

Figure S1. Proteomic workflow of the present study. Schematic representation of the study workflow. Sample collection days: 8 (N=3 sea urchins); tandem MS and pull-downs (N=2).

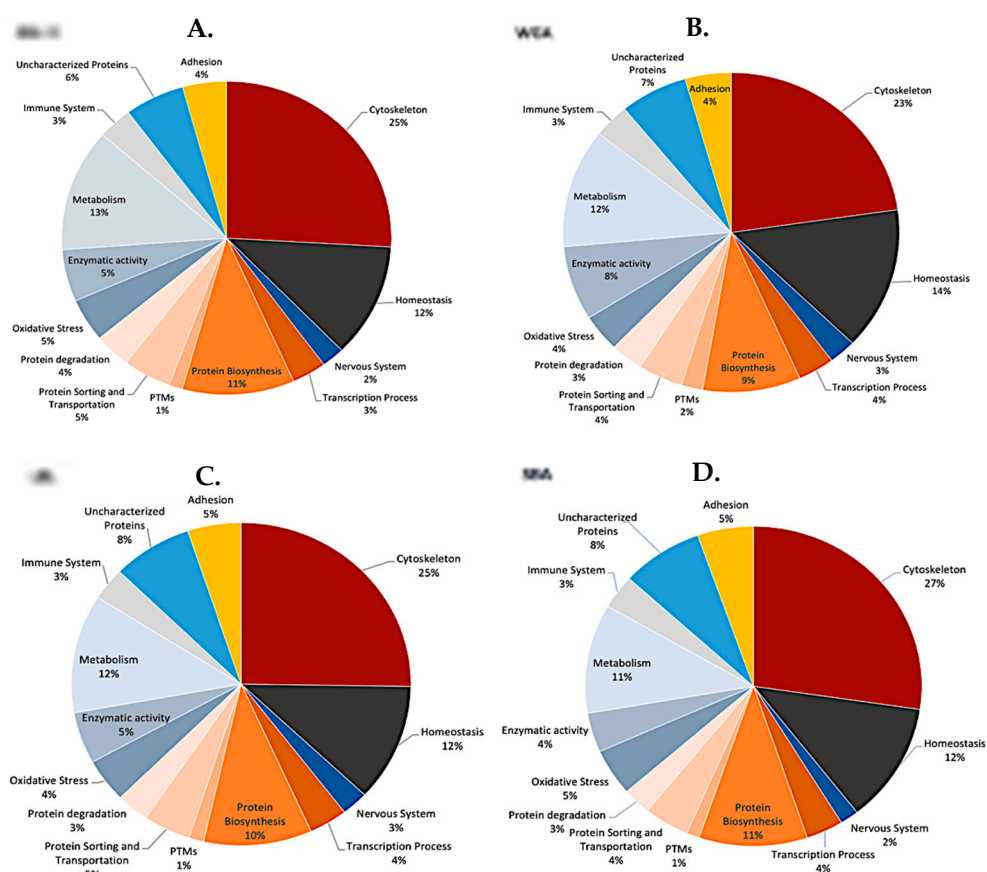


Figure S2. Global protein composition by functional groups of *Paracentrotus lividus* disc proteins pulldown with lectin-bounded agarose beads. GSL II was used to detect the presence of N-acetylglucosamine; WGA and LEL to detect chitobiosis and SBA to detect N-acetylgalactosamine conjugated with proteins (N=2). Abbreviations: GSL II, *Griffonia simplicifolia* lectin II; LEL, *Lycopersicon esculentum* lectin;

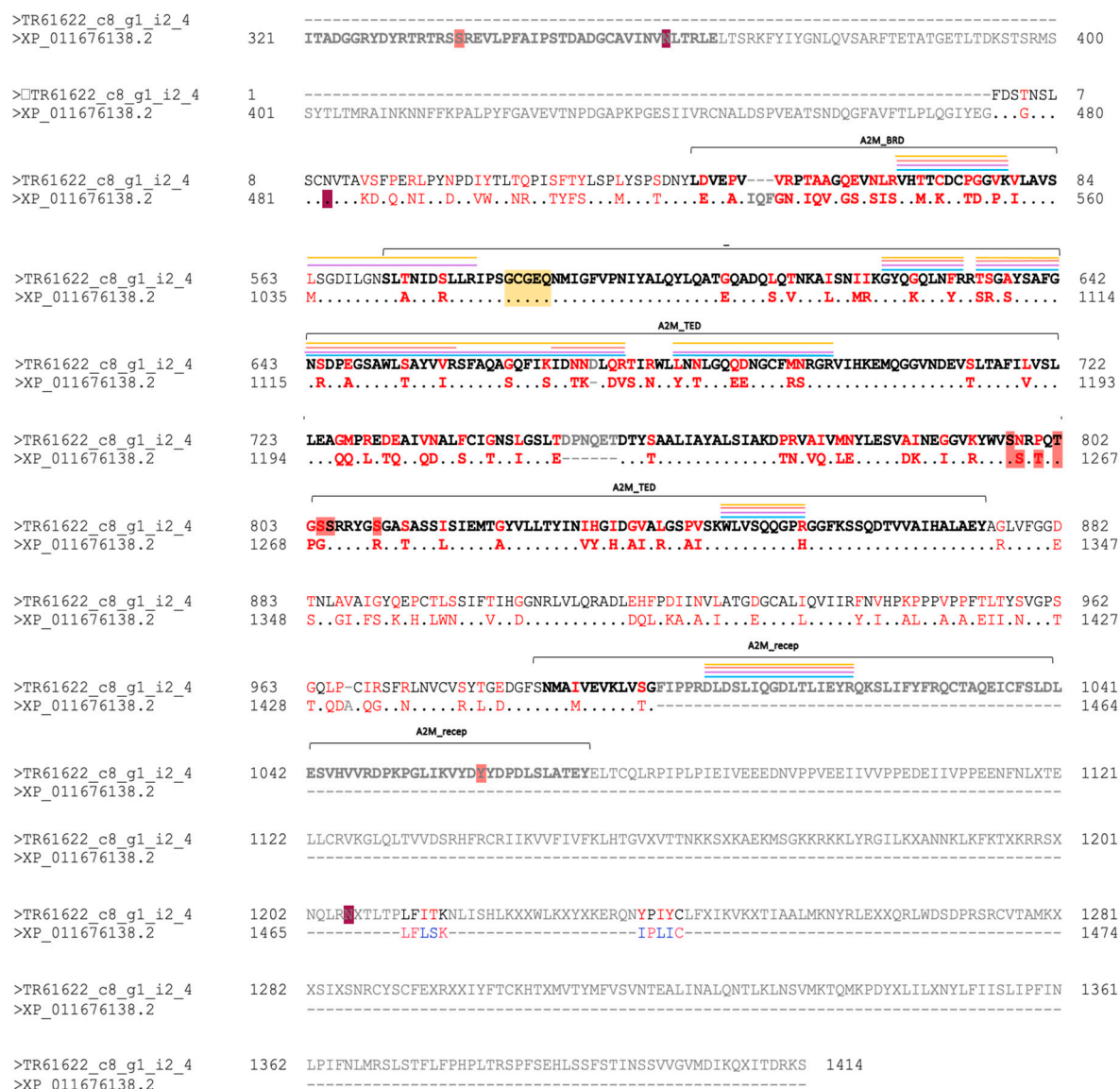


Figure S3. Alpha-2-macroglobulin like sequence alignment. Sequence alignment of *Paracentrotus lividus* alpha-2-macroglobulin and sea urchin *Strongylocentrotus purpuratus* alpha-2-macroglobulin homologous protein. Between sequences, black dots represent equal amino acids, red letters different amino acids in the same position and dash missing amino acids in the aligned sequence. Identified peptides by MS/MS (dashed over the sequences) validated N- (in purple) and O--glycosylation sites. Peptides were found in several lectin-pulldowns specifically GSL II (blue dash), WGA (pink), LEL (purple) and SBA (orange).

Consensus sequence 1	TR46688_c0_g1_i1_6 P L G A V N F M N V H P F S Y I V F G S A P G S P S T W N F P Y P A L S T T V C	42
XP_030852014.1 UP 1201	eitfetpgvlnldgptrfrigladdgtiellklenggg...I...GM.....G.N...S...T.T.N..	1280
Consensus sequence 43	DTQELNIGCPNGQFIDLMYASYGYHPDAISCSEDLPYSCHNENSFSEVLQRCQGIESCFAQVSTGLFSADPCPLTPKS	122
XP_030852014.1 UP 1281	.S.VMS.A...Y...S...SAA.TA...DGOA.A...S...KA...TA.V.NDPCV.M...	1359
Consensus sequence 123	LAIRYRCFSSPIQKTGRTGACIEMCCNGGYCIRSNGAALCRCQSGWTGTHCEISESTCTHYGSSHFTTFDGKHYEFPIS	202
XP_030852014.1 UP 1360	.TV..Q.VAD.S.E...DL..M...F..M..S...PT..ER.AV.S.F..A..M...N.R....	1439
Consensus sequence 203	SNGNEDCTFVLVRHEAHIGETFDVLARNGEITHIEINSRMIKLGEDVRIDGLPVQLDFTdsstPPLFRIDQGNEEFVVEL	282
XP_030852014.1 UP 1440	R...E...SASGES...V...Q...A...S---A...Q.S.K..G..A.T.	1515
Consensus sequence 283	NVGMTIAYKKGILHISMAASAAVSLGCDNNGNINDDFKLANNEITAVPMEFVQEHCTQCTISNTEDECVGQA--QARD	360
XP_030852014.1 UP 1516	...E...T.F.T.TGDA..L...N.D.DADN..E.E.D...LAK...Q..T..PLA...A..SMrd...E	1595
Consensus sequence 361	QCNMFIETDFAACTAAVSSELFLDECSYDVCRSKSYCDLSLEAYVSRCKERNIPLPDWRQTVGCVMECGPNMVYDECSS	440
XP_030852014.1 UP 1596	.SV..SSNL.DN.L.S-EPLVA...RGH...T..EN...N.MP...DS...E..A.	1674
Consensus sequence 441	ACQATCLNPTASANCALPSSCVERCVCQDPFILKSGRCVPMACQFTM---LMTGGEQLGNSP---PAFIP-PSRGSPAP	512
XP_030852014.1 UP 1675	.P..Q...QE...NLP...EAG...A...QpaAEV.FEIVQA.vrqq.VVA.a..PVV...	1752
Consensus sequence 513	VPAP---Q.GMDLQOLFOL--GGQ.PAGQVPVPV-GQPAPSP-----VGQPAFFSV-G	560
XP_030852014.1 UP 1753	.S.v...G.IPN.GSL.A.nq.VPA..PA...A.AS...A.gqfnlapapapaapapapagaQPA...A..p.	1832
Consensus sequence 561	QPVP--PGFSLADMLRNLRGQ.PAPQGPAPGPVSGPAPGPV-----AGPAPVPSPNPQVPSP.PTASVPVQPGPAP	632
XP_030852014.1 UP 1833	.Aa..Q.N..PAPAAP...A.V...A.LNL.SLKLfqlnqp.Q...S.PVAG...P.V.GQVPVSP.VAGQ	1911
Consensus sequence 633	QPVPQFgipilrlfqlgQGPAP.PAGQPVGQGPAP.PVGGQGPAP.PAGQGPAP.PAGQGPAPFAG-----	705
XP_030852014.1 UP 1912	PVPSP...VAGQ.V.SPPVA...V.S.VG...V.S.PV...V.S.PV...I.PAEVPEmcdniy	1977
Consensus sequence	gfdvfarpnycddktvifygdpmqchgdksinylvrvrlepfyvrfyrmgrnmllilvgstvtpttlnetlaisipyr	2057
XP_030852014.1 UP 1978		
Consensus sequence	kgdflavsfqtlvlysytkggtstatilvvdynhvpaiasslpgtttfiterelqekreysimatldcecdgepgqpsidc	2137
XP_030852014.1 UP 2058		
Consensus sequence	nsplgmmsraipdasitsssaiegspasegrlyslvgmlfmggegwaatsesgqwiqvrlnaatnvvgltqggggsgss	2217
XP_030852014.1 UP 2138		
Consensus sequence	qewtsyavqyalgsdmpqyfrddkdmmtgfmngtdketivtnyfwkpvkaevirilpknwssrismrfeylgladnpc	2297
XP_030852014.1 UP 2218		
Consensus sequence 1	TCIMYPTSSIMTYDERQYFFPGEDYVATQTCDENAAESFQV	42
XP_030852014.1 UP 2298	dsspcqngggvc...hdtrt...gymcacqerfsgkmcdeieg...VL.....KNYY...Q.E...S...Q.GQD...	2377
Consensus sequence 43	YVKNIPStDPVSYVPARREIRVELNGKSYELKEKEFYLDGERISLPYIRPNVQVILAGNNFPVLKTDDFGLRVWWDGRRT	122
XP_030852014.1 UP 2378	F.N...A..I.N...V.D.T...A.LNL.SLKLfqlnqp.Q...S.PVAG...P.V.GQVPVSP.VAGQ	2456
Consensus sequence 123	VRIEVPSHHQDMCGLCGNFNDATDDFIMRGSSVASAPAFGFSWASNSPDCPTRCPFCQDPSCDTQIAQLDASSVCS	202
XP_030852014.1 UP 2457	.K...L..K...D.Q...R.QA...LP.A...T.GQQ.TA...NEV...VNNV.K.S.ETI...	2536
Consensus sequence 203	EMNIPFKTCLDAMPNTYMSDCVAGRCAI-QDDDLFCLEMLVNLAYQCEIMGVSVGRWRDAITRCAPITPEGTMYPECLVP	281
XP_030852014.1 UP 2537	...A..A...S...TS.I..Tds.S...SE..V..L...V...P...S..S.	2616
Consensus sequence 282	CTPTCADPGAEKCDLMTCEVGYACSPGLVFNGETCQVTRCCCLVEGKSYDVGESYLIHDCTEQCVCSEGGNMECMPVE	361
XP_030852014.1 UP 2617	...GN.NTA...M...AE...M...I...VN...H...KA...	2696
Consensus sequence 362	CHMDATCAVQGGYTCHCNDGFSGRGLETCCLAINQPIMTQCENEDVTLTCEGLIDVLSVYGGQDGLSECLSSGFLLG	441
XP_030852014.1 UP 2697	...K.S.ME.N.K...A.Q...F.V...ATT...V...AI...V...I.A...A.PT...S	2776
Consensus sequence 442	TCSAEGVLLPVQLQCQGRPECTFTANMFMGEPENGVAKYIRVQHHCQOPLASEVPQTPVRRNMPQGNIMVLECPDGTF	521
XP_030852014.1 UP 2777	.A...T..A..NR...KA...SDV..V...KA...V..E...PEA.G...I...AS...N.Q..E...	2855
Consensus sequence 522	LDIQRARYGRPDREESCFSAEVRVAMCQGLTRCEVDVTDNLGETCEMTNNILEVNFESAQPVDRSTILGHCNEN	601
XP_030852014.1 UP 2856	...V.F...PS..AII..A...Q.Q...VA..T...P..M...S...E...STIM...	2935

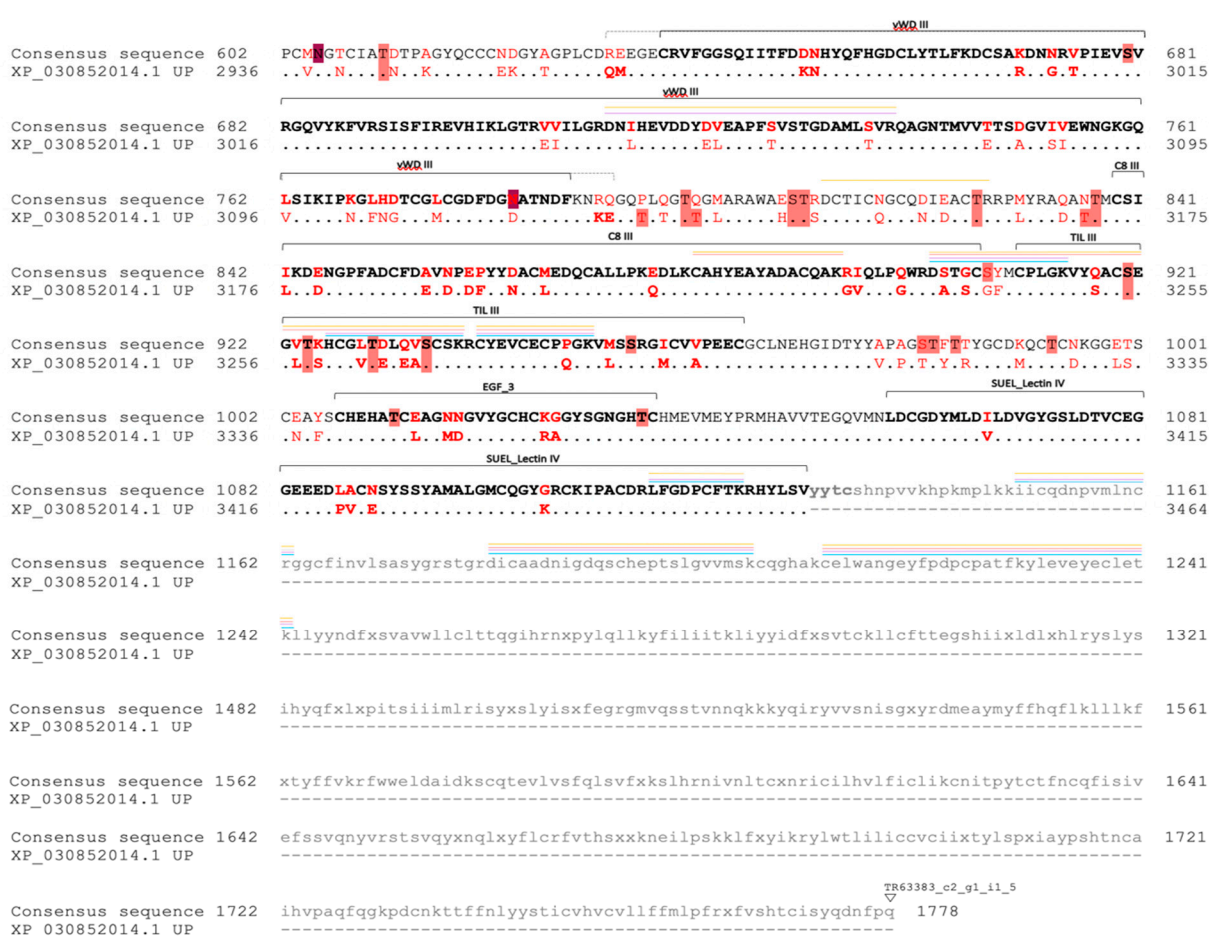


Figure S4. Alpha-tectorin like sequence alignment. Sequence alignment of *Paracentrotus lividus* alpha-tectorin and sea urchin *Strongylocentrotus purpuratus* uncharacterized protein LOC100892803 homologous protein. Between sequences, black dots represent equal amino acids, red letters different amino acids in the same position and dash missing amino acids in the aligned sequence. Identified peptides by MS/MS (dashed over the sequences) validated N- (in purple) and O--glycosylation sites. Peptides were found in several lectin-pulldowns specifically GSL II (blue dash), WGA (pink), LEL (purple) and SBA (orange).

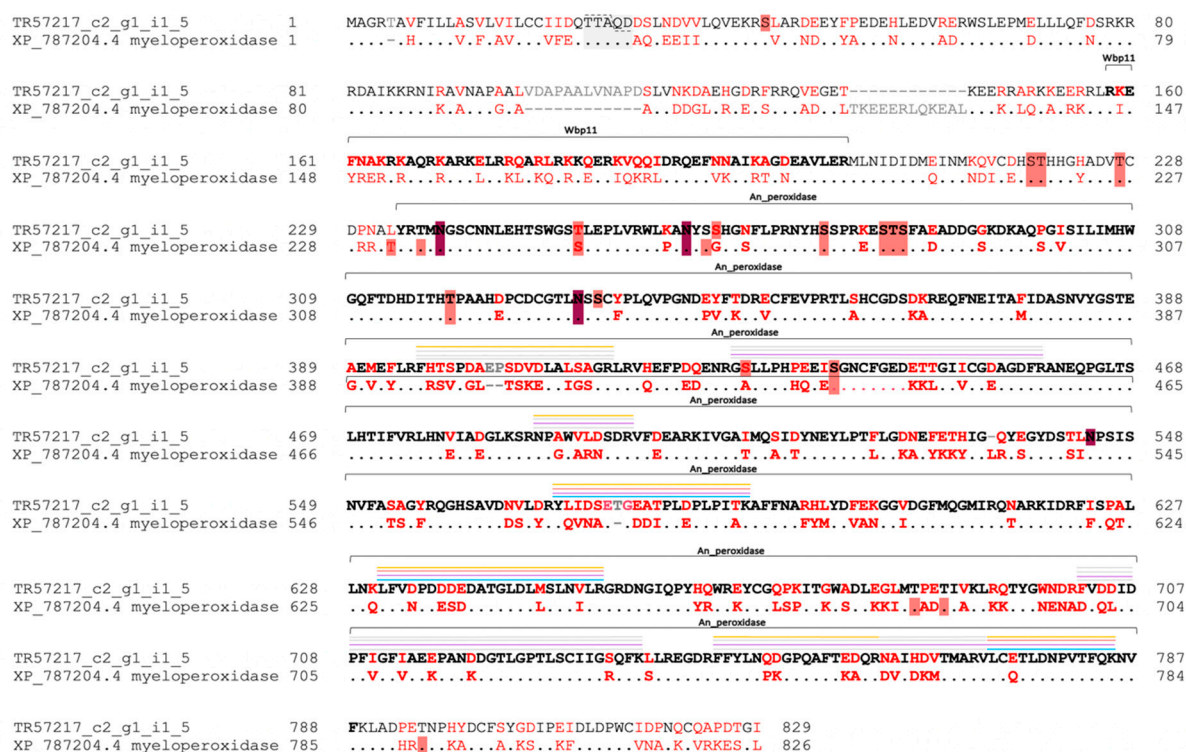


Figure S5. Myeloperoxidase sequence alignment. Sequence alignment of *Paracentrotus lividus* and sea urchin *Strongylocentrotus purpuratus* myeloperoxidase homologous proteins. Between sequences, black dots represent equal amino acids, red letters different amino acids in the same position and dash missing amino acids in the aligned sequence. Identified peptides by MS/MS (dashed over the sequences) validated N- (in purple) and O--glycosylation sites. Peptides were found in several lectin-pulldowns specifically GSL II (blue dash), WGA (pink), LEL (purple) and SBA (orange).

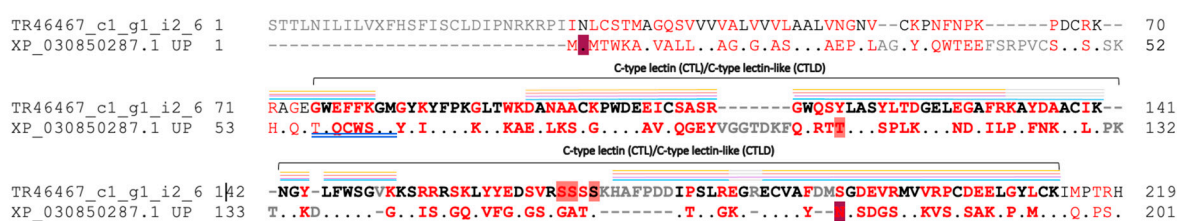
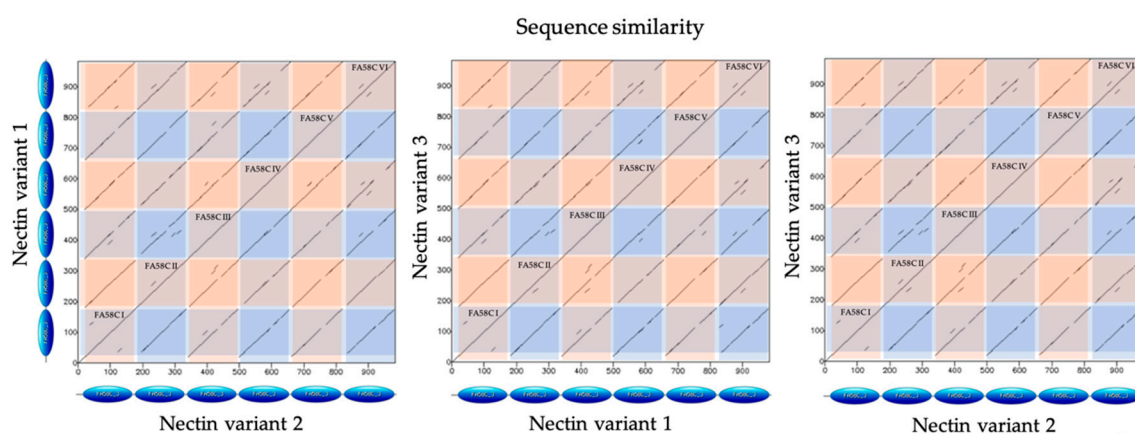


Figure S6. Uncharacterized protein sequence alignment. Sequence alignment of *Paracentrotus lividus* and sea urchin *Strongylocentrotus purpuratus* uncharacterized proteins homologous proteins. Between sequences, black dots represent equal amino acids, red letters different amino acids in the same position and dash missing amino acids in the aligned sequence. Identified peptides by MS/MS (dashed over the sequences) validated N- (in purple) and O--glycosylation sites. Peptides were found in several lectin-pulldowns specifically GSL II (blue dash), WGA (pink), LEL (purple) and SBA (orange).



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Figure S7. Comparison of Nectin variants. Graphical representation of the similarity regions between two protein sequences using EMBOSS Dotmatcher. Local regions of similarity correspond to diagonals in the dotplot. Structural variations are represented as gaps on the diagonal lines (deletion and insertions) or duplication of a sequence segment towards one of the axis (duplication).

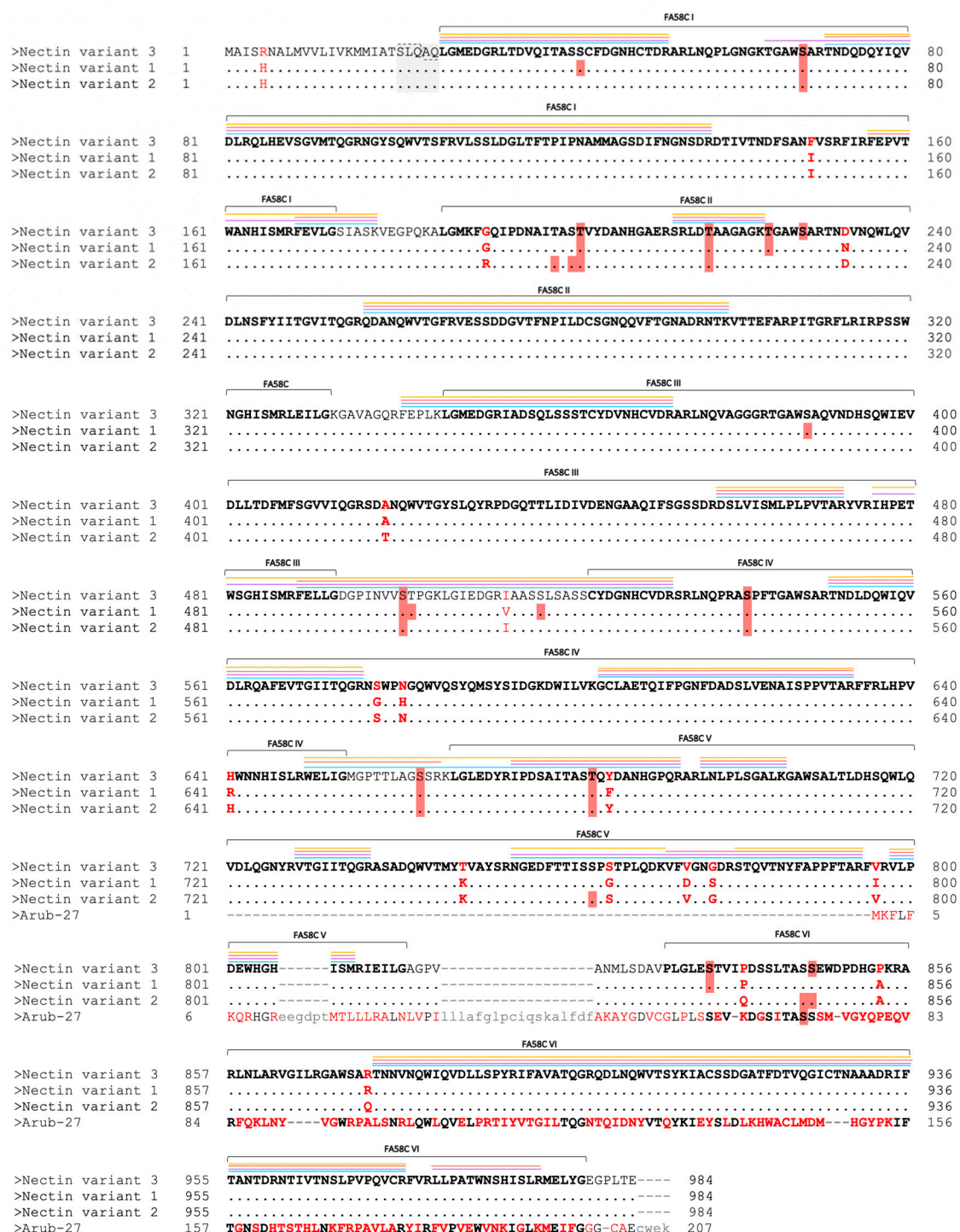


Figure S8. Nectin sequence alignment. Sequence alignment of *Paracentrotus lividus* Nectin variants and sea star *Asteria rubens* Arub-27. Between sequences, black dots represent equal amino acids, red letters different amino acids in the same position and dash missing amino acids in the aligned sequence. Identified peptides by MS/MS (dashed over the sequences) validated N- (in purple) and O- glycosylation sites. Peptides were found in several lectin-pulldowns specifically GSL II (blue dash), WGA (pink), LEL (purple) and SBA (orange).

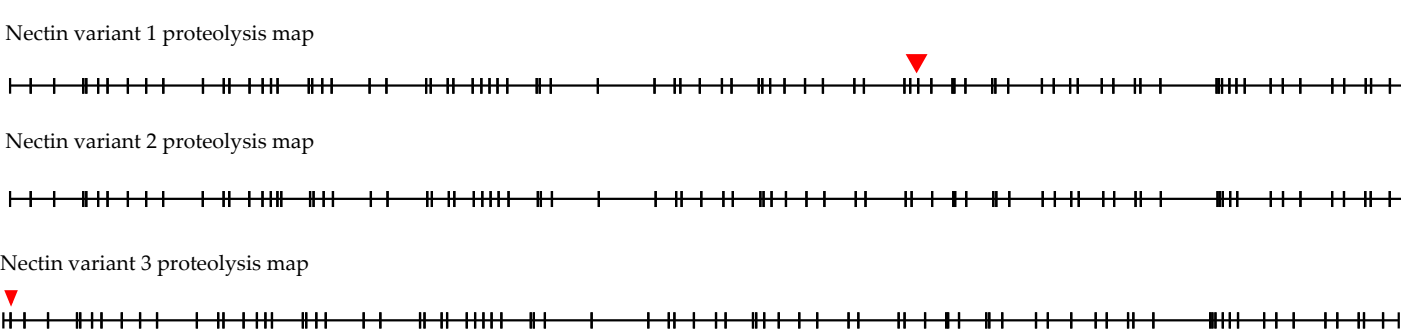


Figure S9. Proteolysis map of Nectin variants. Sites predicted to be cleaved by trypsin were performed with proteolysis mapping tool. Cleavage sites are identified by black lines, while differences between sequences are emphasize as a red arrow.