

Supplementary Materials: Analysis of High Molecular Mass Compounds from the Spider *Pamphobeteus verdolaga* Venom Gland. A Transcriptomic and MS ID Approach

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Supplementary material 3: Prediction of Cys-Cys formation of putative protein ORFs corresponding to phospholipases A₂, phospholipases D, phospholipases B, kunitz-type, hyaluronidases, lycotoxins toxins, CRISP proteins, Hephaestin-like protein and venom metalloproteinase. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Residues highlighted in yellow shows cysteines potentially forming disulfide bridges.

PhospholipaseA₂-1-Pverdolaga:

XLGTGKSPVVAVETIDVFRPDSLWDA^CKMVALGVSAIGQLLIDQATQTDGRVIGRAQAM^CSM
LNIPYYRLNPQLTENVGLD^TTDNKT^LVKMLWETTAYMHSMRQELEQL^CNNYEDSGLD

Sequence inputSeq Length 119 residues

Cysteines in this sequence: 3

Disulfide Connectivity prediction

Step 1: Running PSI-BLAST with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Disulfide bond scores

Cysteine sequence position	Distance	Bond	Score
27 - 60	33	SLWDACKMVAL-RAQAMCSMLNI	0.01102
27 - 110	83	SLWDACKMVAL-ELEQLCNNYED	0.75862
60 - 110	50	RAQAMCSMLNI-ELEQLCNNYED	0.89632

Step 5: Weighted matching

Predicted bonds

60 - 110	RAQAMCSMLNI - ELEQLCNNYED
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Predicted connectivity

2-3

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PhospholipaseA₂-Pverdolaga:

MAAESVADDVLRCCVNLSEFRDFYCPYDIPSVEGPPTPLEFARNWVSPNKPVIFRNAVKHWP
ALKKWTVSYLK

Sequence **inputSeq** Length 74 residues

Cysteines in this sequence: 3

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Disulfide bond scores

Cysteine sequence position	Distance	Bond	Score
13 - 14	1	DDVLRCCVNLS-DVLRCCVNLS	0.01037
13 - 26	13	DDVLRCCVNLS-FRDFYCPYDIP	0.03657
14 - 26	12	DVLRCCVNLS-FRDFYCPYDIP	0.82076

Step 5: Weighted matching

Predicted bonds

14 - 26	DVLRCCVNLS - FRDFYCPYDIP
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Predicted connectivity

2-3

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PhospholipaseA₂-3-Pverdolaga:

MLSLSTHSRFVVSFTLLSLLISSTTSYRIPKRSVRPSPVIFVPGDGGSQLQAKLNKPETVHYYCN
 KKTDYYFDLWLNLELLVPYVLD CWIDNMRLIYDNVTRKTTNAPGVDIRVPGFGNTSTVEWLD
 PSQIAPSA YFVRIVQGLVDEGYTRGVDLKGAPYDYRKAPNEMANYYKNVKQMTEEMYFKLN
 KTRITYV CHSMGCPVMLYFFNRQTQDWK DTHVKALITLGGAWGGAVKAMKAFASGENLGV
 YVINHLLLRKEQRTSPSLAYMTPSDTFWKKDEILVVTEKQNYTIGNYYDFFQDIRFPVGVWEMW
 KDTYNLTRDLIPPGVEVH CMHGVNVSTIERLVYKHLEFPDSNPTLIQGDGDGTVNLRSLGCL
 RWKGNQKQKVVKPLNNVDHMGVLYDDDDVIQYIKQVVSS

Sequence inputSeq Length 415 residues

Cysteines in this sequence: 6

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

65 - 89	TVHYYCNKKTD - PYVLDCWIDNM
197 - 202	RITYVCHSMGC - CHSMGCPVMLY
331 - 374	GVEVHCMHGVN - RSLEGCLRWKG

Predicted connectivity

1-2, 3-4, 5-6

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PhospholipaseA₂-4-Pverdolaga:

XFVNNICTSSVLDTRKGRAGLILNPLRGLSLIPCFNFSPFSPTSPSDDMLFKGLTEAVPTQSKTLY
 LVDGGLTFNLPFPLLRPQRGIDVYLAADFSSRDADH

Sequence inputSeq Length 103 residues

Cysteines in this sequence: 2

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Disulfide bond scores

Cysteine sequence position	Distance	Bond	Score
7 - 34	27	FVNNICTSSVL-LSLIPCFNFSP	0.15031

Step 5: Weighted matching

Predicted bonds

7 - 34	FVNNICTSSVL - LSLIPCFNFSP
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Predicted connectivity

1-2

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PhospholipaseA₂-5-Pverdolaga:

XPSQSKKCTCSFDCSGGDSMEIVPQNCRVLC LDGGGIRGLVLIQLLDQLEKVLGIPVNLCFDWI
 AGTSTGGVLALLLAQGKSVKECRCLYFRLKDRVFVGMRPYDAEPLEKILQKELGYETMMSDV
 TGARVMVTATKSDRHPAELHVFRNYDSPMEILTQEDLDPFHNTPLPKPSEQLVWKVARATGS
 APTYFRAFGAFLDGGLISNNPTLDALTEIHQCNQAYRVTHQEEKIKEIDX

Sequence inputSeq Length 239 residues

Cysteines in this sequence: 9

Disulfide Connectivity prediction

Step 1: Running PSI-BLAST with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

8 - 10	SQSKKCTCSFD - SKKCTCSFDCS
14 - 27	TCSFDCSGGDS - IVPQNCRVLCL
31 - 88	NCRVLCLDGGG - VKECRCLYFRL
60 - 86	IPVNLCFDWIA - KSVKECRCLYF

Predicted connectivity

1-2, 3-4, 5-8, 6-7

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PhospholipaseA₂-6-Pverdolaga:

MTICTSNSKYLFLVQLWIILPFLAFNVRKWANNSSDDCNYYDLQVENDGPVTLDPITFYAVLE
 CASAEHYVYIFQDNAVPPHRIQVDGSTGANVSFVYNANIYRPGVYILKVSFSGMWSPVLVG
 IASTSSTFVISEYIPGSLNISDIKVRNQGGSLYISSGSVTNLTINLHYPSSVYPLLETYSWNVEKDQ
 FITVDPFIYNFTQPGTYRISVSAVARVPVYNVLAVPTQIMKYKWGYFNTVATVKDSMTAVNLT
 GNTYLKHGQLNLDVSCGTGSGPFECWKIFQPFENVTDLTCPSPIVTTKCSFPIIYFQESGNYQ
 VAILVDNYITSIQRNIEVHVYDVSLLKPLSTVILPLVCAVLAIITIGIVIHIRENQQFDIETADFD
 FLQSDVIVVETFWKMYHSILQVLLRREVQSNYYLRIVSPDASSSHYGSVPXIGAVRRIIVTV
 WMIGRCHHVSKSLTAEFLYWFLRLRFQHTVKEKLFDSNPASTWNWPHFRNCNYLLVL

Sequence inputSeq Length 516 residues

Cysteines in this sequence: 11

Disulfide Connectivity prediction

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Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

4 - 39	XXMTICTSNSK - NNSDDCNYYDLQ
65 - 309	YAVLECASAE - IVTTKCSFPII
276 - 464	NLDVSCGTGSGP - WMIGRCHHVSK
300 - 362	VTDLTCPSPIV - ILPLVCAVLAI
417 - 509	ILQVLCLRREV - PHFRNCNYLLV

Predicted connectivity

1-2, 3-7, 4-10, 6-8, 9-11

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PhospholipaseA₂-7-Pverdolaga:

MTLGAPNIRRKIKRDLLDLADMFEELTQLDPTEYIPYGNWCGYGGDGEILDRIDRCCEIHDRCYGKVSENVCSNEQVHIINYQWNRENDTITCDGNTSKCEMEACMCDRDVVLCHKHNGDYSH
 EVRYVDSTKPKTSGVPQWSSMNKDCTKRSDGSEIPLMGRMGNMMSLIFX

Sequence inputSeq Length 173 residues

Cysteines in this sequence: 11

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

56 - 72	DRIDRCCEIHD - VSENVCSNEQV
57 - 100	RIDRCCEIHDR - GNTSKCEMEAC
63 - 93	EIHDRCYGKVS - NDTITCDGNTS
105 - 149	CEMEACMCDRD - SMNKDCTKRSD
107 - 114	MEACMCDRDV - RDVVLCHKHN

Predicted connectivity

2-5, 3-7, 4-6, 8-11, 9-10

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PhospholipaseA₂-8-Pverdolaga:

MGFLLTAALT FILLAGYSPFSAEKPLQIRRNKRS LFDLNDMIKQLTGRSGLDFIGYGN YCGFGGE
 GKPVDIDR CCKMHDICYDFAQNDDCAEDPNVYKIKYGWQKSFQVQCSFSQSKCMKVVC
 CIDVRFAKCLKNYINEYNNSNKHEKDLQELLEEVQQMSK

Sequence inputSeq Length 166 residues

Cysteines in this sequence: 10

Disulfide Connectivity prediction

Step 1: Running PSI-BLAST with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds	
60 - 126	GYGNYCGFGGE - CMKVVCICDVR
75 - 91	DDIDRCCKMHD - AQNDDCAEDPN
76 - 121	DIDRCCKMHDI - FSQSKCMKVVC
82 - 114	KMHDICYDFAQ - SFGVQCSFSQS
128 - 135	KVVCICDVRFA - VRFAKCLKNYI

Predicted connectivity

1-8, 2-5, 3-7, 4-6, 9-10

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Mature protein disulfide pattern

Step 5: Weighted matching	
Predicted bonds	
11 - 77	GYGNYCGFGGE - CMKVVCICDVR
26 - 42	DDIDRCCKMHD - AQNDDCAEDPN
27 - 72	DIDRCCKMHDI - FSQSKCMKVVC
33 - 65	KMHDICYDFAQ - SFGVQCSFSQS
79 - 86	KVVCICDVRFA - VRFAKCLKNYI
Predicted connectivity	
1-8, 2-5, 3-7, 4-6, 9-10	
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PhospholipaseA₂-9-Pverdolaga:

MERKYL^YCAVVLGSFIITYPQSLFAGVKNVLDSVNAIVEEVSLGLRSLSAGLDFVDQFVQTAG
 SEECLFH^CPSGKKLVN^QKYKPVPSG^CGAYGVTLSVKNSPQKEFTECC^NYHDI^CYGTCLSKKEI
^CDEKFDK^CLNKA^CAKQAKEIGEKKFGD^CKMAAKVFYAGTVALG^CKAFLDAQAEA^CICPEA
 WSVRL^CVRSTRQIC^VVYGEDAIAPRTA

Sequence inputSeq Length 216 residues

Cysteines in this sequence: 17

Disulfide Connectivity prediction

Step 1: Running PSI-BLAST with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

9 - 68	KYLLYCAVVLG - AGSEECLEFHCP
72 - 172	ECLFHCPSGKK - TVALGCKAFLD
91 - 111	PVPSGCGAYGV - KEFTECCNYHD
112 - 202	EFTECCNYHDI - STRQICVVYGE
118 - 183	NYHDICYGTCL - AQAEACICPEA
122 - 141	ICYGTCLSKKE - CLNKACAKQAK
136 - 156	EKFDKCLNKAC - KKFGDCKMAAK
185 - 194	AEACICPEAWS - WSVRLCVRSTR

Predicted connectivity

1-2, 3-13, 4-5, 6-17, 7-14, 8-11, 10-12, 15-16

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Mature protein disulfide pattern

Sequence **inputSeq** Length **189** residues

Cysteines in this sequence: **16**

Disulfide Connectivity prediction

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Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

42 - 103	AGSEECLEFHCP - SKKEICDEKFD
46 - 146	ECLFHCPGSGKK - TVALGCKAFLD
65 - 85	PVPSGCGAYGV - KEFTECCNYHD
86 - 176	EFTECCNYHDI - STRQICVVYGE
92 - 157	NYHDICYGTCL - AQAEACICPEA
96 - 115	ICYGTCLSKKE - CLNKACAKQAK
110 - 130	EKFDKCLNKAC - KKFGDCKMAAK
159 - 168	AEACICPEAWS - WSVRLCVRSTR

Predicted connectivity

1-8, 2-12, 3-4, 5-16, 6-13, 7-10, 9-11, 14-15

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PhospholipaseA₂-10-Pverdolaga:

FGYIMVLKNGSLNDSEEVATGENLTMIKILDGNGYLKDADIRCTWSIDMERFDLEGTSINY
 TYYDPGMSYIAVAVFATLPSSKTVFGLFTKELVVKVPVSDITISGNPFIHHNEVLNLNVSWTGTP
 PFEYCWDIINSNETVEGNFTCMVIVTYDTSFPVTRYFQKNGTYTMAIHVSNDVKLVKRNMEIIV
 FSVLPKSQLSTVIPIVCSLLTLVIAIGIAYYRQRRQLIVEVASFDFHDNSDSYRERTFFEQLWDS
 FRCRGCCSPSLSVRSDCLPSENEPLLT

Sequence inputSeq Length 288 residues

Cysteines in this sequence: 8

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

45 - 277	DADIRCTWSID - SVRSDCLPSEN
133 - 263	PPFEYCWDIIN - WDSFRCRGCCS
149 - 266	EGNFTCMVIVT - FRCRGCCSPSL
210 - 267	IIPIVCSLLTL - RCRGCCSPSL

Predicted connectivity

1-8, 2-5, 3-6, 4-7

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PhospholipaseA₂-11-Pverdolaga:

XGDLVDTPDPYVVLKVPGPSNGKKRTKYFNNTINPTWKETFTFVLDPEKNYELEVILMDANYT
 IDQRLGX

No disulfide bonds are possible for this sequence, the prediction will not be attempted

[Clote's structural bioinformatics Lab - Author's homepage](#)

PhospholipaseA₂-12-Pverdolaga:

MSIIRDILGGFRKVSQAQVDDPFRVLEVNVEDYLTVDVVCREDCLVLYKANDRGVMKLEIVVQL
 HINHSSNKNKVVSLHRSEDETNCQILFSQMCQKIPILIDYVPEVGLSKMALQNVSQVIRENLA
 WNAAHIAAHFGYTD CFKYKTMASEISEPCEGTLQTPHVAIKASQFPSVVALVDVMDIV
 DCNNGDSIFHYAATTTKEIIQALSVKPCVPVINMLNHDGHTPLHLACMADKPECVKELLRAGA
 DVNMAISIVDVDEVDRAQAAMPKLLSDVMHHTHAQRLYMDDMKTGGTPLHWSKTSELTAI
 LIEYGCHIDAKNFEGNTALHVMVLNRISC AVTLLSHGANVDIQQADGNTPLHLAVKSGDIY
 LVYAFVAFGANVNAINNKGETPRHILATEKRPGFEEMLYALHIVGAERCQRRTPWC KDGC EP
 GQHFNGIPSENPPVLNKTTLDDLLGAT

Sequence inputSeq Length 464 residues

Cysteines in this sequence: 15

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

39 - 341	TYDVVCREDC - RNRISCAVTLL
43 - 429	VCREDCLVLYK - RRTPWCKDGCE
87 - 235	EDETNCQILFS - PLHLACMADKP
95 - 422	LFSQMCQKIPI - VGAERCQRRTP
142 - 433	FGYTDCFKYKT - WCKDGCPEPGQH
191 - 317	MDIVDCNGDSI - LIEYGCHIDAK
216 - 242	LSVKPCVPVIN - ADKPECVKELL

Predicted connectivity

1-12, 2-14, 3-9, 4-13, 5-15, 7-11, 8-10

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PhospholipaseA₂-13-Pverdolaga:

XRLHELDEPADAELIQNSGLPAKYPSEFKMMLELINNC¹SQLELPVHKVASSIATNQSEPNNTIS
 KWSPWALWNGIVPGTKW²CGVGDIAS³TEELGSQAVVDS⁴CCRAHDH⁵CPVKLKAFRVGYGMI
 NLSFYTKSH⁶CD⁷CDRLFHS⁸CLKQTKNKLANAVGNFYFN⁹FIRVQ¹⁰CLKERKVYV¹¹VENRTDVDGL
 NEC¹²IRWSVDPDSRKX

Sequence inputSeq Length 202 residues

Cysteines in this sequence: 11

Disulfide Connectivity prediction

Step 1: Running PSI-BLAST with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

38 - 110	ELINNCSQLEL - RAHDHCPVKLK
82 - 104	PGTKWCGVGDI - VVDSCCRAHDH
103 - 134	AVVDSCCRAHD - YTKSHCDCDRL
136 - 143	KSHCDCDRLFH - RLFHSCCLKQTK
176 - 189	RKVYVCVENRT - DGLNECIRWSV

Predicted connectivity

1-5, 2-4, 3-6, 7-8, 10-11

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PhospholipaseA₂-14-Pverdolaga:

X C R A H D L C D D T L A P G E T K H N L T N R S T F T K L N C Q C D Q E F Y E C L Q K V D S L V S N S I G N L Y F N V L R
R G C Y E Y D H P L T K C K S Y R T

Sequence inputSeq Length 81 residues

Cysteines in this sequence: 7

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

2 - 32	XXXXXCRAHDL - FTKLNCQCDQE
8 - 65	RAHDLCDDTLA - VLRRGCYEYDH
34 - 41	KLNCQCDQEFY - QEFYECLQKVD

Predicted connectivity

1-3, 2-6, 4-5

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PhospholipaseA₂-15-Pverdolaga:

MPRSQNAFSRNSSLYSSLYTRSVNISKEKRKLLHLHKTYCTSKRSSDLNVSKPSSDKIPGNSIFSTIW
 KSVVVASSMLRPGLSVTPPKSIPIREFISKVGNVSTEEKYSKLLQPYLKLRSVNSEENVROTTEKS
 RTCSKPGVVSQAGNVISGEKESVFEQAAAEWITSANLQEKQENLSNQKEKSENLPKVLISKAS
 LASRSRFLVRSLSACASSQMLRLEEVCKHLLQHPQEKGTLVKEGLIRVALRLRRKSSNTDIQT
 QACVALTLLGYHEPPGGQGIRILSIDGGGTRGLMAIEILRQLQARTGKTVHEMFDYICGVSSGA
 ILTFLGGLRLSPDECESLYRELSLEVFKASGIWGAGRLMWYHAYYDTSMWVDVLRKTFGDK
 MLIDSVKEKSSPKLAAISAVMNLPALRAVFRNYDYPIRVQSQYIGSANYRMWEAIRASGAAP
 GYFEFHLNHLHLDQGGIMINNPTALAIHEARLLWPSDYIQCVFSLGSGRFTPATNTAFTSTTL
 KTKVQKVIDSATDTEAVHISMNDLLSPGTYFRNPYLTEFLHLDENRPDKLHQLKMDAQMYL
 RRNEHKLEQSIKVLTRPRSTLKKINDWIQLQKTLL

Sequence inputSeq Length 614 residues

Cysteines in this sequence: 9

Disulfide Connectivity prediction**Step 1:** Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output**Step 2:** Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output**Step 3:** Disulfide Oxidation State Prediction; click [here](#) to see the results**Warning!** The number of predicted half-cystines is lower than 2.**Step 4:** Disulfide Bonds Prediction using a trained Neural Network**Step 5:** Weighted matching**Predicted bonds**

39 - 211	LHKTYCTSKRS - VRSLSCASSCS
136 - 265	EKSRTCSPKGV - IQTQACVALTL
215 - 493	SCASSCSSQML - SDYIQCVFSLG
226 - 342	RLEEVCKHLLQ - LSPDECESLYR

Predicted connectivity

1-3, 2-6, 4-9, 5-8

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PhospholipaseA₂-16-Pverdolaga:

MAEEYHLMCSILAHGSDIRSVTTSYVPLGGIVTGSRDKTIKLWRPTGTTFTTEEHCMRGASHFIS
 SLCALPPSDQYPDGLILAGSNDCAIYGFSLDSSEPILKLLGHSENVCALVAGNLGTIVSGSWDKT
 ARVWHGQRVATLSGHTQAVWAVALLPDHALVLTGSADKAVFLWNNGKERKFIGHEDC
 VRGLTVISDLEFLSCSNDTTVRRWQTSGECLGIYTGHTDYVYDILSSCREYFISCSEDQTVKVV
 KENVCVQTIKLPKSLWAVTYLYNGDIAVGGSDGSVRVFTKDKSRRASPAAEEARFNEEIVSMN
 SKNMKQNIQDLELDDVPGPDALLQDGTSDGQTQLCKVGNEVSVFQWSVKEHKWLKLGKVL
 DALDNRPAGKKTVEGKEYDYVFTIDVAEGKLLKLPYNDTEDPWLVAHKFIEKHDLNPMFLD
 QIANFIINNSKSAGVQAESMSEFSDPFTGASRYIPSNVGPSSLASNHGDNSSIQELPKSNPTGN
 GDIEKASTGAHFLLTYVTFDTANTNGIRAKLCEFTEKIEKSQQLSIEKIEHMLLLLDYPQAITD
 DQMLSLEKALSWPAEFVFPALDVLRLAVRAEPVNSRVSKDGGVGLINHLLRYVSTGNPVSNQ
 MLVLRTLNFFVCPSGEQLLVSAKKVLSLTRSCASKNKHVQIALATLYANYSVAFQKSTSSE
 DTYCKDMYLNDAVEALKQFNEPEALFRLIVCIGTAVQDKYCLQVAKALKIGEIVQSVLERCEV
 SKIQDFGATLIDIVSN

Sequence inputSeq Length 775 residues
Cysteines in this sequence: 23
Disulfide Connectivity prediction
Step 1: Running PSI-BLAST with input sequence; click here to see the output
Step 2: Predicting secondary structure using PSIPRED ; click here to see the output
Step 3: Disulfide Oxidation State Prediction; click here to see the results
Warning! The number of predicted half-cystines is lower than 2.
Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching	
Predicted bonds	
10 - 88	EYHLMCSILAH - AGSNDCAIYGF
56 - 139	FTEEHCMRGAS - WHGQRCVATLS
68 - 179	FISSLCALPPS - WNNKGCERKFI
112 - 644	HSENVCALVAG - SNFFVCPSGEQ
204 - 259	LEFLSCSNDTT - WKENVCVQTIK
219 - 665	QTSGECLGIYT - SLTRSCCASKN
234 - 238	YVYDICLSSCR - ICLSSCREYFI
245 - 726	EYFISCSSEDQT - FRLIVCIGTAV
352 - 736	GQTQLCKVGNE - VQDKYCLQVAK
537 - 756	IRAKLCEFTEK - SVLERCEVSKI
666 - 699	LTRSCCASKNK - SEDTYCKDMYL
Predicted connectivity	
1-4, 2-6, 3-7, 5-17, 9-14, 10-18, 11-12, 13-21, 15-22, 16-23, 19-20	
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PhospholipaseD-1-Pverdolaga:

MKILKFLGCLIWYQVCVADEVDWRRPVWNIAH MVNANYQIDYYLDMGANSIEFDVAFDNS
 GNARFTFEGVPCDCFRSCVRHEEIEENYLEYMRHLTTPGDPKFQEKLVLLFM DLKVKGLSSRAR
 TNAGFSIARKLVRHYWQNGTSAARAHVLM SIPSDHMEVVRGFRDGLRVEGLSGYINKVGV
 DFGNEDLNSIRRALMSEISDRIWQGDGITNCLPRGTGRLREAIQRRDQPGLTHIEKVYWWTV
 DKMSTMRTLRLSVDAMITNYPRLVSVLDEDEFSGRFRMATIDDNPWSKHELRTSALYALDE
 GPTARGGNITTYFDKEDDELLIIASTITQTMAGINFTRGLEESIPX

Sequence inputSeq Length 358 residues
Cysteines in this sequence: 6
Disulfide Connectivity prediction
Step 1: Running PSI-BLAST with input sequence; click here to see the output
Step 2: Predicting secondary structure using PSIPRED ; click here to see the output
Step 3: Disulfide Oxidation State Prediction; click here to see the results
Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching	
Predicted bonds	
9 - 72	LKFLGCLIWYQ - FHGVPCDCFRS
16 - 74	IWYQVCVADEV - GVPCDCFRSCV
78 - 217	DCFRSCVRHEE - DGITNCLPRGT
Predicted connectivity	
1-3, 2-4, 5-6	
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Mature peptide disulfide pattern

Sequence **inputSeq** Length **332** residues

Cysteines in this sequence: **4**

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

47 - 49	FHGVPCDCFRS - GVPDCFRSCV
53 - 192	DCFRSCVRHEE - DGITNCLPRGT

Predicted connectivity

1-2, 3-4

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PhospholipaseD-2-Pverdolaga:

MANDISDAIYLLDQGANALEFDISFFNNGTVNRVYHGVP**C**DCFR**V**C**C**THEASLPDYLSIRKITD
 PQTGKYSQQMTFQFFDLKLQEVTPWGKYVAGLEIANHVIDYLWGNDTKRQLVRVLFINDES
 DKDVVLGVRNAFLQRGMKKFLDQVGFDGGTGTMKSIKSDMWDSLGRGNLWQGDGIFN**C**LS
 EVYKDDRLREALHIRDSPNGFIDKVYHWTIDSRGRMRMSLRLGVDGMITNLPKDLIDVLNEDP
 YSNIFRLATAKDDPFSRFHPSKSFK

Sequence **inputSeq** Length **275** residues

Cysteines in this sequence: **4**

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds	
40 - 184	YHGVPCDCFRV - DGIFNCLSEVY
42 - 46	GVPCDCFRVCT - DCFRVCTHEAS

Predicted connectivity

1-4, 2-3

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PhospholipaseD-3-Pverdolaga:

EKRSGGYAVTSFVKSFGRIFTECCGNWKTRWLLVKDNFVAYIKPSDGQLKC VLLMDHDFSVK
 SGKAETGKSNLSFISNMSRHLRLKCRSERQATEWAAEIERVVEKSGFEFTKVS RHG SFAPPRPH
 SPCRWIIDGATYFDSVASALDRAKEEIFIADWWLTPEIYLKRPTFHGHYWQLDHILK

Sequence inputSeq Length 184 residues

Cysteines in this sequence: 5

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds	
24 - 51	IFTECCGNWKT - DGQLKCVLLMD
87 - 129	HLRLKCRSERQ - RPHSPCRWIID

Predicted connectivity

2-3, 4-5

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PhospholipaseD-4-Pverdolaga:

XALPISKLDIKRHTSSIVPPPLFPVHKRSRSDSNVMTVPKKNQEFYQSRPHDDYHIKTLLKNIPS
 KPQQPVHKLQAKVKHDENRAKQRWRVAVKKIQAISAFQNLESQVLLEQVRDGAHQDVCLS
 SLPTPADVHRTIQEIALVHLGLERTYRLWHGKDYSNFIFKDLNKLNEPYTDSVNRYETPRMP
 WHDVS CFLQGPAARDVARHFIQRWNFTKLRTAKFDDVYPLLLPKCYEFPDPIPPILSSEVGSIL
 MADCQVLRSTSMWSAGIITTEYSILNAYKDAIMKAEHFIYIENQFFVSLQHGKNDVFNDISEC
 LYQRIMKAHQENKRFVYVIMPLLPAPFEGEVGTGTGTLIQAVTHWNYSSICRGPRSLCQRLA
 KSIQDPLSYISFYGLRNFGVLNNKLVTIELYVHSLKMIVDDKKAIGSANINDRSLLGRRDSEIA
 VLVNDSVFVESVMDGKPYKAGHFCSSLRKALFKEHLGLLGEKHSKVEX

Sequence inputSeq Length 490 residues

Cysteines in this sequence: 9

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cysteines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

123 - 193	AHQDVCLSSLP - WHDVSCFLQGP
232 - 255	LLLPKCYEFPD - ILMADCQVLR
314 - 330	NDISECLYQRI - ENKRFCVYVIM
365 - 372	NYSSICRGPRS - GPRSLCQRLAK

Predicted connectivity

1-2, 3-4, 5-6, 7-8

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PhospholipaseB-1-Pverdolaga:

LEAIVLSLFRDNVVFYGVFAPPRLVSASCSSVSLCMKNLSPEASDWKFCMMLTLWVAIALLV
 HVCAASTEQAAYVTWDSSSYKFTVHSDPVENFVAYATFTNEINATGWSYLEVWTNETFPDSV
 QAYSAGLAEGVLTADLLKKHWYNTVATYCDGEESYCDRLKIFLETNLD FMNYNIARRRKYV
 PYWHQVALALEQLSGLEDGYNNVSGKPHTKLNVTGVL MVNIFGDLEDLEGILNKTVSSRPL
 GSGSCGLIKVLPNNEDLYVSQDSWNTYSSMLRVLKKYNISVHSGMDRGSPVIPGQVMSFSSY
 PGLICSGDDFYTISSGLATMETTIGNGNSSLWKYIRAKGTVLEWLSIVANRMARSGREWSRW
 F SIMNSGTYNQWMVVDYNKFLPGAPLQNDLLWVLEQLPGYIHSDDLTDVLRKQGYWPSY
 NTPYFKDIFNLSGSQENADKYGDWFTYDKTPRALIFKRDHGTVDVKSMIKLMRYNDYTHD
 PLSRCNCTPPYSAENAISARCDLNPANGTYPFGALGHRSHGGIDMKLTTGSLFKNFEFVAFG
 GPTYDSLPPFKWSESDFRITTERHEGHPDLWKFEPIVRKWSQ

Sequence inputSeq Length 598 residues

Cysteines in this sequence: 11

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

30 - 252	IVSASCSSVSL - LGSGSCSGLIK
36 - 315	SSVSLCMKNLS - YPGLICSGDDF
50 - 499	SDWKFCMMLTL - DPLSRCNCTPP
66 - 161	LLVHVCAASTE - GEESYCDRLKI
501 - 515	LSRCNCTPPYS - AISARCDLNPA

Predicted connectivity

1-7, 2-8, 3-9, 4-6, 10-11

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Kunitz-1-Pverdolaga:

MGIRNICIVISVFTVLFVLTVPVFSADKMDICKLPPESCIIDLRAQLKIPRWYFNGRLCTRFVYS
GCDASENNFISRAQCRAKCGQARRRIRVPKT

Sequence inputSeq Length 99 residues	
Cysteines in this sequence: 7	
Disulfide Connectivity prediction	
Step 1: Running PSI-BLAST with input sequence; click here to see the output	
Step 2: Predicting secondary structure using PSIPRED ; click here to see the output	
Step 3: Disulfide Oxidation State Prediction; click here to see the results	
Step 4: Disulfide Bonds Prediction using a trained Neural Network	
Step 5: Weighted matching	
Predicted bonds	
7 - 69	GIRNICIVISV - FVYSGCDASEN
34 - 86	EKMDICKLPPE - QCRAKCGQARR
61 - 82	FNGRLCTRFVY - ISRAQCRAKCG
Predicted connectivity	
1-5, 2-7, 4-6	
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Kunitz-2-Pverdolaga:

MGVRTVFLLFVAFSFAAGDLQNPIRDEVCSLKAEPGIPGKNIMCLAYFPKYFNSAVGYCEKFI
 FGGCGGNANSFSTKEECEFCSDDKR

Sequence inputSeq Length 92 residues	
Cysteines in this sequence: 6	
Disulfide Connectivity prediction	
Step 1: Running PSI-BLAST with input sequence; click here to see the output	
Step 2: Predicting secondary structure using PSIPRED ; click here to see the output	
Step 3: Disulfide Oxidation State Prediction; click here to see the results	
Step 4: Disulfide Bonds Prediction using a trained Neural Network	

Step 5: Weighted matching	
Predicted bonds	
29 - 85	IRDEVCSLKAEE - ECEKFCGSDDK
44 - 68	GKNIMCLAYFP - FIFGGCGGNAN
60 - 81	SAVGYCEKFIF - STKEECEKFCG
Predicted connectivity	
1-6, 2-4, 3-5	
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Kunitz-3-Pverdolaga:

MGIRNICSVISVFTVLFALTFPVFLAGYHLDICRQRPDRGMCLVNMERWFFNGRFCSTFVYGG
CGGNGNNFISKAQCMARCAARG

Sequence inputSeq Length 86 residues

Cysteines in this sequence: 7

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

34 - 82	YHLDICRQRPD - QCMARCARGXX
43 - 65	PDRGMCLVNME - FVYGGCGGNGN
57 - 78	FNGRFCSTFVY - ISKAQCMARCA

Predicted connectivity

2-7, 3-5, 4-6

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Mature peptide disulfide pattern

Step 5: Weighted matching

Predicted bonds

7 - 55	YHLDICRQRPD - QCMARCARGXX
16 - 38	PDRGMCLVNME - FVYGGCGGNGN
30 - 51	FNGRFCSTFVY - ISKAQCMARCA

Predicted connectivity

1-6, 2-4, 3-5

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Kunitz-4-Pverdolaga:

MLLMILVVASFQHSNADANGIDLCELDKEPGSCTSVINRYFFNRYSRRCERFIYTDCCGGNSNNF
 HYEFECCERTCPGDLYIGDVCSLPKKVGPCRAAMPRIYFNKETGRCEFTYGGCSGNYNNFETK
 EQCNSYCFQG

Sequence inputSeq Length 138 residues

Cysteines in this sequence: 12

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

24 - 74	NGIDLCELDKE - ECERTCPGDLY
33 - 57	KEPGSCTSVIN - FIYTDCCGGNSN
49 - 70	RYSRRCERFIY - HYEFECCERTCP
84 - 134	YIGDVCSLPKK - QCNSYCFQGXX
93 - 117	KKVGPCRAAMP - FTYGGCSGNYN
109 - 130	KETGRCEFTY - ETKEQCNSYCF

Predicted connectivity

1-6, 2-4, 3-5, 7-12, 8-10, 9-11

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Kunitz-5-Pverdolaga:

XYFLRNGCPSSSTVCETTHSLGISRGNCCDSINCHLIAKFPNXAEMHFTLACVFSLFCGICFANH
 NVPDTDCLPPDAGMCYAYFPMFFYDAPSGACINFIYGGCGGNANRFWTEEECMNRCAGVG
 GTTKEPADEEKGPVDEGKGTISQKPIDEGKEVIIQKPVDEGKGAIYPQPTGGGKGVIFPQ
 PVAGGKGVIFQQPVGGGKGVTVQHAPQADICNQEKGQPGNCSSQIIRYFDKDSKKCDTFMYS
 GCGKNDNNFNKYKFCERTCSGEHDIGDTCNFKQDSGPCRAFFPRFYFSGESGQCEQFIYGGCQ
 GNHNFKTKEECLQFCTSGKGSPLP

Sequence inputSeq Length 342 residues

Cysteines in this sequence: 26

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

8 - 122	FLRNGCPSSSTV - ECMNRCAGVGG
14 - 72	PSSTVCETTHS - VPDTDCSLPPD
27 - 255	ISRGNCCDSIN - FMYSGCGKNDN
28 - 52	SRGNCCDSINS - HFTLACVFSLF
34 - 58	DSINCHLIAK - VFSLFCGICFA
61 - 268	LFCGICFANH - NYKFECERTCS
81 - 105	PDAGMCYAYFP - FIYGGCGGNAN
97 - 118	APSGACINFIY - WTEEECMNRCA
222 - 272	PQADICNQEKG - ECERTCSGEHD
231 - 315	KQPGNCSSQII - FIYGGCQGNHN
247 - 291	KDSKKCDTFMY - QDSGPCRAFFP
282 - 332	DIGDTCNFKQD - ECLQFCTSGKG
307 - 328	GESGQCEQFIY - KTKEECLQFCT

Predicted connectivity

1-14, 2-9, 3-18, 4-6, 5-7, 8-19, 10-12, 11-13, 15-20, 16-24, 17-22, 21-26, 23-25

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Kunitz-6-Pverdolaga:

VISVFTVLLALTFPPLFSADHHLDI^CELPADSGT^CCVRLHRWYFNGES^CTKFLYRG^CGGNENHF
MTEVE^CMAK^CCGGA

Sequence inputSeq Length 78 residues	
Cysteines in this sequence: 6	
Disulfide Connectivity prediction	
Step 1: Running PSI-BLAST with input sequence; click here to see the output	
Step 2: Predicting secondary structure using PSIPRED ; click here to see the output	
Step 3: Disulfide Oxidation State Prediction; click here to see the results	
Step 4: Disulfide Bonds Prediction using a trained Neural Network	
Step 5: Weighted matching	
Predicted bonds	
26 - 74	HHLDICELPAD - ECMACGGAXX
35 - 57	ADSGTCFVRLH - FLYRGCGGNEN
49 - 70	FNGESCTKFLY - MTEVECMACG
Predicted connectivity	
1-6, 2-4, 3-5	
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Kunitz-7-Pverdolaga:

XTSCCKGIKESCTLDRAEAKEICMMPKEIGPCRGYFHRWYFDVNTLTCTVTFVYGGCRGNNNNF
EFQRDCVVRTCEPLFKASGNEDPSNVSTHDVAQGNSPIDCMVTPWX

Sequence inputSeq Length 108 residues

Cysteines in this sequence: 9

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

11 - 101	GIKESCTLDRA - NSPIDCMVTPW
22 - 72	EAKEICMMPKE - DCVRTCEPLFK
31 - 55	KEIGPCRGYFH - FVYGGCRGNNN
47 - 68	VNTLTCTVTFVY - EFQRDCVRTCE

Predicted connectivity

2-9, 3-8, 4-6, 5-7

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Kunitz-8-Pverdolaga:

DAGTCFASIPRWYFTGSKCRSFIYGGCGGNANNFDTELXMPKEMWKEMKRVTSHFTTETGTA
QNPSSGYLEVFEVRIV

Sequence inputSeq Length 80 residues

Cysteines in this sequence: 3

Disulfide Connectivity prediction

Step 1: Running PSI-BLAST with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Disulfide bond scores

Cysteine sequence position	Distance	Bond	Score
5 - 19	14	XDAGTCFASIP-FTGSKCRSFIY	0.0108
5 - 27	22	XDAGTCFASIP-FIYGGCGGNAN	0.99974
19 - 27	8	FTGSKCRSFIY-FIYGGCGGNAN	0.01567

Step 5: Weighted matching

Predicted bonds

5 - 27	XDAGTCFASIP - FIYGGCGGNAN
--------	---------------------------

Predicted connectivity

1-3

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Kunitz-9-Pverdolaga:

QVATLHPPEAEKENLRNYVQRFTGVVMKSSLGVCELEKNSGPCAASYKRWYYDAISKDCLP
FSYGGCLGNENRFRRTKAACEETCKN

Sequence inputSeq Length 88 residues	
Cysteines in this sequence: 6	
Disulfide Connectivity prediction	
Step 1: Running PSI-BLAST with input sequence; click here to see the output	
Step 2: Predicting secondary structure using PSIPRED ; click here to see the output	
Step 3: Disulfide Oxidation State Prediction; click here to see the results	
Step 4: Disulfide Bonds Prediction using a trained Neural Network	
Step 5: Weighted matching	
Predicted bonds	
35 - 85	SSLGVCELEKN - ACEETCKNXXX
44 - 68	KNSGPCAASYK - FSYGGCLGNEN
60 - 81	AISKDCLPFSY - RTKAACEETCK
Predicted connectivity	
1-6, 2-4, 3-5	
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Kunitz-10-Pverdolaga:

XLKLPPKMMKLLWVNLLLLVLATCLCSEKTDKTNNGICNQRMDSGNGNQIRITHFYDYDTGRQ
KCHFPYPYSGRGGNKNFSTMQECKKRMPP

Sequence **inputSeq** Length 90 residues

Cysteines in this sequence: 5

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Warning! The number of predicted half-cystines is lower than 2.

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds	
26 - 38	LATCLCSEKTD - TNNGICNQRMD
63 - 84	TGRQKCHFPYPY - STMQECKKRMPP

Predicted connectivity

2-3, 4-5

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Kunitz-11-Pverdolaga: MRKSIMGTQVQGFRSSSPGALMSRVMASTTLCCFFSGKVYLQA

No disulfide bonds are possible for this sequence, the prediction will not be attempted

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Kunitz-12-Pverdolaga:

MLLRNDVSRRRIMIKVSRQRFSLTDFLEDFTAKDENNTDCQTLPA GDPTCYDNCMPFYD
TSSSTCMNVEYGGCGGKANRFWTEKECTDQCKNKEDDVANGAASEYSGIVSWLKVKYSPFL

Sequence inputSeq Length 124 residues	
Cysteines in this sequence: 8	
Disulfide Connectivity prediction	
Step 1: Running PSI-BLAST with input sequence; click here to see the output	
Step 2: Predicting secondary structure using PSIPRED ; click here to see the output	
Step 3: Disulfide Oxidation State Prediction; click here to see the results	
Step 4: Disulfide Bonds Prediction using a trained Neural Network	
Step 5: Weighted matching	
Predicted bonds	
32 - 94	DLEDFCTAKDE - ECTDQCKNKED
42 - 69	ENNTDCQTLPA - TSSSTCMNVEY
52 - 77	AGDPTCYDNC - VEYGGCGGKAN
57 - 90	CYDNCMPFY - WTEKECTDQCK
Predicted connectivity	
1-8, 2-5, 3-6, 4-7	
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Kunitz-13-Pverdolaga:

MGIARIFSVVSLFSVFLALTFPPLFSADHHEGTDICYLPPERGVCKAYSEQWHFNGRRCAKFVF
GGCGGNANRFPTKDECIIRRCRKA

Sequence **inputSeq** Length **87** residues

Cysteines in this sequence: **6**

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds

36 - 84	EGTDICYLPPE - ECIRRCRKAXX
45 - 67	PERGVCKAYSE - FVFGGCGGNAN
59 - 80	FNGRRCAKFVF - PTKDECIRRCR

Predicted connectivity

1-6, 2-4, 3-5

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Amino acid sequences of Hyaluronidases translated from *Pamphobeteus verdolaga*. Yellow highlighted residues indicate the cysteine position on hyaluronidase-like sequence (Cys17, Cys176, Cys183, Cys196, Cys218, Cys307, Cys332, Cys337, Cys343, Cys372, Cys374 and Cys383).

Hyaluronidase-1-Pverdolaga:

PRMYQSKLLQGLFPNSKDLPLDSVLLLDSEGA VKVIGH SRLSRVLEDNRG CWIASVIISKEKRG
QGLGKFLMMKTEEYAKVLGLTTAYLNTRDKQGFYEH LGYSY CNPVSPHKGSFSMNGVGHLS
NFHRQVLRRC EEGETNHSGSPVGD PKIAKSSSVSSAKTSTPPLPPPPPPPPSSNVKTD CFTSATG
HNWMKKYL

Sequence inputSeq Length 199 residues
Cysteines in this sequence: 4
Disulfide Connectivity prediction
Step 1: Running PSI-BLAST with input sequence; click [here](#) to see the output
Step 2: Predicting secondary structure using PSIPRED; click [here](#) to see the output
Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results
Warning! The number of predicted half-cystines is lower than 2.
Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching

Predicted bonds	
51 - 135	EDNRGCWIASV - QVLRRC EEGET
106 - 185	LGYSYCNFVSP - NVKTD CFTSAT

Predicted connectivity	
1-3, 2-4	

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Hyaluronidase-2-Pverdolaga:

MSVTLFLLLLLPCYTRQAEDPTVFTVRWNVPTIQCRKTYGMDFVPLLKSYGILVNSGDEFKGEV
 NTIFYESQLGLYPHLDQSGQRVNGGIPQLGDLPEHLKNAREDINKAIPDINFNGLGIIDWESWR
 PVWNFNWVGALKKYQDESFQEALKQHPGWTNDSLWQLAQQEWETSAKNFMLETLRLAQTM
 RPNLWLCYYLFPDCYNYNGQTPREFRCPISIVVTGNNQLSWLWHESKAVCPSLYVADGYLQKY
 TFEQRTWYVDGRLKEALRVAPNSQLYPYIGYGYGVTPGAMVPEDDFWRILAQVASAGSSGTVI
 WGASATLRSKDNCQLLQKYVKDILGPSVTIVKENAERCAKTMNGKGRCTWLNDPNVIAWR
 VYLDNRNKHPPQRSEITCHVEGYSGRYCDVQRRVINQTKLRVSFKLSLDLYTYLRRLLDN

Sequence inputSeq Length 432 residues

Cysteines in this sequence: 13

Disulfide Connectivity prediction

Step 1: Running [PSI-BLAST](#) with input sequence; click [here](#) to see the output

Step 2: Predicting secondary structure using [PSIPRED](#); click [here](#) to see the output

Step 3: Disulfide Oxidation State Prediction; click [here](#) to see the results

Step 4: Disulfide Bonds Prediction using a trained Neural Network

Step 5: Weighted matching**Predicted bonds**

13 - 392	LLLLPCYTRQA - EITCHVEGYSG
35 - 236	VPTIQCRKTYG - ESKAVCPSLYV
194 - 201	PNSLWCYYLFP - YLFPDCYNYNG
214 - 325	PREFRCPSIVV - RSKDNCQLLQK
350 - 361	ENAERCAKTCM - NGKGRCTWLND
355 - 390	CAKTCMNGKGR - RSEITCHVEG

Predicted connectivity

1-12, 2-6, 3-4, 5-7, 8-10, 9-11

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