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# Supplementary Material for

## Molecular architecture of the *Saccharomyces cerevisiae* activated spliceosome

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**This PDF file includes:**



**Other Supplementary Material for this manuscript includes the following:**
(available at www.sciencemag.org/content/science.aag1906/DC1)

Movies S1 and S2

## Materials and Methods

### Yeast growth

The *Saccharomyces cerevisiae* 3.2.AID/CRL2101 strain (*MAT*alpha*, prp2-1, ade2, his3, lys2-801, ura3*) carrying the G360D substitution in the helicase domain of Prp2 (*53*) was kindly provided by Ren-Jang Lin. This mutation renders Prp2 temperature-sensitive at 35 ˚C. Yeast spliceosomes assembled in the presence of this temperature-sensitive Prp2 mutant stop at the stage of the $B^{act}$ complex. Yeast was grown in yeast extract/peptone medium (Formedium™) in a 100 L fermenter to a density of $OD_{600}$ 4. Biomass was collected by centrifugation. Cell pellets were washed with cold water and resuspended in a volume of 1 ml per g cells in AGK buffer (20 mM HEPES-KOH pH 7.5 $_{4°C}$, 200 mM KCl, 1.5 mM $MgCl_2$, 10% v/v glycerol, 0.5 mM DTT, 0.5 mM PMSF) containing protease inhibitors (Roche). Drops of this slurry were frozen in liquid nitrogen.

### Whole-cell extract preparation

Frozen beads were ground at 18,000 rpm in a Retsch ZM200 nitrogen mill. The yeast powder was thawed at room temperature and then centrifuged at 4 ˚C for 30 min in an A27-8x50 rotor (Thermo-Scientific). The supernatant was then centrifuged for 1 hour at 4 ˚C in a T647.5 rotor (Thermo Scientific) at 42,000 rpm. The clear middle phase in each tube was collected (ca. 60–70% of total volume) and dialyzed three times for 2 hours against 5 L each of buffer D (20 mM HEPES-KOH pH 7.5 $_{4°C}$, 50 mM KCl, 0.2 mM EDTA, 20% (v/v) glycerol, 0.5 mM DTT, 0.5 mM PMSF), using SnakeSkin™ dialysis tubing (7000 MW cut-off, Thermo Scientific). After a final centrifugation in an F14-14x50cy rotor (Thermo-Scientific) (10 min at 9500 rpm) aliquots were frozen in liquid

nitrogen and stored at –80 ˚C.

**Aptamer-tagged pre-mRNA substrate**

For affinity purification of $B^{act}$ complexes, cap-free wild-type actin pre-mRNA tagged with three MS2 RNA aptamers (M3-actin) was prepared by T7 runoff transcription in the presence or absence of α-[$^{32}$P]-labeled UTP (*2*). Actin pre-mRNA substrate comprises the end of exon 1, the intron and the 5' end of exon 2 of the yeast actin gene. $B^{act}$ complexes assembled on actin pre-mRNA in the presence of MS2-MBP fusion protein were then purified on amylose affinity columns.

**Splicing reaction and affinity purification of $B^{act}$ complexes**

Splicing reactions were performed in a volume of 36 ml or multiples thereof. Dialyzed prp2-1 extract was thawed in cold water and then incubated at 35 ˚C for 30 min to heat-inactivate the Prp2 protein. For a standard 36 ml reaction a mixture of 0.85 pmol [$^{32}$P]-labeled pre-mRNA and 65 pmol unlabeled actin pre-mRNA (the total pre-mRNA concentration in the reaction was ~1.8 nM, with a specific activity of ~160 cpm/fmol) was pre-incubated with a 15-fold molar excess of MS2-MBP protein in 1.5 ml HEPES-KOH buffer (pH 7.3 $_{4°C}$) on ice for 30 min. The splicing reaction mixture contained 60 mM K-phosphate buffer, pH 7.25 $_{20°C}$, 0.3% (w/v) PEG8000, 2.5 mM $MgCl_2$, 2 mM spermidine, 1.8 nM pre-mRNA, 27 nM MS2-MBP, 2 mM ATP and 14.4 ml dialyzed prp2-1 extract. The reaction was allowed to proceed for 1 hour at 23 ˚C. Thereafter the reaction mixture was centrifuged for 10 min at 9000 rpm in a F14-14x50cy rotor (Thermo Scientific) and the supernatant was applied directly to a 0.6 ml column of Amylose Resin™ affinity matrix (NEB), equilibrated with G75 buffer (20 mM HEPES-KOH pH

7.3 $_{4^{\circ}C}$, 1.5 mM $MgCl_2$, 75 mM KCl, 0.01% NP-40 (v/v), 5% glycerol (v/v), 0.5 mM DTT and 0.5 mM PMSF). After loading under hydrostatic pressure, the matrix was washed with 10 volumes of G75 buffer. $B^{act}$ was eluted from the column with G75 buffer containing 100 mM maltose. HEPES-KOH buffer at pH 7.3 $_{4^{\circ}C}$ had been identified as an optimum buffer for $B^{act}$ complex stability in a thermofluor experiment performed according to Chari *et al.* (*54*).

**Binding of the dominant negative Prp2 G551N protein to the $B^{act\ \Delta Prp2}$ complex**

Unlike the prp2-1 ts-mutant protein, which does not remain in the $B^{act\ \Delta Prp2}$ complex, the G551N Prp2 mutant protein, although it does not support splicing, nevertheless binds tightly to the $B^{act\ \Delta Prp2}$ complex (*55*). For locating Prp2 within the $B^{act\ \Delta Prp2}$ complex, recombinant dominant-negative G551N Prp2 protein (kindly provided by Jana Schmitzovà) was added to the sample after elution from the amylose column. Purified $B^{act\ \Delta Prp2}$ complexes were incubated with 2-fold molar excess of the G551N Prp2 mutant protein. The same molar amount of recombinant wild-type Spp2 was added. After incubation the $B^{act+Prp2}$ complex was loaded directly onto a glycerol gradient.

**Glycerol-gradient sedimentation of the $B^{act}$ complex**

The $B^{act}$ peak from the amylose column was loaded onto a glycerol gradient [10–30% glycerol (v/v) in G75 buffer containing 0.5 mM each of DTT and PMSF]. Native gradients were run using 4.4 ml polyallomer tubes in a TH660 rotor at 4˚ C for 17 hours at 21,000 rpm. When particles were centrifuged under cross-linking conditions, DTT and PMSF were omitted from the gradient, the 30% solution was supplemented with 0.1% EM-grade glutaraldehyde (EMS) and the 10% solution was supplemented with 1 mM

PMPI (Thermo Scientific). After centrifugation, gradients were harvested from bottom to top in 24 fractions of about 180 µl. Crosslinked fractions were immediately quenched with 50 mM each of aspartate and cysteine, pH 7. Before electron cryomicroscopy samples were subjected to a buffer exchange against G75 buffer containing 2 mM IPTG and 0.5 mM DTT, but without glycerol and NP-40.

**Crosslinking of $B^{act}$ complexes and crosslink identification by mass spectrometry**

Approximately 10–20 pmol of purified $B^{act}$ complexes were cross-linked with 150 µM BS3 for 30 min at 25 °C, pelleted by ultracentrifugation and analyzed essentially as described before (*56*), with the following modifications: precipitated material was dissolved in 4 M urea / 50 mM ammonium bicarbonate, reduced with DTT, alkylated with iodoacetamide, diluted to 1 M urea and digested with trypsin (1:20 w/w). Peptides were reverse-phase extracted and fractionated by gel filtration on a Superdex Peptide PC3.2/30 column (GE HealthCare). 50 µl fractions corresponding to an elution volume of 1.2–1.8 ml were analyzed on a Thermo Scientific Orbitrap Fusion Tribrid and on Sciex TripleTOF 5600+ (dataset 1), Thermo Scientific Q Exactive (dataset 2) or Q Exactive HF (dataset 3) mass spectrometers. Protein-protein crosslinks were identified by pLink1.22 or 1.23 search engine and filtered at FDR 1% (pfind.ict.ac.cn/software/pLink) according to the recommendations of the developers (*57*). For simplicity, the crosslink score is represented as a negative value of the common logarithm of the original pLink score, that is Score = $-\log_{10}$("pLink Score"). The crosslinks observed with at least 2 spectral counts are listed in Table S2. For model building, a maximum distance of 3 nm between the Cα-atoms of the crosslinked lysines was allowed. The actual distribution of Cα-Cα distances

between crosslinked residues that can be mapped in the model of the $B^{act}$ complex is shown in Fig. S19.

**EM and image processing**

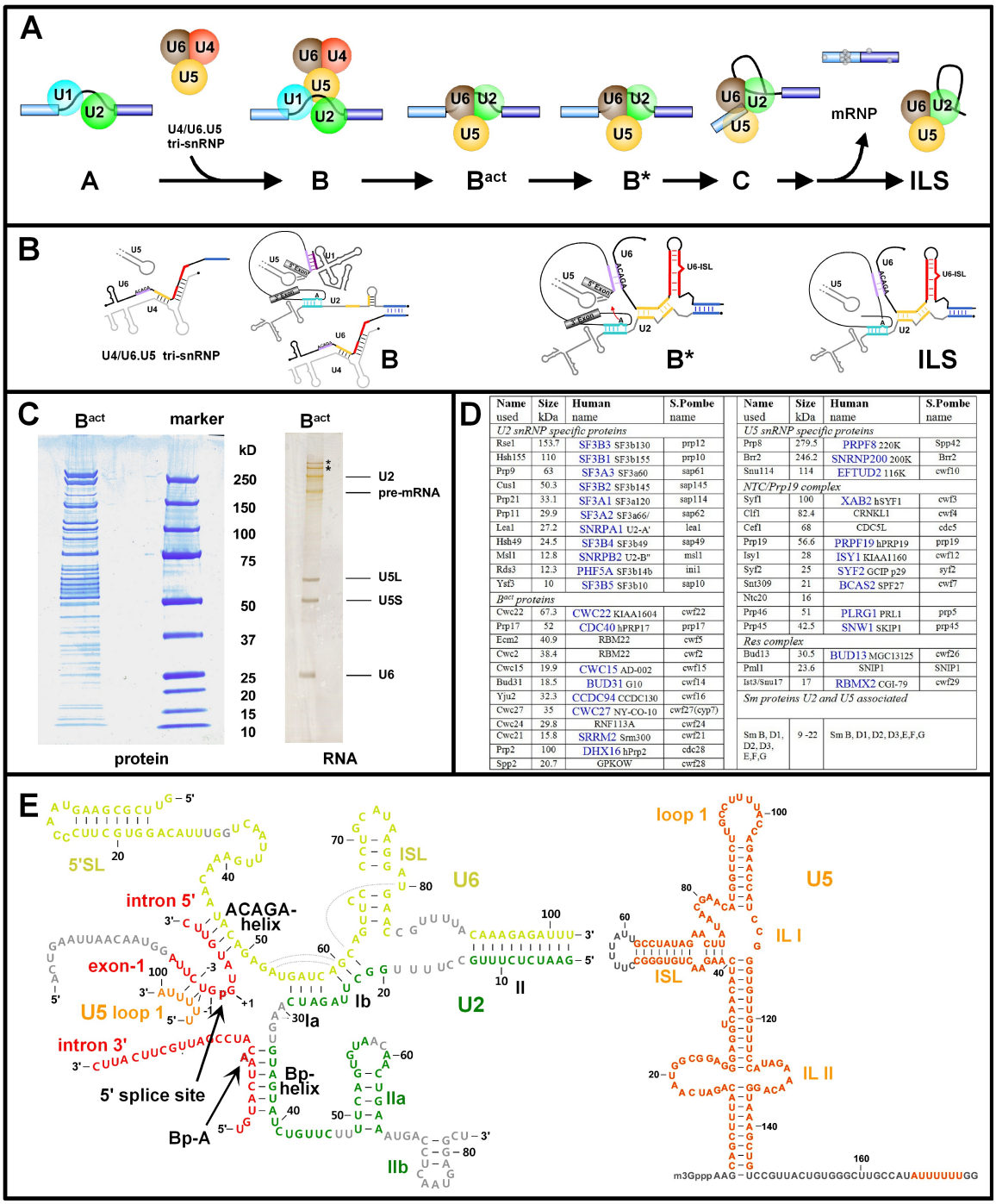
Purified spliceosomes were allowed to adsorb on a thin carbon film prior to rapid plunge freezing into liquid ethane at 100% humidity and 4 ºC. Images were recorded at -193 ºC in a Titan Krios electron microscope (FEI Company, The Netherlands) on a Falcon II direct electron detector at 74.000x magnification resulting in a pixel size of 2 Å on the specimen level. We extracted ~1 million particle images from the micrographs and applied several sorting steps at the 2D and 3D level. The first sorting was based on CTF parameters by applying multivariate statistical analysis and classification to power spectra as implemented in Imagic-5 (*58*). Only particles in classes revealing isotropic Thon rings were used for the subsequent rounds of sorting. 2D multivariate statistics and classification was then applied to the non-aligned particle images and subsequently to the aligned particles. In each round, particles contributing to bad classes were excluded from further processing. The remaining ~650.000 particles were then CTF corrected by CTFFIND (*59*) and applied to 3D classification in RELION (*60*). For the high-resolution structure determination, the ~122.000 particles contributing to the best 3D class were used for refinement revealing an 8Å resolution structure. Roughly 30% of the spliceosome density were not clearly defined at this level of resolution. As these densities largely disappear during the higher-resolution structure calculations, we excluded them with a mask in the final rounds of the refinement. A soft mask with a cut-off of 6 voxel was used for the refinement and for the determination of resolution. We obtained 5.8 Å resolution for the final map by using the Fourier-shell-correlation function calculated

from two independent data sets and a threshold of 0.143. The molecular components which were masked away are indicated in Figures S12, S13 and S17. A local resolution plot revealed that there are indeed areas of high resolution in the catalytic RNP core of the $B^{act}$ complex that approach the maximum achievable resolution limit corresponding to the Nyquist frequency (4 Å). Some peripheral regions have somewhat lower resolution.

**Model fitting and building**

Available X-ray or homology models of proteins were initially fit into the EM density by CHIMERA (*61*). Individual models of substructures (e.g. domains or structural motifs) were further fitted as rigid bodies by COOT (*62*). After visual inspection, the models were adjusted manually in the density, the disordered regions were removed and regions that were reorganized or were not present in the initial models (e.g. loops and various elements of secondary structure) were built in COOT. The detailed processing of protein models incorporated into the $B^{act}$ structure is described in Table S1. Initially, the U5 snRNA model of the *S. cerevisiae* tri-snRNP (*13*), the U2/U6 snRNA catalytic core and the branch-point helix of the *S. pombe* ILS spliceosome (*10*), as well as a 5' group II intron fragment (5'-GUUAU/gu-3')(*23*) were fitted into the 10 Å cryo-EM density by visual inspection in CHIMERA. All further adjustments were done manually by using the COOT program with the 5.8 Å cryo-EM map. The 5' stem-loop of U6 and the U2/U6 helix II were generated by rigid-body fitting of idealized double-stranded RNA helices. Sections of the RNA models that could not be placed unambiguously into a density, or that did not have an associated density because of their high flexibility, are shown in grey in Fig S1 (RNA–RNA interactions). The atomic model was refined by the real space

refinement routines as implemented in PHENIX, using base pairing restraints (*63*). The RNA model was then validated by the MolProbity server (*64*). A summary of the Molprobity scores is shown in Table S3. The Molprobity scores for all individual RNA nucleotides from the final model are provided in a separate HTML file. Final visualization was carried out with CHIMERA and PyMOL (http://www.pymol.org).




| Name used | Size kDa | Human name | S.Pombe name |
|---|---|---|---|
| *U2 snRNP specific proteins* | | | |
| Rse1 | 153.7 | SF3B3 SF3b130 | prp12 |
| Hsh155 | 110 | SF3B1 SF3b155 | prp10 |
| Prp9 | 63 | SF3A3 SF3a60 | sap61 |
| Cus1 | 50.3 | SF3B2 SF3b145 | sap145 |
| Prp21 | 33.1 | SF3A1 SF3a120 | sap114 |
| Prp11 | 29.9 | SF3A2 SF3a66/ | sap62 |
| Lea1 | 27.2 | SNRPA1 U2-A' | lea1 |
| Hsh49 | 24.5 | SF3B4 SF3b49 | sap49 |
| Msl1 | 12.8 | SNRPB2 U2-B" | msl1 |
| Rds3 | 12.3 | PHF5A SF3b14b | ini1 |
| Ysf3 | 10 | SF3B5 SF3b10 | sap10 |
| *Bact proteins* | | | |
| Cwc22 | 67.3 | CWC22 KIAA1604 | cwf22 |
| Prp17 | 52 | CDC40 hPRP17 | prp17 |
| Ecm2 | 40.9 | RBM22 | cwf5 |
| Cwc2 | 38.4 | RBM22 | cwf2 |
| Cwc15 | 19.9 | CWC15 AD-002 | cwf15 |
| Bud31 | 18.5 | BUD31 G10 | cwf14 |
| Yju2 | 32.3 | CCDC94 CCDC130 | cwf16 |
| Cwc27 | 35 | CWC27 NY-CO-10 | cwf27(cyp7) |
| Cwc24 | 29.8 | RNF113A | cwf24 |
| Cwc21 | 15.8 | SRRM2 Srm300 | cwf21 |
| Prp2 | 100 | DHX16 hPrp2 | cdc28 |
| Spp2 | 20.7 | GPKOW | cwf28 |

| Name used | Size kDa | Human name | S.Pombe name |
|---|---|---|---|
| *U5 snRNP specific proteins* | | | |
| Prp8 | 279.5 | PRPF8 220K | Spp42 |
| Brr2 | 246.2 | SNRNP200 200K | Brr2 |
| Snu114 | 114 | EFTUD2 116K | cwf10 |
| *NTC/Prp19 complex* | | | |
| Syf1 | 100 | XAB2 hSYF1 | cwf3 |
| Clf1 | 82.4 | CRNKL1 | cwf4 |
| Cef1 | 68 | CDC5L | cdc5 |
| Prp19 | 56.6 | PRPF19 hPRP19 | prp19 |
| Isy1 | 28 | ISY1 KIAA1160 | cwf12 |
| Syf2 | 25 | SYF2 GCIP p29 | syf2 |
| Snt309 | 21 | BCAS2 SPF27 | cwf7 |
| Ntc20 | 16 | | |
| Prp46 | 51 | PLRG1 PRL1 | prp5 |
| Prp45 | 42.5 | SNW1 SKIP1 | prp45 |
| *Res complex* | | | |
| Bud13 | 30.5 | BUD13 MGC13125 | cwf26 |
| Pml1 | 23.6 | SNIP1 | SNIP1 |
| Ist3/Snu17 | 17 | RBMX2 CGI-79 | cwf29 |
| *Sm proteins U2 and U5 associated* | | | |
| Sm B, D1, D2, D3, E,F,G | 9 -22 | Sm B, D1, D2, D3,E,F,G | |

**Fig. S1**

**Purification and characterization of B$^{act}$ spliceosomes from the yeast *Saccharomyces cerevisiae*.** (**A**) Assembly and remodeling steps of the spliceosome during activation and catalysis of splicing. (**B**) RNA–RNA rearrangements occurring during spliceosome

activation and the catalysis of splicing. (**C**) Proteins and RNA isolated from purified $B^{act}$ complexes were visualized on an SDS-polyacrylamide gel by Coomassie blue staining (left) or by silver staining (right). (**D**) Proteins present in yeast $B^{act}$ complexes and their molecular masses. Proteins were identified by mass spectrometry (*17*). Standard names for human proteins are shown in blue. (**E**) Schematic representation of the secondary structure of RNA in the $B^{act}$ spliceosome. The complete secondary structure of the U5 snRNA is shown on the right. Only selected regions of the pre-mRNA and U2 snRNA are shown. Regions of the RNA that could not be placed unambiguously into the EM density or that did not have an associated density owing to their high flexibility are shown in grey. Tertiary interactions are indicated by stippled lines.

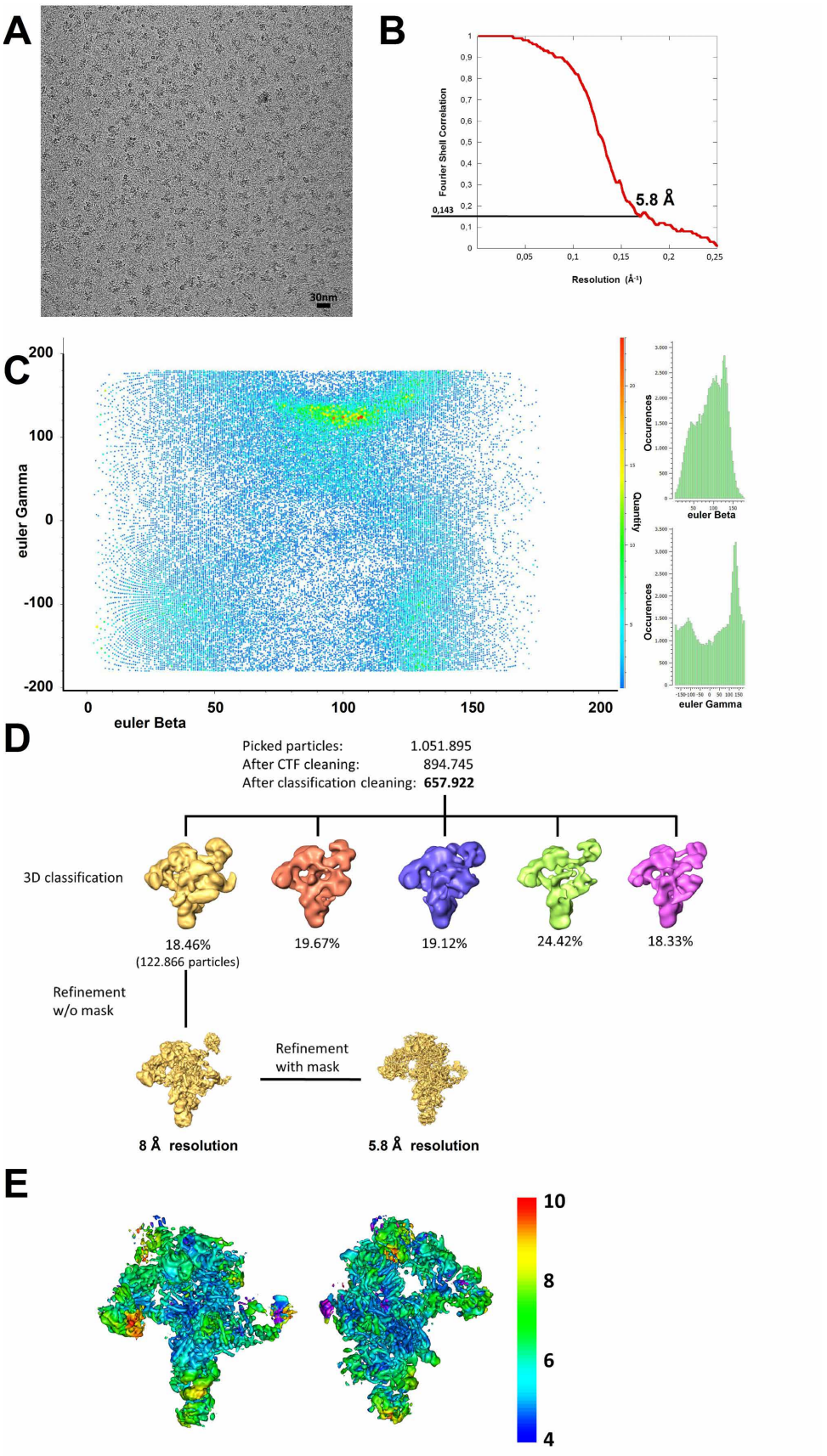

A
30nm
B
Fourier Shell Correlation
0,143
5.8 Å
Resolution (Å⁻¹)
C
euler Gamma
euler Beta
Occurences
Quantity
D
Picked particles: 1.051.895
After CTF cleaning: 894.745
After classification cleaning: 657.922
3D classification
18.46%
(122.866 particles)
19.67%
19.12%
24.42%
18.33%
Refinement
w/o mask
Refinement
with mask
8 Å resolution
5.8 Å resolution
E
10
8
6
4

**Fig. S2**

**Cryo-EM and image-processing of the yeast $B^{act}$ complex.** (**A**) Typical cryo-EM raw image of *S. cerevisiae* $B^{act}$ spliceosomes recorded with a Titan Krios (FEI Company) electron microscope at a nominal magnification of 74,000x with a Falcon II direct electron detector resulting in a pixel size of 2 Å/pixel. (**B**) Fourier-shell correlation function of two independently refined half data sets indicates a global resolution of 5.8Å for the masked $B^{act}$ spliceosome comprising ca. 70% of the density of the whole spliceosome. (**C**) Euler angle distribution of all particle images that contributed to the final 3D map. The coordinates describe the beta and gamma angles. Size and color of the plotted dots indicate the number of particles at any given Euler angle. Although one angular orientation of $B^{act}$ dominated, an almost complete angular coverage was obtained. (**D**) Computational sorting scheme. Roughly 1 million particle images were selected from the micrographs. In a first sorting step ~10% of particle images were discarded based on the quality of Thon rings in local power spectra. Another 15% particles were excluded according to multiple rounds of 2D classifications. The remaining 657,922 particles were separated into 5 classes by 3D classification in RELION (*60*). Images contributing to the best defined spliceosome structure (~18.5%) were then refined to a structure at 8 Å resolution without masking. The final structure at 5.8 Å resolution was obtained by applying a soft mask during the final steps of the refinement process. (**E**) Local resolution plot reveals a resolution distribution from about 4-10 Å with some less well defined parts at the periphery of the complex. Higher resolution regions (in blue, close to 4 Å resolution) were obtained for the centrally-located catalytic core of the spliceosome.

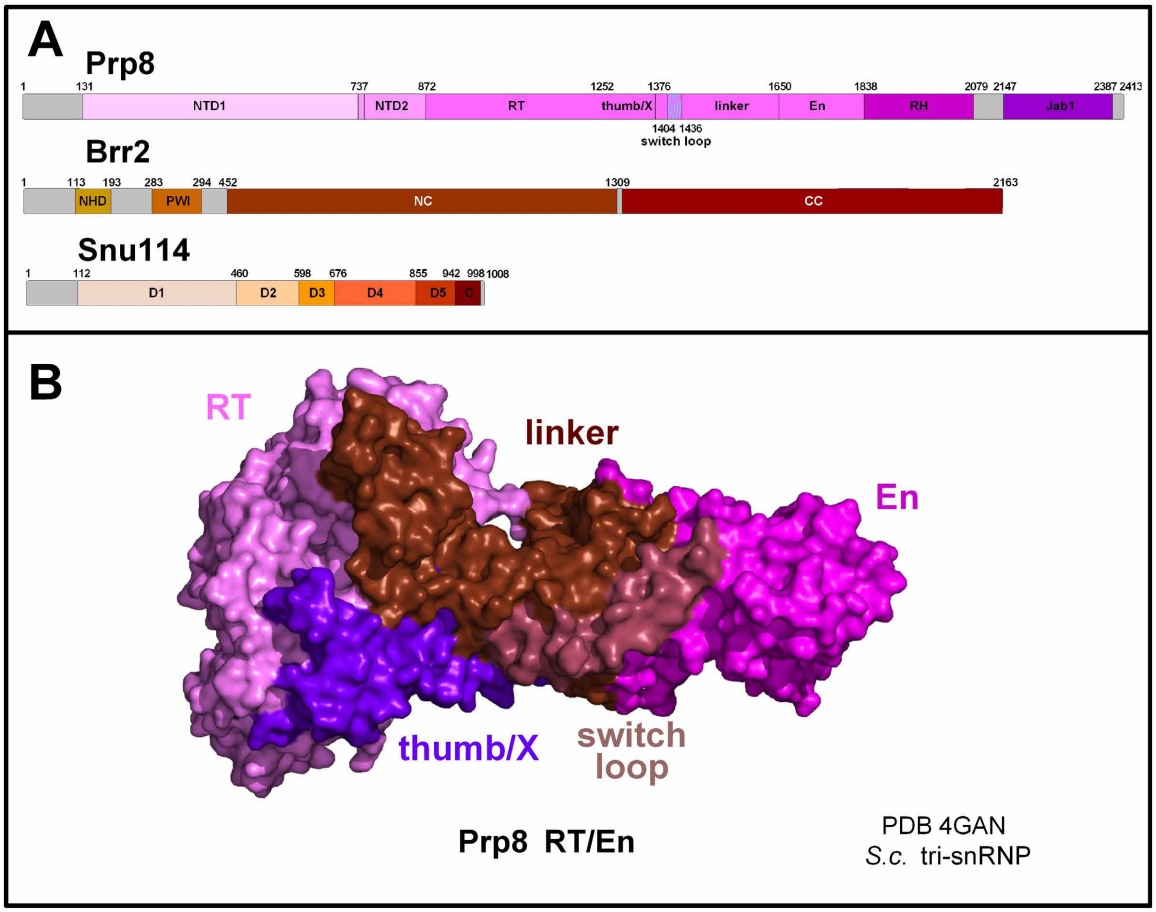



**Fig. S3**

**Structural organization of Prp8, Brr2 and Snu114.** (**A**) Organization of Prp8, Brr2 and Snu114 domains. Prp8, NTD1 and NTD2, N-terminal domains 1 and 2; RT, reverse-transcriptase-like; thumb/X, linker; En, endonuclease-like; RH, RNase H-like; Jab1, Jab1/MPN-like. Brr2, NHD, N-terminal helical domain; PWI, N-terminal, non-canonical PWI domain; NC/CC N-terminal/C-terminal helicase cassette. Snu114, D1–D5 homologous to EF-G/EF-2. (**B**) Three-dimensional organization of the Prp8 RT, thumb/X, linker and En domains in the *S. cerevisiae* tri-snRNP, according to (*11*). The location of the switch loop is also indicated.

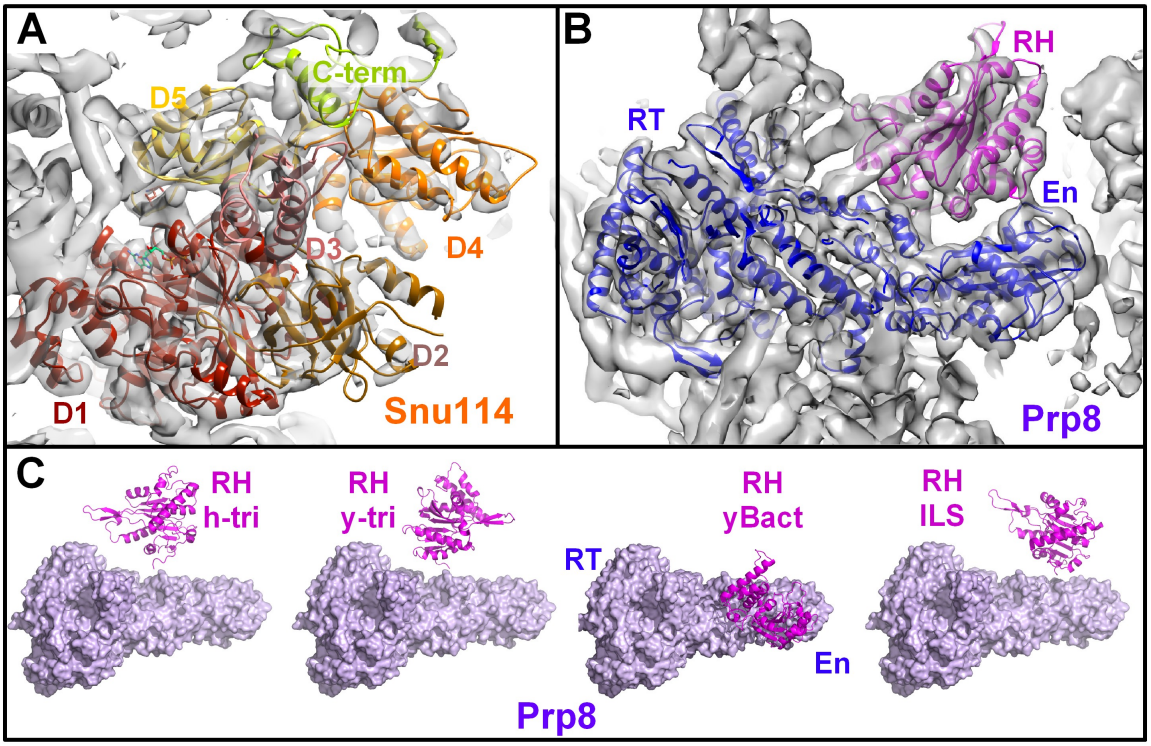



**Fig. S4**

**Structure and location of Snu114 and Prp8 in the yeast B$^{act}$ complex.** (**A**) Density fit of Snu114 domains D1–D5. (**B**) Density fit of Prp8: RT, reverse-transcriptase-like; En, endonuclease-like; RH, RNase H-like domains; (**C**) Variation in the position of Prp8's RH domain (magenta ribbon model) relative to the Prp8 En domain in human (h) and yeast (y) tri-snRNPs, and in the *S. cerevisiae* B$^{act}$ complex and *S. pombe* intron-lariat spliceosome (ILS). The structure of the Prp8 (from *S. cerevisiae* B$^{act}$) RT, thumb/X linker and En domains are shown as a space filling model in grey. In B$^{act}$ the RH domain is closely associated with the "back side" of the En domain, whereby the RH RNA-binding β sheet faces the En domain. The palm edge of the RH domain interacts with the En domain of Prp8 in a region where in the ILS (and tri-snRNPs) the tip of a major β-hairpin-loop (switch loop) is instead located (see also Fig. 2 and text). The density for the

β-hairpin-loop of the RH domain is not well defined in the $B^{act}$ structure, consistent with the possibility that it adopts a more open conformation.

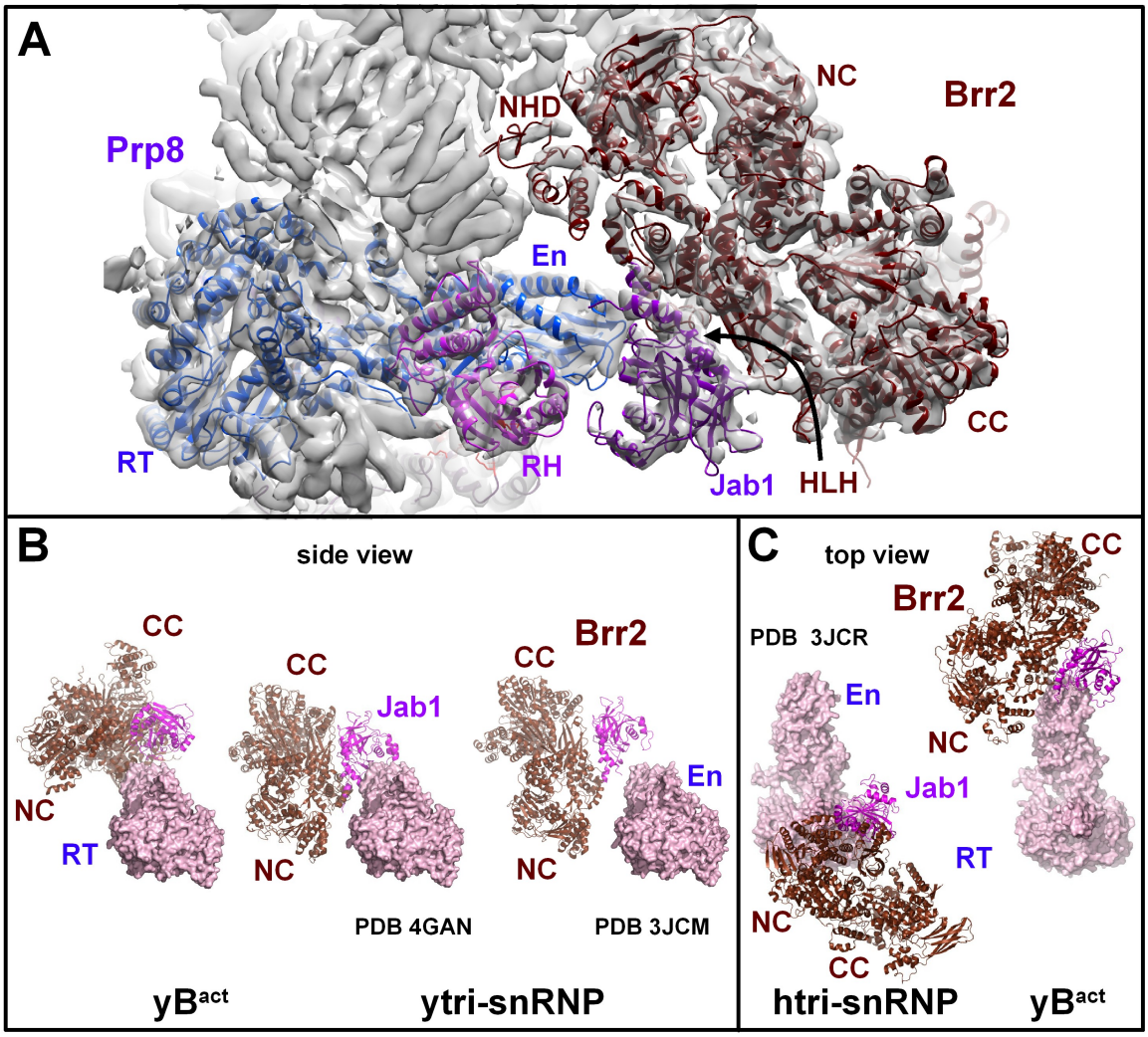



**Fig. S5**

**Structure and location of the RNA helicase Brr2 and Prp8 Jab1 domain.** (**A**) Expanded view of the shallow slope of $B^{act}$ (Fig. 1A) showing the fit of Brr2's helicase region in complex with Prp8's Jab1 domain. The tip of Prp8's En domain interacts with Brr2 through the HLH domain of the NC cassette. (**B**) Brr2 is located at the same end of Prp8's RT/En domain in $B^{act}$ and the yeast tri-snRNP (*13-15*); however, in the two models Brr2 has a different orientation (side views). (**C**) Top view illustrating that Brr2 is located at radically different positions in the human tri-snRNP (*16*) and yeast $B^{act}$ complex. It is found at opposite ends of Prp8's RT/En domain in the two models.

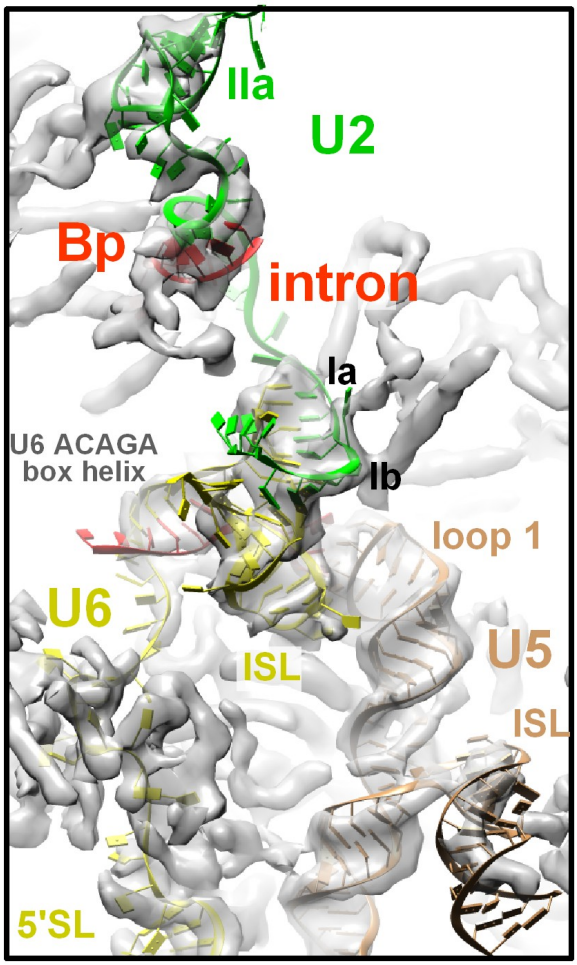



**Fig. S6**

**A close-up view of the central RNA network in the B$^{act}$ spliceosome.** Shown is a slice through the spliceosome showing only the high density elements of the cryo-EM map, comprising U5 RNA, U2/U6 catalytic RNA network, the BS/U2 RNA helix, the U6 ACAGA box helix, the U2 RNA helix IIa and corresponding linker regions.

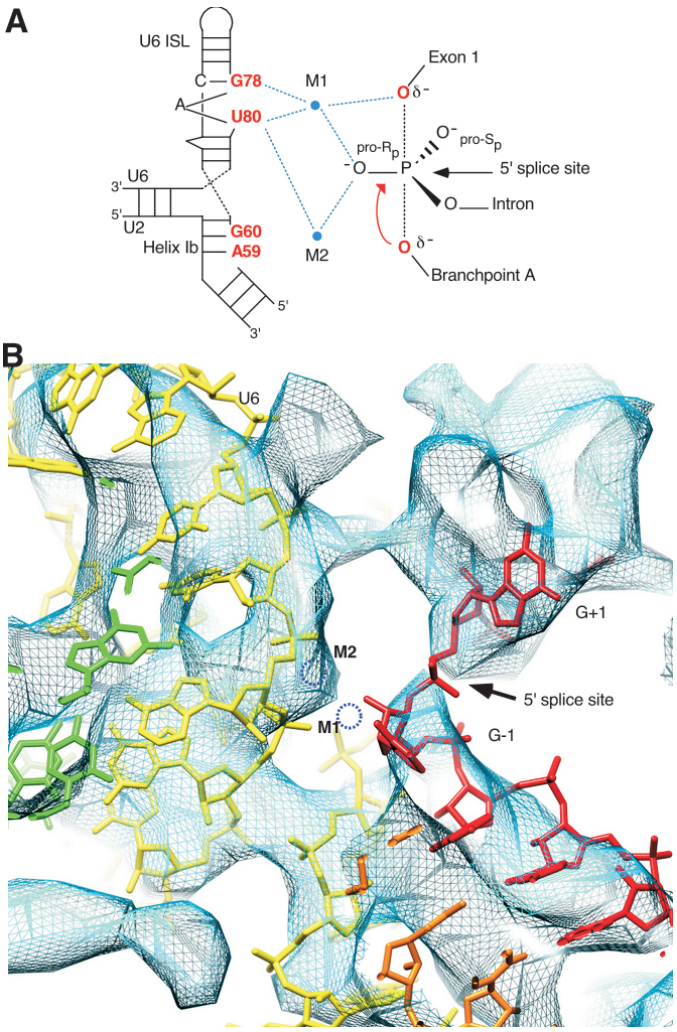



**Fig. S7**

**Putative location of the two catalytic metal ions in the B$^{act}$ complex.** (**A**) Constellation of the catalytic metals for step one of pre-mRNA splicing. The diagram is adapted from (*24*). The scissile phosphate of the pre-mRNA is shown as a pentacovalent transition state and the blue dashed lines depict the coordinations of oxygens directly involved in the reaction (red). M2 is further coordinated by A59 and G60. (**B**) Model of the catalytic RNA-RNA network in the experimental EM map, where U2 snRNA is shown in green, U6 snRNA in yellow, and the pre-mRNA in red. The putative position of the catalytic metal ions are shown as stippled blue circles (see also text).

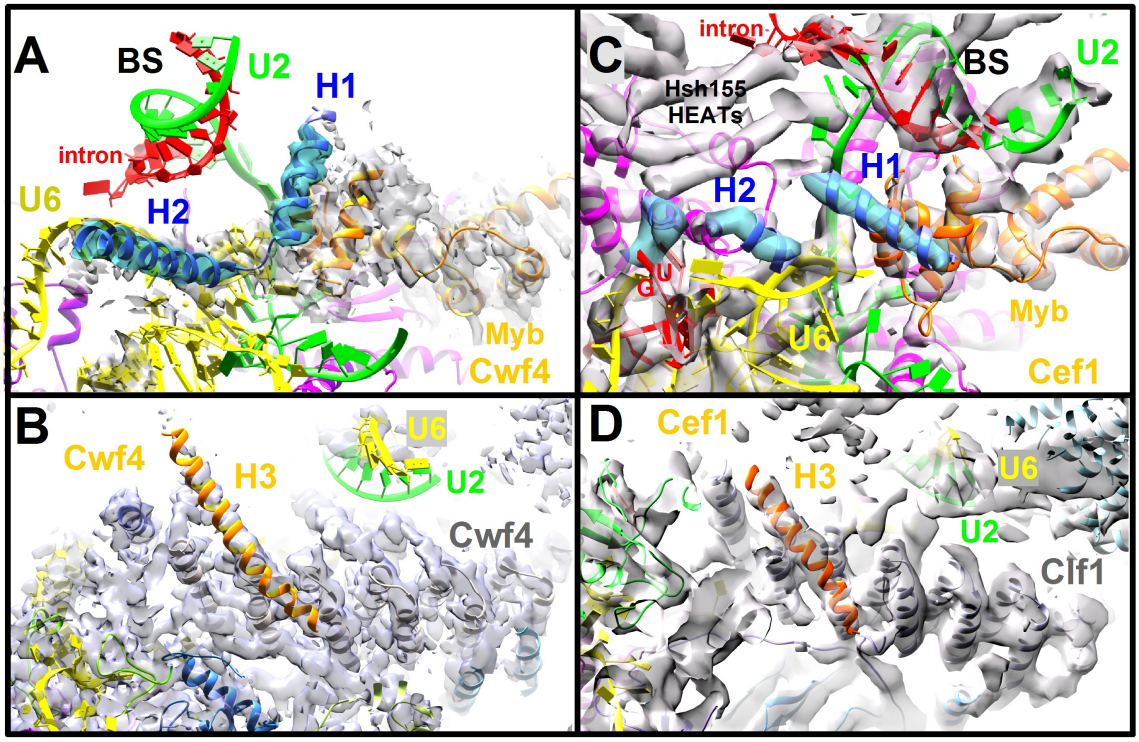



**Fig. S8**

**Differential organization of the N-terminal region of Cef1 (Cdc5) in B$^{act}$ and ILS complexes.** Slices through the *S. pombe* ILS structure showing density elements of the Cryo-EM map (*10*), comprising the N-terminal region of the *S. pombe* Cdc5 protein (*S. cerevisiae* Cef1) including its Myb domains and the more C-terminally located α-helices H1 and H2 (**A**) and H3 (**B**). (**C, D**) Slices through the *S. cervisiae* B$^{act}$ structure showing density elements of the Cryo-EM map comprising the Cef1 Myb domains and the potentially rearranged α-helical elements corresponding to the Cdc5 helices H1 and H2, respectively, and, (**D**), the Cef1 α-helix H3 (corresponding to the *S. pombe* H3 α-helix). For better orientation, the positions of certain U2 and U6 RNA elements in the ILS and B$^{act}$ structures are also indicated in panels A to D. In the *S. cerevisiae* B$^{act}$ complex, the Cef1 Myb domains and α-helix H3 have nearly the same structure and position as in the ILS (see corresponding densities with orange helices shown in panels **A, B** and **C, D,**

respectively), consistent with protein crosslinks (Table S1). Densities for the *S. pombe* H1 and H2 α-helices are clearly missing at corresponding positions in $B^{act}$ (compare blue densities in panels A and C, respectively). One possibility is that both Cdc5 α-helices H1 and H2 are restructured in $B^{act}$ such that H1 is rotated by 110° and H2 corresponds to the kinked α-helical element in $B^{act}$, with its C-terminal part being situated in the density element close to the 5'ss, while the N-terminal part of the kinked helix remains close to the U6 snRNA turn. As an alternative explanation, the regions of Cef1 corresponding to the Cdc5 α-helices H1 and H2 are flexible in the $B^{act}$ structure (and therefore not visible in our EM map) and the density elements close to the 5'ss and the U6 turn, as well as the density element associated with the Myb domains in the $B^{act}$ structure may therefore comprise parts of one or more other proteins. Even if this were true, it does not, however, invalidate our major conclusion that the 5'ss is shielded via its close interaction with a protein element that hinders access of the BS adenosine to the 5'ss. Moreover, our data indicate that the N-terminal region of Cef1(Cdc5) restructures from the $B^{act}$ to ILS transition.

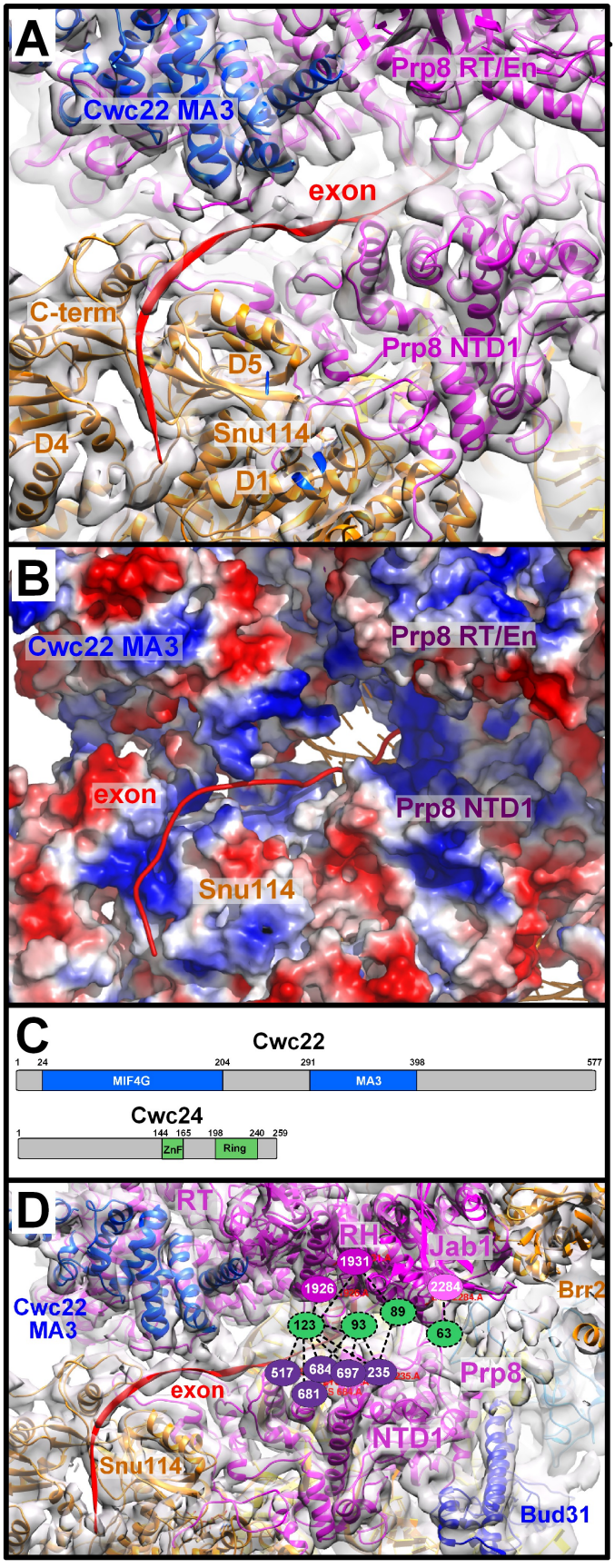

A
Prp8 RT/En
Cwc22 MA3
exon
C-term
Prp8 NTD1
D5
D4
Snu114
D1
B
Cwc22 MA3
Prp8 RT/En
exon
Prp8 NTD1
Snu114
C
Cwc22
1
24
204
291
398
577
MIF4G
MA3
Cwc24
1
144
165
198
240
259
ZnF
Ring
D
RT
RH
Jab1
1931
1926
2284
Brr2
Cwc22
MA3
89
123
93
63
517
684
697
235
Prp8
681
exon
NTD1
Snu114
Bud31

**Fig. S9**

**Crosslinking of Cwc24 to Prp8 domains close to the 5' exon binding channel.** (**A**) Path of the 5' exon binding channel in $B^{act}$ (as in Fig. 4A). (**B**) Electrostatic surface potential of the 5' exon binding channel. The RNA follows the basic patches (blue), whereas acidic patches (red) are avoided. (**C**) Domain structure of Cwc22 and Cwc24. (**D**) Crosslinks of Cwc24 to Prp8's NTD1, RH and Jab1 domains. The crosslinks indicate that the N-terminal region of Cwc24 is located centrally in the cleft between Prp8's RH and NTD1 domains, close to the 5' exon binding channel. Numbers indicate the positions of crosslinked lysine residues (connected by stippled lines) in each protein. Numbers in ovals without borders are residues in the modeled part of the protein, whereas those in ovals with stippled borders are residues within non modeled regions. The latter are arbitrarily placed close (less than 30 Å) to their crosslinking partners observed in our model.

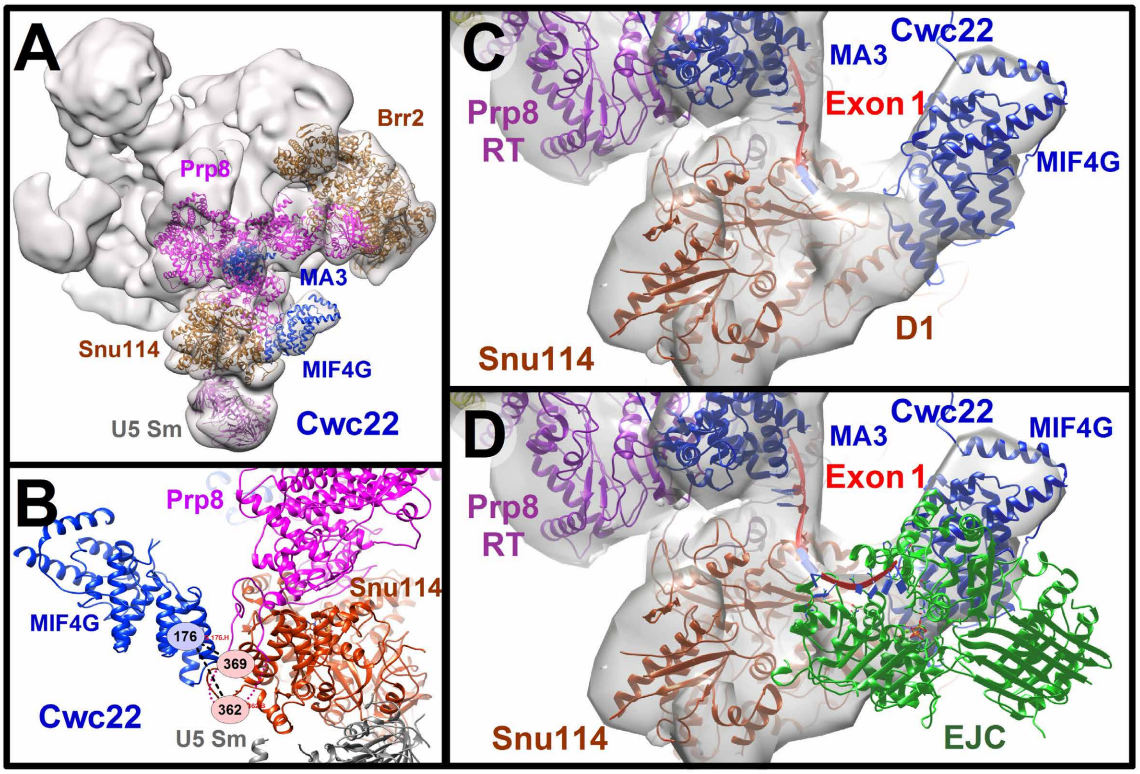



**Fig. S10**

**Position of the Cwc22-MIF4G domain and possible location of the exon junction complex in subsequently formed spliceosomes.** (**A**) Back view of the low resolution $B^{act}$ model with the placement of U5 proteins and Cwc22's MA3 and MIF4G domains. (**B**) Crosslinks between the Cwc22's MIF4G domain and Snu114. Lysine residues 362 and 369 are located in the region of Snu114's D1 domain, which is encircled by the lasso-like protrusion of Prp8's NTD1 domain (*10*). (**C**) Close-up view of the fit of Cwc22's MIF4G domain into the density element close to Snu114's D1 domain, as observed in the low resolution $B^{act}$ model. (**D**) Putative location of the EJC in the spliceosome. The crystal structure used to place Cwc22 contains an EIF4G molecule with its two RecA domains (PDB 4c9b; see Table S2). To determine the putative location of an EJC in the spliceosome, the RecA2 domain of EIF4G from that structure was

superimposed with the RecA2 domain of the EIF4G contained in the EJC structure (PDB codes 2joq and 2jos). The small piece of RNA contained in the EJC structure (red arrow) would be close to the exon channel and has the correct polarity. We note that this is a model for the location of the EJC in spliceosomes from those organisms having an EJC, and that yeast *S. cerevisiae* does not belong to this group. In addition, the EJC is stably recruited to the spliceosme after the first step of splicing as shown for the human spliceosome (*65*).

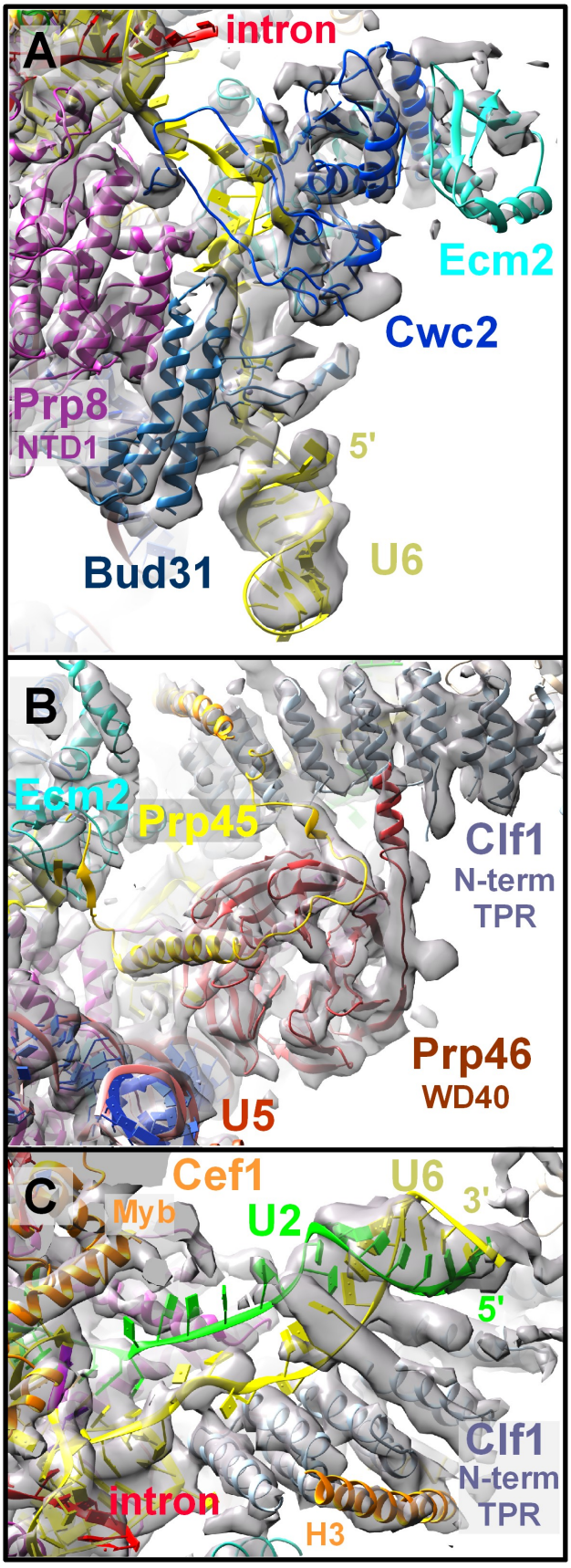

A
intron
Ecm2
Cwc2
Prp8
NTD1
5'
Bud31
U6
B
Ecm2
Prp45
Clf1
N-term
TPR
Prp46
WD40
U5
C
Cef1
Myb
U6
3'
U2
5'
Clf1
N-term
TPR
intron
H3

**Fig. S11**

**Structure and location of the 5'- and 3'-terminal parts of U6 snRNA and the proteins with which they interact.** (**A**) Fit of Cwc2, Ecm2 and Bud31 in the EM density map. All three proteins are in close contact with the 5'-terminal stem-loop (SL) of U6 snRNA. (**B**) The N-terminal TPR repeats of Clf1 and the WD40 domain of Prp46 fit into a pocket formed by the ISL loop of U6 snRNA and stem I of the U5 snRNA in $B^{act}$ as also found in the *S. pombe* ILS. (**C**) Cef1 (Cdc5) α-helix 3 (H3) is located next to the N-terminal TPRs of Clf1 in an almost identical position as in the *S. pombe* ILS, consistent protein crosslinking (Table S2 and Fig. S12B).

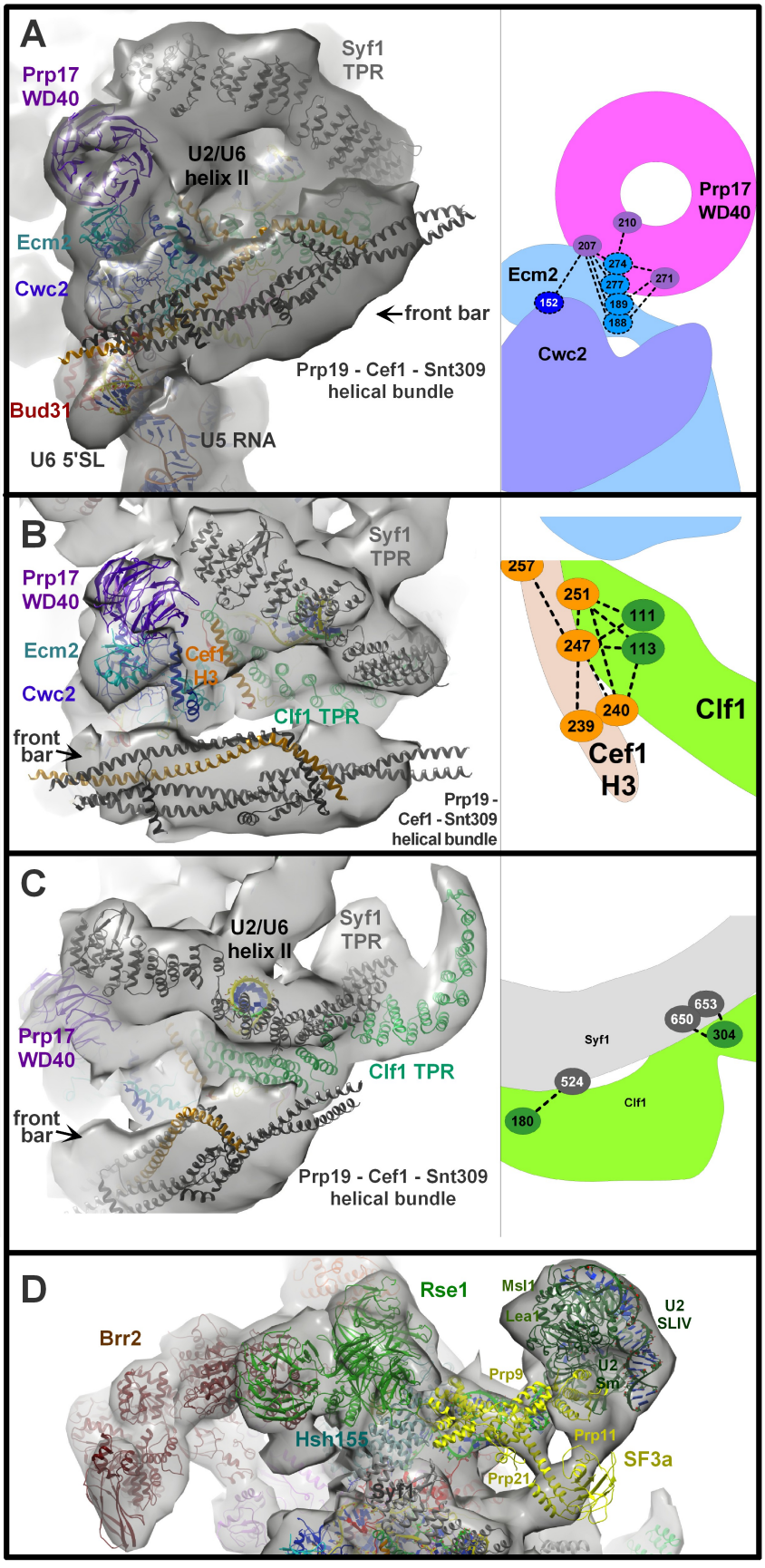

A
Prp17
WD40
Syf1
TPR
U2/U6
helix II
Ecm2
Cwc2
front bar
Prp19 - Cef1 - Snt309
helical bundle
Bud31
U5 RNA
U6 5'SL
Prp17
WD40
210
207
274
271
277
189
188
Ecm2
152
Cwc2
B
Syf1
TPR
Prp17
WD40
Ecm2
Cef1
H3
Cwc2
Clf1 TPR
front
bar
Prp19 -
Cef1 - Snt309
helical bundle
257
251
111
247
113
240
239
Clf1
Cef1
H3
C
U2/U6
helix II
Syf1
TPR
Prp17
WD40
Clf1 TPR
front
bar
Prp19 - Cef1 - Snt309
helical bundle
653
650
304
Syf1
524
Clf1
180
D
Rse1
Msl1
Lea1
U2
SLIV
Brr2
Prp9
U2
Sm
Prp11
Hsh155
SF3a
Prp21
Syf1

**Fig. S12**

**Location and crosslinks of Prp17-WD40 domain, NTC proteins and U2 components in the $B^{act}$ complex.** (**A**) Front view of the low resolution $B^{act}$ model and location of the Prp17-WD40 domain above Ecm2. In the 3D reconstruction of the $B^{act}$ complex generated without masking, the course of the N-terminal TPR repeats of Syf1, connected with structural elements of Cwc2 and Prp17-WD40, can be identified clearly. Right: intermolecular crosslinks between the Prp17-WD40 domain and Ecm2 and Cwc2. The numbers indicate the positions of crosslinked lysine residues in the three proteins. (**B**) Top view of the low resolution $B^{act}$ model and location of the Clf1 TPR repeats and Cef1 (Cdc5) helix3 (H3) (see Table S1). A density element lying perpendicular to the central part of the main body in the front view is sized suitably to accommodate the helical-bundle domain with the Prp19 core (Prp19-Cef1-Snt309 bar). Right: intermolecular crosslinks between the Clf1 TPRs and Cef1 H3. (**C**) Front view of the $B^{act}$ complex showing the long, curved TPR repeats of Syf1 and Clf1, which cross one another and together form a basket-like structural element as shown in the upper part of the *S. pombe* ILS (*10*). Much of the mass of the *S. pombe* proteins can be fit as rigid bodies into the corresponding density regions in the $B^{act}$ spliceosome. Some local adaptations were necessary, but the curvature of the repeats and also the cross-over points are organised in a similar way in the $B^{act}$ complex and the *S. pombe* ILS. As the density of the TPR repeats of Clf1 and Syf1 in the 5.8 Å $B^{act}$ structure breaks off abruptly, this only becomes clear when one also takes into account the non-masked spliceosome model and intermolecular crosslinks that are found between Clf1 and the Syf1 TPRs, as shown on the right. (**D**) Top view of the low resolution $B^{act}$ model and density elements in $B^{act}$ attributed to the U2 Sm core RNP and part of the SF3a protein complex. Within the

density region that was identified at high resolution by masking, the last reliably fit element is stem-loop IIa of the U2 snRNA. In $B^{act}$, this element is connected to a very large density region that is structurally less stable and was masked out to obtain the high resolution structure. The non-masked 3D reconstruction shows that this region has a very large globular structure, bridged to the U2-SF3b complex and the NTC region containing Syf1 and Clf1. Its position with respect to the U2 stem-loop IIa and the SF3b proteins – and also its very large size – indicate that it contains the large 3'-terminal components of U2 snRNP: the U2 Sm ring with the proteins Lea1 und Msl1 associated with stem-loop IV (SLIV). A main connection is likely provided between the 3' terminal U2 snRNP domain and the top domain of $B^{act}$ through the SF3a protein complex. The low resolution in this region prevents exact localization, despite the availability of the crystal structure of the SF3a core complex (*66*).

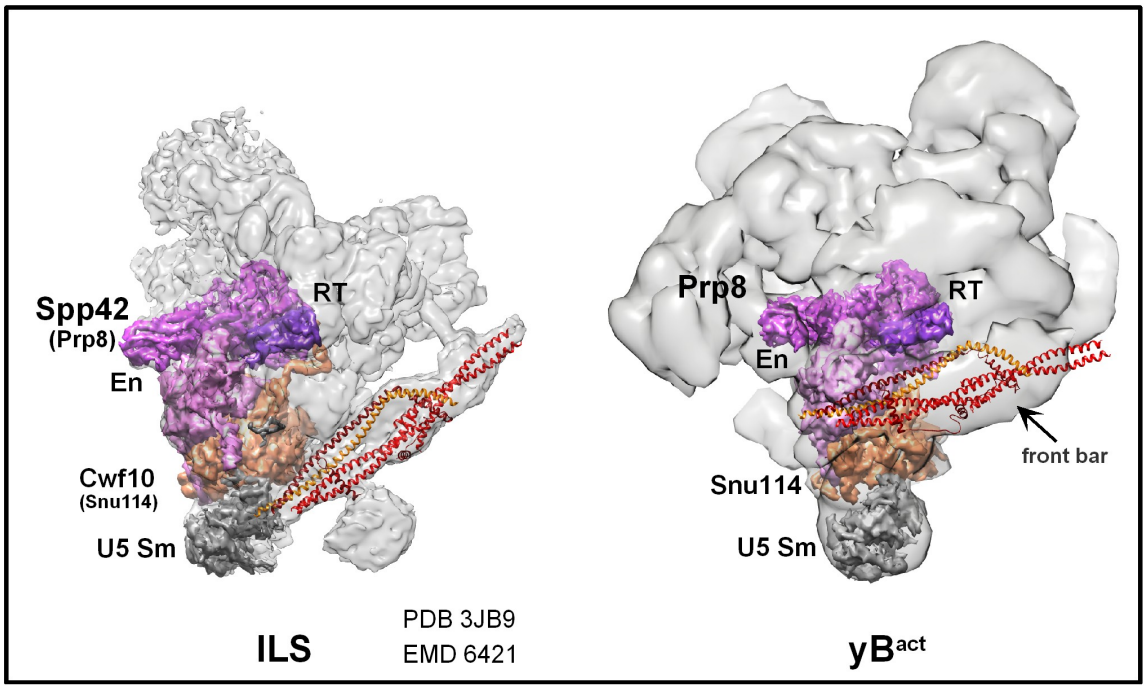



**Fig. S13**

**Prp19's helical bundle is differentially orientated in $B^{act}$ versus the ILS.** EM density maps of the *S. pombe* ILS (EMD 6421) and *S. cerevisiae* $B^{act}$ complexes (front view of the low resolution $B^{act}$ model) with the U5 snRNP proteins Prp8 (purple), Snu114 (orange) and Sm core (grey) indicated. The positions of the U5 snRNP proteins and their structural organisation share many similarities in both spliceosomal complexes. In the *S. pombe* spliceosome the coiled-coil elements of the four copies of Prp19 (red), together with Snt309 (dark purple) and the C-terminal region of Cef1 (Cdc5; dark orange), form a helical bundle that runs, as a self-contained arm II domain, parallel to the main body of the *S. pombe* spliceosome and is only bound to it by thin structural elements (*10*). There is no density at this corresponding position in the $B^{act}$ complex that would correspond to that in the *S. pombe* spliceosome – either in the 5.8 Å model or in the non-masked low resolution $B^{act}$ model shown here. Rather, in the latter model there is a density element that lies orthogonal to the central part of the main body in the front view (called front bar

in Fig. 1A) and is suitably sized to accommodate the helical-bundle domain with the Prp19 core. The non-masked model of $B^{act}$ was aligned by using the U5 proteins with the structure of the *S. pombe* ILS, and the position of the Prp19 helical bundle was deduced.

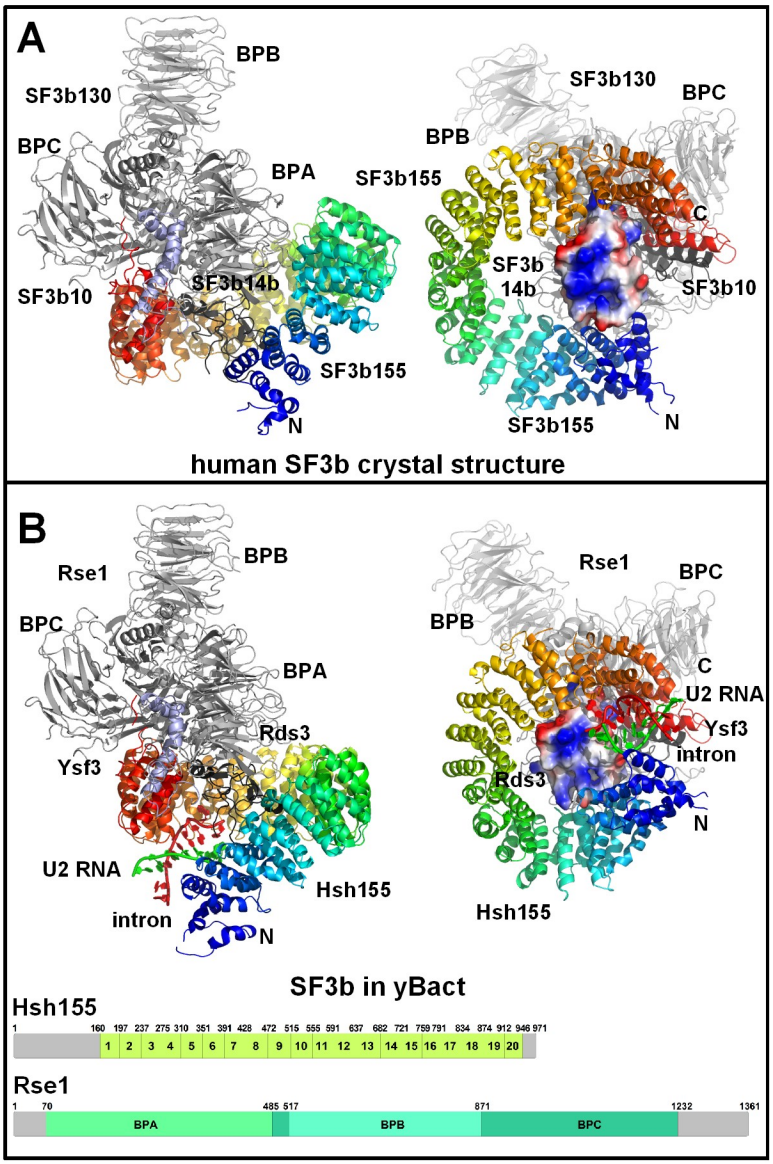



**Fig. S14**

**Structure of the yeast SF3b core complex in the B$^{act}$ spliceosome and in the crystal structure of a protease-resistant human SF3b core complex.** Ribbon representation of SF3b proteins in (**A**) the crystal structure of the human SF3b core complex comprised of SF3B155's entire C-terminal HEAT repeat domain, SF3b130 (yeast Rse1) and the small proteins SF3b14 (yeast Rds3) and SF3b10 (yeast Ysf3) (*37*) and (**B**) in the B$^{act}$ complex. Left: side views, right: bottom views. SF3b14 (yeast Rds3) is shown in blue in a space

filling model in the middle of the structure. Superposition of the HEAT domains from the two orthologs shows that the N-terminal H1–H5 and C-terminal H16–H20 regions are restructured versus the central H6–H15 region. In this way, HEAT repeats H1 and H19 come to lie almost on top of each other and with the distance between them shortened from 24 Å (in the crystal structure) to 18 Å (in $B^{act}$). Given that the isolated yeast SF3b complex has a similar structure, this suggests that the Hsh155 HEAT repeats are restructured after incorporation of SF3b into the spliceosome. SF3b130's (yeast Rse1) three β propeller (WD40) clusters (BPA+ BPB +BPC) are also indicated. An RNA density element consisting of the U2/BS RNA helix is located in the opening between the terminal HEAT repeats of Hsh155 in the $B^{act}$ structure (see below).

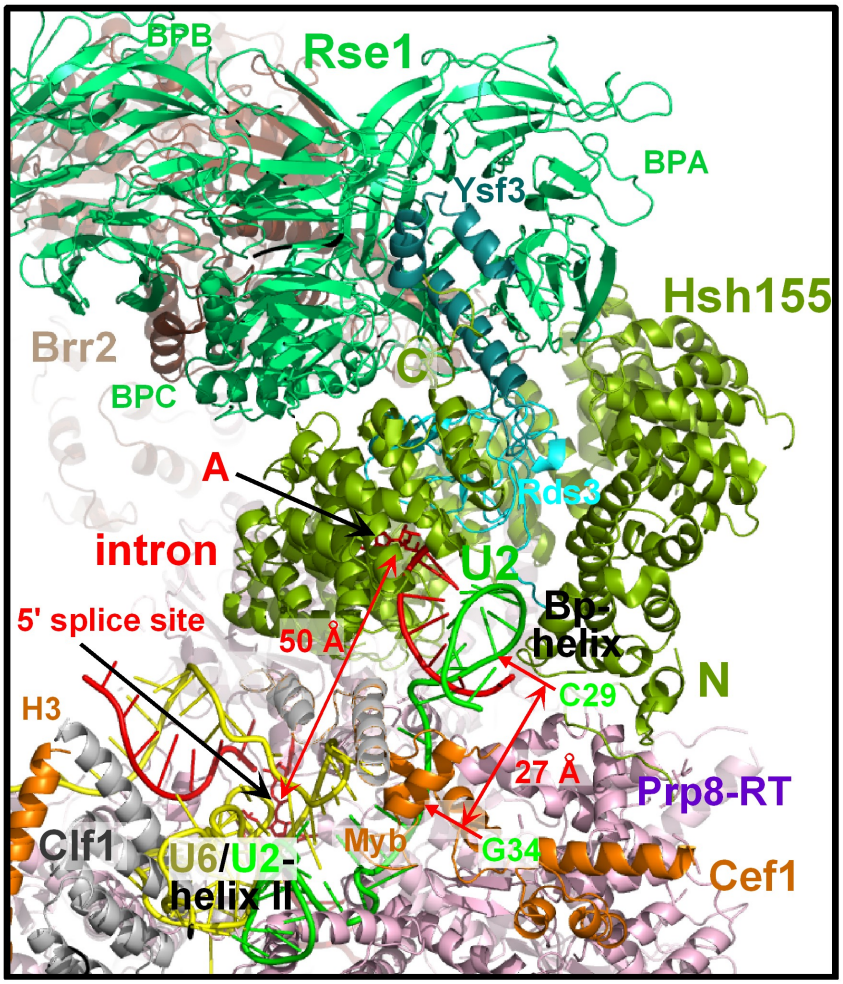



**Fig. S15**

**Location of the U2/BS RNA helix, Hsh155 and the 5' splice site.** The U2/BS RNA helix is located between the terminal HEAT repeats of Hsh155 and the BS adenosine is spatially separated from the scissile bond of the 5'ss by 50 Å. The 5' terminal nucleotides of U2 of the U2/BS helix (U2-C29) is spatially separated from the 3' terminal U2 nucleotides of U2/U6 helix Ia (U2-G34) by 27Å.

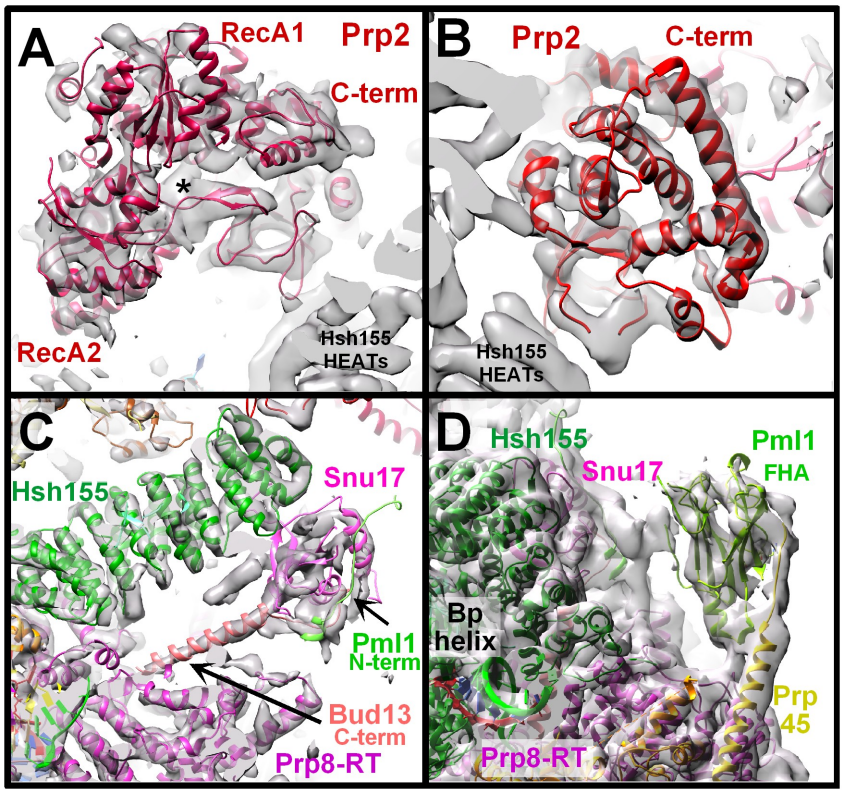



**Fig. S16**

**Location of the Prp2 RNA helicase and the RES proteins.** (**A**) Close-up view of the fit of the Prp2 RecA domains, into the Prp2 density associated with Hsh155's HEAT domain (see also Fig. 6A) in the $B^{act}$ model. The asterisk indicates unassigned density likely to be occupied by parts of Spp2. (**B**) Close-up view of the fit of Prp2's C-terminal domain, including its OB-fold domain, into the corresponding Prp2 density of the $B^{act}$ model. (**C**) Expanded view of the $B^{act}$ steep slope (see Fig. 1A), showing the fit of Hsh155's HEAT repeats, Snu17's RRM and the C-terminal region of Bud13 into the corresponding densities. The Bud13 C-terminal helix occupies a density tube that continues further down to Prp8-RT/En. Two crosslinks of Snu17 to HEAT repeats 7 and 8 of Hsh155 support its location and the orientation of this central part of the RES

complex (Table S1). (**D**) Pml1's N-terminal FHA (forkhead-associated) domain forms a bridge between Snu17 and the C terminus of the Prp8-RT-associated Prp45 helix.

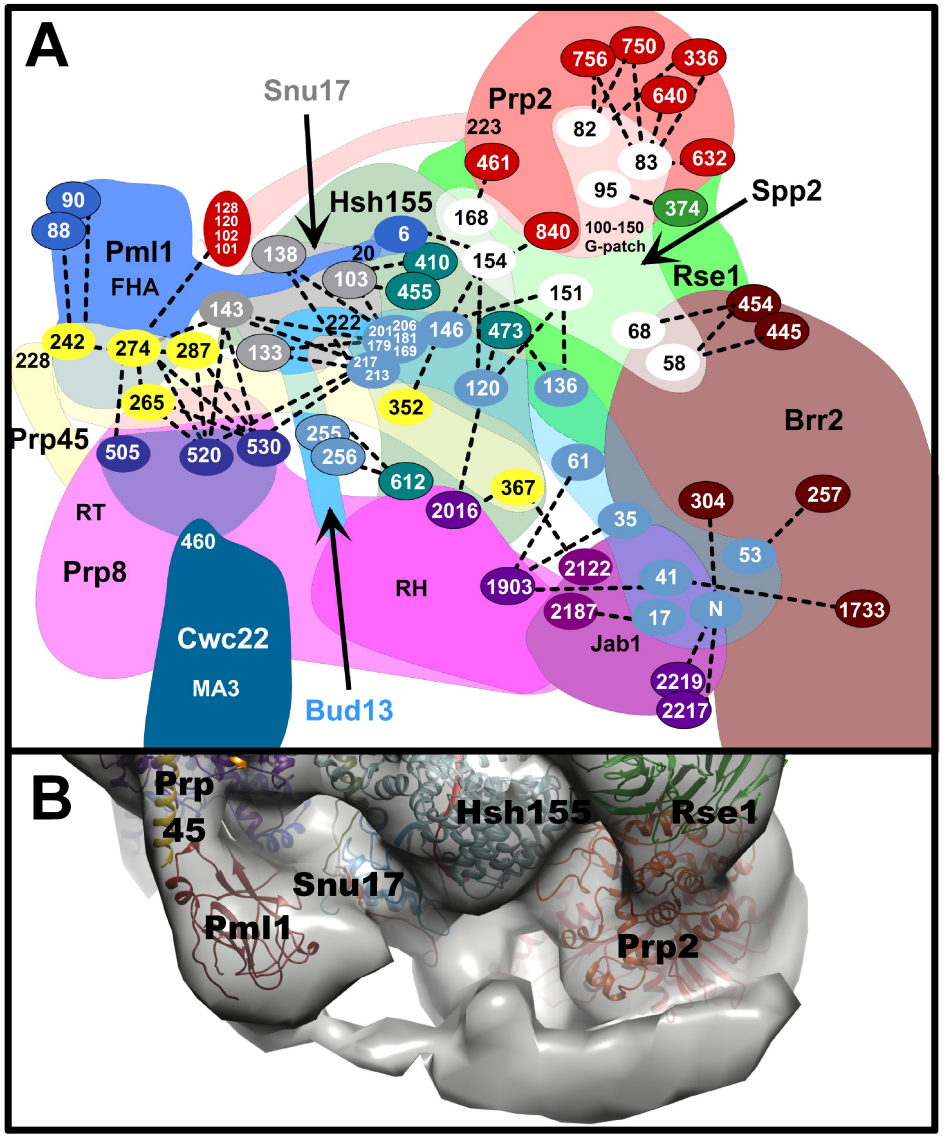



**Fig. S17**

**Intermolecular crosslinks support the juxtaposition of Spp2 with Prp2 and the RES complex, and suggest the position of the C-terminal parts of Cwc22 and Prp45.** (**A**) Schematic diagram of the back of the front view of the $B^{act}$ complex (see Figure 1A). Intermolecular crosslinks between the protein domains are shown. Numbers indicate the positions of crosslinked lysine residues (connected by stippled lines) in each protein. Numbers in ovals with black borders indicate the residues in the modeled parts of the proteins, whereas those in ovals without borders are residues within non-modeled

regions. The latter are arbitrarily placed close (less than 30 Å) to their crosslinking partners observed in our model. Numbers without ovals represent the terminal residues of protein regions modeled in the high resolution $B^{act}$ structure. Red ovals represent Prp2 residues, white – Spp2, green – Rse1, turquoise – Hsh155, brown – Brr2, violet – Prp8, purple – Cwc22, yellow – Prp45, blue – Pml1, light blue – Bud13 and grey – Snu17. Tentative localization of the non-modeled regions of a given protein is indicated by semi-transparent coloring. Although projected onto the plane of the paper, the positions in space of the crosslinked lysines correspond to their positions in the 3D structures of their respective protein domains. The maximum observed length for any crosslink was less than 30 Å. (**B**) Top view shows unassigned regions of the unmasked EM density likely to be occupied by flexible parts of RES, Spp2, Prp2, Hsh155, Cwc22 and Prp45 proteins not resolved in 5.8 Å EM map. Prp45 appears to play a role in stabilizing the various protein-protein interactions.

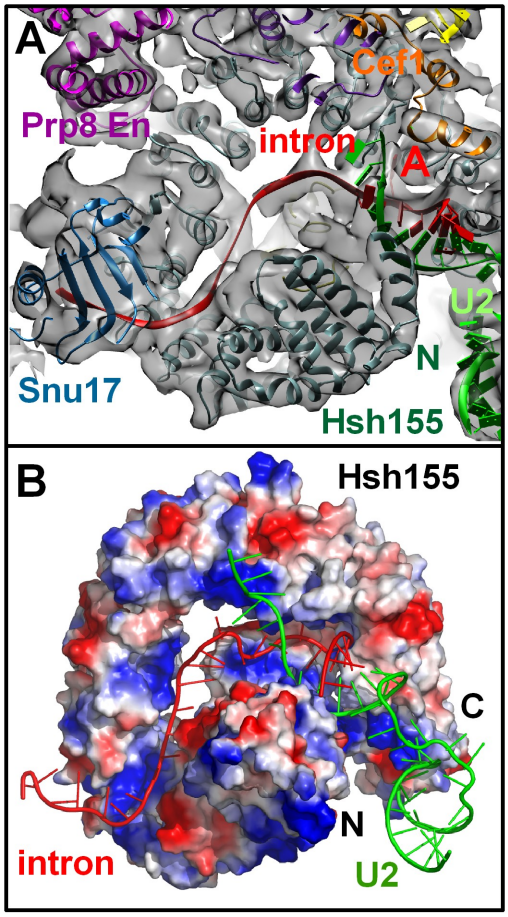



**Fig. S18**

**Path of the intron's 3' end across the Hsh155 HEAT domain in the yeast $B^{act}$ complex. (A)** Path of the intron across the Hsh155 HEAT repeat spiral. Clear densities are present for the intron just after the branch site and Hsh155 HEAT repeat H6 on the opposite site. The density for the central nucleotides of the BS-3'SS region of actin pre-mRNA (UCCGAUU) is not well resolved and thus the placement is ambiguous. **(B)** The electrostatic surface potential of the Hsh155 HEAT domain with the path of the intron's 3' end (red). The RNA lies in a basic channel (blue), well-separated from the red acidic patches. Upon exiting the ring, the RNA passes through a clamp-like structure (bottom left).

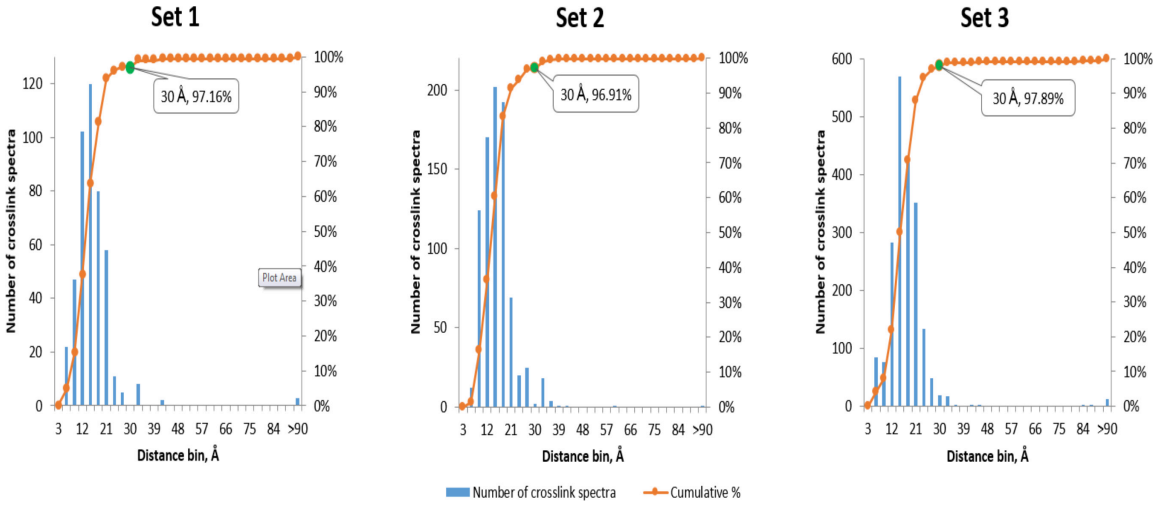



**Fig. S19**

**Distribution of the Cα-Cα distances between BS3-crosslinked residues.** The Euclidian distances were measured in the 5.8 Å model of the yeast $B^{act}$ complex using PyMOL (http://www.pymol.org). More than 95% of all crosslink-assigned spectra correspond to crosslink distances of 30 Å or less.

**Movie S1**
Hsh155 – SF3b HEAT domain transformation

**Movie S2**
y$B^{act}$ rotation

**Table S1.**

**Protein and model building information for all modeled yeast $B^{act}$ proteins**. Protein names, their molecular weight and detailed information about the model building process are provided.

**Table S2.**

**BS3-crosslinks of proteins in the yeast $B^{act}$ complex**. Statistics (Spectral Counts and $Score_{max}$) of the CX-MS data for the proteins of the purified yeast $B^{act}$. “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 methionine residue. Euclidian C**α**-C**α** distances between crosslinked residues are given in Ångström (column "**Å**"). The Table includes crosslinks of all proteins of the $B^{act}$ complex, even if they were not observed/modeled into the EM density.

**Table S3.**
**MolProbity validation of the final RNA model of the yeast $B^{act}$ complex.** For the clash score, a percentile is given with the $100^{th}$ percentile being the best structure among structures of comparable resolution (N=1784, all resolutions).

**Table S1: Positioning of proteins in the cryo-EM structure model of *S. cerevisiae* $B^{act}$**

| Protein | Domain | Positioning |
|---|---|---|
| | | |
| Prp8<br>279.5 kDa<br>2413 aa | NTD1<br>131-737 | The *S. cerevisiae* NTD1 structure (PDB 5GAN), determined as part of the cryo-EM investigation of the *S. cerevisiae* (S.c.) tri-snRNP (*13*) was used for rigid-body fitting followed by refinement with the COOT program (*62*). The position and structure of NTD1 in $B^{act}$ are similar to those observed in the human (*16*) and S.c. tri-snRNP (*13-15*) and the ILS (*10*). |
| | NTD2<br>738-872 | The model of the orthologous *S. pombe* (S.p.) structure (PDB 3JB9) determined by cryo-EM of the S.p. ILS complex (*10*) was used for rigid-body fitting followed by refinement with COOT. The linker between NTD1 and NTD2 was reconstructed with COOT. The position and structure of NTD2 in $B^{act}$ are equivalent to those in the ILS (*10*). |
| | RT/En<br>873-1838 | The RT/En structure (PDB 5GAN) determined by cryo-EM of the S.c. tri-snRNP (*13*) was used for rigid-body fitting followed by refinement with COOT. Several loops (1039–1043, 1201–1213, 1375–1385, 1402–1427,1614–1623) were manually adjusted or rebuilt. RT/En position and structure in $B^{act}$ are similar, but not identical, to those in the ILS (*10*). |
| | RH<br>1839-<br>2078 | The RH structure (PDB 5GAN) determined by cryo-EM of the S.c. tri-snRNP (*13*) was used for rigid-body fitting followed by refinement with COOT. The loops 1831–1839 and 1858–1874 were adjusted or rebuilt manually. The position of RH in $B^{act}$ is different from those observed in the human (*16*) and S.c. tri-snRNP (*13, 15*) and the ILS (*10*). |
| | Jab1<br>2148-<br>2398 | The Jab1-Brr2 complex of the S.c. structure (PDB 5DCA) determined by X-ray analysis of the co-crystal with Brr2 (*19*)was used for rigid-body fitting followed by refinement with COOT. |
| Snu114<br>114.0 kDa<br>1008 aa | D1<br>111–460 | The Snu114 structure (PDB 5GAN) determined by cryo-EM of the S.c. tri-snRNP (*13*) was used for rigid-body fitting followed by refinement with COOT. The Snu114 position and structure in $B^{act}$ are equivalent to those of the human (*16*) and S.c. tri-snRNP (*13, 15*) and the ILS (*10*). |
| | D2<br>461–598 | |
| | D3<br>599–676 | |
| | D4<br>677–852 | |
| | D5<br>853–941 | |
| | C-term<br>942–998 | |
| Brr2<br>246.1 kDa<br>2163 aa | NC-CC<br>453-2163 | For rigid-body fitting of the two helicase cassettes, the structure of the Jab1-Brr2 complex of S.c. (PDB 5DCA) was used (*19*) followed by refinement with COOT. The position of Brr2 in $B^{act}$ is very different from the corresponding position in the human tri-snRNP (*16*), and Brr2 is differently bound and oriented compared with the S.c. tri-snRNP (*13, 15*). |
| | PWI<br>284-294 | For rigid-body fitting of the PWI domain, the Jab1-Brr2 co-crystal (*67*) (PDB 5DCA) was used. The domain was fitted into a density on top of the NC cassette close to the Prp8-Jab1 domain, and this was followed by refinement with COOT. The position of PWI in the $B^{act}$ complex is different from, but close to, the position found in the Brr2-Jab1 crystal structure and in the human tri-snRNP (*16*). |
| | NHD<br>115-191 | To identify the position of the small NHD domain, its position in the human tri-snRNP (PDB 3JCR) relative to the easily locatable Brr2 NC-CC cassettes was used. The density for the NHD domain is well-defined and fits well with the protein's 3D structure; it places the NHD in $B^{act}$ in a location and orientation relative to NC-CC that are similar to the corresponding location and orientation found in the human tri-snRNP. The S.c. structure of NHD |

| | | |
|---|---|---|
| | | (PDB 5DCA) determined by X-ray analysis of a co-crystal with Brr2 (*19*) and modified according the conformation in the human tri-snRNP was used for fitting. |
| U5-Sm | Sm domains of SmB, SmD1, SmD2, SmD3, SmE, SmF, SmG | For rigid-body fitting of the U5-Sm, its structure determined by cryo-EM of the S.c. tri-snRNP (PDB 5GAN) (*13*) was used. The U5-Sm position in $B^{act}$ is equivalent to that of the human (*16*) and S.c. tri-snRNP (*13, 15*) and the ILS (*10*). |
| Cwc2<br>38.4 kDa<br>339 aa | | For rigid body fitting the orthologous S.p. structure (PDB 3JB9) determined by cryo-EM of the ILS complex (*10*) was used, followed by refinement with COOT. The Cwc2 position is equivalent to the one in the ILS (*10*). |
| Ecm2<br>40.9 kDa<br>364 aa | 8–284 | For rigid-body fitting the orthologous model of the S.p. structure (PDB 3JB9) as determined by cryo-EM of the ILS complex (*10*) was used; this was followed by refinement with COOT. The position of Ecm2 is equivalent to its position in the ILS (*10*). For refinement COOT was used. |
| Bud31<br>18.4 kDa<br>157 aa | 17–154 | For rigid-body fitting of Bud31, the S.c. structure (2MY1) determined by crystallography (*68*) was used; this was followed by refinement with COOT. The position of Bud31 in $B^{act}$ is equivalent to its position in the ILS (*10*). |
| Prp17<br>52 kDa<br>455 aa | WD40<br>150–455 | A structural model of the WD40 domain was produced by using the Robetta server. It was placed in such a way into a poorly resolved density of the non-masked low-resolution structure, just above Cwc2 und Ecm2, so that the observed crosslinks with Cwc2 and Ecm2 would be possible. Although exact positioning was not possible, the principal orientation is determined by the crosslinks (see Fig. S12). In the S.p. ILS structure (*10*) the only part of Prp17 identified was a helical N-terminal region not conserved in the S.c. sequence. |
| Prp45(*69*)<br>42.5 kDa<br>379 aa | 31–235 | An orthologous model of the S.p. structure (PDB 3JB9) as determined by cryo-EM of the ILS complex (*10*) was used for rigid-body fitting followed by refinement with COOT. Well-fitting densities for the helical and β-sheet regions were found in the $B^{act}$ structure at positions equivalent to those found in the ILS. The fitted structure ends C-terminally, with a helix tightly attached to the RT end of the Prp8-RT/En domain. The remaining C terminus, which is not present in the ILS model (*10*), on the basis of evidence from crosslinks (see Fig. S17), runs around the back side of the $B^{act}$ complex, passing the RES-complex proteins, and reaches the vicinity of the RH and Jab1 domains of Prp8. A short stretch (229–236) was modeled into a thin thread of density running along the Pml1-FHA domain. |
| Prp46(*69*)<br>50.7 kDa<br>451 aa | WD40<br>107–446 | For rigid-body fitting, an orthologous model of the S.p. structure (PDB 3JB9) as determined by cryo-EM of the ILS complex (*10*) was used, followed by refinement with COOT. The position of Prp46-WD40 is equivalent to its position in the ILS. |
| Cef1<br>67.7 kDa<br>590 aa | tandem Myb<br>12–110 | For rigid-body fitting an orthologous model of the S.p. structure (PDB 3JB9) as determined by cryo-EM of the ILS complex (*10*) was used; this was followed by refinement with COOT. The position of Cef1-Myb is equivalent to its position in the ILS. |

| | | |
|---|---|---|
| | H1<br>143–160<br>H2<br>164–185 | Densities as observed for the *S. pombe* H1 and H2 α-helices are clearly missing in $B^{act}$ and may be restructured instead into a H1 helix rotated by 110 ° and a kinked α-helix (Fig. S8). The C-terminal part of the latter would be situated in a density close to the 5'ss, the N-terminal part instead would remain close to the U6 snRNA turn. However, it cannot be excluded that the parts of Cef1 corresponding to the S. pombe H1 and H2 helices are not visible in the EM map due to high flexibility. Although the conclusion that the 5'ss is clearly shielded by protein elements can be drawn, an unambiguous assignment to a specific protein is not possible. |
| | H3<br>230–259 | In the ILS upstream of H2 a straight, 34-aa-long helix of unknown sequence is positioned on the loop side of the N-terminal Clf1/Syf3 TPRs. In the $B^{act}$ complex a density rod at a similar position, but of shorter length, is also present above the Clf1/Syf3 N-terminal TPRs. Modeling by the Robetta server revealed a long helix downstream of H2. The Clf1/Syf3 internal crosslinks support the presence of a helix between amino acids 230 and 259 (Fig. S12) and the helix model of this stretch fits perfectly into the density rod. Crosslinks to the Clf1 TPR support not only the helix placement but also its orientation with the N terminus to the outside and its C terminus pointing to the catalytic center, as observed in the ILS model. Refinement was performed with COOT. |
| | C-helix<br>500–590 | An orthologous model of the S.p. structure (PDB 3JB9) as determined by cryo-EM of the ILS complex (*10*) was used to model the helical bundle that the C-terminal helix of Cef1/Cdc5 forms with helices of Prp19 and Snt309. The helical bundle fits into the elongated density bar of the front view. This density is present only in the non-masked lower-resolution structure, and an exact placement is not possible. |
| Prp19<br>56.5 kDa<br>503 aa | HD<br>76–140 | An orthologous model of the S.p. structure (PDB 3JB9) as determined by cryo-EM of the ILS complex (*10*) was used to model the helical bundle that four copies of the Prp19 helical domain (HD) form with helices of Cef1/Cdc5 and Snt309. The helical bundle was placed as described above (Cef1/Cdc5, C helix). |
| Snt309<br>20.7 kDa<br>175 aa | 1–175 | An orthologous model of the S.p. structure (PDB 3JB9) as determined by cryo-EM of the ILS complex (*10*) was used to model the helical bundle that Snt309 forms with helices of Cef1/Cdc5 and Prp19. The helical bundle was placed as described above (Cef1/Cdc5, C helix). |
| Syf1<br>100.2 kDa<br>859 aa | TPR<br>393–654 | For modeling the TPR domain of S.c. protein Syf1, the sequence of the human orthologue Xab2 was used to produce a first model with the Robetta server. Xab2 was used because in the S.c. sequence an S.c.-specific insert (170–216) prevents TPR continuity. The Xab2 model was then bent to fit into the non-masked $B^{act}$ density that resembles the Cwcf3/Syf1 density of the S.p. ILS. From the Xab2 structure the S.c. orthologue model was then built. The ILS model of the Cwf3/Syf1 protein covers only a short stretch of sequence (homologous to the S.c. Syf1 sequence position 498–734). From this stretch an orthologous model was created and used to replace the corresponding stretch in the model built with Xab2. A short region (393–654) of Syf1 passes through a density of the masked high-resolution $B^{act}$ structure. Here, the TPRs show excellent fit with TPR-typical densities. Refinement was performed with COOT. |
| Clf1/Syf3<br>82.4 kDa<br>687 aa | TPR<br>39–272 | In the S.p. ILS model (*10*) only for the N-terminal Cwf4/Clf1 TPRs was the sequence (homologous to the S.c. Clf1 sequence 36–291) provided. An orthologous S.c. model was generated and could be fitted with only slight adjustments into TPR-typical densities of the high-resolution $B^{act}$ structure. In the $B^{act}$, the positioning of the N-terminal TPR close to the catalytic center corresponds to the position in the ILS model. For the remaining C-terminal TPRs no high-resolution density is present in the masked structure; density is |

| | | |
|---|---|---|
| | | only found in the lower-resolution structure obtained without application of a mask. For these C-terminal Clf1 TPRs, a model produced by the Robetta server was used; the model was fitted by bending it into the density corresponding to a similar density region in the ILS structure. Crosslinks between Syf1 and Clf1 TPRs (Fig. S12) verify this ILS-based arrangement of the Syf1 and Clf1 TPRs. COOT refinement was applied in areas with sufficient resolution. |
| Cwc22<br>67.3 kDa<br>577 aa | MIF4G<br>11–263 | Using the structure of this domain in the human Cwc22 orthologue (PDB 4C9B), determined by X-ray analysis of the co-crystal with eIF4AIII (*33*), an orthologous model was produced and fitted into a prominent density of the non-masked, low-resolution $B^{act}$ structure. This density protrudes obliquely out of the central main body and has exactly the shape of the MIF4G domain. One strong crosslink (K369 to K176 of Snu144) and a minor one (K362 to K176 of Snu114) verify the position and orientation of the MIF4G domain. The MIF4G is bound to the D1 domain of Snu114, where a lasso-like loop of the Prp8-NTD1 domain encircles a little protrusion of the D1 domain. The sequence region 425–430 of the NTD1 lasso seems to contribute to the Cwc22-MIF4G binding site. Refinement was performed with COOT. |
| | MA3<br>280–533 | A model of the region containing the MA3 domain was produced by the Robetta server and fitted with slight adjustments perfectly into a well-resolved density above the MIF4G domain. It is attached to the linker domain of Prp8-RT/En, with its N-terminal helix in contact with Prp8-RH and its C terminus close to the RES complex region. The extreme C-terminal region of Cwc22 could not be placed into a $B^{act}$ density, but a network of crosslinks places it in the RES complex region (see Fig. S17). |
| Cwc24<br>29.7 kDa<br>259 aa | 63–123 | Submission of the Cwc24 sequence to the Robetta server resulted in the separation of the small Cwc24 protein into several domains. N-terminal amino acids 93, 89 and 123 of Cwc24 form a network of crosslinks to the NTD1 and RH domains of Prp8 (see Fig. S9). Amino acid 63 crosslinks to the Jab1 domain of Prp8. In the high-resolution structure of $B^{act}$ we cannot discern a clear density, which could accommodate this region of the Cwc24 protein. |
| Hsh155<br>110.0 kDa<br>971 aa | HEAT repeats<br>126–960 | The structures of the four S.c. SF3b proteins were modeled according to the crystal structure of the human protease-treated SF3b complex consisting of SF3b155/Hsh155, SF3b130/Rse1, SF3b14b/Rds3 and SF3b10/Ysf3. In the S.c. $B^{act}$ structure well-resolved and well-defined densities are immediately visible for the Hsh155 HEAT repeats forming a spiral of parallel density rods and the Rse1 WD40 domains visible as three similar, protruding ring densities. The entire homology modeled S.c. SF3b complex docks easily into the $B^{act}$ density, but some significant adaptations are necessary. While the central (8–15) HEAT repeats can be docked as a rigid body, the N- and C-terminal repeats have to be moved upward and downward, respectively, and both need to be tilted inwards, thus narrowing the diameter of the spiral. As Rse1 is mainly connected to the C-terminal HEAT repeats it is positioned more sideward compared to the crystal structure. The small Ysf3 protein is part of the Hsh155-Rse1 binding region and its density is well recognizable in the $B^{act}$ structure. In the crystal structure the Rds3 protein has a central position within the Hsh155 spiral. In the equivalent position a well-defined density in the $B^{act}$ structure perfectly fits Rds3. All four protein structures were refined by using COOT. |
| Rse1<br>153.8 kDa<br>1361 aa | 3x WD40<br>56–1331 | |
| Rds3<br>12.3 kDa<br>107 aa | 6–95 | |
| Ysf3<br>10.0 kDa<br>85 aa | 5–73 | |
| U2-Sm | Sm domains of SmB, SmD1, | In the high-resolution structure of $B^{act}$ no other density element apart from the one at the bottom housing U5-Sm has the shape typical of the heptameric Sm ring. In the non-masked lower-resolution $B^{act}$ structure, however, such a density can be observed in the upper right corner of the front view; this density contributes to a large extent to the steep slope. In this density the U2- |

| | | |
|---|---|---|
| | SmD2,<br>SmD3,<br>SmE,<br>SmF,<br>SmG | Sm ring with the two bound U2-specific proteins Lea1 and Msl1 and the SLIV of U2RNA can be placed as the complex structure determined within the S.p. ILS (PDB 3JB9) by cryo-EM (*10*). |
| Lea1<br>27.2 kDa<br>238 aa | 1–185 | |
| Msl1<br>12.8 kDa<br>111 aa | 24–111 | |
| Prp9<br>63.0 kDa<br>530 aa | 1–378 | The structure of a large part of the S.c. SF3a complex was solved by crystallography (*66*). For this large, roughly Y-shaped structure (PDB 4DGW), no matching density is present in the high-resolution structure of the $B^{act}$ complex. In the non-masked lower-resolution $B^{act}$ structure a suitably sized forked density is present that connects the branch-point helix and the region containing U2-SLII of the high-resolution part with the density of the less well-resolved structure into which the U2-Sm complex fits. Since the resolution of the forked density does not allow unambiguous positioning of the arms, the positioning of SF3a is at present arbitrary. |
| Prp11<br>29.9 kDa<br>266 aa | 101–253 | |
| Prp21<br>33.0 kDa<br>280 aa | 89–228 | |
| Snu17/Ist3<br>17.1 kDa<br>148 aa | RRM<br>26–135 | Snu17 is the central RES complex component and binds to the other two RES complex proteins, Pml1 and Bud13 (*70*). The structure of the RRM domain of Snu17 in complex with a short N-terminal sequence of Pml1 (20–43) and a C-terminal sequence (213–246) of Bud13 (PDB 2MKC) has been solved by NMR (*71*). Additionally, the Snu17 structure was also determined within a complex with a longer piece of the Bud13 C terminus (PDB 4UQT) (*10*) that also includes a short helix (240–256) at the C terminus. Merged, the two structures fit well into a density on the back of $B^{act}$. This density is connected to the lower loops of Hsh155 HEAT repeats 7–9 and is framed by Prp8-RT/En, Prp8-RH and Cwc22-MA3. The Bud 13 C-terminal helix occupies a density tube that continues further down to Prp8-RT/En. Two crosslinks of Snu17 to HEAT repeats 7 and 8 (K103 to Hsh155 K410 and K455) support this location and orientation of this central part of the RES complex. |
| Pml1<br>23.6 kDa<br>204 aa | FHA<br>28–42<br>51–204 | The structure of a large part (51–204) of the S.c. protein Pml1 (PDB 2JKD, PDB 3ELV) containing the FHA domain was determined by crystallography (*72, 73*). A well-fitting density is located close to the side of Snu17 where the bound Pml1 N terminus exits. In its position within the $B^{act}$ complex, Pml1 forms a bridge between Snu17 and the C terminus of the Prp8-RT-associated Prp45 helix. Refinement was performed with COOT. |
| Bud13/Cwc26<br>30.5 kDa<br>266 aa | 235–266 | For Bud13 only the structure of a short piece of the C terminus (222–256) is known from the Snu17-Bud13 complex NMR structure (see above, Snu17/Ist3). A network of crosslinks indicates that the large N-terminal part extents from Snu17 up to the Brr2-Jab1 region of the $B^{act}$ complex. The C-terminal helix was further modeled into the density extension (see above, Snu17/Ist3). |
| Prp2<br>99.8 kDa<br>876 aa | RecA1<br>186–397 | The Prp2 RecA domains and the C-terminal domain were modeled with Prp43 as a template (PDB 2XAU) (*74*). The modeled C-terminal domain fits perfectly into a density region connecting the OB-fold of that domain to Hsh155 HEAT repeats 7 and 8. The RecA domains fit into two densities that are attached on the outside of the C-terminal domain which establishes contact with the main body of $B^{act}$. Both RecA domains have no contact to any other high-resolution $B^{act}$ density. The RecA domain densities are in close proximity to the mask applied for producing the high-resolution $B^{act}$ structure and are less well defined than the C-terminal domain is. |
| | RecA2<br>401–575 | |
| | C-term/OB-fold | |

| | | |
|---|---|---|
| | 587–864 | Refinement was performed with COOT. |
| Spp2<br>20.6 kDa<br>185 aa | | The structure of Spp2 has not yet been determined. Not surprisingly, evidence from a network of crosslinks places Spp2 in the $B^{act}$ complex close to Prp2 (see Fig. S17). The N-terminal Spp2 region resides in the vicinity of Brr2, while the C-terminal region is located closer to the RES complex. The central domain seems to be the main Prp2-binding region. The known Prp2-binding sequence, the G-patch domain, links the central domain to the C-terminal domain. No crosslinks are at present available to allow positioning of the G-patch sequence region. |

## Table S2: BS3-crosslinks of proteins in the yeast $B^{act}$ complex

| | | | | | | Spectral count | | | $Score_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | $Score_{max}$ |
| Inter | Brr2 | Bud13/Cwc26 | 71 | 115 | | | | 3 | | | 3,40 | 3 | 3,40 |
| | | | 74 | 115 | | | | 2 | | | 7,06 | 2 | 7,06 |
| | | | 91 | 53 | | | | 1 | | | 3,42 | 1 | 3,42 |
| | | | 304 | 2 | | 5 | | 4 | 14,17 | | 11,82 | 9 | 14,17 |
| | | | | 15 | | | | 2 | | | 5,65 | 2 | 5,65 |
| | | | | 35 | | | | 1 | | | 3,46 | 1 | 3,46 |
| | | | 414 | 64 | | | | 1 | | | 2,20 | 1 | 2,20 |
| | | | 417 | 53 | | | | 1 | | | 7,12 | 1 | 7,12 |
| | | | | 61 | | | | 1 | | | 1,81 | 1 | 1,81 |
| | | | 1733 | 41 | | | 4 | 1 | | 3,26 | 2,82 | 5 | 3,26 |
| | | Cwc24 | 748 | 256 | | 1 | | | 0,20 | | | 1 | 0,20 |
| | | | 2109 | 29 | | | 2 | 2 | | 7,16 | 7,35 | 4 | 7,35 |
| | | Cwc27 | 1504 | 213 | | 1 | | 1 | 0,94 | | 2,00 | 2 | 2,00 |
| | | | 1529 | 225 | | 1 | 3 | 1 | 0,47 | 5,11 | 7,64 | 5 | 7,64 |
| | | Ecm2 | 82 | 356 | | | | 1 | | | 2,03 | 1 | 2,03 |
| | | Hsh155 | 82 | 35 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | Prp17 | 1414 | 153 | | 1 | | | 0,97 | | | 1 | 0,97 |
| | | Prp2 | 2 | 211 | | | | 1 | | | 6,22 | 1 | 6,22 |
| | | | 28 | 211 | | | | 2 | | | 7,29 | 2 | 7,29 |
| | | | 1437 | 45 | | | | 1 | | | 5,60 | 1 | 5,60 |
| | | | 1623 | 2 | | | | 1 | | | 2,31 | 1 | 2,31 |
| | | | 2070 | 2 | | | | 3 | | | 8,79 | 3 | 8,79 |
| | | | 2109 | 2 | | | | 10 | | | 10,91 | 10 | 10,91 |
| | | | 2116 | 2 | | | | 1 | | | 7,51 | 1 | 7,51 |
| | | | 2121 | 2 | | | | 35 | | | 16,89 | 35 | 16,89 |
| | | Prp8 | 2 | 1903 | | | | 2 | | | 9,54 | 2 | 9,54 |
| | | | 25 | 1903 | | 1 | | | 1,15 | | | 1 | 1,15 |
| | | | 31 | 1903 | | 1 | | | 0,32 | | | 1 | 0,32 |
| | | | 50 | 2016 | | | | 1 | | | 7,68 | 1 | 7,68 |
| | | | 74 | 2016 | | | | 3 | | | 8,59 | 3 | 8,59 |
| | | | 91 | 2154 | | | | 1 | | | 8,47 | 1 | 8,47 |
| | | | | 2284 | | | | 1 | | | 1,15 | 1 | 1,15 |
| | | | 304 | 2167 | | | | 1 | | | 6,73 | 1 | 6,73 |
| | | | | 2187 | | | | 1 | | | 6,89 | 1 | 6,89 |
| | | | | 2213 | | | | 2 | | | 5,60 | 2 | 5,60 |
| | | | 1055 | 2108 | | | | 2 | | | 5,65 | 2 | 5,65 |
| | | | | 2149 | 17,5 | | | 1 | | | 5,78 | 1 | 5,78 |
| | | | | 2154 | 16,4 | | 3 | 6 | | 5,43 | 5,02 | 9 | 5,43 |
| | | Prp9 | 152 | 519 | | | 1 | | | 0,14 | | 1 | 0,14 |
| | | Rse1 | 304 | 556 | | | | 2 | | | 6,29 | 2 | 6,29 |
| | | | 414 | 556 | | | | 7 | | | 8,66 | 7 | 8,66 |
| | | | 417 | 556 | | | | 1 | | | 3,42 | 1 | 3,42 |
| | | | 758 | 1269 | | | | 1 | | | 1,69 | 1 | 1,69 |
| | | | 795 | 1269 | | | | 1 | | | 4,89 | 1 | 4,89 |
| | | | 967 | 556 | 83,3 | | | 1 | | | 6,22 | 1 | 6,22 |
| | | SmD2 | 1904 | 59 | | | 1 | | | 2,76 | | 1 | 2,76 |
| | | Snt309 | 748 | 94 | | | 1 | | | 0,55 | | 1 | 0,55 |
| | | Snu114 | 2 | 955 | | | | 1 | | | 5,16 | 1 | 5,16 |
| | | | 7 | 955 | | | | 1 | | | 4,08 | 1 | 4,08 |
| | | Spp2 | 74 | 133 | | | | 1 | | | 6,69 | 1 | 6,69 |
| | | | 85 | 133 | | | | 1 | | | 3,56 | 1 | 3,56 |
| | | | 91 | 58 | | | | 3 | | | 15,52 | 3 | 15,52 |
| | | | | 133 | | 1 | | 5 | 0,62 | | 16,93 | 6 | 16,93 |
| | | | 168 | 38 | | | | 1 | | | 4,12 | 1 | 4,12 |
| | | | 445 | 38 | | | | 1 | | | 5,97 | 1 | 5,97 |
| | | | | 58 | | 1 | | | 3,83 | | | 1 | 3,83 |
| | | | 454 | 38 | | | | 5 | | | 3,46 | 5 | 3,46 |
| | | | | 68 | | 2 | | 1 | 1,65 | | 1,27 | 3 | 1,65 |
| | | | 769 | 38 | | | | 4 | | | 10,34 | 4 | 10,34 |
| | | | | 46 | | | | 1 | | | 4,44 | 1 | 4,44 |
| | | Syf1 | 259 | 362 | | 1 | | | 0,58 | | | 1 | 0,58 |
| | Bud13/Cwc26 | Brr2 | 2 | 304 | | 5 | | 4 | 14,17 | | 11,82 | 9 | 14,17 |
| | | | 15 | 304 | | | | 2 | | | 5,65 | 2 | 5,65 |
| | | | 35 | 304 | | | | 1 | | | 3,46 | 1 | 3,46 |
| | | | 41 | 1733 | | | 4 | 1 | | 3,26 | 2,82 | 5 | 3,26 |
| | | | 53 | 91 | | | | 1 | | | 3,42 | 1 | 3,42 |
| | | | | 417 | | | | 1 | | | 7,12 | 1 | 7,12 |
| | | | 61 | 417 | | | | 1 | | | 1,81 | 1 | 1,81 |
| | | | 64 | 414 | | | | 1 | | | 2,20 | 1 | 2,20 |
| | | | 115 | 71 | | | | 3 | | | 3,40 | 3 | 3,40 |
| | | | | 74 | | | | 2 | | | 7,06 | 2 | 7,06 |
| | | Clf1 | 115 | 458 | | | | 1 | | | 4,06 | 1 | 4,06 |
| | | Cus1 | 255 | 40 | | 1 | | | 0,79 | | | 1 | 0,79 |
| | | Cwc22 | 201 | 520 | | | | 1 | | | 3,45 | 1 | 3,45 |
| | | | 213 | 520 | | | | 2 | | | 6,91 | 2 | 6,91 |
| | | | | 530 | | 2 | | 1 | 3,05 | | 1,61 | 3 | 3,05 |
| | | | 217 | 520 | | | 1 | | | 1,88 | | 1 | 1,88 |
| | | Cwc24 | 115 | 4 | | 1 | | | 3,23 | | | 1 | 3,23 |
| | | | 213 | 100 | | 1 | | | 1,03 | | | 1 | 1,03 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | Hsh155 | 120 | 473 | | | 3 | 1 | | 2,42 | 2,23 | 4 | 2,42 |
| | | | | 511 | | | 2 | | | 4,13 | | 2 | 4,13 |
| | | | 130 | 473 | | | | 4 | | | 9,36 | 4 | 9,36 |
| | | | | 511 | | | | 1 | | | 13,86 | 1 | 13,86 |
| | | | 136 | 473 | | | | 1 | | | 2,03 | 1 | 2,03 |
| | | | 255 | 612 | 20,0 | 1 | 4 | 15 | 4,45 | 7,00 | 8,53 | 20 | 8,53 |
| | | | 256 | 612 | 16,7 | | 2 | 5 | | 0,53 | 5,10 | 7 | 5,10 |
| | | Prp2 | 115 | 567 | | | | 1 | | | 0,09 | 1 | 0,09 |
| | | | 181 | 2 | | | | 1 | | | 6,85 | 1 | 6,85 |
| | | Prp45 | 136 | 367 | | | | 1 | | | 5,55 | 1 | 5,55 |
| | | | 146 | 352 | | 1 | | 1 | 2,53 | | 2,42 | 2 | 2,53 |
| | | Prp8 | 2 | 2217 | | 1 | | | 0,63 | | | 1 | 0,63 |
| | | | | 2219 | | 1 | | 1 | 5,15 | | 1,47 | 2 | 5,15 |
| | | | 15 | 2187 | | | | 2 | | | 11,00 | 2 | 11,00 |
| | | | 17 | 2187 | | 2 | | | 3,68 | | | 2 | 3,68 |
| | | | 35 | 1903 | | 3 | | | 1,92 | | | 3 | 1,92 |
| | | | 41 | 1903 | | 2 | | | 2,22 | | | 2 | 2,22 |
| | | | 53 | 2016 | | | | 1 | | | 8,14 | 1 | 8,14 |
| | | | 61 | 2016 | | | | 1 | | | 2,19 | 1 | 2,19 |
| | | | 68 | 2187 | | | | 2 | | | 4,23 | 2 | 4,23 |
| | | | 120 | 2016 | | | 1 | | | 0,68 | | 1 | 0,68 |
| | | | 181 | 1926 | | | | 2 | | | 4,40 | 2 | 4,40 |
| | | | 255 | 1589 | 33,4 | | | 2 | | | 7,71 | 2 | 7,71 |
| | | Rse1 | 115 | 1269 | | | | 1 | | | 5,69 | 1 | 5,69 |
| | | Snu17/Ist3 | 169 | 133 | | | 2 | 1 | | 4,84 | 2,06 | 3 | 4,84 |
| | | | | 138 | | 4 | 7 | 4 | 3,39 | 6,93 | 8,23 | 15 | 8,23 |
| | | | 179 | 138 | | | 4 | 6 | | 4,88 | 14,63 | 10 | 14,63 |
| | | | | 143 | | 1 | 2 | 4 | 2,73 | 1,41 | 9,46 | 7 | 9,46 |
| | | | 180 | 138 | | | | 2 | | | 6,88 | 2 | 6,88 |
| | | | 181 | 133 | | | 1 | 3 | | 3,77 | 5,55 | 4 | 5,55 |
| | | | | 138 | | 12 | 17 | 48 | 10,00 | 6,95 | 7,94 | 77 | 10,00 |
| | | | | 143 | | | 2 | 2 | | 0,52 | 1,85 | 4 | 1,85 |
| | | | 201 | 138 | | 1 | 4 | 16 | 4,09 | 3,27 | 9,39 | 21 | 9,39 |
| | | | | 143 | | | | 6 | | | 5,09 | 6 | 5,09 |
| | | | 206 | 138 | | 3 | | 4 | 11,35 | | 7,72 | 7 | 11,35 |
| | | | | 143 | | 1 | | | 0,97 | | | 1 | 0,97 |
| | | | 213 | 133 | | 3 | 5 | 3 | 6,15 | 6,66 | 6,20 | 11 | 6,66 |
| | | | | 138 | | 5 | 6 | 5 | 8,35 | 7,00 | 9,39 | 16 | 9,39 |
| | | | | 143 | | 1 | | | 0,90 | | | 1 | 0,90 |
| | | | 244 | 10 | | | 2 | | | 4,43 | | 2 | 4,43 |
| | | Spp2 | 115 | 151 | | | | 8 | | | 10,72 | 8 | 10,72 |
| | | | 120 | 151 | | 13 | | 17 | 12,61 | | 9,30 | 30 | 12,61 |
| | | | | 154 | | 3 | | | 1,97 | | | 3 | 1,97 |
| | | | 136 | 151 | | 3 | | 7 | 7,57 | | 13,17 | 10 | 13,17 |
| | | | | 154 | | | | 1 | | | 5,35 | 1 | 5,35 |
| | | | | 182 | | | | 2 | | | 4,89 | 2 | 4,89 |
| | | | 146 | 151 | | 2 | | 1 | 0,69 | | 2,77 | 3 | 2,77 |
| | | | | 154 | | 1 | | 2 | 1,81 | | 9,42 | 3 | 9,42 |
| | | | 151 | 181 | | | | 1 | | | 2,59 | 1 | 2,59 |
| | Bud31 | Cwc22 | 10 | 495 | | | | 1 | | | 1,53 | 1 | 1,53 |
| | | Cwc27 | 35 | 78 | | | | 2 | | | 4,58 | 2 | 4,58 |
| | | Ecm2 | 40 | 230 | 39,1 | | | 1 | | | 9,34 | 1 | 9,34 |
| | Cef1 | Clf1 | 240 | 113 | 11,1 | 6 | 9 | 4 | 6,06 | 8,32 | 11,14 | 19 | 11,14 |
| | | | 247 | 111 | 14,5 | 2 | 1 | 3 | 7,51 | 2,12 | 8,45 | 6 | 8,45 |
| | | | | 113 | 11,5 | 2 | 1 | | 2,42 | 0,29 | | 3 | 2,42 |
| | | | 251 | 111 | 14,5 | | 1 | | | 1,16 | | 1 | 1,16 |
| | | | | 113 | 13,6 | 2 | 2 | | 10,44 | 4,75 | | 4 | 10,44 |
| | | | 318 | 507 | | | | 1 | | | 2,52 | 1 | 2,52 |
| | | Isy1 | 294 | 42 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | Lea1 | 359 | 205 | | 1 | | | 0,18 | | | 1 | 0,18 |
| | | Ntc20 | 305 | 94 | | | | 2 | | | 3,90 | 2 | 3,90 |
| | | Prp11 | 22 | 36 | | | 1 | | | 1,92 | | 1 | 1,92 |
| | | Prp19 | 444 | 108 | | 5 | | 13 | 4,63 | | 6,83 | 18 | 6,83 |
| | | | 454 | 130 | | 2 | 2 | 2 | 3,58 | 9,32 | 5,03 | 6 | 9,32 |
| | | | | 135 | | | 1 | | | 2,63 | | 1 | 2,63 |
| | | | 496 | 107 | | 3 | 3 | 16 | 8,53 | 2,42 | 8,46 | 22 | 8,53 |
| | | | | 108 | | 3 | 5 | 14 | 1,87 | 7,01 | 5,71 | 22 | 7,01 |
| | | | 500 | 108 | | 21 | 23 | 220 | 14,32 | 14,03 | 16,95 | 264 | 16,95 |
| | | | 558 | 108 | | | 1 | | | 7,46 | | 1 | 7,46 |
| | | Prp2 | 263 | 732 | | | 1 | | | 5,68 | | 1 | 5,68 |
| | | Prp8 | 166 | 98 | | 1 | | | 0,62 | | | 1 | 0,62 |
| | | | 294 | 1910 | | 3 | | 1 | 2,80 | | 1,46 | 4 | 2,80 |
| | | | 496 | 2192 | | 1 | | | 0,46 | | | 1 | 0,46 |
| | | SmB | 187 | 76 | | 1 | | | 0,95 | | | 1 | 0,95 |
| | | SmD3 | 321 | 85 | | 1 | | | 0,46 | | | 1 | 0,46 |
| | | Snt309 | 187 | 26 | | | | 1 | | | 1,36 | 1 | 1,36 |
| | | Syf1 | 293 | 770 | | 3 | 4 | 2 | 3,68 | 4,58 | 3,13 | 9 | 4,58 |
| | | | 294 | 770 | | | 1 | | | 1,22 | | 1 | 1,22 |
| | | | 296 | 770 | | | 1 | | | 0,78 | | 1 | 0,78 |
| | | | 312 | 770 | | 1 | | | 2,91 | | | 1 | 2,91 |
| | | Syf2 | 239 | 173 | | 3 | 1 | | 4,95 | 0,55 | | 4 | 4,95 |
| | | | 240 | 159 | | | | 1 | | | 3,73 | 1 | 3,73 |
| | | | | 173 | | 5 | 6 | 10 | 7,61 | 11,75 | 9,07 | 21 | 11,75 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 247 | 159 | | | 1 | | | 1,07 | | 1 | 1,07 |
| | | | | 173 | | | 4 | 6 | | 3,71 | 6,44 | 10 | 6,44 |
| | | | 251 | 173 | | 2 | 1 | 2 | 4,91 | 1,42 | 8,77 | 5 | 8,77 |
| | | | 259 | 173 | | 1 | | | 0,55 | | | 1 | 0,55 |
| | Clf1 | Bud13/Cwc26 | 458 | 115 | | | | 1 | | | 4,06 | 1 | 4,06 |
| | | Cef1 | 111 | 247 | 14,5 | 2 | 1 | 3 | 7,51 | 2,12 | 8,45 | 6 | 8,45 |
| | | | | 251 | 14,5 | | 1 | | | 1,16 | | 1 | 1,16 |
| | | | 113 | 240 | 11,1 | 6 | 9 | 4 | 6,06 | 8,32 | 11,14 | 19 | 11,14 |
| | | | | 247 | 11,5 | 2 | 1 | | 2,42 | 0,29 | | 3 | 2,42 |
| | | | | 251 | 13,6 | 2 | 2 | | 10,44 | 4,75 | | 4 | 10,44 |
| | | | 507 | 318 | | | | 1 | | | 2,52 | 1 | 2,52 |
| | | Cus1 | 24 | 202 | | 1 | | | 4,36 | | | 1 | 4,36 |
| | | | | 289 | | 2 | | | 2,29 | | | 2 | 2,29 |
| | | Cwc2 | 24 | 236 | | 1 | | | 4,19 | | | 1 | 4,19 |
| | | Cwc21 | 25 | 62 | | | 4 | 1 | | 0,30 | 0,91 | 5 | 0,91 |
| | | Ecm2 | 24 | 164 | | | | 2 | | | 4,54 | 2 | 4,54 |
| | | | 59 | 116 | | | 1 | 2 | | 0,56 | 2,98 | 3 | 2,98 |
| | | | 668 | 230 | | | | 1 | | | 2,55 | 1 | 2,55 |
| | | Isy1 | 529 | 104 | | 1 | | | 3,23 | | | 1 | 3,23 |
| | | Ntc20 | 451 | 121 | | | 2 | 2 | | 3,86 | 6,69 | 4 | 6,69 |
| | | Prp2 | 425 | 10 | | | | 1 | | | 2,46 | 1 | 2,46 |
| | | Prp46 | 273 | 67 | | | 1 | 3 | | 4,33 | 12,55 | 4 | 12,55 |
| | | | | 87 | | | | 3 | | | 9,49 | 3 | 9,49 |
| | | | | 88 | | 1 | | 1 | 5,98 | | 10,44 | 2 | 10,44 |
| | | Rds3 | 640 | 42 | | 1 | 1 | 3 | 3,50 | 0,50 | 5,76 | 5 | 5,76 |
| | | SmG | 668 | 1 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | Snt309 | 670 | 94 | | | | 1 | | | 4,05 | 1 | 4,05 |
| | | Snu114 | 670 | 627 | | | | 1 | | | 0,28 | 1 | 0,28 |
| | | Spp2 | 458 | 151 | | | | 1 | | | 2,99 | 1 | 2,99 |
| | | Syf1 | 180 | 524 | | 3 | 5 | 3 | 5,16 | 2,04 | 5,79 | 11 | 5,79 |
| | | | | 531 | | 2 | | 1 | 2,81 | | 2,27 | 3 | 2,81 |
| | | | 289 | 653 | | | | 1 | | | 8,83 | 1 | 8,83 |
| | | | 304 | 650 | | 8 | 3 | 5 | 16,67 | 5,17 | 6,87 | 16 | 16,67 |
| | | | | 653 | | 12 | 10 | 54 | 17,65 | 11,96 | 13,33 | 76 | 17,65 |
| | | Syf2 | 25 | 173 | | | 4 | 6 | | 2,24 | 4,57 | 10 | 4,57 |
| | | | 113 | 159 | | 7 | 7 | 5 | 4,73 | 2,95 | 7,19 | 19 | 7,19 |
| | | | | 173 | | 4 | | 2 | 10,42 | | 7,42 | 6 | 10,42 |
| | | | 180 | 121 | | | | 8 | | | 9,41 | 8 | 9,41 |
| | Cus1 | Bud13/Cwc26 | 40 | 255 | | 1 | | | 0,79 | | | 1 | 0,79 |
| | | Clf1 | 202 | 24 | | 1 | | | 4,36 | | | 1 | 4,36 |
| | | | 289 | 24 | | 2 | | | 2,29 | | | 2 | 2,29 |
| | | Cwc2 | 436 | 10 | | | | 1 | | | 5,61 | 1 | 5,61 |
| | | Ecm2 | 429 | 203 | | | | 1 | | | 6,37 | 1 | 6,37 |
| | | Hsh155 | 102 | 237 | | 1 | 1 | 1 | 3,85 | 0,69 | 2,42 | 3 | 3,85 |
| | | | | 325 | | | 4 | 1 | | 2,40 | 3,50 | 5 | 3,50 |
| | | | 223 | 722 | | | | 4 | | | 2,31 | 4 | 2,31 |
| | | | 226 | 722 | | | | 5 | | | 5,11 | 5 | 5,11 |
| | | | 236 | 722 | | | 13 | 42 | | 8,32 | 7,90 | 55 | 8,32 |
| | | Hsh49 | 102 | 204 | | | | 1 | | | 2,65 | 1 | 2,65 |
| | | Isy1 | 41 | 59 | | 1 | | | 0,03 | | | 1 | 0,03 |
| | | | 48 | 59 | | | | 1 | | | 3,17 | 1 | 3,17 |
| | | | 317 | 157 | | | | 1 | | | 1,98 | 1 | 1,98 |
| | | Msl1 | 102 | 2 | | | | 2 | | | 6,19 | 2 | 6,19 |
| | | | 128 | 2 | | 1 | | 1 | 8,56 | | 5,86 | 2 | 8,56 |
| | | Prp11 | 223 | 28 | | | | 4 | | | 5,60 | 4 | 5,60 |
| | | | | 48 | | | | 2 | | | 0,99 | 2 | 0,99 |
| | | | | 60 | | | | 2 | | | 3,26 | 2 | 3,26 |
| | | | | 192 | | | | 1 | | | 2,44 | 1 | 2,44 |
| | | | 226 | 11 | | | | 3 | | | 4,34 | 3 | 4,34 |
| | | | | 28 | | | | 2 | | | 5,53 | 2 | 5,53 |
| | | | | 36 | | | 4 | | | 2,17 | | 4 | 2,17 |
| | | | | 48 | | | | 4 | | | 5,15 | 4 | 5,15 |
| | | | | 60 | | | 1 | 2 | | 3,83 | 3,98 | 3 | 3,98 |
| | | | | 192 | | | | 1 | | | 5,00 | 1 | 5,00 |
| | | Prp19 | 357 | 272 | | | 2 | | | 1,11 | | 2 | 1,11 |
| | | Prp2 | 102 | 2 | | | | 1 | | | 6,10 | 1 | 6,10 |
| | | Prp21 | | | | | 1 | | | 0,13 | | 1 | 0,13 |
| | | Prp9 | 128 | 466 | | 1 | 2 | 2 | 3,23 | 1,24 | 2,61 | 5 | 3,23 |
| | | | | 468 | | | 1 | 1 | | 0,38 | 5,52 | 2 | 5,52 |
| | | | | 492 | | | | 1 | | | 3,31 | 1 | 3,31 |
| | | Rse1 | 245 | 1342 | | 2 | 11 | 19 | 1,01 | 7,20 | 11,47 | 32 | 11,47 |
| | | | 246 | 1342 | | 5 | 19 | 8 | 6,41 | 12,16 | 11,56 | 32 | 12,16 |
| | | | 347 | 1149 | | 1 | 2 | | 4,32 | 4,68 | | 3 | 4,68 |
| | | SmB | 79 | 186 | | | | 1 | | | 3,62 | 1 | 3,62 |
| | | | 83 | 138 | | | | 2 | | | 4,68 | 2 | 4,68 |
| | | | | 145 | | | | 1 | | | 2,97 | 1 | 2,97 |
| | | | | 186 | | | | 1 | | | 4,86 | 1 | 4,86 |
| | | | 86 | 138 | | | | 1 | | | 1,97 | 1 | 1,97 |
| | | | 95 | 138 | | | 1 | 2 | | 0,44 | 8,99 | 3 | 8,99 |
| | | | 102 | 138 | | | | 4 | | | 8,02 | 4 | 8,02 |
| | | | | 186 | | | | 1 | | | 7,29 | 1 | 7,29 |
| | | | 128 | 117 | | 1 | | 1 | 1,46 | | 4,59 | 2 | 4,59 |
| | | SmD1 | 83 | 128 | | | | 1 | | | 4,47 | 1 | 4,47 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 102 | 128 | | | | 3 | | | 8,62 | 3 | 8,62 |
| | | SmD3 | 79 | 2 | | | | 17 | | | 9,62 | 17 | 9,62 |
| | | | 83 | 2 | | | | 4 | | | 9,14 | 4 | 9,14 |
| | | | | 86 | | | | 2 | | | 6,19 | 2 | 6,19 |
| | | | 86 | 2 | | | | 2 | | | 4,62 | 2 | 4,62 |
| | | | | 85 | | | | 1 | | | 1,90 | 1 | 1,90 |
| | | | 102 | 2 | | | | 1 | | | 3,26 | 1 | 3,26 |
| | | SmE | 39 | 6 | | 4 | 2 | 10 | 2,02 | 2,30 | 4,35 | 16 | 4,35 |
| | | | 48 | 6 | | 1 | 1 | 16 | 0,86 | 0,64 | 5,50 | 18 | 5,50 |
| | | | 53 | 6 | | | | 1 | | | 1,87 | 1 | 1,87 |
| | | | 58 | 6 | | | | 1 | | | 2,86 | 1 | 2,86 |
| | | | 79 | 6 | | 2 | | | 3,36 | | | 2 | 3,36 |
| | | SmF | 58 | 20 | | | 2 | | | 2,80 | | 2 | 2,80 |
| | | SmG | 2 | 8 | | 2 | | | 1,18 | | | 2 | 1,18 |
| | | | 16 | 24 | | | 2 | 3 | | 2,89 | 8,83 | 5 | 8,83 |
| | | | 79 | 2 | | | 2 | 13 | | 3,68 | 9,91 | 15 | 9,91 |
| | | | | 8 | | 1 | | | 3,97 | | | 1 | 3,97 |
| | | | 83 | 2 | | | | 1 | | | 3,09 | 1 | 3,09 |
| | | | | 8 | | | 1 | 1 | | 1,39 | 2,50 | 2 | 2,50 |
| | | Syf1 | 317 | 146 | | 4 | 5 | 3 | 15,41 | 11,09 | 10,86 | 12 | 15,41 |
| | | | 329 | 146 | | | | 1 | | | 1,31 | 1 | 1,31 |
| | | Ysf3 | 102 | 12 | | | | 1 | | | 3,31 | 1 | 3,31 |
| | | | | 15 | | 1 | | 1 | 0,22 | | 1,15 | 2 | 1,15 |
| | Cwc15 | Cwc24 | 41 | 228 | | 1 | | | 0,36 | | | 1 | 0,36 |
| | | Ecm2 | 16 | 27 | | 1 | | | 1,20 | | | 1 | 1,20 |
| | | Prp45 | 41 | 71 | | 1 | | 1 | 4,39 | | 6,62 | 2 | 6,62 |
| | | | 43 | 71 | | | 1 | | | 1,32 | | 1 | 1,32 |
| | | Prp8 | 151 | 1242 | | | | 1 | | | 5,95 | 1 | 5,95 |
| | | | 172 | 1205 | | | 1 | | | 0,70 | | 1 | 0,70 |
| | | | | 1310 | | 3 | | | 3,49 | | | 3 | 3,49 |
| | | Rse1 | 43 | 557 | | | | 2 | | | 3,38 | 2 | 3,38 |
| | | Snu114 | 140 | 60 | | 1 | | | 5,78 | | | 1 | 5,78 |
| | | | 145 | 59 | | 1 | | | 3,47 | | | 1 | 3,47 |
| | | | | 60 | | 1 | 2 | 1 | 0,63 | 4,30 | 5,72 | 4 | 5,72 |
| | | | 150 | 59 | | | | 2 | | | 3,96 | 2 | 3,96 |
| | | | | 60 | | 4 | 1 | | 4,12 | 0,67 | | 5 | 4,12 |
| | | | | 72 | | 1 | | | 2,10 | | | 1 | 2,10 |
| | | | | 81 | | | | 1 | | | 1,79 | 1 | 1,79 |
| | | | 151 | 59 | | | | 1 | | | 2,82 | 1 | 2,82 |
| | | | | 60 | | 2 | 4 | 3 | 9,75 | 7,80 | 8,57 | 9 | 9,75 |
| | | | | 72 | | | | 4 | | | 13,68 | 4 | 13,68 |
| | | | | 81 | | | | 14 | | | 12,86 | 14 | 12,86 |
| | | Syf2 | 102 | 9 | | 1 | | | 0,13 | | | 1 | 0,13 |
| | Cwc2 | Clf1 | 236 | 24 | | 1 | | | 4,19 | | | 1 | 4,19 |
| | | Cus1 | 10 | 436 | | | | 1 | | | 5,61 | 1 | 5,61 |
| | | Cwc24 | 152 | 93 | | | | 1 | | | 6,93 | 1 | 6,93 |
| | | Ecm2 | 2 | 230 | | 1 | 2 | 11 | 1,27 | 4,41 | 6,91 | 14 | 6,91 |
| | | | | 233 | | 1 | 6 | | 4,08 | 2,53 | | 7 | 4,08 |
| | | | 152 | 188 | | | 2 | 4 | | 5,56 | 11,32 | 6 | 11,32 |
| | | | | 189 | | 29 | 26 | 132 | 14,18 | 8,62 | 14,79 | 187 | 14,79 |
| | | | 236 | 116 | | | | 2 | | | 5,12 | 2 | 5,12 |
| | | | | 119 | 26,3 | | | 6 | | | 6,76 | 6 | 6,76 |
| | | | | 157 | | 3 | 3 | 4 | 4,36 | 1,44 | 6,79 | 10 | 6,79 |
| | | | | 164 | | 2 | 2 | 5 | 8,28 | 3,07 | 10,52 | 9 | 10,52 |
| | | | | 167 | | 1 | 1 | 12 | 15,55 | 3,07 | 12,74 | 14 | 15,55 |
| | | | | 173 | 30,7 | 4 | 2 | 1 | 2,40 | 2,32 | 5,14 | 7 | 5,14 |
| | | | | 247 | 18,7 | 2 | | 2 | 2,21 | | 6,84 | 4 | 6,84 |
| | | Isy1 | 152 | 7 | | 1 | | | 3,83 | | | 1 | 3,83 |
| | | | | 27 | | | | 1 | | | 2,53 | 1 | 2,53 |
| | | | | 40 | | 1 | | | 3,32 | | | 1 | 3,32 |
| | | | | 42 | | | 1 | 1 | | 1,48 | 2,56 | 2 | 2,56 |
| | | Prp17 | 152 | 207 | | 4 | 2 | 1 | 9,51 | 5,81 | 1,66 | 7 | 9,51 |
| | | Prp19 | 286 | 107 | | | | 2 | | | 3,09 | 2 | 3,09 |
| | | | | 108 | | 3 | 3 | 31 | 4,55 | 1,57 | 11,28 | 37 | 11,28 |
| | | | 320 | 108 | | 4 | 4 | 7 | 7,67 | 6,27 | 8,30 | 15 | 8,30 |
| | | Prp46 | 286 | 56 | | 1 | | | 0,65 | | | 1 | 0,65 |
| | | SmG | 310 | 8 | | | 2 | | | 1,04 | | 2 | 1,04 |
| | | Syf1 | 310 | 524 | | | | 2 | | | 4,43 | 2 | 4,43 |
| | | | | 531 | | | | 1 | | | 1,35 | 1 | 1,35 |
| | | | 320 | 424 | | 4 | 1 | 3 | 5,37 | 5,03 | 3,68 | 8 | 5,37 |
| | Cwc21 | Clf1 | 62 | 25 | | | 4 | 1 | | 0,30 | 0,91 | 5 | 0,91 |
| | | Cwc27 | 98 | 234 | | | 3 | | | 0,96 | | 3 | 0,96 |
| | | Prp19 | 98 | 404 | | | | 1 | | | 2,36 | 1 | 2,36 |
| | | Prp2 | 48 | 756 | | | | 1 | | | 10,75 | 1 | 10,75 |
| | | Prp8 | 12 | 351 | | | | 1 | | | 9,11 | 1 | 9,11 |
| | | | | 1205 | | 3 | | 2 | 3,97 | | 4,62 | 5 | 4,62 |
| | | Snu114 | 12 | 955 | | 6 | 2 | 6 | 9,33 | 5,91 | 12,44 | 14 | 12,44 |
| | Cwc22 | Bud13/Cwc26 | 520 | 201 | | | | 1 | | | 3,45 | 1 | 3,45 |
| | | | | 213 | | | | 2 | | | 6,91 | 2 | 6,91 |
| | | | | 217 | | | 1 | | | 1,88 | | 1 | 1,88 |
| | | | 530 | 213 | | 2 | | 1 | 3,05 | | 1,61 | 3 | 3,05 |
| | | Bud31 | 495 | 10 | | | | 1 | | | 1,53 | 1 | 1,53 |
| | | Cwc24 | 294 | 123 | | | | 1 | | | 4,16 | 1 | 4,16 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | Cwc27 | 176 | 295 | | 5 | | | 1,56 | | | 5 | 1,56 |
| | | Ntc20 | 203 | 1 | | | | 1 | | | 0,36 | 1 | 0,36 |
| | | Prp11 | 548 | 28 | | | | 1 | | | 1,68 | 1 | 1,68 |
| | | Prp2 | 520 | 137 | | | | 1 | | | 2,20 | 1 | 2,20 |
| | | Prp45 | 505 | 130 | | 1 | | | 2,06 | | | 1 | 2,06 |
| | | | | 274 | | 5 | 1 | 1 | 6,23 | 3,75 | 4,11 | 7 | 6,23 |
| | | | 520 | 265 | | 1 | 1 | 7 | 5,13 | 4,37 | 11,97 | 9 | 11,97 |
| | | | | 274 | | 18 | 11 | 17 | 11,78 | 9,46 | 14,67 | 46 | 14,67 |
| | | | | 287 | | 4 | 1 | 7 | 2,44 | 0,74 | 3,90 | 12 | 3,90 |
| | | | 530 | 265 | | 4 | 4 | 3 | 6,04 | 6,92 | 7,54 | 11 | 7,54 |
| | | | | 274 | | 16 | 7 | 14 | 8,37 | 3,25 | 7,13 | 37 | 8,37 |
| | | | | 287 | | 4 | 8 | 14 | 5,49 | 4,49 | 7,60 | 26 | 7,60 |
| | | Prp8 | 294 | 1435 | 10,3 | | | 2 | | | 13,19 | 2 | 13,19 |
| | | | 505 | 121 | | 4 | | | 2,82 | | | 4 | 2,82 |
| | | Snu114 | 176 | 369 | 13,8 | 5 | | | 4,02 | | | 5 | 4,02 |
| | | Snu17/Ist3 | 520 | 138 | | | | 1 | | | 4,91 | 1 | 4,91 |
| | | | 530 | 143 | | 1 | | | 2,93 | | | 1 | 2,93 |
| | | Syf1 | 548 | 311 | | | 1 | | | 26,34 | | 1 | 26,34 |
| | | Ysf3 | 203 | 15 | 147,7 | 1 | | | 0,49 | | | 1 | 0,49 |
| | Cwc24 | Brr2 | 29 | 2109 | | | 2 | 2 | | 7,16 | 7,35 | 4 | 7,35 |
| | | | 256 | 748 | | 1 | | | 0,20 | | | 1 | 0,20 |
| | | Bud13/Cwc26 | 4 | 115 | | 1 | | | 3,23 | | | 1 | 3,23 |
| | | | 100 | 213 | | 1 | | | 1,03 | | | 1 | 1,03 |
| | | Cwc15 | 228 | 41 | | 1 | | | 0,36 | | | 1 | 0,36 |
| | | Cwc2 | 93 | 152 | | | | 1 | | | 6,93 | 1 | 6,93 |
| | | Cwc22 | 123 | 294 | | | | 1 | | | 4,16 | 1 | 4,16 |
| | | Cwc27 | 63 | 171 | | | | 2 | | | 6,12 | 2 | 6,12 |
| | | Prp2 | 232 | 870 | | | | 1 | | | 1,61 | 1 | 1,61 |
| | | | 256 | 40 | | | | 2 | | | 1,78 | 2 | 1,78 |
| | | Prp8 | 63 | 2284 | | 3 | | | 2,13 | | | 3 | 2,13 |
| | | | 93 | 235 | | 2 | 2 | 3 | 3,33 | 0,89 | 10,67 | 7 | 10,67 |
| | | | | 517 | | 1 | | | 1,40 | | | 1 | 1,40 |
| | | | | 684 | | 4 | 8 | 6 | 10,33 | 7,89 | 8,80 | 18 | 10,33 |
| | | | | 697 | | 3 | 1 | | 3,79 | 1,77 | | 4 | 3,79 |
| | | | | 1926 | | | | 8 | | | 6,65 | 8 | 6,65 |
| | | | | 1931 | | | | 1 | | | 5,32 | 1 | 5,32 |
| | | | 98 | 235 | 13,5 | 1 | | | 0,69 | | | 1 | 0,69 |
| | | | | 1926 | 28,4 | | | 5 | | | 5,07 | 5 | 5,07 |
| | | | | 1931 | 28,7 | | 1 | 2 | | 0,39 | 4,69 | 3 | 4,69 |
| | | | 123 | 235 | | 3 | 3 | | 1,02 | 0,42 | | 6 | 1,02 |
| | | | | 517 | | 2 | 3 | | 3,45 | 3,27 | | 5 | 3,45 |
| | | | | 681 | | 1 | | | 0,84 | | | 1 | 0,84 |
| | | | | 684 | | 2 | 1 | 1 | 1,46 | 5,97 | 6,15 | 4 | 6,15 |
| | | | | 697 | | 5 | 2 | 2 | 14,16 | 8,26 | 6,08 | 9 | 14,16 |
| | | | | 1435 | | | | 3 | | | 10,51 | 3 | 10,51 |
| | | | | 1926 | | 3 | 1 | 8 | 5,55 | 3,54 | 7,20 | 12 | 7,20 |
| | | | | 1931 | | 2 | | 4 | 3,57 | | 10,66 | 6 | 10,66 |
| | | Rse1 | 182 | 1342 | | | | 3 | | | 3,96 | 3 | 3,96 |
| | | Spp2 | 4 | 151 | | 1 | | | 0,05 | | | 1 | 0,05 |
| | Cwc27 | Brr2 | 213 | 1504 | | 1 | | 1 | 0,94 | | 2,00 | 2 | 2,00 |
| | | | 225 | 1529 | | 1 | 3 | 1 | 0,47 | 5,11 | 7,64 | 5 | 7,64 |
| | | Bud31 | 78 | 35 | | | | 2 | | | 4,58 | 2 | 4,58 |
| | | Cwc21 | 234 | 98 | | | 3 | | | 0,96 | | 3 | 0,96 |
| | | Cwc22 | 295 | 176 | | 5 | | | 1,56 | | | 5 | 1,56 |
| | | Cwc24 | 171 | 63 | | | | 2 | | | 6,12 | 2 | 6,12 |
| | | Prp8 | 123 | 1713 | | | | 6 | | | 11,34 | 6 | 11,34 |
| | | SmD1 | 216 | 140 | | 1 | | | 2,77 | | | 1 | 2,77 |
| | Ecm2 | Brr2 | 356 | 82 | | | | 1 | | | 2,03 | 1 | 2,03 |
| | | Bud31 | 230 | 40 | 39,1 | | | 1 | | | 9,34 | 1 | 9,34 |
| | | Clf1 | 116 | 59 | | | 1 | 2 | | 0,56 | 2,98 | 3 | 2,98 |
| | | | 164 | 24 | | | | 2 | | | 4,54 | 2 | 4,54 |
| | | | 230 | 668 | | | | 1 | | | 2,55 | 1 | 2,55 |
| | | Cus1 | 203 | 429 | | | | 1 | | | 6,37 | 1 | 6,37 |
| | | Cwc15 | 27 | 16 | | 1 | | | 1,20 | | | 1 | 1,20 |
| | | Cwc2 | 116 | 236 | | | | 2 | | | 5,12 | 2 | 5,12 |
| | | | 119 | 236 | 26,3 | | | 6 | | | 6,76 | 6 | 6,76 |
| | | | 157 | 236 | | 3 | 3 | 4 | 4,36 | 1,44 | 6,79 | 10 | 6,79 |
| | | | 164 | 236 | | 2 | 2 | 5 | 8,28 | 3,07 | 10,52 | 9 | 10,52 |
| | | | 167 | 236 | | 1 | 1 | 12 | 15,55 | 3,07 | 12,74 | 14 | 15,55 |
| | | | 173 | 236 | 30,7 | 4 | 2 | 1 | 2,40 | 2,32 | 5,14 | 7 | 5,14 |
| | | | 188 | 152 | | | 2 | 4 | | 5,56 | 11,32 | 6 | 11,32 |
| | | | 189 | 152 | | 29 | 26 | 132 | 14,18 | 8,62 | 14,79 | 187 | 14,79 |
| | | | 230 | 2 | | 1 | 2 | 11 | 1,27 | 4,41 | 6,91 | 14 | 6,91 |
| | | | 233 | 2 | | 1 | 6 | | 4,08 | 2,53 | | 7 | 4,08 |
| | | | 247 | 236 | 18,7 | 2 | | 2 | 2,21 | | 6,84 | 4 | 6,84 |
| | | Prp17 | 188 | 207 | | 4 | 2 | 1 | 3,14 | 2,72 | 4,89 | 7 | 4,89 |
| | | | | 271 | | 1 | | | 4,58 | | | 1 | 4,58 |
| | | | 189 | 207 | | 1 | 2 | 2 | 0,21 | 1,97 | 7,29 | 5 | 7,29 |
| | | | | 271 | | 9 | 4 | 2 | 14,24 | 9,54 | 6,86 | 15 | 14,24 |
| | | | 203 | 207 | | | | 2 | | | 3,11 | 2 | 3,11 |
| | | | 274 | 207 | | 2 | | 2 | 2,15 | | 9,05 | 4 | 9,05 |
| | | | | 210 | | 1 | | | 0,00 | | | 1 | 0,00 |
| | | | | 271 | | | 4 | | | 1,03 | | 4 | 1,03 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 315 | | 1 | | 1 | 2,93 | | 1,87 | 2 | 2,93 |
| | | | 277 | 207 | | 1 | | | 0,15 | | | 1 | 0,15 |
| | | Snu114 | 188 | 111 | | | 1 | | | 0,82 | | 1 | 0,82 |
| | | | 353 | 746 | | 1 | | | 0,46 | | | 1 | 0,46 |
| | | Snu17/Ist3 | 188 | 123 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | Syf2 | 138 | 148 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | Hsh155 | Brr2 | 35 | 82 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | Bud13/Cwc26 | 473 | 120 | | | 3 | 1 | | 2,42 | 2,23 | 4 | 2,42 |
| | | | | 130 | | | | 4 | | | 9,36 | 4 | 9,36 |
| | | | | 136 | | | | 1 | | | 2,03 | 1 | 2,03 |
| | | | 511 | 120 | | | 2 | | | 4,13 | | 2 | 4,13 |
| | | | | 130 | | | | 1 | | | 13,86 | 1 | 13,86 |
| | | | 612 | 255 | 20,0 | 1 | 4 | 15 | 4,45 | 7,00 | 8,53 | 20 | 8,53 |
| | | | | 256 | 16,7 | | 2 | 5 | | 0,53 | 5,10 | 7 | 5,10 |
| | | Cus1 | 237 | 102 | | 1 | 1 | 1 | 3,85 | 0,69 | 2,42 | 3 | 3,85 |
| | | | 325 | 102 | | | 4 | 1 | | 2,40 | 3,50 | 5 | 3,50 |
| | | | 722 | 223 | | | | 4 | | | 2,31 | 4 | 2,31 |
| | | | | 226 | | | | 5 | | | 5,11 | 5 | 5,11 |
| | | | | 236 | | | 13 | 42 | | 8,32 | 7,90 | 55 | 8,32 |
| | | Prp11 | 722 | 11 | | | | 1 | | | 2,24 | 1 | 2,24 |
| | | Prp2 | 237 | 2 | | | | 1 | | | 5,79 | 1 | 5,79 |
| | | Prp8 | 35 | 906 | | 7 | 6 | 27 | 2,85 | 4,13 | 5,79 | 40 | 5,79 |
| | | | | 1007 | | | 1 | 5 | | 1,53 | 5,55 | 6 | 5,55 |
| | | | 51 | 920 | | | | 2 | | | 8,77 | 2 | 8,77 |
| | | | 104 | 1007 | | | | 1 | | | 12,88 | 1 | 12,88 |
| | | | 137 | 956 | 15,3 | 12 | 5 | 10 | 9,03 | 2,25 | 12,45 | 27 | 12,45 |
| | | | 142 | 956 | 21,0 | 1 | 4 | 7 | 6,97 | 7,13 | 7,47 | 12 | 7,47 |
| | | | 151 | 956 | | | | 2 | | | 8,87 | 2 | 8,87 |
| | | | 612 | 1588 | 30,5 | | | 1 | | | 6,21 | 1 | 6,21 |
| | | | | 1589 | 31,6 | | 6 | | | 6,78 | | 6 | 6,78 |
| | | | 696 | 1588 | 9,7 | | 2 | 1 | | 3,56 | 6,15 | 3 | 6,15 |
| | | Rds3 | 276 | 29 | 43,7 | | | 3 | | | 5,61 | 3 | 5,61 |
| | | | 455 | 53 | 20,3 | 3 | | | 10,29 | | | 3 | 10,29 |
| | | | 500 | 53 | 13,5 | 4 | | | 8,27 | | | 4 | 8,27 |
| | | | 511 | 53 | 19,2 | 2 | | 3 | 0,77 | | 8,47 | 5 | 8,47 |
| | | | | 56 | 19,3 | | | 3 | | | 9,22 | 3 | 9,22 |
| | | Rse1 | 511 | 221 | 22,6 | | 2 | 1 | | 0,52 | 2,40 | 3 | 2,40 |
| | | | | 1269 | | | | 4 | | | 6,95 | 4 | 6,95 |
| | | | 595 | 1269 | | | | 5 | | | 15,04 | 5 | 15,04 |
| | | | 632 | 1269 | | | | 2 | | | 4,56 | 2 | 4,56 |
| | | | 713 | 1269 | | | | 4 | | | 7,49 | 4 | 7,49 |
| | | | | 1342 | | | | 1 | | | 5,21 | 1 | 5,21 |
| | | SmB | 223 | 76 | | 1 | | | 0,73 | | | 1 | 0,73 |
| | | | 325 | 186 | | | 2 | | | 3,04 | | 2 | 3,04 |
| | | SmD1 | 158 | 128 | | | | 2 | | | 6,46 | 2 | 6,46 |
| | | | | 129 | | | | 1 | | | 3,09 | 1 | 3,09 |
| | | | 736 | 128 | | 1 | | | 3,09 | | | 1 | 3,09 |
| | | Snu17/Ist3 | 66 | 96 | | 5 | 2 | 5 | 3,20 | 1,92 | 3,46 | 12 | 3,46 |
| | | | 104 | 96 | | | | 2 | | | 4,99 | 2 | 4,99 |
| | | | 410 | 103 | | 14 | | | 15,45 | | | 14 | 15,45 |
| | | | 455 | 103 | 17,8 | 6 | | | 12,69 | | | 6 | 12,69 |
| | | | 500 | 10 | | 2 | | | 14,08 | | | 2 | 14,08 |
| | | Ysf3 | 932 | 4 | | | 2 | | | 0,68 | | 2 | 0,68 |
| | | | | 12 | 12,7 | | 3 | | | 3,56 | | 3 | 3,56 |
| | Hsh49 | Cus1 | 204 | 102 | | | | 1 | | | 2,65 | 1 | 2,65 |
| | | Isy1 | 82 | 87 | | | | 1 | | | 1,16 | 1 | 1,16 |
| | | Msl1 | 130 | 2 | | | 1 | 1 | | 2,16 | 2,53 | 2 | 2,53 |
| | | Prp11 | 42 | 48 | | 1 | | 4 | 0,96 | | 2,59 | 5 | 2,59 |
| | | | 101 | 103 | | | | 2 | | | 2,47 | 2 | 2,47 |
| | | Prp21 | | | | | 2 | | | 1,53 | | 2 | 1,53 |
| | | Prp9 | 39 | 462 | | 1 | | 1 | 1,39 | | 1,59 | 2 | 1,59 |
| | | | 101 | 429 | | | | 1 | | | 2,02 | 1 | 2,02 |
| | | | 147 | 371 | | | | 1 | | | 2,10 | 1 | 2,10 |
| | | | 204 | 468 | | 2 | 4 | 6 | 12,40 | 3,63 | 4,81 | 12 | 12,40 |
| | | | | 475 | | | 1 | 1 | | 0,18 | 2,54 | 2 | 2,54 |
| | | | 208 | 468 | | 2 | 5 | 6 | 3,70 | 4,70 | 5,83 | 13 | 5,83 |
| | | | | 475 | | | 3 | 5 | | 0,70 | 3,61 | 8 | 3,61 |
| | | | | 492 | | 1 | | 13 | 0,15 | | 7,01 | 14 | 7,01 |
| | | Rse1 | 39 | 1176 | | 4 | 2 | 8 | 5,21 | 0,44 | 3,10 | 14 | 5,21 |
| | Isy1 | Cef1 | 42 | 294 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | Clf1 | 104 | 529 | | 1 | | | 3,23 | | | 1 | 3,23 |
| | | Cus1 | 59 | 41 | | 1 | | | 0,03 | | | 1 | 0,03 |
| | | | | 48 | | | | 1 | | | 3,17 | 1 | 3,17 |
| | | | 157 | 317 | | | | 1 | | | 1,98 | 1 | 1,98 |
| | | Cwc2 | 7 | 152 | | 1 | | | 3,83 | | | 1 | 3,83 |
| | | | 27 | 152 | | | | 1 | | | 2,53 | 1 | 2,53 |
| | | | 40 | 152 | | 1 | | | 3,32 | | | 1 | 3,32 |
| | | | 42 | 152 | | | 1 | 1 | | 1,48 | 2,56 | 2 | 2,56 |
| | | Hsh49 | 87 | 82 | | | | 1 | | | 1,16 | 1 | 1,16 |
| | | Prp11 | 27 | 103 | | | | 1 | | | 4,44 | 1 | 4,44 |
| | | | | 126 | | | | 2 | | | 5,64 | 2 | 5,64 |
| | | | | 192 | | | | 1 | | | 2,82 | 1 | 2,82 |
| | | | 56 | 192 | | | | 1 | | | 1,53 | 1 | 1,53 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | Prp21 | | | | 1 | | | 4,84 | | | 1 | 4,84 |
| | | SmB | 106 | 100 | | 1 | | | 1,19 | | | 1 | 1,19 |
| | | SmG | 104 | 8 | | | | 1 | | | 2,89 | 1 | 2,89 |
| | | Syf1 | 7 | 259 | | | | 2 | | | 5,83 | 2 | 5,83 |
| | | | | 328 | | 1 | 3 | 6 | 10,49 | 5,14 | 9,35 | 10 | 10,49 |
| | | | | 424 | | 1 | 2 | 5 | 1,18 | 5,11 | 7,02 | 8 | 7,02 |
| | | | 27 | 328 | | 1 | | | 2,03 | | | 1 | 2,03 |
| | | | 40 | 328 | | 2 | 3 | 7 | 2,37 | 2,44 | 4,75 | 12 | 4,75 |
| | | | 139 | 146 | | 2 | | | 5,57 | | | 2 | 5,57 |
| | | | 143 | 146 | | 2 | 4 | 1 | 5,24 | 4,45 | 4,06 | 7 | 5,24 |
| | | | 157 | 220 | | | 1 | 4 | | 0,70 | 9,62 | 5 | 9,62 |
| | | | | 249 | | | | 1 | | | 3,79 | 1 | 3,79 |
| | | | 161 | 220 | | 3 | 7 | 9 | 2,63 | 2,37 | 4,94 | 19 | 4,94 |
| | | | 171 | 220 | | 9 | 6 | 1 | 4,61 | 5,04 | 2,46 | 16 | 5,04 |
| | | Syf2 | 7 | 26 | | 1 | 4 | 3 | 1,75 | 2,47 | 4,26 | 8 | 4,26 |
| | | | 27 | 26 | | | 1 | 4 | | 1,36 | 4,12 | 5 | 4,12 |
| | | | 42 | 173 | | 1 | 2 | | 5,98 | 1,83 | | 3 | 5,98 |
| | | Yju2/Cwc16 | 103 | 63 | | | 1 | | | 0,27 | | 1 | 0,27 |
| | Lea1 | Cef1 | 205 | 359 | | 1 | | | 0,18 | | | 1 | 0,18 |
| | | Msl1 | 215 | 2 | | | | 1 | | | 3,65 | 1 | 3,65 |
| | | Prp21 | | | | | 1 | | | 0,27 | | 1 | 0,27 |
| | | Prp9 | 2 | 140 | | | | 1 | | | 7,02 | 1 | 7,02 |
| | | | 194 | 115 | | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | 215 | 107 | | | | 1 | | | 1,72 | 1 | 1,72 |
| | | | | 115 | | 3 | 5 | 8 | 3,15 | 2,06 | 11,71 | 16 | 11,71 |
| | | | | 121 | | 1 | | 2 | 3,07 | | 3,26 | 3 | 3,26 |
| | | | 216 | 115 | | | | 1 | | | 1,38 | 1 | 1,38 |
| | | | 232 | 121 | | | | 1 | | | 1,81 | 1 | 1,81 |
| | | SmB | 125 | 76 | | | 3 | 11 | | 1,57 | 8,77 | 14 | 8,77 |
| | | Syf1 | 232 | 32 | | | 1 | 1 | | 2,40 | 1,79 | 2 | 2,40 |
| | Msl1 | Cus1 | 2 | 102 | | | | 2 | | | 6,19 | 2 | 6,19 |
| | | | | 128 | | 1 | | 1 | 8,56 | | 5,86 | 2 | 8,56 |
| | | Hsh49 | 2 | 130 | | | 1 | 1 | | 2,16 | 2,53 | 2 | 2,53 |
| | | Lea1 | 2 | 215 | | | | 1 | | | 3,65 | 1 | 3,65 |
| | | Prp9 | 2 | 115 | | 1 | | 6 | 12,81 | | 10,88 | 7 | 12,81 |
| | | | | 121 | | | | 4 | | | 4,11 | 4 | 4,11 |
| | | | | 124 | | | | 8 | | | 5,13 | 8 | 5,13 |
| | | Rse1 | 2 | 1001 | | 1 | | | 1,63 | | | 1 | 1,63 |
| | | SmB | 2 | 105 | | 2 | | | 1,64 | | | 2 | 1,64 |
| | | | | 114 | | | | 1 | | | 1,59 | 1 | 1,59 |
| | | | | 124 | | | | 1 | | | 1,92 | 1 | 1,92 |
| | | | | 138 | | | | 2 | | | 4,30 | 2 | 4,30 |
| | | | | 186 | | | 1 | | | 0,03 | | 1 | 0,03 |
| | | SmD3 | 2 | 85 | | | | 1 | | | 4,79 | 1 | 4,79 |
| | Ntc20 | Cef1 | 94 | 305 | | | | 2 | | | 3,90 | 2 | 3,90 |
| | | Clf1 | 121 | 451 | | | 2 | 2 | | 3,86 | 6,69 | 4 | 6,69 |
| | | Cwc22 | 1 | 203 | | | | 1 | | | 0,36 | 1 | 0,36 |
| | | Syf1 | 27 | 498 | | 6 | | 2 | 4,07 | | 8,58 | 8 | 8,58 |
| | | | | 558 | | 2 | 2 | 2 | 1,41 | 1,40 | 5,11 | 6 | 5,11 |
| | Pml1 | Prp2 | 6 | 820 | | 1 | | | 0,39 | | | 1 | 0,39 |
| | | Prp45 | 88 | 242 | | 1 | | 1 | 0,50 | | 5,76 | 2 | 5,76 |
| | | | 90 | 242 | | 2 | 8 | 1 | 2,44 | 5,39 | 2,84 | 11 | 5,39 |
| | | Syf1 | 153 | 372 | | | | 1 | | | 1,13 | 1 | 1,13 |
| | Prp11 | Cef1 | 36 | 22 | | | 1 | | | 1,92 | | 1 | 1,92 |
| | | Cus1 | 11 | 226 | | | | 3 | | | 4,34 | 3 | 4,34 |
| | | | 28 | 223 | | | | 4 | | | 5,60 | 4 | 5,60 |
| | | | | 226 | | | | 2 | | | 5,53 | 2 | 5,53 |
| | | | 36 | 226 | | | 4 | | | 2,17 | | 4 | 2,17 |
| | | | 48 | 223 | | | | 2 | | | 0,99 | 2 | 0,99 |
| | | | | 226 | | | | 4 | | | 5,15 | 4 | 5,15 |
| | | | 60 | 223 | | | | 2 | | | 3,26 | 2 | 3,26 |
| | | | | 226 | | | 1 | 2 | | 3,83 | 3,98 | 3 | 3,98 |
| | | | 192 | 223 | | | | 1 | | | 2,44 | 1 | 2,44 |
| | | | | 226 | | | | 1 | | | 5,00 | 1 | 5,00 |
| | | Cwc22 | 28 | 548 | | | | 1 | | | 1,68 | 1 | 1,68 |
| | | Hsh155 | 11 | 722 | | | | 1 | | | 2,24 | 1 | 2,24 |
| | | Hsh49 | 48 | 42 | | 1 | | 4 | 0,96 | | 2,59 | 5 | 2,59 |
| | | | 103 | 101 | | | | 2 | | | 2,47 | 2 | 2,47 |
| | | Isy1 | 103 | 27 | | | | 1 | | | 4,44 | 1 | 4,44 |
| | | | 126 | 27 | | | | 2 | | | 5,64 | 2 | 5,64 |
| | | | 192 | 27 | | | | 1 | | | 2,82 | 1 | 2,82 |
| | | | | 56 | | | | 1 | | | 1,53 | 1 | 1,53 |
| | | Prp2 | 121 | 43 | | | | 1 | | | 8,50 | 1 | 8,50 |
| | | Prp21 | | | | 11 | 26 | 47 | 4,49 | 8,14 | 11,80 | 84 | 11,80 |
| | | Prp8 | 11 | 956 | | | | 1 | | | 7,10 | 1 | 7,10 |
| | | Prp9 | 11 | 58 | | | | 3 | | | 6,61 | 3 | 6,61 |
| | | | | 371 | | | | 1 | | | 12,95 | 1 | 12,95 |
| | | | 173 | 58 | | | | 9 | | | 11,12 | 9 | 11,12 |
| | | | | 61 | | | | 1 | | | 2,35 | 1 | 2,35 |
| | | | 175 | 61 | | | 3 | | | 1,26 | | 3 | 1,26 |
| | | SmB | 103 | 138 | | | | 1 | | | 2,54 | 1 | 2,54 |
| | | | | 145 | | | | 1 | | | 1,21 | 1 | 1,21 |
| | | | 126 | 186 | | | | 1 | | | 2,38 | 1 | 2,38 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | Syf1 | 192 | 424 | | 1 | | 4 | 2,48 | | 7,93 | 5 | 7,93 |
| | | Syf2 | 192 | 26 | | 2 | 3 | 5 | 3,34 | 5,17 | 6,42 | 10 | 6,42 |
| | Prp17 | Brr2 | 153 | 1414 | | 1 | | | 0,97 | | | 1 | 0,97 |
| | | Cwc2 | 207 | 152 | | 4 | 2 | 1 | 9,51 | 5,81 | 1,66 | 7 | 9,51 |
| | | Ecm2 | 207 | 188 | | 4 | 2 | 1 | 3,14 | 2,72 | 4,89 | 7 | 4,89 |
| | | | | 189 | | 1 | 2 | 2 | 0,21 | 1,97 | 7,29 | 5 | 7,29 |
| | | | | 203 | | | | 2 | | | 3,11 | 2 | 3,11 |
| | | | | 274 | | 2 | | 2 | 2,15 | | 9,05 | 4 | 9,05 |
| | | | | 277 | | 1 | | | 0,15 | | | 1 | 0,15 |
| | | | 210 | 274 | | 1 | | | 0,00 | | | 1 | 0,00 |
| | | | 271 | 188 | | 1 | | | 4,58 | | | 1 | 4,58 |
| | | | | 189 | | 9 | 4 | 2 | 14,24 | 9,54 | 6,86 | 15 | 14,24 |
| | | | | 274 | | | 4 | | | 1,03 | | 4 | 1,03 |
| | | | 315 | 274 | | 1 | | 1 | 2,93 | | 1,87 | 2 | 2,93 |
| | | Prp19 | 27 | 170 | | | | 1 | | | 2,99 | 1 | 2,99 |
| | | Prp8 | 404 | 670 | | 1 | | | 0,48 | | | 1 | 0,48 |
| | Prp19 | Cef1 | 107 | 496 | | 3 | 3 | 16 | 8,53 | 2,42 | 8,46 | 22 | 8,53 |
| | | | 108 | 444 | | 5 | | 13 | 4,63 | | 6,83 | 18 | 6,83 |
| | | | | 496 | | 3 | 5 | 14 | 1,87 | 7,01 | 5,71 | 22 | 7,01 |
| | | | | 500 | | 21 | 23 | 220 | 14,32 | 14,03 | 16,95 | 264 | 16,95 |
| | | | | 558 | | | 1 | | | 7,46 | | 1 | 7,46 |
| | | | 130 | 454 | | 2 | 2 | 2 | 3,58 | 9,32 | 5,03 | 6 | 9,32 |
| | | | 135 | 454 | | | 1 | | | 2,63 | | 1 | 2,63 |
| | | Cus1 | 272 | 357 | | | 2 | | | 1,11 | | 2 | 1,11 |
| | | Cwc2 | 107 | 286 | | | | 2 | | | 3,09 | 2 | 3,09 |
| | | | 108 | 286 | | 3 | 3 | 31 | 4,55 | 1,57 | 11,28 | 37 | 11,28 |
| | | | | 320 | | 4 | 4 | 7 | 7,67 | 6,27 | 8,30 | 15 | 8,30 |
| | | Cwc21 | 404 | 98 | | | | 1 | | | 2,36 | 1 | 2,36 |
| | | Prp17 | 170 | 27 | | | | 1 | | | 2,99 | 1 | 2,99 |
| | | Prp21 | | | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | Prp8 | 107 | 1372 | | 2 | | | 1,22 | | | 2 | 1,22 |
| | | | | 1378 | | 1 | | | 1,38 | | | 1 | 1,38 |
| | | | 108 | 1209 | | | | 1 | | | 0,41 | 1 | 0,41 |
| | | SmB | 378 | 55 | | 1 | | | 3,42 | | | 1 | 3,42 |
| | | | | 60 | | 2 | 3 | 1 | 4,83 | 2,16 | 0,94 | 6 | 4,83 |
| | | SmG | 130 | 24 | | 1 | | | 0,98 | | | 1 | 0,98 |
| | | Snt309 | 107 | 25 | | 12 | 3 | 8 | 10,81 | 8,62 | 13,48 | 23 | 13,48 |
| | | | | 32 | | 2 | | 12 | 4,50 | | 13,91 | 14 | 13,91 |
| | | | | 46 | | 1 | 4 | | 1,70 | 10,80 | | 5 | 10,80 |
| | | | | 48 | | 6 | 3 | 11 | 6,46 | 1,19 | 8,82 | 20 | 8,82 |
| | | | | 67 | | 7 | 4 | 10 | 14,65 | 3,43 | 9,05 | 21 | 14,65 |
| | | | | 72 | | | 1 | | | 0,21 | | 1 | 0,21 |
| | | | 108 | 25 | | 15 | 9 | 9 | 14,90 | 10,62 | 17,25 | 33 | 17,25 |
| | | | | 46 | | 9 | 6 | 9 | 9,75 | 5,41 | 5,51 | 24 | 9,75 |
| | | | | 48 | | | | 1 | | | 12,06 | 1 | 12,06 |
| | | | 120 | 25 | | 4 | 2 | 4 | 5,76 | 4,11 | 7,08 | 10 | 7,08 |
| | | | 130 | 26 | | 1 | 1 | 1 | 0,24 | 2,43 | 6,54 | 3 | 6,54 |
| | | | 135 | 11 | | 1 | | | 1,31 | | | 1 | 1,31 |
| | | | 139 | 26 | | 2 | 2 | | 4,21 | 3,59 | | 4 | 4,21 |
| | Prp2 | Brr2 | 2 | 1623 | | | | 1 | | | 2,31 | 1 | 2,31 |
| | | | | 2070 | | | | 3 | | | 8,79 | 3 | 8,79 |
| | | | | 2109 | | | | 10 | | | 10,91 | 10 | 10,91 |
| | | | | 2116 | | | | 1 | | | 7,51 | 1 | 7,51 |
| | | | | 2121 | | | | 35 | | | 16,89 | 35 | 16,89 |
| | | | 45 | 1437 | | | | 1 | | | 5,60 | 1 | 5,60 |
| | | | 211 | 2 | | | | 1 | | | 6,22 | 1 | 6,22 |
| | | | | 28 | | | | 2 | | | 7,29 | 2 | 7,29 |
| | | Bud13/Cwc26 | 2 | 181 | | | | 1 | | | 6,85 | 1 | 6,85 |
| | | | 567 | 115 | | | | 1 | | | 0,09 | 1 | 0,09 |
| | | Cef1 | 732 | 263 | | | 1 | | | 5,68 | | 1 | 5,68 |
| | | Clf1 | 10 | 425 | | | | 1 | | | 2,46 | 1 | 2,46 |
| | | Cus1 | 2 | 102 | | | | 1 | | | 6,10 | 1 | 6,10 |
| | | Cwc21 | 756 | 48 | | | | 1 | | | 10,75 | 1 | 10,75 |
| | | Cwc22 | 137 | 520 | | | | 1 | | | 2,20 | 1 | 2,20 |
| | | Cwc24 | 40 | 256 | | | | 2 | | | 1,78 | 2 | 1,78 |
| | | | 870 | 232 | | | | 1 | | | 1,61 | 1 | 1,61 |
| | | Hsh155 | 2 | 237 | | | | 1 | | | 5,79 | 1 | 5,79 |
| | | Pml1 | 820 | 6 | | 1 | | | 0,39 | | | 1 | 0,39 |
| | | Prp11 | 43 | 121 | | | | 1 | | | 8,50 | 1 | 8,50 |
| | | Prp45 | 2 | 274 | | | | 1 | | | 5,90 | 1 | 5,90 |
| | | | 60 | 274 | | | | 1 | | | 6,27 | 1 | 6,27 |
| | | | 101 | 274 | | 1 | | 2 | 1,35 | | 9,86 | 3 | 9,86 |
| | | | 102 | 265 | | | | 1 | | | 10,38 | 1 | 10,38 |
| | | | | 274 | | 2 | | 2 | 3,95 | | 11,12 | 4 | 11,12 |
| | | | 113 | 265 | | | | 1 | | | 3,13 | 1 | 3,13 |
| | | | | 274 | | | | 2 | | | 6,24 | 2 | 6,24 |
| | | | 120 | 274 | | 2 | | 2 | 0,95 | | 7,59 | 4 | 7,59 |
| | | | 128 | 274 | | 1 | | | 0,80 | | | 1 | 0,80 |
| | | | 130 | 274 | | | | 1 | | | 2,15 | 1 | 2,15 |
| | | | 133 | 274 | | | | 5 | | | 6,22 | 5 | 6,22 |
| | | Prp8 | 40 | 672 | | | | 1 | | | 1,38 | 1 | 1,38 |
| | | | 467 | 1903 | 84,6 | | | 2 | | | 3,45 | 2 | 3,45 |
| | | | 560 | 1903 | 82,5 | | | 2 | | | 3,48 | 2 | 3,48 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 756 | 519 | 155,0 | | | 1 | | | 5,49 | 1 | 5,49 |
| | | | 820 | 817 | | 1 | | | 2,95 | | | 1 | 2,95 |
| | | Prp9 | 83 | 235 | | | 1 | | | 0,94 | | 1 | 0,94 |
| | | Rds3 | 10 | 42 | | | | 3 | | | 3,45 | 3 | 3,45 |
| | | SmD1 | 756 | 128 | | | | 1 | | | 2,24 | 1 | 2,24 |
| | | SmE | 14 | 1 | | 1 | | | 0,82 | | | 1 | 0,82 |
| | | Snu114 | 40 | 115 | | | | 1 | | | 2,34 | 1 | 2,34 |
| | | | 632 | 955 | 149,8 | | | 2 | | | 7,04 | 2 | 7,04 |
| | | | 756 | 749 | 208,0 | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | | 955 | 160,1 | | | 5 | | | 5,61 | 5 | 5,61 |
| | | | 763 | 955 | 147,7 | | | 1 | | | 5,73 | 1 | 5,73 |
| | | | 851 | 955 | 135,7 | | | 3 | | | 6,41 | 3 | 6,41 |
| | | Spp2 | 336 | 82 | | 2 | | 5 | 1,67 | | 7,16 | 7 | 7,16 |
| | | | | 83 | | 1 | | 4 | 2,28 | | 2,76 | 5 | 2,76 |
| | | | 461 | 168 | | 4 | | 6 | 3,34 | | 5,84 | 10 | 5,84 |
| | | | | 181 | | | | 1 | | | 2,80 | 1 | 2,80 |
| | | | 632 | 82 | | | | 1 | | | 3,53 | 1 | 3,53 |
| | | | | 83 | | 2 | | 2 | 7,68 | | 7,77 | 4 | 7,77 |
| | | | 640 | 83 | | 1 | | | 4,92 | | | 1 | 4,92 |
| | | | 750 | 82 | | 1 | | 1 | 1,21 | | 3,93 | 2 | 3,93 |
| | | | 756 | 82 | | 1 | | | 1,91 | | | 1 | 1,91 |
| | | | | 83 | | 1 | | 2 | 3,40 | | 2,90 | 3 | 3,40 |
| | | | | 95 | | | | 1 | | | 5,34 | 1 | 5,34 |
| | | | 840 | 154 | | 1 | | | 2,83 | | | 1 | 2,83 |
| | | Yju2/Cwc16 | 732 | 29 | | 2 | | | 0,44 | | | 2 | 0,44 |
| | Prp21 | Cus1 | 261 | 53 | | | 1 | | | 0,13 | | 1 | 0,13 |
| | | Hsh49 | 175 | 147 | | | 2 | | | 1,53 | | 2 | 1,53 |
| | | Isy1 | 189 | 7 | | 1 | | | 4,84 | | | 1 | 4,84 |
| | | Lea1 | 175 | 194 | | | 1 | | | 0,27 | | 1 | 0,27 |
| | | Prp11 | 68 | 175 | | | | 1 | | | 2,66 | 1 | 2,66 |
| | | | 177 | 175 | | | 4 | | | 3,18 | | 4 | 3,18 |
| | | | 183 | 121 | | | 7 | 1 | | 5,85 | 6,15 | 8 | 6,15 |
| | | | 199 | 126 | | | 1 | 4 | | 1,72 | 3,13 | 5 | 3,13 |
| | | | 205 | 192 | | | | 1 | | | 5,64 | 1 | 5,64 |
| | | | 234 | 139 | | 3 | 6 | 4 | 1,71 | 8,14 | 11,74 | 13 | 11,74 |
| | | | 240 | 11 | | | | 3 | | | 8,58 | 3 | 8,58 |
| | | | | 130 | | | | 1 | | | 2,15 | 1 | 2,15 |
| | | | | 139 | | 4 | 4 | 12 | 4,49 | 5,55 | 11,80 | 20 | 11,80 |
| | | | 247 | 11 | | | | 1 | | | 5,42 | 1 | 5,42 |
| | | | | 192 | | | | 1 | | | 2,90 | 1 | 2,90 |
| | | | 254 | 11 | | | | 3 | | | 2,84 | 3 | 2,84 |
| | | | | 28 | | | | 1 | | | 2,39 | 1 | 2,39 |
| | | | | 126 | | 1 | | | 0,70 | | | 1 | 0,70 |
| | | | | 192 | | 2 | 2 | 7 | 1,31 | 1,07 | 6,91 | 11 | 6,91 |
| | | | | 194 | | | | 1 | | | 2,16 | 1 | 2,16 |
| | | | 256 | 28 | | | | 1 | | | 2,85 | 1 | 2,85 |
| | | | | 36 | | | | 1 | | | 2,56 | 1 | 2,56 |
| | | | | 192 | | 1 | 1 | 2 | 0,02 | 2,23 | 4,18 | 4 | 4,18 |
| | | | 261 | 28 | | | | 1 | | | 2,39 | 1 | 2,39 |
| | | | | 192 | | | 1 | 1 | | 1,00 | 2,27 | 2 | 2,27 |
| | | Prp19 | 177 | 18 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | Prp45 | 175 | 237 | | 1 | | | 0,00 | | | 1 | 0,00 |
| | | Prp8 | 247 | 777 | | | | 1 | | | 2,63 | 1 | 2,63 |
| | | Prp9 | 20 | 47 | | | 3 | | | 1,48 | | 3 | 1,48 |
| | | | | 58 | | | 5 | 2 | | 4,61 | 5,46 | 7 | 5,46 |
| | | | 29 | 58 | | | | 1 | | | 3,99 | 1 | 3,99 |
| | | | 41 | 58 | | | | 1 | | | 5,63 | 1 | 5,63 |
| | | | 68 | 47 | | | 19 | 13 | | 2,14 | 2,37 | 32 | 2,37 |
| | | | | 58 | | 5 | 12 | 81 | 4,47 | 2,84 | 10,51 | 98 | 10,51 |
| | | | | 61 | | | 3 | 2 | | 2,58 | 5,34 | 5 | 5,34 |
| | | | 105 | 107 | | 7 | 2 | 7 | 2,65 | 1,77 | 6,82 | 16 | 6,82 |
| | | | | 115 | | 6 | 13 | 14 | 10,69 | 3,91 | 4,70 | 33 | 10,69 |
| | | | 116 | 107 | | | | 1 | | | 7,28 | 1 | 7,28 |
| | | | | 121 | | 1 | 1 | | 0,68 | 1,32 | | 2 | 1,32 |
| | | | 143 | 107 | | 3 | 7 | 13 | 18,44 | 12,85 | 6,21 | 23 | 18,44 |
| | | | 175 | 371 | | 1 | 7 | 4 | 0,98 | 7,82 | 10,71 | 12 | 10,71 |
| | | SmB | 68 | 194 | | | | 1 | | | 1,62 | 1 | 1,62 |
| | | | 175 | 124 | | | 1 | | | 1,50 | | 1 | 1,50 |
| | | Syf1 | 240 | 424 | | | | 2 | | | 4,63 | 2 | 4,63 |
| | | | 247 | 424 | | | | 1 | | | 4,45 | 1 | 4,45 |
| | | | 254 | 424 | | 3 | | 5 | 3,40 | | 6,01 | 8 | 6,01 |
| | | | 256 | 424 | | 1 | | 4 | 1,06 | | 4,15 | 5 | 4,15 |
| | | Syf2 | 247 | 26 | | | | 1 | | | 4,02 | 1 | 4,02 |
| | | | 254 | 26 | | | 1 | | | 3,40 | | 1 | 3,40 |
| | Prp45 | Bud13/Cwc26 | 352 | 146 | | 1 | | 1 | 2,53 | | 2,42 | 2 | 2,53 |
| | | | 367 | 136 | | | | 1 | | | 5,55 | 1 | 5,55 |
| | | Cwc15 | 71 | 41 | | 1 | | 1 | 4,39 | | 6,62 | 2 | 6,62 |
| | | | | 43 | | | 1 | | | 1,32 | | 1 | 1,32 |
| | | Cwc22 | 130 | 505 | | 1 | | | 2,06 | | | 1 | 2,06 |
| | | | 265 | 520 | | 1 | 1 | 7 | 5,13 | 4,37 | 11,97 | 9 | 11,97 |
| | | | | 530 | | 4 | 4 | 3 | 6,04 | 6,92 | 7,54 | 11 | 7,54 |
| | | | 274 | 505 | | 5 | 1 | 1 | 6,23 | 3,75 | 4,11 | 7 | 6,23 |
| | | | | 520 | | 18 | 11 | 17 | 11,78 | 9,46 | 14,67 | 46 | 14,67 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 530 | | 16 | 7 | 14 | 8,37 | 3,25 | 7,13 | 37 | 8,37 |
| | | | 287 | 520 | | 4 | 1 | 7 | 2,44 | 0,74 | 3,90 | 12 | 3,90 |
| | | | | 530 | | 4 | 8 | 14 | 5,49 | 4,49 | 7,60 | 26 | 7,60 |
| | | Pml1 | 242 | 88 | | 1 | | 1 | 0,50 | | 5,76 | 2 | 5,76 |
| | | | | 90 | | 2 | 8 | 1 | 2,44 | 5,39 | 2,84 | 11 | 5,39 |
| | | Prp2 | 265 | 102 | | | | 1 | | | 10,38 | 1 | 10,38 |
| | | | | 113 | | | | 1 | | | 3,13 | 1 | 3,13 |
| | | | 274 | 2 | | | | 1 | | | 5,90 | 1 | 5,90 |
| | | | | 60 | | | | 1 | | | 6,27 | 1 | 6,27 |
| | | | | 101 | | 1 | | 2 | 1,35 | | 9,86 | 3 | 9,86 |
| | | | | 102 | | 2 | | 2 | 3,95 | | 11,12 | 4 | 11,12 |
| | | | | 113 | | | | 2 | | | 6,24 | 2 | 6,24 |
| | | | | 120 | | 2 | | 2 | 0,95 | | 7,59 | 4 | 7,59 |
| | | | | 128 | | 1 | | | 0,80 | | | 1 | 0,80 |
| | | | | 130 | | | | 1 | | | 2,15 | 1 | 2,15 |
| | | | | 133 | | | | 5 | | | 6,22 | 5 | 6,22 |
| | | Prp21 | | | | 1 | | | 0,00 | | | 1 | 0,00 |
| | | Prp46 | 60 | 319 | 15,4 | 2 | 1 | 5 | 12,63 | 4,95 | 10,91 | 8 | 12,63 |
| | | | 81 | 249 | 15,0 | 1 | | 1 | 1,05 | | 3,50 | 2 | 3,50 |
| | | Prp8 | 129 | 159 | 9,6 | 1 | | | 0,83 | | | 1 | 0,83 |
| | | | 242 | 858 | | 1 | | | 2,89 | | | 1 | 2,89 |
| | | | 274 | 810 | | 1 | | | 1,69 | | | 1 | 1,69 |
| | | | 352 | 2097 | | | | 1 | | | 2,91 | 1 | 2,91 |
| | | | 367 | 1910 | | | | 3 | | | 6,52 | 3 | 6,52 |
| | | | | 2016 | | 2 | | 9 | 5,39 | | 10,16 | 11 | 10,16 |
| | | | | 2122 | | | | 6 | | | 11,41 | 6 | 11,41 |
| | | | 373 | 2016 | | | | 4 | | | 6,17 | 4 | 6,17 |
| | | SmB | 60 | 138 | | | | 4 | | | 5,94 | 4 | 5,94 |
| | | | | 186 | | | | 2 | | | 5,37 | 2 | 5,37 |
| | | | 71 | 131 | | | 2 | | | 1,55 | | 2 | 1,55 |
| | | | | 132 | | 1 | | | 1,09 | | | 1 | 1,09 |
| | | | | 138 | | 2 | 4 | 5 | 7,44 | 5,86 | 9,06 | 11 | 9,06 |
| | | | | 145 | | | | 1 | | | 7,76 | 1 | 7,76 |
| | | Snu17/Ist3 | 287 | 143 | | | | 1 | | | 2,17 | 1 | 2,17 |
| | | Syf2 | 36 | 142 | | | | 1 | | | 1,02 | 1 | 1,02 |
| | | | | 145 | | 15 | 10 | 27 | 13,10 | 3,00 | 5,38 | 52 | 13,10 |
| | | | | 151 | | 4 | 5 | 10 | 12,24 | 4,37 | 18,80 | 19 | 18,80 |
| | | | 71 | 1 | | | | 2 | | | 0,22 | 2 | 0,22 |
| | | Yju2/Cwc16 | 129 | 1 | | 1 | | | 0,59 | | | 1 | 0,59 |
| | Prp46 | Clf1 | 67 | 273 | | | 1 | 3 | | 4,33 | 12,55 | 4 | 12,55 |
| | | | 87 | 273 | | | | 3 | | | 9,49 | 3 | 9,49 |
| | | | 88 | 273 | | 1 | | 1 | 5,98 | | 10,44 | 2 | 10,44 |
| | | Cwc2 | 56 | 286 | | 1 | | | 0,65 | | | 1 | 0,65 |
| | | Prp45 | 249 | 81 | 15,0 | 1 | | 1 | 1,05 | | 3,50 | 2 | 3,50 |
| | | | 319 | 60 | 15,4 | 2 | 1 | 5 | 12,63 | 4,95 | 10,91 | 8 | 12,63 |
| | | SmB | 319 | 138 | | | | 1 | | | 3,70 | 1 | 3,70 |
| | | | | 186 | | | | 1 | | | 4,93 | 1 | 4,93 |
| | | Snu114 | 173 | 81 | | | | 2 | | | 1,64 | 2 | 1,64 |
| | | Syf2 | 56 | 145 | | | | 1 | | | 2,52 | 1 | 2,52 |
| | | | 67 | 145 | | | | 1 | | | 3,17 | 1 | 3,17 |
| | | | 87 | 145 | | 1 | | 3 | 7,44 | | 6,64 | 4 | 7,44 |
| | | | 88 | 145 | | 2 | | | 3,30 | | | 2 | 3,30 |
| | Prp8 | Brr2 | 1903 | 2 | | | | 2 | | | 9,54 | 2 | 9,54 |
| | | | | 25 | | 1 | | | 1,15 | | | 1 | 1,15 |
| | | | | 31 | | 1 | | | 0,32 | | | 1 | 0,32 |
| | | | 2016 | 50 | | | | 1 | | | 7,68 | 1 | 7,68 |
| | | | | 74 | | | | 3 | | | 8,59 | 3 | 8,59 |
| | | | 2108 | 1055 | | | | 2 | | | 5,65 | 2 | 5,65 |
| | | | 2149 | 1055 | 17,5 | | | 1 | | | 5,78 | 1 | 5,78 |
| | | | 2154 | 91 | | | | 1 | | | 8,47 | 1 | 8,47 |
| | | | | 1055 | 16,4 | | 3 | 6 | | 5,43 | 5,02 | 9 | 5,43 |
| | | | 2167 | 304 | | | | 1 | | | 6,73 | 1 | 6,73 |
| | | | 2187 | 304 | | | | 1 | | | 6,89 | 1 | 6,89 |
| | | | 2213 | 304 | | | | 2 | | | 5,60 | 2 | 5,60 |
| | | | 2284 | 91 | | | | 1 | | | 1,15 | 1 | 1,15 |
| | | Bud13/Cwc26 | 1589 | 255 | 33,4 | | | 2 | | | 7,71 | 2 | 7,71 |
| | | | 1903 | 35 | | 3 | | | 1,92 | | | 3 | 1,92 |
| | | | | 41 | | 2 | | | 2,22 | | | 2 | 2,22 |
| | | | 1926 | 181 | | | | 2 | | | 4,40 | 2 | 4,40 |
| | | | 2016 | 53 | | | | 1 | | | 8,14 | 1 | 8,14 |
| | | | | 61 | | | | 1 | | | 2,19 | 1 | 2,19 |
| | | | | 120 | | | 1 | | | 0,68 | | 1 | 0,68 |
| | | | 2187 | 15 | | | | 2 | | | 11,00 | 2 | 11,00 |
| | | | | 17 | | 2 | | | 3,68 | | | 2 | 3,68 |
| | | | | 68 | | | | 2 | | | 4,23 | 2 | 4,23 |
| | | | 2217 | 2 | | 1 | | | 0,63 | | | 1 | 0,63 |
| | | | 2219 | 2 | | 1 | | 1 | 5,15 | | 1,47 | 2 | 5,15 |
| | | Cef1 | 98 | 166 | | 1 | | | 0,62 | | | 1 | 0,62 |
| | | | 1910 | 294 | | 3 | | 1 | 2,80 | | 1,46 | 4 | 2,80 |
| | | | 2192 | 496 | | 1 | | | 0,46 | | | 1 | 0,46 |
| | | Cwc15 | 1205 | 172 | | | 1 | | | 0,70 | | 1 | 0,70 |
| | | | 1242 | 151 | | | | 1 | | | 5,95 | 1 | 5,95 |
| | | | 1310 | 172 | | 3 | | | 3,49 | | | 3 | 3,49 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | Cwc21 | 351 | 12 | | | | 1 | | | 9,11 | 1 | 9,11 |
| | | | 1205 | 12 | | 3 | | 2 | 3,97 | | 4,62 | 5 | 4,62 |
| | | Cwc22 | 121 | 505 | | 4 | | | 2,82 | | | 4 | 2,82 |
| | | | 1435 | 294 | 10,3 | | | 2 | | | 13,19 | 2 | 13,19 |
| | | Cwc24 | 235 | 93 | | 2 | 2 | 3 | 3,33 | 0,89 | 10,67 | 7 | 10,67 |
| | | | | 98 | 13,5 | 1 | | | 0,69 | | | 1 | 0,69 |
| | | | | 123 | | 3 | 3 | | 1,02 | 0,42 | | 6 | 1,02 |
| | | | 517 | 93 | | 1 | | | 1,40 | | | 1 | 1,40 |
| | | | | 123 | | 2 | 3 | | 3,45 | 3,27 | | 5 | 3,45 |
| | | | 681 | 123 | | 1 | | | 0,84 | | | 1 | 0,84 |
| | | | 684 | 93 | | 4 | 8 | 6 | 10,33 | 7,89 | 8,80 | 18 | 10,33 |
| | | | | 123 | | 2 | 1 | 1 | 1,46 | 5,97 | 6,15 | 4 | 6,15 |
| | | | 697 | 93 | | 3 | 1 | | 3,79 | 1,77 | | 4 | 3,79 |
| | | | | 123 | | 5 | 2 | 2 | 14,16 | 8,26 | 6,08 | 9 | 14,16 |
| | | | 1435 | 123 | | | | 3 | | | 10,51 | 3 | 10,51 |
| | | | 1926 | 93 | | | | 8 | | | 6,65 | 8 | 6,65 |
| | | | | 98 | 28,4 | | | 5 | | | 5,07 | 5 | 5,07 |
| | | | | 123 | | 3 | 1 | 8 | 5,55 | 3,54 | 7,20 | 12 | 7,20 |
| | | | 1931 | 93 | | | | 1 | | | 5,32 | 1 | 5,32 |
| | | | | 98 | 28,7 | | 1 | 2 | | 0,39 | 4,69 | 3 | 4,69 |
| | | | | 123 | | 2 | | 4 | 3,57 | | 10,66 | 6 | 10,66 |
| | | | 2284 | 63 | | 3 | | | 2,13 | | | 3 | 2,13 |
| | | Cwc27 | 1713 | 123 | | | | 6 | | | 11,34 | 6 | 11,34 |
| | | Hsh155 | 906 | 35 | | 7 | 6 | 27 | 2,85 | 4,13 | 5,79 | 40 | 5,79 |
| | | | 920 | 51 | | | | 2 | | | 8,77 | 2 | 8,77 |
| | | | 956 | 137 | 15,3 | 12 | 5 | 10 | 9,03 | 2,25 | 12,45 | 27 | 12,45 |
| | | | | 142 | 21,0 | 1 | 4 | 7 | 6,97 | 7,13 | 7,47 | 12 | 7,47 |
| | | | | 151 | | | | 2 | | | 8,87 | 2 | 8,87 |
| | | | 1007 | 35 | | | 1 | 5 | | 1,53 | 5,55 | 6 | 5,55 |
| | | | | 104 | | | | 1 | | | 12,88 | 1 | 12,88 |
| | | | 1588 | 612 | 30,5 | | | 1 | | | 6,21 | 1 | 6,21 |
| | | | | 696 | 9,7 | | 2 | 1 | | 3,56 | 6,15 | 3 | 6,15 |
| | | | 1589 | 612 | 31,6 | | 6 | | | 6,78 | | 6 | 6,78 |
| | | Prp11 | 956 | 11 | | | | 1 | | | 7,10 | 1 | 7,10 |
| | | Prp17 | 670 | 404 | | 1 | | | 0,48 | | | 1 | 0,48 |
| | | Prp19 | 1209 | 108 | | | | 1 | | | 0,41 | 1 | 0,41 |
| | | | 1372 | 107 | | 2 | | | 1,22 | | | 2 | 1,22 |
| | | | 1378 | 107 | | 1 | | | 1,38 | | | 1 | 1,38 |
| | | Prp2 | 519 | 756 | 155,0 | | | 1 | | | 5,49 | 1 | 5,49 |
| | | | 672 | 40 | | | | 1 | | | 1,38 | 1 | 1,38 |
| | | | 817 | 820 | | 1 | | | 2,95 | | | 1 | 2,95 |
| | | | 1903 | 467 | 84,6 | | | 2 | | | 3,45 | 2 | 3,45 |
| | | | | 560 | 82,5 | | | 2 | | | 3,48 | 2 | 3,48 |
| | | Prp21 | | | | | | 1 | | | 2,63 | 1 | 2,63 |
| | | Prp45 | 159 | 129 | 9,6 | 1 | | | 0,83 | | | 1 | 0,83 |
| | | | 810 | 274 | | 1 | | | 1,69 | | | 1 | 1,69 |
| | | | 858 | 242 | | 1 | | | 2,89 | | | 1 | 2,89 |
| | | | 1910 | 367 | | | | 3 | | | 6,52 | 3 | 6,52 |
| | | | 2016 | 367 | | 2 | | 9 | 5,39 | | 10,16 | 11 | 10,16 |
| | | | | 373 | | | | 4 | | | 6,17 | 4 | 6,17 |
| | | | 2097 | 352 | | | | 1 | | | 2,91 | 1 | 2,91 |
| | | | 2122 | 367 | | | | 6 | | | 11,41 | 6 | 11,41 |
| | | Rse1 | 2080 | 1269 | | | | 1 | | | 8,87 | 1 | 8,87 |
| | | | 2097 | 1269 | | | | 1 | | | 7,64 | 1 | 7,64 |
| | | SmB | 90 | 138 | | | | 1 | | | 3,21 | 1 | 3,21 |
| | | | | 186 | | | | 1 | | | 10,12 | 1 | 10,12 |
| | | | 98 | 138 | | | | 1 | | | 8,45 | 1 | 8,45 |
| | | | | 186 | | | 2 | 1 | | 4,22 | 3,66 | 3 | 4,22 |
| | | | 103 | 138 | | | | 1 | | | 6,58 | 1 | 6,58 |
| | | | 159 | 186 | | | | 1 | | | 9,02 | 1 | 9,02 |
| | | | 166 | 186 | | | | 3 | | | 6,94 | 3 | 6,94 |
| | | | 586 | 186 | | | | 2 | | | 6,62 | 2 | 6,62 |
| | | | 743 | 145 | | | | 1 | | | 2,20 | 1 | 2,20 |
| | | | 810 | 186 | | | 1 | 3 | | 2,09 | 5,94 | 4 | 5,94 |
| | | | | 194 | | | | 1 | | | 3,15 | 1 | 3,15 |
| | | SmD1 | 98 | 140 | | | | 1 | | | 3,18 | 1 | 3,18 |
| | | SmG | 846 | 13 | | 1 | | | 0,11 | | | 1 | 0,11 |
| | | Snt309 | 490 | 72 | | | | 1 | | | 0,43 | 1 | 0,43 |
| | | Snu114 | 325 | 173 | 13,1 | 8 | 23 | 13 | 8,22 | 8,13 | 7,04 | 44 | 8,22 |
| | | | 333 | 173 | 18,4 | 4 | 9 | 4 | 7,21 | 8,32 | 5,39 | 17 | 8,32 |
| | | | 334 | 173 | 17,8 | | 1 | 3 | | 6,62 | 8,38 | 4 | 8,38 |
| | | | 810 | 59 | | | 1 | 1 | | 1,49 | 3,17 | 2 | 3,17 |
| | | | | 60 | | | 4 | 1 | | 6,13 | 4,46 | 5 | 6,13 |
| | | | 1209 | 669 | 19,6 | | | 1 | | | 0,95 | 1 | 0,95 |
| | | | 1299 | 955 | 24,0 | | 1 | | | 0,87 | | 1 | 0,87 |
| | | Spp2 | 835 | 14 | | 1 | | | 0,32 | | | 1 | 0,32 |
| | | Syf1 | 300 | 2 | | | 1 | | | 0,08 | | 1 | 0,08 |
| | Prp9 | Brr2 | 519 | 152 | | | 1 | | | 0,14 | | 1 | 0,14 |
| | | Cus1 | 466 | 128 | | 1 | 2 | 2 | 3,23 | 1,24 | 2,61 | 5 | 3,23 |
| | | | 468 | 128 | | | 1 | 1 | | 0,38 | 5,52 | 2 | 5,52 |
| | | | 492 | 128 | | | | 1 | | | 3,31 | 1 | 3,31 |
| | | Hsh49 | 371 | 147 | | | | 1 | | | 2,10 | 1 | 2,10 |
| | | | 429 | 101 | | | | 1 | | | 2,02 | 1 | 2,02 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 462 | 39 | | 1 | | 1 | 1,39 | | 1,59 | 2 | 1,59 |
| | | | 468 | 204 | | 2 | 4 | 6 | 12,40 | 3,63 | 4,81 | 12 | 12,40 |
| | | | | 208 | | 2 | 5 | 6 | 3,70 | 4,70 | 5,83 | 13 | 5,83 |
| | | | 475 | 204 | | | 1 | 1 | | 0,18 | 2,54 | 2 | 2,54 |
| | | | | 208 | | | 3 | 5 | | 0,70 | 3,61 | 8 | 3,61 |
| | | | 492 | 208 | | 1 | | 13 | 0,15 | | 7,01 | 14 | 7,01 |
| | | Lea1 | 107 | 215 | | | | 1 | | | 1,72 | 1 | 1,72 |
| | | | 115 | 194 | | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | | 215 | | 3 | 5 | 8 | 3,15 | 2,06 | 11,71 | 16 | 11,71 |
| | | | | 216 | | | | 1 | | | 1,38 | 1 | 1,38 |
| | | | 121 | 215 | | 1 | | 2 | 3,07 | | 3,26 | 3 | 3,26 |
| | | | | 232 | | | | 1 | | | 1,81 | 1 | 1,81 |
| | | | 140 | 2 | | | | 1 | | | 7,02 | 1 | 7,02 |
| | | Msl1 | 115 | 2 | | 1 | | 6 | 12,81 | | 10,88 | 7 | 12,81 |
| | | | 121 | 2 | | | | 4 | | | 4,11 | 4 | 4,11 |
| | | | 124 | 2 | | | | 8 | | | 5,13 | 8 | 5,13 |
| | | Prp11 | 58 | 11 | | | | 3 | | | 6,61 | 3 | 6,61 |
| | | | | 173 | | | | 9 | | | 11,12 | 9 | 11,12 |
| | | | 61 | 173 | | | | 1 | | | 2,35 | 1 | 2,35 |
| | | | | 175 | | | 3 | | | 1,26 | | 3 | 1,26 |
| | | | 371 | 11 | | | | 1 | | | 12,95 | 1 | 12,95 |
| | | Prp2 | 235 | 83 | | | 1 | | | 0,94 | | 1 | 0,94 |
| | | Prp21 | | | | 23 | 72 | 139 | 18,44 | 12,85 | 10,71 | 234 | 18,44 |
| | | Rse1 | 462 | 1176 | | 1 | 5 | 3 | 0,71 | 6,80 | 8,97 | 9 | 8,97 |
| | | | 492 | 1001 | | | | 3 | | | 6,37 | 3 | 6,37 |
| | | | | 1184 | | | | 4 | | | 5,39 | 4 | 5,39 |
| | | SmB | 235 | 65 | | 1 | | 2 | 1,09 | | 2,35 | 3 | 2,35 |
| | | | | 68 | | | | 1 | | | 4,54 | 1 | 4,54 |
| | | | 238 | 65 | | | | 1 | | | 2,58 | 1 | 2,58 |
| | | | | 68 | | | | 2 | | | 5,17 | 2 | 5,17 |
| | | | 371 | 138 | | | | 3 | | | 7,73 | 3 | 7,73 |
| | | | | 186 | | | | 4 | | | 12,93 | 4 | 12,93 |
| | | | 466 | 117 | | | | 1 | | | 2,87 | 1 | 2,87 |
| | | | 468 | 117 | | | 2 | | | 1,78 | | 2 | 1,78 |
| | | SmD1 | 360 | 128 | | | | 1 | | | 2,35 | 1 | 2,35 |
| | | | 371 | 128 | | | 1 | 5 | | 0,66 | 4,46 | 6 | 4,46 |
| | | | | 129 | | | | 1 | | | 2,25 | 1 | 2,25 |
| | | | | 140 | | | | 4 | | | 4,98 | 4 | 4,98 |
| | | Yju2/Cwc16 | 371 | 68 | | | | 1 | | | 2,32 | 1 | 2,32 |
| | Rds3 | Clf1 | 42 | 640 | | 1 | 1 | 3 | 3,50 | 0,50 | 5,76 | 5 | 5,76 |
| | | Hsh155 | 29 | 276 | 43,7 | | | 3 | | | 5,61 | 3 | 5,61 |
| | | | 53 | 455 | 20,3 | 3 | | | 10,29 | | | 3 | 10,29 |
| | | | | 500 | 13,5 | 4 | | | 8,27 | | | 4 | 8,27 |
| | | | | 511 | 19,2 | 2 | | 3 | 0,77 | | 8,47 | 5 | 8,47 |
| | | | 56 | 511 | 19,3 | | | 3 | | | 9,22 | 3 | 9,22 |
| | | Prp2 | 42 | 10 | | | | 3 | | | 3,45 | 3 | 3,45 |
| | | Ysf3 | 13 | 9 | 16,6 | | 1 | | | 0,14 | | 1 | 0,14 |
| | Rse1 | Brr2 | 556 | 304 | | | | 2 | | | 6,29 | 2 | 6,29 |
| | | | | 414 | | | | 7 | | | 8,66 | 7 | 8,66 |
| | | | | 417 | | | | 1 | | | 3,42 | 1 | 3,42 |
| | | | | 967 | 83,3 | | | 1 | | | 6,22 | 1 | 6,22 |
| | | | 1269 | 758 | | | | 1 | | | 1,69 | 1 | 1,69 |
| | | | | 795 | | | | 1 | | | 4,89 | 1 | 4,89 |
| | | Bud13/Cwc26 | 1269 | 115 | | | | 1 | | | 5,69 | 1 | 5,69 |
| | | Cus1 | 1149 | 347 | | 1 | 2 | | 4,32 | 4,68 | | 3 | 4,68 |
| | | | 1342 | 245 | | 2 | 11 | 19 | 1,01 | 7,20 | 11,47 | 32 | 11,47 |
| | | | | 246 | | 5 | 19 | 8 | 6,41 | 12,16 | 11,56 | 32 | 12,16 |
| | | Cwc15 | 557 | 43 | | | | 2 | | | 3,38 | 2 | 3,38 |
| | | Cwc24 | 1342 | 182 | | | | 3 | | | 3,96 | 3 | 3,96 |
| | | Hsh155 | 221 | 511 | 22,6 | | 2 | 1 | | 0,52 | 2,40 | 3 | 2,40 |
| | | | 1269 | 511 | | | | 4 | | | 6,95 | 4 | 6,95 |
| | | | | 595 | | | | 5 | | | 15,04 | 5 | 15,04 |
| | | | | 632 | | | | 2 | | | 4,56 | 2 | 4,56 |
| | | | | 713 | | | | 4 | | | 7,49 | 4 | 7,49 |
| | | | 1342 | 713 | | | | 1 | | | 5,21 | 1 | 5,21 |
| | | Hsh49 | 1176 | 39 | | 4 | 2 | 8 | 5,21 | 0,44 | 3,10 | 14 | 5,21 |
| | | Msl1 | 1001 | 2 | | 1 | | | 1,63 | | | 1 | 1,63 |
| | | Prp8 | 1269 | 2080 | | | | 1 | | | 8,87 | 1 | 8,87 |
| | | | | 2097 | | | | 1 | | | 7,64 | 1 | 7,64 |
| | | Prp9 | 1001 | 492 | | | | 3 | | | 6,37 | 3 | 6,37 |
| | | | 1176 | 462 | | 1 | 5 | 3 | 0,71 | 6,80 | 8,97 | 9 | 8,97 |
| | | | 1184 | 492 | | | | 4 | | | 5,39 | 4 | 5,39 |
| | | Snt309 | 1057 | 48 | | 1 | | | 1,68 | | | 1 | 1,68 |
| | | Spp2 | 374 | 38 | | | | 6 | | | 12,26 | 6 | 12,26 |
| | | | | 83 | | | | 1 | | | 4,28 | 1 | 4,28 |
| | SmB | Cef1 | 76 | 187 | | 1 | | | 0,95 | | | 1 | 0,95 |
| | | Cus1 | 117 | 128 | | 1 | | 1 | 1,46 | | 4,59 | 2 | 4,59 |
| | | | 138 | 83 | | | | 2 | | | 4,68 | 2 | 4,68 |
| | | | | 86 | | | | 1 | | | 1,97 | 1 | 1,97 |
| | | | | 95 | | | 1 | 2 | | 0,44 | 8,99 | 3 | 8,99 |
| | | | | 102 | | | | 4 | | | 8,02 | 4 | 8,02 |
| | | | 145 | 83 | | | | 1 | | | 2,97 | 1 | 2,97 |
| | | | 186 | 79 | | | | 1 | | | 3,62 | 1 | 3,62 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 83 | | | | 1 | | | 4,86 | 1 | 4,86 |
| | | | | 102 | | | | 1 | | | 7,29 | 1 | 7,29 |
| | | Hsh155 | 76 | 223 | | 1 | | | 0,73 | | | 1 | 0,73 |
| | | | 186 | 325 | | | 2 | | | 3,04 | | 2 | 3,04 |
| | | Isy1 | 100 | 106 | | 1 | | | 1,19 | | | 1 | 1,19 |
| | | Lea1 | 76 | 125 | | | 3 | 11 | | 1,57 | 8,77 | 14 | 8,77 |
| | | Msl1 | 105 | 2 | | 2 | | | 1,64 | | | 2 | 1,64 |
| | | | 114 | 2 | | | | 1 | | | 1,59 | 1 | 1,59 |
| | | | 124 | 2 | | | | 1 | | | 1,92 | 1 | 1,92 |
| | | | 138 | 2 | | | | 2 | | | 4,30 | 2 | 4,30 |
| | | | 186 | 2 | | | 1 | | | 0,03 | | 1 | 0,03 |
| | | Prp11 | 138 | 103 | | | | 1 | | | 2,54 | 1 | 2,54 |
| | | | 145 | 103 | | | | 1 | | | 1,21 | 1 | 1,21 |
| | | | 186 | 126 | | | | 1 | | | 2,38 | 1 | 2,38 |
| | | Prp19 | 55 | 378 | | 1 | | | 3,42 | | | 1 | 3,42 |
| | | | 60 | 378 | | 2 | 3 | 1 | 4,83 | 2,16 | 0,94 | 6 | 4,83 |
| | | Prp21 | | | | | 1 | 1 | | 1,50 | 1,62 | 2 | 1,62 |
| | | Prp45 | 131 | 71 | | | 2 | | | 1,55 | | 2 | 1,55 |
| | | | 132 | 71 | | 1 | | | 1,09 | | | 1 | 1,09 |
| | | | 138 | 60 | | | | 4 | | | 5,94 | 4 | 5,94 |
| | | | | 71 | | 2 | 4 | 5 | 7,44 | 5,86 | 9,06 | 11 | 9,06 |
| | | | 145 | 71 | | | | 1 | | | 7,76 | 1 | 7,76 |
| | | | 186 | 60 | | | | 2 | | | 5,37 | 2 | 5,37 |
| | | Prp46 | 138 | 319 | | | | 1 | | | 3,70 | 1 | 3,70 |
| | | | 186 | 319 | | | | 1 | | | 4,93 | 1 | 4,93 |
| | | Prp8 | 138 | 90 | | | | 1 | | | 3,21 | 1 | 3,21 |
| | | | | 98 | | | | 1 | | | 8,45 | 1 | 8,45 |
| | | | | 103 | | | | 1 | | | 6,58 | 1 | 6,58 |
| | | | 145 | 743 | | | | 1 | | | 2,20 | 1 | 2,20 |
| | | | 186 | 90 | | | | 1 | | | 10,12 | 1 | 10,12 |
| | | | | 98 | | | 2 | 1 | | 4,22 | 3,66 | 3 | 4,22 |
| | | | | 159 | | | | 1 | | | 9,02 | 1 | 9,02 |
| | | | | 166 | | | | 3 | | | 6,94 | 3 | 6,94 |
| | | | | 586 | | | | 2 | | | 6,62 | 2 | 6,62 |
| | | | | 810 | | | 1 | 3 | | 2,09 | 5,94 | 4 | 5,94 |
| | | | 194 | 810 | | | | 1 | | | 3,15 | 1 | 3,15 |
| | | Prp9 | 65 | 235 | | 1 | | 2 | 1,09 | | 2,35 | 3 | 2,35 |
| | | | | 238 | | | | 1 | | | 2,58 | 1 | 2,58 |
| | | | 68 | 235 | | | | 1 | | | 4,54 | 1 | 4,54 |
| | | | | 238 | | | | 2 | | | 5,17 | 2 | 5,17 |
| | | | 117 | 466 | | | | 1 | | | 2,87 | 1 | 2,87 |
| | | | | 468 | | | 2 | | | 1,78 | | 2 | 1,78 |
| | | | 138 | 371 | | | | 3 | | | 7,73 | 3 | 7,73 |
| | | | 186 | 371 | | | | 4 | | | 12,93 | 4 | 12,93 |
| | | SmD1 | 138 | 128 | | | | 2 | | | 3,71 | 2 | 3,71 |
| | | | 186 | 129 | | | | 1 | | | 2,24 | 1 | 2,24 |
| | | SmD2 | 65 | 82 | | | | 10 | | | 3,89 | 10 | 3,89 |
| | | SmD3 | 19 | 79 | 15,3 | | | 1 | | | 2,33 | 1 | 2,33 |
| | | | 39 | 2 | | | | 1 | | | 4,88 | 1 | 4,88 |
| | | | 105 | 2 | | | | 2 | | | 6,85 | 2 | 6,85 |
| | | | | 79 | | | 1 | 1 | | 0,30 | 1,36 | 2 | 1,36 |
| | | | | 85 | | 2 | 5 | 3 | 2,36 | 7,58 | 7,24 | 10 | 7,58 |
| | | | | 86 | | | 5 | 8 | | 3,30 | 4,46 | 13 | 4,46 |
| | | Snu114 | 76 | 60 | | | 1 | | | 1,86 | | 1 | 1,86 |
| | | | 105 | 99 | | | | 2 | | | 7,28 | 2 | 7,28 |
| | | | | 159 | | | 4 | 5 | | 4,15 | 3,67 | 9 | 4,15 |
| | | | 186 | 617 | | | | 1 | | | 4,88 | 1 | 4,88 |
| | | Syf2 | 117 | 14 | | | | 1 | | | 2,79 | 1 | 2,79 |
| | | Yju2/Cwc16 | 105 | 2 | | | | 1 | | | 1,39 | 1 | 1,39 |
| | SmD1 | Cus1 | 128 | 83 | | | | 1 | | | 4,47 | 1 | 4,47 |
| | | | | 102 | | | | 3 | | | 8,62 | 3 | 8,62 |
| | | Cwc27 | 140 | 216 | | 1 | | | 2,77 | | | 1 | 2,77 |
| | | Hsh155 | 128 | 158 | | | | 2 | | | 6,46 | 2 | 6,46 |
| | | | | 736 | | 1 | | | 3,09 | | | 1 | 3,09 |
| | | | 129 | 158 | | | | 1 | | | 3,09 | 1 | 3,09 |
| | | Prp2 | 128 | 756 | | | | 1 | | | 2,24 | 1 | 2,24 |
| | | Prp8 | 140 | 98 | | | | 1 | | | 3,18 | 1 | 3,18 |
| | | Prp9 | 128 | 360 | | | | 1 | | | 2,35 | 1 | 2,35 |
| | | | | 371 | | | 1 | 5 | | 0,66 | 4,46 | 6 | 4,46 |
| | | | 129 | 371 | | | | 1 | | | 2,25 | 1 | 2,25 |
| | | | 140 | 371 | | | | 4 | | | 4,98 | 4 | 4,98 |
| | | SmB | 128 | 138 | | | | 2 | | | 3,71 | 2 | 3,71 |
| | | | 129 | 186 | | | | 1 | | | 2,24 | 1 | 2,24 |
| | | SmD2 | 54 | 82 | | | 1 | 9 | | 0,29 | 4,32 | 10 | 4,32 |
| | | | 111 | 59 | | | | 3 | | | 5,09 | 3 | 5,09 |
| | | | 128 | 27 | | | | 4 | | | 4,84 | 4 | 4,84 |
| | | SmD3 | 128 | 2 | | | | 1 | | | 2,95 | 1 | 2,95 |
| | | Snu114 | 128 | 356 | | 1 | 1 | 1 | 3,03 | 0,60 | 1,77 | 3 | 3,03 |
| | | | | 397 | | 1 | 3 | 3 | 6,12 | 5,66 | 9,82 | 7 | 9,82 |
| | | | 129 | 397 | | | | 1 | | | 4,30 | 1 | 4,30 |
| | | | 140 | 356 | | 2 | | | 1,44 | | | 2 | 1,44 |
| | | | | 397 | | | 4 | 3 | | 3,66 | 5,35 | 7 | 5,35 |
| | | Yju2/Cwc16 | 128 | 74 | | | | 1 | | | 2,94 | 1 | 2,94 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 140 | 74 | | | | 1 | | | 1,97 | 1 | 1,97 |
| | SmD2 | Brr2 | 59 | 1904 | | | 1 | | | 2,76 | | 1 | 2,76 |
| | | SmB | 82 | 65 | | | | 10 | | | 3,89 | 10 | 3,89 |
| | | SmD1 | 27 | 128 | | | | 4 | | | 4,84 | 4 | 4,84 |
| | | | 59 | 111 | | | | 3 | | | 5,09 | 3 | 5,09 |
| | | | 82 | 54 | | | 1 | 9 | | 0,29 | 4,32 | 10 | 4,32 |
| | | Spp2 | 80 | 3 | | | 1 | | | 0,21 | | 1 | 0,21 |
| | SmD3 | Cef1 | 85 | 321 | | 1 | | | 0,46 | | | 1 | 0,46 |
| | | Cus1 | 2 | 79 | | | | 17 | | | 9,62 | 17 | 9,62 |
| | | | | 83 | | | | 4 | | | 9,14 | 4 | 9,14 |
| | | | | 86 | | | | 2 | | | 4,62 | 2 | 4,62 |
| | | | | 102 | | | | 1 | | | 3,26 | 1 | 3,26 |
| | | | 85 | 86 | | | | 1 | | | 1,90 | 1 | 1,90 |
| | | | 86 | 83 | | | | 2 | | | 6,19 | 2 | 6,19 |
| | | Msl1 | 85 | 2 | | | | 1 | | | 4,79 | 1 | 4,79 |
| | | SmB | 2 | 39 | | | | 1 | | | 4,88 | 1 | 4,88 |
| | | | | 105 | | | | 2 | | | 6,85 | 2 | 6,85 |
| | | | 79 | 19 | 15,3 | | | 1 | | | 2,33 | 1 | 2,33 |
| | | | | 105 | | | 1 | 1 | | 0,30 | 1,36 | 2 | 1,36 |
| | | | 85 | 105 | | 2 | 5 | 3 | 2,36 | 7,58 | 7,24 | 10 | 7,58 |
| | | | 86 | 105 | | | 5 | 8 | | 3,30 | 4,46 | 13 | 4,46 |
| | | SmD1 | 2 | 128 | | | | 1 | | | 2,95 | 1 | 2,95 |
| | | SmG | 32 | 9 | 16,5 | | 8 | | | 4,92 | | 8 | 4,92 |
| | | Snu114 | 32 | 558 | 16,1 | | | 2 | | | 5,84 | 2 | 5,84 |
| | | | 85 | 159 | 13,6 | 10 | 15 | 96 | 16,46 | 6,72 | 9,09 | 121 | 16,46 |
| | | | 86 | 159 | | 1 | 4 | 11 | 4,04 | 4,51 | 6,97 | 16 | 6,97 |
| | SmE | Cus1 | 6 | 39 | | 4 | 2 | 10 | 2,02 | 2,30 | 4,35 | 16 | 4,35 |
| | | | | 48 | | 1 | 1 | 16 | 0,86 | 0,64 | 5,50 | 18 | 5,50 |
| | | | | 53 | | | | 1 | | | 1,87 | 1 | 1,87 |
| | | | | 58 | | | | 1 | | | 2,86 | 1 | 2,86 |
| | | | | 79 | | 2 | | | 3,36 | | | 2 | 3,36 |
| | | Prp2 | 1 | 14 | | 1 | | | 0,82 | | | 1 | 0,82 |
| | | SmG | 6 | 8 | | 2 | 7 | 30 | 15,35 | 6,68 | 11,58 | 39 | 15,35 |
| | | | | 13 | | | | 2 | | | 2,85 | 2 | 2,85 |
| | | | | 14 | | 1 | 1 | 1 | 0,94 | 0,01 | 1,72 | 3 | 1,72 |
| | SmF | Cus1 | 20 | 58 | | | 2 | | | 2,80 | | 2 | 2,80 |
| | SmG | Clf1 | 1 | 668 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | Cus1 | 2 | 79 | | | 2 | 13 | | 3,68 | 9,91 | 15 | 9,91 |
| | | | | 83 | | | | 1 | | | 3,09 | 1 | 3,09 |
| | | | 8 | 2 | | 2 | | | 1,18 | | | 2 | 1,18 |
| | | | | 79 | | 1 | | | 3,97 | | | 1 | 3,97 |
| | | | | 83 | | | 1 | 1 | | 1,39 | 2,50 | 2 | 2,50 |
| | | | 24 | 16 | | | 2 | 3 | | 2,89 | 8,83 | 5 | 8,83 |
| | | Cwc2 | 8 | 310 | | | 2 | | | 1,04 | | 2 | 1,04 |
| | | Isy1 | 8 | 104 | | | | 1 | | | 2,89 | 1 | 2,89 |
| | | Prp19 | 24 | 130 | | 1 | | | 0,98 | | | 1 | 0,98 |
| | | Prp8 | 13 | 846 | | 1 | | | 0,11 | | | 1 | 0,11 |
| | | SmD3 | 9 | 32 | 16,5 | | 8 | | | 4,92 | | 8 | 4,92 |
| | | SmE | 8 | 6 | | 2 | 7 | 30 | 15,35 | 6,68 | 11,58 | 39 | 15,35 |
| | | | 13 | 6 | | | | 2 | | | 2,85 | 2 | 2,85 |
| | | | 14 | 6 | | 1 | 1 | 1 | 0,94 | 0,01 | 1,72 | 3 | 1,72 |
| | Snt309 | Brr2 | 94 | 748 | | | 1 | | | 0,55 | | 1 | 0,55 |
| | | Cef1 | 26 | 187 | | | | 1 | | | 1,36 | 1 | 1,36 |
| | | Clf1 | 94 | 670 | | | | 1 | | | 4,05 | 1 | 4,05 |
| | | Prp19 | 11 | 135 | | 1 | | | 1,31 | | | 1 | 1,31 |
| | | | 25 | 107 | | 12 | 3 | 8 | 10,81 | 8,62 | 13,48 | 23 | 13,48 |
| | | | | 108 | | 15 | 9 | 9 | 14,90 | 10,62 | 17,25 | 33 | 17,25 |
| | | | | 120 | | 4 | 2 | 4 | 5,76 | 4,11 | 7,08 | 10 | 7,08 |
| | | | 26 | 130 | | 1 | 1 | 1 | 0,24 | 2,43 | 6,54 | 3 | 6,54 |
| | | | | 139 | | 2 | 2 | | 4,21 | 3,59 | | 4 | 4,21 |
| | | | 32 | 107 | | 2 | | 12 | 4,50 | | 13,91 | 14 | 13,91 |
| | | | 46 | 107 | | 1 | 4 | | 1,70 | 10,80 | | 5 | 10,80 |
| | | | | 108 | | 9 | 6 | 9 | 9,75 | 5,41 | 5,51 | 24 | 9,75 |
| | | | 48 | 107 | | 6 | 3 | 11 | 6,46 | 1,19 | 8,82 | 20 | 8,82 |
| | | | | 108 | | | | 1 | | | 12,06 | 1 | 12,06 |
| | | | 67 | 107 | | 7 | 4 | 10 | 14,65 | 3,43 | 9,05 | 21 | 14,65 |
| | | | 72 | 107 | | | 1 | | | 0,21 | | 1 | 0,21 |
| | | Prp8 | 72 | 490 | | | | 1 | | | 0,43 | 1 | 0,43 |
| | | Rse1 | 48 | 1057 | | 1 | | | 1,68 | | | 1 | 1,68 |
| | Snu114 | Brr2 | 955 | 2 | | | | 1 | | | 5,16 | 1 | 5,16 |
| | | | | 7 | | | | 1 | | | 4,08 | 1 | 4,08 |
| | | Clf1 | 627 | 670 | | | | 1 | | | 0,28 | 1 | 0,28 |
| | | Cwc15 | 59 | 145 | | 1 | | | 3,47 | | | 1 | 3,47 |
| | | | | 150 | | | | 2 | | | 3,96 | 2 | 3,96 |
| | | | | 151 | | | | 1 | | | 2,82 | 1 | 2,82 |
| | | | 60 | 140 | | 1 | | | 5,78 | | | 1 | 5,78 |
| | | | | 145 | | 1 | 2 | 1 | 0,63 | 4,30 | 5,72 | 4 | 5,72 |
| | | | | 150 | | 4 | 1 | | 4,12 | 0,67 | | 5 | 4,12 |
| | | | | 151 | | 2 | 4 | 3 | 9,75 | 7,80 | 8,57 | 9 | 9,75 |
| | | | 72 | 150 | | 1 | | | 2,10 | | | 1 | 2,10 |
| | | | | 151 | | | | 4 | | | 13,68 | 4 | 13,68 |
| | | | 81 | 150 | | | | 1 | | | 1,79 | 1 | 1,79 |
| | | | | 151 | | | | 14 | | | 12,86 | 14 | 12,86 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | Cwc21 | 955 | 12 | | 6 | 2 | 6 | 9,33 | 5,91 | 12,44 | 14 | 12,44 |
| | | Cwc22 | 369 | 176 | 13,8 | 5 | | | 4,02 | | | 5 | 4,02 |
| | | Ecm2 | 111 | 188 | | | 1 | | | 0,82 | | 1 | 0,82 |
| | | | 746 | 353 | | 1 | | | 0,46 | | | 1 | 0,46 |
| | | Prp2 | 115 | 40 | | | | 1 | | | 2,34 | 1 | 2,34 |
| | | | 749 | 756 | 208,0 | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | 955 | 632 | 149,8 | | | 2 | | | 7,04 | 2 | 7,04 |
| | | | | 756 | 160,1 | | | 5 | | | 5,61 | 5 | 5,61 |
| | | | | 763 | 147,7 | | | 1 | | | 5,73 | 1 | 5,73 |
| | | | | 851 | 135,7 | | | 3 | | | 6,41 | 3 | 6,41 |
| | | Prp46 | 81 | 173 | | | | 2 | | | 1,64 | 2 | 1,64 |
| | | Prp8 | 59 | 810 | | | 1 | 1 | | 1,49 | 3,17 | 2 | 3,17 |
| | | | 60 | 810 | | | 4 | 1 | | 6,13 | 4,46 | 5 | 6,13 |
| | | | 173 | 325 | 13,1 | 8 | 23 | 13 | 8,22 | 8,13 | 7,04 | 44 | 8,22 |
| | | | | 333 | 18,4 | 4 | 9 | 4 | 7,21 | 8,32 | 5,39 | 17 | 8,32 |
| | | | | 334 | 17,8 | | 1 | 3 | | 6,62 | 8,38 | 4 | 8,38 |
| | | | 669 | 1209 | 19,6 | | | 1 | | | 0,95 | 1 | 0,95 |
| | | | 955 | 1299 | 24,0 | | 1 | | | 0,87 | | 1 | 0,87 |
| | | SmB | 60 | 76 | | | 1 | | | 1,86 | | 1 | 1,86 |
| | | | 99 | 105 | | | | 2 | | | 7,28 | 2 | 7,28 |
| | | | 159 | 105 | | | 4 | 5 | | 4,15 | 3,67 | 9 | 4,15 |
| | | | 617 | 186 | | | | 1 | | | 4,88 | 1 | 4,88 |
| | | SmD1 | 356 | 128 | | 1 | 1 | 1 | 3,03 | 0,60 | 1,77 | 3 | 3,03 |
| | | | | 140 | | 2 | | | 1,44 | | | 2 | 1,44 |
| | | | 397 | 128 | | 1 | 3 | 3 | 6,12 | 5,66 | 9,82 | 7 | 9,82 |
| | | | | 129 | | | | 1 | | | 4,30 | 1 | 4,30 |
| | | | | 140 | | | 4 | 3 | | 3,66 | 5,35 | 7 | 5,35 |
| | | SmD3 | 159 | 85 | 13,6 | 10 | 15 | 96 | 16,46 | 6,72 | 9,09 | 121 | 16,46 |
| | | | | 86 | | 1 | 4 | 11 | 4,04 | 4,51 | 6,97 | 16 | 6,97 |
| | | | 558 | 32 | 16,1 | | | 2 | | | 5,84 | 2 | 5,84 |
| | Snu17/Ist3 | Bud13/Cwc26 | 10 | 244 | | | 2 | | | 4,43 | | 2 | 4,43 |
| | | | 133 | 169 | | | 2 | 1 | | 4,84 | 2,06 | 3 | 4,84 |
| | | | | 181 | | | 1 | 3 | | 3,77 | 5,55 | 4 | 5,55 |
| | | | | 213 | | 3 | 5 | 3 | 6,15 | 6,66 | 6,20 | 11 | 6,66 |
| | | | 138 | 169 | | 4 | 7 | 4 | 3,39 | 6,93 | 8,23 | 15 | 8,23 |
| | | | | 179 | | | 4 | 6 | | 4,88 | 14,63 | 10 | 14,63 |
| | | | | 180 | | | | 2 | | | 6,88 | 2 | 6,88 |
| | | | | 181 | | 12 | 17 | 48 | 10,00 | 6,95 | 7,94 | 77 | 10,00 |
| | | | | 201 | | 1 | 4 | 16 | 4,09 | 3,27 | 9,39 | 21 | 9,39 |
| | | | | 206 | | 3 | | 4 | 11,35 | | 7,72 | 7 | 11,35 |
| | | | | 213 | | 5 | 6 | 5 | 8,35 | 7,00 | 9,39 | 16 | 9,39 |
| | | | 143 | 179 | | 1 | 2 | 4 | 2,73 | 1,41 | 9,46 | 7 | 9,46 |
| | | | | 181 | | | 2 | 2 | | 0,52 | 1,85 | 4 | 1,85 |
| | | | | 201 | | | | 6 | | | 5,09 | 6 | 5,09 |
| | | | | 206 | | 1 | | | 0,97 | | | 1 | 0,97 |
| | | | | 213 | | 1 | | | 0,90 | | | 1 | 0,90 |
| | | Cwc22 | 138 | 520 | | | | 1 | | | 4,91 | 1 | 4,91 |
| | | | 143 | 530 | | 1 | | | 2,93 | | | 1 | 2,93 |
| | | Ecm2 | 123 | 188 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | Hsh155 | 10 | 500 | | 2 | | | 14,08 | | | 2 | 14,08 |
| | | | 96 | 66 | | 5 | 2 | 5 | 3,20 | 1,92 | 3,46 | 12 | 3,46 |
| | | | | 104 | | | | 2 | | | 4,99 | 2 | 4,99 |
| | | | 103 | 410 | | 14 | | | 15,45 | | | 14 | 15,45 |
| | | | | 455 | 17,8 | 6 | | | 12,69 | | | 6 | 12,69 |
| | | Prp45 | 143 | 287 | | | | 1 | | | 2,17 | 1 | 2,17 |
| | Spp2 | Brr2 | 38 | 168 | | | | 1 | | | 4,12 | 1 | 4,12 |
| | | | | 445 | | | | 1 | | | 5,97 | 1 | 5,97 |
| | | | | 454 | | | | 5 | | | 3,46 | 5 | 3,46 |
| | | | | 769 | | | | 4 | | | 10,34 | 4 | 10,34 |
| | | | 46 | 769 | | | | 1 | | | 4,44 | 1 | 4,44 |
| | | | 58 | 91 | | | | 3 | | | 15,52 | 3 | 15,52 |
| | | | | 445 | | 1 | | | 3,83 | | | 1 | 3,83 |
| | | | 68 | 454 | | 2 | | 1 | 1,65 | | 1,27 | 3 | 1,65 |
| | | | 133 | 74 | | | | 1 | | | 6,69 | 1 | 6,69 |
| | | | | 85 | | | | 1 | | | 3,56 | 1 | 3,56 |
| | | | | 91 | | 1 | | 5 | 0,62 | | 16,93 | 6 | 16,93 |
| | | Bud13/Cwc26 | 151 | 115 | | | | 8 | | | 10,72 | 8 | 10,72 |
| | | | | 120 | | 13 | | 17 | 12,61 | | 9,30 | 30 | 12,61 |
| | | | | 136 | | 3 | | 7 | 7,57 | | 13,17 | 10 | 13,17 |
| | | | | 146 | | 2 | | 1 | 0,69 | | 2,77 | 3 | 2,77 |
| | | | 154 | 120 | | 3 | | | 1,97 | | | 3 | 1,97 |
| | | | | 136 | | | | 1 | | | 5,35 | 1 | 5,35 |
| | | | | 146 | | 1 | | 2 | 1,81 | | 9,42 | 3 | 9,42 |
| | | | 181 | 151 | | | | 1 | | | 2,59 | 1 | 2,59 |
| | | | 182 | 136 | | | | 2 | | | 4,89 | 2 | 4,89 |
| | | Clf1 | 151 | 458 | | | | 1 | | | 2,99 | 1 | 2,99 |
| | | Cwc24 | 151 | 4 | | 1 | | | 0,05 | | | 1 | 0,05 |
| | | Prp2 | 82 | 336 | | 2 | | 5 | 1,67 | | 7,16 | 7 | 7,16 |
| | | | | 632 | | | | 1 | | | 3,53 | 1 | 3,53 |
| | | | | 750 | | 1 | | 1 | 1,21 | | 3,93 | 2 | 3,93 |
| | | | | 756 | | 1 | | | 1,91 | | | 1 | 1,91 |
| | | | 83 | 336 | | 1 | | 4 | 2,28 | | 2,76 | 5 | 2,76 |
| | | | | 632 | | 2 | | 2 | 7,68 | | 7,77 | 4 | 7,77 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 640 | | 1 | | | 4,92 | | | 1 | 4,92 |
| | | | | 756 | | 1 | | 2 | 3,40 | | 2,90 | 3 | 3,40 |
| | | | 95 | 756 | | | | 1 | | | 5,34 | 1 | 5,34 |
| | | | 154 | 840 | | 1 | | | 2,83 | | | 1 | 2,83 |
| | | | 168 | 461 | | 4 | | 6 | 3,34 | | 5,84 | 10 | 5,84 |
| | | | 181 | 461 | | | | 1 | | | 2,80 | 1 | 2,80 |
| | | Prp8 | 14 | 835 | | 1 | | | 0,32 | | | 1 | 0,32 |
| | | Rse1 | 38 | 374 | | | | 6 | | | 12,26 | 6 | 12,26 |
| | | | 83 | 374 | | | | 1 | | | 4,28 | 1 | 4,28 |
| | | SmD2 | 3 | 80 | | | 1 | | | 0,21 | | 1 | 0,21 |
| | Syf1 | Brr2 | 362 | 259 | | 1 | | | 0,58 | | | 1 | 0,58 |
| | | Cef1 | 770 | 293 | | 3 | 4 | 2 | 3,68 | 4,58 | 3,13 | 9 | 4,58 |
| | | | | 294 | | | 1 | | | 1,22 | | 1 | 1,22 |
| | | | | 296 | | | 1 | | | 0,78 | | 1 | 0,78 |
| | | | | 312 | | 1 | | | 2,91 | | | 1 | 2,91 |
| | | Clf1 | 524 | 180 | | 3 | 5 | 3 | 5,16 | 2,04 | 5,79 | 11 | 5,79 |
| | | | 531 | 180 | | 2 | | 1 | 2,81 | | 2,27 | 3 | 2,81 |
| | | | 650 | 304 | | 8 | 3 | 5 | 16,67 | 5,17 | 6,87 | 16 | 16,67 |
| | | | 653 | 289 | | | | 1 | | | 8,83 | 1 | 8,83 |
| | | | | 304 | | 12 | 10 | 54 | 17,65 | 11,96 | 13,33 | 76 | 17,65 |
| | | Cus1 | 146 | 317 | | 4 | 5 | 3 | 15,41 | 11,09 | 10,86 | 12 | 15,41 |
| | | | | 329 | | | | 1 | | | 1,31 | 1 | 1,31 |
| | | Cwc2 | 424 | 320 | | 4 | 1 | 3 | 5,37 | 5,03 | 3,68 | 8 | 5,37 |
| | | | 524 | 310 | | | | 2 | | | 4,43 | 2 | 4,43 |
| | | | 531 | 310 | | | | 1 | | | 1,35 | 1 | 1,35 |
| | | Cwc22 | 311 | 548 | | | 1 | | | 26,34 | | 1 | 26,34 |
| | | Isy1 | 146 | 139 | | 2 | | | 5,57 | | | 2 | 5,57 |
| | | | | 143 | | 2 | 4 | 1 | 5,24 | 4,45 | 4,06 | 7 | 5,24 |
| | | | 220 | 157 | | | 1 | 4 | | 0,70 | 9,62 | 5 | 9,62 |
| | | | | 161 | | 3 | 7 | 9 | 2,63 | 2,37 | 4,94 | 19 | 4,94 |
| | | | | 171 | | 9 | 6 | 1 | 4,61 | 5,04 | 2,46 | 16 | 5,04 |
| | | | 249 | 157 | | | | 1 | | | 3,79 | 1 | 3,79 |
| | | | 259 | 7 | | | | 2 | | | 5,83 | 2 | 5,83 |
| | | | 328 | 7 | | 1 | 3 | 6 | 10,49 | 5,14 | 9,35 | 10 | 10,49 |
| | | | | 27 | | 1 | | | 2,03 | | | 1 | 2,03 |
| | | | | 40 | | 2 | 3 | 7 | 2,37 | 2,44 | 4,75 | 12 | 4,75 |
| | | | 424 | 7 | | 1 | 2 | 5 | 1,18 | 5,11 | 7,02 | 8 | 7,02 |
| | | Lea1 | 32 | 232 | | | 1 | 1 | | 2,40 | 1,79 | 2 | 2,40 |
| | | Ntc20 | 498 | 27 | | 6 | | 2 | 4,07 | | 8,58 | 8 | 8,58 |
| | | | 558 | 27 | | 2 | 2 | 2 | 1,41 | 1,40 | 5,11 | 6 | 5,11 |
| | | Pml1 | 372 | 153 | | | | 1 | | | 1,13 | 1 | 1,13 |
| | | Prp11 | 424 | 192 | | 1 | | 4 | 2,48 | | 7,93 | 5 | 7,93 |
| | | Prp21 | | | | 4 | | 12 | 3,40 | | 6,01 | 16 | 6,01 |
| | | Prp8 | 2 | 300 | | | 1 | | | 0,08 | | 1 | 0,08 |
| | | Syf2 | 362 | 11 | | 3 | 4 | 8 | 7,31 | 2,06 | 5,86 | 15 | 7,31 |
| | | | | 14 | | 1 | | 9 | 10,00 | | 5,80 | 10 | 10,00 |
| | | | 413 | 23 | | 1 | | | 9,20 | | | 1 | 9,20 |
| | | | | 26 | | 2 | 4 | 4 | 4,66 | 3,68 | 5,31 | 10 | 5,31 |
| | | | 424 | 26 | | | 1 | 1 | | 1,10 | 3,29 | 2 | 3,29 |
| | | | 524 | 132 | | | | 1 | | | 0,86 | 1 | 0,86 |
| | | | 531 | 121 | | | | 3 | | | 9,05 | 3 | 9,05 |
| | | Yju2/Cwc16 | 790 | 234 | | 1 | | | 1,32 | | | 1 | 1,32 |
| | Syf2 | Cef1 | 159 | 240 | | | | 1 | | | 3,73 | 1 | 3,73 |
| | | | | 247 | | | 1 | | | 1,07 | | 1 | 1,07 |
| | | | 173 | 239 | | 3 | 1 | | 4,95 | 0,55 | | 4 | 4,95 |
| | | | | 240 | | 5 | 6 | 10 | 7,61 | 11,75 | 9,07 | 21 | 11,75 |
| | | | | 247 | | | 4 | 6 | | 3,71 | 6,44 | 10 | 6,44 |
| | | | | 251 | | 2 | 1 | 2 | 4,91 | 1,42 | 8,77 | 5 | 8,77 |
| | | | | 259 | | 1 | | | 0,55 | | | 1 | 0,55 |
| | | Clf1 | 121 | 180 | | | | 8 | | | 9,41 | 8 | 9,41 |
| | | | 159 | 113 | | 7 | 7 | 5 | 4,73 | 2,95 | 7,19 | 19 | 7,19 |
| | | | 173 | 25 | | | 4 | 6 | | 2,24 | 4,57 | 10 | 4,57 |
| | | | | 113 | | 4 | | 2 | 10,42 | | 7,42 | 6 | 10,42 |
| | | Cwc15 | 9 | 102 | | 1 | | | 0,13 | | | 1 | 0,13 |
| | | Ecm2 | 148 | 138 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | Isy1 | 26 | 7 | | 1 | 4 | 3 | 1,75 | 2,47 | 4,26 | 8 | 4,26 |
| | | | | 27 | | | 1 | 4 | | 1,36 | 4,12 | 5 | 4,12 |
| | | | 173 | 42 | | 1 | 2 | | 5,98 | 1,83 | | 3 | 5,98 |
| | | Prp11 | 26 | 192 | | 2 | 3 | 5 | 3,34 | 5,17 | 6,42 | 10 | 6,42 |
| | | Prp21 | | | | | 1 | 1 | | 3,40 | 4,02 | 2 | 4,02 |
| | | Prp45 | 1 | 71 | | | | 2 | | | 0,22 | 2 | 0,22 |
| | | | 142 | 36 | | | | 1 | | | 1,02 | 1 | 1,02 |
| | | | 145 | 36 | | 15 | 10 | 27 | 13,10 | 3,00 | 5,38 | 52 | 13,10 |
| | | | 151 | 36 | | 4 | 5 | 10 | 12,24 | 4,37 | 18,80 | 19 | 18,80 |
| | | Prp46 | 145 | 56 | | | | 1 | | | 2,52 | 1 | 2,52 |
| | | | | 67 | | | | 1 | | | 3,17 | 1 | 3,17 |
| | | | | 87 | | 1 | | 3 | 7,44 | | 6,64 | 4 | 7,44 |
| | | | | 88 | | 2 | | | 3,30 | | | 2 | 3,30 |
| | | SmB | 14 | 117 | | | | 1 | | | 2,79 | 1 | 2,79 |
| | | Syf1 | 11 | 362 | | 3 | 4 | 8 | 7,31 | 2,06 | 5,86 | 15 | 7,31 |
| | | | 14 | 362 | | 1 | | 9 | 10,00 | | 5,80 | 10 | 10,00 |
| | | | 23 | 413 | | 1 | | | 9,20 | | | 1 | 9,20 |
| | | | 26 | 413 | | 2 | 4 | 4 | 4,66 | 3,68 | 5,31 | 10 | 5,31 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 424 | | | 1 | 1 | | 1,10 | 3,29 | 2 | 3,29 |
| | | | 121 | 531 | | | | 3 | | | 9,05 | 3 | 9,05 |
| | | | 132 | 524 | | | | 1 | | | 0,86 | 1 | 0,86 |
| | | Yju2/Cwc16 | 11 | 22 | | 1 | | | 1,04 | | | 1 | 1,04 |
| | Yju2/Cwc16 | Isy1 | 63 | 103 | | | 1 | | | 0,27 | | 1 | 0,27 |
| | | Prp2 | 29 | 732 | | 2 | | | 0,44 | | | 2 | 0,44 |
| | | Prp45 | 1 | 129 | | 1 | | | 0,59 | | | 1 | 0,59 |
| | | Prp9 | 68 | 371 | | | | 1 | | | 2,32 | 1 | 2,32 |
| | | SmB | 2 | 105 | | | | 1 | | | 1,39 | 1 | 1,39 |
| | | SmD1 | 74 | 128 | | | | 1 | | | 2,94 | 1 | 2,94 |
| | | | | 140 | | | | 1 | | | 1,97 | 1 | 1,97 |
| | | Syf1 | 234 | 790 | | 1 | | | 1,32 | | | 1 | 1,32 |
| | | Syf2 | 22 | 11 | | 1 | | | 1,04 | | | 1 | 1,04 |
| | Ysf3 | Cus1 | 12 | 102 | | | | 1 | | | 3,31 | 1 | 3,31 |
| | | | 15 | 102 | | 1 | | 1 | 0,22 | | 1,15 | 2 | 1,15 |
| | | Cwc22 | 15 | 203 | 147,7 | 1 | | | 0,49 | | | 1 | 0,49 |
| | | Hsh155 | 4 | 932 | | | 2 | | | 0,68 | | 2 | 0,68 |
| | | | 12 | 932 | 12,7 | | 3 | | | 3,56 | | 3 | 3,56 |
| | | Rds3 | 9 | 13 | 16,6 | | 1 | | | 0,14 | | 1 | 0,14 |
| Intra | Brr2 | Brr2 | 1 | 2108 | | | 1 | | | 0,54 | | 1 | 0,54 |
| | | | 2 | 28 | | 1 | | 7 | 4,24 | | 6,67 | 8 | 6,67 |
| | | | | 50 | | | | 6 | | | 10,41 | 6 | 10,41 |
| | | | | 74 | | | | 1 | | | 1,99 | 1 | 1,99 |
| | | | | 304 | | | | 1 | | | 2,17 | 1 | 2,17 |
| | | | | 967 | | | | 1 | | | 4,29 | 1 | 4,29 |
| | | | | 1437 | | | | 2 | | | 2,83 | 2 | 2,83 |
| | | | | 1623 | | | | 1 | | | 2,94 | 1 | 2,94 |
| | | | | 1634 | | | | 4 | | | 9,97 | 4 | 9,97 |
| | | | 7 | 25 | | | | 1 | | | 3,75 | 1 | 3,75 |
| | | | | 50 | | | | 2 | | | 4,06 | 2 | 4,06 |
| | | | | 967 | | | | 1 | | | 1,41 | 1 | 1,41 |
| | | | 9 | 91 | | | | 1 | | | 2,74 | 1 | 2,74 |
| | | | 11 | 720 | | | | 1 | | | 0,99 | 1 | 0,99 |
| | | | 25 | 7 | | | | 1 | | | 3,75 | 1 | 3,75 |
| | | | | 50 | | | 3 | 2 | | 1,47 | 3,50 | 5 | 3,50 |
| | | | | 59 | | | | 1 | | | 2,26 | 1 | 2,26 |
| | | | | 454 | | | 1 | | | 0,74 | | 1 | 0,74 |
| | | | | 1437 | | | | 1 | | | 1,30 | 1 | 1,30 |
| | | | | 1623 | | | 1 | | | 1,37 | | 1 | 1,37 |
| | | | 28 | 2 | | 1 | | 7 | 4,24 | | 6,67 | 8 | 6,67 |
| | | | | 50 | | | 4 | 9 | | 3,74 | 4,89 | 13 | 4,89 |
| | | | | 71 | | | 1 | | | 1,55 | | 1 | 1,55 |
| | | | | 74 | | | | 2 | | | 5,74 | 2 | 5,74 |
| | | | | 82 | | | | 1 | | | 5,97 | 1 | 5,97 |
| | | | | 91 | | | 1 | | | 0,39 | | 1 | 0,39 |
| | | | | 454 | | | 1 | | | 2,58 | | 1 | 2,58 |
| | | | | 967 | | | | 1 | | | 10,20 | 1 | 10,20 |
| | | | 50 | 2 | | | | 6 | | | 10,41 | 6 | 10,41 |
| | | | | 7 | | | | 2 | | | 4,06 | 2 | 4,06 |
| | | | | 25 | | | 3 | 2 | | 1,47 | 3,50 | 5 | 3,50 |
| | | | | 28 | | | 4 | 9 | | 3,74 | 4,89 | 13 | 4,89 |
| | | | | 59 | | 2 | 4 | 57 | 5,07 | 10,06 | 14,40 | 63 | 14,40 |
| | | | | 71 | | | 2 | 8 | | 3,53 | 3,39 | 10 | 3,53 |
| | | | | 74 | | | 2 | 13 | | 7,80 | 9,88 | 15 | 9,88 |
| | | | | 82 | | | | 4 | | | 7,03 | 4 | 7,03 |
| | | | | 85 | | | 1 | 4 | | 0,48 | 6,86 | 5 | 6,86 |
| | | | | 91 | | | 1 | 4 | | 5,34 | 8,41 | 5 | 8,41 |
| | | | | 967 | | | | 1 | | | 1,11 | 1 | 1,11 |
| | | | | 1623 | | | | 1 | | | 3,23 | 1 | 3,23 |
| | | | | 1634 | | | | 1 | | | 4,28 | 1 | 4,28 |
| | | | 59 | 25 | | | | 1 | | | 2,26 | 1 | 2,26 |
| | | | | 50 | | 2 | 4 | 57 | 5,07 | 10,06 | 14,40 | 63 | 14,40 |
| | | | | 74 | | 4 | 9 | 11 | 6,95 | 14,69 | 10,62 | 24 | 14,69 |
| | | | | 82 | | | 1 | 7 | | 0,59 | 9,87 | 8 | 9,87 |
| | | | | 85 | | | 3 | 1 | | 1,78 | 2,87 | 4 | 2,87 |
| | | | | 91 | | | 1 | 7 | | 7,99 | 19,64 | 8 | 19,64 |
| | | | 71 | 28 | | | 1 | | | 1,55 | | 1 | 1,55 |
| | | | | 50 | | | 2 | 8 | | 3,53 | 3,39 | 10 | 3,53 |
| | | | | 82 | | | 7 | 6 | | 6,25 | 5,63 | 13 | 6,25 |
| | | | | 85 | | | 6 | 3 | | 5,97 | 4,96 | 9 | 5,97 |
| | | | | 90 | | | 3 | 1 | | 4,12 | 2,51 | 4 | 4,12 |
| | | | | 91 | | | 4 | 4 | | 5,55 | 9,23 | 8 | 9,23 |
| | | | 74 | 2 | | | | 1 | | | 1,99 | 1 | 1,99 |
| | | | | 28 | | | | 2 | | | 5,74 | 2 | 5,74 |
| | | | | 50 | | | 2 | 13 | | 7,80 | 9,88 | 15 | 9,88 |
| | | | | 59 | | 4 | 9 | 11 | 6,95 | 14,69 | 10,62 | 24 | 14,69 |
| | | | | 85 | | 1 | 6 | 20 | 4,46 | 5,70 | 8,15 | 27 | 8,15 |
| | | | | 90 | | | 2 | 3 | | 0,97 | 4,30 | 5 | 4,30 |
| | | | | 91 | | | 5 | 9 | | 13,71 | 15,07 | 14 | 15,07 |
| | | | 82 | 28 | | | | 1 | | | 5,97 | 1 | 5,97 |
| | | | | 50 | | | | 4 | | | 7,03 | 4 | 7,03 |
| | | | | 59 | | | 1 | 7 | | 0,59 | 9,87 | 8 | 9,87 |
| | | | | 71 | | | 7 | 6 | | 6,25 | 5,63 | 13 | 6,25 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 90 | | | 1 | 12 | | 0,39 | 5,76 | 13 | 5,76 |
| | | | | 91 | | 2 | 6 | 19 | 4,57 | 8,99 | 13,27 | 27 | 13,27 |
| | | | | 1051 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | | 85 | 50 | | | 1 | 4 | | 0,48 | 6,86 | 5 | 6,86 |
| | | | | 59 | | | 3 | 1 | | 1,78 | 2,87 | 4 | 2,87 |
| | | | | 71 | | | 6 | 3 | | 5,97 | 4,96 | 9 | 5,97 |
| | | | | 74 | | 1 | 6 | 20 | 4,46 | 5,70 | 8,15 | 27 | 8,15 |
| | | | | 91 | | 11 | 17 | 30 | 8,76 | 9,01 | 11,41 | 58 | 11,41 |
| | | | | 454 | | | 2 | | | 0,25 | | 2 | 0,25 |
| | | | 90 | 71 | | | 3 | 1 | | 4,12 | 2,51 | 4 | 4,12 |
| | | | | 74 | | | 2 | 3 | | 0,97 | 4,30 | 5 | 4,30 |
| | | | | 82 | | | 1 | 12 | | 0,39 | 5,76 | 13 | 5,76 |
| | | | | 454 | | 1 | 6 | 5 | 1,51 | 2,79 | 4,69 | 12 | 4,69 |
| | | | 91 | 9 | | | | 1 | | | 2,74 | 1 | 2,74 |
| | | | | 28 | | | 1 | | | 0,39 | | 1 | 0,39 |
| | | | | 50 | | | 1 | 4 | | 5,34 | 8,41 | 5 | 8,41 |
| | | | | 59 | | | 1 | 7 | | 7,99 | 19,64 | 8 | 19,64 |
| | | | | 71 | | | 4 | 4 | | 5,55 | 9,23 | 8 | 9,23 |
| | | | | 74 | | | 5 | 9 | | 13,71 | 15,07 | 14 | 15,07 |
| | | | | 82 | | 2 | 6 | 19 | 4,57 | 8,99 | 13,27 | 27 | 13,27 |
| | | | | 85 | | 11 | 17 | 30 | 8,76 | 9,01 | 11,41 | 58 | 11,41 |
| | | | | 431 | | | | 1 | | | 5,50 | 1 | 5,50 |
| | | | | 445 | | | 2 | | | 5,94 | | 2 | 5,94 |
| | | | | 1051 | | 4 | | 2 | 1,74 | | 4,21 | 6 | 4,21 |
| | | | 152 | 190 | 11,8 | | | 20 | | | 21,68 | 20 | 21,68 |
| | | | 168 | 717 | 9,9 | 1 | 2 | 2 | 0,51 | 1,34 | 2,54 | 5 | 2,54 |
| | | | 190 | 152 | 11,8 | | | 20 | | | 21,68 | 20 | 21,68 |
| | | | 271 | 304 | | | 1 | 6 | | 3,22 | 7,63 | 7 | 7,63 |
| | | | | 351 | | | | 1 | | | 1,03 | 1 | 1,03 |
| | | | 276 | 304 | | | | 1 | | | 7,89 | 1 | 7,89 |
| | | | | 380 | | | | 1 | | | 14,08 | 1 | 14,08 |
| | | | | 967 | 52,2 | | | 1 | | | 4,52 | 1 | 4,52 |
| | | | 304 | 2 | | | | 1 | | | 2,17 | 1 | 2,17 |
| | | | | 271 | | | 1 | 6 | | 3,22 | 7,63 | 7 | 7,63 |
| | | | | 276 | | | | 1 | | | 7,89 | 1 | 7,89 |
| | | | | 339 | | 5 | 7 | 3 | 6,02 | 8,77 | 9,54 | 15 | 9,54 |
| | | | | 414 | | | | 2 | | | 1,99 | 2 | 1,99 |
| | | | | 417 | | | 2 | 7 | | 3,17 | 12,29 | 9 | 12,29 |
| | | | | 967 | | | | 1 | | | 1,95 | 1 | 1,95 |
| | | | | 1372 | | | | 1 | | | 12,26 | 1 | 12,26 |
| | | | | 1529 | | | | 2 | | | 10,19 | 2 | 10,19 |
| | | | | 1634 | | | | 1 | | | 2,70 | 1 | 2,70 |
| | | | 339 | 304 | | 5 | 7 | 3 | 6,02 | 8,77 | 9,54 | 15 | 9,54 |
| | | | 351 | 271 | | | | 1 | | | 1,03 | 1 | 1,03 |
| | | | | 398 | | | | 1 | | | 1,86 | 1 | 1,86 |
| | | | | 417 | | | | 1 | | | 1,71 | 1 | 1,71 |
| | | | 364 | 1529 | | | | 1 | | | 6,89 | 1 | 6,89 |
| | | | 380 | 276 | | | | 1 | | | 14,08 | 1 | 14,08 |
| | | | 390 | 398 | | | 1 | | | 0,09 | | 1 | 0,09 |
| | | | | 417 | | | 2 | 2 | | 5,20 | 1,46 | 4 | 5,20 |
| | | | 398 | 351 | | | | 1 | | | 1,86 | 1 | 1,86 |
| | | | | 390 | | | 1 | | | 0,09 | | 1 | 0,09 |
| | | | | 967 | | | | 1 | | | 3,64 | 1 | 3,64 |
| | | | 414 | 304 | | | | 2 | | | 1,99 | 2 | 1,99 |
| | | | | 417 | | 3 | 7 | 10 | 9,40 | 3,59 | 6,31 | 20 | 9,40 |
| | | | | 967 | | 2 | 1 | 13 | 2,60 | 0,39 | 8,45 | 16 | 8,45 |
| | | | 417 | 304 | | | 2 | 7 | | 3,17 | 12,29 | 9 | 12,29 |
| | | | | 351 | | | | 1 | | | 1,71 | 1 | 1,71 |
| | | | | 390 | | | 2 | 2 | | 5,20 | 1,46 | 4 | 5,20 |
| | | | | 414 | | 3 | 7 | 10 | 9,40 | 3,59 | 6,31 | 20 | 9,40 |
| | | | | 967 | | 5 | 10 | 25 | 5,15 | 7,58 | 8,61 | 40 | 8,61 |
| | | | 431 | 91 | | | | 1 | | | 5,50 | 1 | 5,50 |
| | | | 445 | 91 | | | 2 | | | 5,94 | | 2 | 5,94 |
| | | | | 457 | 21,5 | | 2 | | | 1,49 | | 2 | 1,49 |
| | | | 454 | 25 | | | 1 | | | 0,74 | | 1 | 0,74 |
| | | | | 28 | | | 1 | | | 2,58 | | 1 | 2,58 |
| | | | | 85 | | | 2 | | | 0,25 | | 2 | 0,25 |
| | | | | 90 | | 1 | 6 | 5 | 1,51 | 2,79 | 4,69 | 12 | 4,69 |
| | | | 457 | 445 | 21,5 | | 2 | | | 1,49 | | 2 | 1,49 |
| | | | 546 | 549 | 8,3 | 24 | 54 | 12 | 14,56 | 9,53 | 11,58 | 90 | 14,56 |
| | | | 549 | 546 | 8,3 | 24 | 54 | 12 | 14,56 | 9,53 | 11,58 | 90 | 14,56 |
| | | | | 584 | 13,3 | 7 | 4 | 8 | 11,10 | 9,36 | 9,50 | 19 | 11,10 |
| | | | | 1904 | 21,4 | 7 | 8 | 51 | 18,55 | 7,94 | 9,46 | 66 | 18,55 |
| | | | 564 | 611 | 9,9 | | 9 | 8 | | 8,38 | 11,63 | 17 | 11,63 |
| | | | | 1138 | 20,9 | 2 | 8 | 95 | 2,38 | 4,23 | 10,34 | 105 | 10,34 |
| | | | 584 | 549 | 13,3 | 7 | 4 | 8 | 11,10 | 9,36 | 9,50 | 19 | 11,10 |
| | | | | 597 | 13,3 | 2 | 2 | 7 | 6,03 | 8,55 | 15,58 | 11 | 15,58 |
| | | | 597 | 584 | 13,3 | 2 | 2 | 7 | 6,03 | 8,55 | 15,58 | 11 | 15,58 |
| | | | | 1589 | 19,0 | 5 | 6 | 69 | 11,85 | 11,53 | 25,58 | 80 | 25,58 |
| | | | | 1896 | 13,4 | 12 | 10 | 29 | 3,90 | 1,34 | 3,41 | 51 | 3,90 |
| | | | | 1904 | 20,8 | 3 | 13 | 15 | 2,55 | 3,42 | 4,62 | 31 | 4,62 |
| | | | 611 | 564 | 9,9 | | 9 | 8 | | 8,38 | 11,63 | 17 | 11,63 |
| | | | | 1138 | 22,4 | | | 4 | | | 10,10 | 4 | 10,10 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 659 | 967 | 22,4 | | | 1 | | | 2,35 | 1 | 2,35 |
| | | | 717 | 168 | 9,9 | 1 | 2 | 2 | 0,51 | 1,34 | 2,54 | 5 | 2,54 |
| | | | | 720 | 4,9 | 1 | 7 | 9 | 5,58 | 0,65 | 3,77 | 17 | 5,58 |
| | | | 720 | 11 | | | | 1 | | | 0,99 | 1 | 0,99 |
| | | | | 717 | 4,9 | 1 | 7 | 9 | 5,58 | 0,65 | 3,77 | 17 | 5,58 |
| | | | | 748 | 17,1 | | 4 | 10 | | 3,83 | 5,87 | 14 | 5,87 |
| | | | 748 | 720 | 17,1 | | 4 | 10 | | 3,83 | 5,87 | 14 | 5,87 |
| | | | | 758 | 15,6 | | | 2 | | | 7,77 | 2 | 7,77 |
| | | | | 760 | 18,2 | | 1 | | | 3,01 | | 1 | 3,01 |
| | | | | 769 | 25,3 | | 1 | | | 1,75 | | 1 | 1,75 |
| | | | | 795 | 15,6 | 17 | 68 | 128 | 10,40 | 6,59 | 7,71 | 213 | 10,40 |
| | | | | 1088 | 14,8 | | | 2 | | | 1,49 | 2 | 1,49 |
| | | | 758 | 748 | 15,6 | | | 2 | | | 7,77 | 2 | 7,77 |
| | | | | 778 | 16,5 | | 8 | 28 | | 7,79 | 11,55 | 36 | 11,55 |
| | | | | 782 | 16,8 | | 12 | 1 | | 2,09 | 1,53 | 13 | 2,09 |
| | | | | 795 | 9,2 | 11 | 21 | 5 | 7,32 | 4,12 | 3,85 | 37 | 7,32 |
| | | | 760 | 748 | 18,2 | | 1 | | | 3,01 | | 1 | 3,01 |
| | | | 769 | 748 | 25,3 | | 1 | | | 1,75 | | 1 | 1,75 |
| | | | | 778 | 13,2 | | 2 | 1 | | 3,98 | 1,63 | 3 | 3,98 |
| | | | 778 | 758 | 16,5 | | 8 | 28 | | 7,79 | 11,55 | 36 | 11,55 |
| | | | | 769 | 13,2 | | 2 | 1 | | 3,98 | 1,63 | 3 | 3,98 |
| | | | | 795 | 13,5 | 3 | 12 | 9 | 4,65 | 4,52 | 5,37 | 24 | 5,37 |
| | | | 782 | 758 | 16,8 | | 12 | 1 | | 2,09 | 1,53 | 13 | 2,09 |
| | | | | 795 | 10,5 | | 7 | 6 | | 13,60 | 9,20 | 13 | 13,60 |
| | | | 795 | 748 | 15,6 | 17 | 68 | 128 | 10,40 | 6,59 | 7,71 | 213 | 10,40 |
| | | | | 758 | 9,2 | 11 | 21 | 5 | 7,32 | 4,12 | 3,85 | 37 | 7,32 |
| | | | | 778 | 13,5 | 3 | 12 | 9 | 4,65 | 4,52 | 5,37 | 24 | 5,37 |
| | | | | 782 | 10,5 | | 7 | 6 | | 13,60 | 9,20 | 13 | 13,60 |
| | | | 967 | 2 | | | | 1 | | | 4,29 | 1 | 4,29 |
| | | | | 7 | | | | 1 | | | 1,41 | 1 | 1,41 |
| | | | | 28 | | | | 1 | | | 10,20 | 1 | 10,20 |
| | | | | 50 | | | | 1 | | | 1,11 | 1 | 1,11 |
| | | | | 276 | 52,2 | | | 1 | | | 4,52 | 1 | 4,52 |
| | | | | 304 | | | | 1 | | | 1,95 | 1 | 1,95 |
| | | | | 398 | | | | 1 | | | 3,64 | 1 | 3,64 |
| | | | | 414 | | 2 | 1 | 13 | 2,60 | 0,39 | 8,45 | 16 | 8,45 |
| | | | | 417 | | 5 | 10 | 25 | 5,15 | 7,58 | 8,61 | 40 | 8,61 |
| | | | | 659 | 22,4 | | | 1 | | | 2,35 | 1 | 2,35 |
| | | | 1042 | 1055 | 20,3 | | 1 | | | 1,60 | | 1 | 1,60 |
| | | | 1051 | 82 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | | | 91 | | 4 | | 2 | 1,74 | | 4,21 | 6 | 4,21 |
| | | | | 1055 | 5,8 | 1 | 5 | 13 | 2,44 | 2,76 | 6,40 | 19 | 6,40 |
| | | | 1055 | 1042 | 20,3 | | 1 | | | 1,60 | | 1 | 1,60 |
| | | | | 1051 | 5,8 | 1 | 5 | 13 | 2,44 | 2,76 | 6,40 | 19 | 6,40 |
| | | | 1088 | 748 | 14,8 | | | 2 | | | 1,49 | 2 | 1,49 |
| | | | 1138 | 564 | 20,9 | 2 | 8 | 95 | 2,38 | 4,23 | 10,34 | 105 | 10,34 |
| | | | | 611 | 22,4 | | | 4 | | | 10,10 | 4 | 10,10 |
| | | | | 1150 | 14,1 | 1 | 8 | 31 | 3,91 | 9,00 | 14,48 | 40 | 14,48 |
| | | | 1150 | 1138 | 14,1 | 1 | 8 | 31 | 3,91 | 9,00 | 14,48 | 40 | 14,48 |
| | | | | 1187 | 15,1 | | 2 | | | 0,96 | | 2 | 0,96 |
| | | | | 1634 | 57,5 | | 1 | | | 1,42 | | 1 | 1,42 |
| | | | 1158 | 1187 | 13,9 | | 4 | 6 | | 2,27 | 8,41 | 10 | 8,41 |
| | | | 1187 | 1150 | 15,1 | | 2 | | | 0,96 | | 2 | 0,96 |
| | | | | 1158 | 13,9 | | 4 | 6 | | 2,27 | 8,41 | 10 | 8,41 |
| | | | 1372 | 304 | | | | 1 | | | 12,26 | 1 | 12,26 |
| | | | 1392 | 1504 | 12,8 | | | 1 | | | 1,78 | 1 | 1,78 |
| | | | 1437 | 2 | | | | 2 | | | 2,83 | 2 | 2,83 |
| | | | | 25 | | | | 1 | | | 1,30 | 1 | 1,30 |
| | | | | 2116 | 16,9 | | | 3 | | | 6,61 | 3 | 6,61 |
| | | | | 2121 | 16,5 | 7 | 14 | 74 | 14,39 | 7,39 | 13,36 | 95 | 14,39 |
| | | | 1441 | 2121 | 19,1 | | | 2 | | | 15,61 | 2 | 15,61 |
| | | | 1504 | 1392 | 12,8 | | | 1 | | | 1,78 | 1 | 1,78 |
| | | | 1529 | 304 | | | | 2 | | | 10,19 | 2 | 10,19 |
| | | | | 364 | | | | 1 | | | 6,89 | 1 | 6,89 |
| | | | 1589 | 597 | 19,0 | 5 | 6 | 69 | 11,85 | 11,53 | 25,58 | 80 | 25,58 |
| | | | | 1896 | 10,2 | 1 | 4 | 24 | 1,08 | 0,98 | 3,73 | 29 | 3,73 |
| | | | | 1904 | 19,2 | 8 | 11 | 72 | 16,27 | 6,25 | 10,71 | 91 | 16,27 |
| | | | 1600 | 1634 | 14,5 | | | 6 | | | 9,18 | 6 | 9,18 |
| | | | 1603 | 1634 | 14,4 | | 3 | 6 | | 1,02 | 4,62 | 9 | 4,62 |
| | | | 1623 | 2 | | | | 1 | | | 2,94 | 1 | 2,94 |
| | | | | 25 | | | 1 | | | 1,37 | | 1 | 1,37 |
| | | | | 50 | | | | 1 | | | 3,23 | 1 | 3,23 |
| | | | 1634 | 2 | | | | 4 | | | 9,97 | 4 | 9,97 |
| | | | | 50 | | | | 1 | | | 4,28 | 1 | 4,28 |
| | | | | 304 | | | | 1 | | | 2,70 | 1 | 2,70 |
| | | | | 1150 | 57,5 | | 1 | | | 1,42 | | 1 | 1,42 |
| | | | | 1600 | 14,5 | | | 6 | | | 9,18 | 6 | 9,18 |
| | | | | 1603 | 14,4 | | 3 | 6 | | 1,02 | 4,62 | 9 | 4,62 |
| | | | 1896 | 597 | 13,4 | 12 | 10 | 29 | 3,90 | 1,34 | 3,41 | 51 | 3,90 |
| | | | | 1589 | 10,2 | 1 | 4 | 24 | 1,08 | 0,98 | 3,73 | 29 | 3,73 |
| | | | | 1904 | 14,9 | | 4 | 6 | | 3,36 | 5,90 | 10 | 5,90 |
| | | | 1904 | 549 | 21,4 | 7 | 8 | 51 | 18,55 | 7,94 | 9,46 | 66 | 18,55 |
| | | | | 597 | 20,8 | 3 | 13 | 15 | 2,55 | 3,42 | 4,62 | 31 | 4,62 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 1589 | 19,2 | 8 | 11 | 72 | 16,27 | 6,25 | 10,71 | 91 | 16,27 |
| | | | | 1896 | 14,9 | | 4 | 6 | | 3,36 | 5,90 | 10 | 5,90 |
| | | | 2070 | 2115 | 12,7 | | 6 | 8 | | 6,52 | 10,99 | 14 | 10,99 |
| | | | 2108 | 1 | | | 1 | | | 0,54 | | 1 | 0,54 |
| | | | 2115 | 2070 | 12,7 | | 6 | 8 | | 6,52 | 10,99 | 14 | 10,99 |
| | | | | 2121 | 17,3 | | 5 | 4 | | 2,09 | 2,43 | 9 | 2,43 |
| | | | 2116 | 1437 | 16,9 | | | 3 | | | 6,61 | 3 | 6,61 |
| | | | 2121 | 1437 | 16,5 | 7 | 14 | 74 | 14,39 | 7,39 | 13,36 | 95 | 14,39 |
| | | | | 1441 | 19,1 | | | 2 | | | 15,61 | 2 | 15,61 |
| | | | | 2115 | 17,3 | | 5 | 4 | | 2,09 | 2,43 | 9 | 2,43 |
| | Bud13/Cwc26 | Bud13/Cwc26 | 2 | 101 | | | | 1 | | | 3,08 | 1 | 3,08 |
| | | | 15 | 19 | | 1 | | | 0,21 | | | 1 | 0,21 |
| | | | | 21 | | 1 | | | 5,91 | | | 1 | 5,91 |
| | | | 19 | 15 | | 1 | | | 0,21 | | | 1 | 0,21 |
| | | | | 41 | | | | 1 | | | 1,56 | 1 | 1,56 |
| | | | 21 | 15 | | 1 | | | 5,91 | | | 1 | 5,91 |
| | | | 24 | 35 | | | | 3 | | | 3,80 | 3 | 3,80 |
| | | | | 41 | | | | 1 | | | 3,47 | 1 | 3,47 |
| | | | | 53 | | | | 1 | | | 2,49 | 1 | 2,49 |
| | | | 25 | 35 | | 1 | 1 | 2 | 1,20 | 0,84 | 5,34 | 4 | 5,34 |
| | | | | 41 | | | | 1 | | | 2,07 | 1 | 2,07 |
| | | | 28 | 41 | | 1 | | 8 | 6,18 | | 14,29 | 9 | 14,29 |
| | | | | 53 | | | | 6 | | | 6,54 | 6 | 6,54 |
| | | | 35 | 24 | | | | 3 | | | 3,80 | 3 | 3,80 |
| | | | | 25 | | 1 | 1 | 2 | 1,20 | 0,84 | 5,34 | 4 | 5,34 |
| | | | | 53 | | | | 3 | | | 8,98 | 3 | 8,98 |
| | | | | 61 | | | | 1 | | | 3,56 | 1 | 3,56 |
| | | | 41 | 19 | | | | 1 | | | 1,56 | 1 | 1,56 |
| | | | | 24 | | | | 1 | | | 3,47 | 1 | 3,47 |
| | | | | 25 | | | | 1 | | | 2,07 | 1 | 2,07 |
| | | | | 28 | | 1 | | 8 | 6,18 | | 14,29 | 9 | 14,29 |
| | | | | 53 | | | 4 | 9 | | 3,09 | 12,17 | 13 | 12,17 |
| | | | | 61 | | | 3 | 3 | | 3,34 | 7,69 | 6 | 7,69 |
| | | | | 64 | | | 1 | | | 1,88 | | 1 | 1,88 |
| | | | | 68 | | 1 | 1 | 2 | 4,67 | 1,93 | 7,43 | 4 | 7,43 |
| | | | | 72 | | | | 1 | | | 3,22 | 1 | 3,22 |
| | | | 53 | 24 | | | | 1 | | | 2,49 | 1 | 2,49 |
| | | | | 28 | | | | 6 | | | 6,54 | 6 | 6,54 |
| | | | | 35 | | | | 3 | | | 8,98 | 3 | 8,98 |
| | | | | 41 | | | 4 | 9 | | 3,09 | 12,17 | 13 | 12,17 |
| | | | | 68 | | | 1 | 3 | | 1,13 | 5,85 | 4 | 5,85 |
| | | | | 115 | | | | 1 | | | 2,39 | 1 | 2,39 |
| | | | 61 | 35 | | | | 1 | | | 3,56 | 1 | 3,56 |
| | | | | 41 | | | 3 | 3 | | 3,34 | 7,69 | 6 | 7,69 |
| | | | | 66 | | 1 | | | 3,45 | | | 1 | 3,45 |
| | | | | 68 | | 2 | | 7 | 7,24 | | 5,57 | 9 | 7,24 |
| | | | | 72 | | | | 1 | | | 3,68 | 1 | 3,68 |
| | | | | 115 | | | | 3 | | | 4,79 | 3 | 4,79 |
| | | | 64 | 41 | | | 1 | | | 1,88 | | 1 | 1,88 |
| | | | | 68 | | 1 | 5 | 3 | 2,98 | 1,90 | 3,80 | 9 | 3,80 |
| | | | | 97 | | | | 1 | | | 2,58 | 1 | 2,58 |
| | | | 66 | 61 | | 1 | | | 3,45 | | | 1 | 3,45 |
| | | | 68 | 41 | | 1 | 1 | 2 | 4,67 | 1,93 | 7,43 | 4 | 7,43 |
| | | | | 53 | | | 1 | 3 | | 1,13 | 5,85 | 4 | 5,85 |
| | | | | 61 | | 2 | | 7 | 7,24 | | 5,57 | 9 | 7,24 |
| | | | | 64 | | 1 | 5 | 3 | 2,98 | 1,90 | 3,80 | 9 | 3,80 |
| | | | | 97 | | | | 1 | | | 7,93 | 1 | 7,93 |
| | | | 72 | 41 | | | | 1 | | | 3,22 | 1 | 3,22 |
| | | | | 61 | | | | 1 | | | 3,68 | 1 | 3,68 |
| | | | 97 | 64 | | | | 1 | | | 2,58 | 1 | 2,58 |
| | | | | 68 | | | | 1 | | | 7,93 | 1 | 7,93 |
| | | | | 120 | | | | 1 | | | 5,85 | 1 | 5,85 |
| | | | 101 | 2 | | | | 1 | | | 3,08 | 1 | 3,08 |
| | | | | 115 | | 2 | | 5 | 16,70 | | 6,15 | 7 | 16,70 |
| | | | | 120 | | | 2 | 1 | | 1,30 | 4,37 | 3 | 4,37 |
| | | | 115 | 53 | | | | 1 | | | 2,39 | 1 | 2,39 |
| | | | | 61 | | | | 3 | | | 4,79 | 3 | 4,79 |
| | | | | 101 | | 2 | | 5 | 16,70 | | 6,15 | 7 | 16,70 |
| | | | | 120 | | 6 | 10 | 20 | 2,96 | 9,61 | 6,67 | 36 | 9,61 |
| | | | | 130 | | 1 | 2 | 12 | 3,08 | 6,06 | 9,19 | 15 | 9,19 |
| | | | | 136 | | 3 | | 7 | 7,16 | | 9,97 | 10 | 9,97 |
| | | | 120 | 97 | | | | 1 | | | 5,85 | 1 | 5,85 |
| | | | | 101 | | | 2 | 1 | | 1,30 | 4,37 | 3 | 4,37 |
| | | | | 115 | | 6 | 10 | 20 | 2,96 | 9,61 | 6,67 | 36 | 9,61 |
| | | | | 130 | | 3 | 13 | 36 | 11,28 | 6,89 | 10,21 | 52 | 11,28 |
| | | | | 136 | | 3 | 3 | 3 | 7,47 | 3,22 | 2,54 | 9 | 7,47 |
| | | | | 146 | | 1 | 2 | | 8,97 | 5,49 | | 3 | 8,97 |
| | | | | 151 | | 4 | | | 10,35 | | | 4 | 10,35 |
| | | | 130 | 115 | | 1 | 2 | 12 | 3,08 | 6,06 | 9,19 | 15 | 9,19 |
| | | | | 120 | | 3 | 13 | 36 | 11,28 | 6,89 | 10,21 | 52 | 11,28 |
| | | | | 146 | | | | 2 | | | 7,00 | 2 | 7,00 |
| | | | 136 | 115 | | 3 | | 7 | 7,16 | | 9,97 | 10 | 9,97 |
| | | | | 120 | | 3 | 3 | 3 | 7,47 | 3,22 | 2,54 | 9 | 7,47 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 146 | | | 1 | 13 | | 0,49 | 11,34 | 14 | 11,34 |
| | | | | 151 | | 4 | | 2 | 8,47 | | 2,60 | 6 | 8,47 |
| | | | 146 | 120 | | 1 | 2 | | 8,97 | 5,49 | | 3 | 8,97 |
| | | | | 130 | | | | 2 | | | 7,00 | 2 | 7,00 |
| | | | | 136 | | | 1 | 13 | | 0,49 | 11,34 | 14 | 11,34 |
| | | | 151 | 120 | | 4 | | | 10,35 | | | 4 | 10,35 |
| | | | | 136 | | 4 | | 2 | 8,47 | | 2,60 | 6 | 8,47 |
| | | | 179 | 181 | | | 5 | 2 | | 4,64 | 5,41 | 7 | 5,41 |
| | | | | 201 | | | | 1 | | | 5,33 | 1 | 5,33 |
| | | | | 206 | | 5 | 6 | 13 | 6,72 | 8,97 | 6,97 | 24 | 8,97 |
| | | | | 256 | | | 1 | 4 | | 0,05 | 9,52 | 5 | 9,52 |
| | | | 180 | 206 | | | | 1 | | | 7,72 | 1 | 7,72 |
| | | | | 256 | | | | 1 | | | 4,92 | 1 | 4,92 |
| | | | 181 | 179 | | | 5 | 2 | | 4,64 | 5,41 | 7 | 5,41 |
| | | | | 206 | | 6 | 9 | 34 | 19,87 | 5,70 | 8,73 | 49 | 19,87 |
| | | | | 256 | | | | 5 | | | 7,16 | 5 | 7,16 |
| | | | 201 | 179 | | | | 1 | | | 5,33 | 1 | 5,33 |
| | | | | 206 | | 3 | 6 | 24 | 17,55 | 10,00 | 11,33 | 33 | 17,55 |
| | | | | 213 | | | | 7 | | | 9,31 | 7 | 9,31 |
| | | | | 217 | | | | 2 | | | 8,21 | 2 | 8,21 |
| | | | 206 | 179 | | 5 | 6 | 13 | 6,72 | 8,97 | 6,97 | 24 | 8,97 |
| | | | | 180 | | | | 1 | | | 7,72 | 1 | 7,72 |
| | | | | 181 | | 6 | 9 | 34 | 19,87 | 5,70 | 8,73 | 49 | 19,87 |
| | | | | 201 | | 3 | 6 | 24 | 17,55 | 10,00 | 11,33 | 33 | 17,55 |
| | | | | 213 | | | 2 | 2 | | 5,58 | 6,81 | 4 | 6,81 |
| | | | | 217 | | | 3 | 8 | | 4,81 | 8,80 | 11 | 8,80 |
| | | | 213 | 201 | | | | 7 | | | 9,31 | 7 | 9,31 |
| | | | | 206 | | | 2 | 2 | | 5,58 | 6,81 | 4 | 6,81 |
| | | | 217 | 201 | | | | 2 | | | 8,21 | 2 | 8,21 |
| | | | | 206 | | | 3 | 8 | | 4,81 | 8,80 | 11 | 8,80 |
| | | | 256 | 179 | | | 1 | 4 | | 0,05 | 9,52 | 5 | 9,52 |
| | | | | 180 | | | | 1 | | | 4,92 | 1 | 4,92 |
| | | | | 181 | | | | 5 | | | 7,16 | 5 | 7,16 |
| | Bud31 | Bud31 | 5 | 20 | | 1 | | | 2,53 | | | 1 | 2,53 |
| | | | 10 | 20 | | 1 | | | 1,92 | | | 1 | 1,92 |
| | | | 20 | 5 | | 1 | | | 2,53 | | | 1 | 2,53 |
| | | | | 10 | | 1 | | | 1,92 | | | 1 | 1,92 |
| | | | 37 | 44 | 10,2 | | 1 | | | 0,28 | | 1 | 0,28 |
| | | | 44 | 37 | 10,2 | | 1 | | | 0,28 | | 1 | 0,28 |
| | | | 69 | 71 | 5,8 | 1 | | | 0,53 | | | 1 | 0,53 |
| | | | 71 | 69 | 5,8 | 1 | | | 0,53 | | | 1 | 0,53 |
| | Cef1 | Cef1 | 22 | 59 | 12,4 | 1 | 3 | | 2,22 | 6,24 | | 4 | 6,24 |
| | | | 59 | 22 | 12,4 | 1 | 3 | | 2,22 | 6,24 | | 4 | 6,24 |
| | | | 180 | 187 | | | | 1 | | | 7,80 | 1 | 7,80 |
| | | | 187 | 180 | | | | 1 | | | 7,80 | 1 | 7,80 |
| | | | | 201 | | 2 | | | 1,81 | | | 2 | 1,81 |
| | | | 201 | 187 | | 2 | | | 1,81 | | | 2 | 1,81 |
| | | | 239 | 247 | 13,0 | 1 | | 1 | 0,64 | | 3,78 | 2 | 3,78 |
| | | | | 251 | 19,0 | | | 1 | | | 6,43 | 1 | 6,43 |
| | | | 240 | 247 | 11,0 | 7 | 10 | 11 | 6,18 | 3,89 | 4,69 | 28 | 6,18 |
| | | | | 251 | 16,9 | 2 | 6 | 2 | 11,13 | 5,98 | 5,20 | 10 | 11,13 |
| | | | 247 | 239 | 13,0 | 1 | | 1 | 0,64 | | 3,78 | 2 | 3,78 |
| | | | | 240 | 11,0 | 7 | 10 | 11 | 6,18 | 3,89 | 4,69 | 28 | 6,18 |
| | | | | 251 | 6,2 | | 2 | | | 1,16 | | 2 | 1,16 |
| | | | | 257 | 15,3 | | 1 | | | 0,06 | | 1 | 0,06 |
| | | | | 259 | 18,5 | | 1 | | | 0,19 | | 1 | 0,19 |
| | | | 251 | 239 | 19,0 | | | 1 | | | 6,43 | 1 | 6,43 |
| | | | | 240 | 16,9 | 2 | 6 | 2 | 11,13 | 5,98 | 5,20 | 10 | 11,13 |
| | | | | 247 | 6,2 | | 2 | | | 1,16 | | 2 | 1,16 |
| | | | 257 | 247 | 15,3 | | 1 | | | 0,06 | | 1 | 0,06 |
| | | | 259 | 247 | 18,5 | | 1 | | | 0,19 | | 1 | 0,19 |
| | | | 293 | 296 | | 10 | 2 | 33 | 19,98 | 1,64 | 14,00 | 45 | 19,98 |
| | | | 296 | 293 | | 10 | 2 | 33 | 19,98 | 1,64 | 14,00 | 45 | 19,98 |
| | | | | 308 | | | 1 | | | 0,26 | | 1 | 0,26 |
| | | | 305 | 312 | | 2 | | | 4,54 | | | 2 | 4,54 |
| | | | | 314 | | 4 | | | 12,62 | | | 4 | 12,62 |
| | | | | 318 | | | | 2 | | | 6,69 | 2 | 6,69 |
| | | | | 353 | | 1 | 2 | | 1,94 | 1,90 | | 3 | 1,94 |
| | | | | 356 | | | | 1 | | | 4,33 | 1 | 4,33 |
| | | | | 359 | | | 1 | 2 | | 0,23 | 2,73 | 3 | 2,73 |
| | | | 308 | 296 | | | 1 | | | 0,26 | | 1 | 0,26 |
| | | | | 321 | | | | 1 | | | 3,27 | 1 | 3,27 |
| | | | | 353 | | 1 | | 1 | 6,11 | | 3,15 | 2 | 6,11 |
| | | | | 359 | | 1 | | | 2,23 | | | 1 | 2,23 |
| | | | 312 | 305 | | 2 | | | 4,54 | | | 2 | 4,54 |
| | | | | 314 | | 2 | | | 3,18 | | | 2 | 3,18 |
| | | | | 318 | | 4 | | 5 | 5,43 | | 6,08 | 9 | 6,08 |
| | | | | 353 | | | | 2 | | | 8,80 | 2 | 8,80 |
| | | | | 356 | | 1 | | | 0,73 | | | 1 | 0,73 |
| | | | | 359 | | 1 | 1 | | 1,80 | 1,09 | | 2 | 1,80 |
| | | | 314 | 305 | | 4 | | | 12,62 | | | 4 | 12,62 |
| | | | | 312 | | 2 | | | 3,18 | | | 2 | 3,18 |
| | | | | 321 | | 5 | | 1 | 7,68 | | 4,29 | 6 | 7,68 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 318 | 305 | | | | 2 | | | 6,69 | 2 | 6,69 |
| | | | | 312 | | 4 | | 5 | 5,43 | | 6,08 | 9 | 6,08 |
| | | | | 321 | | 2 | 1 | 4 | 1,63 | 3,63 | 4,01 | 7 | 4,01 |
| | | | | 335 | | | | 1 | | | 1,76 | 1 | 1,76 |
| | | | | 353 | | | | 1 | | | 3,81 | 1 | 3,81 |
| | | | 321 | 308 | | | | 1 | | | 3,27 | 1 | 3,27 |
| | | | | 314 | | 5 | | 1 | 7,68 | | 4,29 | 6 | 7,68 |
| | | | | 318 | | 2 | 1 | 4 | 1,63 | 3,63 | 4,01 | 7 | 4,01 |
| | | | 335 | 318 | | | | 1 | | | 1,76 | 1 | 1,76 |
| | | | 353 | 305 | | 1 | 2 | | 1,94 | 1,90 | | 3 | 1,94 |
| | | | | 308 | | 1 | | 1 | 6,11 | | 3,15 | 2 | 6,11 |
| | | | | 312 | | | | 2 | | | 8,80 | 2 | 8,80 |
| | | | | 318 | | | | 1 | | | 3,81 | 1 | 3,81 |
| | | | | 359 | | 1 | 1 | 1 | 0,24 | 1,79 | 2,42 | 3 | 2,42 |
| | | | | 364 | | 2 | 2 | 3 | 0,84 | 0,85 | 1,96 | 7 | 1,96 |
| | | | 356 | 305 | | | | 1 | | | 4,33 | 1 | 4,33 |
| | | | | 312 | | 1 | | | 0,73 | | | 1 | 0,73 |
| | | | | 364 | | | | 1 | | | 1,53 | 1 | 1,53 |
| | | | 359 | 305 | | | 1 | 2 | | 0,23 | 2,73 | 3 | 2,73 |
| | | | | 308 | | 1 | | | 2,23 | | | 1 | 2,23 |
| | | | | 312 | | 1 | 1 | | 1,80 | 1,09 | | 2 | 1,80 |
| | | | | 353 | | 1 | 1 | 1 | 0,24 | 1,79 | 2,42 | 3 | 2,42 |
| | | | 364 | 353 | | 2 | 2 | 3 | 0,84 | 0,85 | 1,96 | 7 | 1,96 |
| | | | | 356 | | | | 1 | | | 1,53 | 1 | 1,53 |
| | Clf1 | Clf1 | 24 | 28 | | | | 5 | | | 2,75 | 5 | 2,75 |
| | | | 25 | 111 | | 1 | | 1 | 0,47 | | 3,22 | 2 | 3,22 |
| | | | 28 | 24 | | | | 5 | | | 2,75 | 5 | 2,75 |
| | | | 111 | 25 | | 1 | | 1 | 0,47 | | 3,22 | 2 | 3,22 |
| | | | 281 | 304 | | 1 | | 1 | 0,19 | | 4,13 | 2 | 4,13 |
| | | | 304 | 281 | | 1 | | 1 | 0,19 | | 4,13 | 2 | 4,13 |
| | | | 352 | 399 | | | | 2 | | | 5,61 | 2 | 5,61 |
| | | | 399 | 352 | | | | 2 | | | 5,61 | 2 | 5,61 |
| | | | 529 | 532 | | 11 | 4 | 9 | 5,44 | 3,71 | 4,44 | 24 | 5,44 |
| | | | 532 | 529 | | 11 | 4 | 9 | 5,44 | 3,71 | 4,44 | 24 | 5,44 |
| | | | 605 | 679 | | 1 | | | 1,17 | | | 1 | 1,17 |
| | | | 635 | 640 | | | | 3 | | | 6,37 | 3 | 6,37 |
| | | | 640 | 635 | | | | 3 | | | 6,37 | 3 | 6,37 |
| | | | | 668 | | | | 1 | | | 2,54 | 1 | 2,54 |
| | | | | 679 | | 2 | | 2 | 5,39 | | 7,80 | 4 | 7,80 |
| | | | 668 | 640 | | | | 1 | | | 2,54 | 1 | 2,54 |
| | | | | 673 | | 5 | 3 | 26 | 11,23 | 4,56 | 9,23 | 34 | 11,23 |
| | | | | 679 | | | | 2 | | | 4,00 | 2 | 4,00 |
| | | | 670 | 679 | | 3 | | 2 | 0,80 | | 3,82 | 5 | 3,82 |
| | | | | 680 | | | | 1 | | | 0,47 | 1 | 0,47 |
| | | | 673 | 668 | | 5 | 3 | 26 | 11,23 | 4,56 | 9,23 | 34 | 11,23 |
| | | | 679 | 605 | | 1 | | | 1,17 | | | 1 | 1,17 |
| | | | | 640 | | 2 | | 2 | 5,39 | | 7,80 | 4 | 7,80 |
| | | | | 668 | | | | 2 | | | 4,00 | 2 | 4,00 |
| | | | | 670 | | 3 | | 2 | 0,80 | | 3,82 | 5 | 3,82 |
| | | | | 682 | | 4 | 3 | 1 | 5,77 | 2,48 | 2,21 | 8 | 5,77 |
| | | | 680 | 670 | | | | 1 | | | 0,47 | 1 | 0,47 |
| | | | 682 | 679 | | 4 | 3 | 1 | 5,77 | 2,48 | 2,21 | 8 | 5,77 |
| | Cus1 | Cus1 | 2 | 58 | | 1 | | | 0,87 | | | 1 | 0,87 |
| | | | 39 | 41 | | 4 | 11 | 22 | 2,49 | 4,59 | 6,67 | 37 | 6,67 |
| | | | | 48 | | 2 | 5 | 18 | 0,94 | 4,56 | 8,19 | 25 | 8,19 |
| | | | | 50 | | | 2 | | | 0,43 | | 2 | 0,43 |
| | | | | 53 | | 1 | 3 | 7 | 1,97 | 1,07 | 5,10 | 11 | 5,10 |
| | | | 40 | 53 | | | | 1 | | | 5,61 | 1 | 5,61 |
| | | | 41 | 39 | | 4 | 11 | 22 | 2,49 | 4,59 | 6,67 | 37 | 6,67 |
| | | | | 50 | | | | 1 | | | 0,80 | 1 | 0,80 |
| | | | | 53 | | 1 | 7 | 16 | 5,65 | 4,56 | 7,37 | 24 | 7,37 |
| | | | 48 | 39 | | 2 | 5 | 18 | 0,94 | 4,56 | 8,19 | 25 | 8,19 |
| | | | | 53 | | 6 | 3 | 22 | 2,64 | 5,74 | 11,98 | 31 | 11,98 |
| | | | | 58 | | 1 | 5 | 1 | 1,95 | 1,58 | 2,06 | 7 | 2,06 |
| | | | | 61 | | | 1 | | | 0,49 | | 1 | 0,49 |
| | | | | 64 | | | | 3 | | | 3,01 | 3 | 3,01 |
| | | | 50 | 39 | | | 2 | | | 0,43 | | 2 | 0,43 |
| | | | | 41 | | | | 1 | | | 0,80 | 1 | 0,80 |
| | | | | 58 | | | 1 | 9 | | 0,41 | 3,33 | 10 | 3,33 |
| | | | | 64 | | | 1 | | | 0,30 | | 1 | 0,30 |
| | | | 53 | 39 | | 1 | 3 | 7 | 1,97 | 1,07 | 5,10 | 11 | 5,10 |
| | | | | 40 | | | | 1 | | | 5,61 | 1 | 5,61 |
| | | | | 41 | | 1 | 7 | 16 | 5,65 | 4,56 | 7,37 | 24 | 7,37 |
| | | | | 48 | | 6 | 3 | 22 | 2,64 | 5,74 | 11,98 | 31 | 11,98 |
| | | | | 61 | | 5 | 11 | 74 | 11,82 | 2,66 | 9,67 | 90 | 11,82 |
| | | | | 64 | | 5 | 9 | 19 | 8,61 | 7,23 | 9,56 | 33 | 9,56 |
| | | | 58 | 2 | | 1 | | | 0,87 | | | 1 | 0,87 |
| | | | | 48 | | 1 | 5 | 1 | 1,95 | 1,58 | 2,06 | 7 | 2,06 |
| | | | | 50 | | | 1 | 9 | | 0,41 | 3,33 | 10 | 3,33 |
| | | | | 64 | | 6 | 9 | 10 | 5,40 | 4,87 | 9,31 | 25 | 9,31 |
| | | | | 83 | | | | 1 | | | 2,06 | 1 | 2,06 |
| | | | 61 | 48 | | | 1 | | | 0,49 | | 1 | 0,49 |
| | | | | 53 | | 5 | 11 | 74 | 11,82 | 2,66 | 9,67 | 90 | 11,82 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 79 | | | | 2 | | | 6,33 | 2 | 6,33 |
| | | | 64 | 48 | | | | 3 | | | 3,01 | 3 | 3,01 |
| | | | | 50 | | | 1 | | | 0,30 | | 1 | 0,30 |
| | | | | 53 | | 5 | 9 | 19 | 8,61 | 7,23 | 9,56 | 33 | 9,56 |
| | | | | 58 | | 6 | 9 | 10 | 5,40 | 4,87 | 9,31 | 25 | 9,31 |
| | | | | 79 | | | | 2 | | | 8,20 | 2 | 8,20 |
| | | | | 83 | | | | 4 | | | 6,60 | 4 | 6,60 |
| | | | 79 | 61 | | | | 2 | | | 6,33 | 2 | 6,33 |
| | | | | 64 | | | | 2 | | | 8,20 | 2 | 8,20 |
| | | | | 86 | | 8 | 1 | 44 | 7,02 | 5,02 | 9,78 | 53 | 9,78 |
| | | | | 95 | | | | 3 | | | 11,01 | 3 | 11,01 |
| | | | 83 | 58 | | | | 1 | | | 2,06 | 1 | 2,06 |
| | | | | 64 | | | | 4 | | | 6,60 | 4 | 6,60 |
| | | | | 95 | | | 3 | 5 | | 1,03 | 3,62 | 8 | 3,62 |
| | | | 86 | 79 | | 8 | 1 | 44 | 7,02 | 5,02 | 9,78 | 53 | 9,78 |
| | | | 95 | 79 | | | | 3 | | | 11,01 | 3 | 11,01 |
| | | | | 83 | | | 3 | 5 | | 1,03 | 3,62 | 8 | 3,62 |
| | | | | 102 | | 3 | 5 | 4 | 16,44 | 3,76 | 11,26 | 12 | 16,44 |
| | | | 102 | 95 | | 3 | 5 | 4 | 16,44 | 3,76 | 11,26 | 12 | 16,44 |
| | | | 202 | 226 | | | 1 | 2 | | 3,89 | 9,01 | 3 | 9,01 |
| | | | | 246 | | 12 | 17 | 41 | 22,72 | 14,98 | 14,75 | 70 | 22,72 |
| | | | | 379 | | | | 2 | | | 7,64 | 2 | 7,64 |
| | | | 223 | 236 | | | | 2 | | | 2,17 | 2 | 2,17 |
| | | | 226 | 202 | | | 1 | 2 | | 3,89 | 9,01 | 3 | 9,01 |
| | | | | 236 | | | 8 | 6 | | 5,33 | 4,01 | 14 | 5,33 |
| | | | 236 | 223 | | | | 2 | | | 2,17 | 2 | 2,17 |
| | | | | 226 | | | 8 | 6 | | 5,33 | 4,01 | 14 | 5,33 |
| | | | | 246 | | | 5 | 2 | | 9,36 | 10,64 | 7 | 10,64 |
| | | | 246 | 202 | | 12 | 17 | 41 | 22,72 | 14,98 | 14,75 | 70 | 22,72 |
| | | | | 236 | | | 5 | 2 | | 9,36 | 10,64 | 7 | 10,64 |
| | | | 317 | 347 | | | 3 | | | 3,78 | | 3 | 3,78 |
| | | | 329 | 347 | | 1 | 4 | | 3,04 | 4,83 | | 5 | 4,83 |
| | | | 347 | 317 | | | 3 | | | 3,78 | | 3 | 3,78 |
| | | | | 329 | | 1 | 4 | | 3,04 | 4,83 | | 5 | 4,83 |
| | | | | 358 | | 3 | 2 | | 2,00 | 0,20 | | 5 | 2,00 |
| | | | 358 | 347 | | 3 | 2 | | 2,00 | 0,20 | | 5 | 2,00 |
| | | | 379 | 202 | | | | 2 | | | 7,64 | 2 | 7,64 |
| | Cwc15 | Cwc15 | 38 | 41 | | 2 | 2 | | 7,21 | 2,26 | | 4 | 7,21 |
| | | | | 43 | | | 1 | | | 0,03 | | 1 | 0,03 |
| | | | 41 | 38 | | 2 | 2 | | 7,21 | 2,26 | | 4 | 7,21 |
| | | | 43 | 38 | | | 1 | | | 0,03 | | 1 | 0,03 |
| | | | 88 | 102 | | 1 | 2 | | 2,13 | 1,13 | | 3 | 2,13 |
| | | | 91 | 104 | | | 1 | | | 0,77 | | 1 | 0,77 |
| | | | 102 | 88 | | 1 | 2 | | 2,13 | 1,13 | | 3 | 2,13 |
| | | | | 108 | | 2 | 2 | 4 | 1,08 | 4,06 | 6,02 | 8 | 6,02 |
| | | | | 118 | | | | 1 | | | 2,99 | 1 | 2,99 |
| | | | 104 | 91 | | | 1 | | | 0,77 | | 1 | 0,77 |
| | | | | 129 | | | | 2 | | | 7,19 | 2 | 7,19 |
| | | | 108 | 102 | | 2 | 2 | 4 | 1,08 | 4,06 | 6,02 | 8 | 6,02 |
| | | | | 129 | | 2 | | | 8,61 | | | 2 | 8,61 |
| | | | 118 | 102 | | | | 1 | | | 2,99 | 1 | 2,99 |
| | | | | 129 | | 6 | 5 | 11 | 8,14 | 7,16 | 9,75 | 22 | 9,75 |
| | | | | 140 | | 1 | 1 | | 1,09 | 2,63 | | 2 | 2,63 |
| | | | 129 | 104 | | | | 2 | | | 7,19 | 2 | 7,19 |
| | | | | 108 | | 2 | | | 8,61 | | | 2 | 8,61 |
| | | | | 118 | | 6 | 5 | 11 | 8,14 | 7,16 | 9,75 | 22 | 9,75 |
| | | | | 137 | | 3 | 1 | | 8,29 | 0,85 | | 4 | 8,29 |
| | | | | 140 | | 4 | 6 | 5 | 6,64 | 9,52 | 7,70 | 15 | 9,52 |
| | | | | 145 | | | 1 | | | 3,95 | | 1 | 3,95 |
| | | | 137 | 129 | | 3 | 1 | | 8,29 | 0,85 | | 4 | 8,29 |
| | | | | 145 | | 2 | | | 3,46 | | | 2 | 3,46 |
| | | | 140 | 118 | | 1 | 1 | | 1,09 | 2,63 | | 2 | 2,63 |
| | | | | 129 | | 4 | 6 | 5 | 6,64 | 9,52 | 7,70 | 15 | 9,52 |
| | | | | 151 | | | 2 | 2 | | 2,07 | 5,16 | 4 | 5,16 |
| | | | 145 | 129 | | | 1 | | | 3,95 | | 1 | 3,95 |
| | | | | 137 | | 2 | | | 3,46 | | | 2 | 3,46 |
| | | | | 151 | | 1 | 2 | 4 | 4,45 | 3,80 | 6,62 | 7 | 6,62 |
| | | | 151 | 140 | | | 2 | 2 | | 2,07 | 5,16 | 4 | 5,16 |
| | | | | 145 | | 1 | 2 | 4 | 4,45 | 3,80 | 6,62 | 7 | 6,62 |
| | Cwc2 | Cwc2 | 2 | 10 | | | 1 | | | 2,02 | | 1 | 2,02 |
| | | | 10 | 2 | | | 1 | | | 2,02 | | 1 | 2,02 |
| | | | | 86 | 13,6 | | | 1 | | | 3,30 | 1 | 3,30 |
| | | | 61 | 86 | 10,5 | | | 1 | | | 1,98 | 1 | 1,98 |
| | | | 86 | 10 | 13,6 | | | 1 | | | 3,30 | 1 | 3,30 |
| | | | | 61 | 10,5 | | | 1 | | | 1,98 | 1 | 1,98 |
| | | | 116 | 152 | | | 3 | | | 3,54 | | 3 | 3,54 |
| | | | 135 | 152 | | | 1 | | | 1,28 | | 1 | 1,28 |
| | | | 152 | 116 | | | 3 | | | 3,54 | | 3 | 3,54 |
| | | | | 135 | | | 1 | | | 1,28 | | 1 | 1,28 |
| | | | | 179 | | | 2 | | | 2,12 | | 2 | 2,12 |
| | | | 179 | 152 | | | 2 | | | 2,12 | | 2 | 2,12 |
| | | | | 236 | 28,0 | | | 2 | | | 11,38 | 2 | 11,38 |
| | | | 185 | 236 | 15,4 | | 2 | | | 1,73 | | 2 | 1,73 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 236 | 179 | 28,0 | | | 2 | | | 11,38 | 2 | 11,38 |
| | | | | 185 | 15,4 | | 2 | | | 1,73 | | 2 | 1,73 |
| | | | 310 | 320 | | 3 | 4 | 7 | 3,22 | 5,82 | 5,67 | 14 | 5,82 |
| | | | 320 | 310 | | 3 | 4 | 7 | 3,22 | 5,82 | 5,67 | 14 | 5,82 |
| | Cwc21 | Cwc21 | 47 | 53 | | 3 | 2 | 4 | 4,27 | 1,64 | 5,88 | 9 | 5,88 |
| | | | 53 | 47 | | 3 | 2 | 4 | 4,27 | 1,64 | 5,88 | 9 | 5,88 |
| | | | | 62 | | 1 | 3 | | 0,66 | 3,71 | | 4 | 3,71 |
| | | | 62 | 53 | | 1 | 3 | | 0,66 | 3,71 | | 4 | 3,71 |
| | | | 97 | 105 | | 19 | 9 | 97 | 13,12 | 10,74 | 20,89 | 125 | 20,89 |
| | | | 98 | 105 | | 35 | 34 | 89 | 11,32 | 6,04 | 16,07 | 158 | 16,07 |
| | | | 105 | 97 | | 19 | 9 | 97 | 13,12 | 10,74 | 20,89 | 125 | 20,89 |
| | | | | 98 | | 35 | 34 | 89 | 11,32 | 6,04 | 16,07 | 158 | 16,07 |
| | Cwc22 | Cwc22 | 294 | 316 | 12,8 | | | 2 | | | 10,65 | 2 | 10,65 |
| | | | 316 | 294 | 12,8 | | | 2 | | | 10,65 | 2 | 10,65 |
| | | | 406 | 444 | 6,3 | | | 1 | | | 9,70 | 1 | 9,70 |
| | | | 444 | 406 | 6,3 | | | 1 | | | 9,70 | 1 | 9,70 |
| | | | 495 | 505 | | | | 5 | | | 3,07 | 5 | 3,07 |
| | | | 496 | 505 | | | | 1 | | | 2,78 | 1 | 2,78 |
| | | | 505 | 495 | | | | 5 | | | 3,07 | 5 | 3,07 |
| | | | | 496 | | | | 1 | | | 2,78 | 1 | 2,78 |
| | | | | 508 | | 6 | | | 2,05 | | | 6 | 2,05 |
| | | | 508 | 505 | | 6 | | | 2,05 | | | 6 | 2,05 |
| | | | 520 | 530 | | 6 | 5 | 7 | 6,60 | 1,97 | 3,93 | 18 | 6,60 |
| | | | 530 | 520 | | 6 | 5 | 7 | 6,60 | 1,97 | 3,93 | 18 | 6,60 |
| | Cwc24 | Cwc24 | 63 | 67 | | 2 | 2 | | 4,00 | 3,97 | | 4 | 4,00 |
| | | | 67 | 63 | | 2 | 2 | | 4,00 | 3,97 | | 4 | 4,00 |
| | | | 93 | 123 | | 4 | 1 | 5 | 3,57 | 3,31 | 7,13 | 10 | 7,13 |
| | | | 123 | 93 | | 4 | 1 | 5 | 3,57 | 3,31 | 7,13 | 10 | 7,13 |
| | | | 148 | 169 | 15,2 | | 5 | 2 | | 4,97 | 3,91 | 7 | 4,97 |
| | | | 169 | 148 | 15,2 | | 5 | 2 | | 4,97 | 3,91 | 7 | 4,97 |
| | | | 186 | 232 | 16,5 | 1 | | 1 | 3,36 | | 5,25 | 2 | 5,25 |
| | | | 194 | 203 | 19,0 | 4 | 3 | 4 | 4,38 | 5,27 | 5,88 | 11 | 5,88 |
| | | | | 256 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | | 203 | 194 | 19,0 | 4 | 3 | 4 | 4,38 | 5,27 | 5,88 | 11 | 5,88 |
| | | | | 229 | 18,7 | 1 | | 2 | 3,05 | | 1,27 | 3 | 3,05 |
| | | | 225 | 229 | 6,6 | | | 1 | | | 1,98 | 1 | 1,98 |
| | | | 229 | 203 | 18,7 | 1 | | 2 | 3,05 | | 1,27 | 3 | 3,05 |
| | | | | 225 | 6,6 | | | 1 | | | 1,98 | 1 | 1,98 |
| | | | 232 | 186 | 16,5 | 1 | | 1 | 3,36 | | 5,25 | 2 | 5,25 |
| | | | 256 | 194 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | Cwc27 | Cwc27 | 36 | 171 | | 3 | | | 2,82 | | | 3 | 2,82 |
| | | | 56 | 146 | | | | 1 | | | 2,68 | 1 | 2,68 |
| | | | 146 | 56 | | | | 1 | | | 2,68 | 1 | 2,68 |
| | | | 171 | 36 | | 3 | | | 2,82 | | | 3 | 2,82 |
| | | | 225 | 234 | | | | 1 | | | 2,94 | 1 | 2,94 |
| | | | 234 | 225 | | | | 1 | | | 2,94 | 1 | 2,94 |
| | | | 278 | 289 | | 3 | | 6 | 7,00 | | 6,15 | 9 | 7,00 |
| | | | 289 | 278 | | 3 | | 6 | 7,00 | | 6,15 | 9 | 7,00 |
| | | | | 295 | | 1 | | | 0,27 | | | 1 | 0,27 |
| | | | | 297 | | 4 | 6 | 14 | 5,00 | 4,97 | 6,99 | 24 | 6,99 |
| | | | 295 | 289 | | 1 | | | 0,27 | | | 1 | 0,27 |
| | | | 297 | 289 | | 4 | 6 | 14 | 5,00 | 4,97 | 6,99 | 24 | 6,99 |
| | Ecm2 | Ecm2 | 47 | 57 | 9,0 | | | 3 | | | 4,44 | 3 | 4,44 |
| | | | 57 | 47 | 9,0 | | | 3 | | | 4,44 | 3 | 4,44 |
| | | | 116 | 138 | | | | 1 | | | 2,97 | 1 | 2,97 |
| | | | | 157 | | | | 1 | | | 1,82 | 1 | 1,82 |
| | | | 119 | 157 | | | | 5 | | | 7,84 | 5 | 7,84 |
| | | | 138 | 116 | | | | 1 | | | 2,97 | 1 | 2,97 |
| | | | | 157 | | | | 5 | | | 5,28 | 5 | 5,28 |
| | | | | 164 | | | | 1 | | | 1,77 | 1 | 1,77 |
| | | | | 167 | | | | 1 | | | 7,61 | 1 | 7,61 |
| | | | 140 | 164 | | | | 1 | | | 5,66 | 1 | 5,66 |
| | | | 157 | 116 | | | | 1 | | | 1,82 | 1 | 1,82 |
| | | | | 119 | | | | 5 | | | 7,84 | 5 | 7,84 |
| | | | | 138 | | | | 5 | | | 5,28 | 5 | 5,28 |
| | | | | 167 | | 4 | 2 | 10 | 8,34 | 3,76 | 12,22 | 16 | 12,22 |
| | | | | 173 | | | | 3 | | | 4,01 | 3 | 4,01 |
| | | | | 247 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | | | 277 | | 1 | | | 0,27 | | | 1 | 0,27 |
| | | | 164 | 138 | | | | 1 | | | 1,77 | 1 | 1,77 |
| | | | | 140 | | | | 1 | | | 5,66 | 1 | 5,66 |
| | | | | 173 | | | | 5 | | | 6,16 | 5 | 6,16 |
| | | | | 337 | | | | 1 | | | 5,06 | 1 | 5,06 |
| | | | 167 | 138 | | | | 1 | | | 7,61 | 1 | 7,61 |
| | | | | 157 | | 4 | 2 | 10 | 8,34 | 3,76 | 12,22 | 16 | 12,22 |
| | | | | 247 | | 3 | 3 | 1 | 5,86 | 4,25 | 5,43 | 7 | 5,86 |
| | | | | 311 | | | | 2 | | | 10,95 | 2 | 10,95 |
| | | | | 318 | | | | 1 | | | 5,27 | 1 | 5,27 |
| | | | | 337 | | | | 1 | | | 8,56 | 1 | 8,56 |
| | | | 173 | 157 | | | | 3 | | | 4,01 | 3 | 4,01 |
| | | | | 164 | | | | 5 | | | 6,16 | 5 | 6,16 |
| | | | | 245 | 18,2 | | | 1 | | | 4,58 | 1 | 4,58 |
| | | | | 247 | 14,2 | 1 | | 2 | 3,56 | | 5,85 | 3 | 5,85 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 311 | | | | 1 | | | 5,13 | 1 | 5,13 |
| | | | 177 | 245 | 12,3 | | 1 | | | 0,94 | | 1 | 0,94 |
| | | | 188 | 274 | | | | 3 | | | 4,38 | 3 | 4,38 |
| | | | 189 | 265 | | | 1 | | | 2,93 | | 1 | 2,93 |
| | | | 198 | 265 | | 5 | 5 | 5 | 28,24 | 10,98 | 8,48 | 15 | 28,24 |
| | | | | 277 | | 1 | | | 1,19 | | | 1 | 1,19 |
| | | | 230 | 233 | | | 4 | 3 | | 4,11 | 4,96 | 7 | 4,96 |
| | | | | 265 | 20,3 | 19 | 12 | 33 | 32,27 | 6,16 | 10,72 | 64 | 32,27 |
| | | | 233 | 230 | | | 4 | 3 | | 4,11 | 4,96 | 7 | 4,96 |
| | | | | 265 | | 1 | | | 0,06 | | | 1 | 0,06 |
| | | | 245 | 173 | 18,2 | | | 1 | | | 4,58 | 1 | 4,58 |
| | | | | 177 | 12,3 | | 1 | | | 0,94 | | 1 | 0,94 |
| | | | 247 | 157 | | | | 1 | | | 1,49 | 1 | 1,49 |
| | | | | 167 | | 3 | 3 | 1 | 5,86 | 4,25 | 5,43 | 7 | 5,86 |
| | | | | 173 | 14,2 | 1 | | 2 | 3,56 | | 5,85 | 3 | 5,85 |
| | | | 265 | 189 | | | 1 | | | 2,93 | | 1 | 2,93 |
| | | | | 198 | | 5 | 5 | 5 | 28,24 | 10,98 | 8,48 | 15 | 28,24 |
| | | | | 230 | 20,3 | 19 | 12 | 33 | 32,27 | 6,16 | 10,72 | 64 | 32,27 |
| | | | | 233 | | 1 | | | 0,06 | | | 1 | 0,06 |
| | | | 274 | 188 | | | | 3 | | | 4,38 | 3 | 4,38 |
| | | | | 318 | | | | 2 | | | 6,59 | 2 | 6,59 |
| | | | | 331 | | | | 1 | | | 2,85 | 1 | 2,85 |
| | | | | 337 | | | | 1 | | | 3,12 | 1 | 3,12 |
| | | | | 342 | | | | 1 | | | 1,44 | 1 | 1,44 |
| | | | 277 | 157 | | 1 | | | 0,27 | | | 1 | 0,27 |
| | | | | 198 | | 1 | | | 1,19 | | | 1 | 1,19 |
| | | | 311 | 167 | | | | 2 | | | 10,95 | 2 | 10,95 |
| | | | | 173 | | | | 1 | | | 5,13 | 1 | 5,13 |
| | | | 318 | 167 | | | | 1 | | | 5,27 | 1 | 5,27 |
| | | | | 274 | | | | 2 | | | 6,59 | 2 | 6,59 |
| | | | 331 | 274 | | | | 1 | | | 2,85 | 1 | 2,85 |
| | | | 337 | 164 | | | | 1 | | | 5,06 | 1 | 5,06 |
| | | | | 167 | | | | 1 | | | 8,56 | 1 | 8,56 |
| | | | | 274 | | | | 1 | | | 3,12 | 1 | 3,12 |
| | | | 342 | 274 | | | | 1 | | | 1,44 | 1 | 1,44 |
| | Hsh155 | Hsh155 | 35 | 45 | | 1 | 1 | 10 | 2,62 | 5,55 | 7,08 | 12 | 7,08 |
| | | | | 51 | | | 1 | 3 | | 0,37 | 5,65 | 4 | 5,65 |
| | | | | 66 | | | | 2 | | | 4,45 | 2 | 4,45 |
| | | | | 72 | | | | 1 | | | 2,34 | 1 | 2,34 |
| | | | 45 | 35 | | 1 | 1 | 10 | 2,62 | 5,55 | 7,08 | 12 | 7,08 |
| | | | | 66 | | | 3 | 1 | | 3,20 | 9,81 | 4 | 9,81 |
| | | | 51 | 35 | | | 1 | 3 | | 0,37 | 5,65 | 4 | 5,65 |
| | | | | 66 | | | 1 | | | 0,81 | | 1 | 0,81 |
| | | | 66 | 35 | | | | 2 | | | 4,45 | 2 | 4,45 |
| | | | | 45 | | | 3 | 1 | | 3,20 | 9,81 | 4 | 9,81 |
| | | | | 51 | | | 1 | | | 0,81 | | 1 | 0,81 |
| | | | 72 | 35 | | | | 1 | | | 2,34 | 1 | 2,34 |
| | | | | 237 | | | 3 | 2 | | 4,63 | 5,77 | 5 | 5,77 |
| | | | 150 | 151 | | | | 1 | | | 1,84 | 1 | 1,84 |
| | | | | 158 | | 2 | 6 | 42 | 2,30 | 5,25 | 11,34 | 50 | 11,34 |
| | | | 151 | 150 | | | | 1 | | | 1,84 | 1 | 1,84 |
| | | | 158 | 150 | | 2 | 6 | 42 | 2,30 | 5,25 | 11,34 | 50 | 11,34 |
| | | | | 191 | | | 8 | 6 | | 9,77 | 5,29 | 14 | 9,77 |
| | | | 172 | 191 | 16,0 | | | 1 | | | 1,81 | 1 | 1,81 |
| | | | 191 | 158 | | | 8 | 6 | | 9,77 | 5,29 | 14 | 9,77 |
| | | | | 172 | 16,0 | | | 1 | | | 1,81 | 1 | 1,81 |
| | | | 237 | 72 | | | 3 | 2 | | 4,63 | 5,77 | 5 | 5,77 |
| | | | | 276 | 10,8 | 12 | 1 | | 8,55 | 1,25 | | 13 | 8,55 |
| | | | 276 | 237 | 10,8 | 12 | 1 | | 8,55 | 1,25 | | 13 | 8,55 |
| | | | 410 | 455 | | 1 | | | 2,56 | | | 1 | 2,56 |
| | | | 455 | 410 | | 1 | | | 2,56 | | | 1 | 2,56 |
| | | | 473 | 521 | 16,9 | | | 3 | | | 5,34 | 3 | 5,34 |
| | | | 521 | 473 | 16,9 | | | 3 | | | 5,34 | 3 | 5,34 |
| | | | 696 | 699 | 9,3 | | 1 | | | 1,39 | | 1 | 1,39 |
| | | | 699 | 696 | 9,3 | | 1 | | | 1,39 | | 1 | 1,39 |
| | Hsh49 | Hsh49 | 1 | 2 | | | | 1 | | | 3,97 | 1 | 3,97 |
| | | | 2 | 1 | | | | 1 | | | 3,97 | 1 | 3,97 |
| | | | 22 | 39 | | 11 | 5 | 16 | 3,26 | 0,85 | 1,87 | 32 | 3,26 |
| | | | | 42 | | 4 | 2 | 2 | 1,36 | 0,20 | 2,19 | 8 | 2,19 |
| | | | 39 | 22 | | 11 | 5 | 16 | 3,26 | 0,85 | 1,87 | 32 | 3,26 |
| | | | 42 | 22 | | 4 | 2 | 2 | 1,36 | 0,20 | 2,19 | 8 | 2,19 |
| | | | 101 | 133 | | | 1 | 1 | | 0,40 | 4,53 | 2 | 4,53 |
| | | | 113 | 193 | | | | 1 | | | 4,87 | 1 | 4,87 |
| | | | 126 | 133 | | | 1 | | | 0,45 | | 1 | 0,45 |
| | | | 130 | 160 | | | 1 | 3 | | 1,53 | 2,99 | 4 | 2,99 |
| | | | | 166 | | 2 | 17 | 2 | 3,42 | 3,45 | 2,68 | 21 | 3,45 |
| | | | 133 | 101 | | | 1 | 1 | | 0,40 | 4,53 | 2 | 4,53 |
| | | | | 126 | | | 1 | | | 0,45 | | 1 | 0,45 |
| | | | | 213 | | | | 1 | | | 5,74 | 1 | 5,74 |
| | | | 160 | 130 | | | 1 | 3 | | 1,53 | 2,99 | 4 | 2,99 |
| | | | 166 | 130 | | 2 | 17 | 2 | 3,42 | 3,45 | 2,68 | 21 | 3,45 |
| | | | 193 | 113 | | | | 1 | | | 4,87 | 1 | 4,87 |
| | | | 204 | 213 | | | | 1 | | | 5,08 | 1 | 5,08 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 213 | 133 | | | | 1 | | | 5,74 | 1 | 5,74 |
| | | | | 204 | | | | 1 | | | 5,08 | 1 | 5,08 |
| | Isy1 | Isy1 | 7 | 27 | | 3 | 2 | 6 | 11,09 | 5,81 | 12,96 | 11 | 12,96 |
| | | | | 42 | | | 2 | 1 | | 0,70 | 1,60 | 3 | 1,60 |
| | | | | 45 | | 1 | 3 | | 0,86 | 3,71 | | 4 | 3,71 |
| | | | | 59 | | 1 | | | 0,47 | | | 1 | 0,47 |
| | | | 27 | 7 | | 3 | 2 | 6 | 11,09 | 5,81 | 12,96 | 11 | 12,96 |
| | | | | 40 | | 7 | 3 | 2 | 4,61 | 1,77 | 2,80 | 12 | 4,61 |
| | | | | 42 | | | 1 | 2 | | 2,63 | 1,73 | 3 | 2,63 |
| | | | | 45 | | 3 | 2 | 4 | 8,36 | 6,79 | 10,44 | 9 | 10,44 |
| | | | | 56 | | 2 | 3 | 11 | 1,01 | 2,43 | 4,30 | 16 | 4,30 |
| | | | | 59 | | | 1 | | | 0,35 | | 1 | 0,35 |
| | | | | 61 | | | | 1 | | | 1,94 | 1 | 1,94 |
| | | | 40 | 27 | | 7 | 3 | 2 | 4,61 | 1,77 | 2,80 | 12 | 4,61 |
| | | | 42 | 7 | | | 2 | 1 | | 0,70 | 1,60 | 3 | 1,60 |
| | | | | 27 | | | 1 | 2 | | 2,63 | 1,73 | 3 | 2,63 |
| | | | 45 | 7 | | 1 | 3 | | 0,86 | 3,71 | | 4 | 3,71 |
| | | | | 27 | | 3 | 2 | 4 | 8,36 | 6,79 | 10,44 | 9 | 10,44 |
| | | | 56 | 27 | | 2 | 3 | 11 | 1,01 | 2,43 | 4,30 | 16 | 4,30 |
| | | | | 61 | | | | 3 | | | 5,35 | 3 | 5,35 |
| | | | 59 | 7 | | 1 | | | 0,47 | | | 1 | 0,47 |
| | | | | 27 | | | 1 | | | 0,35 | | 1 | 0,35 |
| | | | 61 | 27 | | | | 1 | | | 1,94 | 1 | 1,94 |
| | | | | 56 | | | | 3 | | | 5,35 | 3 | 5,35 |
| | | | 121 | 139 | | 9 | 9 | 11 | 5,87 | 5,51 | 6,68 | 29 | 6,68 |
| | | | | 143 | | 1 | 1 | | 2,06 | 0,58 | | 2 | 2,06 |
| | | | 139 | 121 | | 9 | 9 | 11 | 5,87 | 5,51 | 6,68 | 29 | 6,68 |
| | | | 143 | 121 | | 1 | 1 | | 2,06 | 0,58 | | 2 | 2,06 |
| | Lea1 | Lea1 | 194 | 215 | | 2 | 6 | 6 | 4,07 | 0,65 | 4,87 | 14 | 4,87 |
| | | | | 232 | | 2 | 2 | 10 | 5,00 | 3,61 | 4,08 | 14 | 5,00 |
| | | | 205 | 215 | | | 3 | 1 | | 0,95 | 1,30 | 4 | 1,30 |
| | | | | 232 | | | 3 | 6 | | 4,59 | 4,67 | 9 | 4,67 |
| | | | 215 | 194 | | 2 | 6 | 6 | 4,07 | 0,65 | 4,87 | 14 | 4,87 |
| | | | | 205 | | | 3 | 1 | | 0,95 | 1,30 | 4 | 1,30 |
| | | | | 232 | | | | 1 | | | 1,74 | 1 | 1,74 |
| | | | 232 | 194 | | 2 | 2 | 10 | 5,00 | 3,61 | 4,08 | 14 | 5,00 |
| | | | | 205 | | | 3 | 6 | | 4,59 | 4,67 | 9 | 4,67 |
| | | | | 215 | | | | 1 | | | 1,74 | 1 | 1,74 |
| | Msl1 | Msl1 | 2 | 7 | | | | 1 | | | 1,99 | 1 | 1,99 |
| | | | | 8 | | | 3 | 2 | | 1,72 | 3,22 | 5 | 3,22 |
| | | | 7 | 2 | | | | 1 | | | 1,99 | 1 | 1,99 |
| | | | 8 | 2 | | | 3 | 2 | | 1,72 | 3,22 | 5 | 3,22 |
| | Ntc20 | Ntc20 | 85 | 94 | | | | 1 | | | 5,31 | 1 | 5,31 |
| | | | 94 | 85 | | | | 1 | | | 5,31 | 1 | 5,31 |
| | Prp11 | Prp11 | 11 | 28 | | | 2 | 6 | | 4,08 | 11,92 | 8 | 11,92 |
| | | | | 36 | | | | 3 | | | 9,36 | 3 | 9,36 |
| | | | | 60 | | | | 1 | | | 9,75 | 1 | 9,75 |
| | | | | 192 | | | | 3 | | | 6,66 | 3 | 6,66 |
| | | | 28 | 11 | | | 2 | 6 | | 4,08 | 11,92 | 8 | 11,92 |
| | | | | 48 | | | | 2 | | | 9,07 | 2 | 9,07 |
| | | | | 60 | | | | 1 | | | 2,84 | 1 | 2,84 |
| | | | | 192 | | | | 1 | | | 9,70 | 1 | 9,70 |
| | | | 36 | 11 | | | | 3 | | | 9,36 | 3 | 9,36 |
| | | | | 60 | | | | 5 | | | 8,01 | 5 | 8,01 |
| | | | | 126 | | | | 1 | | | 3,24 | 1 | 3,24 |
| | | | | 192 | | | | 3 | | | 4,78 | 3 | 4,78 |
| | | | 48 | 28 | | | | 2 | | | 9,07 | 2 | 9,07 |
| | | | | 126 | | | | 1 | | | 6,08 | 1 | 6,08 |
| | | | | 192 | | | | 2 | | | 3,54 | 2 | 3,54 |
| | | | 60 | 11 | | | | 1 | | | 9,75 | 1 | 9,75 |
| | | | | 28 | | | | 1 | | | 2,84 | 1 | 2,84 |
| | | | | 36 | | | | 5 | | | 8,01 | 5 | 8,01 |
| | | | 103 | 126 | | | 6 | 8 | | 3,96 | 9,95 | 14 | 9,95 |
| | | | 121 | 144 | | | 1 | | | 0,21 | | 1 | 0,21 |
| | | | | 173 | | | | 1 | | | 2,81 | 1 | 2,81 |
| | | | 126 | 36 | | | | 1 | | | 3,24 | 1 | 3,24 |
| | | | | 48 | | | | 1 | | | 6,08 | 1 | 6,08 |
| | | | | 103 | | | 6 | 8 | | 3,96 | 9,95 | 14 | 9,95 |
| | | | | 144 | | | 1 | | | 0,15 | | 1 | 0,15 |
| | | | 144 | 121 | | | 1 | | | 0,21 | | 1 | 0,21 |
| | | | | 126 | | | 1 | | | 0,15 | | 1 | 0,15 |
| | | | | 175 | | | 1 | | | 0,40 | | 1 | 0,40 |
| | | | 173 | 121 | | | | 1 | | | 2,81 | 1 | 2,81 |
| | | | 175 | 144 | | | 1 | | | 0,40 | | 1 | 0,40 |
| | | | 192 | 11 | | | | 3 | | | 6,66 | 3 | 6,66 |
| | | | | 28 | | | | 1 | | | 9,70 | 1 | 9,70 |
| | | | | 36 | | | | 3 | | | 4,78 | 3 | 4,78 |
| | | | | 48 | | | | 2 | | | 3,54 | 2 | 3,54 |
| | Prp17 | Prp17 | 121 | 239 | | 4 | 5 | 6 | 6,28 | 5,94 | 4,87 | 15 | 6,28 |
| | | | 239 | 121 | | 4 | 5 | 6 | 6,28 | 5,94 | 4,87 | 15 | 6,28 |
| | | | 307 | 366 | | 1 | | | 0,79 | | | 1 | 0,79 |
| | | | 366 | 307 | | 1 | | | 0,79 | | | 1 | 0,79 |
| | | | 404 | 422 | | 13 | 17 | 7 | 5,19 | 4,49 | 3,07 | 37 | 5,19 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 427 | | | 1 | | | 0,20 | | 1 | 0,20 |
| | | | 422 | 404 | | 13 | 17 | 7 | 5,19 | 4,49 | 3,07 | 37 | 5,19 |
| | | | 427 | 404 | | | 1 | | | 0,20 | | 1 | 0,20 |
| | | | | 450 | | 8 | 6 | 24 | 16,47 | 10,59 | 13,52 | 38 | 16,47 |
| | | | 450 | 427 | | 8 | 6 | 24 | 16,47 | 10,59 | 13,52 | 38 | 16,47 |
| | Prp19 | Prp19 | 1 | 1 | | 2 | | | 0,09 | | | 2 | 0,09 |
| | | | 107 | 275 | | | 2 | | | 0,53 | | 2 | 0,53 |
| | | | 108 | 120 | | 7 | 13 | 36 | 10,19 | 12,01 | 10,04 | 56 | 12,01 |
| | | | | 139 | | 4 | 2 | 1 | 8,19 | 9,46 | 4,06 | 7 | 9,46 |
| | | | | 170 | | 1 | 4 | | 0,75 | 2,58 | | 5 | 2,58 |
| | | | | 202 | | 1 | | | 1,74 | | | 1 | 1,74 |
| | | | | 275 | | 1 | | | 1,30 | | | 1 | 1,30 |
| | | | | 404 | | 1 | | | 1,37 | | | 1 | 1,37 |
| | | | 120 | 108 | | 7 | 13 | 36 | 10,19 | 12,01 | 10,04 | 56 | 12,01 |
| | | | | 135 | | 3 | 3 | 10 | 2,42 | 3,57 | 5,07 | 16 | 5,07 |
| | | | | 139 | | | 2 | | | 5,92 | | 2 | 5,92 |
| | | | 130 | 139 | | | 2 | | | 6,22 | | 2 | 6,22 |
| | | | 135 | 120 | | 3 | 3 | 10 | 2,42 | 3,57 | 5,07 | 16 | 5,07 |
| | | | | 139 | | 1 | 1 | | 1,67 | 0,39 | | 2 | 1,67 |
| | | | | 272 | | | 1 | 1 | | 0,12 | 3,74 | 2 | 3,74 |
| | | | | 275 | | 1 | 2 | | 1,52 | 0,16 | | 3 | 1,52 |
| | | | 139 | 108 | | 4 | 2 | 1 | 8,19 | 9,46 | 4,06 | 7 | 9,46 |
| | | | | 120 | | | 2 | | | 5,92 | | 2 | 5,92 |
| | | | | 130 | | | 2 | | | 6,22 | | 2 | 6,22 |
| | | | | 135 | | 1 | 1 | | 1,67 | 0,39 | | 2 | 1,67 |
| | | | | 139 | | | 2 | 2 | | 1,94 | 3,41 | 4 | 3,41 |
| | | | | 275 | | 1 | 1 | | 3,68 | 0,16 | | 2 | 3,68 |
| | | | 168 | 433 | | | | 6 | | | 3,63 | 6 | 3,63 |
| | | | | 452 | | 2 | | 3 | 0,33 | | 1,26 | 5 | 1,26 |
| | | | 170 | 108 | | 1 | 4 | | 0,75 | 2,58 | | 5 | 2,58 |
| | | | | 202 | | 6 | 9 | 3 | 9,23 | 2,56 | 2,87 | 18 | 9,23 |
| | | | | 275 | | 1 | | | 1,54 | | | 1 | 1,54 |
| | | | | 452 | | 1 | 1 | 6 | 1,59 | 3,49 | 4,13 | 8 | 4,13 |
| | | | 173 | 202 | | | 1 | | | 1,49 | | 1 | 1,49 |
| | | | | 229 | | 3 | 5 | 6 | 7,09 | 6,18 | 5,53 | 14 | 7,09 |
| | | | | 433 | | 3 | 1 | 15 | 4,59 | 1,24 | 4,51 | 19 | 4,59 |
| | | | | 452 | | 3 | | | 1,90 | | | 3 | 1,90 |
| | | | | 455 | | 1 | 1 | | 14,22 | 3,43 | | 2 | 14,22 |
| | | | 202 | 108 | | 1 | | | 1,74 | | | 1 | 1,74 |
| | | | | 170 | | 6 | 9 | 3 | 9,23 | 2,56 | 2,87 | 18 | 9,23 |
| | | | | 173 | | | 1 | | | 1,49 | | 1 | 1,49 |
| | | | | 226 | | 4 | 6 | 2 | 13,94 | 4,89 | 6,26 | 12 | 13,94 |
| | | | | 229 | | 2 | 5 | 4 | 2,01 | 8,09 | 8,68 | 11 | 8,68 |
| | | | | 272 | | 2 | 3 | 1 | 1,91 | 4,52 | 4,51 | 6 | 4,52 |
| | | | 226 | 202 | | 4 | 6 | 2 | 13,94 | 4,89 | 6,26 | 12 | 13,94 |
| | | | 229 | 173 | | 3 | 5 | 6 | 7,09 | 6,18 | 5,53 | 14 | 7,09 |
| | | | | 202 | | 2 | 5 | 4 | 2,01 | 8,09 | 8,68 | 11 | 8,68 |
| | | | 272 | 135 | | | 1 | 1 | | 0,12 | 3,74 | 2 | 3,74 |
| | | | | 202 | | 2 | 3 | 1 | 1,91 | 4,52 | 4,51 | 6 | 4,52 |
| | | | 275 | 107 | | | 2 | | | 0,53 | | 2 | 0,53 |
| | | | | 108 | | 1 | | | 1,30 | | | 1 | 1,30 |
| | | | | 135 | | 1 | 2 | | 1,52 | 0,16 | | 3 | 1,52 |
| | | | | 139 | | 1 | 1 | | 3,68 | 0,16 | | 2 | 3,68 |
| | | | | 170 | | 1 | | | 1,54 | | | 1 | 1,54 |
| | | | | 404 | | 1 | | | 1,22 | | | 1 | 1,22 |
| | | | 404 | 108 | | 1 | | | 1,37 | | | 1 | 1,37 |
| | | | | 275 | | 1 | | | 1,22 | | | 1 | 1,22 |
| | | | | 452 | | 1 | | | 0,61 | | | 1 | 0,61 |
| | | | | 455 | | 10 | 7 | 1 | 1,72 | 2,98 | 1,86 | 18 | 2,98 |
| | | | 433 | 168 | | | | 6 | | | 3,63 | 6 | 3,63 |
| | | | | 173 | | 3 | 1 | 15 | 4,59 | 1,24 | 4,51 | 19 | 4,59 |
| | | | | 455 | | 3 | 10 | 25 | 2,74 | 4,45 | 4,69 | 38 | 4,69 |
| | | | 452 | 168 | | 2 | | 3 | 0,33 | | 1,26 | 5 | 1,26 |
| | | | | 170 | | 1 | 1 | 6 | 1,59 | 3,49 | 4,13 | 8 | 4,13 |
| | | | | 173 | | 3 | | | 1,90 | | | 3 | 1,90 |
| | | | | 404 | | 1 | | | 0,61 | | | 1 | 0,61 |
| | | | | 455 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | | | 455 | 173 | | 1 | 1 | | 14,22 | 3,43 | | 2 | 14,22 |
| | | | | 404 | | 10 | 7 | 1 | 1,72 | 2,98 | 1,86 | 18 | 2,98 |
| | | | | 433 | | 3 | 10 | 25 | 2,74 | 4,45 | 4,69 | 38 | 4,69 |
| | | | | 452 | | 1 | | | 0,08 | | | 1 | 0,08 |
| | Prp2 | Prp2 | 2 | 40 | | | | 13 | | | 12,82 | 13 | 12,82 |
| | | | | 43 | | | | 6 | | | 10,23 | 6 | 10,23 |
| | | | | 52 | | | | 14 | | | 13,80 | 14 | 13,80 |
| | | | | 60 | | | | 12 | | | 18,06 | 12 | 18,06 |
| | | | | 71 | | | | 1 | | | 9,34 | 1 | 9,34 |
| | | | | 75 | | | | 8 | | | 14,79 | 8 | 14,79 |
| | | | | 83 | | | | 10 | | | 16,56 | 10 | 16,56 |
| | | | | 87 | | | | 3 | | | 3,67 | 3 | 3,67 |
| | | | | 91 | | | | 3 | | | 10,76 | 3 | 10,76 |
| | | | | 101 | | | | 6 | | | 11,26 | 6 | 11,26 |
| | | | | 102 | | | | 3 | | | 11,70 | 3 | 11,70 |
| | | | | 113 | | | | 3 | | | 14,59 | 3 | 14,59 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 120 | | | | 5 | | | 8,80 | 5 | 8,80 |
| | | | | 128 | | | | 2 | | | 14,67 | 2 | 14,67 |
| | | | | 133 | | | | 1 | | | 3,34 | 1 | 3,34 |
| | | | | 211 | | | | 6 | | | 13,57 | 6 | 13,57 |
| | | | | 311 | | | | 3 | | | 7,66 | 3 | 7,66 |
| | | | | 454 | | | | 1 | | | 5,92 | 1 | 5,92 |
| | | | | 560 | | | | 1 | | | 4,74 | 1 | 4,74 |
| | | | | 718 | | | | 2 | | | 3,94 | 2 | 3,94 |
| | | | | 732 | | | | 8 | | | 6,84 | 8 | 6,84 |
| | | | | 756 | | | | 7 | | | 17,20 | 7 | 17,20 |
| | | | | 820 | | | | 1 | | | 3,90 | 1 | 3,90 |
| | | | 10 | 14 | | | | 3 | | | 3,67 | 3 | 3,67 |
| | | | | 45 | | | | 3 | | | 7,09 | 3 | 7,09 |
| | | | | 52 | | | | 2 | | | 8,08 | 2 | 8,08 |
| | | | | 60 | | | | 1 | | | 4,28 | 1 | 4,28 |
| | | | | 75 | | | | 1 | | | 2,04 | 1 | 2,04 |
| | | | | 87 | | | | 1 | | | 6,49 | 1 | 6,49 |
| | | | | 101 | | | | 1 | | | 4,08 | 1 | 4,08 |
| | | | | 102 | | | | 3 | | | 3,09 | 3 | 3,09 |
| | | | | 756 | | | | 1 | | | 1,81 | 1 | 1,81 |
| | | | 14 | 10 | | | | 3 | | | 3,67 | 3 | 3,67 |
| | | | 40 | 2 | | | | 13 | | | 12,82 | 13 | 12,82 |
| | | | | 45 | | | | 28 | | | 11,49 | 28 | 11,49 |
| | | | | 52 | | 2 | | 15 | 1,49 | | 9,58 | 17 | 9,58 |
| | | | | 87 | | | | 1 | | | 2,65 | 1 | 2,65 |
| | | | 43 | 2 | | | | 6 | | | 10,23 | 6 | 10,23 |
| | | | | 52 | | 3 | | 11 | 0,82 | | 8,87 | 14 | 8,87 |
| | | | | 84 | | | | 1 | | | 4,92 | 1 | 4,92 |
| | | | 45 | 10 | | | | 3 | | | 7,09 | 3 | 7,09 |
| | | | | 40 | | | | 28 | | | 11,49 | 28 | 11,49 |
| | | | | 60 | | | | 6 | | | 12,75 | 6 | 12,75 |
| | | | | 71 | | | | 2 | | | 5,80 | 2 | 5,80 |
| | | | | 75 | | | | 2 | | | 4,02 | 2 | 4,02 |
| | | | | 87 | | | | 2 | | | 4,54 | 2 | 4,54 |
| | | | 52 | 2 | | | | 14 | | | 13,80 | 14 | 13,80 |
| | | | | 10 | | | | 2 | | | 8,08 | 2 | 8,08 |
| | | | | 40 | | 2 | | 15 | 1,49 | | 9,58 | 17 | 9,58 |
| | | | | 43 | | 3 | | 11 | 0,82 | | 8,87 | 14 | 8,87 |
| | | | | 60 | | 8 | | 49 | 12,05 | | 9,88 | 57 | 12,05 |
| | | | | 71 | | 3 | | 6 | 5,22 | | 6,45 | 9 | 6,45 |
| | | | | 75 | | | | 8 | | | 8,26 | 8 | 8,26 |
| | | | | 83 | | | | 1 | | | 2,87 | 1 | 2,87 |
| | | | | 84 | | 1 | | 3 | 0,62 | | 5,66 | 4 | 5,66 |
| | | | | 87 | | | | 5 | | | 8,35 | 5 | 8,35 |
| | | | | 91 | | | | 3 | | | 5,24 | 3 | 5,24 |
| | | | | 101 | | | | 5 | | | 9,32 | 5 | 9,32 |
| | | | | 102 | | | | 2 | | | 7,20 | 2 | 7,20 |
| | | | | 130 | | | | 1 | | | 3,97 | 1 | 3,97 |
| | | | | 718 | | 1 | | | 1,79 | | | 1 | 1,79 |
| | | | 60 | 2 | | | | 12 | | | 18,06 | 12 | 18,06 |
| | | | | 10 | | | | 1 | | | 4,28 | 1 | 4,28 |
| | | | | 45 | | | | 6 | | | 12,75 | 6 | 12,75 |
| | | | | 52 | | 8 | | 49 | 12,05 | | 9,88 | 57 | 12,05 |
| | | | | 75 | | 3 | | 34 | 8,01 | | 18,94 | 37 | 18,94 |
| | | | | 83 | | 1 | | 6 | 1,00 | | 9,85 | 7 | 9,85 |
| | | | | 84 | | | | 1 | | | 2,78 | 1 | 2,78 |
| | | | | 87 | | | | 5 | | | 7,52 | 5 | 7,52 |
| | | | | 91 | | | | 3 | | | 18,89 | 3 | 18,89 |
| | | | | 101 | | | | 3 | | | 3,96 | 3 | 3,96 |
| | | | | 102 | | 1 | | 7 | 1,63 | | 10,86 | 8 | 10,86 |
| | | | | 113 | | | | 2 | | | 6,15 | 2 | 6,15 |
| | | | | 211 | | | | 1 | | | 2,25 | 1 | 2,25 |
| | | | | 718 | | 1 | | | 1,82 | | | 1 | 1,82 |
| | | | | 756 | | | | 1 | | | 6,52 | 1 | 6,52 |
| | | | 71 | 2 | | | | 1 | | | 9,34 | 1 | 9,34 |
| | | | | 45 | | | | 2 | | | 5,80 | 2 | 5,80 |
| | | | | 52 | | 3 | | 6 | 5,22 | | 6,45 | 9 | 6,45 |
| | | | | 83 | | 4 | | 7 | 3,81 | | 8,07 | 11 | 8,07 |
| | | | | 84 | | | | 4 | | | 3,69 | 4 | 3,69 |
| | | | | 87 | | 1 | | 8 | 2,44 | | 7,38 | 9 | 7,38 |
| | | | | 91 | | | | 6 | | | 5,36 | 6 | 5,36 |
| | | | | 102 | | | | 2 | | | 9,28 | 2 | 9,28 |
| | | | | 137 | | | | 1 | | | 2,42 | 1 | 2,42 |
| | | | | 560 | | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | | 718 | | 1 | | | 0,88 | | | 1 | 0,88 |
| | | | 75 | 2 | | | | 8 | | | 14,79 | 8 | 14,79 |
| | | | | 10 | | | | 1 | | | 2,04 | 1 | 2,04 |
| | | | | 45 | | | | 2 | | | 4,02 | 2 | 4,02 |
| | | | | 52 | | | | 8 | | | 8,26 | 8 | 8,26 |
| | | | | 60 | | 3 | | 34 | 8,01 | | 18,94 | 37 | 18,94 |
| | | | | 84 | | | | 2 | | | 9,22 | 2 | 9,22 |
| | | | | 87 | | | | 19 | | | 7,46 | 19 | 7,46 |
| | | | | 91 | | 2 | | 11 | 3,86 | | 9,65 | 13 | 9,65 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 101 | | | | 5 | | | 6,24 | 5 | 6,24 |
| | | | | 102 | | | | 2 | | | 12,54 | 2 | 12,54 |
| | | | | 120 | | | | 2 | | | 8,13 | 2 | 8,13 |
| | | | | 128 | | | | 1 | | | 2,49 | 1 | 2,49 |
| | | | | 130 | | | | 1 | | | 1,92 | 1 | 1,92 |
| | | | | 756 | | | | 3 | | | 5,75 | 3 | 5,75 |
| | | | 83 | 2 | | | | 10 | | | 16,56 | 10 | 16,56 |
| | | | | 52 | | | | 1 | | | 2,87 | 1 | 2,87 |
| | | | | 60 | | 1 | | 6 | 1,00 | | 9,85 | 7 | 9,85 |
| | | | | 71 | | 4 | | 7 | 3,81 | | 8,07 | 11 | 8,07 |
| | | | | 87 | | 3 | | 47 | 5,82 | | 10,73 | 50 | 10,73 |
| | | | | 91 | | 1 | | 22 | 8,15 | | 14,13 | 23 | 14,13 |
| | | | | 101 | | | | 9 | | | 6,84 | 9 | 6,84 |
| | | | | 102 | | | | 8 | | | 14,02 | 8 | 14,02 |
| | | | | 113 | | | | 2 | | | 1,82 | 2 | 1,82 |
| | | | | 130 | | | | 4 | | | 6,05 | 4 | 6,05 |
| | | | | 137 | | | | 2 | | | 4,51 | 2 | 4,51 |
| | | | | 211 | | | | 1 | | | 3,67 | 1 | 3,67 |
| | | | | 718 | | 1 | | | 0,95 | | | 1 | 0,95 |
| | | | | 756 | | | | 1 | | | 3,86 | 1 | 3,86 |
| | | | 84 | 43 | | | | 1 | | | 4,92 | 1 | 4,92 |
| | | | | 52 | | 1 | | 3 | 0,62 | | 5,66 | 4 | 5,66 |
| | | | | 60 | | | | 1 | | | 2,78 | 1 | 2,78 |
| | | | | 71 | | | | 4 | | | 3,69 | 4 | 3,69 |
| | | | | 75 | | | | 2 | | | 9,22 | 2 | 9,22 |
| | | | | 91 | | 1 | | | 1,71 | | | 1 | 1,71 |
| | | | | 101 | | 1 | | 10 | 0,64 | | 14,24 | 11 | 14,24 |
| | | | | 102 | | | | 4 | | | 2,53 | 4 | 2,53 |
| | | | | 128 | | | | 1 | | | 3,59 | 1 | 3,59 |
| | | | | 137 | | | | 1 | | | 4,46 | 1 | 4,46 |
| | | | | 211 | | | | 1 | | | 10,64 | 1 | 10,64 |
| | | | 87 | 2 | | | | 3 | | | 3,67 | 3 | 3,67 |
| | | | | 10 | | | | 1 | | | 6,49 | 1 | 6,49 |
| | | | | 40 | | | | 1 | | | 2,65 | 1 | 2,65 |
| | | | | 45 | | | | 2 | | | 4,54 | 2 | 4,54 |
| | | | | 52 | | | | 5 | | | 8,35 | 5 | 8,35 |
| | | | | 60 | | | | 5 | | | 7,52 | 5 | 7,52 |
| | | | | 71 | | 1 | | 8 | 2,44 | | 7,38 | 9 | 7,38 |
| | | | | 75 | | | | 19 | | | 7,46 | 19 | 7,46 |
| | | | | 83 | | 3 | | 47 | 5,82 | | 10,73 | 50 | 10,73 |
| | | | | 101 | | 2 | | 10 | 3,21 | | 8,67 | 12 | 8,67 |
| | | | | 102 | | | | 13 | | | 8,10 | 13 | 8,10 |
| | | | | 113 | | | | 1 | | | 4,56 | 1 | 4,56 |
| | | | | 120 | | | | 2 | | | 4,07 | 2 | 4,07 |
| | | | | 128 | | | | 2 | | | 8,92 | 2 | 8,92 |
| | | | | 130 | | | | 1 | | | 4,39 | 1 | 4,39 |
| | | | | 211 | | | | 2 | | | 8,33 | 2 | 8,33 |
| | | | | 756 | | | | 1 | | | 5,21 | 1 | 5,21 |
| | | | 91 | 2 | | | | 3 | | | 10,76 | 3 | 10,76 |
| | | | | 52 | | | | 3 | | | 5,24 | 3 | 5,24 |
| | | | | 60 | | | | 3 | | | 18,89 | 3 | 18,89 |
| | | | | 71 | | | | 6 | | | 5,36 | 6 | 5,36 |
| | | | | 75 | | 2 | | 11 | 3,86 | | 9,65 | 13 | 9,65 |
| | | | | 83 | | 1 | | 22 | 8,15 | | 14,13 | 23 | 14,13 |
| | | | | 84 | | 1 | | | 1,71 | | | 1 | 1,71 |
| | | | | 102 | | 2 | | 38 | 4,76 | | 24,32 | 40 | 24,32 |
| | | | | 113 | | | | 6 | | | 10,94 | 6 | 10,94 |
| | | | | 120 | | | | 1 | | | 7,13 | 1 | 7,13 |
| | | | | 128 | | | | 1 | | | 2,94 | 1 | 2,94 |
| | | | | 130 | | | | 1 | | | 1,56 | 1 | 1,56 |
| | | | | 133 | | | | 2 | | | 4,48 | 2 | 4,48 |
| | | | | 756 | | | | 2 | | | 6,74 | 2 | 6,74 |
| | | | 101 | 2 | | | | 6 | | | 11,26 | 6 | 11,26 |
| | | | | 10 | | | | 1 | | | 4,08 | 1 | 4,08 |
| | | | | 52 | | | | 5 | | | 9,32 | 5 | 9,32 |
| | | | | 60 | | | | 3 | | | 3,96 | 3 | 3,96 |
| | | | | 75 | | | | 5 | | | 6,24 | 5 | 6,24 |
| | | | | 83 | | | | 9 | | | 6,84 | 9 | 6,84 |
| | | | | 84 | | 1 | | 10 | 0,64 | | 14,24 | 11 | 14,24 |
| | | | | 87 | | 2 | | 10 | 3,21 | | 8,67 | 12 | 8,67 |
| | | | | 113 | | 1 | | 6 | 0,28 | | 5,95 | 7 | 5,95 |
| | | | | 120 | | 1 | | 2 | 1,17 | | 5,59 | 3 | 5,59 |
| | | | | 128 | | 1 | | 1 | 1,99 | | 6,88 | 2 | 6,88 |
| | | | | 130 | | | | 8 | | | 4,46 | 8 | 4,46 |
| | | | | 133 | | | | 12 | | | 10,63 | 12 | 10,63 |
| | | | | 137 | | | | 11 | | | 7,91 | 11 | 7,91 |
| | | | | 454 | | | | 1 | | | 2,37 | 1 | 2,37 |
| | | | | 560 | | | | 2 | | | 4,85 | 2 | 4,85 |
| | | | | 718 | | 1 | | | 1,08 | | | 1 | 1,08 |
| | | | | 732 | | | | 4 | | | 7,01 | 4 | 7,01 |
| | | | | 756 | | | | 1 | | | 3,76 | 1 | 3,76 |
| | | | 102 | 2 | | | | 3 | | | 11,70 | 3 | 11,70 |
| | | | | 10 | | | | 3 | | | 3,09 | 3 | 3,09 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 52 | | | | 2 | | | 7,20 | 2 | 7,20 |
| | | | | 60 | | 1 | | 7 | 1,63 | | 10,86 | 8 | 10,86 |
| | | | | 71 | | | | 2 | | | 9,28 | 2 | 9,28 |
| | | | | 75 | | | | 2 | | | 12,54 | 2 | 12,54 |
| | | | | 83 | | | | 8 | | | 14,02 | 8 | 14,02 |
| | | | | 84 | | | | 4 | | | 2,53 | 4 | 2,53 |
| | | | | 87 | | | | 13 | | | 8,10 | 13 | 8,10 |
| | | | | 91 | | 2 | | 38 | 4,76 | | 24,32 | 40 | 24,32 |
| | | | | 120 | | | | 18 | | | 12,55 | 18 | 12,55 |
| | | | | 128 | | 1 | | 2 | 1,45 | | 4,50 | 3 | 4,50 |
| | | | | 130 | | 1 | | 4 | 0,49 | | 2,61 | 5 | 2,61 |
| | | | | 133 | | | | 2 | | | 5,63 | 2 | 5,63 |
| | | | | 137 | | | | 5 | | | 5,65 | 5 | 5,65 |
| | | | | 211 | | | | 2 | | | 11,21 | 2 | 11,21 |
| | | | | 732 | | | | 2 | | | 4,71 | 2 | 4,71 |
| | | | 113 | 2 | | | | 3 | | | 14,59 | 3 | 14,59 |
| | | | | 60 | | | | 2 | | | 6,15 | 2 | 6,15 |
| | | | | 83 | | | | 2 | | | 1,82 | 2 | 1,82 |
| | | | | 87 | | | | 1 | | | 4,56 | 1 | 4,56 |
| | | | | 91 | | | | 6 | | | 10,94 | 6 | 10,94 |
| | | | | 101 | | 1 | | 6 | 0,28 | | 5,95 | 7 | 5,95 |
| | | | | 128 | | 1 | | 5 | 0,61 | | 6,01 | 6 | 6,01 |
| | | | | 130 | | | | 5 | | | 2,45 | 5 | 2,45 |
| | | | | 133 | | | | 9 | | | 7,71 | 9 | 7,71 |
| | | | | 137 | | | | 1 | | | 3,87 | 1 | 3,87 |
| | | | | 718 | | | | 1 | | | 2,65 | 1 | 2,65 |
| | | | | 732 | | | | 1 | | | 1,77 | 1 | 1,77 |
| | | | 120 | 2 | | | | 5 | | | 8,80 | 5 | 8,80 |
| | | | | 75 | | | | 2 | | | 8,13 | 2 | 8,13 |
| | | | | 87 | | | | 2 | | | 4,07 | 2 | 4,07 |
| | | | | 91 | | | | 1 | | | 7,13 | 1 | 7,13 |
| | | | | 101 | | 1 | | 2 | 1,17 | | 5,59 | 3 | 5,59 |
| | | | | 102 | | | | 18 | | | 12,55 | 18 | 12,55 |
| | | | | 130 | | 1 | | | 0,64 | | | 1 | 0,64 |
| | | | | 133 | | 1 | | 2 | 4,37 | | 4,22 | 3 | 4,37 |
| | | | | 137 | | 1 | | 2 | 0,12 | | 1,69 | 3 | 1,69 |
| | | | | 211 | | | | 1 | | | 5,08 | 1 | 5,08 |
| | | | | 756 | | | | 2 | | | 6,73 | 2 | 6,73 |
| | | | 128 | 2 | | | | 2 | | | 14,67 | 2 | 14,67 |
| | | | | 75 | | | | 1 | | | 2,49 | 1 | 2,49 |
| | | | | 84 | | | | 1 | | | 3,59 | 1 | 3,59 |
| | | | | 87 | | | | 2 | | | 8,92 | 2 | 8,92 |
| | | | | 91 | | | | 1 | | | 2,94 | 1 | 2,94 |
| | | | | 101 | | 1 | | 1 | 1,99 | | 6,88 | 2 | 6,88 |
| | | | | 102 | | 1 | | 2 | 1,45 | | 4,50 | 3 | 4,50 |
| | | | | 113 | | 1 | | 5 | 0,61 | | 6,01 | 6 | 6,01 |
| | | | | 133 | | 6 | | 15 | 6,32 | | 7,13 | 21 | 7,13 |
| | | | | 137 | | 1 | | 11 | 2,73 | | 5,82 | 12 | 5,82 |
| | | | 130 | 52 | | | | 1 | | | 3,97 | 1 | 3,97 |
| | | | | 75 | | | | 1 | | | 1,92 | 1 | 1,92 |
| | | | | 83 | | | | 4 | | | 6,05 | 4 | 6,05 |
| | | | | 87 | | | | 1 | | | 4,39 | 1 | 4,39 |
| | | | | 91 | | | | 1 | | | 1,56 | 1 | 1,56 |
| | | | | 101 | | | | 8 | | | 4,46 | 8 | 4,46 |
| | | | | 102 | | 1 | | 4 | 0,49 | | 2,61 | 5 | 2,61 |
| | | | | 113 | | | | 5 | | | 2,45 | 5 | 2,45 |
| | | | | 120 | | 1 | | | 0,64 | | | 1 | 0,64 |
| | | | | 137 | | 3 | | 9 | 5,88 | | 4,22 | 12 | 5,88 |
| | | | | 211 | | | | 9 | | | 5,07 | 9 | 5,07 |
| | | | | 560 | | | | 1 | | | 3,67 | 1 | 3,67 |
| | | | | 820 | | | | 1 | | | 3,03 | 1 | 3,03 |
| | | | 133 | 2 | | | | 1 | | | 3,34 | 1 | 3,34 |
| | | | | 91 | | | | 2 | | | 4,48 | 2 | 4,48 |
| | | | | 101 | | | | 12 | | | 10,63 | 12 | 10,63 |
| | | | | 102 | | | | 2 | | | 5,63 | 2 | 5,63 |
| | | | | 113 | | | | 9 | | | 7,71 | 9 | 7,71 |
| | | | | 120 | | 1 | | 2 | 4,37 | | 4,22 | 3 | 4,37 |
| | | | | 128 | | 6 | | 15 | 6,32 | | 7,13 | 21 | 7,13 |
| | | | | 211 | | | | 2 | | | 9,86 | 2 | 9,86 |
| | | | | 718 | | | | 1 | | | 3,98 | 1 | 3,98 |
| | | | | 820 | | | | 1 | | | 2,61 | 1 | 2,61 |
| | | | 137 | 71 | | | | 1 | | | 2,42 | 1 | 2,42 |
| | | | | 83 | | | | 2 | | | 4,51 | 2 | 4,51 |
| | | | | 84 | | | | 1 | | | 4,46 | 1 | 4,46 |
| | | | | 101 | | | | 11 | | | 7,91 | 11 | 7,91 |
| | | | | 102 | | | | 5 | | | 5,65 | 5 | 5,65 |
| | | | | 113 | | | | 1 | | | 3,87 | 1 | 3,87 |
| | | | | 120 | | 1 | | 2 | 0,12 | | 1,69 | 3 | 1,69 |
| | | | | 128 | | 1 | | 11 | 2,73 | | 5,82 | 12 | 5,82 |
| | | | | 130 | | 3 | | 9 | 5,88 | | 4,22 | 12 | 5,88 |
| | | | | 211 | | | | 3 | | | 5,38 | 3 | 5,38 |
| | | | | 454 | | | | 6 | | | 3,78 | 6 | 3,78 |
| | | | | 467 | | | | 1 | | | 2,10 | 1 | 2,10 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 485 | | | | 2 | | | 1,97 | 2 | 1,97 |
| | | | | 718 | | 1 | | | 2,09 | | | 1 | 2,09 |
| | | | | 732 | | | | 1 | | | 4,63 | 1 | 4,63 |
| | | | | 820 | | | | 1 | | | 2,10 | 1 | 2,10 |
| | | | 211 | 2 | | | | 6 | | | 13,57 | 6 | 13,57 |
| | | | | 60 | | | | 1 | | | 2,25 | 1 | 2,25 |
| | | | | 83 | | | | 1 | | | 3,67 | 1 | 3,67 |
| | | | | 84 | | | | 1 | | | 10,64 | 1 | 10,64 |
| | | | | 87 | | | | 2 | | | 8,33 | 2 | 8,33 |
| | | | | 102 | | | | 2 | | | 11,21 | 2 | 11,21 |
| | | | | 120 | | | | 1 | | | 5,08 | 1 | 5,08 |
| | | | | 130 | | | | 9 | | | 5,07 | 9 | 5,07 |
| | | | | 133 | | | | 2 | | | 9,86 | 2 | 9,86 |
| | | | | 137 | | | | 3 | | | 5,38 | 3 | 5,38 |
| | | | | 221 | | 14 | | 11 | 10,43 | | 9,69 | 25 | 10,43 |
| | | | | 311 | | | | 2 | | | 6,47 | 2 | 6,47 |
| | | | | 467 | | 1 | | 1 | 5,48 | | 1,33 | 2 | 5,48 |
| | | | | 560 | | 1 | | 3 | 0,29 | | 4,27 | 4 | 4,27 |
| | | | | 756 | | | | 1 | | | 3,80 | 1 | 3,80 |
| | | | 221 | 211 | | 14 | | 11 | 10,43 | | 9,69 | 25 | 10,43 |
| | | | 270 | 316 | 10,5 | | | 7 | | | 3,20 | 7 | 3,20 |
| | | | 300 | 311 | 10,5 | 17 | | 96 | 12,63 | | 8,36 | 113 | 12,63 |
| | | | | 316 | 5,1 | 18 | | 61 | 11,21 | | 8,08 | 79 | 11,21 |
| | | | 311 | 2 | | | | 3 | | | 7,66 | 3 | 7,66 |
| | | | | 211 | | | | 2 | | | 6,47 | 2 | 6,47 |
| | | | | 300 | 10,5 | 17 | | 96 | 12,63 | | 8,36 | 113 | 12,63 |
| | | | | 732 | 15,3 | 19 | | 32 | 10,39 | | 7,35 | 51 | 10,39 |
| | | | 316 | 270 | 10,5 | | | 7 | | | 3,20 | 7 | 3,20 |
| | | | | 300 | 5,1 | 18 | | 61 | 11,21 | | 8,08 | 79 | 11,21 |
| | | | 454 | 2 | | | | 1 | | | 5,92 | 1 | 5,92 |
| | | | | 101 | | | | 1 | | | 2,37 | 1 | 2,37 |
| | | | | 137 | | | | 6 | | | 3,78 | 6 | 3,78 |
| | | | 467 | 137 | | | | 1 | | | 2,10 | 1 | 2,10 |
| | | | | 211 | | 1 | | 1 | 5,48 | | 1,33 | 2 | 5,48 |
| | | | 485 | 137 | | | | 2 | | | 1,97 | 2 | 1,97 |
| | | | | 728 | 20,5 | | | 1 | | | 2,31 | 1 | 2,31 |
| | | | | 732 | 19,4 | 4 | | 18 | 3,26 | | 3,88 | 22 | 3,88 |
| | | | 560 | 2 | | | | 1 | | | 4,74 | 1 | 4,74 |
| | | | | 71 | | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | | 101 | | | | 2 | | | 4,85 | 2 | 4,85 |
| | | | | 130 | | | | 1 | | | 3,67 | 1 | 3,67 |
| | | | | 211 | | 1 | | 3 | 0,29 | | 4,27 | 4 | 4,27 |
| | | | 632 | 640 | 17,0 | | | 14 | | | 9,06 | 14 | 9,06 |
| | | | 640 | 632 | 17,0 | | | 14 | | | 9,06 | 14 | 9,06 |
| | | | | 750 | 13,8 | 1 | | 10 | 10,69 | | 5,47 | 11 | 10,69 |
| | | | | 756 | 22,0 | 3 | | 58 | 4,80 | | 12,53 | 61 | 12,53 |
| | | | 718 | 2 | | | | 2 | | | 3,94 | 2 | 3,94 |
| | | | | 52 | | 1 | | | 1,79 | | | 1 | 1,79 |
| | | | | 60 | | 1 | | | 1,82 | | | 1 | 1,82 |
| | | | | 71 | | 1 | | | 0,88 | | | 1 | 0,88 |
| | | | | 83 | | 1 | | | 0,95 | | | 1 | 0,95 |
| | | | | 101 | | 1 | | | 1,08 | | | 1 | 1,08 |
| | | | | 113 | | | | 1 | | | 2,65 | 1 | 2,65 |
| | | | | 133 | | | | 1 | | | 3,98 | 1 | 3,98 |
| | | | | 137 | | 1 | | | 2,09 | | | 1 | 2,09 |
| | | | 728 | 485 | 20,5 | | | 1 | | | 2,31 | 1 | 2,31 |
| | | | 732 | 2 | | | | 8 | | | 6,84 | 8 | 6,84 |
| | | | | 101 | | | | 4 | | | 7,01 | 4 | 7,01 |
| | | | | 102 | | | | 2 | | | 4,71 | 2 | 4,71 |
| | | | | 113 | | | | 1 | | | 1,77 | 1 | 1,77 |
| | | | | 137 | | | | 1 | | | 4,63 | 1 | 4,63 |
| | | | | 311 | 15,3 | 19 | | 32 | 10,39 | | 7,35 | 51 | 10,39 |
| | | | | 485 | 19,4 | 4 | | 18 | 3,26 | | 3,88 | 22 | 3,88 |
| | | | 750 | 640 | 13,8 | 1 | | 10 | 10,69 | | 5,47 | 11 | 10,69 |
| | | | 756 | 2 | | | | 7 | | | 17,20 | 7 | 17,20 |
| | | | | 10 | | | | 1 | | | 1,81 | 1 | 1,81 |
| | | | | 60 | | | | 1 | | | 6,52 | 1 | 6,52 |
| | | | | 75 | | | | 3 | | | 5,75 | 3 | 5,75 |
| | | | | 83 | | | | 1 | | | 3,86 | 1 | 3,86 |
| | | | | 87 | | | | 1 | | | 5,21 | 1 | 5,21 |
| | | | | 91 | | | | 2 | | | 6,74 | 2 | 6,74 |
| | | | | 101 | | | | 1 | | | 3,76 | 1 | 3,76 |
| | | | | 120 | | | | 2 | | | 6,73 | 2 | 6,73 |
| | | | | 211 | | | | 1 | | | 3,80 | 1 | 3,80 |
| | | | | 640 | 22,0 | 3 | | 58 | 4,80 | | 12,53 | 61 | 12,53 |
| | | | | 763 | 14,1 | 2 | | 40 | 9,09 | | 12,10 | 42 | 12,10 |
| | | | 763 | 756 | 14,1 | 2 | | 40 | 9,09 | | 12,10 | 42 | 12,10 |
| | | | 820 | 2 | | | | 1 | | | 3,90 | 1 | 3,90 |
| | | | | 130 | | | | 1 | | | 3,03 | 1 | 3,03 |
| | | | | 133 | | | | 1 | | | 2,61 | 1 | 2,61 |
| | | | | 137 | | | | 1 | | | 2,10 | 1 | 2,10 |
| | | | | 840 | | | | 1 | | | 2,40 | 1 | 2,40 |
| | | | 828 | 870 | | | | 1 | | | 1,73 | 1 | 1,73 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 840 | 820 | | | | 1 | | | 2,40 | 1 | 2,40 |
| | | | 870 | 828 | | | | 1 | | | 1,73 | 1 | 1,73 |
| | Prp21 | Prp21 | | | | 44 | 68 | 224 | 20,67 | 13,04 | 17,06 | 336 | 20,67 |
| | Prp45 | Prp45 | 60 | 71 | 16,5 | 4 | 4 | 22 | 4,27 | 2,96 | 8,71 | 30 | 8,71 |
| | | | 71 | 60 | 16,5 | 4 | 4 | 22 | 4,27 | 2,96 | 8,71 | 30 | 8,71 |
| | | | 242 | 265 | | | 1 | | | 3,28 | | 1 | 3,28 |
| | | | 262 | 265 | | 22 | 12 | 60 | 16,56 | 13,76 | 15,33 | 94 | 16,56 |
| | | | | 274 | | 15 | 2 | 6 | 16,38 | 4,84 | 11,87 | 23 | 16,38 |
| | | | 264 | 274 | | 11 | 2 | 5 | 11,70 | 5,32 | 9,86 | 18 | 11,70 |
| | | | 265 | 242 | | | 1 | | | 3,28 | | 1 | 3,28 |
| | | | | 262 | | 22 | 12 | 60 | 16,56 | 13,76 | 15,33 | 94 | 16,56 |
| | | | | 274 | | 24 | 14 | 43 | 11,26 | 12,12 | 13,33 | 81 | 13,33 |
| | | | | 287 | | | | 1 | | | 6,89 | 1 | 6,89 |
| | | | 274 | 262 | | 15 | 2 | 6 | 16,38 | 4,84 | 11,87 | 23 | 16,38 |
| | | | | 264 | | 11 | 2 | 5 | 11,70 | 5,32 | 9,86 | 18 | 11,70 |
| | | | | 265 | | 24 | 14 | 43 | 11,26 | 12,12 | 13,33 | 81 | 13,33 |
| | | | | 287 | | 5 | 4 | 9 | 11,49 | 6,89 | 9,14 | 18 | 11,49 |
| | | | 287 | 265 | | | | 1 | | | 6,89 | 1 | 6,89 |
| | | | | 274 | | 5 | 4 | 9 | 11,49 | 6,89 | 9,14 | 18 | 11,49 |
| | Prp46 | Prp46 | 56 | 67 | | 4 | 3 | 7 | 11,92 | 5,84 | 12,61 | 14 | 12,61 |
| | | | | 87 | | 2 | | 2 | 4,54 | | 10,59 | 4 | 10,59 |
| | | | 66 | 88 | | 2 | | | 5,10 | | | 2 | 5,10 |
| | | | 67 | 56 | | 4 | 3 | 7 | 11,92 | 5,84 | 12,61 | 14 | 12,61 |
| | | | | 88 | | 4 | | | 5,27 | | | 4 | 5,27 |
| | | | 87 | 56 | | 2 | | 2 | 4,54 | | 10,59 | 4 | 10,59 |
| | | | | 100 | | 1 | | | 3,30 | | | 1 | 3,30 |
| | | | | 434 | | | | 1 | | | 7,51 | 1 | 7,51 |
| | | | 88 | 66 | | 2 | | | 5,10 | | | 2 | 5,10 |
| | | | | 67 | | 4 | | | 5,27 | | | 4 | 5,27 |
| | | | | 434 | | | | 2 | | | 8,97 | 2 | 8,97 |
| | | | 100 | 87 | | 1 | | | 3,30 | | | 1 | 3,30 |
| | | | 130 | 427 | 5,6 | 1 | | | 1,68 | | | 1 | 1,68 |
| | | | 319 | 409 | 12,6 | 2 | 2 | 1 | 3,03 | 2,00 | 4,05 | 5 | 4,05 |
| | | | 409 | 319 | 12,6 | 2 | 2 | 1 | 3,03 | 2,00 | 4,05 | 5 | 4,05 |
| | | | | 427 | 14,2 | | 3 | | | 2,81 | | 3 | 2,81 |
| | | | 427 | 130 | 5,6 | 1 | | | 1,68 | | | 1 | 1,68 |
| | | | | 409 | 14,2 | | 3 | | | 2,81 | | 3 | 2,81 |
| | | | 434 | 87 | | | | 1 | | | 7,51 | 1 | 7,51 |
| | | | | 88 | | | | 2 | | | 8,97 | 2 | 8,97 |
| | Prp8 | Prp8 | 89 | 96 | | 1 | | 3 | 1,18 | | 2,86 | 4 | 2,86 |
| | | | 90 | 98 | | 10 | 10 | 44 | 11,94 | 5,37 | 8,84 | 64 | 11,94 |
| | | | | 103 | | | 3 | 3 | | 7,29 | 8,18 | 6 | 8,18 |
| | | | 96 | 89 | | 1 | | 3 | 1,18 | | 2,86 | 4 | 2,86 |
| | | | | 98 | | 10 | 12 | 5 | 9,77 | 5,19 | 5,53 | 27 | 9,77 |
| | | | | 103 | | | 5 | | | 3,04 | | 5 | 3,04 |
| | | | 98 | 90 | | 10 | 10 | 44 | 11,94 | 5,37 | 8,84 | 64 | 11,94 |
| | | | | 96 | | 10 | 12 | 5 | 9,77 | 5,19 | 5,53 | 27 | 9,77 |
| | | | 103 | 90 | | | 3 | 3 | | 7,29 | 8,18 | 6 | 8,18 |
| | | | | 96 | | | 5 | | | 3,04 | | 5 | 3,04 |
| | | | | 121 | | | | 1 | | | 0,41 | 1 | 0,41 |
| | | | | 611 | | | | 3 | | | 1,40 | 3 | 1,40 |
| | | | 121 | 103 | | | | 1 | | | 0,41 | 1 | 0,41 |
| | | | 131 | 141 | 19,0 | | | 2 | | | 6,72 | 2 | 6,72 |
| | | | 141 | 131 | 19,0 | | | 2 | | | 6,72 | 2 | 6,72 |
| | | | 152 | 159 | 14,2 | | 1 | | | 2,84 | | 1 | 2,84 |
| | | | 159 | 152 | 14,2 | | 1 | | | 2,84 | | 1 | 2,84 |
| | | | | 555 | 14,3 | | | 2 | | | 4,98 | 2 | 4,98 |
| | | | | 586 | 12,2 | | 1 | 10 | | 6,63 | 11,62 | 11 | 11,62 |
| | | | | 600 | 23,5 | | 1 | | | 0,46 | | 1 | 0,46 |
| | | | 325 | 334 | 13,8 | 1 | 3 | 4 | 3,20 | 7,63 | 6,84 | 8 | 7,63 |
| | | | 334 | 325 | 13,8 | 1 | 3 | 4 | 3,20 | 7,63 | 6,84 | 8 | 7,63 |
| | | | 351 | 519 | 13,2 | 1 | | | 2,41 | | | 1 | 2,41 |
| | | | | 524 | 8,9 | 1 | 4 | 2 | 0,72 | 2,53 | 3,46 | 7 | 3,46 |
| | | | 517 | 524 | 10,5 | | 2 | | | 0,76 | | 2 | 0,76 |
| | | | | 681 | 10,8 | | 1 | 2 | | 0,03 | 5,56 | 3 | 5,56 |
| | | | | 684 | 11,3 | 32 | 39 | 14 | 17,30 | 11,19 | 12,75 | 85 | 17,30 |
| | | | | 697 | 16,6 | 7 | 8 | 1 | 14,38 | 10,61 | 6,39 | 16 | 14,38 |
| | | | 519 | 351 | 13,2 | 1 | | | 2,41 | | | 1 | 2,41 |
| | | | 524 | 351 | 8,9 | 1 | 4 | 2 | 0,72 | 2,53 | 3,46 | 7 | 3,46 |
| | | | | 517 | 10,5 | | 2 | | | 0,76 | | 2 | 0,76 |
| | | | 555 | 159 | 14,3 | | | 2 | | | 4,98 | 2 | 4,98 |
| | | | 586 | 159 | 12,2 | | 1 | 10 | | 6,63 | 11,62 | 11 | 11,62 |
| | | | | 612 | 8,2 | | 1 | | | 0,76 | | 1 | 0,76 |
| | | | | 743 | 24,3 | 4 | 19 | 37 | 4,97 | 4,66 | 8,41 | 60 | 8,41 |
| | | | 600 | 159 | 23,5 | | 1 | | | 0,46 | | 1 | 0,46 |
| | | | | 611 | 15,4 | | 4 | | | 0,86 | | 4 | 0,86 |
| | | | | 743 | 34,6 | | 3 | | | 0,71 | | 3 | 0,71 |
| | | | 608 | 612 | 6,9 | | | 1 | | | 3,91 | 1 | 3,91 |
| | | | 611 | 103 | | | | 3 | | | 1,40 | 3 | 1,40 |
| | | | | 600 | 15,4 | | 4 | | | 0,86 | | 4 | 0,86 |
| | | | 612 | 586 | 8,2 | | 1 | | | 0,76 | | 1 | 0,76 |
| | | | | 608 | 6,9 | | | 1 | | | 3,91 | 1 | 3,91 |
| | | | 681 | 517 | 10,8 | | 1 | 2 | | 0,03 | 5,56 | 3 | 5,56 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 684 | 517 | 11,3 | 32 | 39 | 14 | 17,30 | 11,19 | 12,75 | 85 | 17,30 |
| | | | | 697 | 13,9 | 5 | 21 | 8 | 7,47 | 8,93 | 9,86 | 34 | 9,86 |
| | | | 697 | 517 | 16,6 | 7 | 8 | 1 | 14,38 | 10,61 | 6,39 | 16 | 14,38 |
| | | | | 684 | 13,9 | 5 | 21 | 8 | 7,47 | 8,93 | 9,86 | 34 | 9,86 |
| | | | | 1926 | 24,8 | 1 | | | 0,85 | | | 1 | 0,85 |
| | | | 743 | 586 | 24,3 | 4 | 19 | 37 | 4,97 | 4,66 | 8,41 | 60 | 8,41 |
| | | | | 600 | 34,6 | | 3 | | | 0,71 | | 3 | 0,71 |
| | | | | 847 | 23,9 | | 1 | 3 | | 4,19 | 6,45 | 4 | 6,45 |
| | | | 747 | 847 | 13,7 | | 1 | 3 | | 1,66 | 4,97 | 4 | 4,97 |
| | | | 794 | 819 | 10,7 | | 14 | 4 | | 15,35 | 14,19 | 18 | 15,35 |
| | | | | 847 | 13,1 | | 7 | 3 | | 2,50 | 3,65 | 10 | 3,65 |
| | | | | 1093 | 10,5 | | 9 | 10 | | 14,53 | 11,74 | 19 | 14,53 |
| | | | 810 | 817 | 10,7 | 1 | 14 | 15 | 3,52 | 3,42 | 4,05 | 30 | 4,05 |
| | | | 817 | 810 | 10,7 | 1 | 14 | 15 | 3,52 | 3,42 | 4,05 | 30 | 4,05 |
| | | | 819 | 794 | 10,7 | | 14 | 4 | | 15,35 | 14,19 | 18 | 15,35 |
| | | | | 847 | 15,5 | | 9 | 2 | | 2,71 | 2,90 | 11 | 2,90 |
| | | | 842 | 847 | 8,6 | | 2 | | | 2,62 | | 2 | 2,62 |
| | | | | 1334 | 17,8 | | 1 | 7 | | 1,19 | 6,49 | 8 | 6,49 |
| | | | 846 | 1093 | 15,2 | | 1 | 1 | | 0,14 | 3,04 | 2 | 3,04 |
| | | | 847 | 743 | 23,9 | | 1 | 3 | | 4,19 | 6,45 | 4 | 6,45 |
| | | | | 747 | 13,7 | | 1 | 3 | | 1,66 | 4,97 | 4 | 4,97 |
| | | | | 794 | 13,1 | | 7 | 3 | | 2,50 | 3,65 | 10 | 3,65 |
| | | | | 819 | 15,5 | | 9 | 2 | | 2,71 | 2,90 | 11 | 2,90 |
| | | | | 842 | 8,6 | | 2 | | | 2,62 | | 2 | 2,62 |
| | | | | 858 | 16,6 | | 4 | 4 | | 2,10 | 5,81 | 8 | 5,81 |
| | | | | 1093 | 14,5 | 1 | 16 | 42 | 4,29 | 4,49 | 6,79 | 59 | 6,79 |
| | | | 858 | 847 | 16,6 | | 4 | 4 | | 2,10 | 5,81 | 8 | 5,81 |
| | | | 920 | 1589 | 25,2 | | | 6 | | | 11,44 | 6 | 11,44 |
| | | | 926 | 1330 | 16,4 | | | 2 | | | 2,13 | 2 | 2,13 |
| | | | 956 | 965 | 15,3 | | 1 | 9 | | 7,59 | 8,31 | 10 | 8,31 |
| | | | 965 | 956 | 15,3 | | 1 | 9 | | 7,59 | 8,31 | 10 | 8,31 |
| | | | 1093 | 794 | 10,5 | | 9 | 10 | | 14,53 | 11,74 | 19 | 14,53 |
| | | | | 846 | 15,2 | | 1 | 1 | | 0,14 | 3,04 | 2 | 3,04 |
| | | | | 847 | 14,5 | 1 | 16 | 42 | 4,29 | 4,49 | 6,79 | 59 | 6,79 |
| | | | 1150 | 1294 | 17,6 | | | 3 | | | 4,68 | 3 | 4,68 |
| | | | 1205 | 1310 | 14,1 | 4 | 5 | 6 | 3,84 | 7,76 | 5,90 | 15 | 7,76 |
| | | | | 1416 | 29,2 | | 1 | 3 | | 0,73 | 3,40 | 4 | 3,40 |
| | | | 1209 | 1416 | 23,0 | | | 7 | | | 4,45 | 7 | 4,45 |
| | | | 1294 | 1150 | 17,6 | | | 3 | | | 4,68 | 3 | 4,68 |
| | | | 1310 | 1205 | 14,1 | 4 | 5 | 6 | 3,84 | 7,76 | 5,90 | 15 | 7,76 |
| | | | 1330 | 926 | 16,4 | | | 2 | | | 2,13 | 2 | 2,13 |
| | | | 1334 | 842 | 17,8 | | 1 | 7 | | 1,19 | 6,49 | 8 | 6,49 |
| | | | 1416 | 1205 | 29,2 | | 1 | 3 | | 0,73 | 3,40 | 4 | 3,40 |
| | | | | 1209 | 23,0 | | | 7 | | | 4,45 | 7 | 4,45 |
| | | | 1589 | 920 | 25,2 | | | 6 | | | 11,44 | 6 | 11,44 |
| | | | 1807 | 1938 | 27,3 | | | 6 | | | 11,77 | 6 | 11,77 |
| | | | | 2080 | | 1 | 1 | 3 | 1,57 | 4,98 | 10,34 | 5 | 10,34 |
| | | | | 2089 | | | | 3 | | | 6,25 | 3 | 6,25 |
| | | | 1821 | 2089 | | | 2 | 1 | | 2,04 | 9,85 | 3 | 9,85 |
| | | | | 2097 | | | | 1 | | | 6,01 | 1 | 6,01 |
| | | | 1864 | 1903 | 23,2 | | | 2 | | | 9,16 | 2 | 9,16 |
| | | | | 2016 | 20,0 | | | 2 | | | 8,28 | 2 | 8,28 |
| | | | | 2108 | | | | 3 | | | 5,03 | 3 | 5,03 |
| | | | | 2122 | | 3 | 1 | 39 | 9,51 | 0,36 | 12,14 | 43 | 12,14 |
| | | | 1873 | 1903 | 13,7 | | 1 | 6 | | 2,31 | 5,25 | 7 | 5,25 |
| | | | | 2122 | | | | 3 | | | 8,01 | 3 | 8,01 |
| | | | 1892 | 1910 | 13,5 | | 1 | | | 0,12 | | 1 | 0,12 |
| | | | | 1912 | 11,2 | | 2 | | | 3,97 | | 2 | 3,97 |
| | | | 1903 | 1864 | 23,2 | | | 2 | | | 9,16 | 2 | 9,16 |
| | | | | 1873 | 13,7 | | 1 | 6 | | 2,31 | 5,25 | 7 | 5,25 |
| | | | | 1910 | 13,0 | 1 | 5 | | 5,80 | 5,02 | | 6 | 5,80 |
| | | | | 2122 | | 1 | 1 | 2 | 6,77 | 0,79 | 6,25 | 4 | 6,77 |
| | | | 1910 | 1892 | 13,5 | | 1 | | | 0,12 | | 1 | 0,12 |
| | | | | 1903 | 13,0 | 1 | 5 | | 5,80 | 5,02 | | 6 | 5,80 |
| | | | | 1938 | 10,5 | 1 | 4 | 10 | 6,36 | 4,60 | 4,92 | 15 | 6,36 |
| | | | | 2094 | | | | 1 | | | 2,66 | 1 | 2,66 |
| | | | | 2097 | | | | 1 | | | 2,86 | 1 | 2,86 |
| | | | | 2108 | | 1 | 3 | 4 | 0,68 | 1,28 | 2,72 | 8 | 2,72 |
| | | | | 2122 | | 2 | 1 | 15 | 2,18 | 2,25 | 6,80 | 18 | 6,80 |
| | | | | 2149 | 27,0 | | | 1 | | | 2,68 | 1 | 2,68 |
| | | | 1912 | 1892 | 11,2 | | 2 | | | 3,97 | | 2 | 3,97 |
| | | | 1926 | 697 | 24,8 | 1 | | | 0,85 | | | 1 | 0,85 |
| | | | 1938 | 1807 | 27,3 | | | 6 | | | 11,77 | 6 | 11,77 |
| | | | | 1910 | 10,5 | 1 | 4 | 10 | 6,36 | 4,60 | 4,92 | 15 | 6,36 |
| | | | | 2016 | 20,2 | | | 2 | | | 9,82 | 2 | 9,82 |
| | | | | 2089 | | 1 | 1 | 7 | 0,97 | 1,24 | 8,39 | 9 | 8,39 |
| | | | | 2094 | | | | 4 | | | 4,70 | 4 | 4,70 |
| | | | | 2097 | | | | 3 | | | 8,74 | 3 | 8,74 |
| | | | 2016 | 1864 | 20,0 | | | 2 | | | 8,28 | 2 | 8,28 |
| | | | | 1938 | 20,2 | | | 2 | | | 9,82 | 2 | 9,82 |
| | | | | 2066 | 13,6 | 37 | 22 | 181 | 10,94 | 10,87 | 13,52 | 240 | 13,52 |
| | | | | 2089 | | 14 | 17 | 51 | 10,35 | 7,92 | 10,17 | 82 | 10,35 |
| | | | | 2094 | | 13 | 5 | 19 | 13,88 | 2,39 | 9,90 | 37 | 13,88 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 2097 | | 7 | 8 | 53 | 8,40 | 9,47 | 15,21 | 68 | 15,21 |
| | | | | 2108 | | | | 50 | | | 13,74 | 50 | 13,74 |
| | | | | 2122 | | 13 | 5 | 176 | 13,68 | 10,45 | 18,77 | 194 | 18,77 |
| | | | | 2124 | | | 1 | 27 | | 1,46 | 10,09 | 28 | 10,09 |
| | | | 2066 | 2016 | 13,6 | 37 | 22 | 181 | 10,94 | 10,87 | 13,52 | 240 | 13,52 |
| | | | | 2089 | | 3 | 5 | 1 | 16,26 | 10,47 | 4,79 | 9 | 16,26 |
| | | | | 2094 | | | | 1 | | | 1,43 | 1 | 1,43 |
| | | | | 2097 | | 1 | 1 | 3 | 5,68 | 3,12 | 9,49 | 5 | 9,49 |
| | | | | 2108 | | | | 1 | | | 12,86 | 1 | 12,86 |
| | | | | 2122 | | | | 3 | | | 7,78 | 3 | 7,78 |
| | | | 2080 | 1807 | | 1 | 1 | 3 | 1,57 | 4,98 | 10,34 | 5 | 10,34 |
| | | | | 2094 | | | 1 | | | 0,52 | | 1 | 0,52 |
| | | | 2089 | 1807 | | | | 3 | | | 6,25 | 3 | 6,25 |
| | | | | 1821 | | | 2 | 1 | | 2,04 | 9,85 | 3 | 9,85 |
| | | | | 1938 | | 1 | 1 | 7 | 0,97 | 1,24 | 8,39 | 9 | 8,39 |
| | | | | 2016 | | 14 | 17 | 51 | 10,35 | 7,92 | 10,17 | 82 | 10,35 |
| | | | | 2066 | | 3 | 5 | 1 | 16,26 | 10,47 | 4,79 | 9 | 16,26 |
| | | | | 2097 | | 3 | 4 | 6 | 3,76 | 4,85 | 6,46 | 13 | 6,46 |
| | | | 2094 | 1910 | | | | 1 | | | 2,66 | 1 | 2,66 |
| | | | | 1938 | | | | 4 | | | 4,70 | 4 | 4,70 |
| | | | | 2016 | | 13 | 5 | 19 | 13,88 | 2,39 | 9,90 | 37 | 13,88 |
| | | | | 2066 | | | | 1 | | | 1,43 | 1 | 1,43 |
| | | | | 2080 | | | 1 | | | 0,52 | | 1 | 0,52 |
| | | | | 2097 | | 1 | 2 | 3 | 2,50 | 2,28 | 3,09 | 6 | 3,09 |
| | | | | 2108 | | | | 1 | | | 2,58 | 1 | 2,58 |
| | | | | 2122 | | | | 3 | | | 3,48 | 3 | 3,48 |
| | | | 2097 | 1821 | | | | 1 | | | 6,01 | 1 | 6,01 |
| | | | | 1910 | | | | 1 | | | 2,86 | 1 | 2,86 |
| | | | | 1938 | | | | 3 | | | 8,74 | 3 | 8,74 |
| | | | | 2016 | | 7 | 8 | 53 | 8,40 | 9,47 | 15,21 | 68 | 15,21 |
| | | | | 2066 | | 1 | 1 | 3 | 5,68 | 3,12 | 9,49 | 5 | 9,49 |
| | | | | 2089 | | 3 | 4 | 6 | 3,76 | 4,85 | 6,46 | 13 | 6,46 |
| | | | | 2094 | | 1 | 2 | 3 | 2,50 | 2,28 | 3,09 | 6 | 3,09 |
| | | | | 2108 | | | 3 | 14 | | 8,71 | 13,41 | 17 | 13,41 |
| | | | | 2154 | | | | 3 | | | 8,11 | 3 | 8,11 |
| | | | 2108 | 1864 | | | | 3 | | | 5,03 | 3 | 5,03 |
| | | | | 1910 | | 1 | 3 | 4 | 0,68 | 1,28 | 2,72 | 8 | 2,72 |
| | | | | 2016 | | | | 50 | | | 13,74 | 50 | 13,74 |
| | | | | 2066 | | | | 1 | | | 12,86 | 1 | 12,86 |
| | | | | 2094 | | | | 1 | | | 2,58 | 1 | 2,58 |
| | | | | 2097 | | | 3 | 14 | | 8,71 | 13,41 | 17 | 13,41 |
| | | | | 2154 | | 1 | | 4 | 0,40 | | 12,04 | 5 | 12,04 |
| | | | 2122 | 1864 | | 3 | 1 | 39 | 9,51 | 0,36 | 12,14 | 43 | 12,14 |
| | | | | 1873 | | | | 3 | | | 8,01 | 3 | 8,01 |
| | | | | 1903 | | 1 | 1 | 2 | 6,77 | 0,79 | 6,25 | 4 | 6,77 |
| | | | | 1910 | | 2 | 1 | 15 | 2,18 | 2,25 | 6,80 | 18 | 6,80 |
| | | | | 2016 | | 13 | 5 | 176 | 13,68 | 10,45 | 18,77 | 194 | 18,77 |
| | | | | 2066 | | | | 3 | | | 7,78 | 3 | 7,78 |
| | | | | 2094 | | | | 3 | | | 3,48 | 3 | 3,48 |
| | | | | 2154 | | | | 1 | | | 5,88 | 1 | 5,88 |
| | | | 2124 | 2016 | | | 1 | 27 | | 1,46 | 10,09 | 28 | 10,09 |
| | | | 2149 | 1910 | 27,0 | | | 1 | | | 2,68 | 1 | 2,68 |
| | | | | 2154 | 11,1 | | | 1 | | | 3,72 | 1 | 3,72 |
| | | | 2154 | 2097 | | | | 3 | | | 8,11 | 3 | 8,11 |
| | | | | 2108 | | 1 | | 4 | 0,40 | | 12,04 | 5 | 12,04 |
| | | | | 2122 | | | | 1 | | | 5,88 | 1 | 5,88 |
| | | | | 2149 | 11,1 | | | 1 | | | 3,72 | 1 | 3,72 |
| | Prp9 | Prp9 | 2 | 115 | | | | 9 | | | 8,22 | 9 | 8,22 |
| | | | 89 | 140 | | | 3 | 21 | | 7,09 | 12,66 | 24 | 12,66 |
| | | | 95 | 107 | | | | 8 | | | 5,74 | 8 | 5,74 |
| | | | 107 | 95 | | | | 8 | | | 5,74 | 8 | 5,74 |
| | | | | 115 | | 19 | 18 | 106 | 15,02 | 10,77 | 15,60 | 143 | 15,60 |
| | | | 115 | 2 | | | | 9 | | | 8,22 | 9 | 8,22 |
| | | | | 107 | | 19 | 18 | 106 | 15,02 | 10,77 | 15,60 | 143 | 15,60 |
| | | | | 124 | | 1 | 3 | 16 | 7,42 | 17,05 | 11,60 | 20 | 17,05 |
| | | | 124 | 115 | | 1 | 3 | 16 | 7,42 | 17,05 | 11,60 | 20 | 17,05 |
| | | | 140 | 89 | | | 3 | 21 | | 7,09 | 12,66 | 24 | 12,66 |
| | | | 278 | 290 | | | | 1 | | | 5,55 | 1 | 5,55 |
| | | | 290 | 278 | | | | 1 | | | 5,55 | 1 | 5,55 |
| | | | 302 | 306 | | 3 | 2 | 8 | 2,17 | 0,36 | 4,48 | 13 | 4,48 |
| | | | 306 | 302 | | 3 | 2 | 8 | 2,17 | 0,36 | 4,48 | 13 | 4,48 |
| | | | 468 | 492 | | | | 1 | | | 2,75 | 1 | 2,75 |
| | | | 492 | 468 | | | | 1 | | | 2,75 | 1 | 2,75 |
| | | | | 519 | | 7 | 2 | 35 | 14,33 | 4,31 | 10,25 | 44 | 14,33 |
| | | | 518 | 525 | | | | 3 | | | 11,09 | 3 | 11,09 |
| | | | 519 | 492 | | 7 | 2 | 35 | 14,33 | 4,31 | 10,25 | 44 | 14,33 |
| | | | | 526 | | | 1 | | | 1,71 | | 1 | 1,71 |
| | | | 525 | 518 | | | | 3 | | | 11,09 | 3 | 11,09 |
| | | | 526 | 519 | | | 1 | | | 1,71 | | 1 | 1,71 |
| | Rse1 | Rse1 | 172 | 221 | 11,9 | | | 2 | | | 16,26 | 2 | 16,26 |
| | | | | 1269 | | | | 1 | | | 2,32 | 1 | 2,32 |
| | | | 221 | 172 | 11,9 | | | 2 | | | 16,26 | 2 | 16,26 |
| | | | | 1269 | | | | 1 | | | 9,63 | 1 | 9,63 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 347 | 462 | | | | 1 | | | 7,93 | 1 | 7,93 |
| | | | 352 | 462 | | 2 | | | 6,88 | | | 2 | 6,88 |
| | | | 361 | 948 | 41,6 | 2 | | | 4,89 | | | 2 | 4,89 |
| | | | | 949 | 40,2 | | 1 | 1 | | 0,77 | 2,39 | 2 | 2,39 |
| | | | 462 | 347 | | | | 1 | | | 7,93 | 1 | 7,93 |
| | | | | 352 | | 2 | | | 6,88 | | | 2 | 6,88 |
| | | | 948 | 361 | 41,6 | 2 | | | 4,89 | | | 2 | 4,89 |
| | | | 949 | 361 | 40,2 | | 1 | 1 | | 0,77 | 2,39 | 2 | 2,39 |
| | | | | 1001 | 32,1 | 4 | 6 | 15 | 4,50 | 5,93 | 6,24 | 25 | 6,24 |
| | | | 1001 | 949 | 32,1 | 4 | 6 | 15 | 4,50 | 5,93 | 6,24 | 25 | 6,24 |
| | | | 1007 | 1057 | 13,9 | 1 | 1 | 2 | 4,79 | 1,61 | 6,13 | 4 | 6,13 |
| | | | 1057 | 1007 | 13,9 | 1 | 1 | 2 | 4,79 | 1,61 | 6,13 | 4 | 6,13 |
| | | | 1269 | 172 | | | | 1 | | | 2,32 | 1 | 2,32 |
| | | | | 221 | | | | 1 | | | 9,63 | 1 | 9,63 |
| | | | 1316 | 1342 | | | 13 | 3 | | 14,76 | 21,63 | 16 | 21,63 |
| | | | 1342 | 1316 | | | 13 | 3 | | 14,76 | 21,63 | 16 | 21,63 |
| | SmB | SmB | 2 | 100 | | | | 1 | | | 10,51 | 1 | 10,51 |
| | | | 19 | 100 | 5,7 | | | 2 | | | 3,05 | 2 | 3,05 |
| | | | 55 | 76 | 8,7 | 8 | 12 | 40 | 6,64 | 3,56 | 11,39 | 60 | 11,39 |
| | | | 60 | 65 | | 4 | 4 | 7 | 4,30 | 3,31 | 5,84 | 15 | 5,84 |
| | | | | 68 | | 2 | 3 | 1 | 1,37 | 5,46 | 4,25 | 6 | 5,46 |
| | | | | 76 | | 25 | 18 | 71 | 9,06 | 11,00 | 15,56 | 114 | 15,56 |
| | | | 65 | 60 | | 4 | 4 | 7 | 4,30 | 3,31 | 5,84 | 15 | 5,84 |
| | | | | 76 | | 1 | 1 | 4 | 1,71 | 2,16 | 3,38 | 6 | 3,38 |
| | | | 68 | 60 | | 2 | 3 | 1 | 1,37 | 5,46 | 4,25 | 6 | 5,46 |
| | | | 76 | 55 | 8,7 | 8 | 12 | 40 | 6,64 | 3,56 | 11,39 | 60 | 11,39 |
| | | | | 60 | | 25 | 18 | 71 | 9,06 | 11,00 | 15,56 | 114 | 15,56 |
| | | | | 65 | | 1 | 1 | 4 | 1,71 | 2,16 | 3,38 | 6 | 3,38 |
| | | | | 100 | 25,9 | | 5 | | | 3,05 | | 5 | 3,05 |
| | | | | 186 | | | 1 | | | 0,89 | | 1 | 0,89 |
| | | | 100 | 2 | | | | 1 | | | 10,51 | 1 | 10,51 |
| | | | | 19 | 5,7 | | | 2 | | | 3,05 | 2 | 3,05 |
| | | | | 76 | 25,9 | | 5 | | | 3,05 | | 5 | 3,05 |
| | | | | 117 | | | | 4 | | | 2,62 | 4 | 2,62 |
| | | | | 186 | | | | 1 | | | 4,81 | 1 | 4,81 |
| | | | 105 | 117 | | | 1 | 3 | | 3,86 | 3,45 | 4 | 3,86 |
| | | | 114 | 117 | | | | 1 | | | 3,62 | 1 | 3,62 |
| | | | | 121 | | | | 4 | | | 4,11 | 4 | 4,11 |
| | | | 117 | 100 | | | | 4 | | | 2,62 | 4 | 2,62 |
| | | | | 105 | | | 1 | 3 | | 3,86 | 3,45 | 4 | 3,86 |
| | | | | 114 | | | | 1 | | | 3,62 | 1 | 3,62 |
| | | | | 124 | | | | 4 | | | 2,96 | 4 | 2,96 |
| | | | | 138 | | | | 3 | | | 4,67 | 3 | 4,67 |
| | | | 121 | 114 | | | | 4 | | | 4,11 | 4 | 4,11 |
| | | | | 127 | | | | 5 | | | 5,72 | 5 | 5,72 |
| | | | | 131 | | | | 1 | | | 3,87 | 1 | 3,87 |
| | | | | 138 | | | | 1 | | | 1,87 | 1 | 1,87 |
| | | | 124 | 117 | | | | 4 | | | 2,96 | 4 | 2,96 |
| | | | | 138 | | | 2 | | | 0,87 | | 2 | 0,87 |
| | | | | 186 | | | 1 | | | 0,43 | | 1 | 0,43 |
| | | | 127 | 121 | | | | 5 | | | 5,72 | 5 | 5,72 |
| | | | 131 | 121 | | | | 1 | | | 3,87 | 1 | 3,87 |
| | | | | 138 | | 2 | 6 | 16 | 4,95 | 3,88 | 6,45 | 24 | 6,45 |
| | | | | 186 | | | | 2 | | | 5,10 | 2 | 5,10 |
| | | | 132 | 138 | | 2 | 5 | 6 | 1,64 | 0,84 | 3,47 | 13 | 3,47 |
| | | | | 186 | | | 1 | | | 1,00 | | 1 | 1,00 |
| | | | 138 | 117 | | | | 3 | | | 4,67 | 3 | 4,67 |
| | | | | 121 | | | | 1 | | | 1,87 | 1 | 1,87 |
| | | | | 124 | | | 2 | | | 0,87 | | 2 | 0,87 |
| | | | | 131 | | 2 | 6 | 16 | 4,95 | 3,88 | 6,45 | 24 | 6,45 |
| | | | | 132 | | 2 | 5 | 6 | 1,64 | 0,84 | 3,47 | 13 | 3,47 |
| | | | | 186 | | 1 | 3 | 7 | 3,47 | 5,07 | 7,22 | 11 | 7,22 |
| | | | | 194 | | | | 1 | | | 2,88 | 1 | 2,88 |
| | | | 145 | 186 | | 1 | 1 | 5 | 0,24 | 1,08 | 8,93 | 7 | 8,93 |
| | | | 186 | 76 | | | 1 | | | 0,89 | | 1 | 0,89 |
| | | | | 100 | | | | 1 | | | 4,81 | 1 | 4,81 |
| | | | | 124 | | | 1 | | | 0,43 | | 1 | 0,43 |
| | | | | 131 | | | | 2 | | | 5,10 | 2 | 5,10 |
| | | | | 132 | | | 1 | | | 1,00 | | 1 | 1,00 |
| | | | | 138 | | 1 | 3 | 7 | 3,47 | 5,07 | 7,22 | 11 | 7,22 |
| | | | | 145 | | 1 | 1 | 5 | 0,24 | 1,08 | 8,93 | 7 | 8,93 |
| | | | 194 | 138 | | | | 1 | | | 2,88 | 1 | 2,88 |
| | SmD1 | SmD1 | 1 | 111 | | | | 1 | | | 7,56 | 1 | 7,56 |
| | | | 2 | 111 | | | | 1 | | | 10,15 | 1 | 10,15 |
| | | | | 128 | | | 1 | | | 0,40 | | 1 | 0,40 |
| | | | 8 | 111 | | 1 | 1 | 9 | 0,72 | 2,50 | 6,04 | 11 | 6,04 |
| | | | | 128 | | | | 3 | | | 7,32 | 3 | 7,32 |
| | | | | 129 | | | | 1 | | | 2,81 | 1 | 2,81 |
| | | | | 140 | | | | 1 | | | 1,87 | 1 | 1,87 |
| | | | 9 | 128 | | | | 3 | | | 8,18 | 3 | 8,18 |
| | | | | 129 | | | | 1 | | | 7,12 | 1 | 7,12 |
| | | | 111 | 1 | | | | 1 | | | 7,56 | 1 | 7,56 |
| | | | | 2 | | | | 1 | | | 10,15 | 1 | 10,15 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | | 8 | | 1 | 1 | 9 | 0,72 | 2,50 | 6,04 | 11 | 6,04 |
| | | | | 128 | | | 4 | 10 | | 5,45 | 7,08 | 14 | 7,08 |
| | | | | 140 | | | 1 | 2 | | 0,16 | 3,04 | 3 | 3,04 |
| | | | 128 | 2 | | | 1 | | | 0,40 | | 1 | 0,40 |
| | | | | 8 | | | | 3 | | | 7,32 | 3 | 7,32 |
| | | | | 9 | | | | 3 | | | 8,18 | 3 | 8,18 |
| | | | | 111 | | | 4 | 10 | | 5,45 | 7,08 | 14 | 7,08 |
| | | | | 140 | | 7 | 18 | 37 | 4,55 | 6,31 | 12,00 | 62 | 12,00 |
| | | | 129 | 8 | | | | 1 | | | 2,81 | 1 | 2,81 |
| | | | | 9 | | | | 1 | | | 7,12 | 1 | 7,12 |
| | | | 140 | 8 | | | | 1 | | | 1,87 | 1 | 1,87 |
| | | | | 111 | | | 1 | 2 | | 0,16 | 3,04 | 3 | 3,04 |
| | | | | 128 | | 7 | 18 | 37 | 4,55 | 6,31 | 12,00 | 62 | 12,00 |
| | SmD2 | SmD2 | 53 | 59 | 17,5 | | 10 | | | 6,35 | | 10 | 6,35 |
| | | | | 73 | 8,0 | 11 | 35 | 4 | 6,78 | 6,85 | 5,79 | 50 | 6,85 |
| | | | | 79 | 15,6 | | 1 | | | 0,17 | | 1 | 0,17 |
| | | | 59 | 53 | 17,5 | | 10 | | | 6,35 | | 10 | 6,35 |
| | | | | 73 | 14,7 | | 3 | | | 2,22 | | 3 | 2,22 |
| | | | | 79 | 31,5 | | 4 | | | 1,61 | | 4 | 1,61 |
| | | | | 82 | 38,7 | | 1 | | | 2,37 | | 1 | 2,37 |
| | | | | 93 | 9,7 | 1 | 4 | 1 | 3,38 | 6,61 | 6,73 | 6 | 6,73 |
| | | | 73 | 53 | 8,0 | 11 | 35 | 4 | 6,78 | 6,85 | 5,79 | 50 | 6,85 |
| | | | | 59 | 14,7 | | 3 | | | 2,22 | | 3 | 2,22 |
| | | | 79 | 53 | 15,6 | | 1 | | | 0,17 | | 1 | 0,17 |
| | | | | 59 | 31,5 | | 4 | | | 1,61 | | 4 | 1,61 |
| | | | | 82 | 7,8 | 3 | 8 | 12 | 9,75 | 7,33 | 9,77 | 23 | 9,77 |
| | | | 82 | 59 | 38,7 | | 1 | | | 2,37 | | 1 | 2,37 |
| | | | | 79 | 7,8 | 3 | 8 | 12 | 9,75 | 7,33 | 9,77 | 23 | 9,77 |
| | | | | 93 | 33,8 | | 1 | | | 2,75 | | 1 | 2,75 |
| | | | 93 | 59 | 9,7 | 1 | 4 | 1 | 3,38 | 6,61 | 6,73 | 6 | 6,73 |
| | | | | 82 | 33,8 | | 1 | | | 2,75 | | 1 | 2,75 |
| | SmD3 | SmD3 | 2 | 85 | | 2 | 2 | 7 | 11,37 | 3,17 | 5,24 | 11 | 11,37 |
| | | | | 86 | | 2 | 3 | 12 | 1,53 | 4,23 | 4,37 | 17 | 4,37 |
| | | | 9 | 85 | 13,0 | | | 1 | | | 3,31 | 1 | 3,31 |
| | | | | 86 | | | | 2 | | | 2,13 | 2 | 2,13 |
| | | | 79 | 86 | | 1 | | 1 | 0,24 | | 1,67 | 2 | 1,67 |
| | | | 85 | 2 | | 2 | 2 | 7 | 11,37 | 3,17 | 5,24 | 11 | 11,37 |
| | | | | 9 | 13,0 | | | 1 | | | 3,31 | 1 | 3,31 |
| | | | 86 | 2 | | 2 | 3 | 12 | 1,53 | 4,23 | 4,37 | 17 | 4,37 |
| | | | | 9 | | | | 2 | | | 2,13 | 2 | 2,13 |
| | | | | 79 | | 1 | | 1 | 0,24 | | 1,67 | 2 | 1,67 |
| | SmG | SmG | 8 | 13 | 10,0 | 2 | 5 | 23 | 4,60 | 4,73 | 5,69 | 30 | 5,69 |
| | | | 13 | 8 | 10,0 | 2 | 5 | 23 | 4,60 | 4,73 | 5,69 | 30 | 5,69 |
| | | | 14 | 24 | 13,0 | 2 | 2 | 3 | 6,97 | 11,25 | 12,31 | 7 | 12,31 |
| | | | 24 | 14 | 13,0 | 2 | 2 | 3 | 6,97 | 11,25 | 12,31 | 7 | 12,31 |
| | Snt309 | Snt309 | 46 | 48 | | | 3 | | | 1,72 | | 3 | 1,72 |
| | | | 48 | 46 | | | 3 | | | 1,72 | | 3 | 1,72 |
| | | | 67 | 94 | | 2 | 3 | 8 | 4,52 | 1,90 | 3,38 | 13 | 4,52 |
| | | | 72 | 94 | | | | 1 | | | 0,61 | 1 | 0,61 |
| | | | 94 | 67 | | 2 | 3 | 8 | 4,52 | 1,90 | 3,38 | 13 | 4,52 |
| | | | | 72 | | | | 1 | | | 0,61 | 1 | 0,61 |
| | Snu114 | Snu114 | 59 | 72 | | | | 1 | | | 0,91 | 1 | 0,91 |
| | | | 60 | 81 | | | | 3 | | | 5,77 | 3 | 5,77 |
| | | | 72 | 59 | | | | 1 | | | 0,91 | 1 | 0,91 |
| | | | 81 | 60 | | | | 3 | | | 5,77 | 3 | 5,77 |
| | | | 99 | 111 | | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | | 494 | | 2 | 5 | 15 | 4,52 | 7,48 | 6,92 | 22 | 7,48 |
| | | | 111 | 99 | | | | 1 | | | 1,75 | 1 | 1,75 |
| | | | 115 | 159 | 6,1 | | 3 | 1 | | 1,76 | 3,29 | 4 | 3,29 |
| | | | 159 | 115 | 6,1 | | 3 | 1 | | 1,76 | 3,29 | 4 | 3,29 |
| | | | 494 | 99 | | 2 | 5 | 15 | 4,52 | 7,48 | 6,92 | 22 | 7,48 |
| | | | | 581 | 14,0 | 1 | 3 | 9 | 1,83 | 5,39 | 14,42 | 13 | 14,42 |
| | | | 520 | 583 | 15,2 | | | 1 | | | 2,21 | 1 | 2,21 |
| | | | 558 | 581 | 15,1 | | | 1 | | | 2,51 | 1 | 2,51 |
| | | | 581 | 494 | 14,0 | 1 | 3 | 9 | 1,83 | 5,39 | 14,42 | 13 | 14,42 |
| | | | | 558 | 15,1 | | | 1 | | | 2,51 | 1 | 2,51 |
| | | | 583 | 520 | 15,2 | | | 1 | | | 2,21 | 1 | 2,21 |
| | | | 617 | 665 | 9,5 | 2 | 2 | 6 | 2,29 | 3,34 | 4,49 | 10 | 4,49 |
| | | | 665 | 617 | 9,5 | 2 | 2 | 6 | 2,29 | 3,34 | 4,49 | 10 | 4,49 |
| | | | 730 | 749 | | | 2 | 4 | | 0,50 | 3,11 | 6 | 3,11 |
| | | | | 890 | | 1 | 3 | | 1,96 | 1,07 | | 4 | 1,96 |
| | | | 749 | 730 | | | 2 | 4 | | 0,50 | 3,11 | 6 | 3,11 |
| | | | 804 | 843 | 10,2 | 3 | 1 | | 1,35 | 0,60 | | 4 | 1,35 |
| | | | 843 | 804 | 10,2 | 3 | 1 | | 1,35 | 0,60 | | 4 | 1,35 |
| | | | | 991 | 17,0 | 1 | 1 | 3 | 0,36 | 1,97 | 2,28 | 5 | 2,28 |
| | | | 890 | 730 | | 1 | 3 | | 1,96 | 1,07 | | 4 | 1,96 |
| | | | 947 | 955 | 18,0 | | | 4 | | | 4,69 | 4 | 4,69 |
| | | | 955 | 947 | 18,0 | | | 4 | | | 4,69 | 4 | 4,69 |
| | | | 991 | 843 | 17,0 | 1 | 1 | 3 | 0,36 | 1,97 | 2,28 | 5 | 2,28 |
| | Snu17/Ist3 | Snu17/Ist3 | 96 | 103 | | 4 | 3 | 7 | 10,92 | 7,53 | 10,43 | 14 | 10,92 |
| | | | 103 | 96 | | 4 | 3 | 7 | 10,92 | 7,53 | 10,43 | 14 | 10,92 |
| | | | 123 | 133 | 17,9 | 2 | | 30 | 0,60 | | 9,88 | 32 | 9,88 |
| | | | | 138 | | | | 1 | | | 2,41 | 1 | 2,41 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 133 | 123 | 17,9 | 2 | | 30 | 0,60 | | 9,88 | 32 | 9,88 |
| | | | | 143 | | 2 | 4 | | 2,87 | 2,22 | | 6 | 2,87 |
| | | | 138 | 123 | | | | 1 | | | 2,41 | 1 | 2,41 |
| | | | | 144 | | | 2 | | | 0,88 | | 2 | 0,88 |
| | | | 143 | 133 | | 2 | 4 | | 2,87 | 2,22 | | 6 | 2,87 |
| | | | 144 | 138 | | | 2 | | | 0,88 | | 2 | 0,88 |
| | Spp2 | Spp2 | 7 | 15 | | 1 | | | 7,65 | | | 1 | 7,65 |
| | | | 11 | 15 | | 1 | | | 0,59 | | | 1 | 0,59 |
| | | | 15 | 7 | | 1 | | | 7,65 | | | 1 | 7,65 |
| | | | | 11 | | 1 | | | 0,59 | | | 1 | 0,59 |
| | | | 38 | 52 | | | | 3 | | | 13,55 | 3 | 13,55 |
| | | | | 58 | | | | 1 | | | 7,55 | 1 | 7,55 |
| | | | | 68 | | | | 1 | | | 3,42 | 1 | 3,42 |
| | | | | 74 | | | | 1 | | | 9,31 | 1 | 9,31 |
| | | | | 83 | | | | 2 | | | 4,37 | 2 | 4,37 |
| | | | | 95 | | | | 1 | | | 5,46 | 1 | 5,46 |
| | | | 52 | 38 | | | | 3 | | | 13,55 | 3 | 13,55 |
| | | | 58 | 38 | | | | 1 | | | 7,55 | 1 | 7,55 |
| | | | 68 | 38 | | | | 1 | | | 3,42 | 1 | 3,42 |
| | | | | 70 | | | | 9 | | | 17,04 | 9 | 17,04 |
| | | | 70 | 68 | | | | 9 | | | 17,04 | 9 | 17,04 |
| | | | | 133 | | | | 1 | | | 2,95 | 1 | 2,95 |
| | | | 74 | 38 | | | | 1 | | | 9,31 | 1 | 9,31 |
| | | | 82 | 95 | | | | 4 | | | 3,94 | 4 | 3,94 |
| | | | 83 | 38 | | | | 2 | | | 4,37 | 2 | 4,37 |
| | | | 95 | 38 | | | | 1 | | | 5,46 | 1 | 5,46 |
| | | | | 82 | | | | 4 | | | 3,94 | 4 | 3,94 |
| | | | 124 | 133 | | | | 1 | | | 0,10 | 1 | 0,10 |
| | | | 127 | 133 | | | | 4 | | | 7,30 | 4 | 7,30 |
| | | | 133 | 70 | | | | 1 | | | 2,95 | 1 | 2,95 |
| | | | | 124 | | | | 1 | | | 0,10 | 1 | 0,10 |
| | | | | 127 | | | | 4 | | | 7,30 | 4 | 7,30 |
| | | | | 154 | | | | 1 | | | 13,98 | 1 | 13,98 |
| | | | 154 | 133 | | | | 1 | | | 13,98 | 1 | 13,98 |
| | | | 168 | 181 | | | | 2 | | | 2,64 | 2 | 2,64 |
| | | | 181 | 168 | | | | 2 | | | 2,64 | 2 | 2,64 |
| | Syf1 | Syf1 | 192 | 367 | | | | 1 | | | 4,84 | 1 | 4,84 |
| | | | 220 | 249 | | 2 | 3 | 3 | 5,33 | 5,17 | 3,14 | 8 | 5,33 |
| | | | 249 | 220 | | 2 | 3 | 3 | 5,33 | 5,17 | 3,14 | 8 | 5,33 |
| | | | 367 | 192 | | | | 1 | | | 4,84 | 1 | 4,84 |
| | | | 413 | 419 | 10,4 | 2 | 5 | 7 | 3,53 | 3,25 | 5,41 | 14 | 5,41 |
| | | | | 424 | 21,1 | | 1 | | | 0,40 | | 1 | 0,40 |
| | | | 419 | 413 | 10,4 | 2 | 5 | 7 | 3,53 | 3,25 | 5,41 | 14 | 5,41 |
| | | | 424 | 413 | 21,1 | | 1 | | | 0,40 | | 1 | 0,40 |
| | | | | 439 | | | 1 | | | 2,72 | | 1 | 2,72 |
| | | | 439 | 424 | | | 1 | | | 2,72 | | 1 | 2,72 |
| | | | | 531 | | 9 | 3 | 23 | 9,89 | 6,16 | 9,55 | 35 | 9,89 |
| | | | 524 | 531 | | 8 | 4 | 6 | 4,68 | 4,30 | 15,22 | 18 | 15,22 |
| | | | 531 | 439 | | 9 | 3 | 23 | 9,89 | 6,16 | 9,55 | 35 | 9,89 |
| | | | | 524 | | 8 | 4 | 6 | 4,68 | 4,30 | 15,22 | 18 | 15,22 |
| | | | 770 | 802 | | | 4 | | | 1,78 | | 4 | 1,78 |
| | | | 790 | 798 | | | | 2 | | | 5,42 | 2 | 5,42 |
| | | | 798 | 790 | | | | 2 | | | 5,42 | 2 | 5,42 |
| | | | 802 | 770 | | | 4 | | | 1,78 | | 4 | 1,78 |
| | Syf2 | Syf2 | 23 | 26 | | 9 | 11 | 16 | 3,47 | 6,27 | 8,99 | 36 | 8,99 |
| | | | 26 | 23 | | 9 | 11 | 16 | 3,47 | 6,27 | 8,99 | 36 | 8,99 |
| | | | 121 | 159 | | | | 2 | | | 5,88 | 2 | 5,88 |
| | | | 132 | 142 | | | | 1 | | | 1,66 | 1 | 1,66 |
| | | | 136 | 142 | | | | 4 | | | 4,15 | 4 | 4,15 |
| | | | | 145 | | | | 1 | | | 3,27 | 1 | 3,27 |
| | | | 142 | 132 | | | | 1 | | | 1,66 | 1 | 1,66 |
| | | | | 136 | | | | 4 | | | 4,15 | 4 | 4,15 |
| | | | 145 | 136 | | | | 1 | | | 3,27 | 1 | 3,27 |
| | | | | 151 | | 11 | 4 | 8 | 5,16 | 3,30 | 4,10 | 23 | 5,16 |
| | | | 151 | 145 | | 11 | 4 | 8 | 5,16 | 3,30 | 4,10 | 23 | 5,16 |
| | | | 159 | 121 | | | | 2 | | | 5,88 | 2 | 5,88 |
| | | | 199 | 206 | | 2 | 2 | 4 | 0,86 | 0,65 | 4,86 | 8 | 4,86 |
| | | | 206 | 199 | | 2 | 2 | 4 | 0,86 | 0,65 | 4,86 | 8 | 4,86 |
| | Yju2/Cwc16 | Yju2/Cwc16 | 5 | 68 | | | 1 | | | 3,01 | | 1 | 3,01 |
| | | | 22 | 26 | | 1 | | 1 | 1,17 | | 2,07 | 2 | 2,07 |
| | | | 26 | 22 | | 1 | | 1 | 1,17 | | 2,07 | 2 | 2,07 |
| | | | 32 | 68 | | | 2 | | | 2,62 | | 2 | 2,62 |
| | | | 36 | 68 | | 3 | 7 | 8 | 5,78 | 3,70 | 6,46 | 18 | 6,46 |
| | | | | 74 | | | 4 | | | 3,95 | | 4 | 3,95 |
| | | | | 80 | | 1 | 4 | | 0,96 | 2,88 | | 5 | 2,88 |
| | | | 60 | 120 | | 2 | 2 | 5 | 3,33 | 1,27 | 8,10 | 9 | 8,10 |
| | | | 63 | 68 | | 1 | 2 | 2 | 3,05 | 4,29 | 5,41 | 5 | 5,41 |
| | | | 68 | 5 | | | 1 | | | 3,01 | | 1 | 3,01 |
| | | | | 32 | | | 2 | | | 2,62 | | 2 | 2,62 |
| | | | | 36 | | 3 | 7 | 8 | 5,78 | 3,70 | 6,46 | 18 | 6,46 |
| | | | | 63 | | 1 | 2 | 2 | 3,05 | 4,29 | 5,41 | 5 | 5,41 |
| | | | | 74 | | | 1 | | | 1,18 | | 1 | 1,18 |
| | | | | 80 | | 18 | 9 | 20 | 14,57 | 3,40 | 6,29 | 47 | 14,57 |

| | | | | | | Spectral count | | | Score$_{max}$ | | | Total | Best |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Type | Protein 1 | Protein 2 | Residue 1 | Residue 2 | Å | Set 1 | Set 2 | Set 3 | Set 1 | Set 2 | Set 3 | spectral count | Score$_{max}$ |
| | | | 74 | 36 | | | 4 | | | 3,95 | | 4 | 3,95 |
| | | | | 68 | | | 1 | | | 1,18 | | 1 | 1,18 |
| | | | 80 | 36 | | 1 | 4 | | 0,96 | 2,88 | | 5 | 2,88 |
| | | | | 68 | | 18 | 9 | 20 | 14,57 | 3,40 | 6,29 | 47 | 14,57 |
| | | | 120 | 60 | | 2 | 2 | 5 | 3,33 | 1,27 | 8,10 | 9 | 8,10 |
| | | | 168 | 172 | | 2 | | | 2,42 | | | 2 | 2,42 |
| | | | 172 | 168 | | 2 | | | 2,42 | | | 2 | 2,42 |
| | | | 242 | 253 | | 1 | | | 2,43 | | | 1 | 2,43 |
| | | | 253 | 242 | | 1 | | | 2,43 | | | 1 | 2,43 |
| | | | | 259 | | 1 | 4 | 4 | 8,00 | 5,45 | 6,27 | 9 | 8,00 |
| | | | 255 | 259 | | | 1 | 1 | | 1,22 | 2,43 | 2 | 2,43 |
| | | | 259 | 253 | | 1 | 4 | 4 | 8,00 | 5,45 | 6,27 | 9 | 8,00 |
| | | | | 255 | | | 1 | 1 | | 1,22 | 2,43 | 2 | 2,43 |
| | | | 272 | 275 | | | 1 | 1 | | 0,24 | 6,37 | 2 | 6,37 |
| | | | 275 | 272 | | | 1 | 1 | | 0,24 | 6,37 | 2 | 6,37 |
| | Ysf3 | Ysf3 | 12 | 17 | 7,9 | | 3 | | | 1,89 | | 3 | 1,89 |
| | | | 17 | 12 | 7,9 | | 3 | | | 1,89 | | 3 | 1,89 |

**Table S3: MolProbity validation of the final RNA model of the yeast $B^{act}$ complex**

| Validation | All RNA | % | Pre-mRNA | % | U6 | % | U2 | % | U5 | % |
|---|---|---|---|---|---|---|---|---|---|---|
| All-Atom Contacts | | | | | | | | | | |
| | | | | | | | | | | |
| Clash score | 5 | 94 | 3.45 | 97 | 3 | 98 | 6 | 91 | 6 | 90 |
| | | | | | | | | | | |
| Nucleic Acid Geometry | | | | | | | | | | |
| Probably wrong sugar puckers: | 12 | 3.2 | 0 | 0 | 6 | 5.9 | 2 | 2.5 | 4 | 3 |
| Bad backbone conformations: | 121 | 32 | 28 | 51 | 41 | 40.2 | 21 | 26 | 31 | 22 |
| Bad bonds: | 0 / 8965 | 0 | 0 / 1286 | 0 | 0 / 2427 | 0 | 0 / 1902 | 0 | 0 / 335 | 0 |
| Bad angles: | 0 / 13938 | 0 | 0 / 1995 | 0 | 0 / 3778 | 0 | 0 / 2956 | 0 | 0 / 5209 | 0 |

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