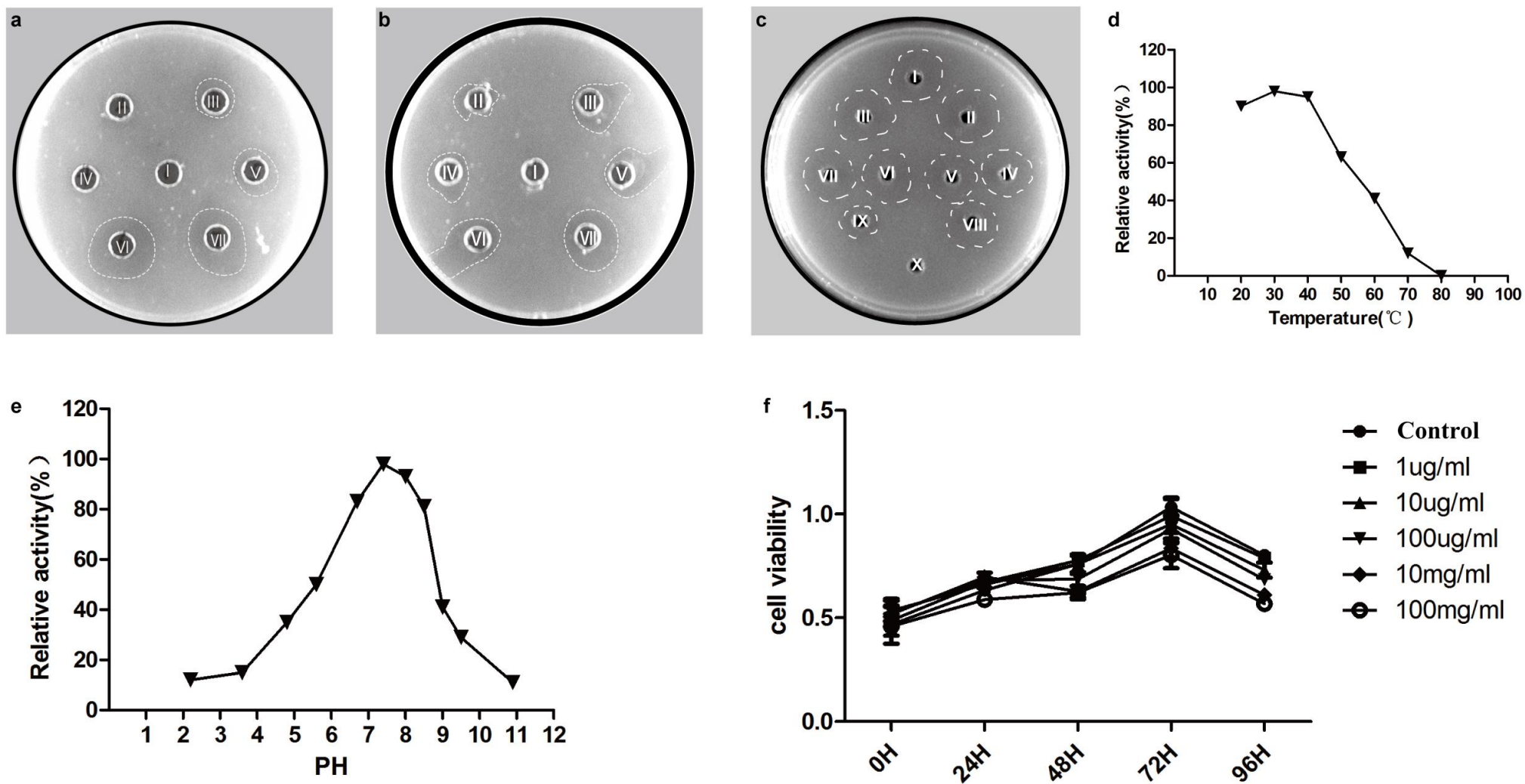
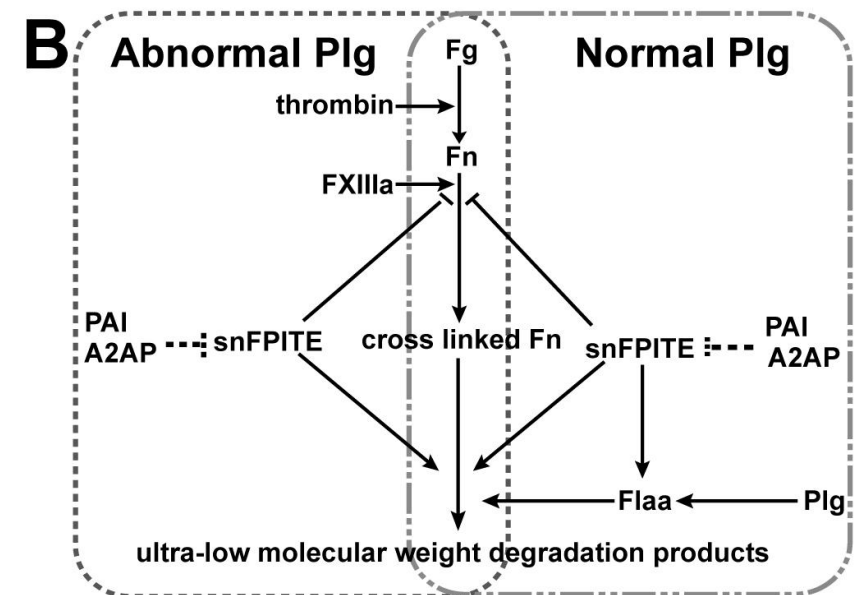
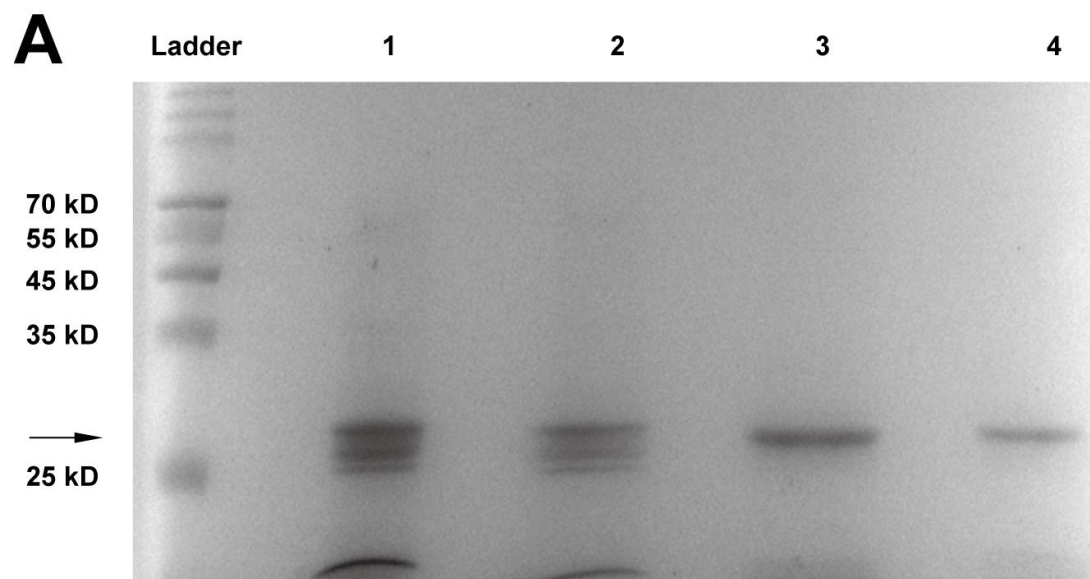
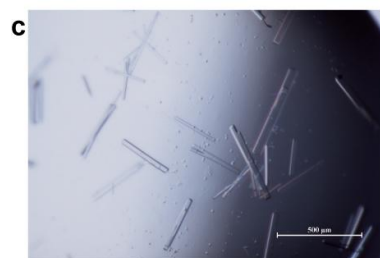
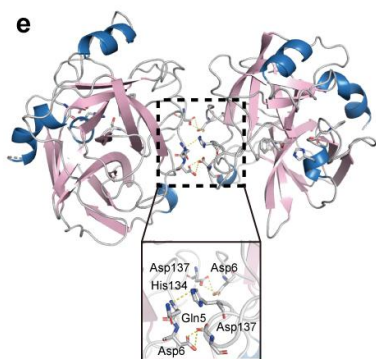
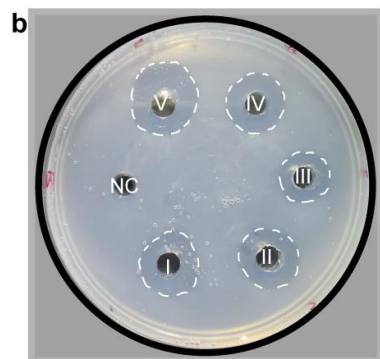
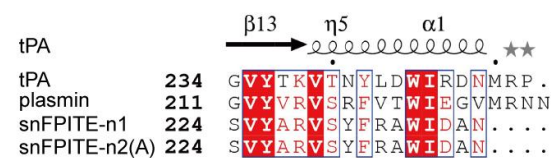
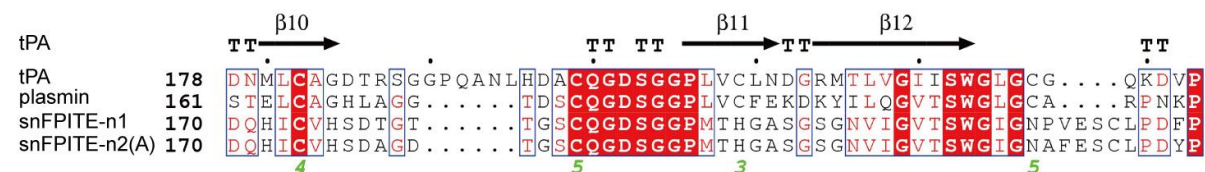
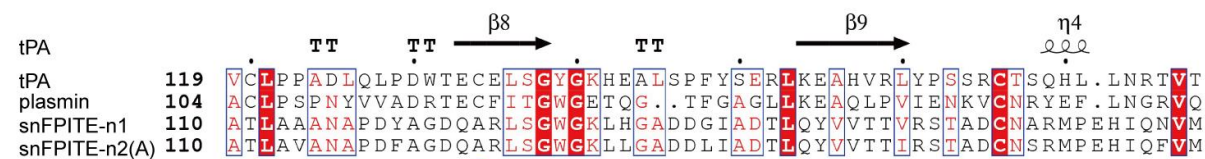
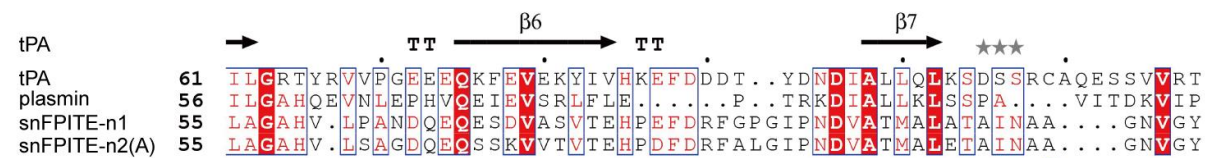
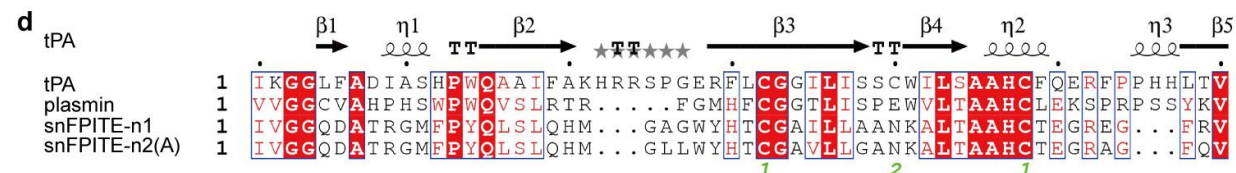
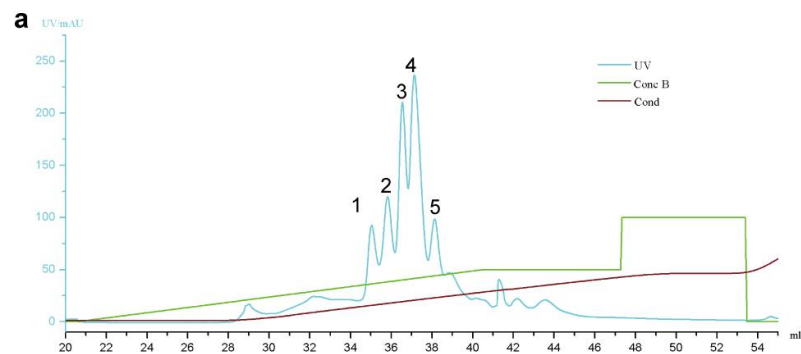




Extended figure 1



Extended figure 2



Extended figure 3

a

fibrinolytic enzyme [Enchytraeus japonensis]Sequence ID: [BAL43185.1](#) Length: 270 Number of Matches: 1Range 1: 33 to 269 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

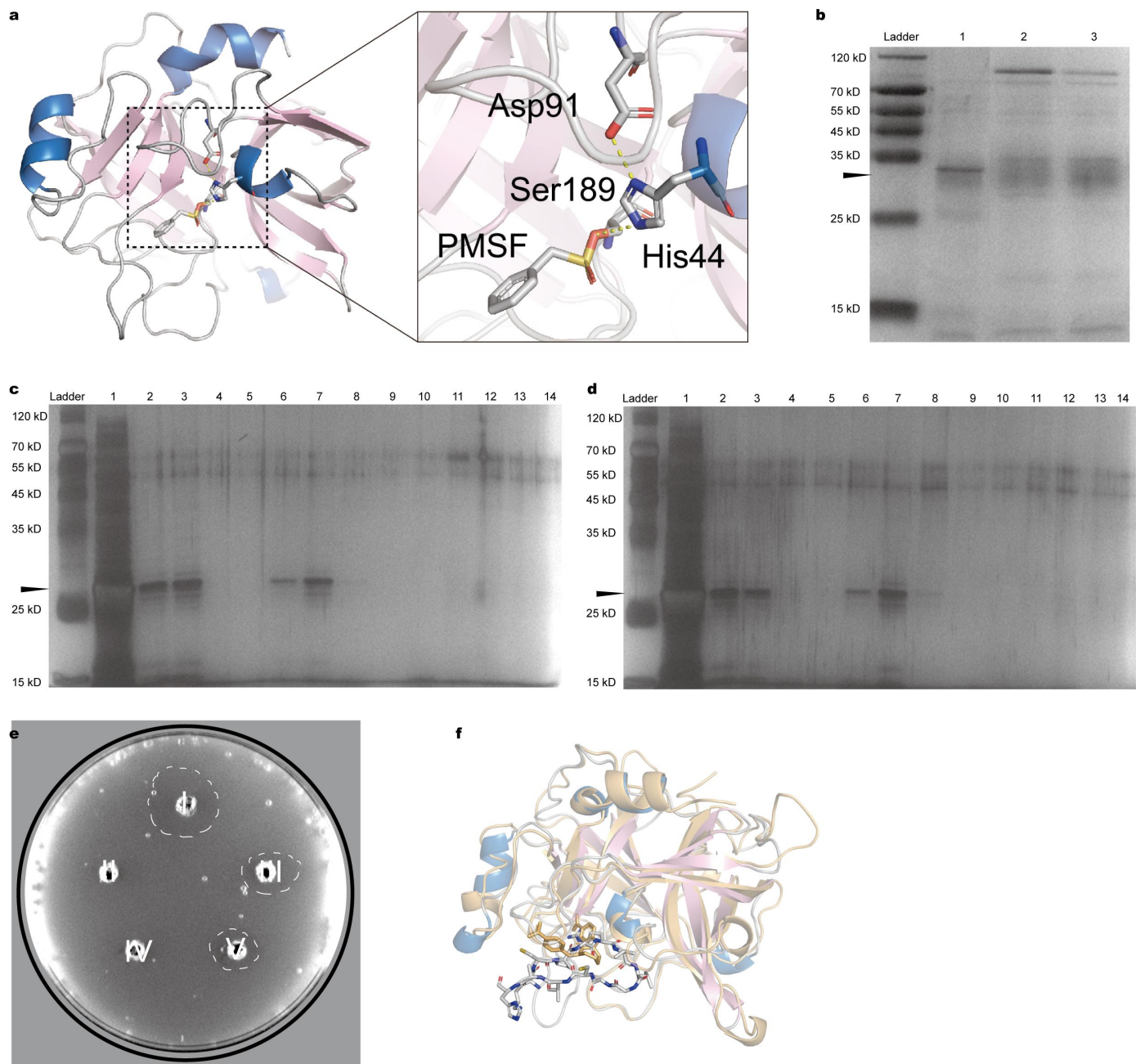
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192 bits(488)	1e-56	Compositional matrix adjust.	107/241(44%)	144/241(59%)	6/241(2%)
Query 1	IVGGQDATRGMFPYQLSLQHMAGWYHTCGAILLAANKALTAAHCTEGREG--FRVLAGA	58			
Sbjct 33	VVGGTDAASPGEFPWQLSQQRLLGGSWSHSCGASLIGATKALSAAHCVGDGASASILRVIAGL	92			
Query 59	HVLPANDQEQESDVASVTEHPEFDRFGPGIPNDVATMALATAINAAGNVGYATLAAANAP	118			
Sbjct 93	HQRSNTAGTQTSNVASYTTTHESYNQGSATFANDVAILNLATAITTTGGNIAFATLAQG-SN	151			
Query 119	DYAGDQARLSGWGKLHGADDGIADTLQYVVTTVRSTADCNARMPEHIQNVMDQHICVHSD	178			
Sbjct 152	DFAGTTTCVISGWGRS-ASNALPDTLQKVSIPVISGTQCQS-LVAGIGTIWDGHICLYDS	209			
Query 179	TGTTGSCQGDSSGPMTHGASGSGNVIGVTSWGIGNPVESCLPDFPSVYARVSYFRAWIDA	238			
Sbjct 210	AGNIGSCNGDSSGPLNCPSSGATVVAGVTSWGI-SSLGVCQRDYPVYTRVSYYYTWIN	268			
Query 239	N	239			
Sbjct 269	H	269			

b

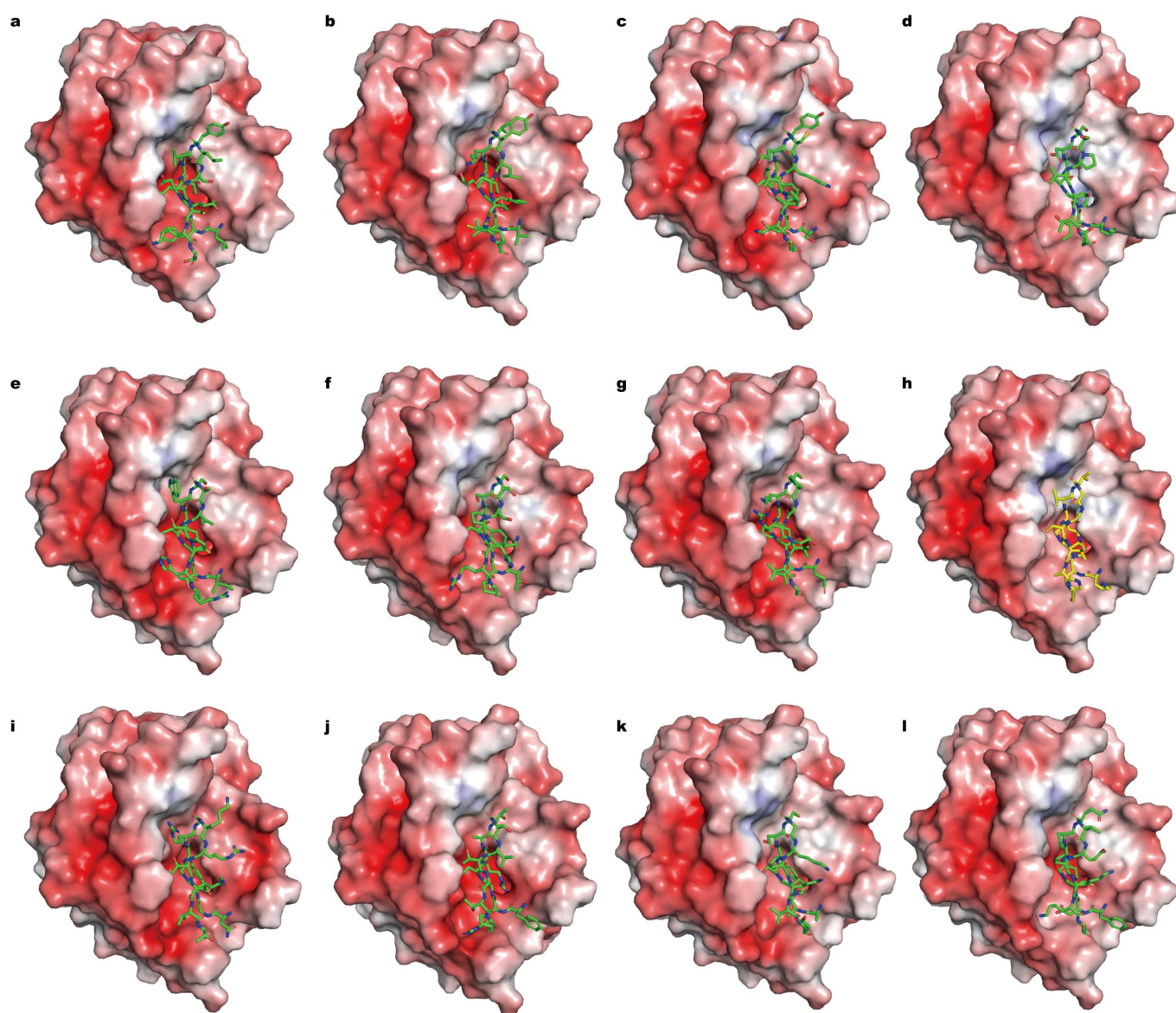
Chain A, Earthworm Fibrinolytic Enzyme [Eisenia fetida]Sequence ID: [1M9U_A](#) Length: 241 Number of Matches: 1[See 2 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)Range 1: 1 to 240 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
162 bits(409)	3e-45	Compositional matrix adjust.	100/242(41%)	137/242(56%)	5/242(2%)
Query 1	IVGGQDATRGMFPYQLSLQHMAGWYHTCGAILLAANKALTAAHCTEG--REGFRVLAGA	58			
Sbjct 1	VIGGTNASPGEFPWQLSQQRQSGWSHSCGASLLSSTSALSASHCVDGVLPNNIRVIAGL	60			
Query 59	HVLPANDQEQESDVASVTEHPEFDRFGPGIPNDVATMALATAINAAGNVGYATLAAANAP	118			
Sbjct 61	WQQSDTSGTQTANVDSYTMHENYAGTASYSNDIAILHLATSISLGGNIQAAVLPANNNN	120			
Query 119	DYAGDQARLSGWGKLHGADDGIADTLQYVVTTVRSTADCNARMPEHIQNVMDQHICVHS	177			
Sbjct 121	DYAGTTTCVISGWGRDGTNN-LPDILQKSSIPVITTAQCTAAMVGVGANIWDNHICVQD	179			
Query 178	DTGTTGSCQGDSSGPMTHGASGSGNVIGVTSWGIGNPVESCLPDFPSVYARVSYFRAWID	237			
Sbjct 180	PAGNTGACNGDSSGGL-NCPDGGTRVVGVTSSVSSGLGACLPDYPVYTRVSAYLWIG	238			
Query 238	AN	239			
Sbjct 239	DN	240			

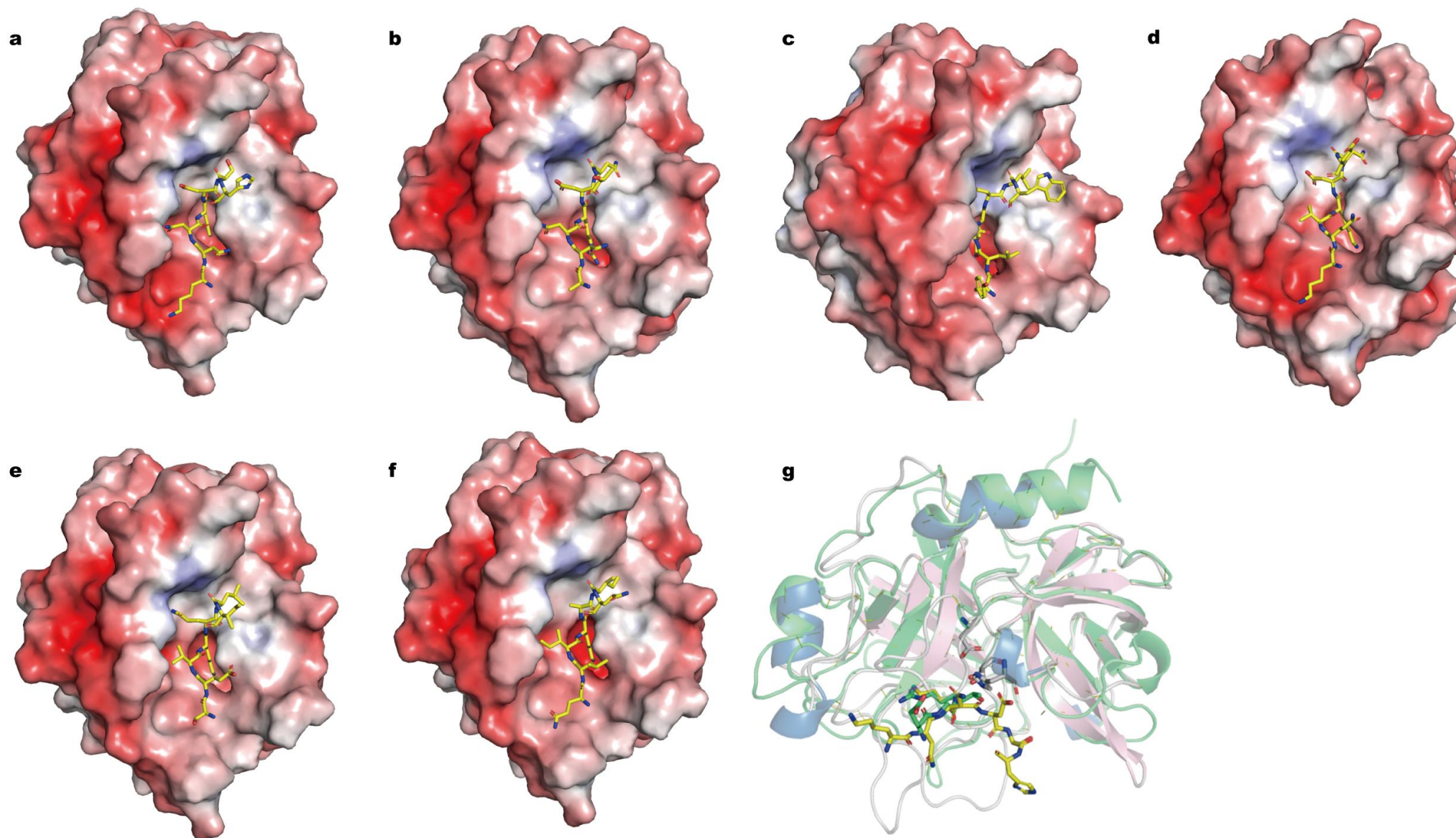
Extended figure 4



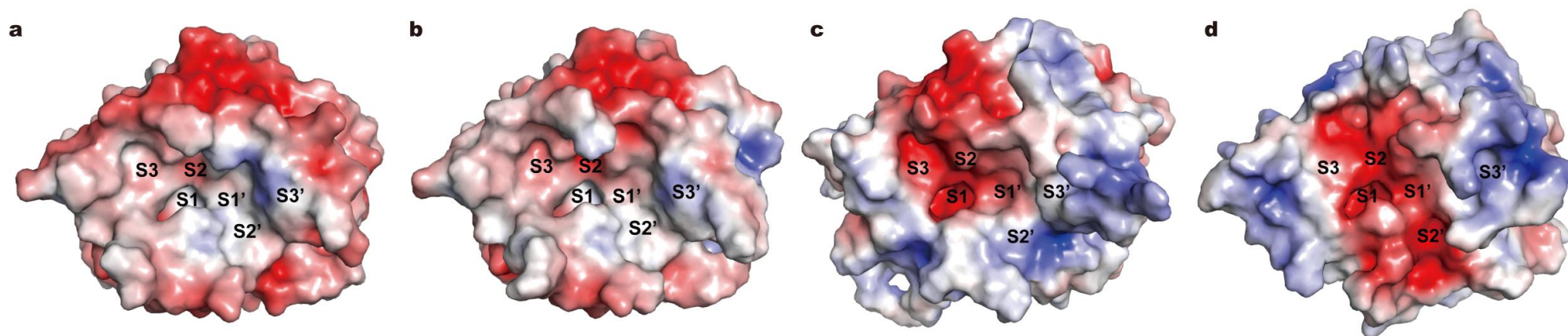
Extended figure 5



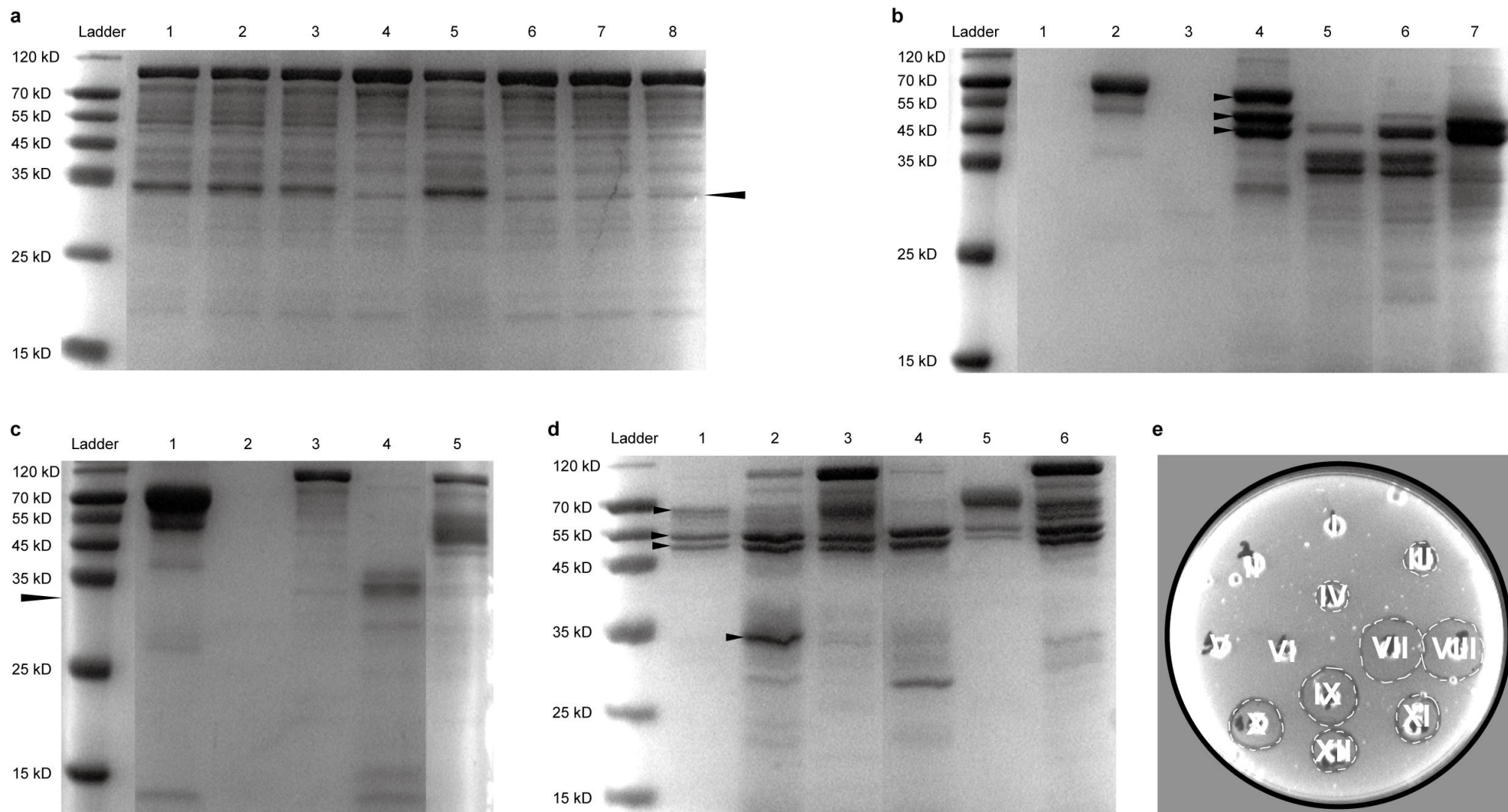
Extended figure 6



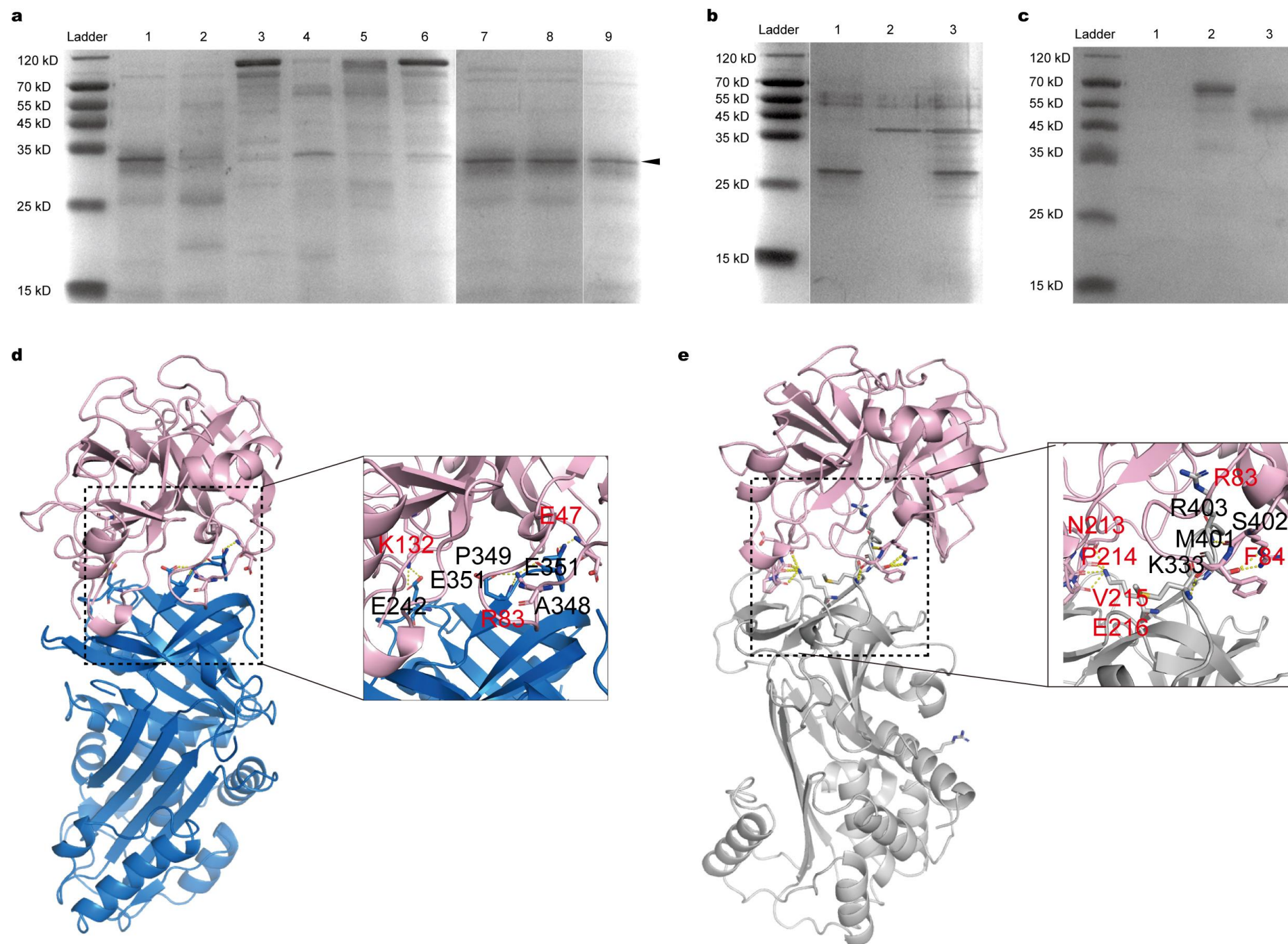
Extended figure 7



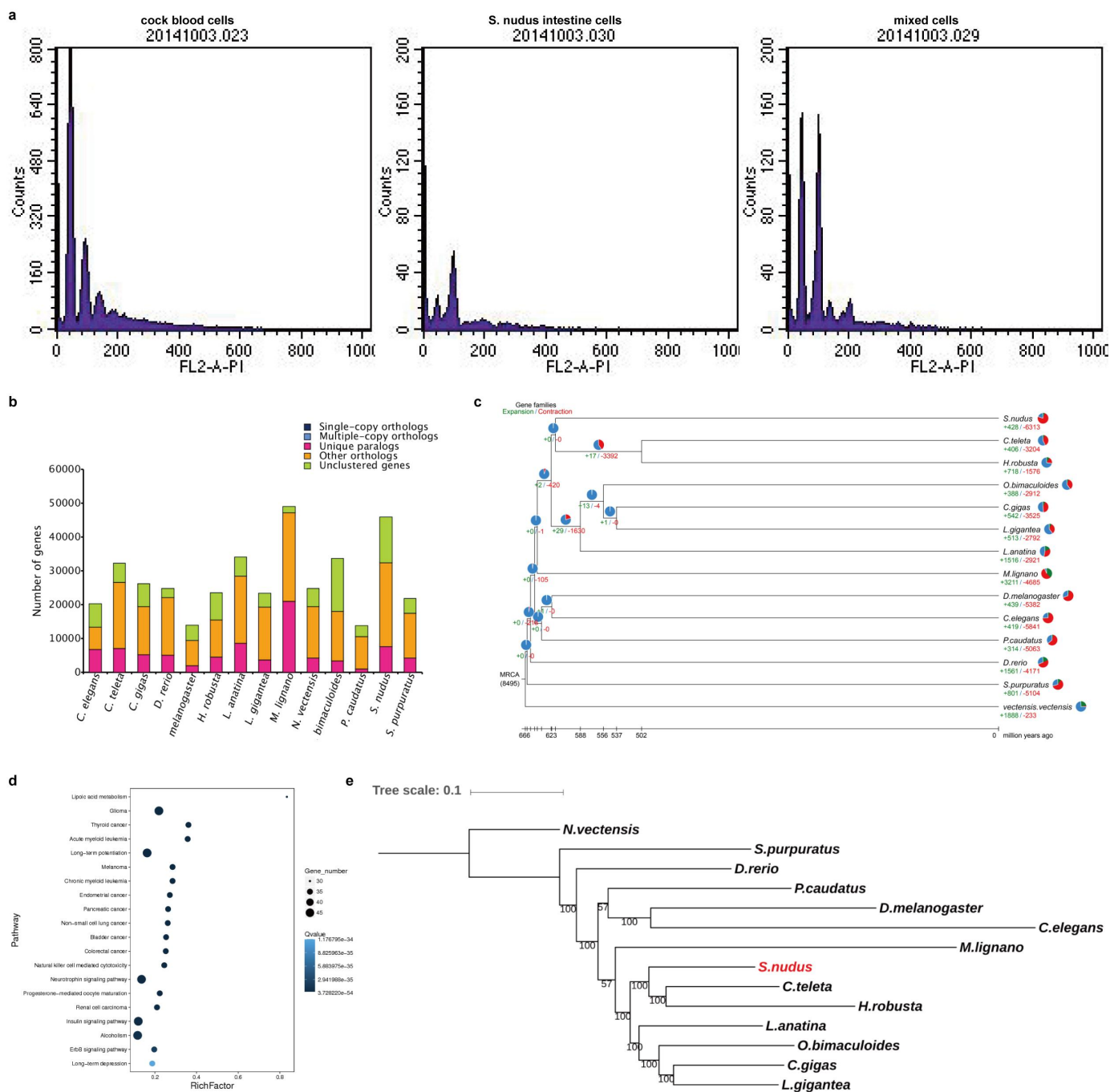
Extended figure 8



Extended figure 9



Extended figure 10



Extended figure 12

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      1      10      20      30      40      50      60      70      80
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snFPITE4 .....IVGGQEATRGMPFYQLSLNLMG..ADWYHTCGAAILLGANKALTAHAHCTDG
snFPITE3 .....MWKILLVAILAAVEARPKSN.LFVSFQNPRIVGGQEASRGMPFYQLSLQHLMG..TDWYHTCGAAILLGANKALTAHAHCTEG
snFPITE7 .....MLFYTVTEARPRTE.FYASFVPRIVGGSPASKGDFPHQLSLQHNN..GGWYHTCGASLISASKALTAHAHCTQG
snFPITE15 .....MWKILALCFLAAVEARPRSQ.FFASFDPRIVNGSPASKGQFFPYQLSLQYDNWFFGYSHTCGASLLSSRKALTAHAHCTDG
snFPITE9 MVSRSQSPRTTGTGMTWITILALCFLAAVEARPRTE.FFASFDPRIVNGSPASKGQFFPYQLSLQYDDFWFGYSHTCGASLLSSRKALTAHAHCTDG
snFPITE12 .....
snFPITE10 .....
snFPITE11 .....IIGGTPVSKGRWPWQLSLQICS..FGCGHTCGAVLLSSSKALTAHAHCTTG
snFPITE8 .....
snFPITE1 .....
snFPITE5 .....
snFPITE6 .....
snFPITE14 .....
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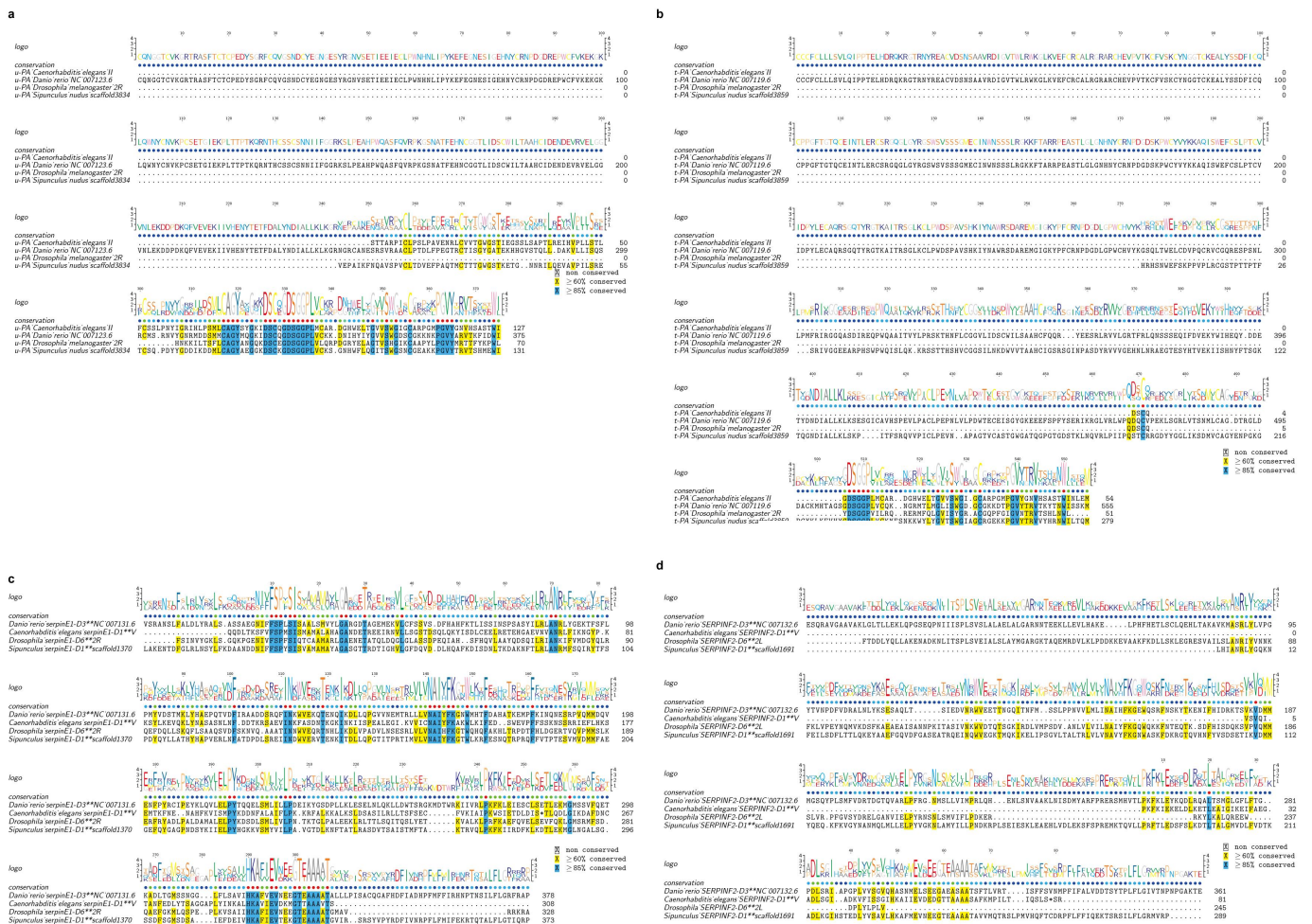
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snFPITE4 RVGFRVLGAGHVLASAG.DQEQQSDVATTTEHPDFDRFGDGIPNDVATMALLS.SAINAGGNVGYATLAANAP...NYAGDQVRLSGWGKLRGAD
snFPITE3 RDGFRVLGAGHVLASAN.DQEQVAEVASTTEHPEFDRFGDGIPNDVATMALLS.SAINAGGNVGYATLAANAP...DYAGDQVRLSGWGKLRGAD
snFPITE7 RSGFRVRAGATRLSPS.DHEGEASVAAIIEHPGYDSSGASGIPNDIATLHLIS.SSISGGGIGYASLPSSGAG...SYAGNSVYISGWGKTGMD
snFPITE15 RWGFRVRAGATRLSPS.DHEQAATISTITEHPNYSSGSAAGIPNDVCTLGGLG.STINSSGGSVAYASLPSSAS...SYAGNTAFISGWGKTGTGA
snFPITE9 RVGFRVRAGATRLSPS.NHEQAATVSSITEHPNYSSGSAAGIPNDVCTLGGLG.SNINAGGSVGYASLPSSAS...SYAGNSAFISGWGKTGGA
snFPITE12 .....STDEAETIDAKNLQHPRYSSGSSPGVPNDIATLRLAD.SARTVSGVVEFARLANSNFPITENYVGATTCYISGWGRTDSSG
snFPITE10 .....QHPLYSSGAPGVPNDIATMALSESATPVSGIIVEFASLASVGS...DWVGSTCYISGWGRTSSG
snFPITE11 .....QHPLYSSGAPGVPNDIATMALSESATPVSGIIVEFASLASVGS...DWVGSTCYISGWGRTSSG
snFPITE8 RSGFQILLGASQIDGS.DAEQTIEISSTTEHPGYSSGAPGIPNDIATMALSESANPVSGIIVEFASLASVGS...DWVGSTCYISGWGRTSSG
snFPITE1 .....QHPLYSSGAPGIPNDIATMALSESATPVSGIIVEFASLASVGS...DWVGSTCYISGWGRTSSG
snFPITE5 .....QHPLYSSGAPGIPNDIATMALSESATPVSGIIVEFASLASVGS...DWVGSTCYISGWGRTSSG
snFPITE6 .....QHPLYSSGAPGIPNDIATMALSESATPVSGIIVEFASLASVGS...DWVGSTCYISGWGRTSSG
snFPITE14 .....QHPLYSSGAPGIPNDIATMALSESATPVSGIIVEFASLASVGS...DWVGSTCYISGWGRTSSG
snFPITE2 RSGFRILAGASNIGASPDHEAESLVSSSTTEHPGFDRFAPGIPNDVGTLLALA.TAVNAGGAILYASLAPETGGP...DYAGNECWASGWGRLLGDN

      180      190      200      210      220      230      240      250      260
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snFPITE4 EGIADTLQYVVTVVRS.TADCN.NARMP.EHIOF.VRDEH.CVHSD.DASS.GSCSG.GDSGGPMT.HGSTGAGNVI.GVTSWGI.CGNPLE.SCLT.HDF.SVYARVS
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snFPITE7 DGGSNVLNQVRRITV.ISETD.CNRNGMP.GSLGSGISAMH.CIFLS..GNSGSGSG.GDSGGPMT.HASNG..LMIGVTSWVGCI.NIFD.SCLT.EY.SVYARVS
snFPITE15 SSGSNILNYAATTILSTTD.CNARMPS.NLGDG.ISSMH.CVHG..GGSGSGSG.GDSGGPMT.HGNSG..LMIGVTSWVGTS.ESDT.TCMTAY.SVYARVS
snFPITE9 SSGSNVLNFAQTIIILSTTE.CNANMPS.NLGGGISMH.CVHG..GGSGSGSG.GDSGGPMT.HGNSG..LMIGVTSWVGTS.ESDT.TCMTAY.SVYARVS
snFPITE12 GSLPSTLQ.EALVDHIDTAE.CNRMPI.NLADGLNDSH.CVHTNTRTR.GSGSGSGSG.GDSGGP.VCCNNG.SWTV.CGVTSWVGSI.VNFS.SCLT.TY.SVYARVS
snFPITE10 GSLPTGLREALVDHVD.TAE.CNRMPI.NLADGVTDNH.CVHTSTGT.GSGSGSGSG.GDSGGP.VCCS.SWTV.CGVTSWVGSI.VNFS.SCLT.TY.SVYARVS
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snFPITE5 GSLPTGLREALVDHLD.TAE.CNRMPI.NLADGVTDNH.CVHTNTGT.GSGSGSGSG.GDSGGP.VCCS.SWTV.CGVTSWVGSI.VNFS.SCLT.TY.SVYARVS
snFPITE6 GSLPTGLREALVDHVD.TAE.CNRMPI.NLADGVTDNH.CVHTNTGT.GSGSGSGSG.GDSGGP.VCCS.SWTV.CGVTSWVGSI.VNFS.SCLT.TY.SVYARVS
snFPITE14 DDLPDTLQELQIDALT.NDE.CNRMPI.NLREGVLDQH.CVHGN.GTRGAC.GDSGGP.LNC.RDGSFLVVGVTSWVGS.FDDT.CMTAY.NAYARVT
snFPITE2 GP.LPDQLQ.EVRIDALT.NAE.CSRMPE.NLQENVL.DQH.CVHGN.GNCGAC.GDSGGP.LNC.RDGSFLVVGVTSWVGS.MDS.SCLT.EY.NVYARVS

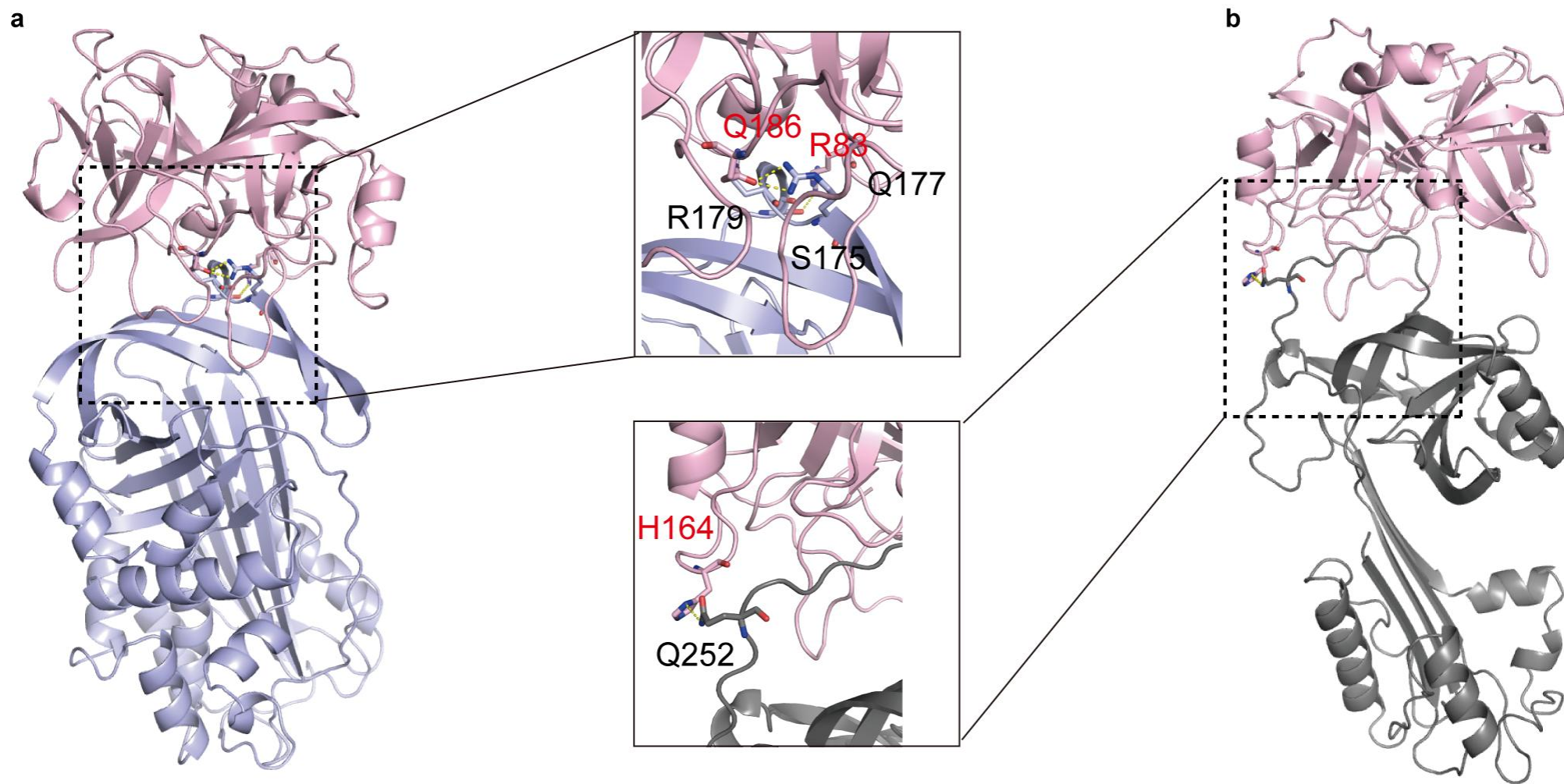
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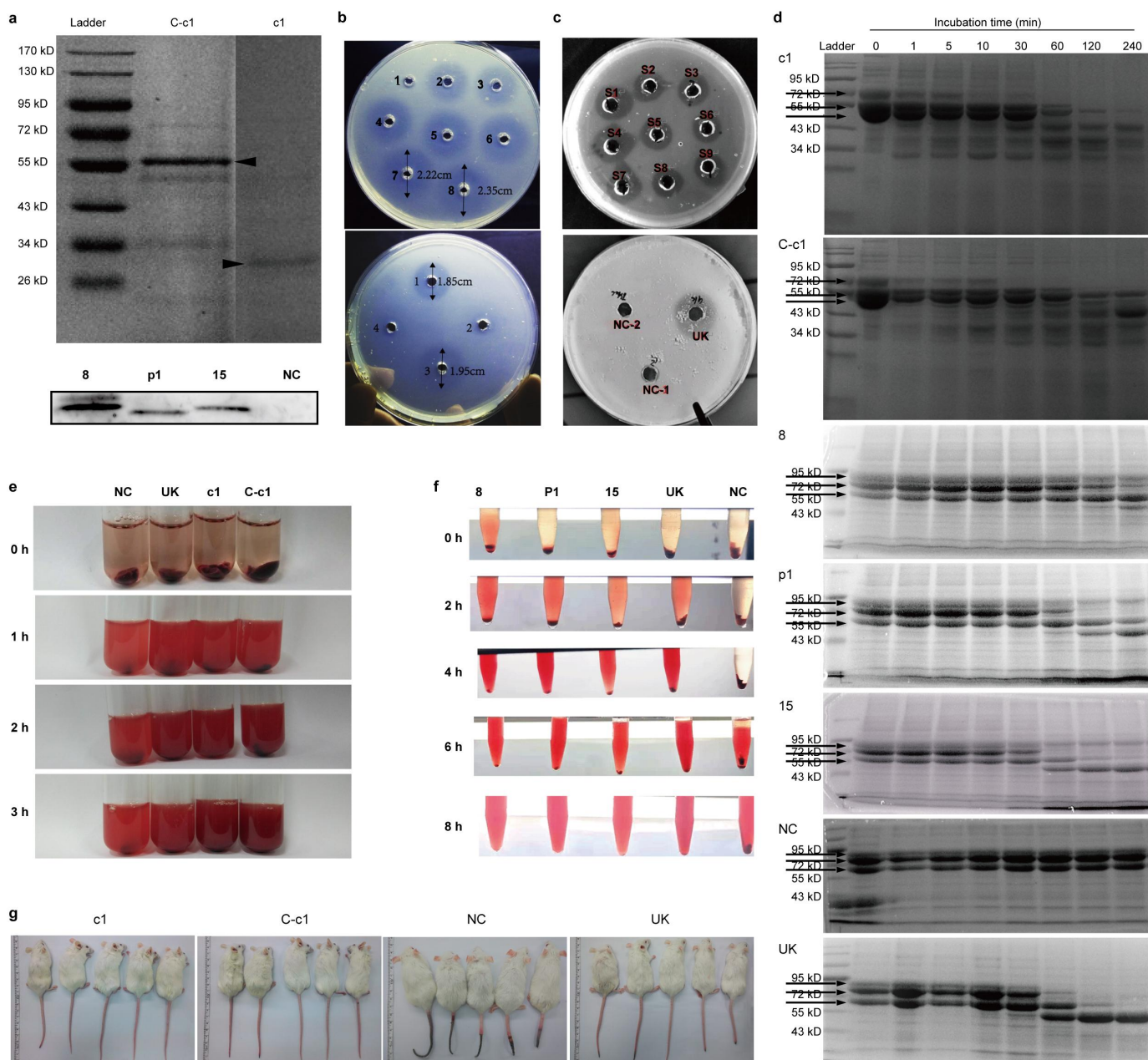
Extended figure 13



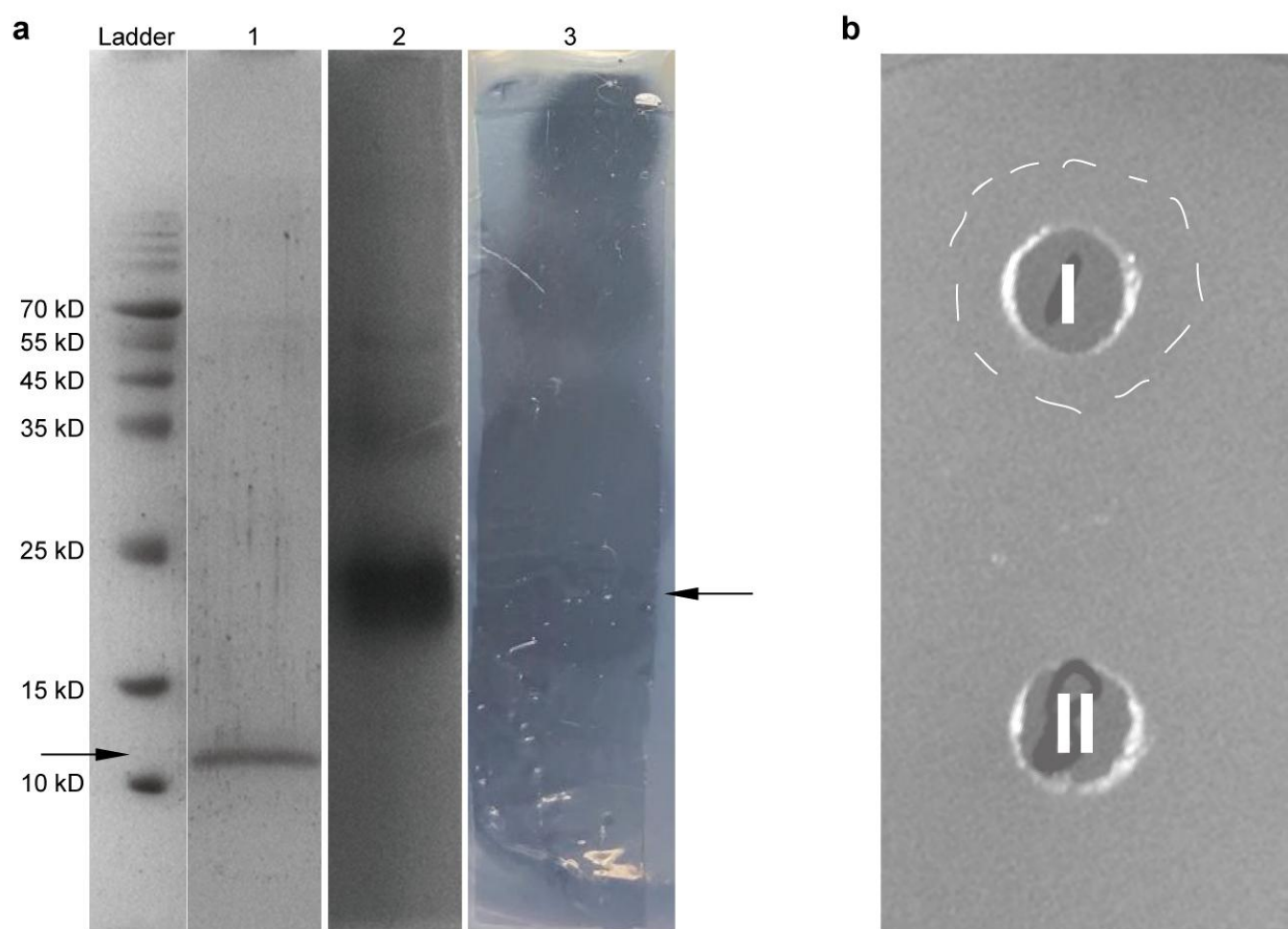
Extended figure 14



Extended figure 15



Extended figure 16



Extended figure 17