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Data Article

Data on the identity of non-canonical complexes formed from proteasome subunits in vivo

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ABSTRACT

The dataset presented here represents analysis supplied by the local proteomics core facility on samples submitted to it in support of the article “Assembly of proteasome subunits into non-canonical complexes in vivo” Hammack and Kusmierczyk (2016) [1]. This article provides the detailed protein contents of gel slices, cut from non-denaturing polyacrylamide gels, containing distinct protein complexes visualized following gel staining. The identification of the protein contents of these complexes was carried out by liquid chromatography tandem mass-spectrometry (LC–MS/MS).

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Specifications Table

| | |
|----------------------------|---|
| Subject area | <i>Biology</i> |
| More specific subject area | <i>Molecular biology</i> |
| Type of data | <i>Excel files, word document</i> |
| How data was acquired | <i>The local proteomics core facility provides fee-for-service protein identification analysis by liquid chromatography tandem mass-spectrometry.</i> |
| Data format | <i>Processed</i> |

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| | |
|-----------------------|---|
| Experimental factors | <i>Purified protein complexes isolated from various yeast strains were separated by native PAGE and stained to identify individual bands.</i> |
| Experimental features | <i>Gel slices, representing individual bands identified on non-denaturing polyacrylamide gels, were cut out and submitted for protein identification.</i> |
| Data source location | <i>Department of Biology; Indiana University-Purdue University Indianapolis; Indianapolis, IN, USA</i> |
| Data accessibility | <i>The processed data in Excel format, as supplied by the core facility, is with this article. The mass-spectrometry raw data collected by the proteomics core facility remains with the facility and was not provided to the researcher as part of the fee-for-service analysis.</i> |

Value of the data

- The data support the identification of novel protein complexes comprised of proteasome subunits.
- Novel protein complexes identified invite additional experiments to further characterize them.
- Data also identify proteins associated with these novel protein complexes.

1. Data

The data contained here (Tables 1–8) are from the Excel files provided to the authors by the local proteomics core facility as part of the fee-for-service analysis of samples submitted ([see Appendix](#)).

Table 1
Protein content of Band 1.

| Accession | Description | Score | Coverage | # Unique Peptides | # Peptides | # PSMs |
|-----------|---|--------|----------|-------------------|------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 236.09 | 78.74 | 3 | 16 | 90 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 228.60 | 79.37 | 1 | 16 | 114 |
| 93279388 | Chain U, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 201.77 | 88.07 | 22 | 22 | 78 |
| 323337524 | Pre9p [Saccharomyces cerevisiae Vin13] | 197.22 | 73.64 | 19 | 19 | 58 |
| 93279386 | Chain S, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 183.95 | 83.69 | 19 | 19 | 60 |
| 256274381 | Pba1p [Saccharomyces cerevisiae JAY291] | 153.63 | 61.96 | 12 | 12 | 54 |
| 93279382 | Chain O, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 152.91 | 52.00 | 12 | 12 | 65 |
| 178847521 | Chain T, Yeast 20s Proteasome:glidobactin A-Complex | 142.44 | 60.98 | 16 | 16 | 49 |
| 323309416 | Pup3p [Saccharomyces cerevisiae FostersO] | 135.74 | 46.60 | 8 | 8 | 38 |
| 444302412 | Chain R, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 109.18 | 59.62 | 17 | 17 | 34 |
| 403071955 | Chain 2, Near-Atomic Resolution Structural Model Of The Yeast 26s Proteasome | 103.01 | 31.80 | 9 | 9 | 69 |
| 151941458 | conserved protein [Saccharomyces cerevisiae YJM789] | 72.71 | 31.84 | 9 | 9 | 27 |
| 151944720 | 22.6 kDa proteasome subunit [Saccharomyces cerevisiae YJM789] | 53.84 | 47.47 | 10 | 10 | 20 |
| 93279393 | Chain Z, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 31.84 | 35.14 | 5 | 5 | 12 |
| 323305986 | Ump1p [Saccharomyces cerevisiae FostersB] | 31.83 | 22.97 | 3 | 3 | 22 |
| 207340308 | YPR103Wp-like protein [Saccharomyces cerevisiae AWRI1631] | 29.60 | 33.10 | 8 | 8 | 9 |
| 323337162 | Pfk26p [Saccharomyces cerevisiae Vin13] | 28.55 | 13.68 | 9 | 9 | 9 |
| 207345674 | YFL007Wp-like protein [Saccharomyces cerevisiae AWRI1631] | 26.43 | 4.62 | 6 | 6 | 8 |
| 741845 | peptidyl-Glu protease | 23.26 | 34.72 | 6 | 6 | 7 |
| 259146995 | Ecm29p [Saccharomyces cerevisiae EC1118] | 15.98 | 4.13 | 5 | 5 | 5 |
| 736313 | unknown [Saccharomyces cerevisiae] | 14.84 | 10.44 | 5 | 5 | 5 |
| 226279 | mitochondrial assembly factor | 11.90 | 7.17 | 3 | 3 | 4 |
| 323304344 | Tdh2p [Saccharomyces cerevisiae FostersB] | 11.63 | 20.98 | 3 | 3 | 4 |

This table pertains to Band 1 from Fig. 2 in the referenced manuscript.

Table 2
Protein content of Band 2.

| Accession | Description | Score | Coverage | # Unique Peptides | # Pep-tides | # PSMs |
|-----------|---|--------|----------|-------------------|-------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 206.36 | 77.56 | 2 | 13 | 113 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 182.00 | 78.17 | 1 | 13 | 82 |
| 323337524 | Pre9p [Saccharomyces cerevisiae Vin13] | 144.66 | 77.27 | 18 | 18 | 43 |
| 93279388 | Chain U, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 141.43 | 83.13 | 19 | 19 | 57 |
| 323309416 | Pup3p [Saccharomyces cerevisiae FostersO] | 96.26 | 46.60 | 8 | 8 | 27 |
| 151946074 | proteasome component Y7 [Saccharomyces cerevisiae YJM789] | 94.51 | 37.20 | 11 | 11 | 40 |
| 403071955 | Chain 2, Near-Atomic Resolution Structural Model Of The Yeast 26s Proteasome | 67.94 | 31.03 | 7 | 7 | 41 |
| 172136 | 6-phosphofructo-2-kinase [Saccharomyces cerevisiae] | 43.50 | 18.62 | 12 | 12 | 13 |
| 151944720 | 22.6 kDa proteasome subunit [Saccharomyces cerevisiae YJM789] | 40.65 | 46.46 | 7 | 7 | 15 |
| 349577910 | K7_Blm10p [Saccharomyces cerevisiae Kyokai no. 7] | 39.81 | 6.35 | 11 | 11 | 13 |
| 259148570 | Erg6p [Saccharomyces cerevisiae EC1118] | 28.84 | 23.76 | 6 | 6 | 8 |
| 256270485 | Pdc1p [Saccharomyces cerevisiae JAY291] | 27.82 | 20.89 | 6 | 6 | 11 |
| 171457 | enolase [Saccharomyces cerevisiae] | 26.17 | 20.82 | 6 | 6 | 7 |
| 323336942 | Ssc1p [Saccharomyces cerevisiae Vin13] | 24.65 | 12.64 | 6 | 6 | 8 |
| 741845 | peptidyl-Glu protease | 24.17 | 36.27 | 6 | 6 | 8 |
| 259149737 | Rpn8p [Saccharomyces cerevisiae EC1118] | 24.00 | 16.57 | 4 | 4 | 7 |
| 323303909 | Acs2p [Saccharomyces cerevisiae FostersB] | 21.18 | 9.15 | 4 | 4 | 8 |
| 312258 | PUP2 [Saccharomyces cerevisiae] | 18.90 | 29.23 | 6 | 6 | 6 |
| 323355426 | Rpn3p [Saccharomyces cerevisiae VL3] | 18.64 | 15.48 | 5 | 5 | 6 |
| 223142 | dehydrogenase isozyme 1,alcohol | 15.41 | 15.77 | 4 | 4 | 5 |
| 323352105 | Eft2p [Saccharomyces cerevisiae VL3] | 15.16 | 7.87 | 4 | 4 | 5 |
| 1103917 | D-arabinono-1,4-lactone oxidase [Saccharomyces cerevisiae] | 14.25 | 11.41 | 5 | 5 | 5 |
| 323333957 | Rpn9p [Saccharomyces cerevisiae AWR1796] | 13.22 | 13.80 | 3 | 3 | 4 |
| 323305986 | Ump1p [Saccharomyces cerevisiae FostersB] | 12.80 | 15.54 | 2 | 2 | 8 |

This table pertains to Band 2 from Fig. 2 in the referenced manuscript.

Each Excel file corresponds to a band cut out of a non-denaturing polyacrylamide gel in the referenced article [1]. Each Excel file includes information to direct the reader to the appropriate band that was analyzed. The Excel files contain details of the proteins identified in each sample submitted to the core facility, including: the number and sequence of each identified peptide, any modifications of each peptide, spectral counts, and coverage, etc. The title of each Excel file is meant to direct the reader to the actual band that was analyzed in the referenced article [1]. Additional Excel files are found in [Appendix](#).

2. Experimental design, materials and methods

Non-denaturing polyacrylamide gel electrophoresis was carried out as described [1]. Bands (gel slices) were excised and submitted for analysis to the Indiana University School of Medicine Proteomics Core Facility. The facility carried out protein identification and provided processed data as Excel files. The Excel files were accompanied by a copy of a Word document that outlined the experimental procedure carried out by the core facility, and the subsequent data analysis, to identify the proteins within the sample. A copy of this word document is included in the [Appendix](#).

Table 3
Protein content of Band 3.

| Accession | Description | Score | Coverage | # Unique Peptides | # Peptides | # PSMs |
|-----------|---|--------|----------|-------------------|------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 625.80 | 67.72 | 2 | 16 | 313 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 575.74 | 68.25 | 3 | 16 | 277 |
| 298508455 | Chain U, Proteasome Activator Complex | 487.69 | 67.40 | 2 | 14 | 174 |
| 93279388 | Chain U, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 188.85 | 89.71 | 22 | 22 | 75 |
| 93279386 | Chain S, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 119.42 | 78.11 | 14 | 14 | 37 |
| 323337524 | Pre9p [Saccharomyces cerevisiae Vin13] | 119.35 | 77.27 | 18 | 18 | 34 |
| 93279382 | Chain O, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 117.98 | 52.00 | 11 | 11 | 48 |
| 323309416 | Pup3p [Saccharomyces cerevisiae FostersO] | 92.81 | 41.88 | 9 | 9 | 29 |
| 390980863 | Chain T, Structure Of Yeast 20s Open-Gate Proteasome With Compound 34 | 90.73 | 51.65 | 9 | 9 | 27 |
| 403071955 | Chain 2, Near-Atomic Resolution Structural Model Of The Yeast 26s Proteasome | 72.80 | 46.74 | 7 | 7 | 47 |
| 256274381 | Pba1p [Saccharomyces cerevisiae JAY291] | 70.73 | 57.25 | 11 | 11 | 19 |
| 312258 | PUP2 [Saccharomyces cerevisiae] | 58.77 | 44.23 | 13 | 13 | 15 |
| 151944720 | 22.6 kDa proteasome subunit [Saccharomyces cerevisiae YJM789] | 45.95 | 47.47 | 8 | 8 | 14 |
| 323305986 | Ump1p [Saccharomyces cerevisiae FostersB] | 35.64 | 41.89 | 5 | 5 | 20 |
| 323337162 | Pfk26p [Saccharomyces cerevisiae Vin13] | 35.29 | 16.54 | 10 | 10 | 10 |
| 93279395 | Chain 2, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 34.81 | 65.31 | 8 | 8 | 12 |
| 93279393 | Chain Z, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 32.74 | 35.59 | 6 | 6 | 11 |
| 151941458 | conserved protein [Saccharomyces cerevisiae YJM789] | 31.70 | 31.46 | 7 | 7 | 10 |
| 207340308 | YPR103Wp-like protein [Saccharomyces cerevisiae AWRI1631] | 30.22 | 25.09 | 6 | 6 | 10 |
| 93279394 | Chain 1, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 23.31 | 27.04 | 3 | 3 | 7 |
| 226279 | mitochondrial assembly factor | 19.36 | 15.03 | 6 | 6 | 6 |
| 190407817 | conserved hypothetical protein [Saccharomyces cerevisiae RM11-1a] | 15.53 | 35.81 | 3 | 3 | 5 |
| 166007292 | Chain E, Crystal Structure Of A Novel Chaperone Complex For Yeast 20s Proteasome Assembly | 13.50 | 36.24 | 3 | 3 | 4 |
| 207345674 | YFL007Wp-like protein [Saccharomyces cerevisiae AWRI1631] | 12.97 | 2.78 | 4 | 4 | 4 |

This table pertains to Band 3 from Fig. 2 in the referenced manuscript.

Table 4
Protein content of Band 4.

| Accession | Description | Score | Coverage | # Unique Peptides | # Peptides | # PSMs |
|-----------|---|--------|----------|-------------------|------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 592.98 | 66.14 | 2 | 17 | 354 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 538.85 | 66.67 | 2 | 17 | 281 |
| 93279388 | Chain U, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 504.52 | 92.59 | 30 | 30 | 198 |
| 298508455 | Chain U, Proteasome Activator Complex | 417.71 | 65.64 | 2 | 15 | 145 |
| 323348418 | Pre9p [Saccharomyces cerevisiae Lalvin QA23] | 268.96 | 91.09 | 22 | 22 | 84 |
| 178847521 | Chain T, Yeast 20s Proteasome:glidobactin A-Complex | 214.58 | 62.72 | 14 | 14 | 72 |
| 93279382 | Chain O, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 197.26 | 52.00 | 12 | 12 | 70 |
| 403071955 | Chain 2, Near-Atomic Resolution Structural Model Of The Yeast 26s Proteasome | 184.91 | 58.62 | 13 | 13 | 85 |
| 323309416 | Pup3p [Saccharomyces cerevisiae FostersO] | 176.76 | 42.93 | 8 | 8 | 49 |
| 93279386 | Chain S, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 166.90 | 82.83 | 17 | 17 | 57 |
| 151944720 | 22.6 kDa proteasome subunit [Saccharomyces cerevisiae YJM789] | 115.04 | 43.94 | 9 | 9 | 48 |
| 256274381 | Pba1p [Saccharomyces cerevisiae JAY291] | 92.42 | 57.25 | 11 | 11 | 28 |
| 312258 | PUP2 [Saccharomyces cerevisiae] | 86.96 | 61.54 | 17 | 17 | 25 |
| 323305986 | Ump1p [Saccharomyces cerevisiae FostersB] | 70.97 | 45.95 | 5 | 5 | 51 |
| 349577910 | K7_Blm10p [Saccharomyces cerevisiae Kyokai no. 7] | 53.82 | 7.89 | 13 | 13 | 17 |
| 166007287 | Chain B, Crystal Structure Of A Novel Chaperone Complex For Yeast 20s Proteasome Assembly | 51.61 | 76.54 | 9 | 9 | 12 |
| 123624 | RecName: Full=Heat shock protein SSA2 | 45.22 | 27.70 | 3 | 11 | 13 |
| 323306163 | Ssa1p [Saccharomyces cerevisiae FostersB] | 41.81 | 24.18 | 1 | 10 | 12 |
| 151941458 | conserved protein [Saccharomyces cerevisiae YJM789] | 38.90 | 28.09 | 6 | 6 | 13 |
| 171541 | glyceraldehyde-3-phosphate dehydrogenase (G3PD) [Saccharomyces cerevisiae] | 35.39 | 33.73 | 6 | 6 | 11 |
| 323337162 | Pfk26p [Saccharomyces cerevisiae Vin13] | 35.23 | 16.54 | 10 | 10 | 10 |
| 190407817 | conserved hypothetical protein [Saccharomyces cerevisiae RM11-1a] | 29.15 | 37.16 | 5 | 5 | 10 |
| 190408474 | conserved hypothetical protein [Saccharomyces cerevisiae RM11-1a] | 25.09 | 5.06 | 6 | 6 | 8 |
| 323334738 | Pre7p [Saccharomyces cerevisiae AWRI796] | 24.16 | 18.48 | 2 | 2 | 6 |
| 3114294 | Chain Z, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution | 16.06 | 25.00 | 5 | 5 | 5 |
| 121575 | RecName: Full=78 kDa glucose-regulated protein homolog; Short=GRP-78; AltName: Full=Immunoglobulin heavy chain-binding protein homolog; Short=BiP; Flags: Precursor | 13.13 | 7.62 | 3 | 4 | 4 |

This table pertains to Band 4 from Fig. 2 in the referenced manuscript.

Table 5
Protein content of Band 5.

| Accession | Description | Score | Coverage | # Unique Peptides | # Peptides | # PSMs |
|-----------|---|---------|----------|-------------------|------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 1411.77 | 69.69 | 2 | 19 | 724 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 1244.29 | 70.24 | 3 | 19 | 546 |
| 298508455 | Chain U, Proteasome Activator Complex | 1056.66 | 69.60 | 2 | 17 | 344 |
| 323352352 | Pre6p [Saccharomyces cerevisiae VL3] | 771.05 | 65.24 | 1 | 16 | 235 |
| 93279388 | Chain U, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 114.49 | 79.01 | 17 | 17 | 47 |
| 323309416 | Pup3p [Saccharomyces cerevisiae FostersO] | 82.42 | 51.83 | 10 | 10 | 24 |
| 151944720 | 22.6 kDa proteasome subunit [Saccharomyces cerevisiae YJM789] | 80.43 | 47.47 | 10 | 10 | 27 |
| 123624 | RecName: Full=Heat shock protein SSA2 | 79.71 | 34.59 | 5 | 16 | 26 |
| 323306163 | Ssa1p [Saccharomyces cerevisiae FostersB] | 78.44 | 30.93 | 2 | 14 | 24 |
| 984187 | transcription factor [Saccharomyces cerevisiae] | 65.14 | 32.41 | 12 | 12 | 27 |
| 312258 | PUP2 [Saccharomyces cerevisiae] | 62.46 | 58.08 | 14 | 14 | 20 |
| 93279393 | Chain Z, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 43.29 | 31.08 | 5 | 5 | 14 |
| 93279386 | Chain S, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 41.02 | 60.94 | 10 | 10 | 12 |
| 93279382 | Chain O, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 35.16 | 44.00 | 7 | 7 | 10 |
| 93279395 | Chain 2, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 34.28 | 39.80 | 8 | 8 | 11 |
| 390980863 | Chain T, Structure Of Yeast 20s Open-Gate Proteasome With Compound 34 | 24.33 | 31.40 | 6 | 6 | 10 |
| 121575 | RecName: Full=78 kDa glucose-regulated protein homolog; Short=GRP-78; AltName: Full=Immunoglobulin heavy chain-binding protein homolog; Short=BiP; Flags: Precursor | 24.28 | 11.44 | 5 | 6 | 8 |
| 93279392 | Chain Y, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 19.31 | 25.47 | 4 | 4 | 6 |
| 403071955 | Chain 2, Near-Atomic Resolution Structural Model Of The Yeast 26s Proteasome | 18.70 | 21.46 | 3 | 3 | 10 |
| 151941041 | proteasome biogenesis-associated [Saccharomyces cerevisiae YJM789] | 17.59 | 11.59 | 3 | 3 | 6 |
| 93279394 | Chain 1, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 16.80 | 6.44 | 1 | 1 | 5 |
| 323353866 | Ubi4p [Saccharomyces cerevisiae VL3] | 15.90 | 54.47 | 3 | 3 | 5 |

This table pertains to Band 5 from Fig. 2 in the referenced manuscript.

Table 6
Protein content of Band 6.

| Accession | Description | Score | Coverage | # Unique Peptides | # Peptides | # PSMs |
|-----------|---|---------|----------|-------------------|------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 1382.37 | 73.23 | 2 | 21 | 763 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 1239.14 | 73.81 | 3 | 20 | 651 |
| 298508455 | Chain U, Proteasome Activator Complex | 1003.49 | 73.57 | 2 | 19 | 352 |
| 323352352 | Pre6p [Saccharomyces cerevisiae VL3] | 722.91 | 69.05 | 1 | 17 | 221 |
| 417149 | RecName: Full=Heat shock protein SSA1; AltName: Full=Heat shock protein YG100 | 201.34 | 59.03 | 8 | 34 | 61 |
| 123624 | RecName: Full=Heat shock protein SSA2 | 194.83 | 55.40 | 5 | 32 | 58 |
| 93279388 | Chain U, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 160.69 | 79.42 | 20 | 20 | 63 |
| 151944720 | 22.6 kDa proteasome subunit [Saccharomyces cerevisiae YJM789] | 131.89 | 47.47 | 9 | 9 | 49 |
| 323309416 | Pup3p [Saccharomyces cerevisiae FostersO] | 105.70 | 46.60 | 8 | 8 | 31 |
| 984187 | transcription factor [Saccharomyces cerevisiae] | 98.23 | 50.64 | 21 | 21 | 30 |
| 312258 | PUP2 [Saccharomyces cerevisiae] | 84.62 | 56.54 | 14 | 14 | 26 |
| 121575 | RecName: Full=78 kDa glucose-regulated protein homolog; Short=GRP-78; AltName: Full=Immunoglobulin heavy chain-binding protein homolog; Short=BIP; Flags: Precursor | 83.13 | 29.62 | 14 | 15 | 22 |
| 256274381 | Pba1p [Saccharomyces cerevisiae JAY291] | 71.41 | 45.65 | 8 | 8 | 19 |
| 390980834 | Chain S, Structure Of Yeast 20s Open-Gate Proteasome With Compound 20 | 50.61 | 62.66 | 10 | 10 | 16 |
| 93279393 | Chain Z, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 47.35 | 39.64 | 6 | 6 | 18 |
| 93279382 | Chain O, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 37.34 | 44.00 | 8 | 8 | 13 |
| 403071955 | Chain 2, Near-Atomic Resolution Structural Model Of The Yeast 26s Proteasome | 33.68 | 37.16 | 7 | 7 | 13 |
| 390980863 | Chain T, Structure Of Yeast 20s Open-Gate Proteasome With Compound 34 | 32.65 | 31.40 | 6 | 6 | 10 |
| 93279395 | Chain 2, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 31.38 | 59.18 | 8 | 8 | 10 |
| 171457 | enolase [Saccharomyces cerevisiae] | 19.63 | 16.25 | 5 | 5 | 6 |
| 93279392 | Chain Y, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 18.74 | 25.47 | 5 | 5 | 6 |
| 166007292 | Chain E, Crystal Structure Of A Novel Chaperone Complex For Yeast 20s Proteasome Assembly | 18.72 | 44.97 | 4 | 4 | 5 |
| 323353866 | Ubi4p [Saccharomyces cerevisiae VL3] | 13.64 | 54.47 | 3 | 3 | 4 |
| 256270485 | Pdc1p [Saccharomyces cerevisiae JAY291] | 11.03 | 9.39 | 2 | 2 | 3 |
| 171541 | glyceraldehyde-3-phosphate dehydrogenase (G3PD) [Saccharomyces cerevisiae] | 10.12 | 17.17 | 3 | 3 | 6 |

This table pertains to Band 6 from Fig. 2 in the referenced manuscript.

Table 7
Protein content of Band 7.

| Accession | Description | Score | Coverage | # Unique Peptides | # Peptides | # PSMs |
|-----------|---|--------|----------|-------------------|------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 402.40 | 62.99 | 3 | 15 | 176 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 369.19 | 63.49 | 1 | 15 | 200 |
| 323337524 | Pre9p [Saccharomyces cerevisiae Vin13] | 15.59 | 9.09 | 1 | 1 | 4 |
| 323309416 | Pup3p [Saccharomyces cerevisiae FostersO] | 14.74 | 24.08 | 3 | 3 | 4 |
| 340707865 | Chain A, Crystal Structure Of Yeast Hsp70 (BipKAR2) ATPASE DOMAIN | 12.47 | 12.31 | 4 | 4 | 4 |
| 390980863 | Chain T, Structure Of Yeast 20s Open-Gate Proteasome With Compound 34 | 12.10 | 14.88 | 3 | 3 | 4 |

This table pertains to Band 7 from Fig. 3 in the referenced manuscript.

Table 8
Protein content of Band 8.

| Accession | Description | Score | Coverage | # Unique Peptides | # Pep-tides | # PSMs |
|-----------|---|--------|----------|-------------------|-------------|--------|
| 444302411 | Chain Q, Yeast 20s Proteasome In Complex With The Vinyl Sulfone Lu112 | 612.56 | 55.12 | 2 | 12 | 323 |
| 323307097 | Pre6p [Saccharomyces cerevisiae FostersO] | 537.41 | 55.56 | 2 | 12 | 334 |
| 298508455 | Chain U, Proteasome Activator Complex | 417.38 | 53.30 | 2 | 10 | 130 |
| 417149 | RecName: Full=Heat shock protein SSA1; AltName: Full=Heat shock protein YG100 | 96.44 | 38.01 | 5 | 17 | 26 |
| 123624 | RecName: Full=Heat shock protein SSA2 | 92.78 | 33.18 | 3 | 16 | 24 |
| 256270485 | Pdc1p [Saccharomyces cerevisiae JAY291] | 30.17 | 16.67 | 5 | 5 | 8 |
| 93279388 | Chain U, Crystal Structure Of The Yeast 20s Proteasome In Complex With Bortezomib | 21.66 | 20.16 | 4 | 4 | 6 |
| 121575 | RecName: Full=78 kDa glucose-regulated protein homolog; Short=GRP-78; AltName: Full=Immunoglobulin heavy chain-binding protein homolog; Short=BiP; Flags: Precursor | 15.44 | 8.80 | 3 | 4 | 4 |
| 323333274 | Fur1p [Saccharomyces cerevisiae AWRI796] | 10.70 | 20.77 | 3 | 3 | 3 |

This table pertains to Band 8 from Fig. 3 in the referenced manuscript.

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Transparency document. Supplementary material

Transparency data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2016.11.048>.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2016.11.048>.

Reference

- [1] L.J. Hammack, A.R. Kusmierczyk, Assembly of proteasome subunits into non-canonical complexes in vivo, *Biochem. Biophys. Res. Commun.* (2016), <http://dx.doi.org/10.1016/j.bbrc.2016.11.024>.