**Supporting table S1:** Mass spectrometry analysis of recombinant P-L complex preparations. Most abundant (iBAQ ≥109) proteins identified by mass spectrometry are shown.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Majority protein IDs** | **Description** | **Mol. weight [kDa]** | **Sequence coverage [%]** | **Razor + unique peptides** | **Intensity** | **MS/MS Count** | **iBAQa** |
| **MeV P** | **RdRP cofactor** | **56** | **95** | **78** | **7.81×1011** | **1715** | **3.12×1010** |
| **MeV L** | **RdRP**  | **248** | **84** | **208** | **6.74×1011** | **1359** | **6.48×109** |
| A0A2H1X3Z3 | mRNA cleavage factor complex\* | 18 | 87 | 8 | 4.37×1010 | 87 | **1.09×1010** |
| A0A2H1WRK1 | mRNA cleavage factor complex\* | 26 | 92 | 28 | 1.23×1011 | 285 | **1.02×1010** |
| A0A2H1VAM0 | mRNA cleavage factor complex\* | 55 | 35 | 14 | 8.85×1010 | 96 | **5.53×109** |
| A0A2H1VKI1 | Thioredoxin-like\* | 47 | 66 | 36 | 1.04×1011 | 161 | **5.45×109** |
| A0A2H1WKT6 | SCD6 protein-related, RNA metabolism\* | 57 | 66 | 29 | 7.23×1010 | 211 | **4.52×109** |
| A0A2H1WFA2 | Heat-Shock Protein | 72 | 87 | 56 | 1.14×1011 | 253 | **3.56×109** |
| A0A2H1W5E0 | Scaffold protein\* | 30 | 87 | 18 | 4.08×1010 | 131 | **2.72×109** |
| A0A2H1VCM4 | Peroxiredoxin\* | 40 | 43 | 18 | 6.25×1010 | 82 | **2.72×109** |
| A0A2H1WKS6 | Ubiquitin-associated protein 2-like\* | 63 | 73 | 17 | 2.62×1010 | 123 | **2.02×109** |
| Q962T8 | 60S ribosomal protein L27a | 17 | 46 | 10 | 1.59×1010 | 25 | **1.98×109** |
| A0A2H1VM87 | Scaffold protein with Ubiquitin-associated domain\* | 41 | 51 | 15 | 2.43×1010 | 93 | **1.87×109** |
| A0A2H1WQZ8 | 40S ribosomal protein S9\* | 18 | 35 | 14 | 1.69×1010 | 22 | **1.69×109** |
| A0A2H1WFG2 | Metal ion transmembrane transporter activity\* | 38 | 58 | 14 | 9.32×109 | 62 | **1.55×109** |
| P17501;A0A097PUZ4;Q65336 | Baculovirus Major envelope glycoprotein  | 59 | 52 | 27 | 3.52×1010 | 130 | **1.53×109** |
| A0A2H1WX17;Q8I866 | Heat-Shock Protein | 73 | 75 | 43 | 4.56×1010 | 167 | **1.52×109** |
| A0A2H1VC46 | Ataxin-2-like protein\* | 67 | 64 | 29 | 3.74×1010 | 132 | **1.50×109** |
| A0A2H1WWH2 | Protein yippee-like | 14 | 58 | 6 | 9.80×109 | 18 | **1.40×109** |
| A0A2H1VDL3 | Thioredoxin-like\* | 24 | 78 | 11 | 1.62×1010 | 50 | **1.35×109** |
| A0A2H1VXJ0 | LSM12-like protein\* | 22 | 79 | 18 | 1.38×1010 | 51 | **1.25×109** |
| S5G646;P41432 | Baculovirus late expression factor 6 | 20 | 67 | 13 | 1.21×1010 | 57 | **1.21×109** |
| A0A2H1WJQ0 | L-lactate dehydrogenase\* | 27 | 71 | 13 | 1.19×1010 | 39 | **1.19×109** |
| A0A2H1VF70 | Nuclear Transport Factor 2-like | 25 | 78 | 14 | 1.17×1010 | 58 | **1.17×109** |
| A0A2H1W9M2 | Scaffold protein\* | 40 | 91 | 22 | 1.66×1010 | 82 | **1.11×109** |
| A0A2H1W5D9 | Scaffold protein\* | 34 | 29 | 7 | 1.71×1010 | 30 | **1.00×109** |
| A0A2H1VWC5 | Lupus La protein-like\* | 84 | 69 | 50 | 4.31×1010 | 136 | **1.00×109** |
| *a*: Intensity Based Absolute Quantification |  |  |  |  |
| \*: predicted by molecular domain or sequence homology |  |  |  |  |  |  |