Mosalaganti et al., https://doi.org/10.1083/jcb.201611060

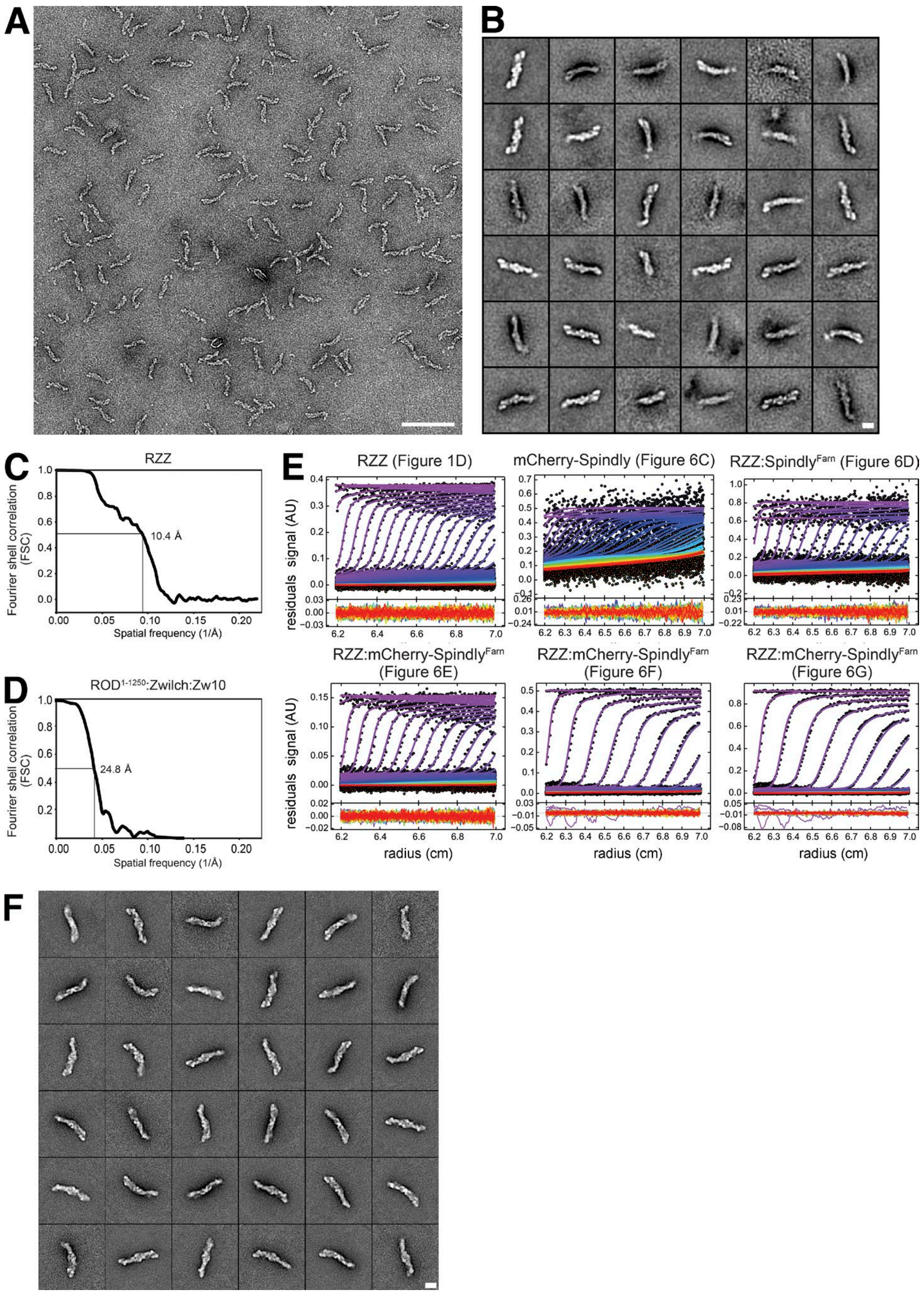


Figure S1. **Additional EM data.** (A) Raw micrograph area of the negatively stained RZZ complex, displaying elongated particles. (B) Gallery of m obtained from the ISAC procedure implemented in SPARX. (C) FSC for cryo-EM reconstruction of the RZZ complex. The FSC0.5 value is shown. (D) FSC curve for the negative stain reconstruction of the ROD1$^{1-1,250}$ZZ complex. FSC0.5 value is shown. (E) Sedimentation velocity absorbance profiles of the indicated species, with residuals of the fit showing the deviation of the c(S) model from the observed signals. AU, arbitrary units. (F) Class averages of negatively stained RZZ–Spindly as calculated by ISAC. Compared with class averages of negatively stained RZZ, no additional density can be readily observed. Bars: (A) 100 nm; (B and F) 10 nm.

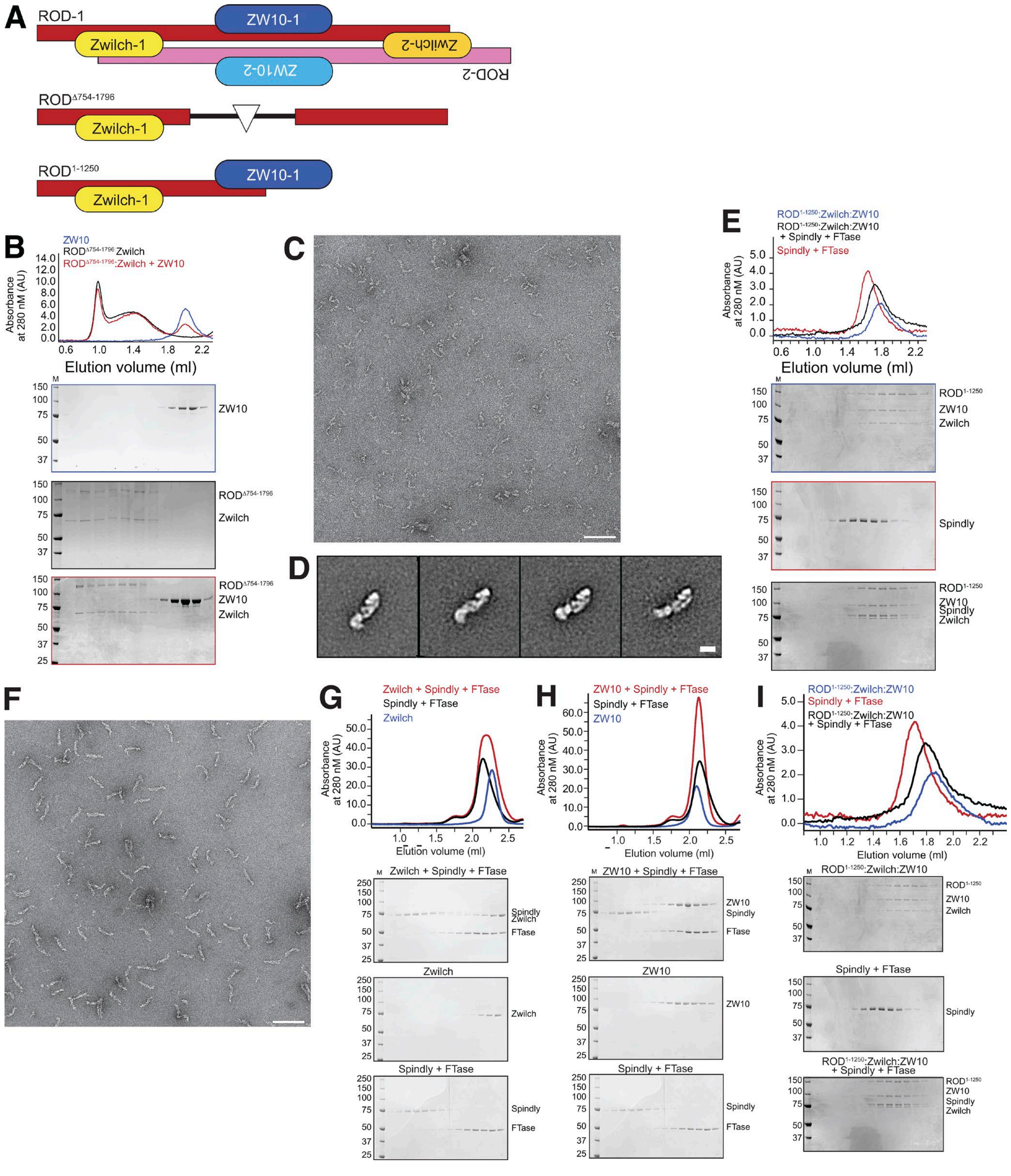


Figure S2. **Structural organization and biochemical properties of RZZ mutants and further characterization of RZZ–Spindly interaction.** (A) Schematic view of the full-length RZZ complex and of the ROD$^{\Delta 754-1,796}$ and ROD$^{1-1,250}$ constructs. (B) SEC analysis of ROD$^{\Delta 754-1,796}$–Zwilch, ZW10, and their stoichiometric combination shows a lack of binding interaction. (C) Micrograph area of the negatively stained ROD$^{1-1,250}$ZZ complex. (D) Typical class averages of the ROD$^{1-1250}$ZZ complex. (E) SEC analysis of ROD$^{1-1,250}$ZZ, Spindly (after treatment with FTase and Fpp), and their stoichiometric combination shows binding, with Spindly interacting stoichiometrically with ROD$^{1-1,250}$ZZ. (F) Digital micrograph of negatively stained RZZ–Spindly^{Farn} complexes. Bars: (C and F) 100 nm; (D) 10 nm. (G–I) SEC and SDS-PAGE analysis of the indicated species. For the control sample indicated as Spindly + FTase, the same SEC elution profile and SDS-PAGE are displayed in G and H. AU, arbitrary units; M, molecular weight marker.

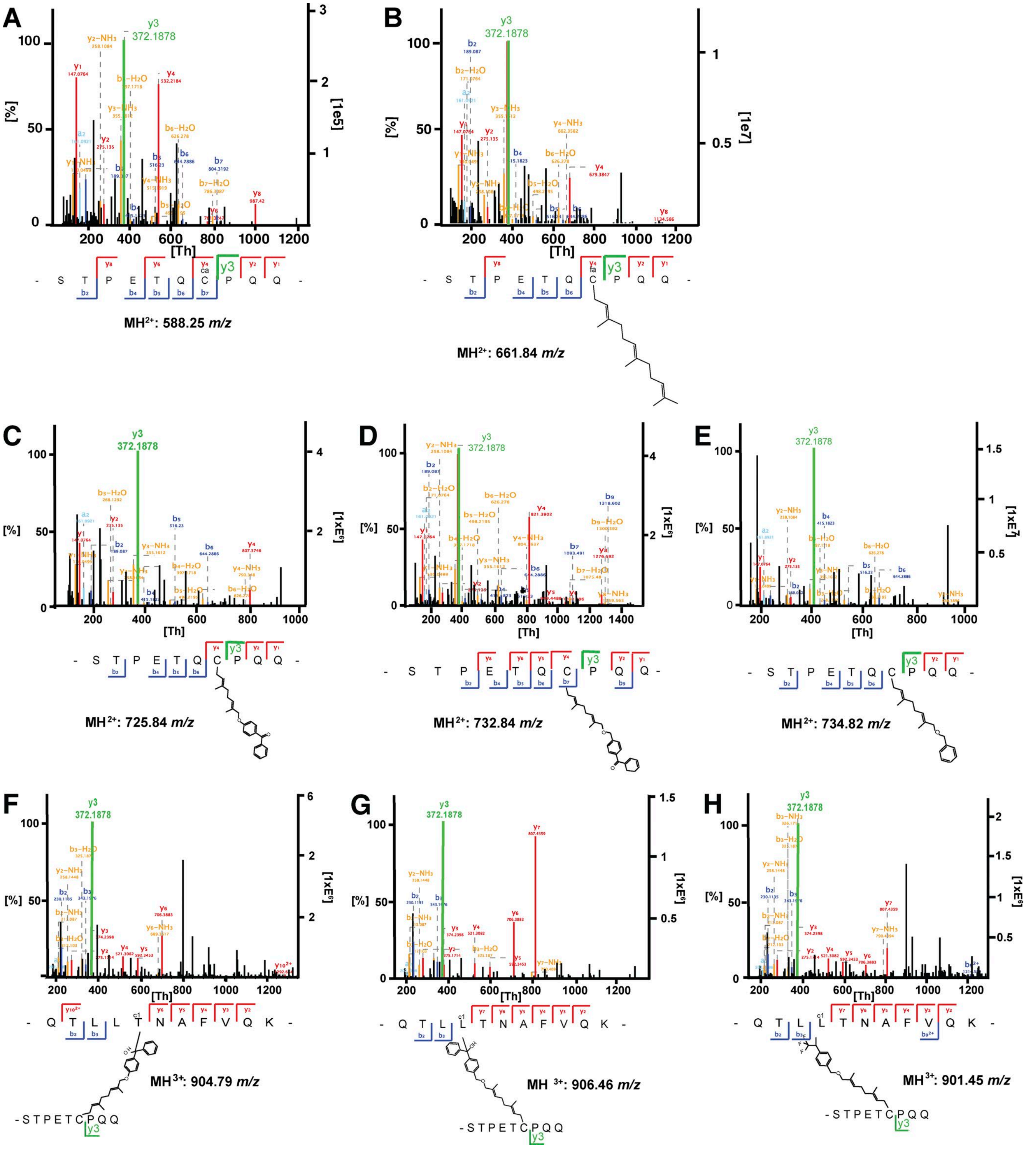


Figure S3. **MS/MS spectra of identified cross-links between farnesylated Spindly and RZZ.** (A and B) Spindly that was in vitro farnesylated or not, digested, and subjected to mass spectrometric analysis. MS/MS spectrum of the unmodified (A) and modified (B) C-terminal peptide of Spindly (aa 596–605). (C–H) Examples of MS/MS spectra for the C-terminal tryptic peptide (residues 596–605) of Spindly farnesylated with BPP1 (C); BPP2 (D); and diazirine (E); the bottom series (F–H) shows examples of MS/MS spectra for the identified cross-link between farnesylated spindly and ROD Leu120 (within the peptide 117–127) with the same order of UV-photoactivatable cross-linkers as in A–C. For every spectrum, the sequence, identified b and y ions, and the *m/z* mass of the corresponding MS peak are indicated in each spectrum. The y3 ion fragment is indicated in green because it was used as diagnostic peak to identify cross-links and to highlight its presence in all spectra.

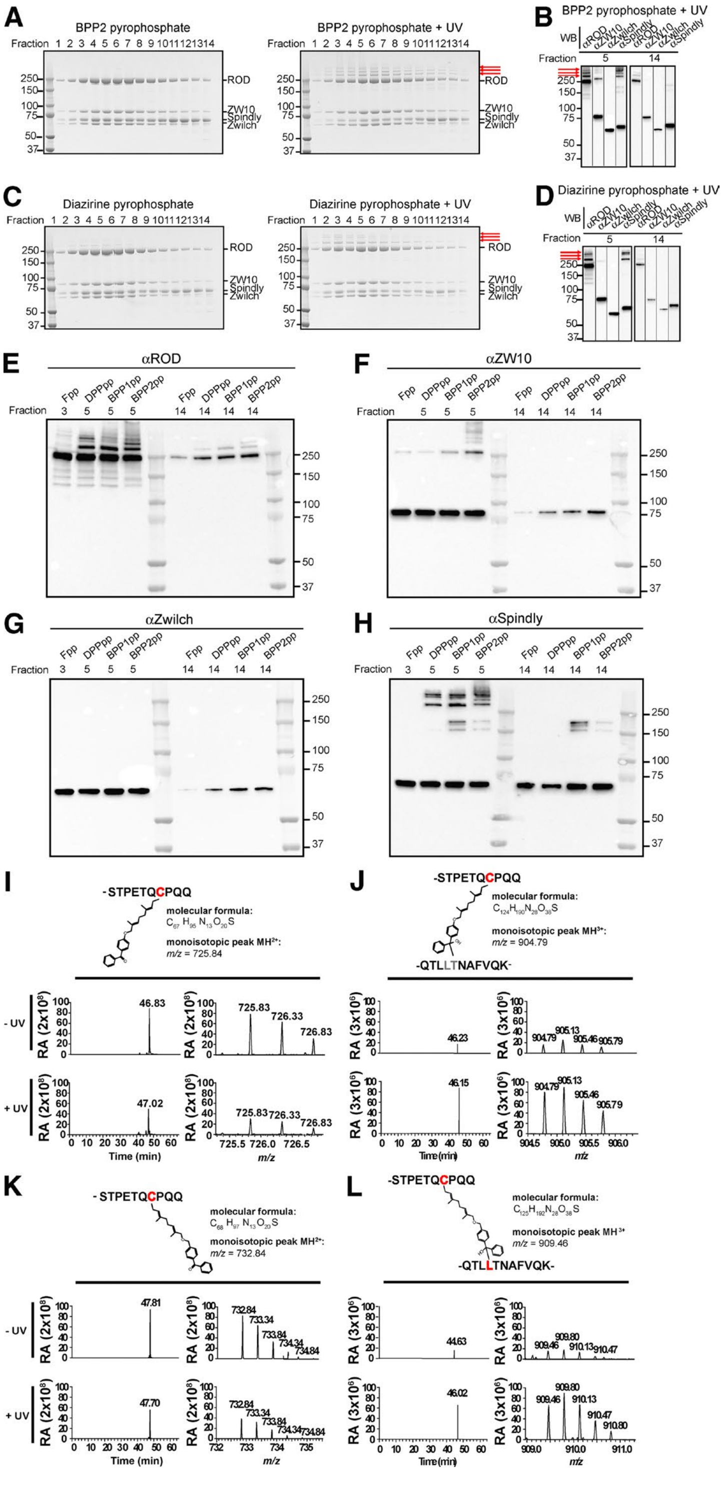
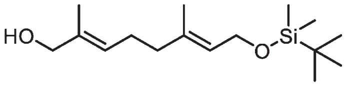


Figure S4. **Cross-links between the farnesyl-modified spindly and RZZ and MS analysis of UV-photoactivated cross-links.** (A and C) Spindly (in the presence of RZZ) was incubated with FTase and Fpp variants carrying BPP2 or diazirine. After separation by SEC, elution fractions were subjected to UV irradiation and visualized by Coomassie staining of SDS-PAGE gels. UV-induced extra bands (the most prominent of which are indicated by red arrows) appear. Equivalent experiments with BPP1 are shown in Fig. 7 C. (B and D) Western blotting analysis of indicated selected fractions (from SDS-PAGE in A and C) with antibodies against ROD, ZW10, Zwilch, and Spindly. (E–H) The complete Western blots from B and D in this figure and from Fig. 7 D were obtained. Molecular mass is indicated in kilodaltons. (I and J) Spindly was farnesylated in vitro with farnesyl derivatives containing the photoreactive cross-linker BPP1 (I) and BPP2 (J). Farnesylated Spindly in complex with RZZ was digested before UV irradiation and analyzed by MS. C-terminal tryptic peptides (residues 596–605) of farnesylated Spindly were found to be modified with BPP1 (I) or BPP2 (J). (K and L) Cross-link between the C-terminal tryptic peptide of farnesylated Spindly and a tryptic peptide of ROD spanning aa 117–127 with BPP1 (K) and BPP2 (L). At the top of each panel is a scheme of the peptide, and the attached farnesyl derivative is depicted together with the elemental composition and the calculated monoisotopic peak. All amino acids with identified cross-links are marked in red. For each panel, left traces show the chromatographic peak, and right traces show the isotopic pattern of the corresponding peptide identified in the MS survey scan. Upper traces represent samples before UV treatment, and lower traces represent samples after UV treatment. RA, relative abundance.

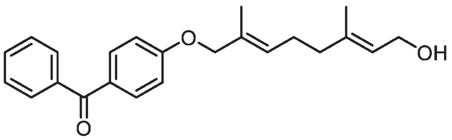
A

8-Hydroxy-geranyl-t-butyldimethylsilylether (1)



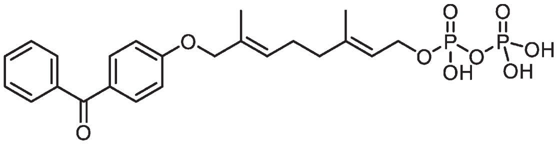
B

8-(4-Benzoylphenyloxy)-geraniol (2)



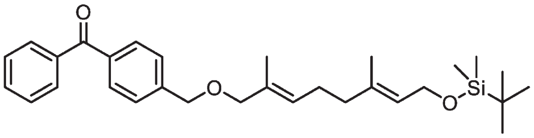
C

8-(4-Benzoylphenyloxy)-geranyl-1-diphosphate (3)



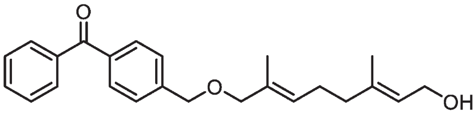
D

8-(3-(Methyl)-benzophenone)-geranyl-t-butyldimethylsilylether (4)



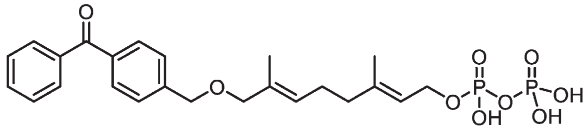
E

8-(3-(Methyl)-benzophenone)-geraniol (5)



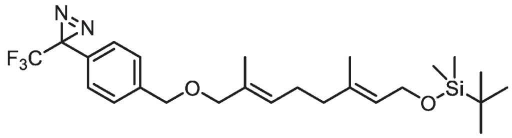
F

8-(3-(Methyl)-benzophenone)-geranyl-1-diphosphate (6)



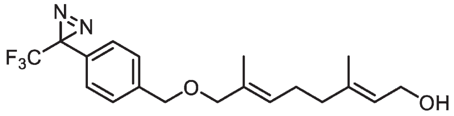
G

8-(3-Trifluoromethyl-3-phenyl-diazirine)-geranyl-t-butyldimethylsilylether (7)



H

8-(3-Trifluoromethyl-3-phenyl-diazirine)-geraniol (8)



I

8-(3-Trifluoromethyl-3-phenyl-diazirine)-geranyl-1-diphosphate (9)

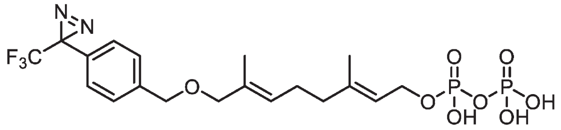


Figure S5. **Synthesis of photoactivatable probes.** (A–I) Structures of the chemicals used to generate photoactivatable probes as described in the Synthesis of the photoactivatable probes section of Materials and methods are shown as follows: 8-hydroxy-geranyl-*t*-butyldimethylsilylether (A), 8-(4-benzoylphenyloxy)-geraniol (B), 8-(4-benzoylphenyloxy)-geranyl-1-diphosphate (C), 8-(3-(methyl)-benzophenone)-geranyl-*t*-butyldimethylsilylether (D), 8-(3-(methyl)-benzophenone)-geraniol (E), 8-(3-(methyl)-benzophenone)-geranyl-1-diphosphate (F), 8-(3-trifluoromethyl-3-phenyl-diazirine)-geranyl-*t*-butyldimethylsilylether (G), 8-(3-trifluoromethyl-3-phenyl-diazirine)-geraniol (H), and 8-(3-trifluoromethyl-3-phenyl-diazirine)-geranyl-1-diphosphate (I).

Video 1. **Montage of cryo-EM RZZ class averages with similar orientations shows considerable flexibility.** The class averages were calculated in Relion 1.4 and show large-scale movement of the two arms. Most notably, the arms are independently flexible. The central region of RZZ seems to be more rigid, although slight deformations are also observable in this region. This video was shot at 20 frames per second.

Video 2. **Fitting of molecular model into the EM density.** This video was shot at 24 and 96 frames per second.

Table S1. **Summary of homology modeling of ROD and ZW10 subunits**

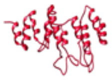
Residues in ROD or ZW10	**Template**	**PDB chain**	**Residues in template**	**Sequence identity**	**Confidence Hhpred**	**Confidence Phyre**	**Multi-item plate modeling**	**Models**
				%	%	%		
ROD								
1–376	Sec31	2PM9_A	5–405	15	100	96	Yes	
	COPI β'	4J73_A	21–290	13	100	97		
396–582	COPI α	3MKQ_B	649–780	15	93	ND	Yes	
	COPI β'	3MKQ_A	655–786	17	85	74		
582–1,190	Sec39	3K8P_D	10–671	12	100	100	No	
1,319–1,797	Clathrin HC	1XI4_A	814–1,198	15	56	ND	No	
1,798–2,192	Nup155	5A9Q_A	776–1,110	15	76	ND	Yes	
	Nup145	4XMM_A	319–575	16	64	74		
ZW10								
475–779	Dsl1	3K8P_C	429–675	14	100	100	No	
54–345	Dsl1	2ETV_A	16–307	13	98	97	Yes	
16–767	Tip20	3FHN_A	11–701	10	96	97		

Table S2. **Model fitting into cryo-EM maps**

Correlation	**Mean map value**	**Inside**
Fitting of Zw10		
0.8776	2.877	0.662
0.8316	2.634	0.604
0.8192	2.514	0.539
0.8171	2.579	0.588
0.8117	2.628	0.577
0.8090	2.431	0.539
0.8074	2.777	0.565
0.8069	2.478	0.553
0.8047	2.579	0.596
0.8022	2.513	0.551
0.8011	2.444	0.557
0.8010	2.395	0.525
0.8007	2.338	0.521
0.8006	2.433	0.524
Fitting of Zwilch		
0.9154	2.654	0.699
0.8895	2.895	0.780
0.8884	3.113	0.869
0.8872	2.855	0.785
0.8868	2.875	0.813
0.8860	3.025	0.735
0.8842	2.981	0.846
0.8811	2.992	0.760
0.8749	2.788	0.745
0.8731	2.539	0.723
0.8721	2.544	0.727

0.8719	2.690	0.766
0.8681	2.683	0.723
0.8679	2.580	0.712
Fitting of ROD$^{396–1,191}$		
0.8352	2.546	0.515
0.8348	2.547	0.515
0.8214	2.280	0.471
0.8214	2.758	0.528
0.8214	2.280	0.471
0.8214	2.758	0.528
0.8189	2.540	0.519
0.8188	2.541	0.520
0.8174	2.435	0.501
0.8173	2.436	0.499
0.8119	2.540	0.491
0.8118	2.469	0.492
0.8106	2.343	0.481
0.8106	2.343	0.483
Fitting of ROD$^{1,319–1,797}$		
0.8980	3.363	0.662
0.8980	3.362	0.661
0.8976	3.369	0.660
0.8975	3.369	0.658
0.8956	3.451	0.694
0.8956	3.449	0.690
0.8956	3.449	0.690
0.8956	3.451	0.694
0.8895	3.420	0.710
0.8893	3.419	0.708
0.8891	3.424	0.700
0.8891	3.424	0.700
0.8887	3.330	0.690
0.8887	3.330	0.690
Fitting of RZZ		
0.8655	2.796	0.487
0.8655	2.796	0.487
0.5497	1.184	0.205
0.5479	1.181	0.205
0.5408	1.248	0.219
0.5357	1.117	0.206
0.5288	1.101	0.201
0.5281	1.123	0.190
0.5280	1.116	0.190
0.5243	0.998	0.175
0.5204	1.009	0.181
0.5192	0.993	0.173
0.5128	1.023	0.185
0.5126	1.028	0.185

Homology models of ROD (segments 396–1,191 and 1,319–1,797), ZW10, and the crystallographic structure of Zwilch (PDB ID: 3IF8) were automatically fitted in the density using UCSF Chimera Fit in Map tool. Individual rigid-body fittings were performed using the systematic global search option starting from 10,000 random initial placements of a simulated 10.5-Å map of the proteins within the cryo-EM map. The correlation score between the simulated map and the cryo-EM map was used as a fitting metric. For each of the placements, local optimization was performed. This table reports the results for the best fits for each search model. “Correlation” is the correlation score between the simulated map and the reference map. “Mean map value” is the density map value averaged over the center positions of all the fit atoms. A higher value means the atoms sit in higher density. “Inside” corresponds to the proportion of fit map grid points that are inside the reference map contour surface. For each model, the position was attributed to the fitting structure that had the best correlation score. Additional models of ROD (segments 1–376 and 1,798–2,189) were manually fitted in the residual density.

Table S3. Table of XL-MS data

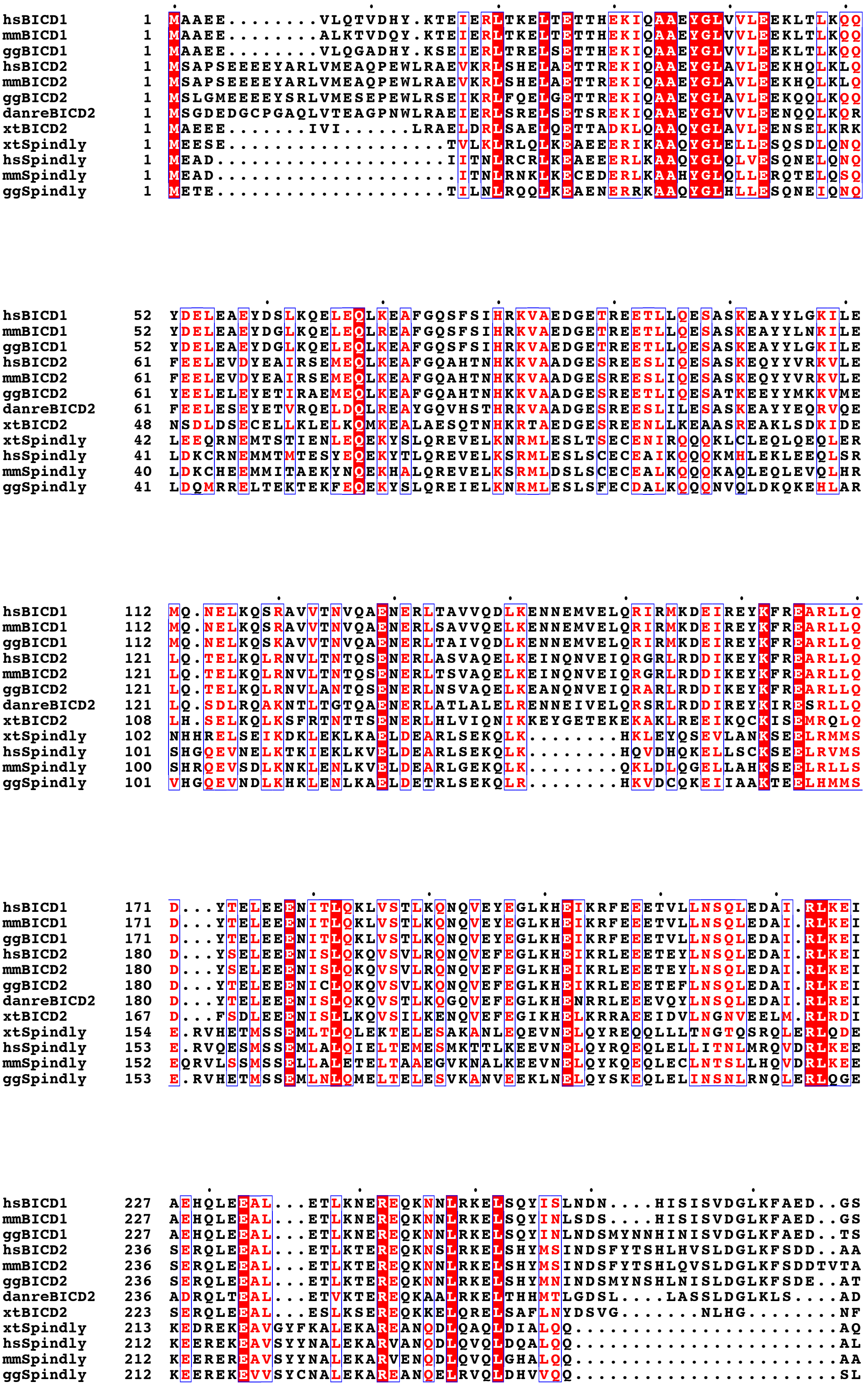
Sequence of cross-linked peptides	**Protein 1**	**Protein 2**	**Position 1**	**Position 2**	**Distance**
					Å
A. Intrasubunit cross-links (RZZ)					
KCFDLK-LL**K**SR	ZW10	ZW10	152	74	30.53
RHP**K**LLAK-HL**K**SYR	ROD	ROD	1493	1560	n.d.
CL**K**LLK-**K**CFDLK	ZW10	ZW10	946	152	25.90

LDGFGDST**K**K-LF**K**VR	Zwilch	Zwilch	317	341	n.d.
LL**K**LTQAK-KL**K**PK	ROD	ROD	1653	1648	8.51
LFGETTLV**K**SR-E**K**AVIFIR	ROD	ROD	1307	1318	n.d.
LEEAQ**K**CLK-LL**K**SR	ZW10	ZW10	143	74	25.79
EQHI**K**AHEVAQAK-SPSMES**K**LHR	ROD	ROD	1021	1051	14.37
RE**K**AEALLK-**K**LHIQYR	ROD	ROD	1731	1738	10.81
LL**K**LTQAK-**K**LKPK	ROD	ROD	1653	1646	11.03
H**K**PGSTPEPIAAEVR-DGNI**K**TALKK	ROD	ROD	1031	1081	25.88
LFGETTLV**K**SR-HVVMEL**K**EK	ROD	ROD	1307	1316	n.d.
KEHGTALYQVDLLVK-LLH**K**HR	ROD	ROD	24	406	56.97
AD**K**NYSVNLENLK-NLYQSE**K**PQK	Zwilch	Zwilch	176	527	16.82
RHQQI**K**NFLGSCDPQVILK-SLILNNIIN**K**K	ROD	ROD	2093	2135	11.79
H**K**PGSTPEPIAAEVR-SPSMES**K**LHR	ROD	ROD	1031	1051	29.61
KDTEVETL**K**HDTAAVDR-LF**K**VR	Zwilch	Zwilch	326	341	n.d.
RE**K**AEALLK-**K**LHIQYRR	ROD	ROD	1731	1738	10.81
RVEEI**K**GEVCNMISK-LL**K**SR	ZW10	ZW10	35	74	26.38
ILCDIQ**K**DNLQK-RHPKLLA**K**	ROD	ROD	971	1493	39.94
DTEVETL**K**HDTAAVDR-LF**K**VR	Zwilch	Zwilch	326	341	n.d.
RHHLSTVTS**K**GFAQYELFK-VEIYSGQ**K**K	Zwilch	Zwilch	201	540	10.60
RVEEI**K**GEVCNMISK-**K**CFDLK	ZW10	ZW10	35	152	32.14
HQQI**K**NFLGSCDPQVILK-SLILNNIIN**K**K	ROD	ROD	2093	2135	11.79
NDP**K**LSEDSVSVLVLR-ISSE**K**ASLNPK	ROD	ROD	377	43	n.d.
H**K**PGSTPEPIAAEVR-LALQEEPDHS**K**EGK	ROD	ROD	1031	946	26.27
V**K**LLQESYK-**K**LKPK	ROD	ROD	829	1646	44.94
LTQA**K**SSTLINK-**K**YNCK	ROD	ROD	1658	701	50.43
KDTEVETLK-LF**K**VR	Zwilch	Zwilch	318	341	n.d.
HHLSTVTS**K**GFAQYELFK-VEIYSGQ**K**K	Zwilch	Zwilch	201	540	10.60
AHEVAQA**K**HKPGSTPEPIAAEVR-SPSMES**K**LHR	ROD	ROD	1029	1051	23.32
E**K**AEALLK-**K**LHIQYR	ROD	ROD	1731	1738	10.81
HP**K**LLAK-HL**K**SYR	ROD	ROD	1493	1560	n.d.
DLHVSTGEFTDL**K**QQLER-LSEDIDLL**K**SR	ZW10	ZW10	96	74	10.26
EQHI**K**AHEVAQAK-AL**K**DGNIK	ROD	ROD	1021	1076	10.90
VLAPELIPSILE**K**FIR-KYNC**K**LALSDFEK	ROD	ROD	739	705	10.05
VLAPELIPSILE**K**FIR-YNC**K**LALSDFEK	ROD	ROD	739	705	10.05
AHEVAQA**K**HKPGSTPEPIAAEVR-DGNI**K**TALKK	ROD	ROD	1029	1081	20.13
SGTEAVLIAH**K**LNTEEYLR-LTQA**K**SSTLINK	ROD	ROD	1756	1658	38.64
AHEVAQA**K**HKPGSTPEPIAAEVR-**K**CSDLFK	ROD	ROD	1029	1086	23.71
AHEVAQA**K**HKPGSTPEPIAAEVR-AL**K**DGNIK	ROD	ROD	1029	1076	23.64
H**K**PGSTPEPIAAEVR-EQHI**K**AHEVAQAK	ROD	ROD	1031	1021	19.67
ED**K**TALIYSDGLK-TRLL**K**K	ROD	ROD	503	499	9.78
AHEVAQAKH**K**PGSTPEPIAAEVR-DGNI**K**TALK	ROD	ROD	1031	1081	25.88
YQEEVPVYVP**K**WMPFK-AQ**K**GELLER	ZW10	ZW10	719	597	23.51
QALALQMS**K**QELEAELTLR-**K**CSDLFK	ROD	ROD	1063	1086	15.05
DGNI**K**TALK-**K**CSDLFK	ROD	ROD	1081	1086	8.48
ENATTLLH**K**VFNCR-LID**K**AWQNYDK	ROD	ROD	1333	1367	n.d.
WLQNIPSQDE**K**REK-AEALL**K**KLHIQYR	ROD	ROD	1728	1737	16.97
VIG**K**PAHLIVSLYEHPSINQR-AEALL**K**K	ROD	ROD	1768	1737	13.79
AHEVAQAKH**K**PGSTPEPIAAEVR-**K**CSDLFK	ROD	ROD	1031	1086	31.02
MFD**K**VLAPELIPSILEK-YNC**K**LALSDFEK	ROD	ROD	726	705	20.76
NFLGSCDPQVIL**K**QLEEHMNTGQLAGFSHQIR-T**K**YFQMLK	ROD	ROD	2106	2145	9.50
MFD**K**VLAPELIPSILEK-KYNC**K**LALSDFEK	ROD	ROD	726	705	20.76
AHEVAQA**K**HKPGSTPEPIAAEVR-LALQEEPDHS**K**EGK	ROD	ROD	1029	946	21.48
AD**K**NYSVNLENLK-**K**RHHLSTVTSK	Zwilch	Zwilch	176	191	29.36
AHEVAQAKH**K**PGSTPEPIAAEVR-LALQEEPDHS**K**EGK	ROD	ROD	1031	946	26.27
LALQEEPDHS**K**EGK-MSVA**K**TSVDILK	ROD	ROD	946	957	9.08
LQQYEEIIQSTEEFENAL**K**EMR-FL**K**GDTTDLLK	ZW10	ZW10	376	382	n.d.
HHLSTVTS**K**GFAQYELFK-WRVEIYSGQ**K**K	Zwilch	Zwilch	201	540	10.60
WLQNIPSQDE**K**REK-AEALLK**K**LHIQYR	ROD	ROD	1728	1738	16.62
GQPNPL**K**NILNENDIVFIVEK-HHLSTVTS**K**GFAQYELFK	Zwilch	Zwilch	52	201	14.98
TVMDEGPQVFAPLSEES**K**NK-**K**YQEEVPVYVPK	ZW10	ZW10	705	708	7.38
AHEVAQA**K**HKPGSTPEPIAAEVR-QALALQMS**K**QELEAELTLR	ROD	ROD	1029	1063	34.58
QALALQMS**K**QELEAELTLR-H**K**PGSTPEPIAAEVR	ROD	ROD	1063	1031	40.98
AQWITYETTQEMLNYA**K**TR-ED**K**TALIYSDGLK	ROD	ROD	494	503	13.64
SSTLIN**K**EITK-LL**K**LTQAK	ROD	ROD	1665	1653	18.11
AHEVAQAKH**K**PGSTPEPIAAEVR-QALALQMS**K**QELEAELTLR	ROD	ROD	1031	1063	40.98
WLQNIPSQDE**K**R-E**K**AEALLK	ROD	ROD	1728	1731	10.61
KYQEEVPVYVP**K**WMPFK-AQ**K**GELLER	ZW10	ZW10	719	597	23.51
LALSDFE**K**ENTTTIVFR-MFD**K**VLAPELIPSILEK	ROD	ROD	713	726	24.01
AISSIHSLWQVPYFS**K**AWQR-KED**K**TALIYSDGLK	ROD	ROD	2016	503	36.59

TVMDEGPQVFAPLSEES**K**NK-NLMTSEIHNTV**K**IIPDSK	ZW10	ZW10	705	424	n.d.
NFLGSCDPQVIL**K**QLEEHMNTGQLAGFSHQIR-EFGILA**K**TK	ROD	ROD	2106	2143	13.80
MFD**K**VLAPELIPSILEK-**K**YNCKLALSDFEK	ROD	ROD	726	701	13.98
TVMDEGPQVFAPLSEES**K**NKK-NLMTSEIHNTV**K**IIPDSK	ZW10	ZW10	705	424	n.d.
EQHI**K**AHEVAQAK-EG**K**AWR	ROD	ROD	1021	949	29.00
IIDLIDREQGEDCLLLL**K**SLPPAEAEK-TSVDIL**K**ILCDIQK	ROD	ROD	916	964	13.71
DTEVETL**K**HDTAAVDR-LDGFGDST**K**K	Zwilch	Zwilch	326	317	n.d.
IIDLIDREQGEDCLLLL**K**SLPPAEAEK-ILCDIQ**K**DNLQK	ROD	ROD	916	971	10.44
QHLEMDHP**K**VK-LL**K**LTQAK	ROD	ROD	829	1653	48.63
SAVELVQEFLNDLNKLDGFGDST**K**K-DTEVETL**K**HDTAAVDR	Zwilch	Zwilch	317	326	n.d.
RHQQI**K**NFLGSCDPQVILK-SLILNNIIN**K**KEFGILAK	ROD	ROD	2093	2135	11.79
TVWQLSDSSPIDHLNFH**K**PDFSELTLNGSLEER-AD**K**NYSVNLENLK	Zwilch	Zwilch	561	176	n.d.
B. Intersubunit cross-links (RZZ)					
EVNLLN**K**EIMR-**K**YVTGAQR	ROD	ZW10	859	130	50.56
LIVW**K**FPPSK-RHP**K**LLAK	ZW10	ROD	188	1493	58.45
ITNININQALSIL**K**HLK-LIVW**K**FPPSK	ROD	ZW10	1557	188	n.d.
NFSNMDDEENYSAAS**K**AVR-H**K**PGSTPEPIAAEVR	ZW10	ROD	624	1031	59.73
GDTTDLL**K**YAR-LFGETTLV**K**SR	ZW10	ROD	390	1307	n.d.
KRHHLSTVTSK-WEPDSS**K**K	Zwilch	ROD	191	239	23.92
IIDLIDREQGEDCLLLL**K**SLPPAEAEK-AAALA**K**IK	ROD	ZW10	916	777	32.34
FSGSSWIEFLNNEDDL**K**DIFLQLK-VEIYSGQ**K**K	ROD	Zwilch	550	540	36.76
MSSSVISYQDLV**K**CFTLIIQSLQR-LE**K**EDLGTR	Zwilch	ZW10	368	17	40.64
KRHHLSTVTSK-LLH**K**HR	Zwilch	ROD	191	406	30.00
NFSNMDDEENYSAASKAVR-KCSDLFKYHCNADTGK	ZW10	ROD	624	1092	22.65
AHEVAQAKH**K**PGSTPEPIAAEVR-NFSNMDDEENYSAAS**K**AVR	ROD	ZW10	1029	624	52.84
QALALQMS**K**QELEAELTLR-QVLHQL**K**R	ROD	ZW10	1063	634	40.81
NFSNMDDEENYSAAS**K**AVR-CSDLF**K**YHCNADTGK	ZW10	ROD	624	1092	22.65
KYSEFLPSMQSAQGLITQVDK-EVNLLN**K**EIMR	ZW10	ROD	45	859	28.13
QLQEFSTAIEEYNCALTE**K**K-EVNLLN**K**EIMR	ZW10	ROD	129	859	51.06
NFSNMDDEENYSAASKAVR-QALALQMSKQELEAELTLR	ZW10	ROD	624	1063	29.04
AHEVAQAKH**K**PGSTPEPIAAEVR-NFSNMDDEENYSAAS**K**AVR	ROD	ZW10	1031	624	59.73
GDTTDLL**K**YAR-LFGETTLV**K**SR	ZW10	ROD	390	1307	n.d.
KRHHLSTVTSK-**K**GMTVK	Zwilch	ROD	191	240	22.56
DTEVETL**K**HDTAAVDR-VLAPELIPSILE**K**FIR	Zwilch	ROD	326	739	n.d.
NIFHLFHDVVPTYH**K**ENLQK-CSDLF**K**YHCNADTGK	ZW10	ROD	528	1092	22.46
CSDLF**K**YHCNADTGK-QVLHQL**K**R	ROD	ZW10	1092	634	30.00
AWRMSVA**K**TSVDILK-LIAEV**K**GKK	ROD	Spc25	957	90	n.d.
C. Intersubunit cross-links (RZZ–Spindly$^{\text{Farn}}$)					
AHEVAQAKH**K**PGSTPEPIAAEVR-LE**K**EDLGTR	ROD	Zw10	1031	17	n.d.
EVNLLN**K**EIMR-**K**YVTGAQR	ROD	Zw10	859	130	n.d.
AHEVAQA**K**HKPGSTPEPIAAEVR-LE**K**EDLGTR	ROD	Zw10	1029	17	n.d.
LAAES**K**LQTEVK-LLH**K**HR	Spindly	ROD	563	406	n.d.
LQTEV**K**EGK-LLH**K**HR	Spindly	ROD	569	406	n.d.
EGKETSS**K**LEK-LLH**K**HR	Spindly	ROD	577	406	n.d.
VIG**K**PAHLIVSLYEHPSINQR-**K**LFANER	ROD	Spindly	1768	409	n.d.
IIDLIDREQGEDCLLLL**K**SLPPAEAEK-AAALA**K**IK	ROD	Zw10	916	777	n.d.
NFSNMDDEENYSAAS**K**AVR-H**K**PGSTPEPIAAEVR	Zw10	ROD	624	1031	n.d.
HCG**K**PVPPDTAPCEILK-NLYQSE**K**PQK	ROD	Zwilch	2189	523	n.d.
AHEVAQA**K**HKPGSTPEPIAAEVR-NFSNMDDEENYSAAS**K**AVR	ROD	Zw10	1029	624	n.d.
NFSNMDDEENYSAAS**K**AVR-QALALQMS**K**QELEAELTLR	Zw10	ROD	624	1063	n.d.
GLW**K**NHSHESMAVR-EVEL**K**SR	ROD	Spindly	1952	69	n.d.
NFSNMDDEENYSAAS**K**AVR-CSDLF**K**YHCNADTGK	Zw10	ROD	624	1092	n.d.
EG**K**ETSSKLEK-LLH**K**HR	Spindly	ROD	572	406	n.d.
AL**K**DGNIK-NL**K**KR	ROD	Zwilch	1076	189	n.d.
TVPEGQIILA**K**WLEQAAR-LLAMLEQ**K**NGEIK	ROD	Spindly	625	326	n.d.
H**K**PGSTPEPIAAEVR-EIEST**K**GELSIQR	ROD	Spindly	1031	386	n.d.

Raw data for this dataset can be accessed from the web site, http://www.ebi.ac.uk/pride/archive/login, with username: reviewer92658@ebi.ac.uk and password: LGNXY7lI. Values in the “Distance” column are Cα–Cα distances of cross-linked lysine residue pairs, calculated from the RZZ model. 31 Å is an arbitrary threshold that includes the maximal overall distance for the Lys Cα-to-Lys Cα pair plus the crosslinker (24 Å) plus an “allowance” that accounts for potential structural changes and for the limited resolution of the maps in which the model was built. Cross-links that could not be annotated on our model are indicated as n.d.

Table S4 *MAFFT sequence alignment of the indicated BicD2 and Spindly sequences*



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ggBICD1       1   MAAEE........VLQGADHY.KSEIERLTRELSETTHEKIQAAEYGLVVLEEKLTLKQQ
hsBICD2       1   MSAPSEEEEYARLVMEAQPEWLRAEVKRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQ
mmBICD2       1   MSAPSEEEEYARLVMEAQPEWLRAEVKRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQ
ggBICD2       1   MSLGMEEEEYSRLVMESEPEWLRSEIKRLFQELGETTREKIQAAEYGLAVLEEKQQLKQQ
danreBICD2    1   MSGDEDGCPGAQLVTEAGPNWLRAEIERLSRELSETSREKIQAAEYGLVVLEENQQLKQR
xtBICD2       1   MAEEE.......IVI......LRAELDRLSAELQETTADKLQAAQYGLAVLEENSELKRK
xtSpindly     1   MEESE...................TVLKLRLQLKEAEEERIKAAQYGLELLESQSDLQNQ
hsSpindly     1   MEAD....................IITNLRCRLKEAEEERLKAAQYGLQLVESQNELQNQ
mmSpindly     1   MEAD.....................ITNLRNKLKECEDERLKAAHYGLQLLERQTELQSQ
ggSpindly     1   METE....................TILNLRQQLKEAENERRKAAQYGLHLLESQNEIQNQ

hsBICD1      52   YDELEAEYDSLKQELEQLKEAFGQSFSIHRKVAEDGETREETLLQESASKEAYYLGKILE
mmBICD1      52   YDELEAEYDGLKQELEQLREAFGQSFSIHRKVAEDGETREETLLQESASKEAYYLNKILE
ggBICD1      52   YDELEAEYDGLKQELEQLKEAFGQSFSIHRKVAEDGETREETLLQESASKEAYYLGKILE
hsBICD2      61   FEELEVDYEAIRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYYVRKVLE
mmBICD2      61   FEELEVDYEAIRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYYVRKVLE
ggBICD2      61   YEELELEYETIRAEMEQLKEAFGQAHTNHKKVAADGESREETLIQESATKEEYYMKKVME
danreBICD2   61   FEELESEYETVRQELDQLREAYGQVHSTHRKVAADGESREESLILESASKEAYYEQRVQE
xtBICD2      48   NSDLDSECELLKLELKQMKEALAESQTNHKRTAEDGESREENLLKEAASREAKLSDKIDE
xtSpindly    42   LEEQRNEMTSTIENLEQEKYSLQREVELKNRMLESLTSECENIRQQQKLCLEQLQEQLER
hsSpindly    41   LDKCRNEMMTMTESYEQEKYTLQREVELKSRMLESLSCECEAIKQQQKMHLEKLEEQLSR
mmSpindly    40   LDKCHEEMMITAEKYNQEKHALQREVELKSRMLDSLSCECEALKQQQKAQLEQLEVQLHR
ggSpindly    41   LDQMRRELTEKTEKFEQEKYSLQREIELKNRMLESLSFECDALKQQQNVQLDKQKEHLAR

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mmBICD1     112   MQ.NELKQSRAVVTNVQAENERLSAVVQELKENNEMVELQRIRMKDEIREYKFREARLLQ
ggBICD1     112   MQ.NELKQSKAVVTNVQAENERLTAIVQDLKENNEMVELQRIRMKDEIREYKFREARLLQ
hsBICD2     121   LQ.TELKQLRNVLTNTQSENERLASVAQELKEINQNVEIQRGRLRDDIKEYKFREARLLQ
mmBICD2     121   LQ.TELKQLRNVLTNTQSENERLTSVAQELKEINQNVEIQRGRLRDDIKEYKFREARLLQ
ggBICD2     121   LQ.TELKQLRNVLANTQSENERLNSVAQELKEANQNVEIQRARLRDDIKEYKFREARLLQ
danreBICD2  121   LQ.SDLRQAKNTLTGTQAENERLATLALELRENNEIVELQRSRLRDDIREYKIRESRLLQ
xtBICD2     108   LH.SELKQLKSFRTNTTSENERLHLVIQNIKKEYGETEKEKAKLREEIKQCKISEMRQLQ
xtSpindly   102   NHHRELSEIKDKLEKLKAELDEARLSEKQLK........HKLEYQSEVLANKSEELRMMS
hsSpindly   101   SHGQEVNELKTKIEKLKVELDEARLSEKQLK........HQVDHQKELLSCKSEELRVMS
mmSpindly   100   SHRQEVSDLKNKLENLKVELDEARLGEKQLK........QKLDLQGELLAHKSEELRLLS
ggSpindly   101   VHGQEVNDLKHKLENLKAELDETRLSEKQLR........HKVDCQKEIIAAKTEELHMMS

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mmBICD1     171   D...YTELEEENITLQKLVSTLKQNQVEYEGLKHEIKRFEEETVLLNSQLEDAI.RLKEI
ggBICD1     171   D...YTELEEENITLQKLVSTLKQNQVEYEGLKHEIKRFEEETVLLNSQLEDAI.RLKEI
hsBICD2     180   D...YSELEEENISLQKQVSVLRQNQVEFEGLKHEIKRLEEETEYLNSQLEDAI.RLKEI
mmBICD2     180   D...YSELEEENISLQKQVSVLRQNQVEFEGLKHEIKRLEEETEYLNSQLEDAI.RLKEI
ggBICD2     180   D...YTELEEENICLQKQVSVLKQNQVEFEGLKHEIKRLEEETEFLNSQLEDAI.RLKEI
danreBICD2  180   D...YTELEEENISLQKQVSTLKQGQVEFEGLKHENRRLEEEVQYLNSQLEDAI.RLREI
xtBICD2     167   D...FSDLEEENISLLKQVSILKENQVEFEGIKHELKRRAEEIDVLNGNVEELM.RLRDI
xtSpindly   154   E.RVHETMSSEMLTLQLEKTELESAKANLEQEVNELQYREQQLLLTNGTQSRQLERLQDE
hsSpindly   153   E.RVQESMSSEMLALQIELTEMESMKTTLKEEVNELQYRQEQLELLITNLMRQVDRLKEE
mmSpindly   152   EQRVLSSMSSELLALETELTAAEGVKNALKEEVNELQYKQEQLECLNTSLLHQVDRLKEE
ggSpindly   153   E.RVHETMSSEMLNLQMELTELESVKANVEEKLNELQYSKEQLELINSNLRNQLERLQGE

hsBICD1     227   AEHQLEEAL...ETLKNEREQKNNLRKELSQYISLNDN....HISISVDGLKFAED..GS
mmBICD1     227   AEHQLEEAL...ETLKNEREQKNNLRKELSQYINLSDS....HISISVDGLKFAED..GS
ggBICD1     227   AEHQLEEAL...ETLKNEREQKNNLRKELSQYINLNDSMYNNHINISVDGLKFAED..TS
hsBICD2     236   SERQLEEAL...ETLKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDD..AA
mmBICD2     236   SERQLEEAL...ETLKTEREQKNNLRKELSHYMSINDSFYTSHLQVSLDGLKFSDDTVTA
ggBICD2     236   SERQLEEAL...ETLKTEREQKNNLRKELSHYMNINDSMYNSHLNISLDGLKFSDE..AT
danreBICD2  236   ADRQLTEAL...ETVKTEREQKAALRKELTHHMTLGDSL....LASSLDGLKLS....AD
xtBICD2     223   SERQLEEAL...ESLKSEREQKKELQRELSAFLNYDSVG.......NLHG........NF
xtSpindly   213   KEDREKEAVGYFKALEKAREANQDLQAQLDIALQQ.....................AQ
hsSpindly   212   KEEREKEAVSYYNALEKARVANQDLQVQLDQALQQ.....................AL
mmSpindly   212   KEERERE AVSYYNALEKARVENQDLQVQLGHALQQ.....................AA
ggSpindly   212   KEEREKEVVSYCNALEKAREANQELRVQLDHVVQQ.....................SL
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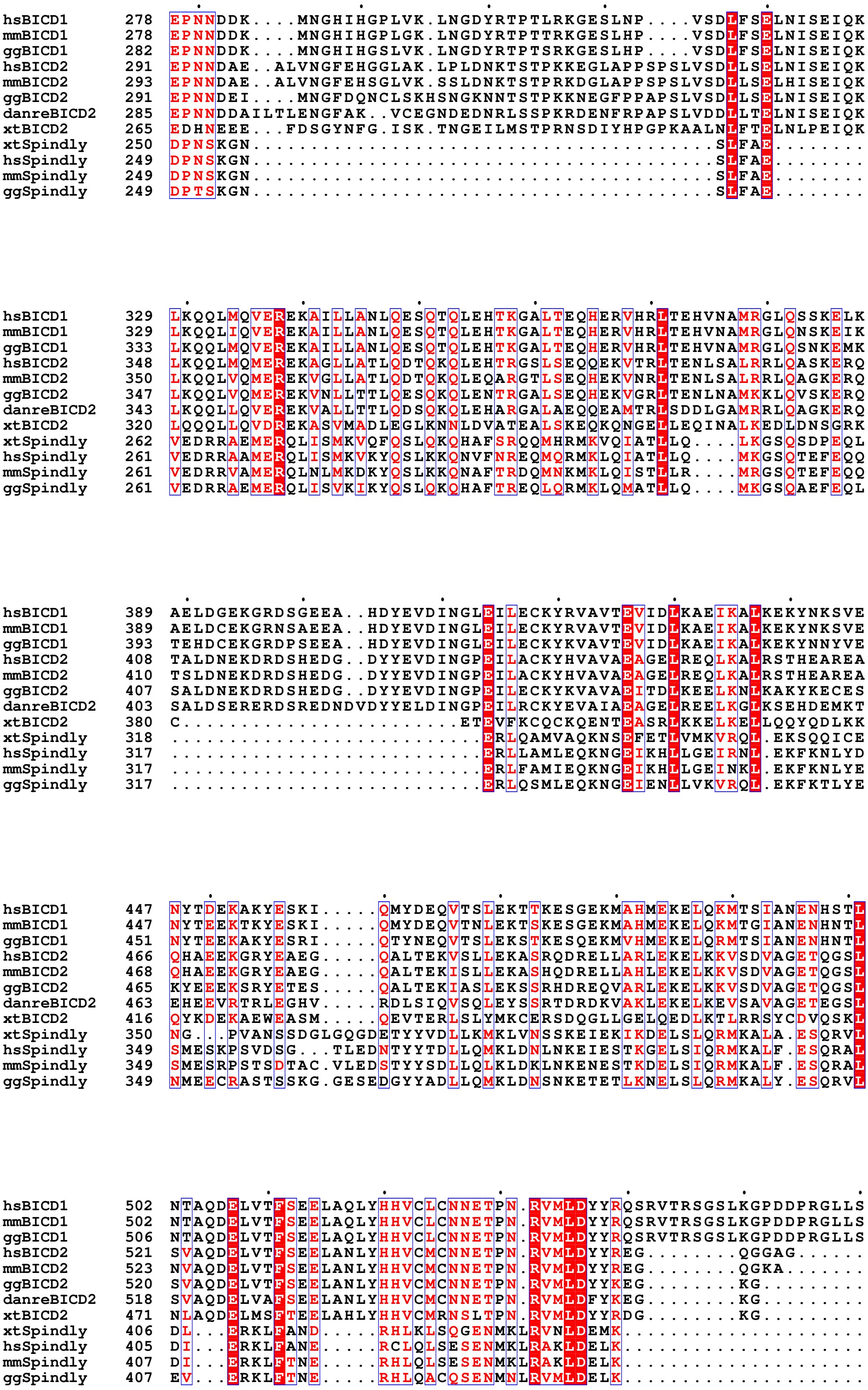

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mmBICD1       278  EPNNDDK....MNGHIHGPLGK.LNGDYRTPTTRKGESLHP....VSDLFSELNISEIQK
ggBICD1       282  EPNNDDK....MNGHIHGSLVK.LNGDYRTPTSRKGESLHP....VSDLFSELNISEIQK
hsBICD2       291  EPNNDAE..ALVNGFEHGGLAK.LPLDNKTSTPKKEGLAPPSPSLVSDLLSELNISEIQK
mmBICD2       293  EPNNDAE..ALVNGFEHSGLVK.SSLDNKTSTPRKDGLAPPSPSLVSDLLSELHISEIQK
ggBICD2       291  EPNNDEI....MNGFDQNCLSKHSNGKNNTSTPKKNEGFPPAPSLVSDLLSELNISEIQK
danreBICD2    285  EPNNDDAILTLENGFAK..VCEGNDEDNRLSSPKRDENFRPAPSLVDDLLTELNISEIQK
xtBICD2       265  EDHNEEE...FDSGYNFG.ISK.TNGEILMSTPRNSDIYHPGPKAALNLFTELNLPEIQK
xtSpindly     250  DPNSKGN........................................SLFAE........
hsSpindly     249  DPNSKGN........................................SLFAE........
mmSpindly     249  DPNSKGN........................................SLFAE........
ggSpindly     249  DPTSKGN........................................SLFAE........

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mmBICD1       329  LKQQLIQVEREKAILLANLQESQTQLEHTKGALTEQHERVHRLTEHVNAMRGLQNSKEIK
ggBICD1       333  LKQQLMQVEREKAILLANLQESQTQLEHTKGALTEQHERVHRLTEHVNAMRGLQSNKEMK
hsBICD2       348  LKQQLMQMEREKAGLLATLQDTQKQLEHTRGSLSEQQEKVTRLTENLSALRRLQASKERQ
mmBICD2       350  LKQQLVQMEREKVGLLATLQDTQKQLEQARGTLSEQHEKVNRLTENLSALRRLQAGKERQ
ggBICD2       347  LKQQLVQMEREKVNLLTTLQESQKQLENTRGALSEQHEKVGRLTENLNAMKKLQVSKERQ
danreBICD2    343  LKQQLLQVEREKVALLTTLQDSQKQLEHARGALAEQQEAMTRLSDDLGAMRRLQAGKERQ
xtBICD2       320  LQQQLLQVDREKASVMADLEGLKNNLDVATEALSKEQKQNGELLEQINALKEDLDNSGRK
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hsSpindly     261  VEDRRAAMERQLISMKVKYQSLKKQNVFNREQMQRMKLQIATLLQ....MKGSQTEFEQQ
mmSpindly     261  VEDRRVAMERQLNLMKDKYQSLKKQNAFTRDQMNKMKLQISTLLR....MRGSQTEFEQQ
ggSpindly     261  VEDRRAEMERQLISVKIKYQSLQKQHAFTREQLQRMKLQMATLLQ....MKGSQAEFEQL

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mmBICD1       389  AELDCEKGRNSAEEA..HDYEVDINGLEILECKYRVAVTEVIDLKAEIKALKEKYNKSVE
ggBICD1       393  TEHDCEKGRDPSEEA..HDYEVDINGLEILECKYKVAVTEVIDLKAEIKALKEKYNNYVE
hsBICD2       408  TALDNEKDRDSHEDG..DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREA
mmBICD2       410  TSLDNEKDRDSHEDG..DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREA
ggBICD2       407  SALDNEKDRDSHEDG..DYYEVDINGPEILECKYKVAVAEITDLKEELKNLKAKYKECES
danreBICD2    403  SALDSERERDSREDNDVDYYELDINGPEILRCKYEVAIAEAGELREELKGLKSEHDEMKT
xtBICD2       380  C........................ETEVFKCQCKQENTEASRLKKELKELLQQYQDLKK
xtSpindly     318  ...........................ERLQAMVAQKNSEFETLVMKVRQL.EKSQQICE
hsSpindly     317  ...........................ERLLAMLEQKNGEIKHLLGEIRNL.EKFKNLYD
mmSpindly     317  ...........................ERLFAMIEQKNGEIKHLLGEINKL.EKFKNLYE
ggSpindly     317  ...........................ERLQSMLEQKNGEIENLLVKVRQL.EKFKTLYE

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ggBICD1       451  NYTEEKAKYESRI.....QTYNEQVTSLEKSTKESQEKMVHMEKELQRMTSIANENHNTL
hsBICD2       466  QHAEEKGRYEAEG.....QALTEKVSLLEKASRQDRELLARLEKELKKVSDVAGETQGSL
mmBICD2       468  QHAEEKGRYEAEG.....QALTEKISLLEKASHQDRELLAHLEKELKKVSDVAGETQGSL
ggBICD2       465  KYEEEKSRYETES.....QALTEKIASLEKSSRHDREQVARLEKELKKVSDVAGETQGSL
danreBICD2    463  EHEEVRTRLEGHV.....RDLSIQVSQLEYSSRTDRDKVAKLEKELKEVSAVAGETEGSL
xtBICD2       416  QYKDEKAEWEASM.....QEVTERLSLYMKCERSDQGLLGELQEDLKTLRRSYCDVQSKL
xtSpindly     350  NG...PVANSSDGLGQGDETYYVDLLKMKLVNSSKEIEKIKDELSLQRMKALA.ESQRVL
hsSpindly     349  SMESKPSVDSG...TLEDNTYYTDLLQMKLDNLNKEIESTKGELSIQRMKALF.ESQRAL
mmSpindly     349  SMESRPSTSDTAC.VLEDSTYYSDLLQLKLDKLNKENESTKDELSIQRMKALF.ESQRAL
ggSpindly     349  NMEECRASTSSKG.GESEDGYYADLLQMKLDNSNKETETLKNELSLQRMKALY.ESQRVL

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mmBICD1       502  NTAQDELVTFSEELAQLYHHVCLCNNETPN.RVMLDYYRQSRVTRSGSLKGPDDPRGLLS
ggBICD1       506  NTAQDELVTFSEELAQLYHHVCLCNNETPN.RVMLDYYRQSRVTRSGSLKGPDDPRGLLS
hsBICD2       521  SVAQDELVTFSEELANLYHHVCMCNNETPN.RVMLDYYREG........QGGAG......
mmBICD2       523  NVAQDELVTFSEELANLYHHVCMCNNETPN.RVMLDYYREG........QGKA.......
ggBICD2       520  SVAQDELVTFSEELANLYHHVCMCNNETPN.RVMLDYYKEG........KG.........
danreBICD2    518  SVAQDELVAFSEELANLYHHVCMCNNETPN.RVMLDFYKEG........KG.........
xtBICD2       471  NLAQDELMSFTEELAHLYHHVCMRNSLTPN.RVMLDYYRDG........KG.........
xtSpindly     406  DL...ERKLFAND.....RHLKLSQGENMKLRVNLDEMK.....................
hsSpindly     405  DI...ERKLFANE.....RCLQLSESENMKLRAKLDELK.....................
mmSpindly     407  DI...ERKLFTNE.....RHLQLSESENMKLRAKLDELK.....................
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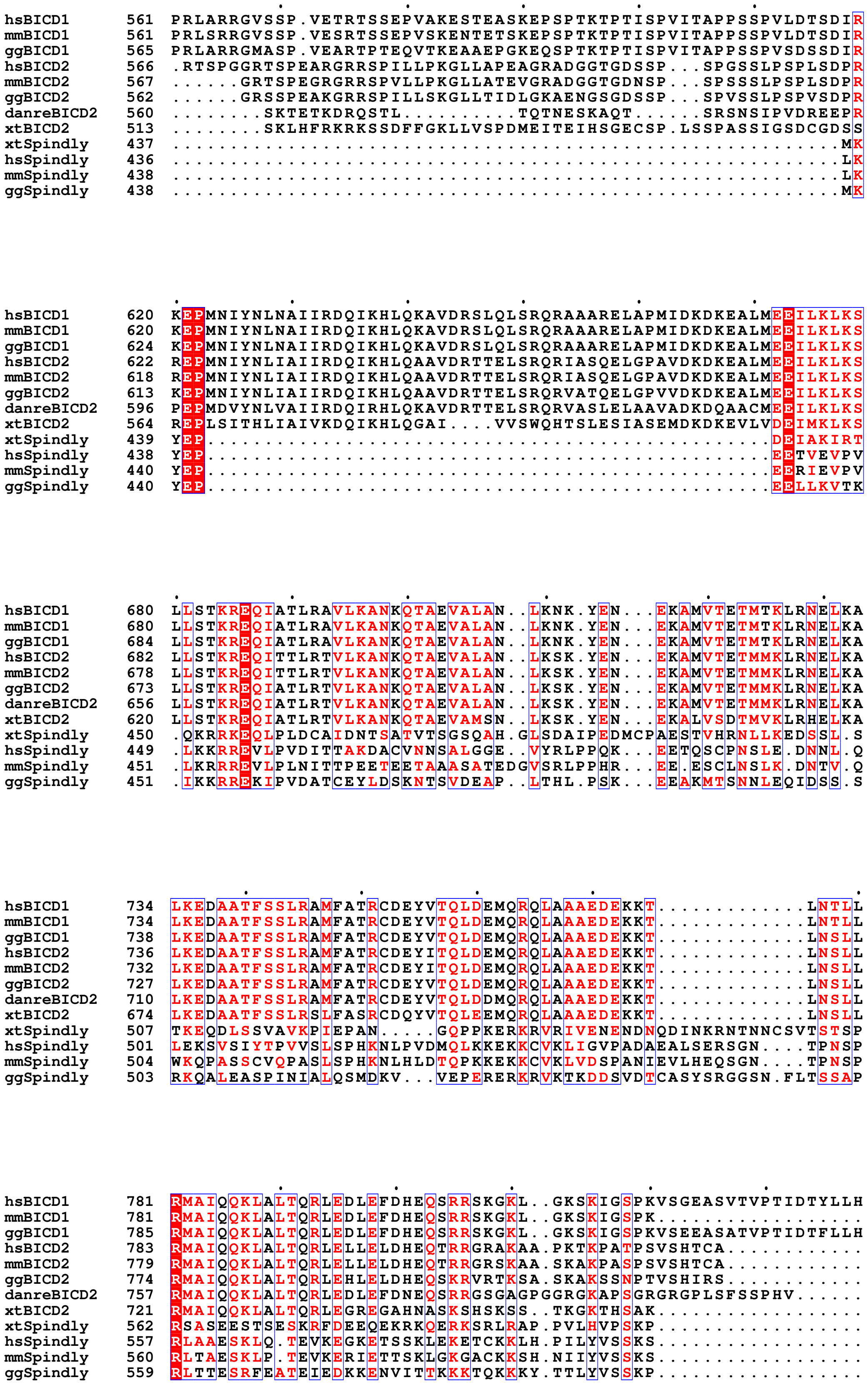

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ggBICD1     565  PRLARRGMASP.VEARTPTEQVTKEAAEPGKEQSPTKTPTISPVITAPPSSPVSDSSDIR
hsBICD2     566  .RTSPGGRTSPEARGRRSPILLPKGLLAPEAGRADGGTGDSSP...SPGSSLPSPLSDPR
mmBICD2     567  ......GRTSPEGRGRRSPVLLPKGLLATEVGRADGGTGDNSP...SPSSSLPSPLSDPR
ggBICD2     562  ......GRSSPEAKGRRSPILLSKGLLTIDLGKAENGSGDSSP...SPVSSLPSPVSDPR
danreBICD2  560  ........SKTETKDRQSTL..........TQTNESKAQT......SRSNSIPVDREEPR
xtBICD2     513  ........SKLHFRKRKSSDFFGKLLVSPDMEITEIHSGECSP.LSSPASSIGSDCGDSS
xtSpindly   437  ..........................................................MK
hsSpindly   436  ..........................................................LK
mmSpindly   438  ..........................................................LK
ggSpindly   438  ..........................................................MK

hsBICD1     620  KEPMNIYNLNAIIRDQIKHLQKAVDRSLQLSRQRAAARELAPMIDKDKEALMEEILKLKS
mmBICD1     620  KEPMNIYNLNAIIRDQIKHLQKAVDRSLQLSRQRAAARELAPMIDKDKEALMEEILKLKS
ggBICD1     624  KEPMNIYNLNAIIRDQIKHLQKAVDRSLQLSRQRAAARELAPMIDKDKEALMEEILKLKS
hsBICD2     622  REPMNIYNLIAIIRDQIKHLQAAVDRTTELSRQRIASQELGPAVDKDKEALMEEILKLKS
mmBICD2     618  REPMNIYNLIAIIRDQIKHLQAAVDRTTELSRQRIASQELGPAVDKDKEALMEEILKLKS
ggBICD2     613  KEPMNIYNLIAIIRDQIKHLQAAVDRTTELSRQRVATQELGPVVDKDKEALMEEILKLKS
danreBICD2  596  PEPMDVYNLVAIIRDQIRHLQKAVDRTTELSRQRVASLELAAVADKDQAACMEEILKLKS
xtBICD2     564  REPLSITHLIAIVKDQIKHLQGAI....VVSWQHTSLESIASEMDKDKEVLVDEIMKLKS
xtSpindly   439  YEP.................................................DEIAKIRT
hsSpindly   438  YEP.................................................EETVEVPV
mmSpindly   440  YEP.................................................EERIEVPV
ggSpindly   440  YEP.................................................EELLKVTK

hsBICD1     680  LLSTKREQIATLRAVLKANKQTAEVALAN..LKNK.YEN...EKAMVTETMTKLRNELKA
mmBICD1     680  LLSTKREQIATLRAVLKANKQTAEVALAN..LKNK.YEN...EKAMVTETMTKLRNELKA
ggBICD1     684  LLSTKREQIATLRAVLKANKQTAEVALAN..LKNK.YEN...EKAMVTETMTKLRNELKA
hsBICD2     682  LLSTKREQITTLRTVLKANKQTAEVALAN..LKSK.YEN...EKAMVTETMMKLRNELKA
mmBICD2     678  LLSTKREQITTLRTVLKANKQTAEVALAN..LKSK.YEN...EKAMVTETMMKLRNELKA
ggBICD2     673  LLSTKREQIATLRTVLKANKQTAEVALAN..LKSK.YEN...EKAMVTETMMKLRNELKA
danreBICD2  656  LLSTKREQIATLRTVLKANKQTAEVALAN..LKSK.YEN...EKAMVTETMMKLRNELKA
xtBICD2     620  LLSTKREQIATLRTVLKANKQTAEVAMSN..LKSK.YEN...EKALVSDTMVKLRHELKA
xtSpindly   450  .QKRRKEQLPLDCAIDNTSATVTSGSQAH.GLSDAIPEDMCPAESTVHRNLLKEDSSL.S
hsSpindly   449  .LKKRREVLPVDITTAKDACVNNSALGGE..VYRLPPQK...EETQSCPNSLE.DNNL.Q
mmSpindly   451  .LKRRREVLPLNITTPEETEETAAASATEDGVSRLPPHR...EE.ESCLNSLK.DNTV.Q
ggSpindly   451  .IKKRREKIPVDATCEYLDSKNTSVDEAP..LTHL.PSK...EEAKMTSNNLEQIDSS.S

hsBICD1     734  LKEDAATFSSLRAMFATRCDEYVTQLDEMQRQLAAAEDEKKT.............LNTLL
mmBICD1     734  LKEDAATFSSLRAMFATRCDEYVTQLDEMQRQLAAAEDEKKT.............LNTLL
ggBICD1     738  LKEDAATFSSLRAMFATRCDEYVTQLDEMQRQLAAAEDEKKT.............LNSLL
hsBICD2     736  LKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDEKKT.............LNSLL
mmBICD2     732  LKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDEKKT.............LNSLL
ggBICD2     727  LKEDAATFSSLRAMFATRCDEYVTQLDEMQRQLAAAEDEKKT.............LNSLL
danreBICD2  710  LKEDAATFSSLRAMFATRCDEYVTQLDDMQRQLAAAEDEKKT.............LNSLL
xtBICD2     674  LKEDAATFSSLRSLFASRCDQYVTQLEEMQRQLAAAEDEKKT.............LNSLL
xtSpindly   507  TKEQDLSSVAVKPIEPAN.....GQPPKERKRVRIVENENDNQDINKRNTNNCSVTSTSP
hsSpindly   501  LEKSVSIYTPVVSLSPHKNLPVDMQLKKEKKCVKLIGVPADAEALSERSGN....TPNSP
mmSpindly   504  WKQPASSCVQPASLSPHKNLHLDTQPKKEKKCVKLVDSPANIEVLHEQSGN....TPNSP
ggSpindly   503  RKQALEASPINIALQSMDKV...VEPERERKRVKTKDDSVDTCASYSRGGSN.FLTSSAP

hsBICD1     781  RMAIQQKLALTQRLEDLEFDHEQSRRSKGKL..GKSKIGSPKVSGEASVTVPTIDTYLLH
mmBICD1     781  RMAIQQKLALTQRLEDLEFDHEQSRRSKGKL..GKSKIGSPK..................
ggBICD1     785  RMAIQQKLALTQRLEDLEFDHEQSRRSKGKL..GKSKIGSPKVSEEASATVPTIDTFLLH
hsBICD2     783  RMAIQQKLALTQRLELLELDHEQTRRGRAKAA.PKTKPATPSVSHTCA............
mmBICD2     779  RMAIQQKLALTQRLELLELDHEQTRRGRSKAA.SKAKPASPSVSHTCA............
ggBICD2     774  RMAIQQKLALTQRLEHLELDHEQSKRVRTKSA.SKAKSSNPTVSHIRS............
danreBICD2  757  RMAIQQKLALTQRLEDLEFDNEQSRRGSGAGPGGRGKAPSGRGRGPLSFSSPHV......
xtBICD2     721  RMAIQQKLALTQRLEGREGAHNASKSHSKSS..TKGKTHSAK..................
xtSpindly   562  RSASEESTSESKRFDEEQEKRKQERKSRLRAP.PVLHVPSKP..................
hsSpindly   557  RLAAESKLQ.TEVKEGKETSSKLEKETCKKLH.PILYVSSKS..................
mmSpindly   560  RLTAESKLP.TEVKERIETTSKLGKGACKKSH.NIIYVSSKS..................
ggSpindly   559  RLTTESRFEATEIEDKKENVITTKKKTQKKKY.TTLYVSSKP..................
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hsBICD1      839  SQGPQTPNIRVSSGTQRKRQFSPSLCDQSRPRTSGASYLQNLLRVPPDPTSTESFLLKGP
mmBICD1           ............................................................
ggBICD1      843  SQGPQQPNLLVSSGTQRKRLFSPSLCDQSHPRTSG.TYLQKLLRAPPHPASTESYLLRGP
hsBICD2      830  .........................CASDRAEGTG.......L..ANQVFCSEKHSIY..
mmBICD2      826  .........................CASERAEGAG.......L..ANQVFCSEKHSIY..
ggBICD2      821  .........................C.GDRPEGSV.......L..NNQVFCSEKYKIY..
danreBICD2   811  ..SPRLP..................C.KNRPQPHG.......LIGSPAVFCSEKYKIL..
xtBICD2      761  ....................................................SKYI....
xtSpindly    603  .............................................AATTQCPQQ......
hsSpindly    597  .............................................TPETQCPQQ......
mmSpindly    600  .............................................APETQCSQQ......
ggSpindly    600  .............................................TPETQCAQQ......

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hsBICD1      899  PSMSEFIQGHRLSKEKRLTVAPP.......DCQQPAASVPPQCSQLAGRQDCPTVSPDTA
mmBICD1      821  .......SGH.........................................CPQ......
ggBICD1      902  PSMSEFIHGHRLSKEKRLTVATPVLVLFQKSSHIPALSVPLSTVSLSLLL.TPNLHMQRK
hsBICD2      854  ...................................................CD.......
mmBICD2      850  ...................................................CD.......
ggBICD2      844  ...................................................CD.......
danreBICD2   841  ...................................................CDTGSD...
xtBICD2           ............................................................
xtSpindly         ............................................................
hsSpindly         ............................................................
mmSpindly         ............................................................
ggSpindly         ............................................................

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hsBICD1      952  LPEEQP..HSSS.QCAPLHCLSKP...PHP
mmBICD1           ..............................
ggBICD1      961  RKRKQSGVHATKVRVVPSERVDNPALLPHR
hsBICD2           ..............................
mmBICD2           ..............................
ggBICD2           ..............................
danreBICD2        ..............................
xtBICD2           ..............................
xtSpindly         ..............................
hsSpindly         ..............................
mmSpindly         ..............................
ggSpindly         ..............................
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