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Supplementary Table 1 | Protein and model building information for all modelled human C* proteins.

The common names of each protein, their molecular weight, number of amino acids and chain ID are shown in the first column. The boundaries of the domains or regions of each protein that are modelled into the C* EM map are indicated in the second column.

Human Protein	Domain/region in C* model	Positioning
Prp8 **U5-220K** 273.6 kDa 2335 aa Chain A	NTD1 aa 26-662	The human structure was generated by homology modelling using the SWISS-MODEL software package[62], based on its *S. pombe* (S.p.) orthologue, whose structure was determined by cryo-EM of the ILS (PDB 3JB9, ref. 14). The resulting model was used for rigid-body fitting into EM density, followed by minor refinement in Coot. Residues 178, 219 and 283 - 293 were ab-initio modelled in Coot. The position and structure of NTD1 in C* are similar to those observed in the human[18] and the *S. cerevisiae* (S.c.) tri-snRNP[16,17], as well as in the S.c. B^{act} and C complex, and S.p. ILS[14,19-22].
	NTDL NTD2 aa 663-798	A homology model was generated as described for the human Prp8 NTD1, and was used for rigid-body fitting followed by refinement in Coot. The position and structure of NTD2 in C* are equivalent to those in the S.c. B^{act} and C complex, and S.p. ILS[14,19-22].
	RT/En aa 799-1775	A homology model was generated for most residues as described for the human Prp8 NTD1, and was used for rigid-body fitting followed by refinement in Coot. Several loops and residues (1204, 1509-1515, 1756-1761) were manually adjusted or rebuilt with Coot. As the switch loop (aa 1334–1356) has a different orientation and structural appearance compared to those in the S.p., its S.c. C complex orthologue (PDB 5LJ3, ref. 22) was used for homology modelling. The position and structure of the RT/En domain in C* are otherwise very similar to those in the S.c. C complex and the S.p. ILS[14,19-22].
	RH aa 1776-1990	The high resolution, closed conformation *H. sapiens* (H.s.) RH structure (PDB 4JK7) determined by X-ray crystallography[71] was used for rigid-body fitting. Due to the excellent fit of this domain, no further manual refinement was necessary.
Snu114 **U5-116K** **EFTUD2** 109.4 kDa 972 aa Chain B	aa 56 -957	A homology model was generated based on the S.p. orthologue as described above for the human Prp8 NTD1, and was used for rigid-body fitting, followed by minor adjustments in Coot. The position and structure of Snu114 in C* are equivalent to those in the human[18] and S.c. tri-snRNP[16,17], as well as those in the S.c. B^{act} and C complex, and S.p. ILS[14,19-22].

Human Protein	Domain/region in C* model	Positioning
U5-40K 39.3 kDa 357 aa Chain F	WD40 aa 51–357	A structural model of the human U5-40K WD40 domain was obtained from the SpliProt3D database[63] and fitted into well-defined density at a position identical to that of its S.p. orthologue (Cwf17) in the ILS (PDB 3JB9, ref. 14). Minor refinement and adjustments of loop elements in the structure were necessary and performed with Coot. The correct orientation of the ring-shaped structure could be determined by fitting characteristic loop elements into the EM density, as well as based on the position of multiple crosslinks to e.g. Cdc5, Prp19, Spf27, Prp8, Rbm22 or Skip (see Supplementary Table 2).
U5 Sm ca 94 kDa 857 aa Chains f, g, a, e, c, b, d	Sm domains of SmB, SmD1, SmD2, SmD3, SmE, SmF, SmG	The crystal structure of a human U4 Sm ring (PDB 4WZJ, ref. 72), including the highly conserved RNA bound by the Sm-proteins, was used for rigid-body fitting into the circular EM density at the foot of the C* main body. The correct orientation of the Sm ring was verified by fitting characteristic density elements (e.g. protruding beta-fingers) and by corresponding crosslinks (Supplementary Table 2). The position of the U5 Sm ring in the C* complex is comparable to that in the H.s. (ref. 18) and S.c. tri-snRNP[16,17], as well as that of the S.c. B^{act} and C complexes, and S.p. ILS[14,19-22].
Rbm22 46.9 kDa 420 aa Chain P	aa 19-308	As the complete structure of Rbm22 is currently not known, it was modelled into the EM density based on structural homology to regions of its apparent yeast orthologues Ecm2 and Cwc2 (ref. 24), secondary structure predictions and protein-protein crosslinks (Supplementary Table 2). AA 19-126, including two zinc-finger domains, were homology modelled according to S.p. Ecm2 aa 18-125 (PDB 3JB9, ref. 14) and could be fitted into the EM density without major adjustments at a position very similar to that were this region of Ecm2 is found in the S.p. ILS. AA 127-163 were fit according to secondary structure predictions made available through the SpliProt3D database[63], where a predicted short α-helix (aa 143-150) could be very well placed into an appropriately thickened density element within the EM map. The following zinc-finger domain encompassing aa 164-190 was homology modelled to S.p. Cwf2 (Cwc2 in S.c.) aa 116-142 (PDB 3JB9, ref. 14) and docked into a well-suited, nearby density element just above a strand of U6 snRNA proximal to its 5' SL. Tracing the adjacent density further, Rbm22 aa 191-232 were fit by introducing a short α-helical element from aa 196-200 and a SpliProt3D secondary structure predicted α-helix (aa 207-217). The adjacent RNA

Human Protein	Domain/region in C* model	Positioning
		recognition motif (RRM) encompassing aa 201-308 was homology modelled according to its counterpart in S.p., Cwf2 (aa 149-259), (PDB 3JB9, ref. 14) and rigid body docked into an characteristically-shaped, but less well-resolved density element that contacts Ppil1 and is in close proximity to Aquarius. It is thus located at a different position compared to that of the Cwf2 (Cwc2) RRM in the S.p. ILS. The placement of Rbm22 domains was further supported by intra- and inter-molecular protein crosslinks (Supplementary Table 2). To name just a few examples, Rbm22 aa 315 (not modelled but in very close proximity to the RRM-domain) crosslinks to multiple positions of Aquarius, consistent with the modelled position of the RRM. Furthermore, Rbm22 aa 76, 139 and 286 crosslink to the same Lys 193 of Skip/hPrp45, Rbm22 aa 76 to Skip/hPrp45 aa 108 and 193, as well as Rbm22 aa 40 to Skip/hPrp45 aa 153, all in agreement with distances and orientations observed in the model. All available Rbm22 intra-molecular crosslinks are also in very good agreement with the present model.
G10 **Bud31** 17.0 kDa 144 aa Chain Q	aa 3-144	The human Bud31 structure was generated by homology modelling using the SWISS-MODEL software package[62], based on its *S.p.* orthologue, whose structure was determined by cryo-EM of the ILS (PDB 3JB9, ref. 14), and was used for rigid-body fitting followed by minor adjustments particularly of loop regions using Coot. The Bud31 position and structure in C* are equivalent to those of its orthologue in the S.c. B^{act} and C complex, and S.p. ILS[14,19-22].
Prp17 65.5 kDa 579 aa Chain E	N-terminal domain aa 117–138	A short α-helical element of human Prp17's N-terminal domain, in accordance with secondary structure predictions from SpliProt3D database[63], was fit into an appropriately shaped, unambiguous density element that contacts U6 snRNA, Bud31, Rbm22, the N-terminal helix of Prp8, Skip and U5-40K. Its position is in excellent agreement with the corresponding region of its Prp17 counterpart in the S.p. ILS (PDB 3JB9, ref. 14). Additionally, Prp17 aa 151 and 161, which are in very close proximity to the modelled α-helical element, are crosslinked to Prp8 aa 36, in agreement with the modelled position.
	WD40 aa 273–579	A structural model of the human Prp17 WD40 domain was obtained from the SpliProt3D database[63] and fit into well-defined density, followed by minor adjustments in Coot. The correct orientation of the ring-shaped structure could be determined by fitting characteristic loop elements into appropriately shaped density, and was consistent with the position of several crosslinks to Cdc5 and Syf3 (for details see Supplementary Table 2).

Human Protein	Domain/region in C* model	Positioning
Skip **Prp45** 61.5 kDa 536 aa Chain C	aa 95–311	A homology model was generated based on the structure of the S.p. orthologue (PDB 3JB9) that was determined by cryo-EM of the ILS[14] and was used for rigid-body fitting followed by refinement with Coot. Well-fitting densities for the helical and ß-sheet regions were found in the C* structure at positions equivalent to those where the corresponding regions of the S. pombe protein are located in the ILS. The modelled position is supported by various crosslinks (Supplementary Table 2). AA 185-192 were added to the model and fit using Coot, tracing the EM density. The fitted structure ends C-terminally with a modelled helix comprising aa 282-310 that interacts with the RT end of the Prp8-RT/En domain and Prp22. The remaining C-terminal aa could not be modelled with sufficient confidence. However, according to our crosslinking data, they must closely interact with Prp22/DHX8 and Prp8 RT/En and RNase H like domains.
Prl1 **Prp46** 57.2 kDa 514 aa Chain D	WD40 aa 186–500	The available crystal structure (PDB 4YVD) was rigid-body fit into well-suited density according to the position of its orthologue in the S.p. ILS (PDB 3JB9, ref. 14) followed by subsequent minor refinement of loop regions with Coot. AA 453–461, 191 –168 and 493–500 were originally missing in the crystal structure and eventually modelled into appropriately shaped density using Coot. The position and structure of human Prl1's WD40 domain in C* are also similar to those of its orthologues found in the S.c. B^{act} and C complex[19-22].
Cdc5 92.3 kDa 802 aa Chain L	tandem Myb aa 10–111	The human structure was generated by homology modelling, using the SWISS-MODEL software package[61], based on the structure of its S.p. orthologue in the ILS that was determined by cryo-EM (PDB 3JB9, ref. 14). The model was fit as a rigid body into appropriately shaped density followed by refinement in Coot. Crosslinks to adjacent proteins, like Skip, Syf1 and Syf2, confirm its position (see Supplementary Table 2). The position and structure of the human Cdc5 Myb domains modelled in the C* complex are equivalent to those of its orthologues found in the S.c. B^{act} and C complex, and S.p. ILS[14,19-22].
	H1 aa 143–161	The human helix 1 (H1) structure was modelled, fit and refined as described above for the tandem Myb domain. The position and structure of the human H1 domain modelled in the C* complex are equivalent to those of the corresponding region of its orthologues found in the S.c. C complex and S.p ILS[14,21,22].
	H2 aa 164–194	The human structure again was modelled, fit and refined as described above for the tandem Myb domain. The structure and position of H2 is similar to those of its orthologues found in the S.c. C complex and in the S.p. ILS[14,21,22]. The unstructured

Human Protein	Domain/region in C* model	Positioning
	Linker H2–H3 aa 195–233	linker between H2 and H3 was in part (aa 195–214) threaded through a density element at a position very similar, but not identical to that found in the S.c. C complex[21,22]. Remaining amino acids were modelled into C* density at a position comparable to that where they are found in the above mentioned S.c. complexes, i.e., flanking the Syf3 HAT-side that faces the main body. Multiple crosslinks to adjacent proteins, like Syf3 and Prp17, further support the modelled positions (see Supplementary Table 2).
	H3 aa 234–245 Linker H3–H4 aa 246–254 H4 aa 255–269	Upon tracing the unstructured linker sequence originating at H2, helix 3 (H3) becomes clearly visible in the C* EM density. Whereas all available yeast models to date (see above) show helices originating at the same position, but with variable lengths, the human C* complex, judging from the density, only harbors a shorter helical element at the otherwise structurally conserved N-terminal origin of H3. This helical density in the map is then connected to a short thread of continuous, unstructured density followed by another short element of helical density. In good agreement with the less conserved nature of the sequence between species at this position, secondary structure predictions made available through the SpliProt3D database[63] show two short α-helical elements (H3 and H4) connected by an unstructured loop at the position in question in the human Cdc5 protein. Consequently, the above mentioned, predicted secondary structure elements were introduced into the C* model in good agreement with their fit to the map. Minor adjustments, primarily concerning the course of the H3-H4 connecting loop region, were necessary and performed with Coot. A crosslink between the N-terminus of H4 and Syf3, further validates the modelled positions (see Supplementary Table 2).
	C-helix aa 689–795	The structure of this C-terminal element in the human protein was homology modelled using the SWISS-MODEL software package[62], based on the structure of its S.p. orthologue in the ILS that was determined by cryo-EM (PDB 3JB9, ref. 14). The resulting model was fit as a rigid body into appropriately shaped density, followed by refinement in Coot. A large number of crosslinks to adjacent proteins in the Prp19 helical bundle, including Spf27, as well as to U5-40K further support its orientation and position (Supplementary Table 2).
Prp19 55.2 kDa	aa 3–137	Four copies of the human Prp19 protein, each comprised of a long α-helical and U-Box motif, were homology modelled based on its S.p. orthologue in the ILS (PDB 3JB9, ref. 14), using the SWISS-MODEL software package[62]. The resulting models were fit as a rigid body into the density, followed by refinement in Coot. A large

Human Protein	Domain/region in C* model	Positioning
504 aa Chain G,H,I,J		number of crosslinks to adjacent proteins like Spf27 and the C-helix of Cdc5, as well as to U5-40K and Ppil1, further support the orientation and position of the human protein (Supplementary Table 2).
Spf27 26.1 kDa 225 aa Chain K	aa 14–225	Several α-helical elements and connective loops were homology modelled using the SWISS-MODEL software package[62], based on its S.p. orthologue (Cwc7) whose structure was determined by cryo-EM of the ILS (PDB 3JB9, ref. 14). The resulting model was fit as a rigid body into appropriately shaped density, followed by refinement in Coot. A large number of crosslinks to adjacent proteins like Prp19 and the C-helix of Cdc5 as well as to U5-40K and Ppil1 further justify the orientation and position of Spf27 in the C* complex (Supplementary Table 2).
Syf1 **Xab2** 100.0 kDa 855 aa Chain M	HAT aa 1–738	To model the HAT domain of H.s. Syf1, several reference structures (as described below) were used and combined in order to fit human Syf1 into to the C* EM map. Due to major variations in the sequence and the presence of insertions in the available yeast structures, only the N-terminal HAT repeat region (aa 1-254) could be homology modelled using the SWISS-MODEL software package[62], according to its S.c. orthologue in the spliceosomal C complex whose structure was determined by cryo-EM (PDB 5LJ3, ref. 22). Amino acids 255-738 were modelled by a 3D comparative modelling approach using the Robetta server (http://robetta.bakerlab.org/). The resulting model showed a typical HAT appearance and could be fit into the well-defined EM map. Good resolution, especially towards the C-terminal end of Syf1, allowed us to determine the HAT register with confidence. All refinement and model editing was performed with Coot. Distinctive crosslinks to Aquarius, Cdc5, Syf3, as well as U2 core proteins, validate its position (Supplementary Table 2).
Syf2 **GCIP p29** 28.7 kDa 243 aa Chain N	aa 128–242	The structure of most parts of the human protein was homology modelled, using the SWISS-MODEL software package[62], according to its S.c. orthologue in the C complex whose structure was determined by cryo-EM (PDB 5GMK, ref. 21). The resulting model was fit as a rigid body into appropriately shaped density. However, several adjustments that adapted secondary structure features to the EM map were necessary and performed with Coot. The following describes the modelling procedures based on the S.c. reference structure. In agreement with the sequence alignment of the S.c. and H.s. proteins, and, most importantly, the fit of the latter into the EM map, the N-terminal-most α-helical element was split into two helices and modelled into the well-resolved density. Into a directly connected density

Human Protein	Domain/region in C* model	Positioning
		element, an unstructured loop of approximately 20 aa (not fully modelled in the S.c. structure) was modelled. The next α-helical element (aa 192 – 211) was elongated at its N-terminus and shortened at its C-terminus with respect to the S.c. structure in order to fit the EM density. An additional loop of ca 15 amino acids could be traced through appropriately shaped density that contacts U2 and U6 snRNA just below U2-U6 helix II and leads to a final α-helical element comprised of aa 227 – 240, which again is, structurally and by sequence alignment, in very good agreement with the S.c. reference model from the C complex. A number of crosslinks to adjacent proteins like Syf3, Skip, Cdc5 and Prp8 additionally validate the modelled orientation and position (see Supplementary Table 2).
Syf3 **Crnkl1** 100.5 kDa 848 aa Chain O	N-terminal aa 175–217 HAT aa 218–738	The human structure was built up from three components, an N-terminal part (aa 175–215), the very well conserved central HAT part (aa 216–428) and the also regularly-structured HAT containing C-terminal part (aa 429–738). As the central HAT containing part is structurally very well conserved between species, the corresponding H.s. structure was homology modelled using the SWISS-MODEL software package[62] according to the structure of its S.c. orthologue in the C complex that was determined by cryo-EM (PDB 5GMK, ref. 21). After rigid body docking, only minor refinement with Coot was necessary. The domain's position and structure in C* are equivalent to those found in the S.c. B^{act}, C complexes, and S.p. ILS[14,19-22]. Due to some differences in sequence conservation between yeast and human, the C-terminal HAT part was comparatively modelled utilizing the Robetta server (http://robetta.bakerlab.org/). The helical elements of the characteristic HAT-containing model that was obtained were rigid body docked into appropriate C* density, followed by refinement of loop regions with Coot. As the H.s. C* map clearly showed additional, distinctive density elements at the modelled proteins's N-terminus, the latter was extended by 42 aa using the secondary structure predicted sequence available through the SpliProt3D database[63]. The predicted α-helical element comprised of aa 190–202 exhibited an excellent fit into the EM map and allowed for the adjacent, unstructured loop elements to be fit with confidence. In addition, the position of this helix appears to be in good agreement with that of a helical element of equal size but unknown amino acid identity modelled in the S.p. ILS (PDB 3JB9, ref. 14). Crosslinks, in particular those contacting appropriate residues of Cdc5, Prp17, Skip, Syf1 and Syf2, further validate the structure and position of human Syf3 (Supplementary Table 2).
Ad002		The structure of human Cwc15 was homology modelled using the SWISS-MODEL

Human Protein	Domain/region in C* model	Positioning
Cwc15 26.6 kDa 229 aa Chain R	aa 23–76 aa 186–229	software package[62], according to the structure of its S.p. orthologue in the ILS that was determined by cryo-EM (PDB 3JB9, ref. 14). The resulting model was fit as a rigid body, followed by minor refinement in Coot. The position and structure of the modelled domain in the H.s. C* complex are equivalent to those found for its orthologue in the referenced S.p. ILS model. N-terminal aa 23–30, not modelled in the ILS complex, were additionally fit into the density using Coot. Crosslinks to Skip, Rbm22, Prp8 and Prl1 further support the domain's orientation and position (Supplementary Table 2).
SRm300 299.6 kDa 2752 aa Chain S	aa 1–30	The human structure was homology modelled using the SWISS-MODEL software package[62], according to the structure of its S.c. orthologue Cwc21 in the C complex that was determined by cryo-EM (PDB 5LJ3, ref. 22). The resulting model was fit as a rigid body, followed by minor refinement with Coot. Due to an almost complete sequence conservation between the N-terminal parts of Cwc21 and SRm300, a high degree of structural homology is also assumed for this region. In fact, the homology modelled N-terminal SRm300 structure fits very well into the H.s. C* density at an equivalent position to that in the S.c. B^{act} and C complexes, contacting exon 1, Prp8 and Cwc22 in a similar way as Cwc21 in the S.c. B^{act} and C complexes[19-22].
Cwc22 105.5 kDa 908 aa Chain T	MIF4G aa 149–406	The human structure of this domain was obtained from the co-crystal structure of Cwc22 MIF4G and the eIF4AIII helicase domain (PDB 4C9B, ref. 73). Specifically, using the less well-resolved, unmasked EM-density map (no particle mask was applied during refinement), the MIF4G domain was docked into an appropriately shaped density element (UPD2) just below the exit tunnel of exon 1, contacting Prp8 and Snu114. The domain's position and orientation are very similar to those of its orthologues found in the S.c. B^{act} and C complex[19-22]. Specific crosslinks to Prp8 and Snu114 further validate its position (Supplementary Table 2).
	MA3 aa 450–651	The human structure of this generally well-conserved domain of Cwc22 was homology modelled using the SWISS-MODEL software package[62], according to the structure of its S.c. orthologue in the C complex that was determined by cryo-EM (PDB 5GMK, ref. 21). The resulting model was fit as a rigid body, followed by minor refinement in Coot. The position and structure of this domain in the C* complex are equivalent to those found in the S.c. B^{act} and C complex[19-22]. A crosslink to the lysine 1222 of Prp8 further validate the domain's position (Supplementary Table 2).
Aquarius IBP160	aa 19–1381	The 2.3 Å crystal structure of the entire H.s. Aquarius protein (PDB 4PJ3, ref. 74) was used and docked into appropriately shaped density, contacting the peripheral

Human Protein	Domain/region in C* model	Positioning
171.3 kDa 1485 aa Chain U		HAT side of Syf1. Crosslinks to Syf1 and Rbm22 validate the position and orientation of the protein in C* (Supplementary Table 2). The position of the H.s. Aquarius helicase in the C* complex appears to be comparable to the position of its S.p. orthologue in the ILS[14].
Ppil1 18.2 kDa 166 aa Chain V	aa 11–165	The human structure was homology modelled using the SWISS-MODEL software package[62], according to its S.p. orthologue in the ILS whose structure was determined by Cryo-EM[14]. The resulting model was rigid body fitted into appropriately-shaped density, followed by minor refinement with Coot. The position and structure of the modelled Ppil1 in the H.s. C* complex are equivalent to those of its orthologue in the referenced S.p. ILS model. Crosslinks to Prp19, Spf27 and Skip, as well as to residues that were not modelled, but close to modelled residues of Prl1 and U5-40K validate the protein's general orientation and position (Supplementary Table 2).
U2 Sm ca 94 kDa 857 aa Chains m, n, h, l, j, i, k	Sm domains of SmB, SmD1, SmD2, SmD3, SmE, SmF, SmG	The crystal structure of a human U4 Sm assembly (PDB 4WZJ, ref. 72), including the highly conserved RNA contacted by the Sm proteins, was used for rigid-body fitting into a ring-shaped density adjacent to the Prp17 WD40 domain. The correct orientation of the Sm ring assembly could be determined by fitting characteristic extensions of certain Sm proteins and evaluating crosslinks to adjacent proteins. Even though the resolution at the U2 Sm position is poorer than that at the RNP core of the C* complex, it is sufficient to unequivocally fit the characteristic doughnut-shaped assembly. Furthermore, the position of the neighbouring U2 snRNP proteins A' and B'' (see below), as well as U2 snRNA helical elements adjacent to the U2 Sm ring, aided its positioning within the complex. The position of the U2 Sm ring in C* is comparable to that in the S.p. ILS (PDB 3JB9, ref. 14).
U2-A' 28.4 kDa 255 aa Chain W	aa 2-163	The entire 2.4 Å crystal structure of the H.s. spliceosomal U2-A' and B'' proteins, including a small stretch of the U2 snRNA to which they bind (PDB 1A9N, ref. 75), was used and docked into appropriately shaped density that, as expected, contacts the U2 Sm ring. The H.s. U2-A' and B'' assembly in the C* complex appears to be located at position comparable to that of its S.p. orthologues in the ILS (PDB 3JB9, ref. 14).
U2-B'' 25.5 kDa 225 aa Chain X	aa 6-99	
eIF4AIII	RecA1 aa 21–242	The human RecA1 domain structure was obtained from its co-crystal with RecA2 and Cwc22 MIF4G (PDB 4C9B, ref. 73) and rigid body docked into the unmasked

Human Protein	Domain/region in C* model	Positioning
46.9 kDa 411 aa Chain p		EM-density map at the UPD2 position. Since the domain does not fit into the C* density in its co-crystalized conformation (Extended Data Figure 7), it was shifted as a rigid-body into a less well-resolved but prominent density element (in the unmasked structure) directly adjacent to RecA2 (see below). Intramolecular crosslinks, in particular between RecA1 aa 60 and RecA2 aa 374, as well as RecA1 aa 70 and RecA2 aa 374, further support the partially open conformation of both RecA domains within the C* complex. Intermolecular crosslinks to Snu114 and Cwc22 MIF4G also support the modelled position (Supplementary Table 2).
	RecA2 aa 245–411	The crystal structure of the human RecA2 helicase domain (see RecA1 and Cwc22 MIF4G above), in conjunction with its co-crystalized Cwc22 MIF4G domain, was rigid body docked into unmasked EM-density map at the UPD2 position. As the RecA2 domain was not separated from the co-crystalized MIF4G domain during docking procedures, RecA2 was oriented within the density by positioning the larger MIF4G domain (see Cwc22 MIF4G above). Using this co-docking procedure the best fit for RecA2 within the density could be achieved (Extended Data Figure 7). Several crosslinks between RecA2 and Cwc22 MIF4G additionally validated its position.
Prp22 **DHX8** 139.3 kDa 1220 aa Chain q	RecA1 aa 558-743 RecA2 aa 744-914 CTD aa 915–1184	Prp22 is a multi-domain protein with a helicase core domain, which consists of two structurally conserved RecA-like domains (DEXDc, HELICc) and a distinct C-terminal domain (CTD)[76]. The crystal structure of the human CTD (aa 948-1184, PDB 3I4U, ref. 76) was used for rigid body docking into an appropriately shaped density element present in the UPD3 region of the less well resolved, unmasked EM map. The presence of an adjacent, high resolution density element harboring a long protruding α-helix of the Skip protein (see above), which directly connects UPD3 to the main body of the spliceosomal complex, in conjunction with numerous crosslinks (see table S2), supported the position and orientation of the Prp22 CTD. For positioning of the two RecA-like domains a Prp22 helicase model with homology modelled RecA domains was obtained from the SpliProt3D Database[63]. This allowed a confident placement of the RecA-like domains relative to the CTD within the remaining density of UPD3. The fully reconstructed Prp22 helicase domain therefore forms a typical barrel-like arrangement that fits well into our unmasked C* density at the described position.

Human Protein	Domain/region in C* model	Positioning
CypE **PPIE** 33.4 kDa 301 aa Chain o	N-terminal aa 1–81 C-terminal aa 141–301	Crosslinks indicate the proximity of CypE to Prp17 WD40, U2-A', U2-B" and SmD1 (see Supplementary Table 2). In fact, the less well resolved, unmasked EM map of the C* complex shows a distinct, but not well-resolved density element that additionally contacts the U2 snRNA approximately 8 nts downstream of the U2 Sm binding site. Using comparatively modelled structures of the N- and C-terminal domain obtained from the SpliProt3D database[63], we were able to fit both domains into the density element in a way that maximized agreement with crosslinks and fit to the EM map. Interestingly, the best fitting configuration of both domains results in a patch of distinctly positively-charged residues running along the proposed U2 snRNA contact side. However, due to the low resolution of the map used for fitting such a small, compactly shaped factor like CypE, it is difficult to determine its exact orientation within the C* complex.

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Supplementary Table 2 | BS3-crosslinks of abundant proteins in the human C* complex.

Statistics (Spectral Counts and $Score_{max}$) of the CX-MS data for the proteins of the purified human C^* complex. "Inter" and "Intra" indicate inter-protein and intra-protein crosslinks, respectively. Numbers in the Residue 1 and 2 columns indicate the position of the crosslinked lysine or N-terminal residue.

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
Inter	**Ad002**	Q9P013	**Aquarius**	O60306	**40**	1045	1	3.87
			Prl1	O43660	**18**	363	17	12.83
					74	237	6	3.27
					205	237	1	1.72
			Prp22	Q14562	**147**	315	2	4.99
			Prp8	Q6P2Q9	**40**	465	3	1.81
					91	1132	7	6.27
						1144	82	9.15
					92	1144	1	0.59
					205	1158	5	4.10
					226	1132	6	5.76
			Rbm22	Q9NW64	**18**	40	3	2.16
						76	52	18.01
					28	40	4	1.53
			Skip	Q13573	**18**	153	44	9.55
					28	153	1	2.05
					152	311	4	5.34
			SmB/B'	P14678	**222**	1	1	0.83
			Snu114	Q15029	**91**	951	7	3.50
					147	951	2	2.04
			U5-40K	Q96DI7	**226**	18	2	2.44
						270	2	1.71
	Aquarius	O60306	**Ad002**	Q9P013	**1045**	40	1	3.87
			Cdc5	Q99459	**124**	733	1	1.64
			CypE	Q9UNP9	**1234**	88	1	0.71
			Isy1	Q9ULR0	**367**	7	1	5.36
					493	7	1	7.13
					524	7	2	2.79
						127	7	6.26
						138	3	2.11
					604	92	5	7.68
						101	35	10.26
						105	15	9.44
						121	1	3.65
			Prl1	O43660	**63**	181	1	0.08
			Rbm22	Q9NW64	**493**	315	27	9.88
					576	313	1	0.36
						315	8	5.17
					604	229	3	2.92
						286	1	0.67
					1234	315	10	5.97
						416	18	4.68
					1256	315	2	4.96
						416	7	2.80
			Skip	Q13573	**493**	344	1	0.01
					576	48	1	1.20
			SmE	P62304	**56**	80	1	0.63
			SmF	P62306	**63**	2	1	0.30
			Syf1	Q9HCS7	**950**	62	1	3.16
					954	2	5	3.65
					1002	2	1	1.21
	Brr2	O75643	**CCDC12**	Q8WUD4	**1146**	123	20	1.90
			Cdc5	Q99459	**1034**	601	2	1.29
			Cwc22/KIAA1604	Q9HCG8	**55**	243	1	3.05
					1142	243	1	2.05
					1146	243	4	2.76
					1715	783	12	3.14
						788	1	2.87
			Isy1	Q9ULR0	**440**	266	1	0.93
					2091	259	1	0.94
			NY-CO-10	Q6UX04	**60**	432	1	0.81
					155	197	1	1.51
					695	324	6	2.81
					1134	35	1	2.39
						84	4	3.71
					1176	35	1	0.45

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						193	1	0.37
					1874	84	11	4.46
					1878	35	3	3.50
						84	1	0.81
			Ppil3	Q9H2H8	**1142**	69	2	3.10
			Prp17	O60508	**1878**	314	1	0.98
			Prp19	Q9UMS4	**1172**	192	1	0.87
			Prp8	Q6P2Q9	**14**	1344	1	4.61
					696	1993	1	3.37
					729	2049	4	2.80
					733	2031	4	2.90
						2034	3	2.35
						2049	2	0.25
					770	2034	2	2.23
						2049	7	8.95
					1039	2034	2	5.91
						2049	7	7.32
						2070	47	8.75
					1049	1831	1	2.50
						2034	3	4.86
						2049	12	19.08
						2070	32	14.33
					1134	1831	5	3.81
						2249	2	3.56
					1142	2049	3	1.67
					1145	2070	9	3.42
					1146	2034	8	11.82
						2049	19	7.82
						2070	2	5.24
			SmB/B'	P14678	**440**	50	1	0.47
			SmD2	P62316	**1146**	2	2	2.47
			SmD3	P62318	**1544**	67	1	0.21
			SRm300	Q9UQ35	**155**	131	1	1.13
					1134	169	13	1.66
			U2-A'	P09661	**733**	221	1	0.29
			U2-B"	P08579	**343**	17	1	3.84
					1421	47	1	0.55
	CBP20	P52298	**CBP80**	Q09161	**34**	17	1	0.89
						20	3	6.14
					38	654	2	1.72
						657	8	5.48
					67	607	65	4.70
						654	14	4.02
					68	607	211	14.32
					78	511	18	11.08
			Prp8	Q6P2Q9	**151**	366	3	3.19
			SmD3	P62318	**68**	67	5	2.28
			Snu114	Q15029	**151**	244	9	4.26
	CBP80	Q09161	**CBP20**	P52298	**17**	34	1	0.89
					20	34	3	6.14
					511	78	18	11.08
					607	67	65	4.70
						68	211	14.32
					654	38	2	1.72
						67	14	4.02
					657	38	8	5.48
			Cwc22/KIAA1604	Q9HCG8	**41**	243	9	2.32
					67	163	4	5.66
					330	243	1	1.34
						250	5	4.12
						330	9	5.66
					342	243	20	6.04
			SRm300	Q9UQ35	**511**	108	5	7.15
					698	131	1	1.85
					707	131	1	0.84
			Syf1	Q9HCS7	**327**	69	1	1.74
			Syf3	Q9BZJ0	**671**	776	3	1.83
	CCDC12	Q8WUD4	**Brr2**	O75643	**123**	1146	20	1.90
			Cdc5	Q99459	**23**	500	2	1.05
						601	1	1.24
						626	3	2.46
					28	500	3	1.88
						623	3	0.84
					32	522	18	6.47

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						708	1	0.07
					34	522	14	5.27
						708	1	0.29
					40	522	10	10.53
					42	522	20	3.32
					53	522	2	3.32
					85	187	1	1.66
					111	312	2	2.30
					126	500	11	2.80
					128	500	3	1.19
					144	500	27	13.51
			Isy1	Q9ULR0	**85**	24	7	3.14
			Prp19	Q9UMS4	**23**	179	4	1.60
						192	1	0.82
						244	5	1.53
						266	2	1.36
						380	6	5.58
					28	192	3	1.21
						244	2	1.45
						266	1	0.13
						380	2	2.05
					32	179	4	6.26
						192	3	3.35
						244	2	2.34
						266	4	2.85
					34	179	1	2.95
						192	3	3.66
					40	179	6	4.35
					42	179	8	1.74
						244	7	1.57
						266	1	1.08
					144	192	1	2.36
						244	1	2.85
			Prp8	Q6P2Q9	**123**	1636	1	0.62
						2049	4	1.66
			Snu114	Q15029	**78**	694	1	0.61
			Syf1	Q9HCS7	**23**	420	14	5.05
						532	3	1.45
					28	420	5	3.13
						532	3	1.05
					32	420	1	0.85
						532	6	2.88
					34	532	5	2.03
					40	532	2	1.35
					42	532	2	1.34
					70	393	1	1.00
					78	532	1	3.52
					87	590	1	4.09
					94	590	4	7.76
						708	2	3.94
			Syf2/GCIP p29	O95926	**23**	49	3	2.00
						85	1	1.44
					28	71	3	3.53
					70	80	27	8.27
						84	1	2.83
					78	80	1	2.10
						84	11	6.42
			Syf3	Q9BZJ0	**117**	607	9	2.67
					126	549	1	0.54
					144	587	18	10.47
						627	2	4.56
	Cdc5	Q99459	**Aquarius**	O60306	**733**	124	1	1.64
			Brr2	O75643	**601**	1034	2	1.29
			CCDC12	Q8WUD4	**187**	85	1	1.66
					312	111	2	2.30
					500	23	2	1.05
						28	3	1.88
						126	11	2.80
						128	3	1.19
						144	27	13.51
					522	32	18	6.47
						34	14	5.27
						40	10	10.53
						42	20	3.32

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						53	2	3.32
					601	23	1	1.24
					623	28	3	0.84
					626	23	3	2.46
					708	32	1	0.07
						34	1	0.29
			Cwc22/KIAA1604	Q9HCG8	**708**	119	3	2.06
			CypE	Q9UNP9	**264**	147	1	0.59
					294	218	3	7.05
					630	83	3	4.50
			Isy1	Q9ULR0	**106**	180	2	2.58
					187	7	3	4.08
						24	3	3.22
						55	21	9.55
			Prl1	O43660	**522**	135	1	0.71
					576	19	9	3.61
					598	66	1	0.99
					601	62	3	2.82
						66	7	0.90
						68	27	21.98
					685	113	1	0.52
					708	68	8	4.26
						135	1	1.04
					712	66	1	2.45
						68	4	2.16
						113	6	1.79
					718	135	1	4.05
			Prp17	O60508	**187**	333	5	3.38
					200	228	2	3.45
						333	44	12.32
						374	6	8.88
						398	4	2.77
			Prp19	Q9UMS4	**487**	192	1	1.97
					500	244	1	0.40
					522	179	1	2.74
						192	5	3.74
						244	7	2.97
						425	2	2.31
					570	122	8	6.95
					601	179	4	4.17
						425	3	0.75
					623	122	2	2.38
					631	122	10	7.66
						244	4	4.79
					685	179	12	5.87
						192	6	1.91
						244	2	1.43
						266	16	2.99
						425	1	1.85
					686	179	1	1.44
					694	192	1	2.48
					708	179	2	0.97
						192	5	6.57
						244	2	0.88
					771	244	4	5.79
					782	179	1	2.21
						192	2	3.42
						244	18	4.66
						266	1	2.55
					795	192	4	8.01
						244	9	6.06
			Prp22	Q14562	**124**	1194	1	1.25
					135	1194	3	1.18
			Prp8	Q6P2Q9	**290**	727	1	1.91
					576	2034	1	0.67
			Rbm22	Q9NW64	**718**	40	1	1.99
			Skip	Q13573	**28**	266	2	8.65
					135	441	1	1.60
			SmD2	P62316	**201**	6	1	0.95
					623	98	1	0.47
			Spf27	O75934	**623**	177	2	0.32
					685	97	34	2.58
					771	177	159	15.36
					782	191	27	5.59

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					795	218	2	0.99
					799	218	1	1.32
			SRm300	Q9UQ35	**187**	845	1	2.16
			Syf1	Q9HCS7	**106**	721	30	13.84
						794	6	5.56
					264	708	1	1.80
					271	708	1	6.77
					290	654	31	9.67
						708	3	4.75
					294	654	70	17.61
						708	6	15.61
					312	654	3	3.47
					522	504	2	3.55
						532	72	5.89
			Syf2/GCIP p29	O95926	**59**	234	1	3.44
					70	234	3	5.32
					166	60	3	0.57
					290	63	3	8.27
						228	5	9.17
					294	63	8	4.81
						228	5	2.90
						234	3	5.53
			Syf3	Q9BZJ0	**7**	175	1	1.81
						182	25	7.23
					174	213	5	6.79
						229	3	5.40
					200	229	32	12.04
					201	229	1	4.42
					255	213	18	1.91
					264	213	3	2.83
					312	527	4	1.49
						531	2	0.59
						569	5	7.02
						607	3	0.77
					432	569	16	5.94
					466	568	9	3.72
					500	587	22	7.21
					601	607	1	0.52
			U5-40K	Q96DI7	**757**	18	6	8.42
					771	1	2	7.92
						8	2	2.02
						18	27	7.33
					782	8	2	3.57
						18	13	7.02
						275	9	6.86
						322	17	4.57
					795	270	56	6.97
					799	270	1	1.18
	Cwc22/KIAA1604	Q9HCG8	**Brr2**	O75643	**243**	55	1	3.05
						1142	1	2.05
						1146	4	2.76
					783	1715	12	3.14
					788	1715	1	2.87
			CBP80	Q09161	**163**	67	4	5.66
					243	41	9	2.32
						330	1	1.34
						342	20	6.04
					250	330	5	4.12
					330	330	9	5.66
			Cdc5	Q99459	**119**	708	3	2.06
			eIF4AIII	P38919	**116**	374	13	12.28
					118	252	1	10.18
						374	3	6.87
					243	19	10	4.28
						374	12	3.53
					250	60	16	6.01
					330	60	5	3.05
						70	3	1.90
					344	152	1	3.02
			NY-CO-10	Q6UX04	**243**	429	1	0.92
						455	1	2.74
					250	434	1	0.04
					330	434	6	6.69
			Prp17	O60508	**724**	380	1	1.36

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
			Prp22	Q14562	**149**	102	1	1.59
			Prp8	Q6P2Q9	**2**	1925	3	1.51
					243	366	1	0.47
					330	366	35	12.38
					584	1222	4	5.87
			SmE	P62304	**745**	80	5	0.85
			Snu114	Q15029	**330**	359	2	5.93
					344	359	1	1.93
			SRm300	Q9UQ35	**402**	217	2	0.17
	CypE	Q9UNP9	**Aquarius**	O60306	**88**	1234	1	0.71
			Cdc5	Q99459	**83**	630	3	4.50
					147	264	1	0.59
					218	294	3	7.05
			Isy1	Q9ULR0	**45**	101	1	2.08
					83	138	7	2.03
					88	138	2	1.16
					104	138	1	1.24
			Prp17	O60508	**88**	244	5	2.53
						314	9	4.25
					104	238	1	1.88
						244	5	2.36
						314	4	3.95
			Prp19	Q9UMS4	**104**	244	1	0.74
			Syf1	Q9HCS7	**147**	708	5	5.29
					218	2	3	3.33
						794	2	3.23
					284	794	6	4.36
			Syf2/GCIP p29	O95926	**147**	49	30	9.50
						63	1	3.79
					151	63	1	1.64
					218	49	1	5.15
					284	49	3	5.65
			Syf3	Q9BZJ0	**123**	175	2	0.67
					147	175	1	0.91
			U2-A'	P09661	**104**	30	8	1.97
					147	129	2	2.04
					218	30	1	0.76
						56	11	10.57
						129	4	4.12
					284	129	1	0.91
			U2-B"	P08579	**104**	57	7	2.64
						93	1	3.95
						111	4	4.13
					123	111	3	5.89
	eIF4AIII	P38919	**Cwc22/KIAA1604**	Q9HCG8	**19**	243	10	4.28
					60	250	16	6.01
						330	5	3.05
					70	330	3	1.90
					152	344	1	3.02
					252	118	1	10.18
					374	116	13	12.28
						118	3	6.87
						243	12	3.53
			NY-CO-10	Q6UX04	**60**	434	4	7.59
					70	434	7	2.62
						455	2	2.74
						463	1	3.12
					74	455	7	6.38
					374	434	18	8.23
			Prp8	Q6P2Q9	**252**	1951	1	0.18
			Snu114	Q15029	**152**	244	1	0.74
						359	2	4.72
			SRm300	Q9UQ35	**19**	108	9	6.38
					74	131	1	1.02
	G10	P41223	**Prp8**	Q6P2Q9	**125**	36	13	6.97
						43	1	1.22
			SmD1	P62314	**3**	41	1	0.24
	Isy1	Q9ULR0	**Aquarius**	O60306	**7**	367	1	5.36
						493	1	7.13
						524	2	2.79
					92	604	5	7.68
					101	604	35	10.26
					105	604	15	9.44
					121	604	1	3.65

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					127	524	7	6.26
					138	524	3	2.11
			Brr2	O75643	**259**	2091	1	0.94
					266	440	1	0.93
			CCDC12	Q8WUD4	**24**	85	7	3.14
			Cdc5	Q99459	**7**	187	3	4.08
					24	187	3	3.22
					55	187	21	9.55
					180	106	2	2.58
			CypE	Q9UNP9	**101**	45	1	2.08
					138	83	7	2.03
						88	2	1.16
						104	1	1.24
			Prp17	O60508	**7**	333	13	6.80
						551	13	11.02
					41	289	1	1.92
						314	5	6.26
						333	21	7.60
						374	2	3.79
						551	5	7.99
					92	228	10	8.48
						333	10	8.19
					101	333	2	3.26
					127	314	1	0.23
			Prp8	Q6P2Q9	**7**	1570	2	7.94
						1838	5	3.01
			Rbm22	Q9NW64	**2**	286	1	0.68
					7	185	1	2.56
			Skip	Q13573	**7**	48	15	7.34
			SmD1	P62314	**138**	86	4	5.96
			Snu114	Q15029	**105**	581	1	0.69
			Syf1	Q9HCS7	**7**	420	16	8.12
						423	4	3.33
					24	420	9	4.48
					26	420	2	1.34
					41	420	4	4.03
					44	420	2	1.89
					138	212	2	0.48
					188	83	3	3.71
					190	2	5	3.90
					238	62	4	6.19
			Syf2/GCIP p29	O95926	**7**	49	13	10.77
						63	1	1.92
						85	2	2.57
					24	49	3	2.01
					41	63	4	5.84
					55	63	20	8.67
					56	63	2	9.77
					92	49	7	10.68
					260	49	1	1.90
			Syf3	Q9BZJ0	**112**	213	3	4.51
					127	213	47	9.56
					138	213	11	7.63
			U2-A'	P09661	**259**	205	3	4.17
					260	56	1	5.02
						205	50	9.96
						221	2	6.75
					266	2	19	17.91
						3	11	16.59
						56	178	12.85
						129	4	0.75
						179	28	14.69
						191	30	11.14
						192	3	5.47
						193	94	18.08
						221	95	16.88
	NY-CO-10	Q6UX04	**Brr2**	O75643	**35**	1134	1	2.39
						1176	1	0.45
						1878	3	3.50
					84	1134	4	3.71
						1874	11	4.46
						1878	1	0.81
					193	1176	1	0.37
					197	155	1	1.51

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					324	695	6	2.81
					432	60	1	0.81
			Cwc22/KIAA1604	Q9HCG8	**429**	243	1	0.92
					434	250	1	0.04
						330	6	6.69
					455	243	1	2.74
			eIF4AIII	P38919	**434**	60	4	7.59
						70	7	2.62
						374	18	8.23
					455	70	2	2.74
						74	7	6.38
					463	70	1	3.12
			Prp19	Q9UMS4	**193**	192	2	4.16
						244	2	1.68
			Prp8	Q6P2Q9	**318**	1838	3	1.03
						1866	1	0.96
			SmB/B'	P14678	**162**	50	4	1.45
					184	50	1	5.65
					186	50	2	4.63
					193	57	25	10.19
						64	3	3.09
			SmD2	P62316	**193**	79	3	4.69
					331	8	4	0.99
					340	8	1	0.49
			Syf2/GCIP p29	O95926	**372**	192	1	2.84
			Syf3	Q9BZJ0	**331**	569	1	3.21
			U5-40K	Q96DI7	**193**	8	2	3.78
						18	1	0.48
	Ppil1	Q9Y3C6	**Prl1**	O43660	**80**	68	1	0.50
						135	4	7.77
					161	113	1	0.35
						135	3	1.86
			Prp17	O60508	**161**	63	5	1.57
			Prp19	Q9UMS4	**80**	122	9	4.84
						179	1	3.37
						192	1	5.84
			Skip	Q13573	**80**	193	1	1.36
					158	97	53	10.02
			Spf27	O75934	**80**	168	85	11.31
					161	151	20	6.13
						158	20	6.16
			Syf2/GCIP p29	O95926	**52**	99	1	0.09
			U5-40K	Q96DI7	**80**	1	17	3.68
						8	30	13.61
						18	26	6.01
					158	18	6	2.67
					161	1	1	3.77
						8	1	2.27
						18	4	2.13
	Ppil3	Q9H2H8	**Brr2**	O75643	**69**	1142	2	3.10
			Prp8	Q6P2Q9	**80**	2244	6	3.18
						2249	1	1.68
					120	2244	7	4.43
						2249	2	8.16
	Prl1	O43660	**Ad002**	Q9P013	**237**	74	6	3.27
						205	1	1.72
					363	18	17	12.83
			Aquarius	O60306	**181**	63	1	0.08
			Cdc5	Q99459	**19**	576	9	3.61
					62	601	3	2.82
					66	598	1	0.99
						601	7	0.90
						712	1	2.45
					68	601	27	21.98
						708	8	4.26
						712	4	2.16
					113	685	1	0.52
						712	6	1.79
					135	522	1	0.71
						708	1	1.04
						718	1	4.05
			Ppil1	Q9Y3C6	**68**	80	1	0.50
					113	161	1	0.35
					135	80	4	7.77

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						161	3	1.86
			Prp19	Q9UMS4	**1**	122	12	6.31
						179	1	4.20
						244	3	4.92
					2	122	7	6.55
					135	122	1	7.43
					180	32	5	2.91
					320	122	1	2.85
						244	1	1.40
			Prp8	Q6P2Q9	**180**	2113	1	0.26
			Skip	Q13573	**113**	48	4	6.27
					135	48	8	11.07
					180	95	1	0.96
					363	108	4	2.16
						153	4	3.15
			SmF	P62306	**510**	1	2	1.23
			Spf27	O75934	**135**	168	9	7.55
					320	168	2	3.95
			Syf1	Q9HCS7	**113**	420	6	5.51
						423	1	4.32
						458	6	5.46
					135	420	7	4.27
			Syf3	Q9BZJ0	**68**	397	2	3.80
					173	397	6	6.11
					510	377	1	1.16
	Prp17	O60508	**Brr2**	O75643	**314**	1878	1	0.98
			Cdc5	Q99459	**228**	200	2	3.45
					333	187	5	3.38
						200	44	12.32
					374	200	6	8.88
					398	200	4	2.77
			Cwc22/KIAA1604	Q9HCG8	**380**	724	1	1.36
			CypE	Q9UNP9	**238**	104	1	1.88
					244	88	5	2.53
						104	5	2.36
					314	88	9	4.25
						104	4	3.95
			Isy1	Q9ULR0	**228**	92	10	8.48
					289	41	1	1.92
					314	41	5	6.26
						127	1	0.23
					333	7	13	6.80
						41	21	7.60
						92	10	8.19
						101	2	3.26
					374	41	2	3.79
					551	7	13	11.02
						41	5	7.99
			Ppil1	Q9Y3C6	**63**	161	5	1.57
			Prp19	Q9UMS4	**42**	380	1	0.33
			Prp8	Q6P2Q9	**151**	36	4	4.59
					161	36	7	5.30
			Rbm22	Q9NW64	**333**	170	1	0.54
			SmD3	P62318	**244**	84	2	1.31
			SmE	P62304	**538**	12	5	5.03
			Syf3	Q9BZJ0	**547**	213	13	2.63
					551	213	3	6.74
			U2-B"	P08579	**233**	111	1	1.01
					244	111	3	13.23
					314	111	1	6.84
	Prp19	Q9UMS4	**Brr2**	O75643	**192**	1172	1	0.87
			CCDC12	Q8WUD4	**179**	23	4	1.60
						32	4	6.26
						34	1	2.95
						40	6	4.35
						42	8	1.74
					192	23	1	0.82
						28	3	1.21
						32	3	3.35
						34	3	3.66
						144	1	2.36
					244	23	5	1.53
						28	2	1.45
						32	2	2.34

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						42	7	1.57
						144	1	2.85
					266	23	2	1.36
						28	1	0.13
						32	4	2.85
						42	1	1.08
					380	23	6	5.58
						28	2	2.05
			Cdc5	Q99459	**122**	570	8	6.95
						623	2	2.38
						631	10	7.66
					179	522	1	2.74
						601	4	4.17
						685	12	5.87
						686	1	1.44
						708	2	0.97
						782	1	2.21
					192	487	1	1.97
						522	5	3.74
						685	6	1.91
						694	1	2.48
						708	5	6.57
						782	2	3.42
						795	4	8.01
					244	500	1	0.40
						522	7	2.97
						631	4	4.79
						685	2	1.43
						708	2	0.88
						771	4	5.79
						782	18	4.66
						795	9	6.06
					266	685	16	2.99
						782	1	2.55
					425	522	2	2.31
						601	3	0.75
						685	1	1.85
			CypE	Q9UNP9	**244**	104	1	0.74
			NY-CO-10	Q6UX04	**192**	193	2	4.16
					244	193	2	1.68
			Ppil1	Q9Y3C6	**122**	80	9	4.84
					179	80	1	3.37
					192	80	1	5.84
			Prl1	O43660	**32**	180	5	2.91
					122	1	12	6.31
						2	7	6.55
						135	1	7.43
						320	1	2.85
					179	1	1	4.20
					244	1	3	4.92
						320	1	1.40
			Prp17	O60508	**380**	42	1	0.33
			Prp22	Q14562	**428**	403	3	1.45
			Prp8	Q6P2Q9	**179**	36	1	2.03
					200	68	2	1.52
			Skip	Q13573	**179**	48	5	5.65
					192	193	1	0.33
					244	48	3	2.39
			SmB/B'	P14678	**179**	57	12	4.53
					192	50	2	2.56
						57	11	2.41
					244	50	1	1.36
						57	12	4.16
					266	57	13	6.07
			SmD1	P62314	**244**	44	3	1.50
			SmD2	P62316	**192**	51	6	1.32
						118	2	7.18
					244	88	1	1.75
					266	8	1	0.45
			Spf27	O75934	**122**	168	1	4.22
					179	158	3	6.93
						168	8	7.29
						218	3	2.14
					192	168	16	9.13

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						218	8	3.42
					244	168	11	7.71
						177	3	4.45
						218	17	5.87
					266	168	11	9.18
						218	9	3.46
					425	97	2	0.72
			SRm300	Q9UQ35	**265**	101	1	0.16
			Syf1	Q9HCS7	**266**	458	7	7.65
			Syf3	Q9BZJ0	**192**	607	1	1.54
			U5-40K	Q96DI7	**32**	18	1	0.93
					122	1	11	9.53
						8	25	9.00
						18	19	9.37
						270	1	1.13
						275	14	6.55
					179	8	2	5.96
						18	5	5.44
						270	1	0.38
					192	18	3	2.14
						270	11	2.34
						275	26	19.57
					244	1	7	4.52
						8	1	2.93
						18	1	1.23
						270	4	1.13
						275	11	7.19
					261	275	2	3.66
					266	275	1	5.03
					425	275	8	1.46
	Prp22	Q14562	**Ad002**	Q9P013	**315**	147	2	4.99
			Cdc5	Q99459	**1194**	124	1	1.25
						135	3	1.18
			Cwc22/KIAA1604	Q9HCG8	**102**	149	1	1.59
			Prp19	Q9UMS4	**403**	428	3	1.45
			Prp8	Q6P2Q9	**399**	833	3	1.69
					1118	837	2	3.44
					1194	837	2	1.59
			Skip	Q13573	**161**	339	5	2.90
					252	379	2	1.00
					315	311	1	1.71
						339	2	3.18
					330	311	1	2.19
						344	2	2.47
					1053	339	4	3.54
						344	10	9.93
					1080	339	68	14.41
						344	10	8.46
					1090	339	17	9.95
					1098	323	7	1.40
					1105	317	12	8.52
						319	8	4.28
						323	13	5.15
						339	2	7.26
						379	1	1.70
	Prp8	Q6P2Q9	**Ad002**	Q9P013	**465**	40	3	1.81
					1132	91	7	6.27
						226	6	5.76
					1144	91	82	9.15
						92	1	0.59
					1158	205	5	4.10
			Brr2	O75643	**1344**	14	1	4.61
					1831	1049	1	2.50
						1134	5	3.81
					1993	696	1	3.37
					2031	733	4	2.90
					2034	733	3	2.35
						770	2	2.23
						1039	2	5.91
						1049	3	4.86
						1146	8	11.82
					2049	729	4	2.80
						733	2	0.25
						770	7	8.95

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						1039	7	7.32
						1049	12	19.08
						1142	3	1.67
						1146	19	7.82
					2070	1039	47	8.75
						1049	32	14.33
						1145	9	3.42
						1146	2	5.24
					2249	1134	2	3.56
			CBP20	P52298	**366**	151	3	3.19
			CCDC12	Q8WUD4	**1636**	123	1	0.62
					2049	123	4	1.66
			Cdc5	Q99459	**727**	290	1	1.91
					2034	576	1	0.67
			Cwc22/KIAA1604	Q9HCG8	**366**	243	1	0.47
						330	35	12.38
					1222	584	4	5.87
					1925	2	3	1.51
			eIF4AIII	P38919	**1951**	252	1	0.18
			G10	P41223	**36**	125	13	6.97
					43	125	1	1.22
			Isy1	Q9ULR0	**1570**	7	2	7.94
					1838	7	5	3.01
			NY-CO-10	Q6UX04	**1838**	318	3	1.03
					1866	318	1	0.96
			Ppil3	Q9H2H8	**2244**	80	6	3.18
						120	7	4.43
					2249	80	1	1.68
						120	2	8.16
			Prl1	O43660	**2113**	180	1	0.26
			Prp17	O60508	**36**	151	4	4.59
						161	7	5.30
			Prp19	Q9UMS4	**36**	179	1	2.03
					68	200	2	1.52
			Prp22	Q14562	**833**	399	3	1.69
					837	1118	2	3.44
						1194	2	1.59
			Rbm22	Q9NW64	**68**	301	3	1.57
			Skip	Q13573	**36**	193	5	11.29
					43	193	23	11.36
					48	193	1	1.69
					702	236	13	4.09
						246	1	0.79
					1258	468	1	1.30
					1505	441	2	5.35
					1838	503	1	1.79
			SmD2	P62316	**1955**	118	2	2.94
					1993	71	4	2.04
			SmG	P62308	**442**	16	3	0.99
			Snu114	Q15029	**218**	405	49	12.93
						409	18	5.00
					366	358	2	1.38
						359	48	11.42
			Spf27	O75934	**1514**	155	1	0.87
			Syf2/GCIP p29	O95926	**727**	228	4	4.21
						234	1	4.60
			U2-B"	P08579	**1838**	211	2	0.82
			U5-40K	Q96DI7	**29**	286	10	6.05
					36	286	4	2.99
					43	286	13	5.52
					48	349	6	1.26
					50	349	2	1.50
	Rbm22	Q9NW64	**Ad002**	Q9P013	**40**	18	3	2.16
						28	4	1.53
					76	18	52	18.01
			Aquarius	O60306	**229**	604	3	2.92
					286	604	1	0.67
					313	576	1	0.36
					315	493	27	9.88
						576	8	5.17
						1234	10	5.97
						1256	2	4.96
					416	1234	18	4.68
						1256	7	2.80

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
			Cdc5	Q99459	**40**	718	1	1.99
			Isy1	Q9ULR0	**185**	7	1	2.56
					286	2	1	0.68
			Prp17	O60508	**170**	333	1	0.54
			Prp8	Q6P2Q9	**301**	68	3	1.57
			Skip	Q13573	**38**	153	1	1.74
					40	153	8	2.03
					76	108	10	3.79
						193	8	5.58
					104	452	1	0.22
					139	81	1	2.26
						193	9	5.96
					286	81	42	15.12
						193	9	4.18
					315	48	8	6.96
					416	193	8	13.25
			U5-40K	Q96DI7	**76**	1	1	1.81
						18	4	3.23
					286	18	4	4.19
	Skip	Q13573	**Ad002**	Q9P013	**153**	18	44	9.55
						28	1	2.05
					311	152	4	5.34
			Aquarius	O60306	**48**	576	1	1.20
					344	493	1	0.01
			Cdc5	Q99459	**266**	28	2	8.65
					441	135	1	1.60
			Isy1	Q9ULR0	**48**	7	15	7.34
			Ppil1	Q9Y3C6	**97**	158	53	10.02
					193	80	1	1.36
			Prl1	O43660	**48**	113	4	6.27
						135	8	11.07
					95	180	1	0.96
					108	363	4	2.16
					153	363	4	3.15
			Prp19	Q9UMS4	**48**	179	5	5.65
						244	3	2.39
					193	192	1	0.33
			Prp22	Q14562	**311**	315	1	1.71
						330	1	2.19
					317	1105	12	8.52
					319	1105	8	4.28
					323	1098	7	1.40
						1105	13	5.15
					339	161	5	2.90
						315	2	3.18
						1053	4	3.54
						1080	68	14.41
						1090	17	9.95
						1105	2	7.26
					344	330	2	2.47
						1053	10	9.93
						1080	10	8.46
					379	252	2	1.00
						1105	1	1.70
			Prp8	Q6P2Q9	**193**	36	5	11.29
						43	23	11.36
						48	1	1.69
					236	702	13	4.09
					246	702	1	0.79
					441	1505	2	5.35
					468	1258	1	1.30
					503	1838	1	1.79
			Rbm22	Q9NW64	**48**	315	8	6.96
					81	139	1	2.26
						286	42	15.12
					108	76	10	3.79
					153	38	1	1.74
						40	8	2.03
					193	76	8	5.58
						139	9	5.96
						286	9	4.18
						416	8	13.25
					452	104	1	0.22
			Snu114	Q15029	**344**	355	2	1.44

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
			Spf27	O75934	**48**	168	6	7.44
			Syf2/GCIP p29	O95926	**236**	228	1	0.52
					240	228	52	8.92
						234	1	3.74
			Syf3	Q9BZJ0	**236**	377	14	3.28
						381	10	6.64
			U5-40K	Q96DI7	**141**	18	3	1.43
					153	1	9	4.65
						8	1	1.73
						18	3	4.15
						349	1	2.24
					170	349	12	6.13
					193	1	11	8.18
						8	5	7.00
						18	18	7.07
	SmB/B'	P14678	**Ad002**	Q9P013	**1**	222	1	0.83
			Brr2	O75643	**50**	440	1	0.47
			NY-CO-10	Q6UX04	**50**	162	4	1.45
						184	1	5.65
						186	2	4.63
					57	193	25	10.19
					64	193	3	3.09
			Prp19	Q9UMS4	**50**	192	2	2.56
						244	1	1.36
					57	179	12	4.53
						192	11	2.41
						244	12	4.16
						266	13	6.07
			SmD1	P62314	**1**	2	1	1.87
					2	86	2	1.90
					5	1	3	3.93
						2	2	3.74
						41	52	8.42
						86	4	1.83
					8	41	49	10.20
					54	44	2	2.86
			SmD2	P62316	**50**	79	2	4.55
			SmD3	P62318	**5**	87	2	3.83
					32	84	9	2.67
					88	84	15	2.52
						87	6	0.73
			Syf2/GCIP p29	O95926	**5**	49	1	0.77
			U2-A'	P09661	**57**	172	8	6.41
			U2-B"	P08579	**88**	57	5	6.96
			U5-40K	Q96DI7	**8**	1	1	2.61
					50	8	2	2.90
						18	2	3.18
					88	1	1	6.56
						8	6	8.71
						18	3	3.46
	SmD1	P62314	**G10**	P41223	**41**	3	1	0.24
			Isy1	Q9ULR0	**86**	138	4	5.96
			Prp19	Q9UMS4	**44**	244	3	1.50
			SmB/B'	P14678	**1**	5	3	3.93
					2	1	1	1.87
						5	2	3.74
					41	5	52	8.42
						8	49	10.20
					44	54	2	2.86
					86	2	2	1.90
						5	4	1.83
			SmD2	P62316	**1**	37	4	1.53
						57	8	7.74
					2	57	1	5.03
					48	50	1	0.80
					86	18	10	2.16
			Syf1	Q9HCS7	**41**	50	1	0.56
						76	78	3.69
						83	20	2.67
					86	212	5	1.84
			U5-40K	Q96DI7	**44**	8	1	1.06
						18	1	2.46
	SmD2	P62316	**Brr2**	O75643	**2**	1146	2	2.47
			Cdc5	Q99459	**6**	201	1	0.95

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					98	623	1	0.47
			NY-CO-10	Q6UX04	**8**	331	4	0.99
						340	1	0.49
					79	193	3	4.69
			Prp19	Q9UMS4	**8**	266	1	0.45
					51	192	6	1.32
					88	244	1	1.75
					118	192	2	7.18
			Prp8	Q6P2Q9	**71**	1993	4	2.04
					118	1955	2	2.94
			SmB/B'	P14678	**79**	50	2	4.55
			SmD1	P62314	**18**	86	10	2.16
					37	1	4	1.53
					50	48	1	0.80
					57	1	8	7.74
						2	1	5.03
			SRm300	Q9UQ35	**18**	920	1	1.80
			U2-B"	P08579	**1**	47	1	0.46
	SmD3	P62318	**Brr2**	O75643	**67**	1544	1	0.21
			CBP20	P52298	**67**	68	5	2.28
			Prp17	O60508	**84**	244	2	1.31
			SmB/B'	P14678	**84**	32	9	2.67
						88	15	2.52
					87	5	2	3.83
						88	6	0.73
			Syf2/GCIP p29	O95926	**2**	60	1	0.01
			U2-B"	P08579	**8**	1	1	0.20
					31	101	13	3.94
						111	17	13.08
					78	101	1	1.02
					84	101	17	6.49
	SmE	P62304	**Aquarius**	O60306	**80**	56	1	0.63
			Cwc22/KIAA1604	Q9HCG8	**80**	745	5	0.85
			Prp17	O60508	**12**	538	5	5.03
			SmG	P62308	**12**	10	20	6.01
						11	17	6.28
						15	8	5.13
						16	21	5.00
	SmF	P62306	**Aquarius**	O60306	**2**	63	1	0.30
			Prl1	O43660	**1**	510	2	1.23
	SmG	P62308	**Prp8**	Q6P2Q9	**16**	442	3	0.99
			SmE	P62304	**10**	12	20	6.01
					11	12	17	6.28
					15	12	8	5.13
					16	12	21	5.00
			Snu114	Q15029	**10**	341	3	2.39
			U2-B"	P08579	**10**	111	1	1.06
	Snu114	Q15029	**Ad002**	Q9P013	**951**	91	7	3.50
						147	2	2.04
			CBP20	P52298	**244**	151	9	4.26
			CCDC12	Q8WUD4	**694**	78	1	0.61
			Cwc22/KIAA1604	Q9HCG8	**359**	330	2	5.93
						344	1	1.93
			eIF4AIII	P38919	**244**	152	1	0.74
					359	152	2	4.72
			Isy1	Q9ULR0	**581**	105	1	0.69
			Prp8	Q6P2Q9	**358**	366	2	1.38
					359	366	48	11.42
					405	218	49	12.93
					409	218	18	5.00
			Skip	Q13573	**355**	344	2	1.44
			SmG	P62308	**341**	10	3	2.39
			Syf3	Q9BZJ0	**609**	175	1	1.18
	Spf27	O75934	**Cdc5**	Q99459	**97**	685	34	2.58
					177	623	2	0.32
						771	159	15.36
					191	782	27	5.59
					218	795	2	0.99
						799	1	1.32
			Ppil1	Q9Y3C6	**151**	161	20	6.13
					158	161	20	6.16
					168	80	85	11.31
			Prl1	O43660	**168**	135	9	7.55
						320	2	3.95

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
			Prp19	Q9UMS4	**97**	425	2	0.72
					158	179	3	6.93
					168	122	1	4.22
						179	8	7.29
						192	16	9.13
						244	11	7.71
						266	11	9.18
					177	244	3	4.45
					218	179	3	2.14
						192	8	3.42
						244	17	5.87
						266	9	3.46
			Prp8	Q6P2Q9	**155**	1514	1	0.87
			Skip	Q13573	**168**	48	6	7.44
			U2-A'	P09661	**85**	191	1	1.24
			U5-40K	Q96DI7	**158**	18	2	5.63
					168	1	1	2.44
						8	1	4.83
						18	27	9.16
						275	13	10.42
					177	1	1	1.74
						18	19	5.39
						275	27	5.92
					191	275	41	15.05
	SRm300	Q9UQ35	**Brr2**	O75643	**131**	155	1	1.13
					169	1134	13	1.66
			CBP80	Q09161	**108**	511	5	7.15
					131	698	1	1.85
						707	1	0.84
			Cdc5	Q99459	**845**	187	1	2.16
			Cwc22/KIAA1604	Q9HCG8	**217**	402	2	0.17
			eIF4AIII	P38919	**108**	19	9	6.38
					131	74	1	1.02
			Prp19	Q9UMS4	**101**	265	1	0.16
			SmD2	P62316	**920**	18	1	1.80
	Syf1	Q9HCS7	**Aquarius**	O60306	**2**	954	5	3.65
						1002	1	1.21
					62	950	1	3.16
			CBP80	Q09161	**69**	327	1	1.74
			CCDC12	Q8WUD4	**393**	70	1	1.00
					420	23	14	5.05
						28	5	3.13
						32	1	0.85
					532	23	3	1.45
						28	3	1.05
						32	6	2.88
						34	5	2.03
						40	2	1.35
						42	2	1.34
						78	1	3.52
					590	87	1	4.09
						94	4	7.76
					708	94	2	3.94
			Cdc5	Q99459	**504**	522	2	3.55
					532	522	72	5.89
					654	290	31	9.67
						294	70	17.61
						312	3	3.47
					708	264	1	1.80
						271	1	6.77
						290	3	4.75
						294	6	15.61
					721	106	30	13.84
					794	106	6	5.56
			CypE	Q9UNP9	**2**	218	3	3.33
					708	147	5	5.29
					794	218	2	3.23
						284	6	4.36
			Isy1	Q9ULR0	**2**	190	5	3.90
					62	238	4	6.19
					83	188	3	3.71
					212	138	2	0.48
					420	7	16	8.12
						24	9	4.48

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						26	2	1.34
						41	4	4.03
						44	2	1.89
					423	7	4	3.33
			Prl1	O43660	**420**	113	6	5.51
						135	7	4.27
					423	113	1	4.32
					458	113	6	5.46
			Prp19	Q9UMS4	**458**	266	7	7.65
			SmD1	P62314	**50**	41	1	0.56
					76	41	78	3.69
					83	41	20	2.67
					212	86	5	1.84
			Syf2/GCIP p29	O95926	**393**	80	20	8.29
					590	97	1	2.09
						99	7	13.01
						118	2	4.94
					794	49	15	8.60
			Syf3	Q9BZJ0	**482**	388	11	2.71
						427	18	4.90
						475	2	3.82
					572	475	1	1.90
					794	771	4	7.17
						776	2	4.76
						781	2	2.89
						787	3	4.06
			U2-A'	P09661	**2**	205	3	5.21
					36	2	1	2.59
						3	1	1.30
	Syf2/GCIP p29	O95926	**CCDC12**	Q8WUD4	**49**	23	3	2.00
					71	28	3	3.53
					80	70	27	8.27
						78	1	2.10
					84	70	1	2.83
						78	11	6.42
					85	23	1	1.44
			Cdc5	Q99459	**60**	166	3	0.57
					63	290	3	8.27
						294	8	4.81
					228	290	5	9.17
						294	5	2.90
					234	59	1	3.44
						70	3	5.32
						294	3	5.53
			CypE	Q9UNP9	**49**	147	30	9.50
						218	1	5.15
						284	3	5.65
					63	147	1	3.79
						151	1	1.64
			Isy1	Q9ULR0	**49**	7	13	10.77
						24	3	2.01
						92	7	10.68
						260	1	1.90
					63	7	1	1.92
						41	4	5.84
						55	20	8.67
						56	2	9.77
					85	7	2	2.57
			NY-CO-10	Q6UX04	**192**	372	1	2.84
			Ppil1	Q9Y3C6	**99**	52	1	0.09
			Prp8	Q6P2Q9	**228**	727	4	4.21
					234	727	1	4.60
			Skip	Q13573	**228**	236	1	0.52
						240	52	8.92
					234	240	1	3.74
			SmB/B'	P14678	**49**	5	1	0.77
			SmD3	P62318	**60**	2	1	0.01
			Syf1	Q9HCS7	**49**	794	15	8.60
					80	393	20	8.29
					97	590	1	2.09
					99	590	7	13.01
					118	590	2	4.94
			Syf3	Q9BZJ0	**118**	388	3	4.26
					140	381	72	6.17

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						388	87	17.42
					143	388	2	4.06
					217	199	1	1.23
			U5-40K	Q96DI7	**155**	18	1	1.39
	Syf3	Q9BZJ0	**CBP80**	Q09161	**776**	671	3	1.83
			CCDC12	Q8WUD4	**549**	126	1	0.54
					587	144	18	10.47
					607	117	9	2.67
					627	144	2	4.56
			Cdc5	Q99459	**175**	7	1	1.81
					182	7	25	7.23
					213	174	5	6.79
						255	18	1.91
						264	3	2.83
					229	174	3	5.40
						200	32	12.04
						201	1	4.42
					527	312	4	1.49
					531	312	2	0.59
					568	466	9	3.72
					569	312	5	7.02
						432	16	5.94
					587	500	22	7.21
					607	312	3	0.77
						601	1	0.52
			CypE	Q9UNP9	**175**	123	2	0.67
						147	1	0.91
			Isy1	Q9ULR0	**213**	112	3	4.51
						127	47	9.56
						138	11	7.63
			NY-CO-10	Q6UX04	**569**	331	1	3.21
			Prl1	O43660	**377**	510	1	1.16
					397	68	2	3.80
						173	6	6.11
			Prp17	O60508	**213**	547	13	2.63
						551	3	6.74
			Prp19	Q9UMS4	**607**	192	1	1.54
			Skip	Q13573	**377**	236	14	3.28
					381	236	10	6.64
			Snu114	Q15029	**175**	609	1	1.18
			Syf1	Q9HCS7	**388**	482	11	2.71
					427	482	18	4.90
					475	482	2	3.82
						572	1	1.90
					771	794	4	7.17
					776	794	2	4.76
					781	794	2	2.89
					787	794	3	4.06
			Syf2/GCIP p29	O95926	**199**	217	1	1.23
					381	140	72	6.17
					388	118	3	4.26
						140	87	17.42
						143	2	4.06
	U2-A'	P09661	**Brr2**	O75643	**221**	733	1	0.29
			CypE	Q9UNP9	**30**	104	8	1.97
						218	1	0.76
					56	218	11	10.57
					129	147	2	2.04
						218	4	4.12
						284	1	0.91
			Isy1	Q9ULR0	**2**	266	19	17.91
					3	266	11	16.59
					56	260	1	5.02
						266	178	12.85
					129	266	4	0.75
					179	266	28	14.69
					191	266	30	11.14
					192	266	3	5.47
					193	266	94	18.08
					205	259	3	4.17
						260	50	9.96
					221	260	2	6.75
						266	95	16.88
			SmB/B'	P14678	**172**	57	8	6.41

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
			Spf27	O75934	**191**	85	1	1.24
			Syf1	Q9HCS7	**2**	36	1	2.59
					3	36	1	1.30
					205	2	3	5.21
			U2-B"	P08579	**30**	111	3	10.15
					129	225	1	1.62
	U2-B"	P08579	**Brr2**	O75643	**17**	343	1	3.84
					47	1421	1	0.55
			CypE	Q9UNP9	**57**	104	7	2.64
					93	104	1	3.95
					111	104	4	4.13
						123	3	5.89
			Prp17	O60508	**111**	233	1	1.01
						244	3	13.23
						314	1	6.84
			Prp8	Q6P2Q9	**211**	1838	2	0.82
			SmB/B'	P14678	**57**	88	5	6.96
			SmD2	P62316	**47**	1	1	0.46
			SmD3	P62318	**1**	8	1	0.20
					101	31	13	3.94
						78	1	1.02
						84	17	6.49
					111	31	17	13.08
			SmG	P62308	**111**	10	1	1.06
			U2-A'	P09661	**111**	30	3	10.15
					225	129	1	1.62
	U5-40K	Q96DI7	**Ad002**	Q9P013	**18**	226	2	2.44
					270	226	2	1.71
			Cdc5	Q99459	**1**	771	2	7.92
					8	771	2	2.02
						782	2	3.57
					18	757	6	8.42
						771	27	7.33
						782	13	7.02
					270	795	56	6.97
						799	1	1.18
					275	782	9	6.86
					322	782	17	4.57
			NY-CO-10	Q6UX04	**8**	193	2	3.78
					18	193	1	0.48
			Ppil1	Q9Y3C6	**1**	80	17	3.68
						161	1	3.77
					8	80	30	13.61
						161	1	2.27
					18	80	26	6.01
						158	6	2.67
						161	4	2.13
			Prp19	Q9UMS4	**1**	122	11	9.53
						244	7	4.52
					8	122	25	9.00
						179	2	5.96
						244	1	2.93
					18	32	1	0.93
						122	19	9.37
						179	5	5.44
						192	3	2.14
						244	1	1.23
					270	122	1	1.13
						179	1	0.38
						192	11	2.34
						244	4	1.13
					275	122	14	6.55
						192	26	19.57
						244	11	7.19
						261	2	3.66
						266	1	5.03
						425	8	1.46
			Prp8	Q6P2Q9	**286**	29	10	6.05
						36	4	2.99
						43	13	5.52
					349	48	6	1.26
						50	2	1.50
			Rbm22	Q9NW64	**1**	76	1	1.81
					18	76	4	3.23

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						286	4	4.19
			Skip	Q13573	**1**	153	9	4.65
						193	11	8.18
					8	153	1	1.73
						193	5	7.00
					18	141	3	1.43
						153	3	4.15
						193	18	7.07
					349	153	1	2.24
						170	12	6.13
			SmB/B'	P14678	**1**	8	1	2.61
						88	1	6.56
					8	50	2	2.90
						88	6	8.71
					18	50	2	3.18
						88	3	3.46
			SmD1	P62314	**8**	44	1	1.06
					18	44	1	2.46
			Spf27	O75934	**1**	168	1	2.44
						177	1	1.74
					8	168	1	4.83
					18	158	2	5.63
						168	27	9.16
						177	19	5.39
					275	168	13	10.42
						177	27	5.92
						191	41	15.05
			Syf2/GCIP p29	O95926	**18**	155	1	1.39
Intra	**Ad002**	Q9P013	**Ad002**	Q9P013	**91**	74	1	2.21
						147	1	4.94
						199	18	6.82
					183	147	4	7.29
						152	3	3.04
	Aquarius	O60306	**Aquarius**	O60306	**9**	36	8	1.95
						52	15	8.18
						56	4	2.73
					29	38	3	1.62
						44	7	9.57
						52	20	7.15
					36	38	9	8.20
					114	37	1	2.26
						38	74	12.18
					115	38	61	12.98
					189	202	2	4.09
					192	202	4	3.35
					195	188	4	4.90
						189	9	5.08
						192	5	1.82
						202	51	4.82
					201	188	3	7.60
					202	195	1	6.04
					206	195	20	10.27
					246	228	64	7.03
					493	571	1	0.68
						576	11	3.96
					558	1025	7	8.57
						1051	7	6.60
					734	762	11	10.62
					762	192	65	6.25
						195	14	13.75
					865	796	30	6.34
					890	796	19	3.04
					954	950	17	5.80
					1003	796	25	16.21
					1033	1003	4	13.74
					1045	558	1	3.30
						660	3	5.28
						662	19	6.56
						1025	63	16.66
						1051	214	17.59
					1051	1025	23	12.39
					1105	660	1	0.94
						662	19	4.89
						1234	16	3.69

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					1234	660	10	5.59
						662	62	7.19
						1256	38	9.02
					1256	660	7	2.74
						662	25	7.31
						1234	36	4.71
	Brr2	O75643	**Brr2**	O75643	**14**	46	19	8.81
						55	2	3.04
						60	23	9.73
						83	1	0.76
						349	4	6.65
						487	2	3.20
						1557	1	2.95
						1603	17	7.25
						1874	10	9.66
						2059	1	0.62
					46	55	54	5.04
						60	58	14.25
						107	2	1.90
						256	1	3.41
						349	1	0.19
						1556	2	6.11
						1557	5	5.19
						1603	8	8.97
						1874	3	4.62
					60	55	31	3.61
						107	2	0.95
						1874	3	4.14
					83	60	4	5.06
						73	1	1.58
						107	8	3.83
					85	60	3	6.42
						73	3	1.36
						107	13	1.68
					103	55	3	1.96
						60	5	10.32
						83	2	2.56
						107	17	3.42
					144	177	3	5.53
					155	60	18	10.46
						147	3	1.09
						151	29	3.31
					177	60	1	1.39
						151	2	1.99
					178	107	1	1.05
					254	256	45	12.33
					285	1874	8	4.44
					294	349	32	12.84
					319	256	7	10.15
					349	975	15	8.25
					358	256	11	4.84
					368	46	2	3.92
						55	2	1.15
						255	5	6.82
						256	29	6.24
						975	7	9.52
						1556	1	0.28
						1557	1	3.09
						1603	23	8.47
					426	46	1	1.53
						55	3	3.09
						60	4	3.26
						285	1	3.06
						349	1	0.42
						368	1	1.69
						944	6	6.12
					440	696	1	0.16
					451	469	1	2.01
						479	2	3.08
					453	469	2	1.98
						479	20	4.04
						487	31	4.17
					466	451	2	1.09
						479	63	6.07

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						487	16	2.01
					479	557	29	13.51
					577	599	7	1.08
						1567	2	1.22
					592	599	1	1.62
					671	487	27	4.86
					695	60	4	2.84
						284	1	0.52
						285	4	7.28
						440	21	3.71
					733	696	1	1.89
					745	440	16	11.47
					770	729	1	1.74
						1134	33	13.63
					944	14	1	11.08
						46	11	6.74
						55	2	0.14
						60	10	11.80
						256	5	3.82
						368	21	9.82
					966	1544	1	1.95
						1552	1	1.82
					971	1711	143	10.63
					975	255	1	4.36
						256	1	6.03
						971	32	8.63
					1134	1120	36	6.62
						1172	10	5.68
					1141	1146	11	9.17
					1146	1142	23	2.15
					1176	1134	260	16.28
					1242	1567	2	2.31
					1404	1404	4	2.05
						1421	63	20.50
					1421	1404	1	2.59
						2059	3	5.41
					1443	1440	4	0.50
						2080	5	7.22
					1544	971	1	1.01
						975	3	5.27
					1552	971	213	9.67
						975	43	11.24
						1557	4	5.63
						1711	62	7.78
					1556	55	2	0.68
						60	1	6.46
						256	1	3.45
						975	3	8.03
					1557	55	2	2.12
						349	1	1.94
						975	2	5.04
					1595	46	4	4.23
					1603	60	4	7.32
						255	1	6.09
						256	9	5.94
						285	5	8.32
						349	1	6.91
					1610	1595	97	18.35
					1883	1874	1	1.67
					1961	1874	28	5.79
					1977	1972	1	0.69
					2059	1404	15	9.87
						1417	41	5.92
						1421	176	11.67
					2080	1440	3	3.14
						2087	1	6.90
						2089	3	1.11
	CBP20	P52298	**CBP20**	P52298	**34**	120	29	14.45
					38	34	6	3.85
						120	6	4.65
					78	75	14	4.89
					120	68	1	1.32
	CBP80	Q09161	**CBP80**	Q09161	**17**	67	14	3.07
						330	3	3.37

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					20	17	22	13.35
						67	30	2.61
					41	330	16	14.98
						342	22	9.96
					557	511	4	8.48
					568	511	27	11.49
						607	22	14.65
					574	698	12	9.96
					654	647	7	1.89
						665	4	2.67
					657	647	3	3.40
						650	85	8.02
					665	671	2	2.33
						684	3	3.84
					684	665	42	5.36
						671	6	1.83
						698	7	9.37
					698	647	9	2.13
						650	8	5.79
						654	91	10.00
						657	3	6.20
						663	1	1.36
						665	14	3.34
						684	2	6.50
	CCDC12	Q8WUD4	**CCDC12**	Q8WUD4	**23**	28	1	1.79
					32	23	14	2.90
						42	12	3.83
						85	4	2.01
					34	23	12	2.72
						42	29	4.78
					40	23	9	6.15
					42	23	3	1.78
						28	3	1.64
					53	28	4	1.71
						40	2	0.85
					70	28	1	1.74
						32	1	1.15
						42	4	6.24
						78	10	2.87
					71	23	1	2.73
						42	2	2.97
						78	3	1.47
					78	28	1	0.45
						34	4	1.41
						40	6	2.58
						42	7	2.20
					85	28	2	3.55
					87	78	16	10.13
					94	85	1	1.08
					126	23	1	1.30
						122	14	4.43
	Cdc5	Q99459	**Cdc5**	Q99459	**7**	44	1	2.61
					20	28	46	7.94
						60	6	6.55
					28	47	1	0.47
					59	20	1	2.32
						70	7	7.59
					60	70	1	2.70
					70	59	3	4.43
					106	76	51	6.67
					124	7	1	2.13
					200	187	22	12.88
					255	268	1	1.83
					264	255	1	0.92
					270	264	16	5.42
						268	18	2.86
					271	264	23	5.97
						268	15	2.43
					290	294	3	1.93
					291	294	1	1.70
					294	271	1	1.61
						290	40	12.34
						291	3	2.22
					447	432	16	20.18

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					466	432	37	15.23
					532	522	2	3.80
					539	626	14	4.53
						630	9	3.61
					598	708	31	4.03
						712	12	3.04
					601	522	12	2.86
						694	5	3.46
						708	92	11.12
						712	23	2.68
					623	532	18	4.57
						539	21	5.11
						630	8	1.71
					626	522	1	2.42
						532	39	4.09
						535	7	2.82
						539	188	11.16
						543	11	6.04
					630	539	10	8.63
					631	626	34	6.66
					694	685	6	6.24
					708	712	42	6.38
					718	708	16	7.38
						718	2	1.05
					771	782	25	6.12
	Cwc22/KIAA1604	Q9HCG8	**Cwc22/KIAA1604**	Q9HCG8	**9**	243	4	0.93
					116	118	86	20.39
						119	197	22.03
						138	66	9.66
						163	4	6.33
						164	2	3.16
						243	15	6.24
					117	119	23	10.45
					118	138	50	8.88
						163	6	5.66
						164	2	5.52
						243	38	6.19
					119	138	27	9.84
						163	14	7.54
						164	1	5.82
						243	40	7.32
					138	119	24	8.65
						163	4	3.00
						164	23	4.45
					149	138	46	8.04
						399	1	0.31
					724	728	1	2.66
					732	720	4	5.15
						724	12	6.33
						745	2	1.16
						766	1	2.29
					783	820	3	1.06
						841	8	7.56
						894	2	3.62
					788	841	1	3.70
					815	783	3	2.34
						788	1	1.56
						841	16	4.82
						881	2	1.02
						894	3	1.48
					841	820	5	6.10
						860	2	4.16
						881	12	6.99
					881	894	4	6.41
	CypE	Q9UNP9	**CypE**	Q9UNP9	**83**	88	8	5.36
						104	12	6.42
					114	103	14	9.04
						104	38	8.87
					123	104	13	3.94
					147	185	119	8.92
						291	8	10.60
					151	289	7	7.07
					212	218	1	2.34
					218	104	2	3.30

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					291	287	4	1.64
	eIF4AIII	P38919	**eIF4AIII**	P38919	**19**	70	3	3.12
						374	1	1.10
					60	70	7	1.78
						374	6	4.97
					70	242	8	4.33
					195	321	1	2.18
					252	374	22	11.43
					314	321	31	8.23
					374	242	5	4.46
					382	289	6	9.33
	G10	P41223	**G10**	P41223	**9**	80	13	10.88
						86	9	4.85
					28	40	4	2.00
					66	68	11	5.79
	Isy1	Q9ULR0	**Isy1**	Q9ULR0	**7**	24	4	4.74
						55	14	11.34
						121	1	3.55
					24	44	14	3.98
						55	6	6.03
					26	44	2	2.27
						55	1	2.33
						190	1	2.07
					41	7	14	10.00
						24	22	8.06
						26	1	0.63
					44	26	1	1.15
					55	24	3	3.32
						26	15	2.16
						44	7	3.78
					56	7	4	3.53
						24	1	1.33
						79	23	10.53
					79	7	2	5.27
						56	9	4.35
					84	121	87	10.31
					92	84	2	3.77
					101	7	5	6.64
						84	13	7.21
						121	19	8.02
					105	7	5	8.64
						84	37	11.96
						92	11	6.05
						121	36	10.25
					112	84	4	6.18
						101	1	1.60
						121	4	5.11
						127	35	8.22
						138	36	8.11
					127	105	2	4.19
					138	112	2	1.69
						121	4	6.13
						127	24	9.57
					179	190	5	2.63
					238	190	3	0.72
	NY-CO-10	Q6UX04	**NY-CO-10**	Q6UX04	**84**	35	14	3.91
					160	184	5	2.90
						186	13	3.42
						193	1	0.17
					162	186	3	5.01
						192	1	2.03
						193	4	2.56
					186	193	7	5.16
					192	197	5	3.52
					291	308	6	6.48
					298	308	13	4.05
					307	291	1	2.34
						331	2	2.76
					331	291	3	4.95
						308	2	3.11
						318	2	4.29
						334	23	5.33
					340	331	5	6.29
					455	462	1	1.91

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						463	12	2.97
	Ppil1	Q9Y3C6	**Ppil1**	Q9Y3C6	**80**	34	51	5.79
						37	30	8.73
					158	52	244	7.17
	Ppil3	Q9H2H8	**Ppil3**	Q9H2H8	**133**	47	5	6.41
	Prl1	O43660	**Prl1**	O43660	**41**	62	3	1.91
						66	1	1.14
						68	4	3.38
					62	68	63	8.72
					113	66	5	4.34
					135	62	4	5.29
						66	4	0.65
						68	11	8.54
					173	181	1	0.99
					320	279	18	8.33
					505	180	11	2.92
						181	24	9.40
						187	8	5.17
					510	180	35	6.62
						181	12	8.47
	Prp17	O60508	**Prp17**	O60508	**214**	203	7	2.51
						333	5	3.75
						374	2	6.52
					228	333	49	11.28
					233	314	2	4.06
						333	50	9.71
					238	314	4	6.10
					289	333	56	4.13
					312	233	1	2.62
						238	9	5.91
						289	1	0.04
					333	374	10	3.35
					398	374	31	10.71
					531	547	3	1.15
					538	500	9	5.04
					541	278	2	4.94
					551	289	61	6.68
	Prp19	Q9UMS4	**Prp19**	Q9UMS4	**56**	64	142	12.31
					64	64	25	5.24
						244	3	3.43
					122	265	6	1.56
						380	3	4.62
						425	19	3.58
					179	122	28	10.87
						265	6	3.43
					192	122	40	9.19
						179	46	10.16
						189	23	1.54
						192	35	15.27
						244	22	12.01
						261	11	7.90
						265	3	0.85
						380	9	2.25
						423	5	2.96
						425	10	1.94
					244	122	39	11.28
						179	31	12.25
						244	11	5.03
						261	213	13.27
						265	3	1.97
						380	1	2.49
						425	1	0.53
					261	122	22	11.63
						179	14	6.25
						244	3	2.28
						380	2	1.08
					265	244	4	4.04
					266	122	47	10.69
						179	9	8.83
						192	17	10.68
						244	139	13.65
						261	11	8.56
						265	6	1.09
						425	5	1.70

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					380	425	5	5.07
					428	122	7	7.78
						244	4	8.22
	Prp22	Q14562	**Prp22**	Q14562	**2**	2	1	1.04
					59	107	1	1.37
					72	116	1	10.71
					97	107	2	0.94
						109	1	0.82
					114	107	3	3.26
					116	107	1	0.46
						109	4	3.14
					147	1105	1	4.01
					161	1105	3	2.79
					252	161	4	2.81
						236	8	5.40
						240	33	8.83
						320	4	1.02
					330	1105	2	3.36
					403	1105	3	5.29
					507	539	4	0.71
						863	1	2.21
						1024	1	3.60
					539	490	8	5.06
						547	40	8.48
						553	2	4.38
					547	553	38	14.99
						569	3	3.50
						628	19	8.74
					553	540	8	7.13
						547	32	8.00
						569	12	5.56
						628	19	8.16
					569	552	1	5.74
					628	540	1	0.36
						552	1	3.12
					798	490	2	2.16
					1034	1031	10	3.84
					1053	1080	46	9.84
						1098	3	2.00
					1056	330	1	7.89
						1080	18	11.89
					1098	1105	2	3.05
					1105	399	1	1.47
						1194	1	2.04
					1188	1194	12	2.88
	Prp8	Q6P2Q9	**Prp8**	Q6P2Q9	**29**	36	28	8.43
					43	48	2	2.71
					50	480	2	3.34
					278	449	7	2.65
					442	609	117	12.64
					480	85	1	1.00
					486	1514	1	0.04
					511	533	1	0.25
						666	6	2.12
						670	6	4.02
					525	536	1	0.15
					623	442	23	8.54
						609	5	8.33
					721	774	4	3.04
					746	774	8	3.64
					769	853	14	9.04
					853	769	1	0.94
						773	9	5.16
					932	833	53	5.87
					987	1158	4	7.57
					1020	774	12	3.04
					1144	1144	2	1.65
					1158	983	29	9.10
					1258	769	1	2.76
						853	4	2.01
					1262	769	130	6.15
						773	3	1.68
						853	1	1.14
					1320	853	2	1.79

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					1344	1132	46	7.60
						1735	3	12.63
						1838	2	2.26
					1449	769	21	4.44
						1258	16	6.37
					1463	853	2	3.65
					1636	1831	2	2.50
					1649	1838	5	0.95
					1732	1838	23	8.28
					1735	1838	8	2.50
					1801	1831	14	6.20
						1898	10	7.99
					1820	1840	8	9.38
					1831	1838	25	6.46
					1859	2034	4	10.59
						2249	5	8.06
					1866	1838	134	6.45
						2034	1	3.87
					1898	1951	1	3.03
					1901	1955	12	4.35
					1955	1901	1	2.31
					1958	1901	2	4.78
						2244	6	4.05
					1994	2034	6	9.14
					2031	1838	23	5.58
						1993	13	7.84
					2034	1831	11	6.19
						1838	37	5.78
						1993	23	10.40
					2049	1831	4	4.09
						1838	29	4.95
						1859	2	4.95
						1951	2	6.53
						1955	1	1.68
						1993	10	6.04
						2031	7	2.95
						2034	25	21.20
						2108	3	4.48
						2244	18	8.37
						2249	34	23.01
						2293	7	10.49
					2070	2031	3	2.07
						2034	8	15.46
						2244	24	9.01
					2244	1838	3	2.33
					2249	1831	1	1.29
						1838	13	3.26
						1993	3	2.03
						2031	5	3.33
						2034	17	12.83
	Rbm22	Q9NW64	**Rbm22**	Q9NW64	**139**	76	2	1.32
						104	1	1.30
						286	45	8.03
					149	104	1	0.87
						286	15	7.06
						290	27	13.75
						301	36	6.20
					185	185	1	0.19
					301	313	11	5.16
					313	301	1	1.13
					315	301	19	6.71
						416	2	1.83
	Skip	Q13573	**Skip**	Q13573	**141**	153	34	5.16
					153	146	6	2.70
					170	153	26	7.91
					193	48	1	7.35
						153	5	8.24
						170	5	7.77
						217	1	1.03
					323	315	20	5.22
						330	35	6.18
						376	1	0.58
						379	1	1.65
					330	323	13	8.54

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					339	323	2	0.23
						330	15	4.08
						376	4	2.71
						379	14	1.55
						476	2	3.71
					344	323	1	0.93
						330	7	4.05
						379	1	0.58
					376	379	11	3.70
						468	2	5.10
					416	441	9	5.36
						476	2	8.72
					441	379	7	1.72
						452	1	2.13
						468	9	1.62
						476	15	9.94
					452	441	32	13.12
						468	4	1.08
					456	441	29	13.88
						468	11	2.79
						476	9	6.62
					476	468	2	1.39
						509	4	4.42
						531	4	3.44
					503	379	2	1.33
						468	3	0.90
						476	5	5.79
						531	4	2.85
					509	476	1	1.14
	SmB/B'	P14678	**SmB/B'**	P14678	**36**	5	48	3.30
					57	50	15	9.29
						52	1	3.70
					64	50	2	3.90
					88	5	1	1.09
						32	14	3.78
	SmD1	P62314	**SmD1**	P62314	**86**	1	2	4.02
	SmD2	P62316	**SmD2**	P62316	**37**	18	17	2.06
						57	8	2.51
						118	12	5.24
					57	118	1	3.63
					71	51	59	3.15
						118	155	13.17
					79	50	1	0.94
						92	2	1.54
					88	118	2	6.08
					98	57	2	1.90
					118	51	26	8.91
						88	25	7.34
	SmE	P62304	**SmE**	P62304	**67**	72	13	2.46
	SmG	P62308	**SmG**	P62308	**10**	15	6	2.34
	Snu114	Q15029	**Snu114**	Q15029	**352**	355	13	7.64
						359	91	14.41
					359	355	2	3.19
					602	609	8	1.21
	Spf27	O75934	**Spf27**	O75934	**151**	158	2	1.24
	SRm300	Q9UQ35	**SRm300**	Q9UQ35	**90**	101	90	14.39
						131	3	1.69
					101	131	10	1.80
					108	131	26	2.42
					130	101	5	7.41
						108	9	10.97
					1186	1165	2	1.72
	Syf1	Q9HCS7	**Syf1**	Q9HCS7	**50**	76	5	3.22
						83	9	7.14
					62	2	1	2.22
					83	50	1	2.19
						76	21	5.77
					420	458	22	9.92
					427	393	1	2.17
					458	423	22	8.06
					539	572	5	4.00
					549	590	6	8.31
					590	654	4	4.57
					637	654	4	3.97

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	Score$_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
					654	677	1	6.13
					708	721	209	15.59
						794	29	6.96
					721	794	7	6.73
					770	708	26	10.46
						794	2	5.92
	Syf2/GCIP p29	O95926	**Syf2/GCIP p29**	O95926	**60**	63	3	4.00
						71	10	4.85
					80	85	1	4.10
						86	4	7.09
					118	118	3	5.36
						140	4	5.48
					143	188	1	3.24
	Syf3	Q9BZJ0	**Syf3**	Q9BZJ0	**182**	175	4	0.91
					213	256	13	7.34
					256	224	8	4.95
					388	357	35	5.61
						381	1	1.93
					445	437	30	8.16
						475	27	10.44
					475	460	15	9.10
					485	445	42	8.14
					527	531	8	2.74
					568	602	18	5.45
					602	569	16	7.40
					740	730	42	5.60
						776	52	10.45
						823	10	4.06
						827	4	7.05
					748	781	7	5.50
					771	776	7	6.25
					787	827	1	0.63
					823	730	4	5.18
						827	25	7.71
					827	730	15	5.54
						740	2	1.60
						776	10	1.86
						781	1	1.27
						823	27	3.44
					832	730	10	2.62
						740	26	5.55
						776	10	2.25
						781	3	0.61
						823	23	2.49
	U2-A'	P09661	**U2-A'**	P09661	**2**	56	6	6.22
						191	4	2.71
						193	2	7.27
						221	7	12.15
					3	56	63	12.27
						191	5	3.47
						193	19	9.53
						221	7	16.37
					30	191	3	3.77
						193	11	7.98
						221	8	10.90
					56	172	14	9.99
					129	172	2	4.12
					138	172	29	8.03
						193	7	6.21
					160	129	32	5.93
					163	129	2	2.39
					172	128	5	7.53
						129	33	4.84
						160	2	2.53
						163	2	2.86
					179	56	121	10.79
						128	20	5.68
						129	81	5.39
						138	11	8.00
						172	176	9.70
						192	3	4.94
						193	70	20.00
						221	20	11.15
					191	56	71	17.59

Type	Protein 1		Protein 2		Residue1	Residue2	Spectral Count	$Score_{max}$
	Name	Uniprot ID	Name	Uniprot ID				
						128	1	4.40
						129	20	6.54
						172	34	13.06
						193	49	21.84
					192	56	3	5.26
					193	56	32	9.29
						128	11	5.05
						129	14	5.53
						172	30	8.88
					205	56	4	4.90
						129	3	1.14
						172	4	2.10
						179	18	12.83
						191	24	8.05
						192	1	0.92
						221	74	20.60
					221	56	46	11.58
						129	14	3.07
						172	10	7.69
						193	17	15.49
	U2-B"	P08579	**U2-B"**	P08579	**57**	93	39	5.81
						101	13	1.84
						111	1	6.91
					85	111	10	11.16
					93	101	6	6.40
					111	85	4	6.17
						93	4	4.80
						101	13	4.92
						103	3	4.95
						224	2	3.45
						225	6	3.34
					211	111	2	5.92
					219	111	9	4.62
	U5-40K	Q96DI7	**U5-40K**	Q96DI7	**8**	1	27	5.92
						6	15	3.50
					18	1	12	6.87
						6	2	1.03
					270	1	4	1.87
						8	7	2.27
						226	9	3.62
					275	1	29	6.09
						6	2	1.24
						8	66	13.26
						18	78	17.98
						270	72	10.95
					322	1	6	3.62
						8	5	10.01
						18	22	6.48
					349	18	12	7.79