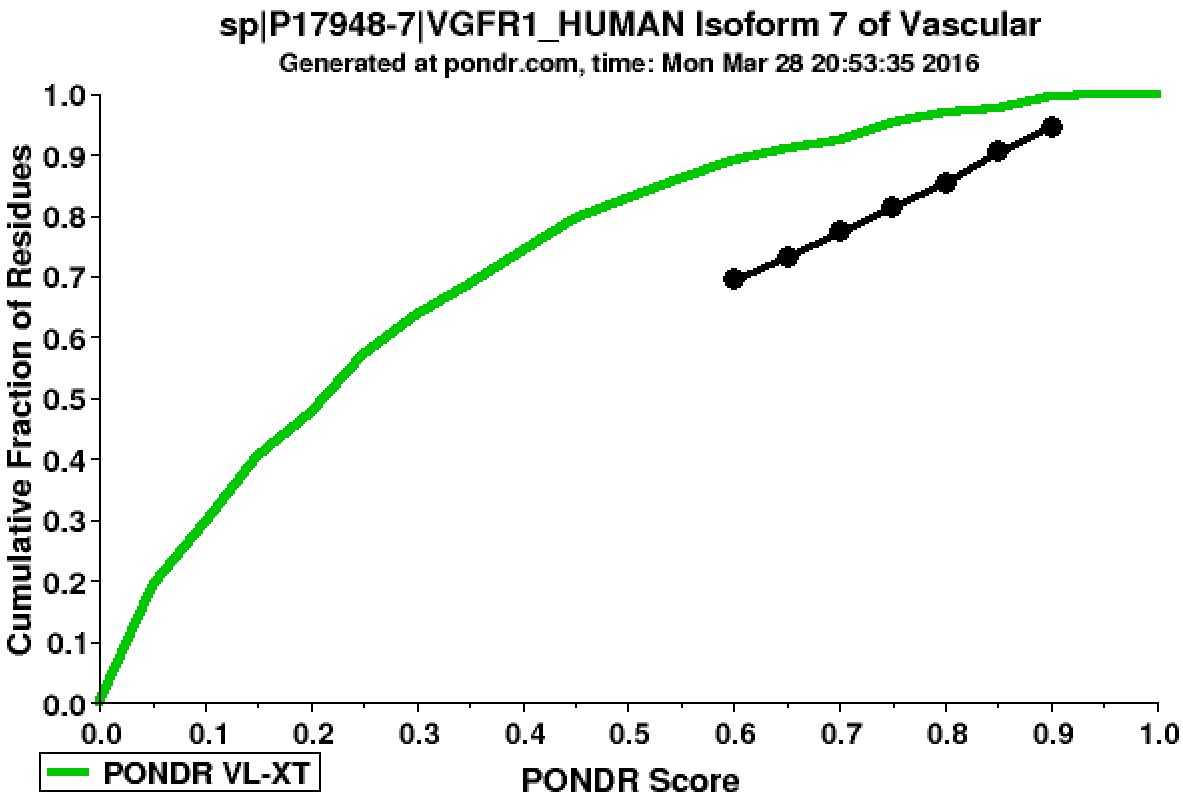
=======================VL3 NNP STATISTICS===============================
Predicted residues: 463                      Number Disordered Regions: 2
Number residues disordered: 123              Longest Disordered Region: 68
Overall percent disordered: 26.57     Average Prediction Score: 0.3651
Predicted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

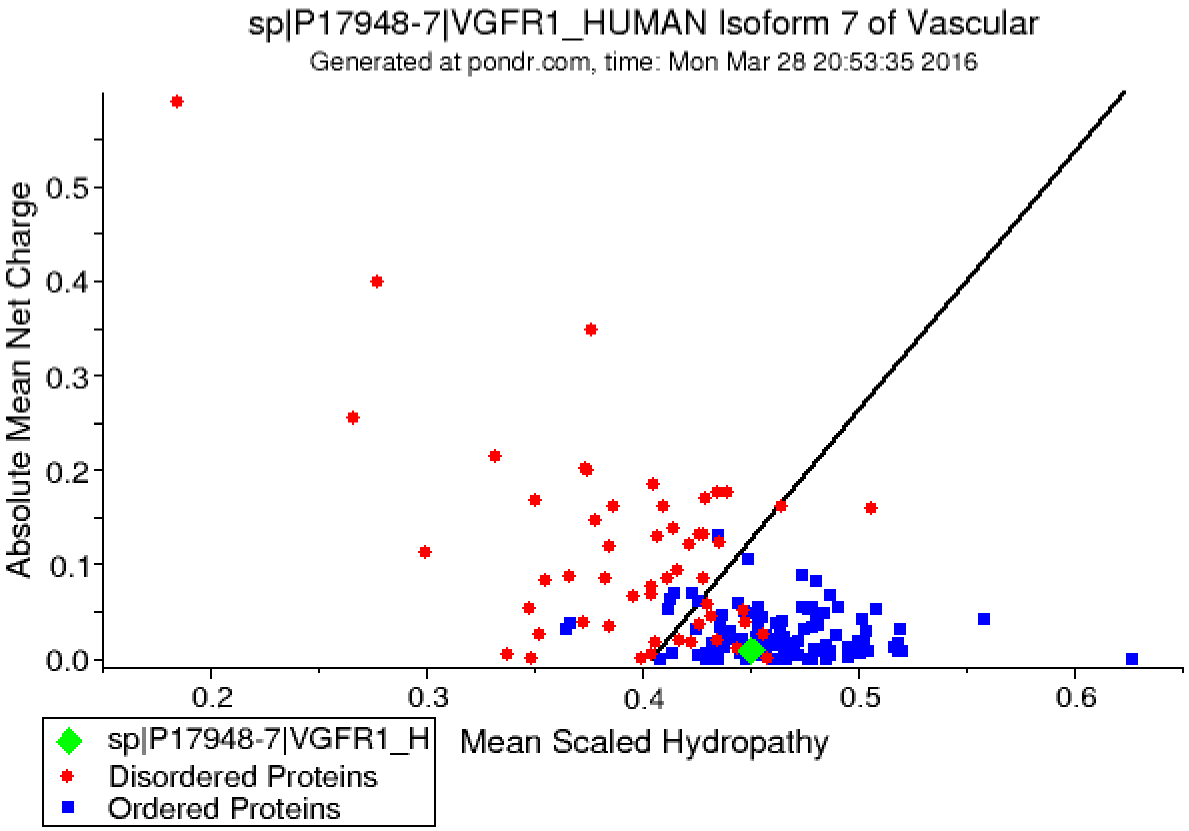
======================VSL2 NNP STATISTICS===============================
Predicted residues: 463                      Number Disordered Regions: 6
Number residues disordered: 175              Longest Disordered Region: 72
Overall percent disordered: 37.80     Average Prediction Score: 0.4656
Predicted 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
SCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI









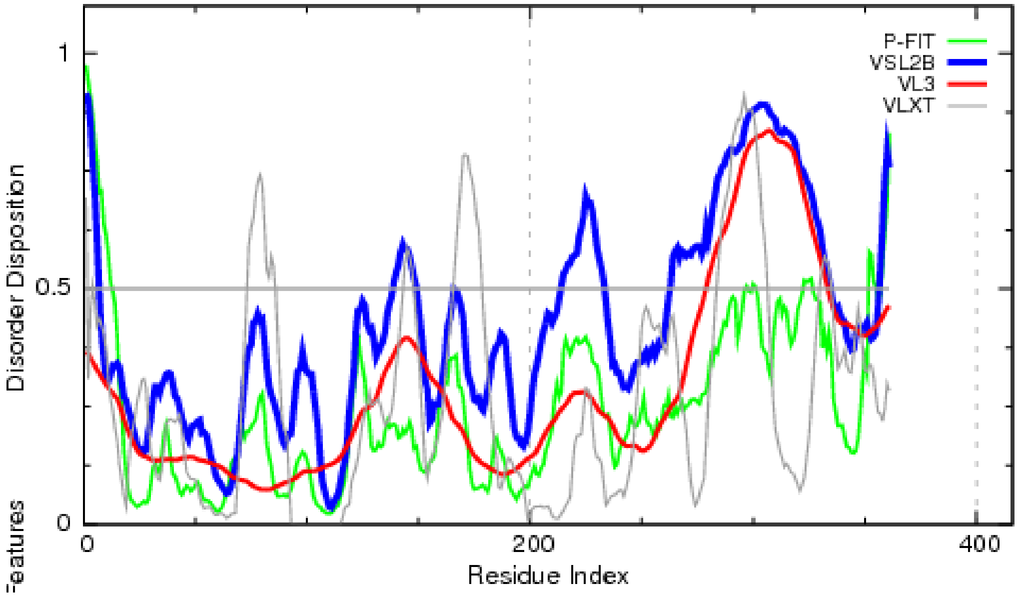
```
======================VLXT NNP STATISTICS===============================
Predicted residues: 343                      Number Disordered Regions: 5
Number residues disordered: 59         Longest Disordered Region: 23
```

```
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

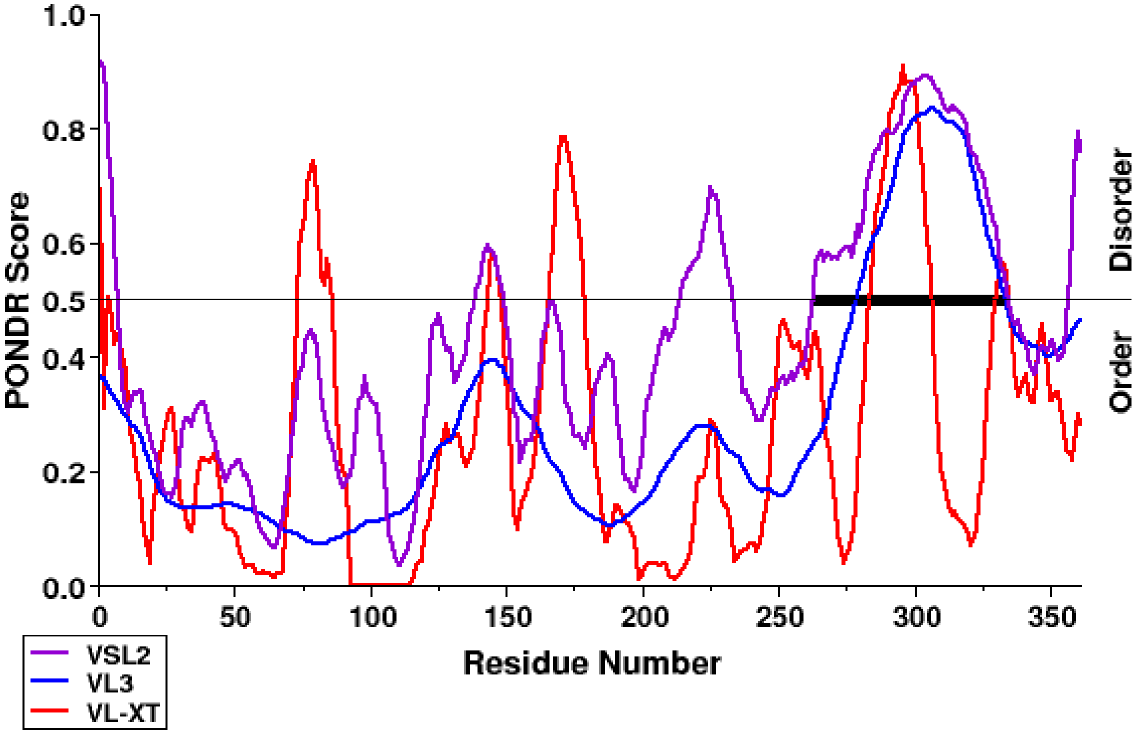
=======================VSL2 NNP STATISTICS===============================
Predicted residues: 343                       Number Disordered Regions: 5
Number residues disordered: 113               Longest Disordered Region: 72
Overall percent disordered: 32.94     Average Prediction Score: 0.4304
Predicted 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
```

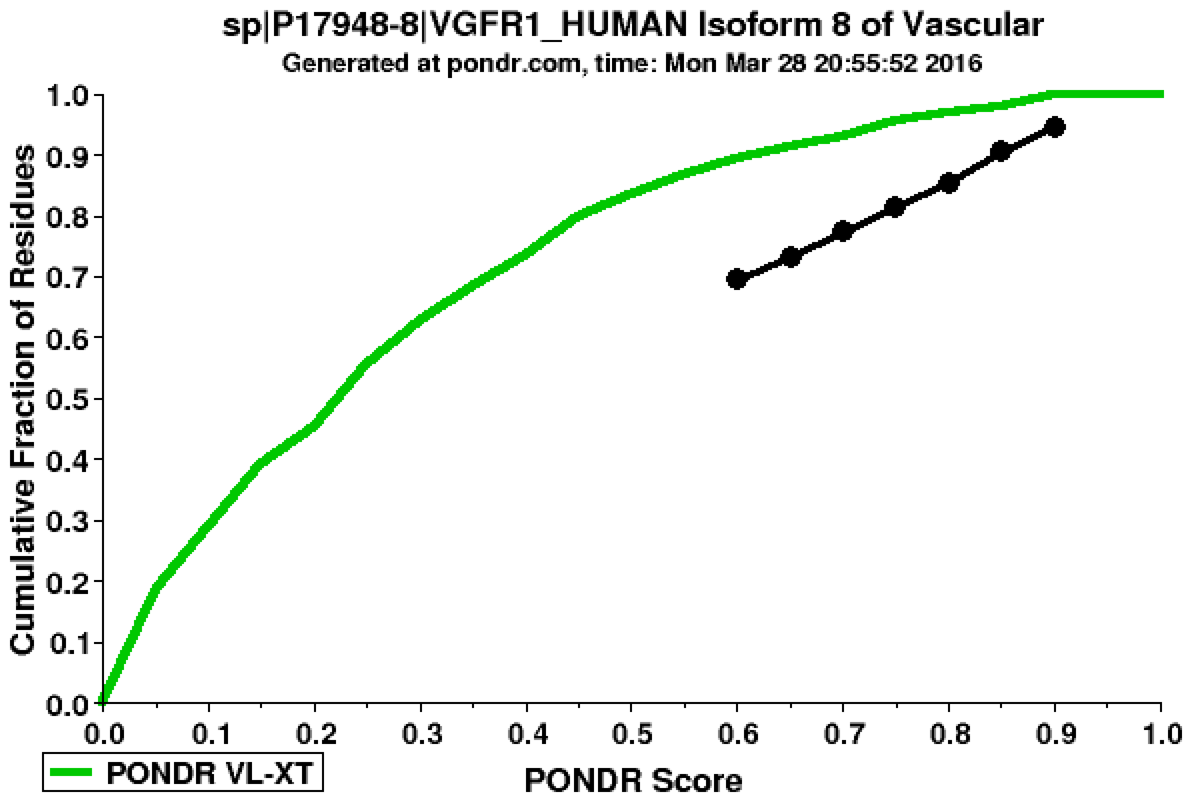
```
>sp|P17948-8|VGFR1_HUMAN Isoform 8 of Vascular endothelial growth factor
receptor 1 OS=Homo sapiens GN=FLT1
MNSDLLVDSDGFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVK
ICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGG
SPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDL
LQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFNSGSSDDVRYVNAF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

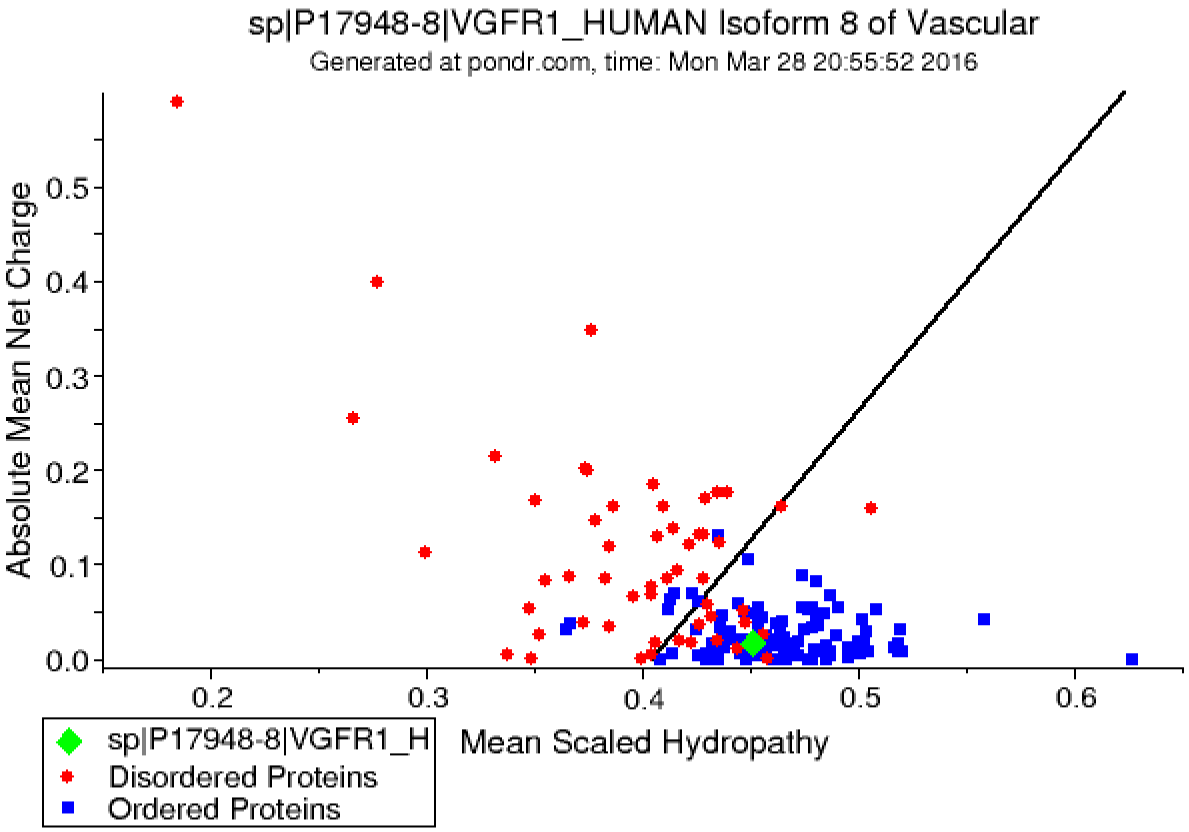


sp|P17948-8|VGFR1_HUMAN Isoform 8 of Vascular

Generated at pondr.com, time: Mon Mar 28 20:55:52 2016







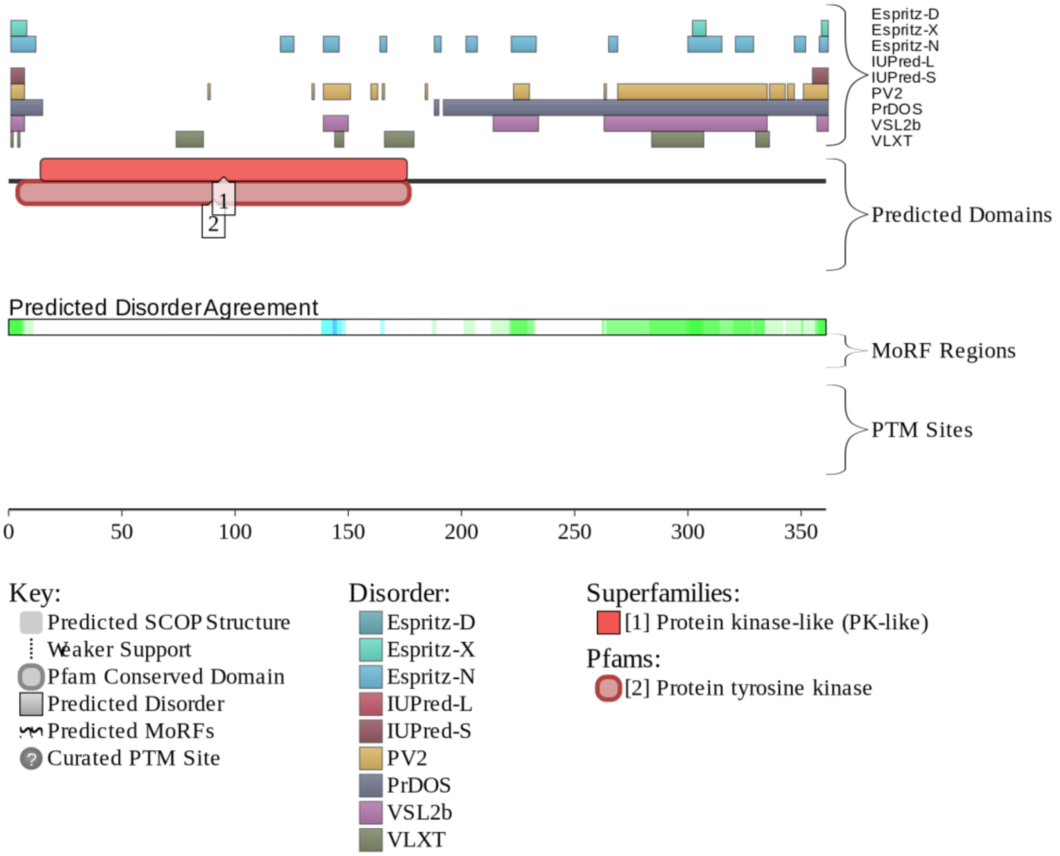
```
=======================VLXT NNP STATISTICS===============================
Predicted residues: 361                       Number Disordered Regions: 6
Number residues disordered: 60         Longest Disordered Region: 23
```

```
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
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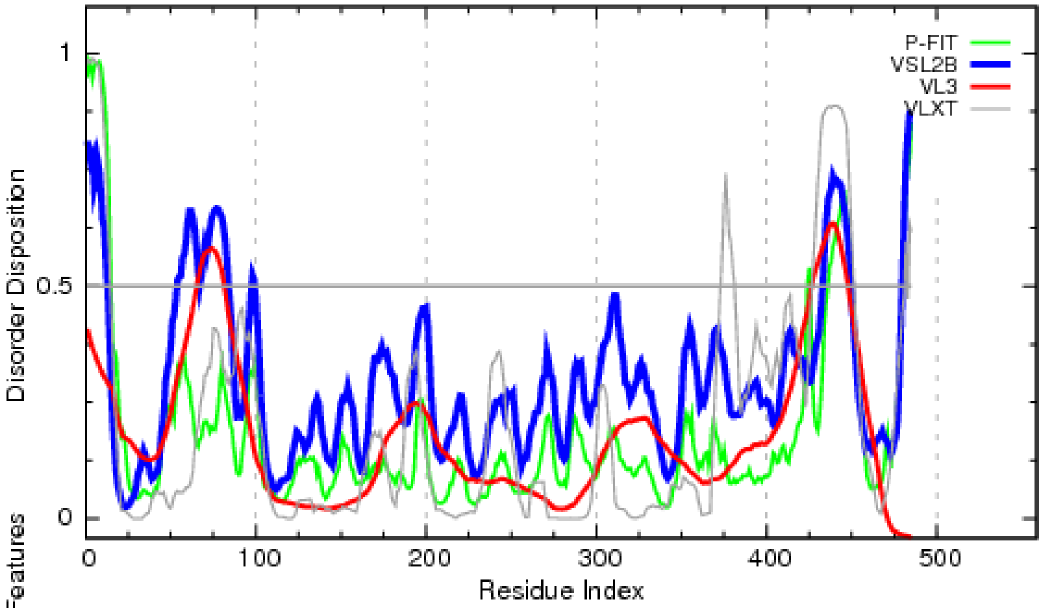

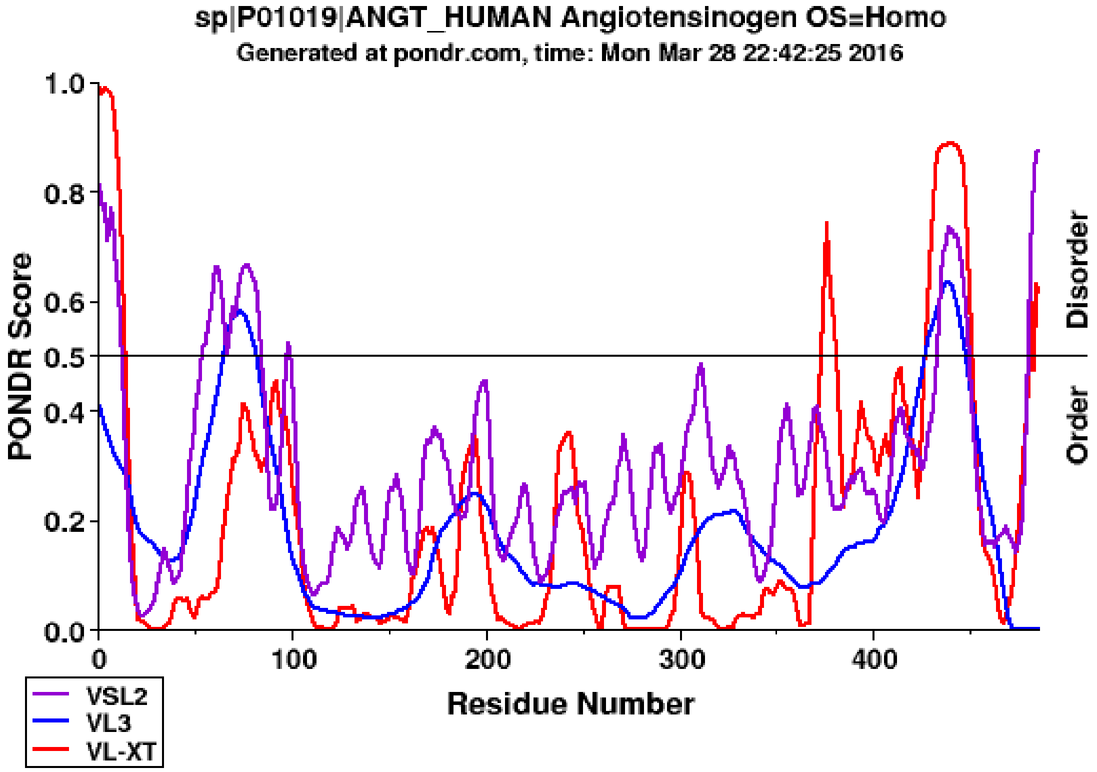
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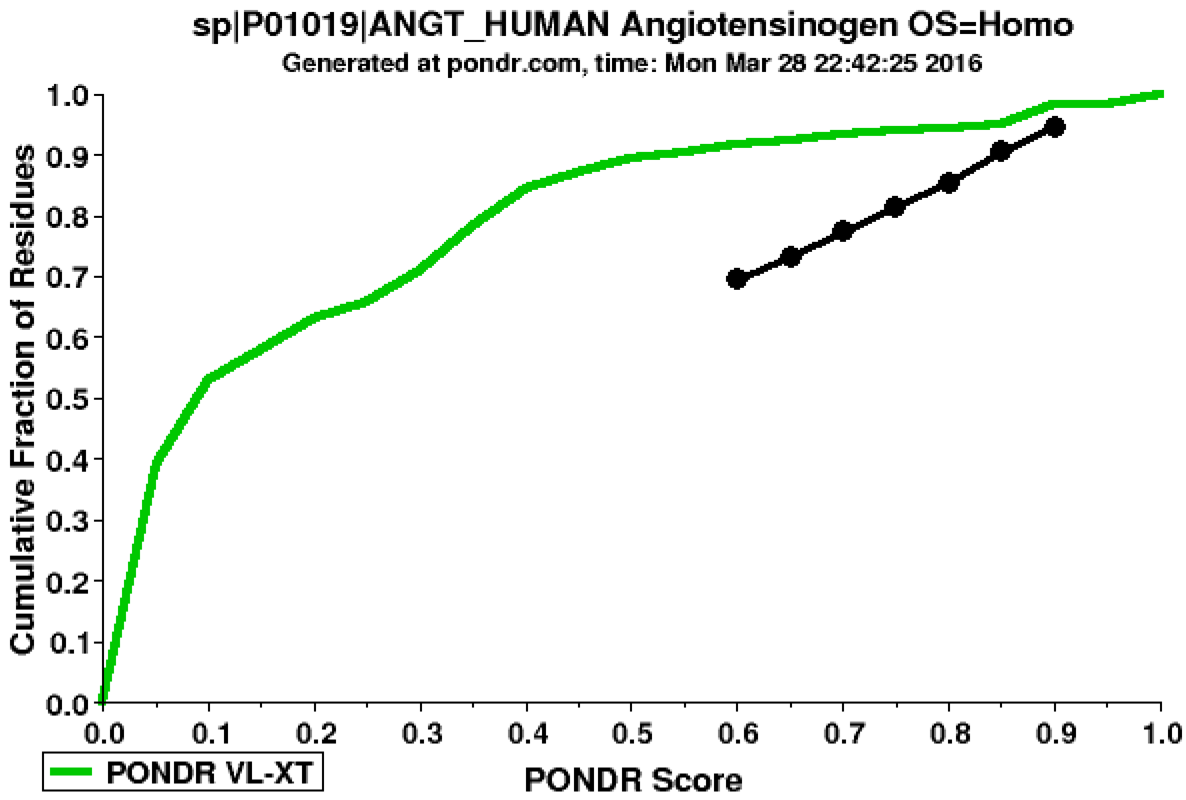

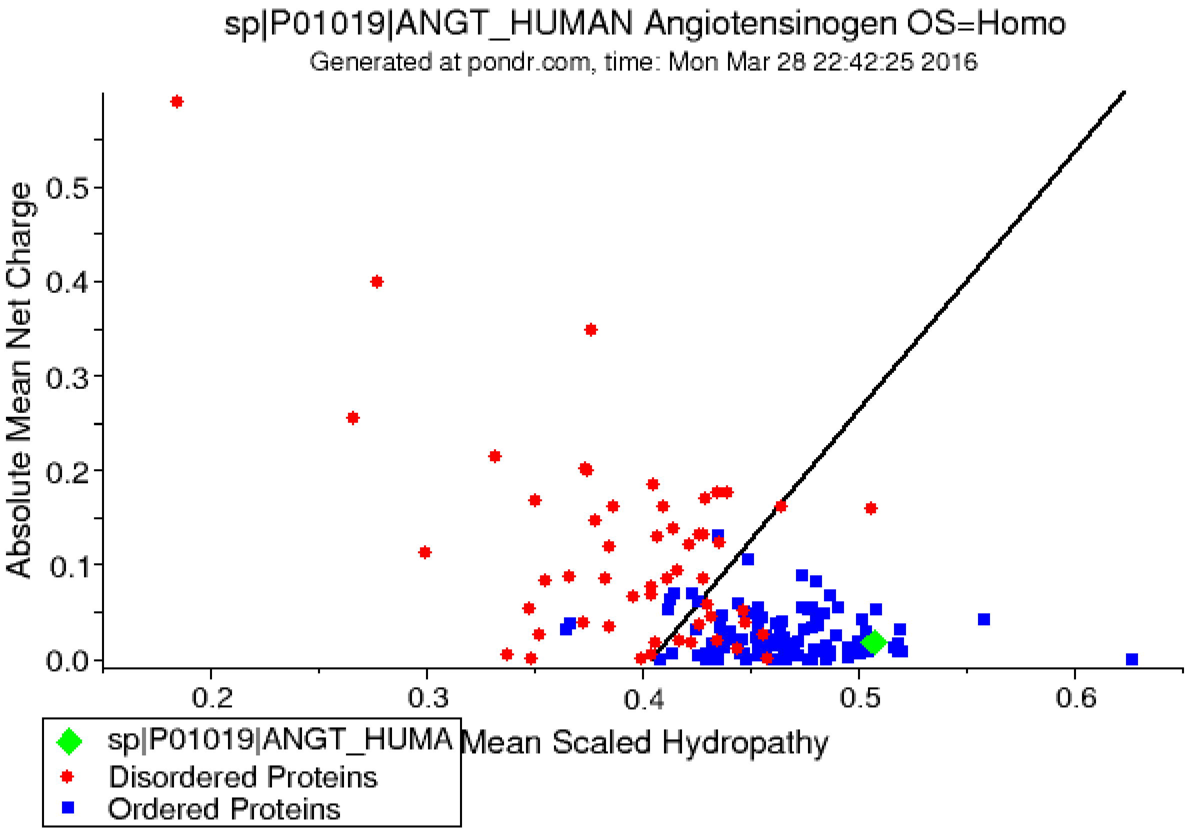

```
======================VLXT NNP STATISTICS===============================
Predicted residues: 485                        Number Disordered Regions: 5
Number residues disordered: 51          Longest Disordered Region: 25
```

```
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
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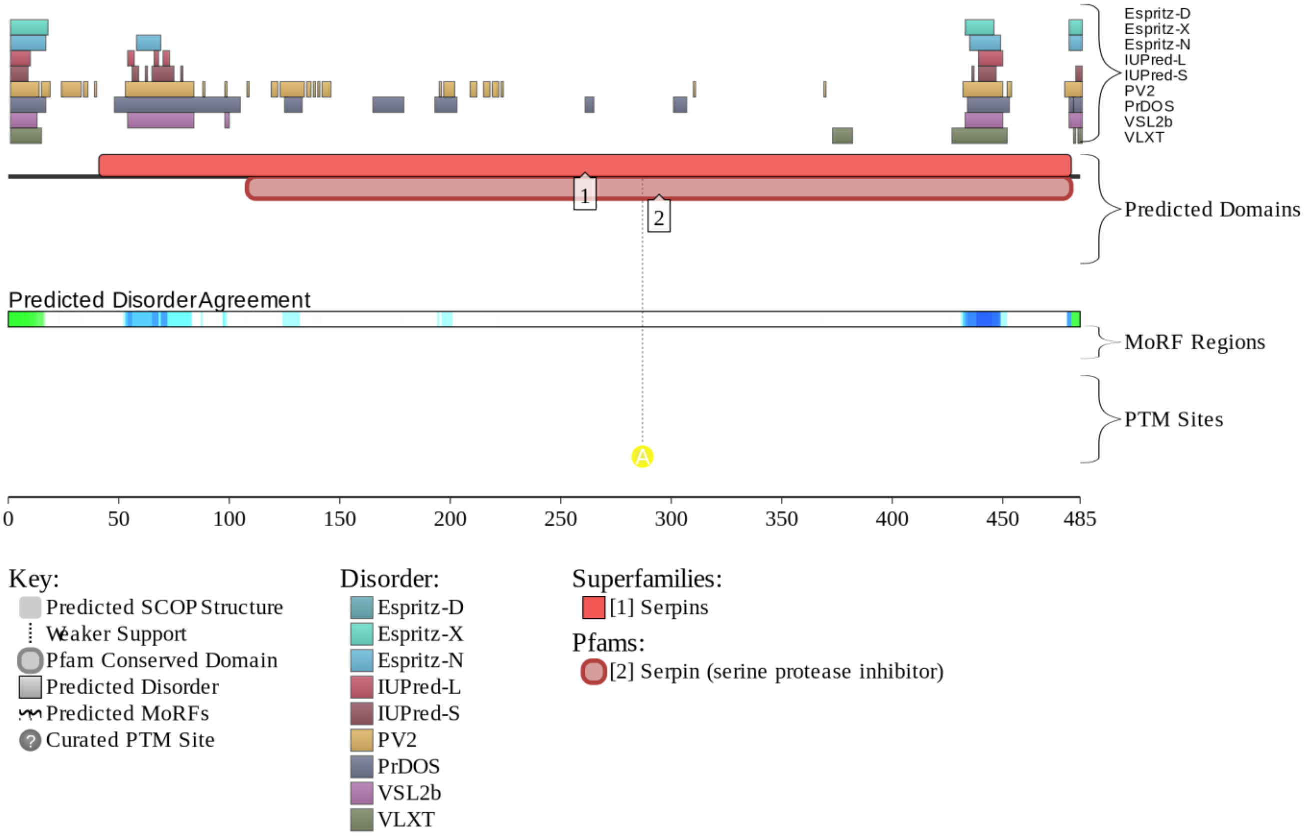
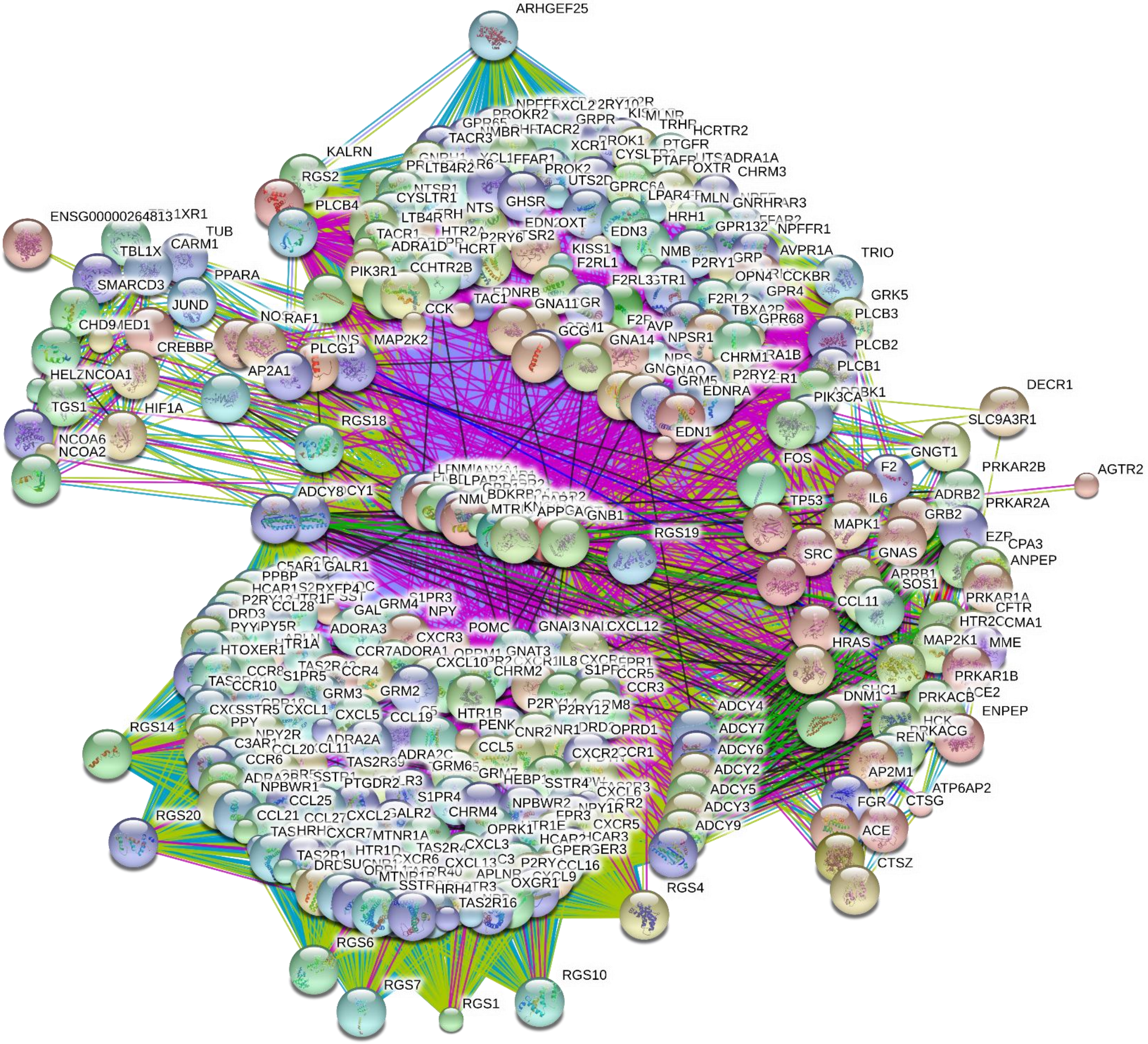
ENSP00000355627

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GPR65
NMBR
TACR2
GRPR
TRHR
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TACR3
XCR1
PROK1
PTGFR
KALRN
LTB4R2
FFAR1
PROK2
CYSLTR2
PTAFR
ADRA1A
OXTR
CHRM3
RGS2
UTS2D
GPRC6A
LPAR4
MLN
GNRHR
NTSR1
CYSLTR1
PLCB4
NTS
GHSR
LTB4R
TRH
HTR2A
EDN2
OXT
HRH1
NPFFR1
GPR132
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ADRA1D
HCRT
SR2
EDN3
KISS1
NMB
P2RY1
GRP
AVPR1A
TRIO
F2RL1
PPARA
SMARCD3
JUND
PIK3R1
HTR2B
OPN4
CCKBR
GPR4
GRK5
CCK
TAC1
EDNRB
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GR
F2RL3
F2RL2
TBXA2R
GPR68
PLCB3
NO
RAF1
CHD9
MED1
F2R
AVP
NPSR1
CREBBP
MAP2K2
GCG
GNA14
PLCG1
CHRM1
PLCB2
INS
AP2A1
HELZ
NCOA1
GNAQ
GRM5
P2RY2
PLCB1
EDNRA
PIK3CA
DECR1
TGS1
HIF1A
EDN1
SLC9A3R1
NCOA6
RGS18
NCOA2
FOS
GNGT1
PRKAR2B
AGTR2
F2
ADRB2
PRKAR2A
ADCY8
ADCY1
TP53
IL6
LPAR2
NMU
BDKRB2
MTR
APP
GNB1
MAPK1
GRB2
RGS19
EZR
CPA3
SRC
GNAS
ANPEP
C5AR1
GALR1
PPBP
HCAR1
ARRB1
SOS1
P2RY13
HTR1F
SST
S1PR3
CCL11
PRKAR1A
CFTR
DRD3
CCL28
GAL
GRM4
NPY
HTR2C
CMA1
PYY
NPY5R
ADORA3
CXCR3
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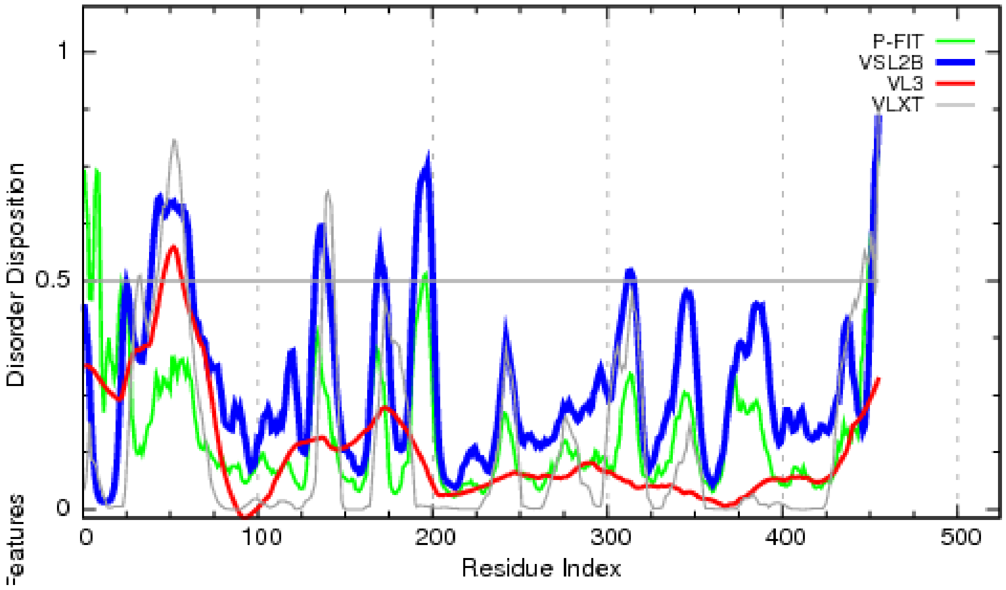
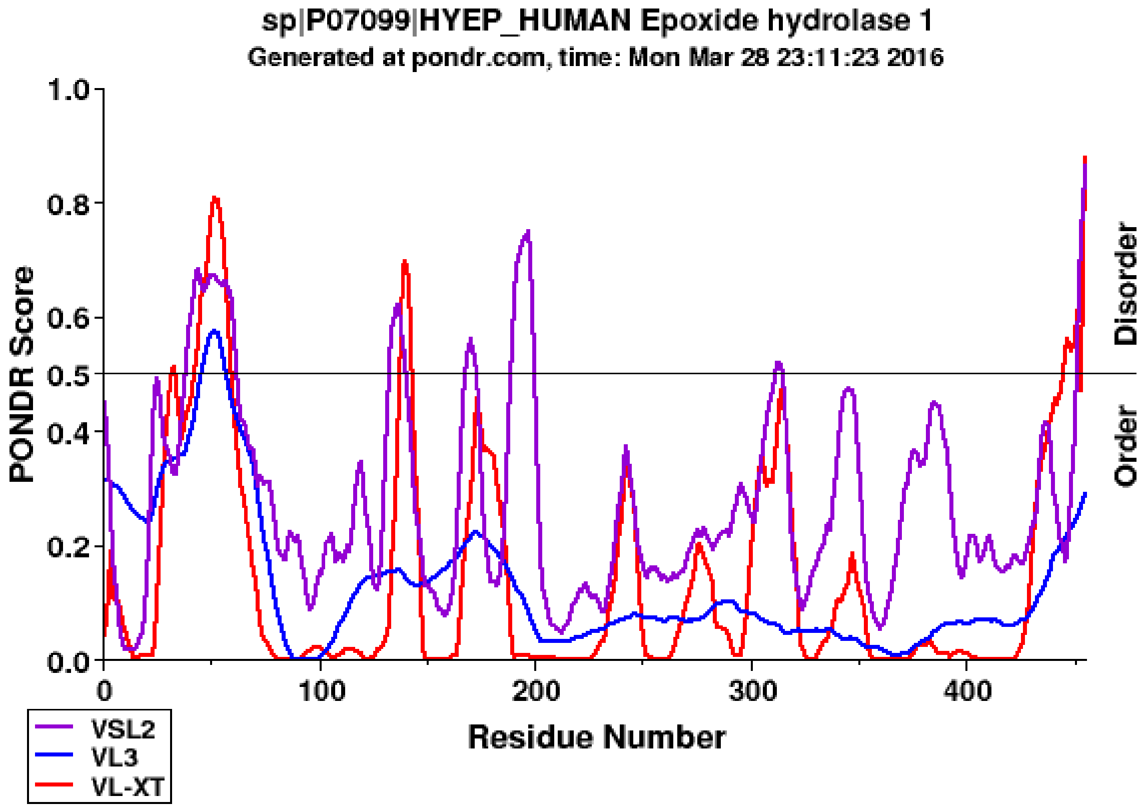
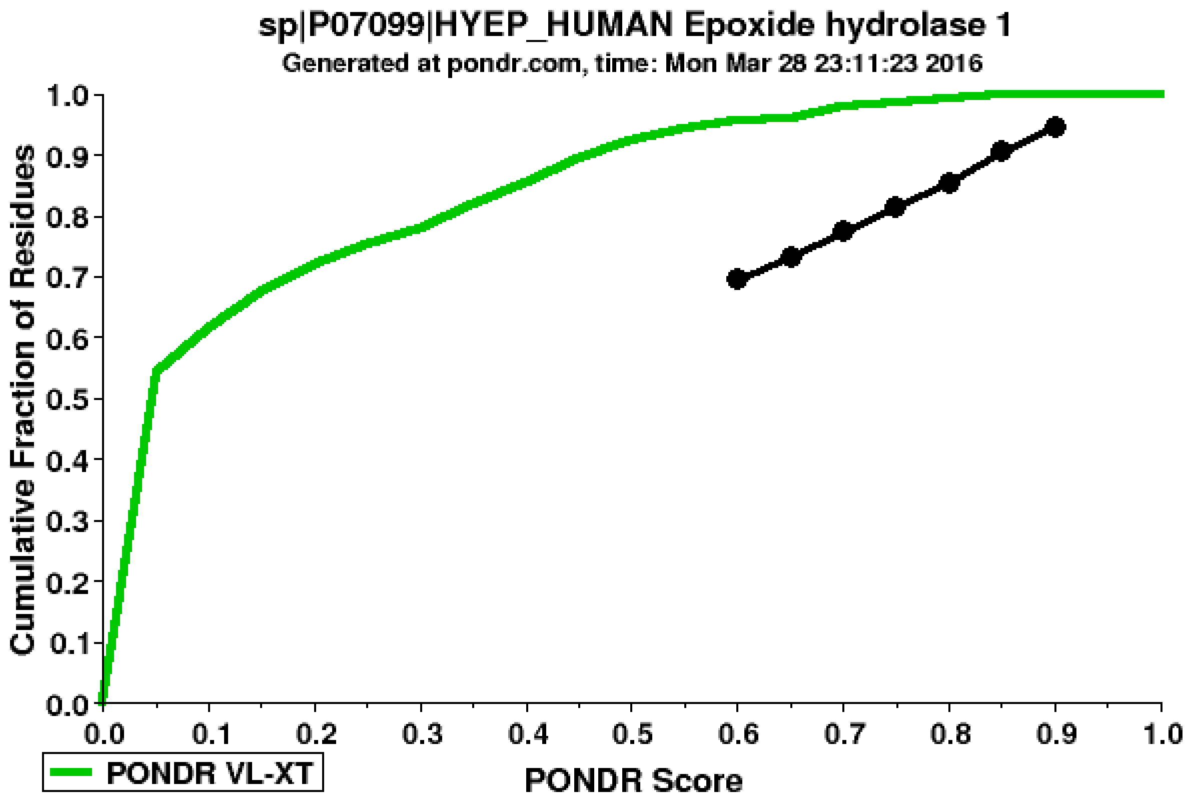
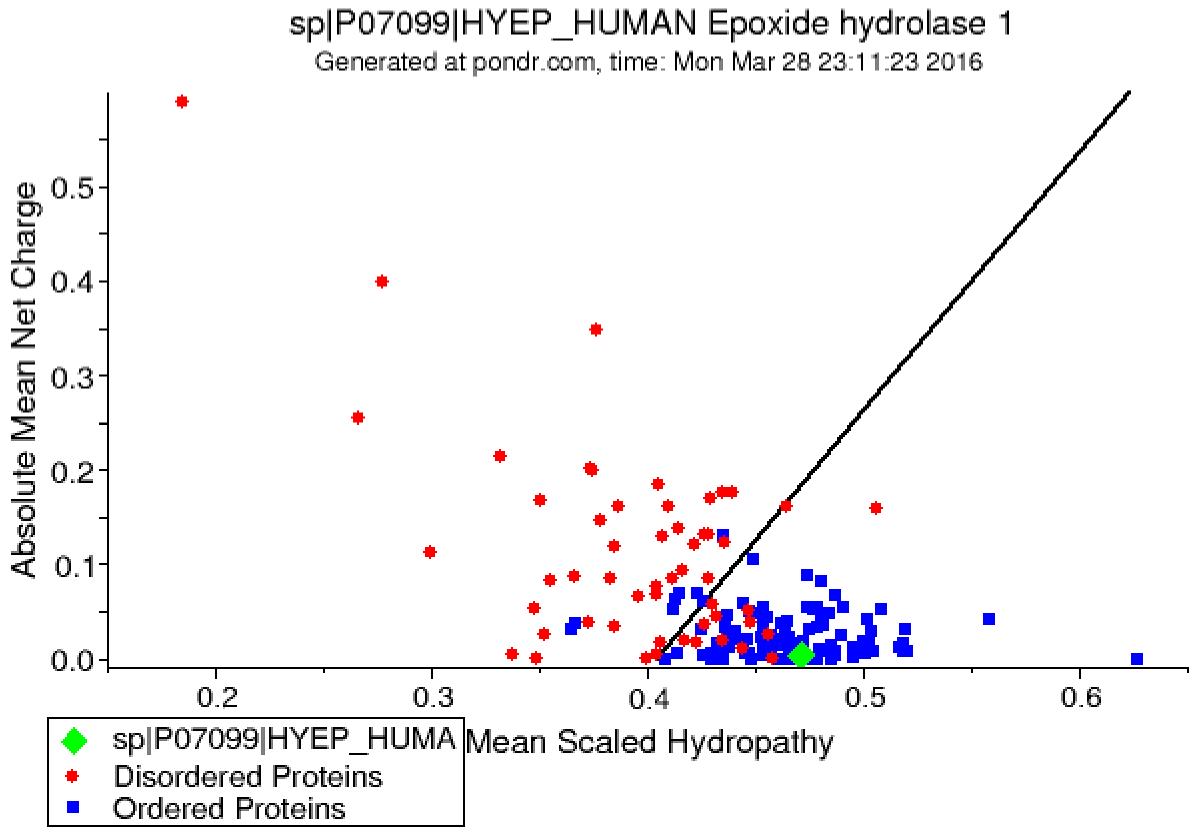
CCR3
DNM1
PRKACB
ACE2
ENPEP
GRM3
GRM2
SSTR5
CXCL1
CXCL5
CCL19
HTR1B
P2RY14
P2RY12
GRM8
ADCY4
RGS14
PPY
PENK
CNR2
DRD
OPRD1
ADCY7
HCK
REN
PRKACG
NPY2R
ADRA2A
C3AR1
CCL20
CCL5
CXCR2
CCR1
ADCY6
CCR6
TAS2R39
ADRA2C
GRM6
ADCY2
AP2M1
SSTR1
PTGDR2
HEBP1
SSTR4
NPBWR1
ADCY5
ATP6AP2
CCL25
S1PR4
CHRM4
NPBWR2
CXCL6
FGR
CTSG
ADCY3
RGS20
CCL21
CCL27
CXCL2
GALR2
NPY1R
ACE
FPR3
CXCR7
MTNR1A
OPRK1
HTR1E
CXCR5
ADCY9
HCAR2
HCAR3
CXCL3
HTR1D
TAS2R4
GPER
TAS2R1
CXCR6
CXCL13
C3
P2RY
CCL16
CTSZ
RGS4
MTNR1B
APLNR
CXCL9
SSTR
HRH4
OXGR1
TAS2R16
RGS6
RGS7
RGS1
RGS10

```
>sp|P07099|HYEP_HUMAN Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1
SV=1
MWLEILLTSVLGFAIYWFISRDKEETLPLEDGWWGPGTRSAAREDDSIRPFKVETSDEEI
HDLHQRIDKFRFTPPLEDSCFHYGFNSNYLKKVISYWRNEFDWKKQVEILNRYPHFKTKI
EGLDIHFIHVKPPQLPAGHTPKPLLMVHGWPGSFYEFYKIIPLLTDPKNHGLSDEHVFEV
ICPSIPGYGFSEASSKKGFNSVATARIFYKLMLRLGFQEFYIQGGDWGSLICTNMAQLVP
SHVKGLHLNMALVLSNFSTLTLLLGQRFGRFLGLTERDVELLYPVKEKVFYSLMRESGYM
HIQCTKPDTVGSALNDSPVGLAAYILEKFSTWTNTEFRYLEDGGLERKFSLDDLLTNVML
YWTTGTIISSQRFYKENLGQGWMTQKHERMKVYVPTGFSAFPFELLHTPEKWVRFKYPKL
ISYSYMVRGGHFAAFEEPELLAQDIRKFLSVLERQ
```









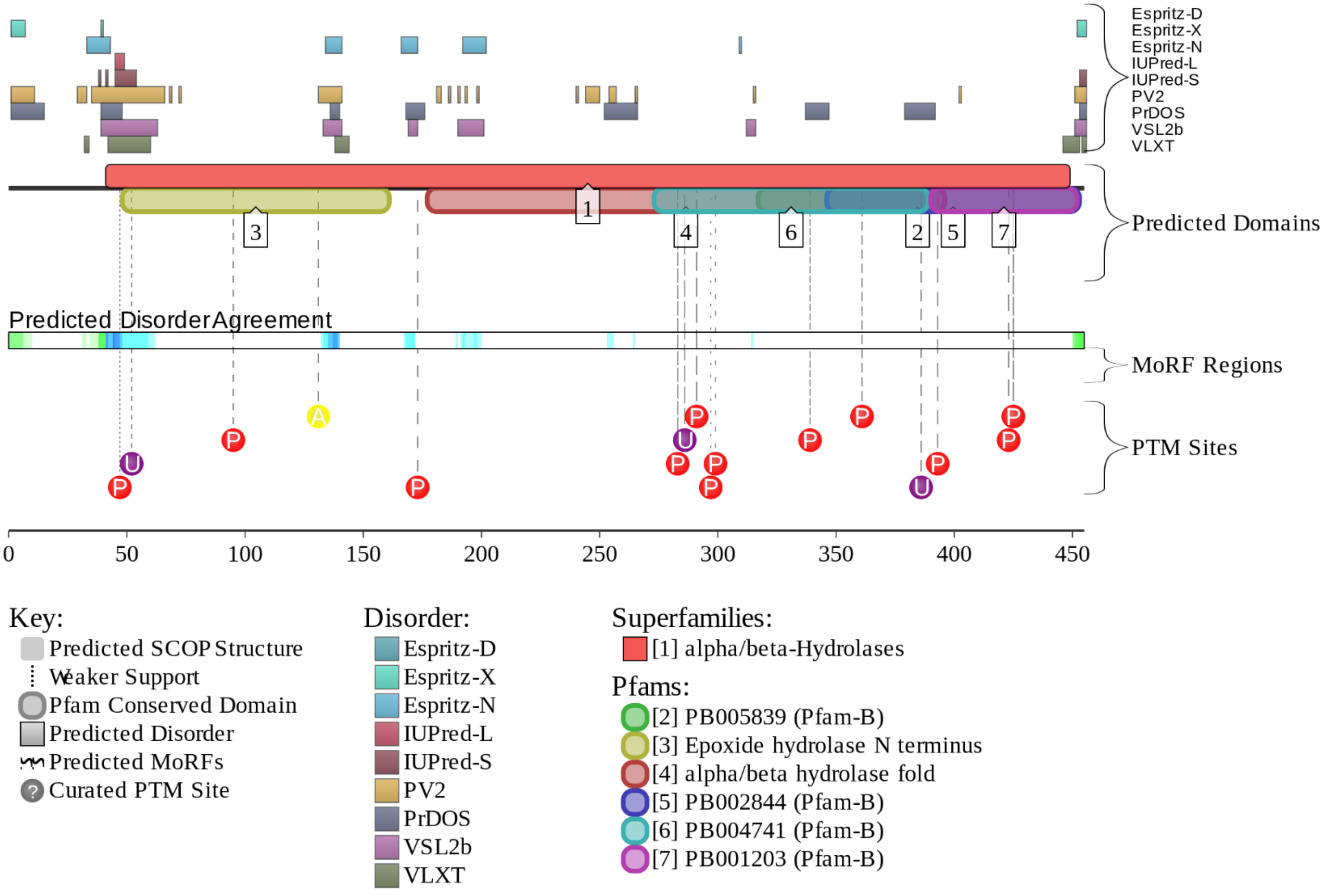
```
======================VLXT NNP STATISTICS===============================
Predicted residues: 455                      Number Disordered Regions: 5
Number residues disordered: 35            Longest Disordered Region: 18
```

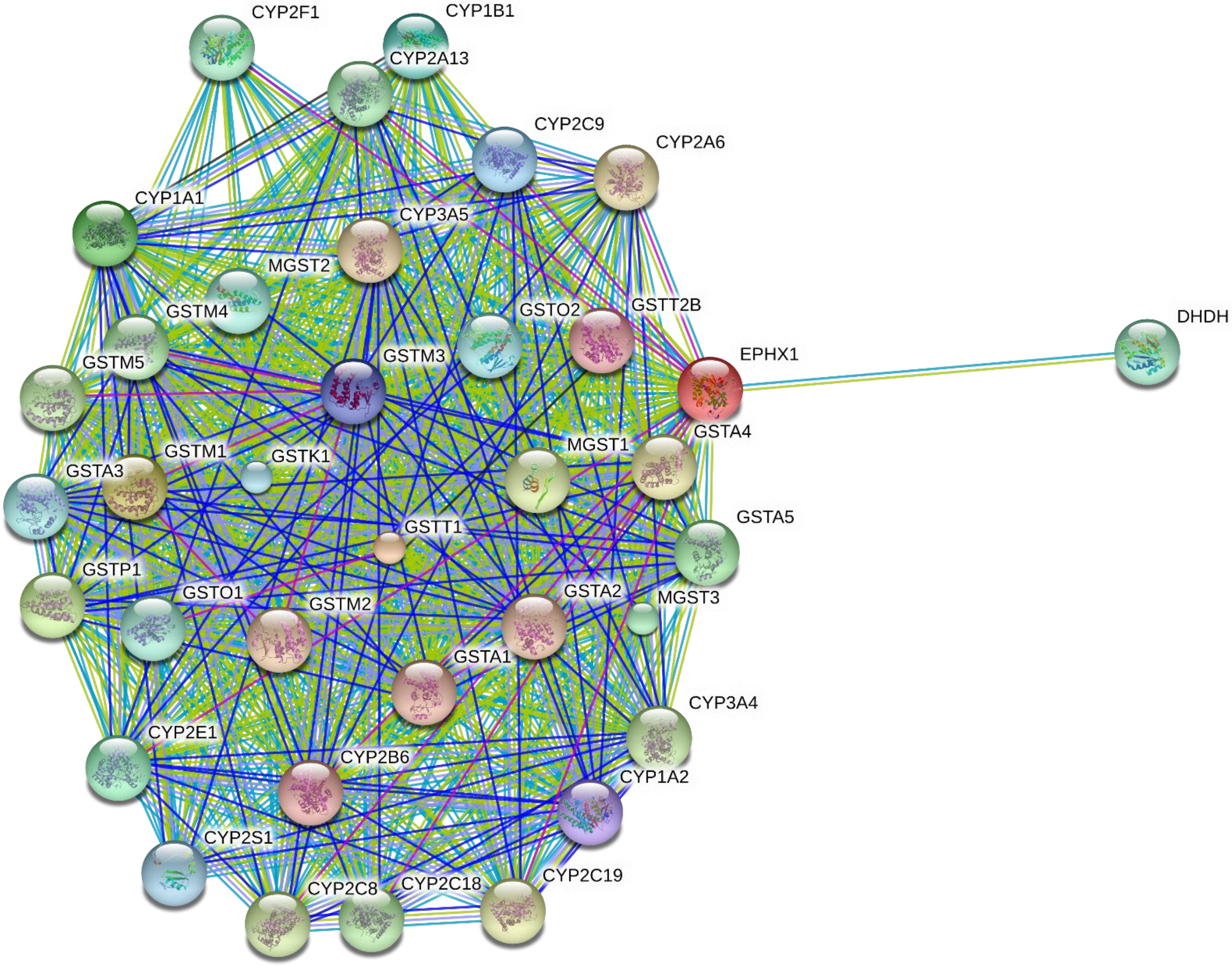
```
Overall percent disordered: 7.69      Average Prediction Score: 0.1461
Predicted disorder segment [32]-[33]  Average Strength= 0.5110
Predicted disorder segment [42]-[59]  Average Strength= 0.6712
Predicted disorder segment [138]-[143]Average Strength= 0.6445
Predicted disorder segment [446]-[452]Average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

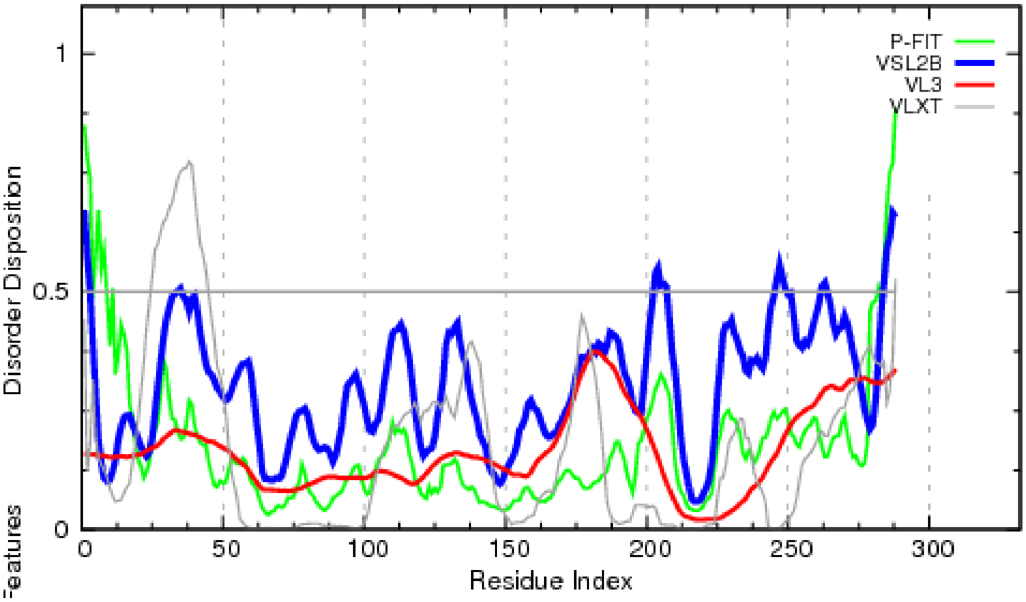
======================VSL2 NNP STATISTICS================================
Predicted residues: 455                        Number Disordered Regions: 6
Number residues disordered: 56        Longest Disordered Region: 24
Overall percent disordered: 12.31     Average Prediction Score: 0.2772
Predicted disorder 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
```

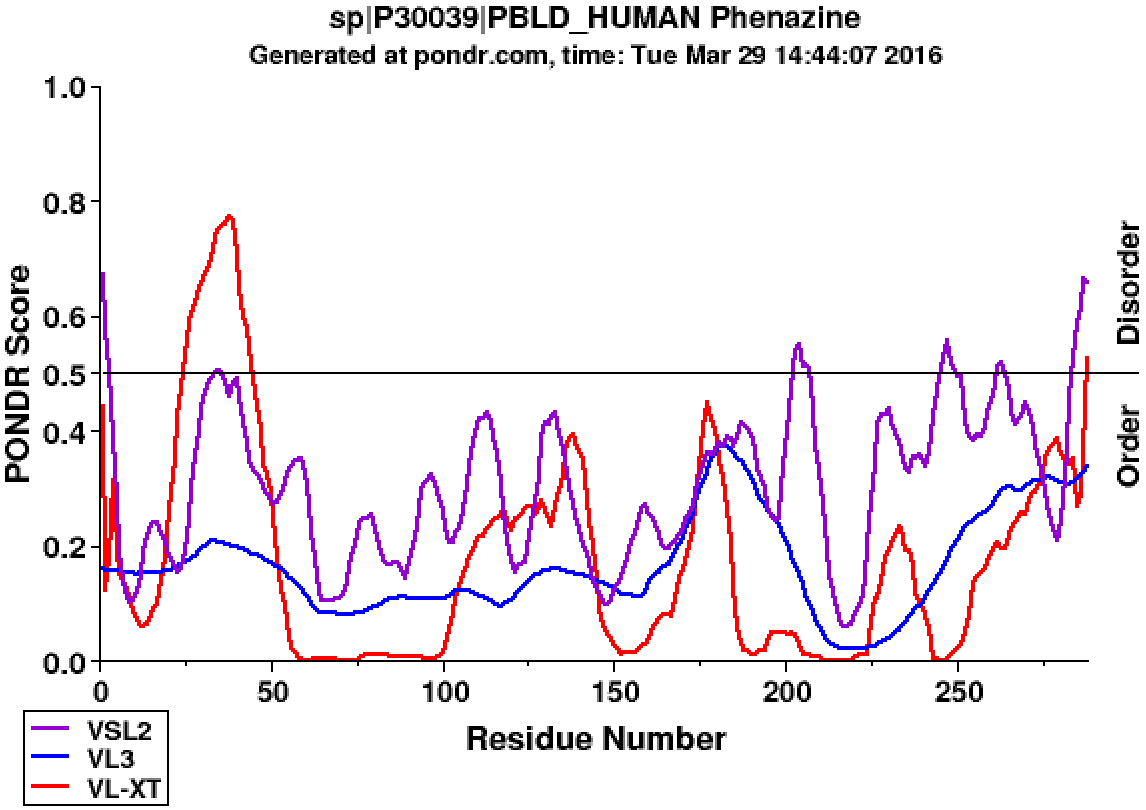
ENSP00000355802, ENSP00000272167

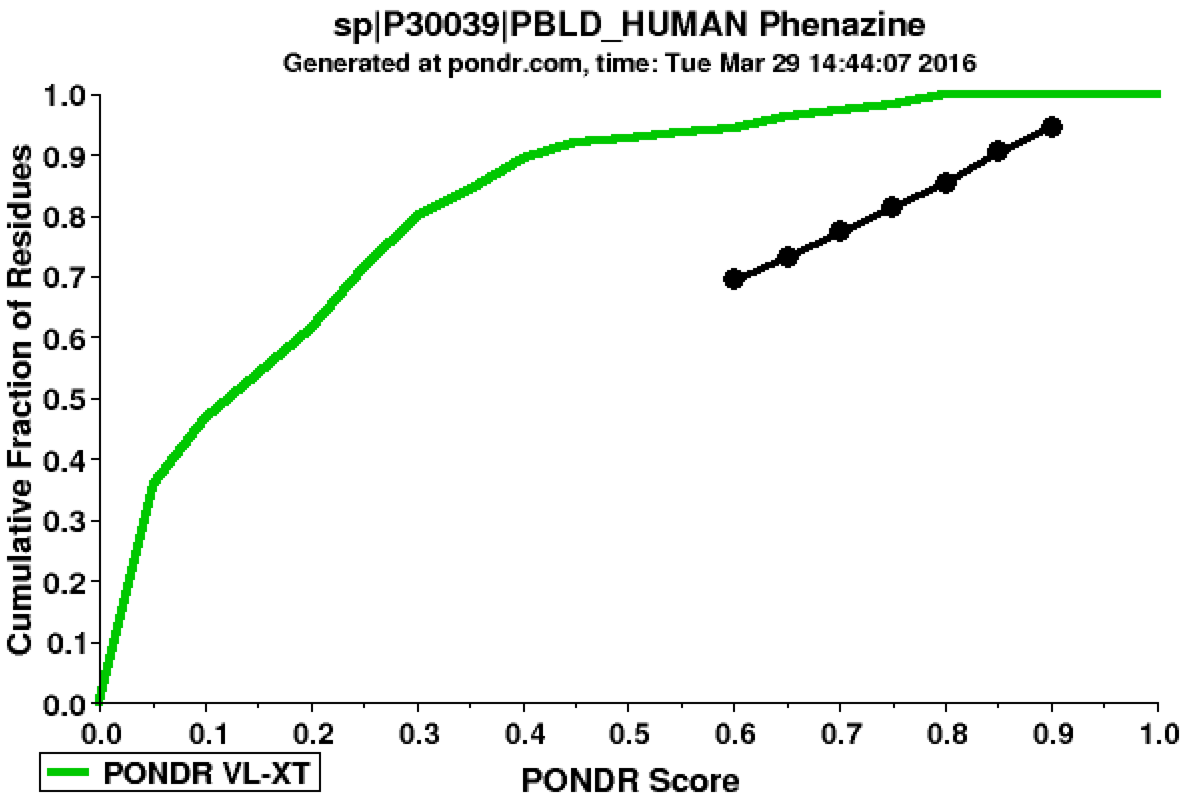


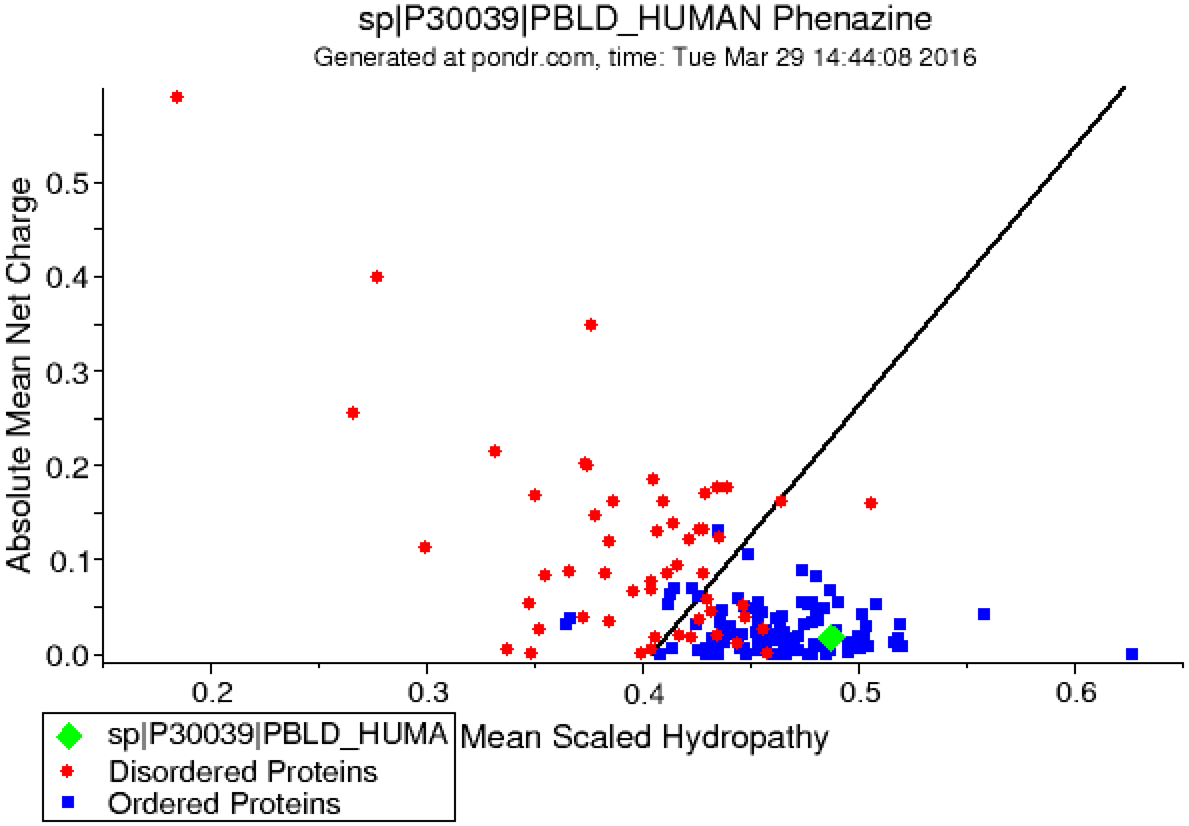

CYP2F1
CYP1B1
CYP2A13
CYP2C9
CYP2A6
CYP1A1
CYP3A5
MGST2
GSTM4
GSTO2
GSTT2B
DHDH
EPHX1
GSTM5
GSTM3
GSTA4
MGST1
GSTM1
GSTK1
GSTA3
GSTA5
GSTT1
GSTP1
GSTO1
GSTA2
MGST3
GSTM2
GSTA1
CYP3A4
CYP2E1
CYP2B6
CYP1A2
CYP2S1
CYP2C8
CYP2C18
CYP2C19

```
>sp|P30039|PBLD_HUMAN Phenazine biosynthesis-like domain-containing
protein OS=Homo sapiens GN=PBLD PE=1 SV=2
MKLPIFIADAFTARAFRGNPAAVCLLENELDEDMHQKIAREMNLSETAFIRKLHPTDNFA
QSSCFGLRWFTPASEVPLCGHATLASAAVLFHKIKNMNSTLTFVTLSGELRARRAEDGIV
LDLPLYPAHPQDFHEVEDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSFLENLKVN
TENLLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSY
WSQHLGKKEMHAFQCSHRGGELGISLRPDGRVDIRGGAAVVLEGTLTA
```





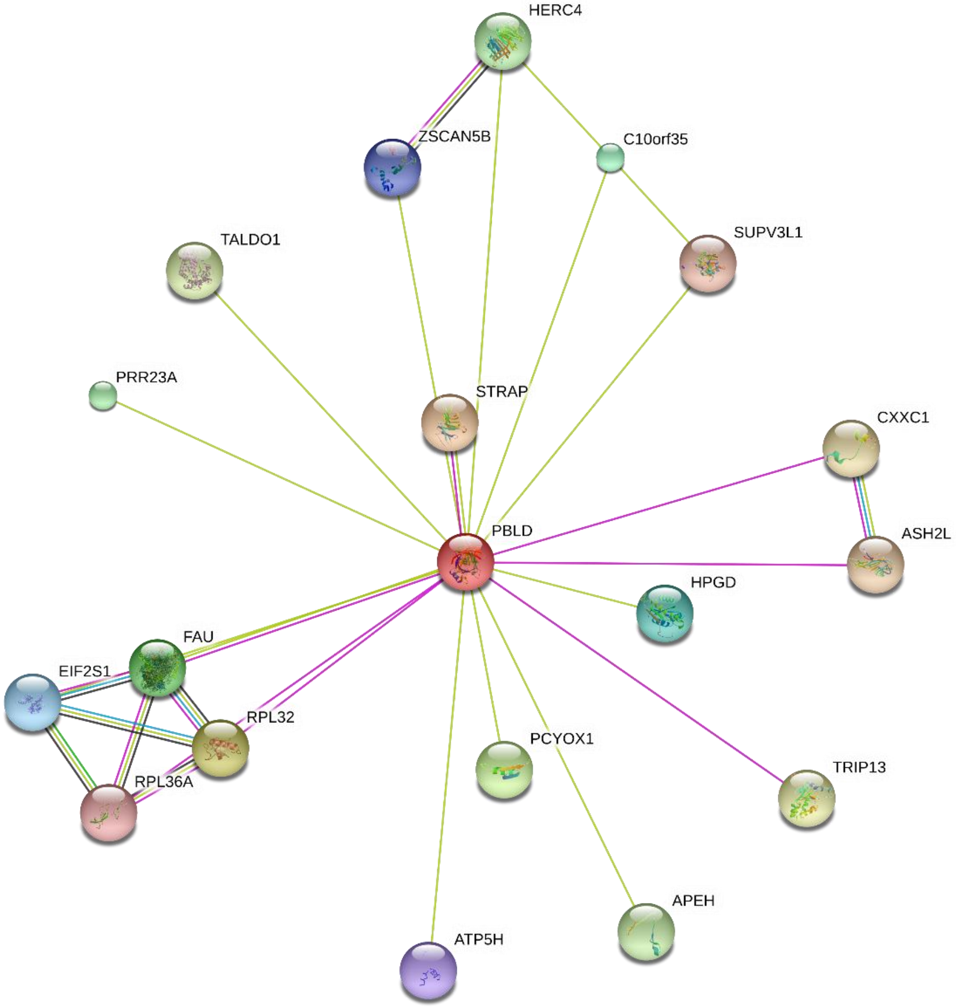

sp|P30039|PBLD_HUMAN Phenazine
Generated at pondr.com, time: Tue Mar 29 14:44:07 2016
Cumulative Fraction of Residues
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
PONDR VL-XT
PONDR Score


sp|P30039|PBLD_HUMAN Phenazine
Generated at pondr.com, time: Tue Mar 29 14:44:08 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
sp|P30039|PBLD_HUMA
Disordered Proteins
Ordered Proteins

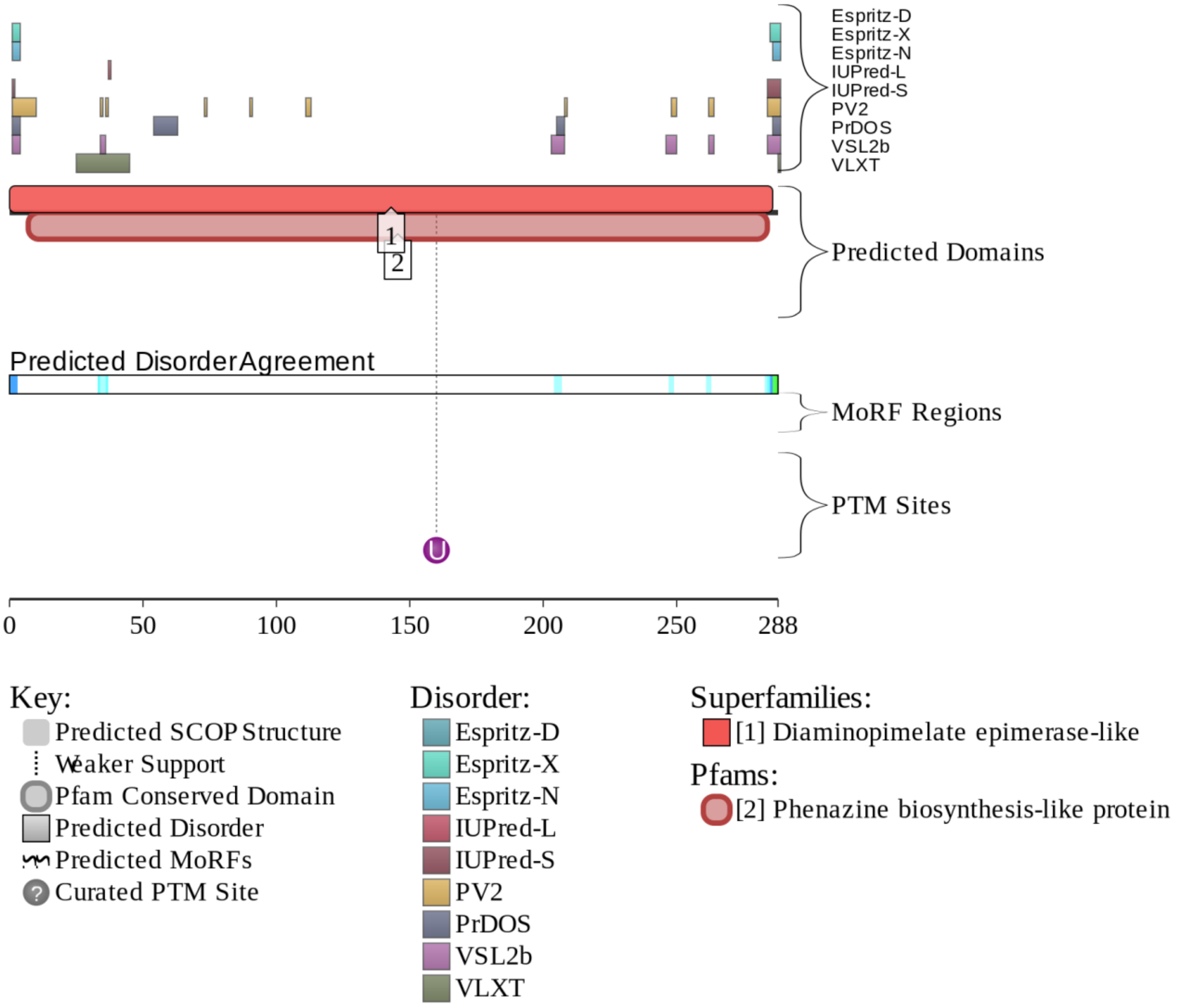
```
========================VLXT NNP STATISTICS================================
Predicted residues: 288                       Number Disordered Regions: 2
Number residues disordered: 21        Longest Disordered Region: 20
Overall percent disordered: 7.29      Average Prediction Score: 0.1771
Predicted 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

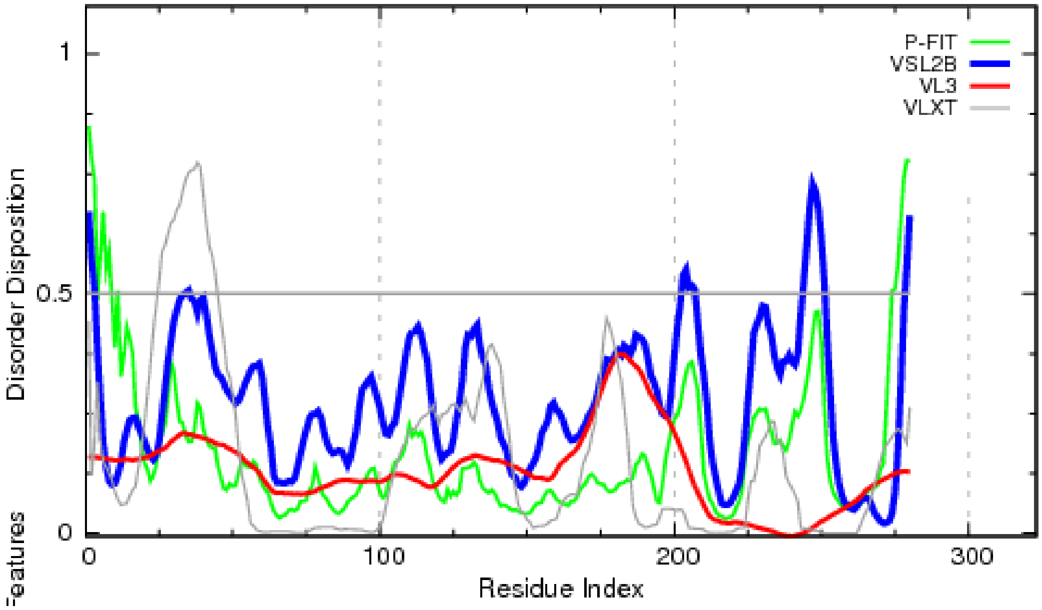
========================VSL2 NNP STATISTICS================================
Predicted residues: 288                       Number Disordered Regions: 6
Number residues disordered: 21        Longest Disordered Region: 5
Overall percent disordered: 7.29      Average Prediction Score: 0.3056
Predicted disorder 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
```

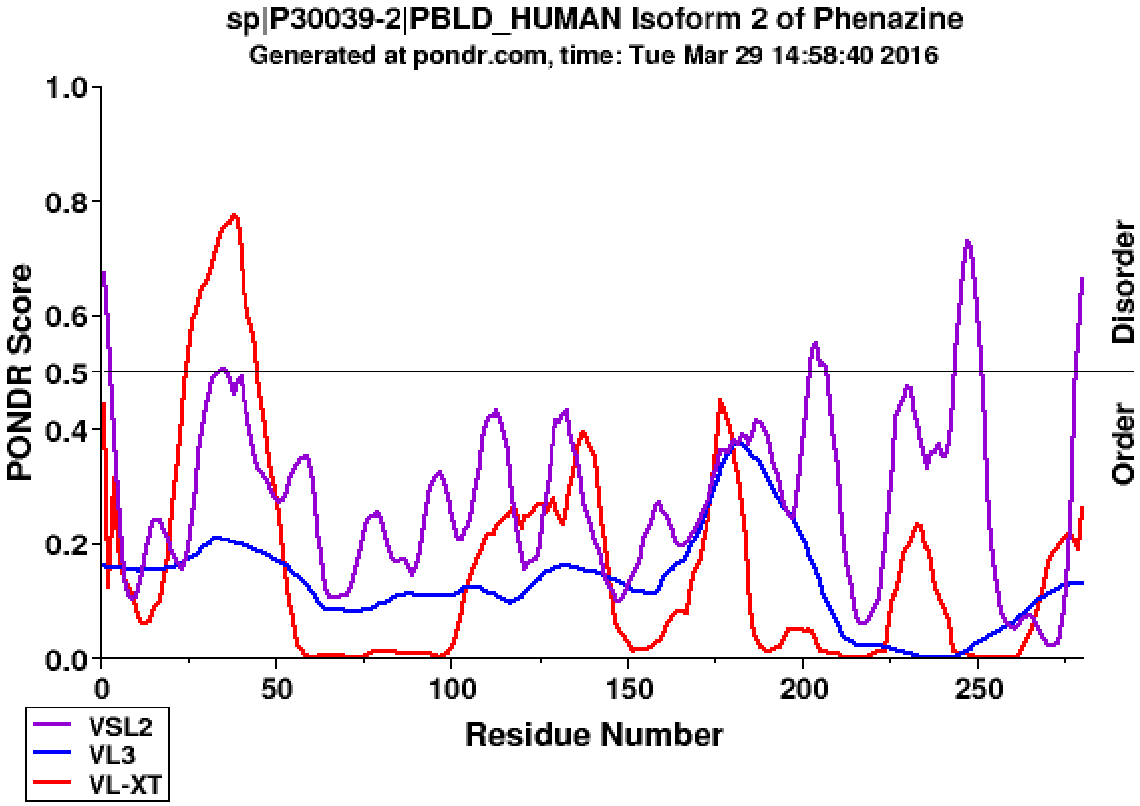


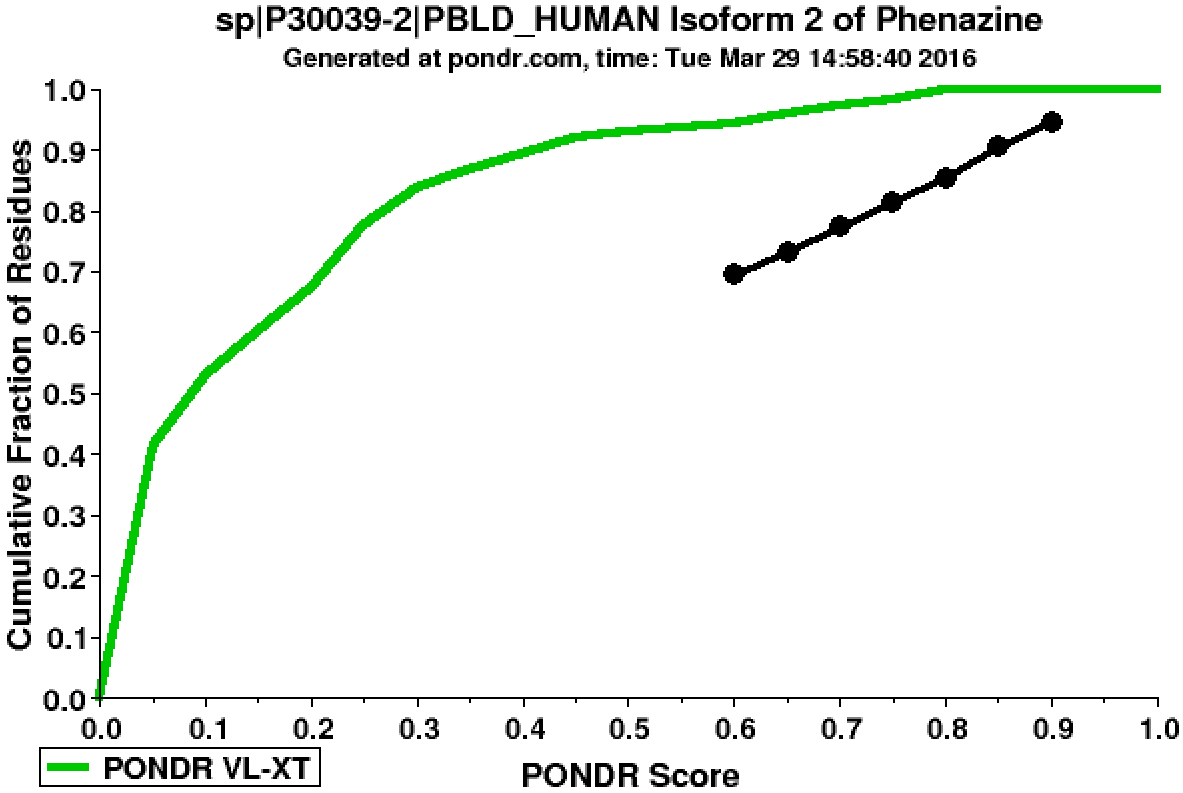
ENSP00000351619, ENSP00000308466

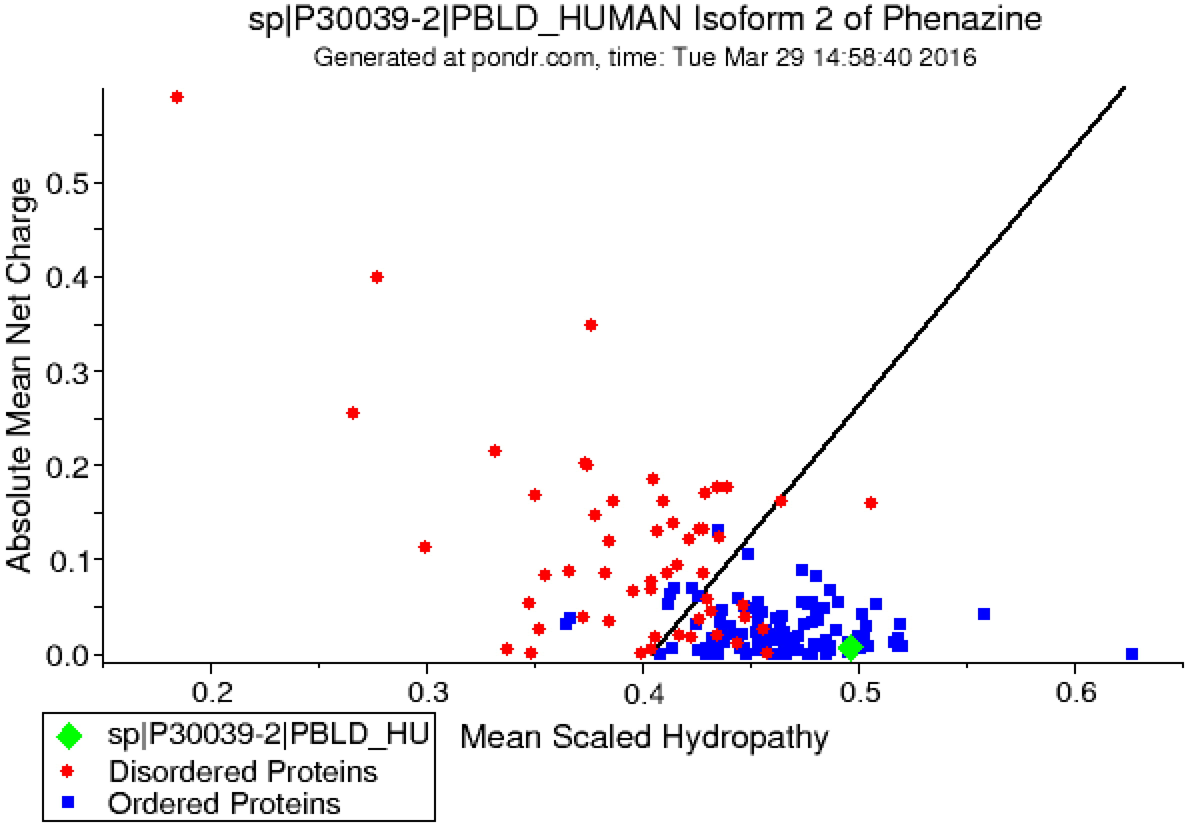


>sp|P30039-2|PBLD_HUMAN Isoform 2 of Phenazine biosynthesis-like domain-containing protein OS=Homo sapiens GN=PBLD
MKLPIFIADAFTARAFRGNPAAVCLLENELDEDMHQKIAREMNLSETAFIRKLHPTDNFA
QSSCFGLRWFTPASEVPLCGHATLASAAVLFHKIKNMNSTLTFVTLSGELRARRAEDGIV
LDLPLYPAHPQDFHEVEDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSFLENLKVN
TENLLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSY
WSQHLGKKEMHGRTALYQFLFYLPNSKLVFLLICTIPLKM






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
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|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
```