

Supporting Information for Microfluidic Flow Cell for Sequential Digestion of Immobilized Proteoliposomes

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Abstract

The supporting information presented here describes the punched-out tape used for flow cell assembly, the derivation of the equation describing the flow profile in the flow cell channel, protein classification search terms, and a summary of proteins identified with sequential and single tryptic digestions of immobilized CHO proteoliposomes.

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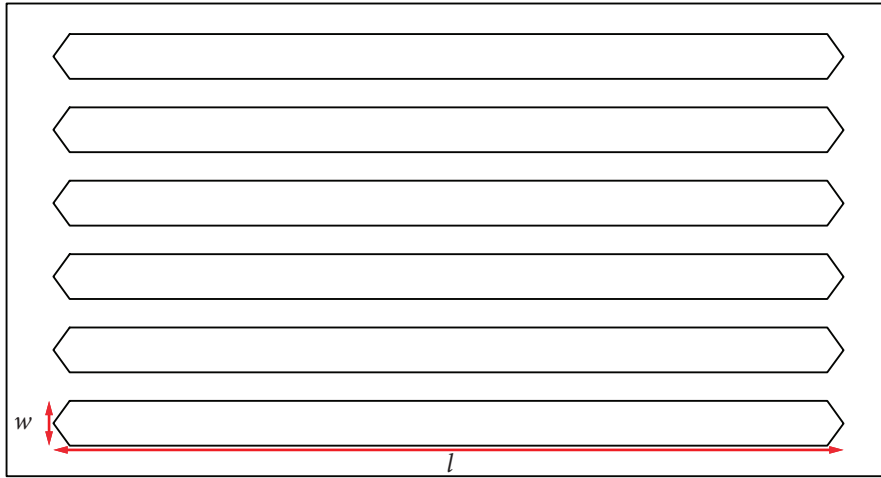
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Flow Cell Assembly

The flow cell is assembled by pressing two polymer substrates [glycol-modified poly(ethylene terephthalate)] together on each side of a 50 μm thick punched-out tape, shown in Figure S-1.

Figure S-1: The punched-out tape used for flow cell assembly, determining channel geometry with width $w = 5$ mm, and length $l = 95$ mm. The height of the channel is determined by the thickness of the tape, $h = 50$ μm . Each flow cell contains six channels for proteoliposome immobilization.



Derivation of the Flow Profile for the Flow Cell Channel

The flow profile in the flow cell channel can be estimated by the Navier-Stokes equation. As water is an incompressible fluid, with a constant density ρ , and the Reynolds number is small, the inertial terms in the Navier-Stokes equation are neglected. The equation describing the flow profile is thus

$$\nabla p = \mu \nabla^2 \mathbf{v}, \quad \nabla \cdot \mathbf{v} = 0, \quad (1)$$

where p is the pressure, μ the viscosity of the liquid, and \mathbf{v} its velocity. Assuming a flow between two infinite parallel plates ($h \ll w < L$), where h , w and L is the height, width, and length of the flow cell channel, respectively, no-slip conditions on the stationary walls, and a Cartesian coordinate system with x , y and z as length-, width- and height-coordinates, respectively; Equation 1 simplifies

into the ordinary differential equation

$$\frac{\partial^2 v_x(z)}{\partial z^2} = -\frac{\Delta p}{\mu L}, \quad (2a)$$

$$v_x(0) = 0, \quad v_x(h) = 0. \quad (2b)$$

The solution to Equation 2 is given by the parabolic function

$$v_x(z) = \frac{\Delta p}{2\mu L} (h - z) z, \quad (3)$$

hence, the volume flow Q , through a rectangular channel is found as

$$Q = \int_0^h \int_0^w v_x(z) dy dz = \frac{h^3 w}{12\mu L} \Delta p. \quad (4)$$

Combining Equation 3 and Equation 4, the flow profile is given as

$$v_x(z) = \frac{6Q}{h^3 w} (h - z) z, \quad (5)$$

where $v_x(z)$ is the flow velocity as a function of height.

Protein Classification

Proteins are classified by database searching in UniProtKB and with Gene ontology terms, as membrane-associated proteins (of which transmembrane, lipid-anchored and peripheral are subclasses), or as nonmembrane-associated, (Figure S-2).

Membrane-Associated Proteins

Proteins are classified as membrane-associated proteins, if any of the search terms in Table S-1 are found.

Figure S-2: Overview of protein classification.

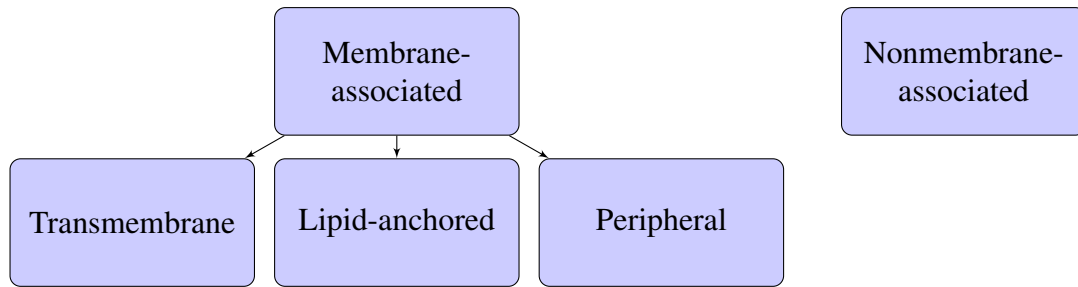


Table S-1: Gene ontology terms for class "Membrane-associated".

| Identifier | Description |
|------------|--|
| GO:0000139 | Golgi membrane |
| GO:0000299 | integral to membrane of membrane fraction |
| GO:0005624 | membrane fraction |
| GO:0005635 | nuclear envelope |
| GO:0005637 | nuclear inner membrane |
| GO:0005639 | integral to nuclear inner membrane |
| GO:0005640 | nuclear outer membrane |
| GO:0005741 | mitochondrial outer membrane |
| GO:0005743 | mitochondrial inner membrane |
| GO:0005779 | integral to peroxisomal membrane |
| GO:0005789 | endoplasmic reticulum membrane |
| GO:0005886 | plasma membrane |
| GO:0005887 | integral to plasma membrane |
| GO:0009274 | peptidoglycan-based cell wall |
| GO:0009275 | Gram-positive-bacterium-type cell wall |
| GO:0009276 | Gram-negative-bacterium-type cell wall |
| GO:0009279 | cell outer membrane |
| GO:0009288 | bacterial-type flagellum |
| GO:0010008 | endosome membrane |
| GO:0015412 | molybdate transmembrane-transporting ATPase activity |
| GO:0015628 | type II protein secretion complex |
| GO:0016020 | membrane |
| GO:0016021 | integral to membrane |
| GO:0019861 | flagellum |
| GO:0019866 | organelle inner membrane |
| GO:0019867 | outer membrane |
| GO:0030173 | integral to Golgi membrane |
| GO:0030176 | integral to endoplasmic reticulum membrane |
| GO:0030257 | type III protein secretion system complex |
| GO:0030285 | integral to synaptic vesicle membrane |
| GO:0030288 | outer membrane-bounded periplasmic space |
| GO:0030313 | cell envelope |
| GO:0030867 | rough endoplasmic reticulum membrane |
| GO:0030868 | smooth endoplasmic reticulum membrane |
| GO:0031165 | integral to contractile vacuolar membrane |
| GO:0031166 | integral to vacuolar membrane |
| GO:0031225 | anchored to membrane |

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Table S-1 – Continued

| Identifier | Description |
|------------|---|
| GO:0031230 | intrinsic to cell outer membrane |
| GO:0031236 | extrinsic to external side of plasma membrane, in periplasmic space |
| GO:0031237 | intrinsic to external side of plasma membrane, in periplasmic space |
| GO:0031244 | extrinsic to cell outer membrane |
| GO:0031300 | intrinsic to organelle membrane |
| GO:0031301 | integral to organelle membrane |
| GO:0031303 | integral to endosome membrane |
| GO:0031305 | integral to mitochondrial inner membrane |
| GO:0031307 | integral to mitochondrial outer membrane |
| GO:0031309 | integral to nuclear outer membrane |
| GO:0031351 | integral to plastid membrane |
| GO:0031353 | integral to plastid inner membrane |
| GO:0031355 | integral to plastid outer membrane |
| GO:0031357 | integral to chloroplast inner membrane |
| GO:0031359 | integral to chloroplast outer membrane |

Transmembrane Proteins

Proteins are classified as transmembrane proteins, if any of the search terms in Table S-2 and Table S-3 are found.

Table S-2: UniProtKB terms for class "Transmembrane".

| Search term | Fields |
|-------------|--------------------------|
| single-pass | Subcellular Localization |
| multi-pass | Subcellular Localization |
| transmem | Keywords Topology |
| integral | GO annotations |

Table S-3: Gene ontology terms for class "Transmembrane".

| Identifier | Description |
|------------|--|
| GO:0000299 | integral to membrane of membrane fraction |
| GO:0005639 | integral to nuclear inner membrane |
| GO:0005779 | integral to peroxisomal membrane |
| GO:0005887 | integral to plasma membrane |
| GO:0016021 | integral to membrane |
| GO:0030173 | integral to Golgi membrane |
| GO:0030176 | integral to endoplasmic reticulum membrane |
| GO:0030285 | integral to synaptic vesicle membrane |
| GO:0031165 | integral to contractile vacuolar membrane |
| GO:0031166 | integral to vacuolar membrane |
| GO:0031301 | integral to organelle membrane |
| GO:0031303 | integral to endosome membrane |
| GO:0031305 | integral to mitochondrial inner membrane |
| GO:0031307 | integral to mitochondrial outer membrane |
| GO:0031309 | integral to nuclear outer membrane |
| GO:0031351 | integral to plastid membrane |
| GO:0031353 | integral to plastid inner membrane |
| GO:0031355 | integral to plastid outer membrane |
| GO:0031357 | integral to chloroplast inner membrane |
| GO:0031359 | integral to chloroplast outer membrane |
| GO:0031361 | integral to thylakoid membrane |
| GO:0032592 | integral to mitochondrial membrane |
| GO:0045203 | integral to cell outer membrane |

Lipid-Anchored Proteins

Proteins are classified as lipid-anchored proteins, if any of the search terms in Table S-4 and Table S-5 are found.

Table S-4: UniProtKB terms for class "Lipid-anchored".

| Search term | Fields |
|-------------|--------------------------------------|
| lipid | Subcellular Localization Topology |
| lipoprotein | Keywords |
| GPI-anchor | Subcellular Localization Topology |

Table S-5: Gene ontology terms for class "Lipid-anchored".

| Identifier | Description |
|------------|-----------------------------|
| GO:0031225 | anchored to membrane |
| GO:0046658 | anchored to plasma membrane |

Peripheral Proteins

If a protein is "Membrane-associated", but is not classified as transmembrane or lipid-anchored, the protein falls into the class "Peripheral".

Nonmembrane-Associated Proteins

If a protein is not "Membrane-associated", the protein falls into the class "Nonmembrane-associated".

Proteins Identified with Sequential and Single Tryptic Digestions of Immobilized CHO Proteoliposomes

A list of proteins detected with sequential and single tryptic digestion of immobilized CHO proteoliposomes is found in Table S-6 and Table S-7, respectively. Number of unique peptides, sequence coverage and MASCOT score is given for each protein ID.

Table S-6: Proteins detected with single digestion.

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|--------------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|
| A1E3K3_CRIGR | 2 | 12.5 | 163.08 | 2 | 17.11 | 122.56 | 3 | 22.92 | 284.41 | 2 | 17.11 | 174.41 | 2 | 17.11 | 127.87 | - | - | - |
| ASHUN3_CRIGR | 3 | 17.11 | 144.29 | 3 | 10.03 | 38.62 | 3 | 11.98 | 204.78 | 2 | 17.11 | 174.41 | 2 | 17.11 | 127.87 | - | - | - |
| BAIP2_CRIGR | 2 | 10.03 | 43.56 | 2 | 10.03 | 38.62 | 3 | 11.98 | 104.61 | 2 | 17.11 | 174.41 | 2 | 17.11 | 127.87 | - | - | - |
| BASI_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| BST2_CRIGR | 2 | 8.63 | 203.06 | 2 | 12.81 | 117.32 | 2 | 15.66 | 139.54 | 3 | 19.68 | 176.82 | 2 | 4.22 | 33.27 | - | - | - |
| CUSX9_CRIGR | 4 | 9.39 | 230.61 | 7 | 16.59 | 230.95 | 5 | 9.36 | 91.61 | 3 | 13.27 | 181.48 | 4 | 7.96 | 220.63 | 2 | 9.36 | 113.94 |
| CD44_CRIGR | 3 | 9.39 | 230.61 | 4 | 7.18 | 171.21 | 3 | 11.28 | 167.41 | 6 | 9.39 | 278.51 | 2 | 10.22 | 352.51 | 2 | 6.63 | 132.69 |
| CH60_CRIGR | 2 | 13.64 | 146.57 | 4 | 14.66 | 256.41 | - | - | - | 3 | 13.96 | 227.1 | 2 | 6.98 | 56.86 | - | - | - |
| COPE_CRIGR | 4 | 12.55 | 281.52 | 5 | 27.92 | 179.18 | 3 | 17.21 | 198.11 | 4 | 16.88 | 127.86 | 6 | 16.88 | 127.86 | 6 | 25.32 | 388.63 |
| EF1A1_CRIGR | 2 | 12.55 | 281.52 | 8 | 21 | 389.23 | 5 | 14.5 | 255.71 | 3 | 15.58 | 319.91 | 8 | 25.11 | 428.55 | 7 | 21.21 | 172.21 |
| EP2_CRIGR | - | - | - | - | 5.01 | 31.96 | 2 | 13.77 | 55.81 | - | - | - | - | - | - | - | - | - |
| F7J0L1_CRIGR | - | - | - | - | - | - | 2 | 11.29 | 95.82 | - | - | - | - | - | - | - | - | - |
| F7J0L2_CRIGR | 2 | 9.45 | 75.69 | 4 | 13.93 | 178.57 | 3 | 11.29 | 95.82 | - | - | - | - | - | - | - | - | - |
| F7J0L3_CRIGR | 2 | 8.7 | 88.63 | 3 | 6.6 | 101.69 | - | - | - | 2 | 7.41 | 90.02 | 3 | 10.45 | 99.17 | 2 | 4.98 | 80.44 |
| FXR1_CRIGR | 2 | 8.7 | 88.63 | 3 | 6.6 | 101.69 | - | - | - | 2 | 7.41 | 90.02 | 3 | 10.45 | 99.17 | 2 | 4.98 | 80.44 |
| GGR93_CRIGR | - | - | - | - | 6.83 | 106.52 | - | - | - | - | - | - | - | - | - | - | - | - |
| GGR95_CRIGR | - | - | - | - | 6.83 | 106.52 | - | - | - | - | - | - | - | - | - | - | - | - |
| GGRB9_CRIGR | - | - | - | - | 6.83 | 106.52 | - | - | - | - | - | - | - | - | - | - | - | - |
| GGRD7_CRIGR | 5 | 5.95 | 258.96 | 6 | 5.95 | 363.43 | 2 | 1.92 | 70.03 | 2 | 1.46 | 81.49 | - | - | - | - | - | - |
| GGRE1_CRIGR | 5 | 20.92 | 201.66 | 2 | 12.32 | 69.28 | 7 | 7.91 | 509.38 | 7 | 7.47 | 369.98 | 7 | 7.33 | 375.47 | 7 | 9.51 | 313.74 |
| GGRE5_CRIGR | 5 | 2.3 | 129.85 | 2 | 12.32 | 69.28 | 3 | 18.62 | 124.3 | 2 | 18.91 | 184.7 | 2 | 12.31 | 118.82 | 2 | 19.49 | 76.89 |
| GGRH9_CRIGR | 3 | 7.84 | 275.02 | 3 | 5.78 | 114.41 | 3 | 4.8 | 158.63 | 3 | 3.62 | 160.98 | 8 | 30.09 | 353.79 | 7 | 30.66 | 447.21 |
| GGRI6_CRIGR | 6 | 16.49 | 142.47 | 3 | 5.78 | 114.41 | 3 | 4.8 | 158.63 | - | - | - | 3 | 2.13 | 78.6 | 2 | 2.13 | 78.6 |
| GGRX2_CRIGR | 3 | 3.49 | 103.56 | 5 | 9.24 | 392.26 | 3 | 20.21 | 204.13 | 3 | 4.66 | 65.17 | - | - | - | 2 | 13.83 | 197.24 |
| GGSN1_CRIGR | 3 | 16.49 | 142.47 | 4 | 8.12 | 108.07 | 4 | 7.42 | 108.07 | 3 | 16.49 | 152.46 | 9 | 16.6 | 391.17 | 2 | 13.83 | 197.24 |
| GGSN4_CRIGR | 6 | 14.2 | 456.73 | 6 | 15.26 | 608.52 | 4 | 13.44 | 322.42 | 7 | 16.62 | 608.03 | 4 | 13.44 | 564.24 | 4 | 8.67 | 150.63 |
| GGSM1_CRIGR | 2 | 7.63 | 134.71 | 2 | 7.63 | 210.36 | 6 | 7.63 | 109.89 | 7 | 10.08 | 196.5 | 5 | 10.35 | 257.73 | 4 | 10.12 | 355.70 |
| GGSM4_CRIGR | 4 | 10.17 | 299.27 | 2 | 5.15 | 226.55 | 6 | 11.62 | 433.58 | 3 | 13.08 | 334.13 | 3 | 10.35 | 257.73 | 2 | 7.63 | 36.95 |
| GGSN8_CRIGR | 2 | 2.33 | 119.44 | 2 | 3.13 | 58.06 | 4 | 4.15 | 290.4 | 5 | 13.08 | 334.13 | 5 | 10.04 | 275.01 | 2 | 4.76 | 207.42 |
| GGSN8_CRIGR | - | - | - | - | 3.76 | 123.15 | 2 | 3.76 | 123.15 | - | - | - | - | - | - | - | - | - |
| GGSP0_CRIGR | 2 | 16.18 | 318.22 | 2 | 6.25 | 40.65 | 2 | 3.76 | 123.15 | - | - | - | - | - | - | - | - | - |
| GGSW3_CRIGR | 9 | 15.61 | 223.6 | 16 | 28.7 | 566.69 | 16 | 24.91 | 642.14 | 14 | 6.46 | 42.73 | 11 | 20.1 | 480.23 | 15 | 24.27 | 664.3 |
| GGT05_CRIGR | 3 | 15.65 | 266 | 2 | 9.76 | 105.68 | 2 | 11.71 | 155.66 | 2 | 9.76 | 108.04 | 2 | 9.76 | 161.58 | 2 | 9.76 | 136.94 |
| GGT06_CRIGR | 3 | 15.65 | 266 | 3 | 15.65 | 170.88 | 3 | 15.65 | 170.88 | 2 | 10.87 | 159.9 | 2 | 10.87 | 136.35 | 2 | 10.87 | 176.76 |
| GGT52_CRIGR | 3 | 1.38 | 63.48 | 2 | 6.53 | 76.91 | 2 | 6.53 | 100.4 | 3 | 10.2 | 80.84 | 3 | 2.24 | 55.14 | - | - | - |
| GGTA2_CRIGR | 3 | 10.2 | 109.06 | 2 | 6.53 | 76.91 | 2 | 3.2 | 127.39 | 2 | 4.45 | 91.21 | 2 | 3.54 | 32.58 | 2 | 3.2 | 81.39 |
| GGT15_CRIGR | 2 | 2.17 | 71.1 | 3 | 6.7 | 136.56 | 2 | 4.29 | 55.28 | 2 | 5.06 | 141.6 | 2 | 3.57 | 108.85 | 2 | 3.2 | 81.39 |
| GGTM5_CRIGR | - | - | - | - | 18.25 | 311.54 | 4 | 6.85 | 71.04 | 3 | 17.87 | 185.37 | 4 | 22.43 | 215.27 | 3 | 15.97 | 210.66 |
| GGTN7_CRIGR | 2 | 12.17 | 233.32 | 3 | 18.25 | 311.54 | 2 | 6.85 | 71.04 | - | - | - | - | - | - | - | - | - |
| GGTS6_CRIGR | - | - | - | - | 32.65 | 566.03 | 2 | 37.11 | 799.72 | 2 | 5.57 | 83.99 | - | - | - | - | - | - |
| GGTV9_CRIGR | - | - | - | - | 14.79 | 1436.85 | 11 | 12.2 | 1280.83 | 12 | 40.21 | 741.61 | 12 | 39.52 | 798.31 | 12 | 38.83 | 818.78 |
| GGTX5_CRIGR | 10 | 33.68 | 537.85 | 8 | 32.65 | 566.03 | 11 | 37.11 | 799.72 | 12 | 40.21 | 741.61 | 12 | 39.52 | 798.31 | 12 | 38.83 | 818.78 |
| GGU30_CRIGR | 18 | 9.86 | 806.93 | 26 | 23.9 | 306.95 | 23 | 12.2 | 1280.83 | 24 | 12.93 | 1327.75 | 26 | 15.3 | 1808.13 | 26 | 15.96 | 1555.02 |
| GGU75_CRIGR | 5 | 19.12 | 317.15 | 6 | 5.32 | 161.51 | 6 | 24.26 | 331.49 | 6 | 30.15 | 527.63 | 6 | 30.88 | 273 | 7 | 33.09 | 310.26 |
| GGU82_CRIGR | 3 | 7.64 | 146.63 | 2 | 5.32 | 161.51 | 2 | 5.32 | 152.42 | 3 | 7.64 | 169.4 | 3 | 7.64 | 322.15 | 2 | 5.32 | 191.28 |
| GGUB3_CRIGR | - | - | - | - | 6.66 | 78.3 | - | - | - | - | - | - | - | - | - | - | - | - |
| GGUH8_CRIGR | 3 | 3.09 | 161.79 | 3 | 1.33 | 97.73 | 2 | 1.33 | 87.22 | 3 | 3.38 | 93.06 | 5 | 5.68 | 300.4 | 2 | 1.97 | 128.49 |
| GGUM5_CRIGR | 3 | 6.46 | 227.22 | 4 | 4.74 | 368.91 | 5 | 4.96 | 140.77 | 3 | 3.38 | 93.06 | 5 | 5.68 | 300.4 | 6 | 7.33 | 313.17 |
| GGU09_CRIGR | 3 | 10.11 | 220.17 | 4 | 6.33 | 231.88 | 4 | 6.33 | 278.07 | 5 | 8.1 | 294.28 | 4 | 8.23 | 279.94 | 4 | 10.63 | 157.57 |
| GGU36_CRIGR | - | - | - | - | 6.33 | 231.88 | 4 | 7.07 | 169.42 | 2 | 5.3 | 177.49 | 2 | 5.3 | 177.49 | 4 | 12.63 | 261.25 |
| GGU52_CRIGR | 3 | 52.78 | 318.71 | - | - | - | 3 | 41.67 | 275.45 | 3 | 3.72 | 99.47 | - | - | - | - | - | - |
| GGU82_CRIGR | 3 | 4.35 | 137.06 | 2 | 3.65 | 99.42 | 2 | 3.18 | 147.04 | 3 | 4.94 | 230.58 | 2 | 3.65 | 127.28 | 4 | 6.24 | 243.08 |
| GGUX2_CRIGR | 3 | 4.37 | 137.06 | 2 | 3.65 | 99.42 | 2 | 3.18 | 147.04 | 3 | 4.94 | 230.58 | 2 | 3.65 | 127.28 | 4 | 6.24 | 243.08 |
| GGUY5_CRIGR | 2 | 4.37 | 137.06 | 2 | 3.65 | 99.42 | 2 | 3.18 | 147.04 | 3 | 4.94 | 230.58 | 2 | 3.65 | 127.28 | 4 | 6.24 | 243.08 |
| GGV27_CRIGR | 2 | 7.1 | 92.57 | - | - | - | - | - | - | 2 | 6.22 | 49.6 | - | - | - | 2 | 14.4 | 44.15 |
| GGW47_CRIGR | 7 | 14.39 | 237.35 | 6 | 13.65 | 344.69 | 4 | 10.7 | 226.59 | 5 | 13.65 | 277.36 | 7 | 16.42 | 287.68 | 7 | 15.13 | 365.7 |
| GGW85_CRIGR | - | - | - | - | 13.65 | 344.69 | 4 | 10.7 | 226.59 | 5 | 13.65 | 277.36 | 7 | 16.42 | 287.68 | 7 | 15.13 | 365.7 |
| GGWA8_CRIGR | - | - | - | - | 13.65 | 344.69 | 4 | 10.7 | 226.59 | 5 | 13.65 | 277.36 | 7 | 16.42 | 287.68 | 7 | 15.13 | 365.7 |
| GGVB5_CRIGR | - | - | - | - | 13.65 | 344.69 | 4 | 10.7 | 226.59 | 5 | 13.65 | 277.36 | 7 | 16.42 | 287.68 | 7 | 15.13 | 365.7 |
| GGVD0_CRIGR | - | - | - | - | 13.65 | 344.69 | 4 | 10.7 | 226.59 | 5 | 13.65 | 277.36 | 7 | 16.42 | 287.68 | 7 | 15.13 | 365.7 |
| GGV05_CRIGR | 5 | 45.33 | 1355.17 | 5 | 42.67 | 1352.64 | 2 | 10.14 | 83.76 | - | - | - | - | - | - | - | - | - |
| GGV66_CRIGR | 3 | 6.52 | 208.23 | 3 | 4.5 | 160.86 | 6 | 49.33 | 2484.42 | 6 | 42.67 | 1514.49 | 5 | 42.67 | 1529.21 | 6 | 45.07 | 1893.79 |
| GGW67_CRIGR | 4 | 14.92 | 305.64 | 6 | 29.58 | 274.49 | 6 | 5.74 | 211.51 | 4 | 5.85 | 187.35 | 3 | 4.61 | 188.85 | 3 | 4.61 | 105.91 |
| GGVH8_CRIGR | 2 | 7.64 | 72.89 | 2 | 7.64 | 72.89 | 6 | 29.58 | 486.49 | 6 | 25.65 | 389.79 | 6 | 28.27 | 269.45 | 6 | 23.3 | 378.57 |
| GGVL0_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGWL7_CRIGR | 2 | 7.47 | 79.22 | 3 | 23.53 | 61.98 | 2 | 23.53 | 61.98 | 2 | 5.56 | 99.21 | 2 | 5.56 | 99.21 | 2 | 5.56 | 99.21 |
| GGWL7_CRIGR | 2 | 7.47 | 79.22 | 3 | 12.44 | 157.9 | 3 | 12.44 | 157.9 | 2 | 32.68 | 52.26 | 2 | 32.68 | 52.26 | 2 | 7.47 | 129.4 |

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Table S-6 – Continued

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|-------------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|
| GGW01.CRIGR | - | - | - | - | - | - | - | 2.8 | 50.76 | - | - | - | - | - | - | - | - | - |
| GGW07.CRIGR | 2 | 8.66 | 81.01 | 2 | 11.66 | 85.6 | 2 | 8.59 | 71.23 | - | - | - | - | 18.71 | 141.84 | - | - | - |
| GGW10.CRIGR | 4 | 16.87 | 227.5 | 3 | 12.7 | 173.69 | 2 | 8.59 | 71.23 | 3 | 8.59 | 141.84 | 2 | 9.92 | 215.11 | 2 | 8.59 | 66.31 |
| GGW14.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGW16.CRIGR | 2 | 7.54 | 118.34 | 2 | 9.84 | 121.81 | 2 | - | - | 3 | - | - | 3 | - | - | - | - | - |
| GGW00.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | 1.46 | 167.77 | - | - | - |
| GGW01.CRIGR | 2 | 5.56 | 166.23 | - | - | - | - | - | - | 2 | - | - | - | - | - | - | - | - |
| GGW06.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGW01.CRIGR | 3 | 2.84 | 234.51 | 2 | 1.74 | 194.04 | 4 | 3.58 | 355.14 | 4 | 3.58 | 355.14 | 2 | 2.65 | 196.07 | 2 | 7.28 | 60.65 |
| GGX17.CRIGR | 7 | 19.44 | 471.22 | 10 | 18.32 | 395.45 | 7 | 19.63 | 669.78 | 9 | 19.63 | 669.78 | 5 | 20.56 | 431.39 | 5 | 14.77 | 341.32 |
| GGX54.CRIGR | 2 | 20.45 | 42.69 | 2 | 3.85 | 48.42 | 2 | 3.51 | 66.11 | 2 | 3.51 | 66.11 | 2 | - | - | 2 | 2.95 | 56.04 |
| GGX57.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGX59.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGX07.CRIGR | 2 | 4.96 | 206.07 | 2 | 5.33 | 247.48 | 3 | 6.17 | 210.88 | - | - | - | 3 | 2.65 | 196.07 | 4 | 2.92 | 214.32 |
| GGX02.CRIGR | 2 | 7.47 | 272.3 | 10 | 8.13 | 604.3 | 12 | 11.78 | 686.57 | - | - | - | 2 | 4.44 | 203.59 | 4 | 2.92 | 214.32 |
| GGX03.CRIGR | 9 | 7.19 | 378.15 | 4 | 4.76 | 101.33 | 5 | 26.21 | 348.56 | 6 | 30.34 | 330.86 | 2 | 4.96 | 203.59 | 2 | 7.26 | 175.86 |
| GGX18.CRIGR | 5 | 30.34 | 280.89 | 3 | 21.38 | 181.35 | 3 | 11.33 | 210.6 | 6 | 30.34 | 330.86 | 2 | 4.98 | 74.37 | 3 | 6.52 | 66.05 |
| GGX03.CRIGR | 3 | 16.18 | 194.55 | 3 | 15.53 | 239.9 | 3 | 3.73 | 41.9 | 2 | 7.77 | 228.78 | 9 | 7.55 | 329.22 | 8 | 6.52 | 378.68 |
| GGX04.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGX07.CRIGR | 11 | 11.44 | 489.16 | 10 | 12.44 | 355.53 | 3 | 2.4 | 143.42 | 12 | 14.68 | 491.31 | 10 | 10.61 | 371.67 | 7 | 9.87 | 422.95 |
| GGY17.CRIGR | 4 | 28.8 | 173.2 | 2 | 21.2 | 86.63 | 3 | 23.37 | 141.27 | 6 | 46.2 | 233.01 | 3 | 19.02 | 160.01 | 2 | 12.62 | 165.07 |
| GGY22.CRIGR | 2 | 21.2 | 86.63 | 3 | 23.37 | 141.27 | 6 | 46.2 | 233.01 | 3 | 19.02 | 160.01 | 2 | 12.62 | 165.07 | 7 | 9.87 | 422.95 |
| GGY25.CRIGR | 34 | 27.18 | 2967.23 | 30 | 30.41 | 3294.51 | 32 | 26.72 | 2818.5 | 40 | 26.72 | 2818.5 | 35 | 32.89 | 3808.86 | 35 | 27.28 | 2569.93 |
| GGY44.CRIGR | 4 | 22.07 | 242.9 | 9 | 32.12 | 299.53 | 6 | 32.41 | 309.5 | 6 | 32.41 | 309.5 | 4 | 25.82 | 2810.06 | 3 | 27.52 | 378.43 |
| GGY55.CRIGR | 2 | 1.87 | 135.83 | 9 | 7.36 | 167.87 | 2 | 3.12 | 95.65 | 2 | 3.12 | 95.65 | 2 | 3.12 | 95.65 | 2 | 5.36 | 74.25 |
| GGY70.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGY75.CRIGR | 10 | 37.33 | 612.81 | 11 | 34.26 | 529.94 | 11 | 40.67 | 325.83 | 8 | 31.2 | 468.04 | 7 | 28.69 | 485.34 | 7 | 28.69 | 406.93 |
| GGY11.CRIGR | 3 | 3.87 | 82.86 | 3 | 10.02 | 131.66 | 3 | 10.02 | 131.66 | 3 | 10.02 | 131.66 | 3 | 6.83 | 59.81 | 3 | 6.83 | 59.81 |
| GGY15.CRIGR | 3 | 21.51 | 129.07 | 2 | 2.74 | 48.7 | 2 | 2.1 | 92.12 | 2 | 2.58 | 83.06 | 4 | 4.75 | 84.63 | 2 | 13.96 | 294.97 |
| GGYK8.CRIGR | 4 | 24.52 | 407.65 | 7 | 34.13 | 623.3 | 7 | 18.49 | 229.32 | 3 | 19.25 | 194.84 | 3 | 19.25 | 194.84 | 2 | 38.46 | 663.83 |
| GGYV8.CRIGR | 5 | 21.92 | 99.52 | 5 | 21.92 | 99.52 | 2 | 9.25 | 57.7 | 2 | 9.25 | 57.7 | 2 | 23.56 | 525.29 | 7 | 38.46 | 663.83 |
| GGYX1.CRIGR | 2 | 8.74 | 259.51 | 2 | 14.16 | 155.79 | 2 | 14.16 | 130.23 | 2 | 8.74 | 149.04 | 2 | 14.16 | 180.45 | 2 | 14.16 | 88.83 |
| GGYX2.CRIGR | 4 | 23.3 | 101.74 | 4 | 23.3 | 101.74 | 4 | 8.48 | 279.43 | 2 | 4.88 | 217.34 | 2 | 4.88 | 217.34 | 4 | 8.23 | 183.18 |
| GGYX4.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGYZ1.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGYZ1.CRIGR | 2 | 11.69 | 139.83 | 3 | 7.71 | 233.45 | 3 | 7.71 | 233.45 | 2 | 2.93 | 145.67 | 2 | 2.93 | 145.67 | 2 | 4.42 | 104.72 |
| GGZ17.CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GGZ54.CRIGR | 5 | 10.77 | 410.79 | 5 | 7.67 | 254.76 | 6 | 10.4 | 348.67 | 4 | 9.41 | 175.43 | 6 | 10.52 | 274.01 | 2 | 24.24 | 160.65 |
| GGZ72.CRIGR | 2 | 3.47 | 95.03 | 2 | 3.98 | 126.64 | 2 | 8.48 | 279.43 | 2 | 4.277 | 126.77 | 2 | 4.277 | 126.77 | 6 | 4.23 | 74.57 |
| GGZ81.CRIGR | 2 | 27.73 | 89.59 | 2 | 1.84 | 117.04 | 2 | 8.52 | 145.53 | 2 | 13.46 | 129.95 | 3 | 2.35 | 93.58 | 3 | 2.35 | 126.14 |
| GGZ83.CRIGR | 3 | 7.59 | 149.73 | 3 | 12.69 | 156.77 | 3 | 8.52 | 145.53 | 2 | 13.46 | 129.95 | 2 | 14.24 | 506.9 | 5 | 10.28 | 491.06 |
| GGZ05.CRIGR | 3 | 6.8 | 288.87 | 3 | 7.12 | 136.9 | 3 | 6.8 | 371.24 | 2 | 11.39 | 606.85 | 6 | 14.24 | 506.9 | 5 | 10.28 | 491.06 |
| GGZH5.CRIGR | 18 | 19.39 | 1171.19 | 10 | 8.55 | 784.54 | 26 | 27.15 | 1875.78 | 18 | 17.89 | 1999.87 | 26 | 25.46 | 1543.41 | 18 | 17.17 | 1125.48 |
| GGZH6.CRIGR | 2 | 4.93 | 105.67 | 2 | 5.37 | 318.04 | 2 | 7.46 | 264.57 | 3 | 5.37 | 244.66 | 3 | 7.76 | 215.04 | 3 | 31.91 | 218.67 |
| GGZ16.CRIGR | 2 | 21.99 | 168.75 | 2 | 6.95 | 89.01 | 2 | 4.01 | 110.06 | 2 | 21.99 | 113.67 | 2 | 6.95 | 101.05 | 3 | 31.91 | 218.67 |
| GGZ08.CRIGR | 2 | 6.92 | 261.15 | 2 | 6.92 | 228.05 | 2 | 4.01 | 110.06 | 2 | 4.01 | 110.06 | 2 | 6.95 | 101.05 | 2 | 6.95 | 101.05 |
| GGZ08.CRIGR | 2 | 16.7 | 331.6 | 2 | 12.11 | 327.72 | 3 | 9.81 | 214.47 | 2 | 4.01 | 110.06 | 2 | 6.95 | 101.05 | 2 | 6.95 | 101.05 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 6.47 | 185.78 | 4 | 12.11 | 248.52 | 2 | 14.2 | 227.7 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9 | 3 | 4.65 | 148.76 |
| GGZ19.CRIGR | 2 | 3.19 | 136.13 | 2 | 3.19 | 150.24 | 2 | 3.19 | 206.63 | 2 | 3.19 | 217.14 | 3 | 4.79 | 198.9</ | | | |

Table S-6 – Continued

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|--------------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|--------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|
| GSH193_CRIGR | - | - | - | - | - | 72.79 | - | - | - | 2 | 7.67 | 63.91 | - | - | - | 2 | 6.24 | 66.64 |
| GSH194_CRIGR | 2 | 19.1 | 75.36 | 3 | 29.21 | 96.31 | - | - | - | - | - | - | - | - | - | - | 29.21 | 269.21 |
| GSH196_CRIGR | 8 | 36.27 | 439.63 | 7 | 35.78 | 355.21 | 9 | 42.16 | 568.62 | 8 | 38.73 | 381.98 | 4 | 31.58 | 444.54 | 4 | 29.21 | 407.46 |
| GSH197_CRIGR | 2 | 8.26 | 37.57 | - | - | - | 3 | 13.5 | 142.55 | 3 | 9.14 | 54.52 | 3 | 12.98 | 450.41 | 8 | 38.73 | 407.46 |
| GSH198_CRIGR | 4 | 22.09 | 222.01 | - | - | - | 2 | 9.21 | 75.85 | 2 | - | - | 2 | - | 116.71 | 2 | 10.12 | 101.27 |
| GSH199_CRIGR | - | - | - | - | - | - | 2 | 15.57 | 115.57 | - | - | - | 2 | - | - | 2 | 9.21 | 177.82 |
| GSH200_CRIGR | - | - | - | - | - | - | 2 | 15.73 | 219.42 | - | - | - | - | - | - | - | - | - |
| GSH201_CRIGR | 2 | 6.69 | 52.72 | - | - | 99.83 | 2 | 8.55 | 46.37 | 3 | 11.15 | 71.38 | - | - | - | - | - | - |
| GSH202_CRIGR | 5 | 31.87 | 272.03 | 4 | 27.5 | 238.62 | 4 | 27.5 | 177.75 | 5 | 20.63 | 166.91 | 5 | 25 | 133.32 | 4 | 28.13 | 179.62 |
| GSH203_CRIGR | 3 | 22.99 | 163.85 | 5 | 17.43 | 186.13 | 2 | 15.71 | 144.8 | 2 | 11.14 | 73.42 | 2 | 14 | 50.41 | 4 | 9.71 | 46.89 |
| GSH204_CRIGR | 3 | 21.53 | 365.79 | 5 | 31.02 | 398.43 | 5 | 31.02 | 398.43 | 4 | 17.88 | 330.65 | 6 | 21.17 | 371.9 | 6 | 32.12 | 236.49 |
| GSH205_CRIGR | 2 | 5.19 | 179.86 | 10 | 16.89 | 669.88 | 2 | 5.63 | 264.47 | 5 | 13.13 | 462.83 | 7 | 10.49 | 263.87 | 7 | 11.59 | 315.56 |
| GSH206_CRIGR | 2 | - | - | 2 | 6.2 | 73.1 | 2 | 73.1 | 121.29 | - | - | - | 2 | - | - | 2 | 6.2 | 59.63 |
| GSH207_CRIGR | 2 | 1.75 | - | 3 | 3.09 | 189.76 | 4 | 6.48 | 148.71 | - | - | - | - | - | - | - | - | - |
| GSH208_CRIGR | - | - | - | 2 | 4.96 | 75.91 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH209_CRIGR | 3 | 17.54 | - | 2 | 13.74 | 68.16 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH210_CRIGR | 2 | 2.43 | 42.47 | 3 | 3.55 | 127.1 | 2 | 3.55 | 127.1 | - | - | - | - | - | - | - | - | - |
| GSH211_CRIGR | 2 | - | - | 3 | 8.87 | 110.92 | 2 | 12.41 | 84.27 | 2 | 8.87 | 96.3 | 2 | 8.87 | 111.43 | 3 | 14.18 | 76.26 |
| GSH212_CRIGR | - | - | - | 3 | 3.46 | 44.63 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH213_CRIGR | - | - | - | 2 | 3.21 | 100.03 | 2 | 2.97 | 55.04 | 2 | 25.38 | 358.16 | 2 | 3.33 | 50.94 | 3 | 7.38 | 45.16 |
| GSH214_CRIGR | 5 | 20.05 | 289.26 | 6 | 28.68 | 334.75 | 2 | 9.39 | 180.01 | 6 | 40.48 | 532.89 | 4 | 18.02 | 427.5 | 4 | 17.26 | 108.55 |
| GSH215_CRIGR | - | - | - | 2 | 34.13 | 871.1 | 4 | - | - | 4 | 6.05 | 175.03 | 5 | 8.96 | 163.72 | 5 | 39.68 | 1372.33 |
| GSH216_CRIGR | - | - | - | 2 | 3.86 | 53.16 | - | - | - | 2 | 4.21 | 51.19 | 2 | 8.96 | 163.72 | 2 | 3.86 | 75.46 |
| GSH217_CRIGR | 2 | 6.05 | 92.52 | 3 | 11.32 | 212.09 | 2 | 11.32 | 212.09 | 2 | 6.05 | 175.03 | 3 | 11.05 | 218.74 | 6 | 21.05 | 315.6 |
| GSH218_CRIGR | 58 | 16.75 | 3422.41 | 70 | 21.99 | 4130.94 | 52 | 25.47 | 142.25 | 71 | 14.35 | 2848.78 | 61 | 21.06 | 3844.64 | 61 | 18.75 | 3992.38 |
| GSH219_CRIGR | 2 | 25.47 | 78.22 | 2 | 25.47 | 104.5 | 2 | 25.47 | 142.25 | 2 | 25.47 | 229.46 | 2 | 25.47 | 208.91 | 2 | 25.47 | 208.91 |
| GSH220_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH221_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH222_CRIGR | 3 | 7.24 | 121.21 | 3 | 6.71 | 115.91 | 3 | 11.5 | 106.58 | 2 | 7 | 144.06 | 2 | 2.19 | 120.3 | - | - | - |
| GSH223_CRIGR | 3 | 4.92 | 281.29 | 5 | 8.57 | 172 | 2 | 23.19 | 146.52 | 3 | 7.24 | 120.74 | 3 | 9.36 | 175.25 | 3 | 9.36 | 175.25 |
| GSH224_CRIGR | 3 | 20.87 | 257.81 | 3 | 11.65 | 155.21 | 3 | 5.26 | 243.13 | 5 | 8.74 | 223.34 | 6 | 10.1 | 418.47 | 6 | 10.27 | 365.22 |
| GSH225_CRIGR | 2 | 4.11 | 77.02 | 4 | 8.1 | 280.7 | 3 | 6.68 | 231.03 | 3 | 16.99 | 249.55 | 3 | 16.99 | 198.36 | 3 | 16.99 | 262.85 |
| GSH226_CRIGR | 14 | 40.68 | 750.36 | 13 | 40.89 | 970.66 | 11 | 37.71 | 883.37 | 12 | 40.04 | 976.16 | 10 | 35.17 | 1220.73 | 8 | 31.14 | 898.25 |
| GSH227_CRIGR | - | - | - | 2 | 4.85 | 93.17 | - | - | - | 2 | 4.53 | 69.19 | 2 | 5.5 | 57.07 | 2 | 2.38 | 43.25 |
| GSH228_CRIGR | 2 | 18.01 | 111.6 | 2 | 18.01 | 98.53 | 3 | 18.01 | 97.67 | 2 | 18.01 | 81.29 | 2 | 18.01 | 70.1 | 2 | 18.01 | 40.51 |
| GSH229_CRIGR | 2 | 29.35 | 205.34 | - | - | - | 2 | 29.35 | 306.95 | 2 | 29.35 | 358.19 | 2 | 29.35 | 393.64 | 2 | 29.35 | 155.94 |
| GSH230_CRIGR | 3 | 19.71 | 115.45 | 3 | 17.39 | 274.65 | 2 | 19.71 | 239.45 | 2 | 29.35 | 358.19 | 2 | 29.35 | 393.64 | 2 | 29.35 | 245.87 |
| GSH231_CRIGR | 4 | 9.8 | 183.02 | 2 | 6.76 | 144.7 | 3 | 7.6 | 154.98 | 4 | 9.29 | 126.02 | 3 | 7.6 | 166.85 | 3 | 17.39 | 180.14 |
| GSH232_CRIGR | 3 | 7.52 | 145.06 | 3 | 7.26 | 89.05 | 2 | 5.8 | 59.11 | 4 | 9.08 | 89.52 | 3 | 7.39 | 38.64 | 3 | 7.26 | 111.2 |
| GSH233_CRIGR | - | - | - | 3 | 21.61 | 392.92 | 4 | 14.29 | 83.53 | 2 | 28.39 | 387.8 | 2 | 6.12 | 72.03 | 2 | 7.94 | 83.78 |
| GSH234_CRIGR | - | - | - | 3 | 18.93 | 272.47 | - | - | - | 2 | 16.56 | 210.54 | 2 | 21.89 | 236.23 | 3 | 29.24 | 349.95 |
| GSH235_CRIGR | 7 | 18.14 | 321.57 | 7 | 18.93 | 272.47 | 7 | 17.35 | 419.63 | 6 | 16.56 | 210.54 | 4 | 11.04 | 277.69 | 6 | 16.4 | 298.47 |
| GSH236_CRIGR | 4 | 14.95 | 194.74 | - | - | 184.85 | 5 | 20.25 | 243.05 | 2 | 20.25 | 243.05 | 2 | 23.89 | 126.66 | 2 | 12.15 | 193.78 |
| GSH237_CRIGR | 3 | 4.91 | 197.16 | 2 | 3.21 | 185.3 | 4 | 7.43 | 57.41 | 3 | 6.2 | 193.92 | 3 | 1.84 | 178.06 | 3 | 12.15 | 193.78 |
| GSH238_CRIGR | 3 | 24.64 | 613.77 | 2 | 17.87 | 526.24 | 3 | 5.07 | 201.19 | 4 | 26.09 | 681.15 | 2 | 3.21 | 109.69 | 2 | 2.78 | 109.73 |
| GSH239_CRIGR | 2 | 2.55 | 92.79 | 2 | 2.55 | 92.79 | 2 | 23.67 | 700.84 | 2 | 2.55 | 141.19 | 3 | 28.5 | 569.1 | 2 | 17.87 | 500.92 |
| GSH240_CRIGR | 2 | 16.77 | 186.94 | 4 | 23.79 | 335.26 | 3 | 17.42 | 162.73 | 4 | 12.33 | 162.73 | 4 | 23.35 | 249.71 | 2 | 2.55 | 238.56 |
| GSH241_CRIGR | 2 | 16.77 | 186.94 | 2 | 16.77 | 128.9 | 2 | 17.42 | 96.89 | 2 | 12.33 | 162.73 | 2 | 16.77 | 208.37 | 2 | 16.77 | 141.4 |
| GSH242_CRIGR | 9 | 6.18 | 345.38 | 14 | 10.14 | 570.67 | 10 | 7.5 | 468.4 | 11 | 8.5 | 469.11 | 9 | 6.76 | 347.28 | 10 | 8.29 | 405.22 |
| GSH243_CRIGR | 3 | 11.45 | 109.2 | 3 | 20 | 419.4 | 3 | 20 | 720.88 | 3 | 20 | 631.98 | 4 | 26.43 | 503.88 | 2 | 17.86 | 246.12 |
| GSH244_CRIGR | 2 | 50.65 | 89.45 | 3 | 11.54 | 78.04 | 3 | 9.76 | 73.45 | 2 | 50.65 | 81.9 | 2 | 50.65 | 81.9 | - | - | - |
| GSH245_CRIGR | 4 | 7.27 | 241.03 | 4 | 7.27 | 167.18 | 2 | 5.17 | 149.8 | 3 | 5.33 | 186.57 | 2 | 5.33 | 198.52 | 6 | 12.28 | 249.22 |
| GSH246_CRIGR | 2 | 9.29 | 115.19 | 2 | 1.63 | 62.6 | 3 | 9.76 | 73.45 | 3 | 13.02 | 69.1 | 3 | 5.33 | 198.52 | 6 | 12.28 | 249.22 |
| GSH247_CRIGR | 4 | 19.38 | 205.24 | 4 | 23.75 | 241.72 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH248_CRIGR | 2 | 7.03 | 66.4 | 3 | 10.33 | 151.46 | 3 | 18.75 | 187.27 | - | - | - | 3 | 18.75 | 175.56 | 2 | 9.29 | 97.1 |
| GSH249_CRIGR | 3 | 2.44 | 236 | 3 | 2.56 | 204.61 | 3 | 2.5 | 272.69 | 3 | 8.56 | 198.73 | 2 | 7.05 | 160.09 | 2 | 9.38 | 71.75 |
| GSH250_CRIGR | 2 | 3.87 | 48.24 | 2 | 2.56 | 204.61 | 4 | 3.72 | 288.1 | 3 | 3.72 | 288.1 | 3 | 2.99 | 244.7 | 3 | 2.08 | 209.87 |
| GSH251_CRIGR | 5 | 10.15 | 239.91 | - | - | - | 2 | 4.93 | 164.07 | 2 | 5.08 | 73.01 | 4 | 8.09 | 170.44 | 2 | 4.53 | 94.69 |

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Table S-6 – Continued

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|--------------|-----------------|-----------------------|--------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|--------|-----------------|-----------------------|--------|-----------------|-----------------------|--------|
| GSH6U2_CRIGR | 2 | 5.52 | 36.18 | 5 | 17.23 | 238.19 | 5 | 18.57 | 202.96 | 7 | 24.83 | 332.7 | 5 | 17.9 | 137.16 | 4 | 19.24 | - |
| GSH6W0_CRIGR | 5 | 21.7 | 235.97 | - | - | - | - | - | - | 2 | 0.85 | 48.74 | - | - | - | - | - | - |
| GSH6X6_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 5.41 | 123.18 | - | - | - | - | - | - |
| GSH742_CRIGR | - | - | - | 2 | 2.05 | 68.12 | 2 | 2.11 | 84.24 | 2 | 2.05 | 61.77 | 2 | 3.6 | 187.62 | 2 | 2.11 | 68.35 |
| GSH761_CRIGR | 5 | 6.53 | 249.02 | 6 | 7.28 | 354.23 | 4 | 5.77 | 219.23 | 6 | 7.85 | 428.08 | 5 | 16.7 | 253 | 7 | 10.03 | 338.81 |
| GSH7A8_CRIGR | 4 | 17.8 | 112.64 | 4 | 18.02 | 308.37 | 4 | 15.82 | 358.4 | 5 | 15.16 | 349.7 | 3 | 21.76 | 315.71 | - | - | - |
| GSH7D4_CRIGR | 2 | 27.08 | 113.81 | 4 | 27.08 | 114.27 | 3 | 20.99 | 398.06 | 3 | 16.41 | 312.38 | 3 | 21.76 | 315.71 | 3 | 31.68 | 303.3 |
| GSH7H4_CRIGR | 3 | 16.41 | 331.16 | 4 | 25.95 | 115.63 | 3 | 7.21 | 232.26 | 4 | 9.61 | 183.53 | 4 | 10.35 | 203.44 | 4 | 10.35 | 254.01 |
| GSH7K5_CRIGR | 4 | 10.35 | 184.44 | 2 | 7.21 | 255.65 | 3 | 7.81 | 126.74 | 3 | 6.25 | 127.3 | 3 | 8.79 | 130.94 | - | - | - |
| GSH7M8_CRIGR | 3 | 8.79 | 167.59 | 2 | 5.86 | 119.41 | 3 | 7.81 | 126.74 | 3 | 6.25 | 127.3 | 3 | 8.79 | 130.94 | - | - | - |
| GSH7T9_CRIGR | 2 | 15.33 | 171.29 | 2 | 15.33 | 124.36 | 3 | 24.9 | 160.28 | 2 | 15.33 | 318.25 | 3 | 25.29 | 242.49 | 2 | 0.84 | 217.51 |
| GSH7U0_CRIGR | 2 | 10.05 | 428.2 | 10 | 11.93 | 575.38 | 3 | 3.65 | 150.42 | 3 | 3.65 | 150.42 | 2 | 2.11 | 140.48 | 2 | 2.11 | 140.48 |
| GSH7Y0_CRIGR | 9 | 9.12 | 97.45 | 2 | 4.15 | 44.55 | 12 | 13.97 | 638.57 | 14 | 15.6 | 642.33 | 11 | 14.05 | 751.83 | 18 | 19.85 | 955.17 |
| GSH830_CRIGR | 2 | 16.57 | 226.02 | 2 | 12.43 | 196.17 | 2 | 3.25 | 83.96 | 2 | 2.58 | 44.9 | 2 | 2.58 | 44.9 | 2 | 4.15 | 60.04 |
| GSH8B8_CRIGR | 4 | 22.8 | 76.37 | 2 | 18.65 | 76.08 | 2 | 10.83 | 132.13 | 2 | 10.83 | 124.78 | 3 | 16.24 | 54.44 | 2 | 6.84 | 69.14 |
| GSH8D0_CRIGR | 3 | 30.77 | 55 | - | - | - | 2 | 18.65 | 117.99 | 3 | 15.68 | 164.84 | 2 | 18.65 | 65.7 | 2 | 18.65 | 394.66 |
| GSH8I3_CRIGR | 2 | 17.21 | 102.61 | 2 | 14.42 | 132.83 | - | - | - | 2 | 30.77 | 43.01 | - | - | - | 2 | 5.97 | 82.92 |
| GSH8K3_CRIGR | - | - | - | - | - | - | 2 | 14.42 | 57.07 | 3 | 26.05 | 199.76 | - | - | - | 2 | 14.42 | 89.15 |
| GSH8L7_CRIGR | - | - | - | - | - | - | 2 | 12.24 | 269.55 | - | - | - | - | - | - | 3 | 11.54 | 177.73 |
| GSH8N3_CRIGR | - | - | - | - | - | - | 2 | 5.24 | 89.4 | 3 | 5.45 | 64.83 | - | - | - | - | - | - |
| GSH8N4_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 3.56 | 46.67 | - | - | - | - | - | - |
| GSH8P7_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 0.57 | 16.59 | - | - | - | - | - | - |
| GSH8Y0_CRIGR | 8 | 26.39 | 945.27 | 6 | 22.77 | 1050.43 | 9 | 17.72 | 611.67 | 5 | 17.59 | 716.17 | 6 | 20.57 | 912.03 | 7 | 24.58 | 966.92 |
| GSH910_CRIGR | 2 | 8.92 | 109.04 | 3 | 6.4 | 89.54 | 2 | 7.08 | 56.63 | 4 | 21.23 | 128.33 | 4 | 4.55 | 70.34 | 4 | 15.69 | 164.74 |
| GSH945_CRIGR | 2 | 4.49 | 118.03 | 2 | 4.55 | 59.15 | 2 | 4.55 | 59.15 | 2 | 4.55 | 59.15 | 2 | 4.55 | 59.15 | 2 | 4.55 | 59.15 |
| GSH973_CRIGR | 4 | 7.36 | 426.81 | 3 | 3.8 | 138.32 | 8 | 9.24 | 864.23 | 4 | 5.24 | 176.3 | 5 | 5.38 | 330.9 | 5 | 4.28 | 215.41 |
| GSH982_CRIGR | 7 | 7.36 | 426.81 | 8 | 9.02 | 671.03 | 9 | 9.24 | 864.23 | 8 | 8.49 | 711.5 | 10 | 10.89 | 688.86 | 4 | 4.21 | 325.73 |
| GSH9H7_CRIGR | - | - | - | 2 | 22.84 | 31.1 | 2 | 5.41 | 150.34 | - | - | - | 2 | 5.67 | 63.13 | 3 | 9.02 | 119.67 |
| GSH9I7_CRIGR | 3 | 24.49 | 155.07 | 3 | 25.17 | 111.81 | 3 | 26.53 | 230.19 | 3 | 25.17 | 220.71 | 2 | 19.73 | 95.35 | 3 | 24.49 | 192.65 |
| GSH9I8_CRIGR | 2 | 3.73 | 148.44 | 2 | 2.7 | 122.26 | 2 | 3.73 | 130.09 | 2 | 3.33 | 60.31 | 2 | 2.7 | 93.73 | 2 | 25.45 | 91.32 |
| GSH9J0_CRIGR | 2 | 31.58 | 85.37 | 2 | 3.22 | 33.68 | 2 | 3.22 | 60.01 | 2 | 4.42 | 57.94 | 2 | 3.12 | 58.54 | 2 | 3.12 | 58.54 |
| GSH9N7_CRIGR | 2 | 6.67 | 179.15 | 2 | 7.85 | 88.6 | 2 | 6.88 | 66.03 | 2 | 33.33 | 36.32 | - | - | - | - | - | - |
| GSH9O9_CRIGR | 3 | 18.06 | 51.22 | 2 | 6.8 | 93.71 | - | - | - | 4 | 6.88 | 66.03 | 4 | 9.14 | 73.46 | 2 | 4.52 | 38 |
| GSH9T1_CRIGR | 2 | 2.18 | 158.41 | 2 | 2.18 | 158.41 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH9Z1_CRIGR | 2 | 43.08 | 158.41 | 3 | 66.15 | 327.03 | 2 | 2.28 | 112.09 | 2 | 1.17 | 61.53 | 2 | 2.28 | 173.51 | 2 | 6.84 | 88.08 |
| GSHA11_CRIGR | 2 | 4.62 | 112.18 | 2 | 2.43 | 83 | 3 | 18.6 | 414.01 | 2 | 1.17 | 61.53 | 2 | 2.28 | 173.51 | 2 | 2.28 | 95.45 |
| GSHA69_CRIGR | 2 | 8.11 | 783.51 | 3 | 12.28 | 260.53 | 3 | 66.15 | 339.95 | 3 | 12.28 | 225.22 | 4 | 17.89 | 248.23 | 3 | 12.28 | 136.58 |
| GSHA82_CRIGR | 3 | 4.62 | 112.18 | 2 | 2.43 | 83 | 3 | 5.35 | 175.34 | 4 | 2.93 | 43.75 | 2 | 4.97 | 55.79 | 3 | 6.2 | 225.36 |
| GSHA83_CRIGR | 15 | 12.65 | 140.75 | 17 | 9.19 | 1001.89 | 21 | 11.43 | 1318.56 | 18 | 8.03 | 237.57 | 4 | 10.31 | 942.76 | 16 | 9.09 | 889.55 |
| GSHAQ2_CRIGR | 2 | 13.81 | 51.34 | 2 | 17.14 | 115.05 | - | - | - | - | - | - | 2 | 12.63 | 66.19 | 2 | 13.06 | 45.06 |
| GSHB27_CRIGR | 2 | 8.88 | 195.86 | 2 | 8.88 | 195.86 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSHB62_CRIGR | 4 | 8.74 | 230.88 | 3 | 6.55 | 116.25 | 2 | 5.34 | 88.75 | 3 | 9.54 | 182.01 | 4 | 11.64 | 180.22 | 4 | 11.64 | 188.87 |
| GSHB69_CRIGR | 3 | 14.63 | 256.33 | 5 | 17.07 | 202.61 | 4 | 18.82 | 304.36 | 3 | 10.42 | 178.33 | 3 | 9.92 | 243.88 | 2 | 6.39 | 118.42 |
| GSHB65_CRIGR | 3 | 11.95 | 253.33 | 3 | 19.71 | 455.09 | 4 | 16.56 | 343.87 | 3 | 12.89 | 194.64 | 2 | 16.98 | 326.56 | 3 | 14.63 | 269.98 |
| GSHB15_CRIGR | 3 | 3.75 | 72.31 | 8 | 29.01 | 447.77 | 3 | 19.45 | 520.57 | 4 | 9.43 | 202.3 | 4 | 5.86 | 94.8 | 3 | 11.95 | 178.61 |
| GSHB18_CRIGR | 2 | 25.6 | 361.45 | 2 | 14.78 | 316.43 | 3 | 19.45 | 520.57 | 5 | 18.77 | 394.28 | 6 | 26.96 | 567.32 | 6 | 19.45 | 604.03 |
| GSHB22_CRIGR | 2 | 11.69 | 49.87 | 3 | 14.78 | 316.43 | 2 | 16.35 | 287.76 | 2 | 16.35 | 287.76 | - | - | - | - | - | - |
| GSHB26_CRIGR | 2 | 8.71 | 42.98 | 2 | 8.71 | 26.11 | 2 | 4.61 | 67.51 | - | - | - | - | - | - | - | - | - |
| GSHB28_CRIGR | 2 | 43.1 | 286.1 | 3 | 43.1 | 266.05 | 3 | 43.1 | 279.82 | 3 | 16.39 | 369.08 | 3 | 21.64 | 619.82 | 2 | 8.71 | 37.52 |
| GSHC03_CRIGR | 3 | 12.84 | 419.58 | 2 | 10.95 | 191.07 | 2 | 9.12 | 79.9 | 3 | 43.1 | 233.8 | 3 | 43.1 | 301.04 | 3 | 12.79 | 715.16 |
| GSHC45_CRIGR | 8 | 19.9 | 344.37 | 8 | 29.37 | 369.92 | 7 | 26.94 | 440.97 | 8 | 31.55 | 540.71 | 6 | 23.79 | 307.8 | 4 | 9.46 | 387.64 |
| GSHC84_CRIGR | 2 | 4.03 | 49.66 | 2 | 1.68 | 74.05 | 2 | 3.16 | 146.22 | 9 | 31.55 | 540.71 | 6 | 23.79 | 307.8 | 8 | 29.37 | 415.66 |
| GSHCD3_CRIGR | 2 | 4.03 | 49.66 | 2 | 1.68 | 74.05 | 2 | 3.16 | 146.22 | 2 | 3.16 | 146.22 | 3 | 2.55 | 143.24 | 2 | 2.42 | 87.42 |
| GSHCD5_CRIGR | 2 | 4.03 | 49.66 | 2 | 1.68 | 74.05 | 2 | 3.16 | 146.22 | 2 | 3.16 | 146.22 | 3 | 2.55 | 143.24 | 2 | 2.42 | 87.42 |
| GSHC10_CRIGR | 2 | 16.89 | 246.49 | 2 | 5.68 | 137.83 | 2 | 8.64 | 39.99 | 2 | 5.68 | 98.05 | 2 | 19.74 | 438.13 | 2 | 5.68 | 135.23 |
| GSHCM4_CRIGR | 5 | 16.89 | 246.49 | 5 | 16.23 | 222.6 | 5 | 16.01 | 383.13 | 2 | 16.23 | 296.75 | 6 | 19.74 | 438.13 | 6 | 20.83 | 408.25 |
| GSHCS4_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSHCPL_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |

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Table S-6 – Continued

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|--------------|-----------------|-----------------------|--------|-----------------|-----------------------|--------|-----------------|-----------------------|---------|-----------------|-----------------------|--------|-----------------|-----------------------|---------|-----------------|-----------------------|--------|
| GSHCU8_CRIGR | 5 | 23.17 | 394.3 | 5 | 23.17 | 303.93 | 5 | 23.17 | 322.76 | 5 | 20.33 | 291.13 | 6 | 27.19 | 439.73 | 6 | 25.3 | 314.39 |
| GSHCW0_CRIGR | 2 | 3.38 | 99.53 | 2 | 18.5 | 341.17 | 7 | 23.23 | 239.83 | 4 | 4.74 | 149.32 | 2 | 4.74 | 170.3 | 2 | 15.94 | 315.58 |
| GSHCX7_CRIGR | 4 | 15.55 | 268.21 | 6 | 18.5 | 341.17 | 7 | 23.23 | 239.83 | 4 | 16.14 | 330.39 | 4 | 15.94 | 196.75 | 5 | 15.94 | 315.58 |
| GSHD22_CRIGR | - | - | - | - | - | - | - | - | - | - | 5.99 | 92.66 | - | - | - | - | - | - |
| GSHD44_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSHD51_CRIGR | 2 | 2.42 | 51.01 | - | - | - | - | 3.33 | 66.01 | 2 | 18.56 | 94.75 | 2 | 1.57 | 104.33 | 4 | 4.18 | 246.53 |
| GSHD63_CRIGR | 3 | 45.92 | 87.28 | - | - | - | - | - | - | 2 | 35.71 | 68.01 | 3 | 46.94 | 114.99 | 2 | 3.8 | 84.58 |
| GSHDA0_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 3.63 | 48.73 | 2 | 2.74 | 49.85 | - | - | - |
| GSHDD7_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 3.45 | 92.37 | 2 | 2.74 | 49.85 | - | - | - |
| GSHDR8_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 11.78 | 280.39 | 4 | 15.41 | 238.53 | - | - | - |
| GSHDT6_CRIGR | 4 | 15.11 | 251.17 | 5 | 15.12 | 382.96 | 2 | 7.33 | 67.84 | 2 | 11.78 | 280.39 | 4 | 15.41 | 238.53 | - | - | - |
| GSHD16_CRIGR | 4 | 15.12 | 169.04 | 4 | 20.73 | 180.19 | 5 | 17.32 | 355.79 | 2 | 9.02 | 260.86 | 4 | 11.46 | 168.12 | 4 | 17.82 | 564.35 |
| GSHD31_CRIGR | 3 | 6.35 | 148.1 | 3 | 20.73 | 180.19 | 5 | 17.32 | 355.79 | 3 | 6.35 | 154.77 | 3 | 4.29 | 129.92 | 4 | 11.95 | 208.32 |
| GSHD36_CRIGR | 3 | 9.13 | 78.94 | - | - | - | - | 6.35 | 72.31 | 3 | 6.35 | 154.77 | 2 | 4.29 | 129.92 | 3 | 7.2 | 70.39 |
| GSHD4_CRIGR | 3 | 9.29 | 71.85 | 2 | 5.95 | 47.94 | 2 | 3.33 | 66.01 | 2 | 18.56 | 94.75 | 2 | 7.06 | 46.53 | 3 | 11.9 | 198.27 |
| GSHD83_CRIGR | 13 | 20.49 | 890.4 | 10 | 15.86 | 815.13 | 17 | 26.98 | 1066.45 | 15 | 22.66 | 972.07 | 18 | 26.98 | 1244.07 | 18 | 27.81 | 938.35 |
| GSHD88_CRIGR | 3 | 5.93 | 64.34 | 4 | 10.43 | 152.37 | 8 | 3.89 | 293.66 | 2 | 3.89 | 62.39 | 2 | 4.7 | 81.62 | 5 | 11.66 | 315.88 |
| GSHD89_CRIGR | 2 | 5.14 | 95.06 | 2 | 5.14 | 109.07 | 3 | 7.82 | 122.89 | 4 | 9.88 | 108.39 | 3 | 7.2 | 115.11 | - | - | - |
| GSHD92_CRIGR | 2 | 14.39 | 87.99 | 2 | 7.76 | 201.13 | 2 | 14.39 | 109.71 | 2 | 14.39 | 93.93 | - | - | - | - | - | - |
| GSHD94_CRIGR | 2 | 11.74 | 126.3 | 2 | 11.74 | 107.3 | 2 | 11.74 | 107.3 | 5 | 64.29 | 356.65 | 3 | 51.79 | 162.05 | 2 | 13.64 | 107.64 |
| GSHD96_CRIGR | 2 | 64.29 | 338.6 | 2 | 52.68 | 246.56 | 5 | 64.29 | 451.76 | 5 | 64.29 | 356.65 | 3 | 51.79 | 162.05 | 4 | 11.74 | 67.4 |
| GSHD97_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 3.42 | 104.06 | 2 | 2.67 | 203.85 | 2 | 64.29 | 484.61 |
| GSHD98_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 3.42 | 104.06 | 2 | 2.67 | 203.85 | 2 | 64.29 | 484.61 |
| GSHD99_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 18.63 | 113.32 | 2 | 3.7 | 106.06 | 4 | 8.64 | 145.28 |
| GSHD00_CRIGR | - | - | - | - | - | - | - | - | - | 4 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD01_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD02_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD03_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD04_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD05_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD06_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD07_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD08_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD09_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD10_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD11_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD12_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD13_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD14_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD15_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD16_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD17_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD18_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD19_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD20_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD21_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD22_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD23_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD24_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD25_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD26_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD27_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD28_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD29_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD30_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD31_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD32_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD33_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD34_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD35_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD36_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD37_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD38_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD39_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD40_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD41_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD42_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD43_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD44_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD45_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD46_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD47_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD48_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD49_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD50_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD51_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD52_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD53_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD54_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD55_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD56_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD57_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD58_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD59_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD60_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD61_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD62_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD63_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD64_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD65_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD66_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD67_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD68_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD69_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD70_CRIGR | - | - | - | - | - | - | - | - | - | 3 | 8.05 | 137.11 | - | - | - | - | - | - |
| GSHD71_CRIGR | | | | | | | | | | | | | | | | | | |

Table S-6 – Continued

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|--------------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|
| GSHIA4_CRIGR | 2 | 25.68 | 87.37 | 2 | 25.68 | 73.91 | 2 | 25.68 | 181.69 | 2 | 25.68 | 109.5 | 2 | 25.68 | 90.34 | 2 | 15.52 | 83.22 |
| GSHIA9_CRIGR | 2 | 14.37 | 75.51 | 2 | 14.37 | 85.98 | 2 | 15.52 | 122.09 | 2 | 29.93 | 143.18 | 5 | 34.31 | 148.87 | 4 | 29.93 | 232.58 |
| GSHID8_CRIGR | 5 | 32.85 | 307.22 | 3 | 21.9 | 240.82 | 5 | 32.12 | 269.68 | 5 | 29.93 | 143.18 | 4 | 20.96 | 228.92 | 2 | 11.76 | 116.58 |
| GSHIP0_CRIGR | 2 | 9.56 | 84.06 | 2 | 2.17 | 72.37 | 2 | 16.54 | 70.99 | 2 | 2.17 | 145.32 | 4 | 20.96 | 228.92 | 2 | 11.76 | 116.58 |
| GSHIS0_CRIGR | 2 | 2.17 | 72.37 | 2 | 2.17 | 72.37 | 2 | 16.54 | 70.99 | 2 | 2.17 | 145.32 | 4 | 20.96 | 228.92 | 2 | 11.76 | 116.58 |
| GSHIS5_CRIGR | 2 | 1.44 | 95.35 | 2 | 1.44 | 95.35 | 2 | 2.32 | 99.38 | 2 | 7.44 | 42.28 | 3 | 7.44 | 42.28 | 2 | 6.27 | 48.99 |
| GSHIU0_CRIGR | 2 | 9.21 | 70.3 | 2 | 9.21 | 70.3 | 2 | 2.32 | 99.38 | 2 | 5.67 | 238.12 | 2 | 5.67 | 238.12 | 2 | 4.76 | 231.76 |
| GSHIV5_CRIGR | 2 | 5.14 | 64.5 | 2 | 5.14 | 64.5 | 2 | 2.32 | 99.38 | 2 | 5.67 | 238.12 | 2 | 5.67 | 238.12 | 2 | 4.76 | 231.76 |
| GSHK00_CRIGR | 2 | 5.14 | 64.5 | 2 | 5.14 | 64.5 | 2 | 2.32 | 99.38 | 2 | 5.67 | 238.12 | 2 | 5.67 | 238.12 | 2 | 4.76 | 231.76 |
| GSHK56_CRIGR | 2 | 5.14 | 64.5 | 2 | 5.14 | 64.5 | 2 | 2.32 | 99.38 | 2 | 5.67 | 238.12 | 2 | 5.67 | 238.12 | 2 | 4.76 | 231.76 |
| GSHK57_CRIGR | 4 | 5.86 | 118.5 | 3 | 3.87 | 126.84 | 3 | 3.44 | 82.31 | 2 | 8.33 | 91.56 | 2 | 3.95 | 107.96 | 2 | 5.36 | 110.86 |
| GSHK64_CRIGR | 2 | 13.56 | 120.31 | 2 | 13.56 | 218.91 | 2 | 4.75 | 188.51 | 2 | 5.14 | 91.64 | 2 | 8.07 | 329.34 | 2 | 14.69 | 95.18 |
| GSHK90_CRIGR | 2 | 36.74 | 1001.63 | 13 | 37.12 | 1138.51 | 8 | 27.65 | 1198.46 | 13 | 37.88 | 807.82 | 14 | 39.77 | 1664.77 | 12 | 37.12 | 1201.87 |
| GSHK88_CRIGR | 2 | 7.63 | 220.96 | 2 | 7.63 | 362.3 | 2 | 15.09 | 478.11 | 6 | 15.28 | 267.58 | 9 | 21.32 | 577.59 | 9 | 22.26 | 453.72 |
| GSHK08_CRIGR | 8 | 4.02 | 217.19 | 5 | 5.19 | 193.53 | 5 | 4.1 | 185.35 | 6 | 15.28 | 267.58 | 9 | 3.94 | 177.23 | 4 | 5.86 | 280.7 |
| GSHK33_CRIGR | 2 | 4.68 | 140.53 | 2 | 2.61 | 53.92 | 2 | 2.22 | 63.23 | 2 | 14.83 | 205.87 | 2 | 2.61 | 37.98 | 2 | 12.17 | 98.93 |
| GSHK38_CRIGR | 2 | 4.68 | 140.53 | 2 | 2.61 | 53.92 | 2 | 2.22 | 63.23 | 2 | 14.83 | 205.87 | 2 | 2.61 | 37.98 | 2 | 12.17 | 98.93 |
| GSHK44_CRIGR | 7 | 10.38 | 286.56 | 9 | 13.57 | 448.47 | 12 | 18.89 | 662.41 | 12 | 17.19 | 611.89 | 11 | 16.97 | 298.7 | 12 | 16.9 | 402.72 |
| GSHKX1_CRIGR | 2 | 9.64 | 225.86 | 2 | 8.85 | 219.59 | 2 | 19.53 | 227.69 | 2 | 14.83 | 205.87 | 2 | 8.85 | 219.53 | 2 | 12.17 | 98.93 |
| GSHK13_CRIGR | 4 | 4.68 | 140.53 | 2 | 2.61 | 53.92 | 2 | 2.22 | 63.23 | 2 | 14.83 | 205.87 | 2 | 2.61 | 37.98 | 2 | 12.17 | 98.93 |
| GSHL15_CRIGR | 4 | 4.68 | 140.53 | 2 | 2.61 | 53.92 | 2 | 2.22 | 63.23 | 2 | 14.83 | 205.87 | 2 | 2.61 | 37.98 | 2 | 12.17 | 98.93 |
| GSHL18_CRIGR | 3 | 4.63 | 157.37 | 3 | 4.63 | 157.37 | 3 | 5.14 | 147.24 | 5 | 8.13 | 267.86 | 4 | 6.79 | 250.85 | 3 | 3.08 | 34.73 |
| GSHL14_CRIGR | 2 | 13.85 | 52.29 | 2 | 13.85 | 52.29 | 2 | 44.34 | 188.97 | 3 | 43.06 | 413.6 | 3 | 13.42 | 169.20 | 2 | 16.12 | 357.71 |
| GSHL40_CRIGR | 5 | 42.59 | 344 | 4 | 31.94 | 528.65 | 7 | 27.62 | 578.1 | 5 | 25.58 | 1091.42 | 10 | 28.39 | 948.5 | 10 | 32.48 | 956.78 |
| GSHLX0_CRIGR | 2 | 9.98 | 1156.19 | 9 | 22.84 | 147.38 | 7 | 7.98 | 172.71 | 2 | 11.81 | 152.89 | 3 | 16.41 | 142.4 | 6 | 22.84 | 321.04 |
| GSHL22_CRIGR | 2 | 51.19 | 90.96 | 2 | 38.1 | 81.99 | 2 | 34.52 | 84.97 | 2 | 38.1 | 48.52 | 3 | 38.1 | 59.25 | 2 | 12.92 | 227.33 |
| GSHM00_CRIGR | 4 | 21.24 | 171.37 | 4 | 21.24 | 171.37 | 4 | 16.99 | 160.73 | 2 | 11.2 | 109.7 | 2 | 11.2 | 36.87 | 2 | 1.89 | 179.82 |
| GSHM03_CRIGR | 3 | 2.46 | 204.66 | 3 | 2.86 | 111.49 | 3 | 2.98 | 99.33 | 3 | 2.86 | 218.9 | 3 | 2.52 | 247.05 | 2 | 15.71 | 74.9 |
| GSHMA7_CRIGR | 2 | 28.8 | 157.75 | 2 | 15.71 | 115.76 | 2 | 10.99 | 45.45 | 3 | 15.71 | 90.67 | 3 | 21.99 | 150.43 | 2 | 18.5 | 194.33 |
| GSHMB2_CRIGR | 4 | 8.81 | 213.21 | 2 | 7.73 | 116.49 | 2 | 7.73 | 101.1 | 2 | 11.45 | 162.13 | 2 | 7.73 | 182.1 | 3 | 18.5 | 139.07 |
| GSHMD6_CRIGR | 7 | 47.73 | 495.33 | 8 | 48.48 | 488.58 | 10 | 58.33 | 777.75 | 9 | 57.58 | 510.61 | 10 | 58.33 | 510.4 | 8 | 56.06 | 566.24 |
| GSHMG4_CRIGR | 5 | 30.98 | 225.25 | 5 | 30.98 | 358.56 | 4 | 5.54 | 124.62 | 3 | 8.78 | 131.16 | 3 | 9.47 | 76.64 | 2 | 5.54 | 61.92 |
| GSHMS8_CRIGR | 6 | 11.55 | 417.21 | 7 | 13.39 | 415.76 | 4 | 26.63 | 246.56 | 4 | 28.54 | 210.67 | 4 | 26.63 | 244.23 | 5 | 30.98 | 365.33 |
| GSHMU4_CRIGR | 2 | 16.11 | 44.71 | 3 | 25.84 | 360.17 | 3 | 25.28 | 343.17 | 3 | 17.42 | 293.76 | 2 | 12.92 | 227.33 | 4 | 25.84 | 252.9 |
| GSHMV2_CRIGR | 3 | 16.85 | 199.65 | 3 | 3.73 | 270.29 | 6 | 4.74 | 476.61 | 2 | 1.84 | 218.98 | 6 | 4.51 | 366.54 | 7 | 4.05 | 460.12 |
| GSHN02_CRIGR | 2 | 5.54 | 113.4 | 2 | 12.64 | 35.44 | 2 | 12.64 | 35.44 | 2 | 1.84 | 218.98 | 6 | 4.51 | 366.54 | 7 | 4.05 | 460.12 |
| GSHN14_CRIGR | 5 | 3.73 | 263.82 | 5 | 3.73 | 270.29 | 6 | 4.74 | 476.61 | 2 | 1.84 | 218.98 | 6 | 4.51 | 366.54 | 7 | 4.05 | 460.12 |
| GSHN37_CRIGR | 2 | 5.54 | 113.4 | 2 | 12.64 | 35.44 | 2 | 12.64 | 35.44 | 2 | 1.84 | 218.98 | 6 | 4.51 | 366.54 | 7 | 4.05 | 460.12 |
| GSHN65_CRIGR | 3 | 14.12 | 263.91 | 2 | 7.44 | 225.72 | 4 | 7.63 | 192.1 | 3 | 7.44 | 168.08 | 2 | 3.44 | 100.62 | 2 | 14.8 | 80.18 |
| GSHN88_CRIGR | 2 | 4.13 | 70.19 | 2 | 12.12 | 179.76 | 2 | 7.41 | 110.43 | 5 | 18.86 | 343.89 | 2 | 3.8 | 79.53 | 2 | 16.16 | 407.93 |
| GSHN92_CRIGR | 5 | 18.86 | 315.33 | 3 | 17.45 | 135.58 | 2 | 19.15 | 68.3 | 5 | 32.77 | 76.44 | 4 | 18.3 | 58.78 | 2 | 10.58 | 120.03 |
| GSHN94_CRIGR | 2 | 13.69 | 123.2 | 3 | 17.45 | 135.58 | 2 | 14.67 | 139.33 | 5 | 9.05 | 107.2 | 3 | 23.47 | 300.24 | 4 | 23.72 | 264.82 |
| GSHN98_CRIGR | 2 | 18.96 | 91.65 | 2 | 18.96 | 91.65 | 2 | 14.67 | 139.33 | 5 | 9.05 | 107.2 | 3 | 23.47 | 300.24 | 4 | 23.72 | 264.82 |
| GSHNY2_CRIGR | 2 | 3.13 | 81.46 | 2 | 2.06 | 113.57 | 2 | 1.72 | 47.68 | 2 | 2.54 | 80.56 | 2 | 4.91 | 210.77 | 2 | 3.09 | 35.33 |
| GSHP24_CRIGR | 3 | 7.45 | 175.64 | 4 | 7.45 | 175.64 | 4 | 6.43 | 147.73 | 5 | 8.12 | 142.29 | 5 | 8.12 | 193.04 | 6 | 6.27 | 48.99 |
| GSHP44_CRIGR | 2 | 3.13 | 81.46 | 2 | 2.06 | 113.57 | 2 | 1.72 | 47.68 | 2 | 2.54 | 80.56 | 2 | 4.91 | 210.77 | 2 | 3.09 | 35.33 |
| GSHP69_CRIGR | 4 | 7.45 | 175.64 | 4 | 7.45 | 175.64 | 4 | 6.43 | 147.73 | 5 | 8.12 | 142.29 | 5 | 8.12 | 193.04 | 6 | 6.27 | 48.99 |
| GSHP71_CRIGR | 2 | 35.81 | 365.15 | 6 | 38.6 | 231.6 | 3 | 31.16 | 353.01 | 2 | 4.13 | 103.83 | 2 | 5.25 | 200.25 | 2 | 36.28 | 278.23 |
| GSHP75_CRIGR | 5 | 29.15 | 522.62 | 6 | 31.66 | 498.82 | 5 | 24.43 | 582.14 | 5 | 22.9 | 646.04 | 7 | 29.65 | 696.52 | 5 | 19.47 | 781.5 |
| GSHP80_CRIGR | 2 | 9.18 | 169.97 | 2 | 9.18 | 169.97 | 2 | 9.18 | 169.97 | 2 | 9.18 | 169.97 | 2 | 9.18 | 169.97 | 2 | 9.18 | 169.97 |
| GSHPV6_CRIGR | 6 | 12.46 | 267.44 | 3 | 10.9 | 192.11 | 4 | 12.11 | 318.57 | 3 | 10.9 | 237.55 | 2 | 5.71 | 228.52 | 2 | 5.36 | 110.86 |
| GSHPZ6_CRIGR | 4 | 7.74 | 134.17 | 2 | 7.74 | 166.11 | 2 | 7.74 | 152.9 | 2 | 7.74 | 91.53 | 2 | 7.74 | 158.79 | 2 | 7.74 | 158.79 |
| GSHQ01_CRIGR | 2 | 7.74 | 134.17 | 2 | 7.74 | 166.11 | 2 | 7.74 | 152.9 | 2 | 7.74 | 91.53 | 2 | 7.74 | 158.79 | 2 | 7.74 | 158.79 |
| GSHQ32_CRIGR | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 |
| GSHQ86_CRIGR | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 |
| GSHQ97_CRIGR | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 | 2 | 5.09 | 156.85 |

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Table S-6 – Continued

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|--------------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|
| GSHOK4_CRIGR | 2 | 4.68 | 87.11 | 3 | 6.44 | 127.45 | 1 | 5.11 | 280.12 | 2 | 3.36 | 153.32 | 2 | 4.68 | 163.66 | 2 | 4.68 | 107.67 |
| GSHOM6_CRIGR | 3 | 5.85 | 223.67 | 2 | 5.02 | 147.91 | 3 | 9.09 | 141.48 | 4 | 14.11 | 192.1 | 4 | 7.1 | 301.22 | 4 | 7.1 | 217.42 |
| GSHOP7_CRIGR | 6 | 23.44 | 303.04 | 2 | 10.84 | 342.18 | 5 | 12.74 | 271.96 | 6 | 16.7 | 257.11 | 7 | 22.73 | 308.22 | 2 | 8.85 | 219.77 |
| GSHOS9_CRIGR | 2 | 7.17 | 401.89 | 4 | 3.82 | 661.4 | 3 | 8.83 | 271.96 | 3 | 8.83 | 257.11 | 6 | 18.76 | 338.94 | 4 | 11.02 | 206.27 |
| GSHR05_CRIGR | 2 | 7.17 | 70.61 | 2 | 9.8 | 103.11 | 3 | 5.41 | 125.01 | 4 | 5.41 | 112.98 | 4 | 4.05 | 94.56 | 2 | 3.96 | 89.35 |
| GSHR69_CRIGR | - | - | - | 2 | 4.43 | 148.8 | 2 | 3.35 | 96.72 | 2 | 2.44 | 73.47 | 2 | 3.35 | 107.6 | 2 | 3.35 | 67.04 |
| GSHR92_CRIGR | - | - | - | 3 | 4.43 | 148.8 | 2 | 3.35 | 96.72 | 2 | 2.44 | 73.47 | 2 | 3.35 | 107.6 | 2 | 3.35 | 152.75 |
| GSHR95_CRIGR | - | - | - | 3 | 4.43 | 148.8 | 2 | 3.35 | 96.72 | 2 | 2.44 | 73.47 | 2 | 3.35 | 107.6 | 2 | 3.35 | - |
| GSHRC5_CRIGR | - | - | - | 2 | 1.87 | 146.91 | - | - | - | 2 | 2.11 | 85.42 | - | - | - | - | - | - |
| GSHRH4_CRIGR | - | - | - | 3 | 3.86 | 90.69 | - | - | - | 2 | 2.11 | 85.42 | - | - | - | - | - | - |
| GSHR17_CRIGR | 3 | 3.86 | 90.69 | 2 | 15.35 | 152.65 | 3 | 21.86 | 260.14 | 2 | 18.14 | 207.91 | 2 | 13.02 | 155.22 | - | - | 176.07 |
| GSHRK4_CRIGR | 2 | 5.81 | 55.09 | 8 | 26.97 | 282.31 | 10 | 36.89 | 351.79 | 5 | 19.29 | 289.97 | 9 | 36.14 | 603.4 | 2 | 15.35 | 335.1 |
| GSHRN0_CRIGR | 2 | 49.67 | 529.37 | 3 | 39.74 | 339.33 | 7 | 7.5 | 726.97 | 7 | 44.37 | 379.46 | 5 | 39.74 | 618.55 | 9 | 34.08 | 674.27 |
| GSHR04_CRIGR | 8 | 49.67 | 529.37 | 3 | 39.74 | 339.33 | 7 | 7.5 | 726.97 | 7 | 44.37 | 379.46 | 5 | 39.74 | 618.55 | 9 | 34.08 | 674.27 |
| GSHR06_CRIGR | - | - | - | 2 | 10.75 | 65.75 | 2 | 19.1 | 122.24 | 2 | 19.1 | 71.74 | 2 | 7.16 | 162.83 | 2 | 7.16 | 57.22 |
| GSHR5_CRIGR | 2 | 8.66 | 135.03 | 2 | 13.57 | 110.96 | 3 | 19.1 | 122.24 | 3 | 19.1 | 71.74 | 2 | 13.57 | 201.83 | 3 | 19.1 | 128.08 |
| GSHRW8_CRIGR | - | - | - | 2 | 4.26 | 272.75 | - | - | - | 2 | 4.26 | 272.75 | - | - | - | 2 | 4.26 | - |
| GSHR01_CRIGR | - | - | - | 2 | 6.95 | 55.35 | - | - | - | 2 | 6.95 | 55.35 | - | - | - | 2 | 6.95 | 58.71 |
| GSHS46_CRIGR | - | - | - | 2 | 18.67 | 170.38 | - | - | - | 2 | 18.67 | 170.38 | - | - | - | 2 | 18.67 | 179.21 |
| GSHS67_CRIGR | - | - | - | 2 | 14.59 | 248.58 | - | - | - | 2 | 14.59 | 248.58 | - | - | - | 2 | 14.59 | 173.85 |
| GSHS85_CRIGR | 4 | 6.12 | 151.68 | 2 | 12.22 | 352.38 | 7 | 5.58 | 287.27 | 2 | 2.9 | 141.53 | 2 | 14.29 | 102.9 | 2 | 14.29 | 246.52 |
| GSHS2_CRIGR | 6 | 1.36 | 347.04 | 2 | 19.09 | 493.7 | 3 | 27.27 | 478.18 | 13 | 22.76 | 490.72 | 4 | 5.88 | 673.34 | 5 | 8.26 | 207.53 |
| GSHS4_CRIGR | 2 | 19.09 | 493.7 | 2 | 19.09 | 493.7 | 3 | 27.27 | 478.18 | 3 | 27.27 | 480.68 | 2 | 17.82 | 673.34 | 3 | 28.18 | 394.77 |
| GSHS8_CRIGR | - | - | - | 2 | 6.35 | 52.1 | - | - | - | 2 | 6.35 | 55.85 | - | - | - | 2 | 6.35 | 37.65 |
| GSHS4_CRIGR | - | - | - | 2 | 6.35 | 52.1 | - | - | - | 2 | 6.35 | 55.85 | - | - | - | 2 | 6.35 | 37.65 |
| GSHS84_CRIGR | - | - | - | 2 | 12.45 | 49.31 | - | - | - | 2 | 12.45 | 49.31 | - | - | - | 2 | 12.45 | 166.15 |
| GSHS88_CRIGR | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 166.15 |
| GSHS83_CRIGR | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 166.15 |
| GSHS77_CRIGR | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 166.15 |
| GSHS74_CRIGR | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 118.88 | - | - | - | 2 | 2.28 | 166.15 |
| GSHS24_CRIGR | - | - | - | 2 | 2.34 | 74.71 | - | - | - | 2 | 2.34 | 74.71 | - | - | - | 2 | 2.34 | 74.86 |
| GSHT22_CRIGR | 2 | 1.84 | 100.27 | 3 | 3.03 | 102.17 | - | - | - | 3 | 3.03 | 102.17 | - | - | - | 3 | 3.03 | 141.09 |
| GSHT77_CRIGR | 2 | 10.2 | 115.39 | 2 | 20.94 | 350.71 | - | - | - | 2 | 20.94 | 350.71 | - | - | - | 2 | 20.94 | 212.99 |
| GSHTD4_CRIGR | - | - | - | 6 | 16.43 | 311.71 | - | - | - | 6 | 16.43 | 311.71 | - | - | - | 6 | 16.43 | 108.26 |
| GSHTE5_CRIGR | - | - | - | 6 | 16.43 | 311.71 | - | - | - | 6 | 16.43 | 311.71 | - | - | - | 6 | 16.43 | 108.26 |
| GSHTF7_CRIGR | 6 | 16.43 | 311.71 | 6 | 20.94 | 350.71 | 7 | 22.38 | 318.08 | 6 | 20.94 | 350.71 | 7 | 22.38 | 318.08 | 5 | 17.25 | 102.11 |
| GSHTG4_CRIGR | - | - | - | 2 | 2.65 | 66.56 | - | - | - | 2 | 2.65 | 66.56 | - | - | - | 2 | 2.65 | 59.71 |
| GSHTG6_CRIGR | 2 | 2.65 | 69.45 | 2 | 2.65 | 66.56 | 2 | 2.65 | 77.94 | 2 | 2.65 | 77.94 | 2 | 3.4 | 55.46 | 2 | 2.65 | 81.87 |
| GSHTG2_CRIGR | - | - | - | 6 | 11.98 | 340.63 | 5 | 10.41 | 409.37 | 4 | 7.5 | 325.6 | 7 | 14.89 | 317.09 | 5 | 11.53 | 309.68 |
| GSHTL1_CRIGR | 6 | 12.21 | 390.27 | 6 | 11.98 | 340.63 | 5 | 10.41 | 409.37 | 4 | 7.5 | 325.6 | 7 | 14.89 | 317.09 | 5 | 11.53 | 309.68 |
| GSHTM8_CRIGR | - | - | - | 5 | 10.86 | 383.14 | 4 | 6.67 | 194.36 | 3 | 8.38 | 99.36 | 5 | 11.62 | 290.68 | 3 | 6.86 | 145.01 |
| GSHTN5_CRIGR | 2 | 1.29 | 51.52 | 5 | 10.86 | 383.14 | 4 | 6.67 | 194.36 | 3 | 8.38 | 99.36 | 5 | 11.62 | 290.68 | 3 | 6.86 | 145.01 |
| GSHTW7_CRIGR | 5 | 10.67 | 193.25 | 5 | 10.86 | 383.14 | 4 | 6.67 | 194.36 | 3 | 8.38 | 99.36 | 5 | 11.62 | 290.68 | 3 | 6.86 | 145.01 |
| GSHU28_CRIGR | 4 | 12.53 | 209.12 | 2 | 11.25 | 111.21 | 2 | 11.25 | 177.34 | 3 | 16.88 | 142.74 | 4 | 20.46 | 112.66 | 2 | 10.85 | 47.79 |
| GSHU7_CRIGR | 3 | 0.93 | 85.86 | 2 | 11.25 | 111.21 | 2 | 0.59 | 69.01 | 3 | 16.88 | 142.74 | 4 | 20.46 | 112.66 | 2 | 10.85 | 47.79 |
| GSHUL2_CRIGR | - | - | - | 4 | 8.86 | 310 | - | - | - | 3 | 5.61 | 211.47 | - | - | - | 3 | 5.61 | 122.58 |
| GSHU07_CRIGR | 3 | 6.2 | 326.94 | - | - | - | 4 | 8.86 | 310 | - | - | - | 3 | 45.36 | 122.58 | - | - | - |
| GSHU2_CRIGR | 2 | 2.49 | 89.07 | - | - | - | 4 | 8.86 | 310 | - | - | - | 3 | 45.36 | 122.58 | - | - | - |
| GSHU3_CRIGR | 2 | 2.49 | 89.07 | - | - | - | 4 | 8.86 | 310 | - | - | - | 3 | 45.36 | 122.58 | - | - | - |
| GSHU13_CRIGR | 3 | 2.12 | 168.84 | - | - | - | 2 | 1.15 | 119.26 | - | - | - | 2 | 6.8 | 100.68 | - | - | - |
| GSHV44_CRIGR | 3 | 5.62 | 116.41 | - | - | - | 2 | 3.52 | 90.75 | - | - | - | 2 | 6.8 | 100.68 | - | - | - |
| GSHV48_CRIGR | 2 | 15.92 | 320.92 | 4 | 6.96 | 118.42 | 2 | 1.15 | 119.26 | 2 | 3.52 | 90.75 | 4 | 8.7 | 196.55 | 3 | 6.61 | 71.9 |
| GSHV48_CRIGR | 5 | 9.45 | 303.89 | 2 | 9.45 | 303.89 | 6 | 20.65 | 470.9 | 2 | 3.52 | 90.75 | 4 | 8.7 | 196.55 | 3 | 6.61 | 71.9 |
| GSHV80_CRIGR | 2 | 4.61 | 290.12 | 2 | 15.45 | 155.23 | 6 | 20.65 | 470.9 | 4 | 16.92 | 426.7 | 3 | 4.58 | 106.04 | 2 | 4.58 | 103.69 |
| GSHWC3_CRIGR | 2 | 4.61 | 290.12 | 2 | 15.45 | 155.23 | 6 | 20.65 | 470.9 | 4 | 16.92 | 426.7 | 3 | 4.58 | 106.04 | 2 | 4.58 | 103.69 |
| GSHWF3_CRIGR | 2 | 3.46 | 69.28 | 2 | 17.36 | 610.59 | 5 | 7.85 | 193.77 | 3 | 6.14 | 183.35 | 3 | 19.55 | 215.29 | 4 | 23.38 | 221.85 |
| GSHW12_CRIGR | 5 | 22.64 | 747.6 | 4 | 17.36 | 610.59 | 5 | 7.85 | 193.77 | 3 | 6.14 | 183.35 | 3 | 19.55 | 215.29 | 4 | 23.38 | 221.85 |
| GSHW13_CRIGR | 18 | 36.97 | 3269.72 | 17 | 38.18 | 3466.19 | 18 | 38.42 | 4415.41 | 16 | 35.04 | 3668.22 | 17 | 38.61 | 4321.18 | 17 | 37.5 | 4177.36 |
| GSHVK4_CRIGR | - | - | - | 2 | 11.45 | 88.74 | 3 | 16.5 | 148.49 | 2 | 6.5 | 166.92 | 4 | 14.81 | 205.18 | 2 | 7.41 | 106.46 |
| GSHV11_CRIGR | 2 | 11.45 | 88.74 | 3 | 16.5 | 148.49 | 2 | 6.5 | 166.92 | 4 | 14.81 | 205.18 | 2 | 7.41 | 106.46 | 2 | 7.41 | 106.46 |
| GSHV16_CRIGR | 5 | 17.26 | 279.29 | 6 | 18.24 | 285.15 | 5 | 15.31 | 252.65 | 2 | 17.2 | 62.81 | 4 | 11.4 | 262.49 | 3 | 11.4 | 146.44 |
| GSHWP9_CRIGR | 6 | 16.67 | 102.97 | 2 | 10.65 | 94.54 | 5 | 15.31 | 252.65 | 2 | 17.2 | 62.81 | 4 | 11.4 | 262.49 | 3 | 11.4 | 146.44 |
| GSHWS3_CRIGR | 3 | 16.67 | 102.97 | 2 | 10.65 | 94.54 | 5 | 15.31 | 252.65 | 2 | 17.2 | 62.81 | 4 | 11.4 | 262.49 | 3 | 11.4 | 146.44 |
| GSHWW4_CRIGR | - | - | - | 2 | 10.26 | 62.51 | - | - | - | 2 | 7.03 | 85.35 | - | - | - | 2 | 10.65 | 47.59 |
| GSHWX8_CRIGR | - | - | - | 2 | 10.26 | 62.51 | - | - | - | 2 | 7.03 | 85.35 | - | - | - | 2 | 10.65 | 47.59 |
| GSHX40_CRIGR | 3 | 31.9 | 163.21 | 3 | 31.9 | 68.05 | 4 | 31.9 | 123.4 | 2 | 24.14 | 113.39 | 5 | 50.86 | 250.24 | 5 | 50.86 | 243.71 |
| GSHX69_CRIGR | 8 | 20.95 | 517.7 | 11 | 26.22 | 610.97 | 6 | 16.73 | 470.27 | 6 | 16.73 | 470.27 | 9 | 19.1 | 668.19 | 8 | 15.02 | 407.83 |
| GSHX83_CRIGR | 4 | 32.56 | 425.13 | 5 | 37.67 | 515.12 | 6 | 44.65 | 309.94 | 6 | 38.6 | 562.98 | 4 | 37.67 | 230.01 | 6 | 43.26 | 383.93 |
| GSHX93_CRIGR | - | - | - | 2 | 3.43 | 44.06 | - | - | - | 2 | 3.43 | 44.06 | - | - | - | 2 | 3.43 | 44.06 |
| GSHXA2_CRIGR | 3 | 11.89 | 85.55 | 4 | 16.5 | 218.73 | 4 | 14.08 | 323.96 | 3 | 14.08 | 230.16 | 3 | 8.74 | 203.83 | 5 | 20.63 | 277.47 |

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Table S-6 – Continued

| Protein ID | Unique Peptides | Single 1 Coverage (%) | Score | Unique Peptides | Single 2 Coverage (%) | Score | Unique Peptides | Single 3 Coverage (%) | Score | Unique Peptides | Single 4 Coverage (%) | Score | Unique Peptides | Single 5 Coverage (%) | Score | Unique Peptides | Single 6 Coverage (%) | Score |
|---------------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|-----------------|-----------------------|---------|
| GSHXF2_CRIGR | 4 | 22.03 | 236.15 | 2 | 10.59 | 81.71 | 2 | 10.59 | 82.72 | 3 | 17.8 | 201.17 | 2 | 10.59 | 192.78 | 4 | 25.42 | 237.4 |
| GSHXL1_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSHXR8_CRIGR | - | - | - | 2 | 6.62 | 58.05 | 2 | 6.62 | 58.05 | 2 | 6.62 | 80.06 | 2 | 8.15 | 144.55 | - | - | - |
| GSHXW9_CRIGR | - | - | - | 3 | 23.67 | 317.94 | 3 | 23.67 | 317.94 | 3 | 17.82 | 232.9 | - | - | - | - | - | - |
| GSHXB3_CRIGR | 2 | 6.01 | 154.95 | 4 | 2.37 | 75.78 | 3 | 4.07 | 90.27 | 2 | 2.37 | 85.33 | - | - | - | 3 | 14.1 | 252.85 |
| GSHYG7_CRIGR | 2 | 16.67 | 136.43 | 2 | 8.02 | 269 | 2 | 8.02 | 184.64 | 2 | 8.02 | 253.94 | 2 | 8.02 | 350.64 | 4 | 12.83 | 375.25 |
| GSHYH7_CRIGR | 3 | 16.67 | 136.43 | 2 | 15.79 | 59.89 | 2 | 16.67 | 86.93 | 2 | 10.53 | 142.43 | 2 | 30.7 | 107.04 | 2 | 5.29 | 81.24 |
| GSHYL0_CRIGR | 2 | 10.58 | 180 | 2 | 6.9 | 165.77 | 3 | 9.45 | 267.91 | 5 | 8.43 | 221.11 | 2 | 4.21 | 234.05 | 5 | 30.7 | 210.07 |
| GSHYU5_CRIGR | 2 | 10.58 | 180 | 8 | 10.05 | 421.7 | 7 | 10.58 | 198.93 | 2 | 8.64 | 565.29 | 2 | 10.58 | 173.33 | 7 | 10.3 | 543.12 |
| GSHZ17_CRIGR | 2 | 22.13 | 212.67 | 2 | 2.85 | 261.62 | 2 | 2.85 | 219.73 | 2 | 3.97 | 302.14 | 2 | 3.97 | 288.22 | 2 | 3.97 | 158.75 |
| GSHZ34_CRIGR | 2 | 18.64 | 124.96 | 2 | 22.13 | 129.21 | 3 | 35.25 | 196.49 | 3 | 35.25 | 288.22 | 2 | 35.25 | 288.22 | 2 | 35.25 | 351.19 |
| GSHZ36_CRIGR | 4 | 16.64 | 117.37 | 4 | 22.46 | 321.34 | 4 | 30.51 | 229.46 | 4 | 18.64 | 205.46 | 4 | 18.64 | 205.46 | 4 | 24.59 | 351.19 |
| GSHZ42_CRIGR | 5 | 16.64 | 117.37 | 6 | 18.88 | 369.11 | 5 | 17.38 | 267.22 | 3 | 17.38 | 267.22 | 3 | 8.22 | 250.11 | 4 | 24.59 | 287.05 |
| GSHZ55_CRIGR | 3 | 5.39 | 186.94 | 2 | 4.14 | 168.15 | 2 | 4.14 | 58.4 | 2 | 4.14 | 58.4 | 2 | 3.76 | 138.3 | 2 | 4.01 | 499.3 |
| GSHZD7_CRIGR | - | - | - | - | - | - | - | - | - | - | 2.66 | 76.99 | - | - | - | - | - | - |
| GSHZG6_CRIGR | 2 | 4.41 | 69.58 | - | - | - | - | - | - | - | 2.13 | 34.03 | 2 | 4.41 | 90.78 | - | - | - |
| GSHZU2_CRIGR | 4 | 4.41 | 181.72 | 3 | 3.65 | 282.07 | 3 | 2.89 | 129.94 | 2 | 2.13 | 34.03 | 3 | 4.03 | 159.96 | 5 | 5.4 | 334.13 |
| GSHZV0_CRIGR | 2 | 18.8 | 38.45 | - | - | - | - | 15.79 | 48.48 | 2 | 16.54 | 39.93 | - | - | - | - | - | - |
| GSHZW3_CRIGR | 4 | 33.09 | 1579.76 | 4 | 36.03 | 1555.61 | 4 | 36.03 | 1621.94 | 5 | 44.85 | 1332.11 | 6 | 44.85 | 1401.38 | 5 | 37.5 | 1833.97 |
| GSHZY1_CRIGR | 4 | 32.48 | 186.94 | 3 | 20.51 | 104.88 | 2 | 16.24 | 65.64 | 3 | 23.08 | 66.39 | 4 | 26.5 | 121.12 | 3 | 5.41 | 176.83 |
| GSH003_CRIGR | 4 | 6.96 | 183.24 | 4 | 17.09 | 211.06 | 5 | 21.52 | 201.11 | 2 | 9.45 | 41.56 | 5 | 21.52 | 230.79 | 3 | 12.66 | 152.24 |
| GSH004_CRIGR | 2 | 6.96 | 183.24 | 4 | 21.56 | 174.52 | 2 | 17.81 | 210.87 | 7 | 36.35 | 368.84 | 3 | 12.5 | 165.8 | 4 | 21.56 | 246.08 |
| GSH018_CRIGR | 5 | 23.75 | 180.38 | 3 | 22.13 | 559.93 | 3 | 22.13 | 379.84 | 3 | 22.13 | 238.98 | 3 | 22.13 | 266.52 | 3 | 22.13 | 461.22 |
| GSH078_CRIGR | 3 | 22.13 | 537.33 | 2 | 6.92 | 101.21 | 2 | 6.92 | 101.21 | - | - | - | - | - | - | - | - | - |
| GSH0C0_CRIGR | 2 | 24 | 191.47 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH0D8_CRIGR | 3 | 17.94 | 199.25 | 5 | 21.93 | 430.25 | 8 | 40.53 | 744.86 | 5 | 21.93 | 402.97 | 5 | 21.26 | 632.06 | 7 | 31.56 | 628.64 |
| GSH0N2_CRIGR | 2 | 20.87 | 242.13 | 2 | 20.87 | 244.58 | 2 | 20.87 | 271.09 | 2 | 3.92 | 94.26 | 2 | 20.87 | 216.63 | 2 | 20.87 | 348.76 |
| GSH0O8_CRIGR | 3 | 5.3 | 209.24 | 3 | 5.3 | 229.68 | 3 | 4.8 | 253.09 | 2 | 3.45 | 140.13 | 3 | 5.3 | 222.32 | 2 | 34.95 | 78.09 |
| GSH102_CRIGR | 2 | 46.6 | 136.25 | 2 | 56.31 | 229.68 | 2 | 24.27 | 151.37 | 2 | 16.22 | 87.46 | 2 | 56.31 | 211.28 | 2 | 34.95 | 78.09 |
| GSH100_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH142_CRIGR | 2 | 19.68 | 155.56 | 2 | 3.28 | 70.99 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH179_CRIGR | 3 | 19.68 | 155.56 | 3 | 22.26 | 80.43 | 4 | 30.65 | 122.42 | 3 | 16.77 | 117.07 | 3 | 23.23 | 162.88 | 2 | 18.06 | 157.16 |
| GSH185_CRIGR | 3 | 19.68 | 155.56 | 3 | 22.26 | 80.43 | 3 | 21.89 | 145.6 | 3 | 21.89 | 145.6 | 3 | 23.23 | 162.88 | 2 | 18.06 | 157.16 |
| GSH1H4_CRIGR | 12 | 25.38 | 622.14 | 14 | 31.38 | 730.85 | 10 | 25.1 | 666.47 | 12 | 27.83 | 1052.53 | 13 | 28.51 | 914.91 | 13 | 28.51 | 714.89 |
| GSH1N0_CRIGR | 3 | 2.76 | 250.04 | 3 | 11.26 | 205.04 | 3 | 2.62 | 246.37 | 4 | 3.26 | 202.56 | 4 | 3.26 | 139.37 | 2 | 2.12 | 370.95 |
| GSH1T4_CRIGR | 7 | 24.69 | 268.83 | 3 | 14.81 | 193.66 | 6 | 23.46 | 426.07 | 9 | 29.32 | 394.46 | 4 | 16.67 | 252.98 | 3 | 12.35 | 277.74 |
| GSH220_CRIGR | 3 | 8.05 | 103.24 | 2 | 2.6 | 59.9 | 2 | 3.83 | 114.01 | - | - | - | - | - | - | - | - | - |
| GSH278_CRIGR | 3 | 8.05 | 103.24 | 3 | 8.05 | 103.24 | 4 | 8.05 | 88.23 | 3 | 7.12 | 93.6 | - | - | - | - | - | - |
| GSH2B6_CRIGR | 2 | 2.71 | 117.67 | 2 | 11.03 | 135.43 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH2D3_CRIGR | 2 | 2.71 | 117.67 | 2 | 11.03 | 135.43 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH2D8_CRIGR | 2 | 45.27 | 392.89 | 4 | 38.81 | 385.63 | 3 | 33.33 | 327.07 | - | - | - | - | - | - | - | - | - |
| GSH2E9_CRIGR | 15 | 39.95 | 1187.98 | 12 | 31.76 | 874.09 | 14 | 36.97 | 1420.26 | 5 | 51.24 | 474.26 | 4 | 41.79 | 330.33 | 4 | 41.79 | 349.66 |
| GSH2M1_CRIGR | 5 | 15.82 | 362.6 | 5 | 13.37 | 299.48 | 6 | 19.4 | 303.28 | 9 | 35.24 | 1024.71 | 9 | 25.31 | 918.49 | 11 | 28.04 | 826.27 |
| GSH2N1_CRIGR | 2 | 10.39 | 105.17 | 5 | 25.11 | 174.7 | 4 | 16.45 | 112.99 | 4 | 21.65 | 226.47 | 7 | 18.83 | 535.64 | 7 | 22.41 | 590.41 |
| GSH2N4_CRIGR | - | - | - | - | - | - | - | 12.23 | 162.19 | 4 | 20.69 | 169.69 | 3 | 17.87 | 149 | 4 | 11.6 | 186.73 |
| GSH2P6_CRIGR | 3 | 2.64 | 103.8 | 2 | 12.93 | 244.57 | 2 | 7.99 | 512.77 | 3 | 11.99 | 363.01 | 3 | 4.78 | 241.65 | 3 | 5.14 | 232.2 |
| GSH300_CRIGR | 4 | 9.28 | 381.91 | 3 | 7.79 | 439.09 | 8 | 8.98 | 455.72 | 4 | 8.05 | 302.96 | 4 | 9.08 | 448.53 | 3 | 9.28 | 555.24 |
| GSH310_CRIGR | 2 | 4.62 | 54.23 | 2 | 3.74 | 431.13 | 3 | 5.77 | 34.6 | 4 | 5.94 | 135.14 | 4 | 12.47 | 222.06 | 2 | 7.83 | 49.18 |
| GSH341_CRIGR | 2 | 32.31 | 352.14 | 2 | 7.84 | 190.67 | 2 | 5.77 | 34.6 | 2 | 26.92 | 328.4 | 2 | 7.84 | 222.06 | 2 | 7.83 | 219.33 |
| GSH351_CRIGR | 5 | 32.31 | 352.14 | 5 | 37.69 | 325.93 | 6 | 33.08 | 337.45 | 4 | 26.92 | 328.4 | 5 | 27.69 | 426.43 | 4 | 26.15 | 234.89 |
| GSH358_CRIGR | 2 | 0.99 | 119.27 | 2 | 1.07 | 151.66 | 2 | 0.89 | 66.59 | - | - | - | - | - | - | - | - | - |
| GSH3A8_CRIGR | 2 | 24.08 | 164.72 | 2 | 0.89 | 226.01 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH3B5_CRIGR | 3 | 8.23 | 442.04 | 3 | 7.13 | 303.16 | 4 | 32.98 | 198.6 | 3 | 32.98 | 162.1 | 3 | 24.08 | 99.56 | 3 | 1.49 | 201.35 |
| GSH3C7_CRIGR | 6 | 85.22 | 1467.94 | 7 | 93.91 | 2368.74 | 8 | 94.78 | 1905.23 | 2 | 8.23 | 329.11 | 2 | 7.13 | 315.21 | 3 | 8.09 | 495.93 |
| GSH3H2_CRIGR | 3 | 6.5 | 107.28 | 2 | 12.93 | 244.57 | 2 | 9.7 | 132.56 | 3 | 3.94 | 113.53 | 7 | 76.52 | 1877.7 | 5 | 66.96 | 2130.8 |
| GSH3I0_CRIGR | 2 | 11.07 | 44.42 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH3I35_CRIGR | 2 | 11.07 | 44.42 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH3W0_CRIGR | 3 | 17.57 | 160.84 | 4 | 24.32 | 304.75 | 4 | 24.32 | 216.11 | 3 | 17.57 | 214.82 | 4 | 24.32 | 128.43 | 4 | 24.32 | 321.61 |
| GSH3W6_CRIGR | 3 | 17.57 | 160.84 | 4 | 4.59 | 129.82 | 4 | 4.67 | 179.64 | 3 | 4.67 | 179.64 | 3 | 3.88 | 86.4 | 4 | 4.67 | 97.46 |
| GSH449_CRIGR | - | - | - | 3 | 4.59 | 129.82 | 3 | 12.84 | 92.04 | - | - | - | - | - | - | - | - | - |
| GSH4B7_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH4C8_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH4H6_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH4I9_CRIGR | 15 | 31.82 | 704.1 | 20 | 41.11 | 1129.99 | 2 | 9.62 | 65.1 | 13 | 25.67 | 598.1 | 17 | 28.57 | 702.22 | 17 | 38.1 | 857.33 |
| GSH501_CRIGR | 3 | 3.4 | 198.58 | 2 | 2.66 | 294.62 | 2 | 11.86 | 194.07 | 2 | 11.86 | 194.07 | 2 | 11.86 | 194.07 | 2 | 11.86 | 189.91 |
| GSH505_CRIGR | 3 | 3.4 | 198.58 | 2 | 2.66 | 294.62 | 3 | 3.25 | 392.12 | 4 | 2.66 | 305.63 | 4 | 4.36 | 443.76 | 3 | 2.88 | 208.82 |
| GSH531_CRIGR | 3 | 7.17 | 123.14 | 3 | 7.17 | 123.14 | - | - | - | - | - | - | - | - | - | - | - | - |

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Table S-6 – Continued

| Protein ID | Single 1 | | | Single 2 | | | Single 3 | | | Single 4 | | | Single 5 | | | Single 6 | | |
|--------------|-----------------|---------|--------------|-----------------|---------|--------------|-----------------|-------|--------------|-----------------|-------|--------------|-----------------|--------|--------------|-----------------|--------|--------------|
| | Unique Peptides | Score | Coverage (%) | Unique Peptides | Score | Coverage (%) | Unique Peptides | Score | Coverage (%) | Unique Peptides | Score | Coverage (%) | Unique Peptides | Score | Coverage (%) | Unique Peptides | Score | Coverage (%) |
| GNAS_CRIGR | - | - | - | 2 | 167.32 | - | - | - | - | - | - | - | 2 | 187.76 | - | 2 | 124.17 | - |
| GOSRT_CRIGR | 3 | 214.85 | 20.4 | 4 | 141.57 | 24 | 9.9 | - | - | - | - | - | 4 | 279.53 | 23.2 | 3 | 411.32 | 14.8 |
| GSLGI_CRIGR | 3 | 110.11 | 3.36 | 3 | 133.71 | 4.14 | 3.28 | 3 | 132.27 | 3 | 3.62 | 4 | 172.12 | 3.62 | 3 | 87.23 | 3.88 | |
| HS90A_CRIGR | 2 | 635.95 | 11.73 | 3 | 566.11 | 14.46 | 19.35 | 3 | 592.07 | 8 | 19.35 | 3 | 669.73 | 22.76 | 5 | 340.62 | 9.55 | |
| HSPTC_CRIGR | 9 | 568.46 | 18.89 | 12 | 517.76 | 24.46 | 5.45 | 8 | 577.7 | 2 | 5.84 | 11 | 113.87 | 5.84 | 12 | 849.31 | 25.7 | |
| IMDH2_CRIGR | - | - | - | 2 | 123.69 | 3.29 | - | - | - | - | - | - | - | - | - | - | - | - |
| MDRI_CRIGR | 2 | 117.91 | 3.29 | 2 | 192.5 | 3.29 | - | - | - | - | - | - | - | - | - | - | - | - |
| NSF_CRIGR | 7 | 362.26 | 11.29 | 11 | 459.08 | 19.62 | 9.27 | 4 | 270.49 | 4 | 9.27 | 10 | 447.35 | 19.09 | 12 | 446.16 | 21.91 | |
| OS8679_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| PLEC_CRIGR | 53 | 5244.83 | 24.17 | 59 | 5067.71 | 26.02 | 24.68 | 50 | 5771.01 | 45 | 24.68 | 24.17 | 6203.17 | 24.17 | 2 | 61.33 | 3.38 | |
| Q06B08_CRIGR | 6 | 166.7 | 11.45 | 4 | 97.01 | 15.06 | 5.42 | 2 | 102.01 | 5 | 5.42 | 19.28 | 152.85 | 19.28 | 57 | 5626.72 | 26.31 | |
| Q3HR12_CRIGR | - | - | - | 2 | 127.97 | 13.84 | 29.08 | 4 | 191.44 | - | - | - | - | - | - | 4 | 148.19 | 16.87 |
| Q4F888_CRIGR | 3 | 731.17 | 28.41 | 4 | 705.34 | 26.17 | 48.44 | 4 | 889.96 | 5 | 29.08 | 5 | 933.38 | 31.1 | - | - | - | |
| Q5VLK2_CRIGR | - | - | - | 2 | 2890.2 | 45.33 | 48.44 | 2 | 2958.29 | 3 | 51.56 | 3 | 2647.18 | 51.56 | - | - | - | |
| Q60455_CRIGR | 2 | 2499.94 | 44.14 | 2 | 2919.01 | 40.09 | 53.15 | 3 | 2664.88 | 3 | 53.15 | 44.14 | 2557.05 | 44.14 | 2 | 2777.7 | 863 | |
| Q60456_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| Q60456_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| Q76G10_CRIGR | 3 | 212.63 | 24.18 | 5 | 280.73 | 19.4 | 9.32 | 2 | 207.22 | 2 | 9.32 | 3 | 81.17 | 15.62 | 4 | 52 | 29.17 | |
| Q80Z93_CRIGR | 3 | 372.76 | 14.66 | 3 | 312.53 | 18.59 | 23.82 | 5 | 381.91 | 3 | 23.82 | 14.66 | 230.49 | 14.66 | 3 | 228.35 | 20.65 | |
| Q8MH04_CRIGR | - | - | - | 2 | 161.19 | 10.92 | 10.92 | 2 | 166.34 | 2 | 10.92 | 2 | 102.61 | 10.92 | 2 | 233.61 | 14.66 | |
| Q8R4U5_CRIGR | - | - | - | 3 | 244.28 | 19.57 | - | - | - | - | - | - | - | - | - | - | - | - |
| Q8R4V8_CRIGR | 2 | 227.22 | 14.5 | 2 | 123.09 | 14.5 | - | - | - | - | - | - | - | - | - | - | - | - |
| Q9EPP7_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| Q9EPP7_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| Q9EPP7_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| RLI3_CRIGR | 9 | 534.17 | 34.12 | 8 | 839.73 | 28.91 | 6.26 | 2 | 798.22 | 2 | 6.26 | 60.73 | 680.54 | 29.86 | 3 | 701.71 | 17.97 | |
| RSL7_CRIGR | 4 | 509.08 | 31.15 | 5 | 702.59 | 31.15 | 29.86 | 8 | 648.52 | 8 | 29.86 | 840.13 | 680.54 | 29.86 | 8 | 701.71 | 29.86 | |
| RSL7_CRIGR | 5 | 509.08 | 31.15 | 5 | 702.59 | 31.15 | 30.13 | 5 | 648.52 | 5 | 30.13 | 48.48 | 43.48 | 31.15 | 5 | 502.17 | 31.15 | |
| RSL7_CRIGR | 12 | 560.77 | 34.88 | 11 | 549.7 | 33.7 | 34.73 | 4 | 491.73 | 5 | 34.73 | 491.73 | 43.48 | 31.15 | 5 | 502.17 | 31.15 | |
| RSL7_CRIGR | 12 | 560.77 | 34.88 | 11 | 549.7 | 33.7 | 34.73 | 4 | 491.73 | 5 | 34.73 | 491.73 | 43.48 | 31.15 | 5 | 502.17 | 31.15 | |
| SVK_CRIGR | 3 | 96.20 | 10.39 | 5 | 167.83 | 10.75 | 13.07 | 12 | 681.37 | 13 | 34.73 | 681.37 | 827.91 | 39.54 | 9 | 831.27 | 28.14 | |
| TBB5_CRIGR | 5 | 3096.81 | 43.69 | 7 | 3649.83 | 52.25 | 59.23 | 7 | 2989.5 | 7 | 59.23 | 218.33 | 327.95 | 15.08 | 9 | 831.27 | 28.14 | |
| TCPA_CRIGR | 4 | 123.82 | 8.09 | 5 | 163.51 | 15.47 | 14.93 | 5 | 3269.03 | 7 | 14.93 | 2989.5 | 3245.56 | 50.23 | 7 | 3381.17 | 47.07 | |
| TSN_CRIGR | - | - | - | 5 | 338.21 | 15.47 | 14.93 | 5 | 338.21 | 5 | 14.93 | 390.61 | 3245.56 | 50.23 | 5 | 3381.17 | 47.07 | |
| XPRI_CRIGR | - | - | - | 2 | 170.69 | 6.32 | - | - | - | - | - | - | 55.63 | 10.09 | 2 | 309.18 | 15.83 | |

Table S-7: Proteins detected with sequential digestion.

| Protein ID | Sequential 1 Unique Peptides | Sequential 1 Best Score | Sequential 2 Unique Peptides | Sequential 2 Coverage (%) | Sequential 3 Best Score | Sequential 3 Unique Peptides | Sequential 3 Coverage (%) | Sequential 4 Best Score | Sequential 4 Unique Peptides | Sequential 4 Coverage (%) | Sequential 5 Best Score | Sequential 5 Unique Peptides | Sequential 5 Coverage (%) | Sequential 6 Unique Peptides | Sequential 6 Coverage (%) | Best Score |
|--------------|---------------------------------|----------------------------|---------------------------------|------------------------------|----------------------------|---------------------------------|------------------------------|----------------------------|---------------------------------|------------------------------|----------------------------|---------------------------------|------------------------------|---------------------------------|------------------------------|------------|
| A1E3K3_CRIGR | 2 | 97.34 | 2 | 12.5 | 96.39 | 2 | 13.54 | 176.67 | 2 | 13.54 | 210.54 | 2 | 13.54 | 2 | 189.74 | 79.1 |
| ASHUN3_CRIGR | 3 | 13.37 | 2 | 9.19 | 58.49 | 4 | 8.55 | 51.82 | 2 | 15.13 | 35.77 | 2 | 15.13 | 4 | 74.12 | 147.54 |
| A1MP1_CRIGR | 3 | 6.14 | 2 | 9.19 | 68.03 | 4 | 16.71 | 124.68 | 4 | 18.38 | 103.28 | 2 | 16.71 | 4 | 74.12 | 147.54 |
| BAIP2_CRIGR | 3 | 43.04 | 4 | 9.19 | 68.03 | 4 | 8.64 | 78.48 | 3 | 6.53 | 34.82 | 2 | 9.19 | 2 | 27.05 | 54.91 |
| BASI_CRIGR | 4 | 17.73 | 4 | 17.73 | 82.41 | 4 | 18.23 | 146.92 | 3 | 16.26 | 85.93 | 3 | 11.65 | 2 | 27.05 | 54.91 |
| BST2_CRIGR | 7 | 15.04 | 4 | 17.73 | 203.55 | 8 | 18.14 | 239.6 | 7 | 15.93 | 269.15 | 8 | 18.14 | 8 | 227.95 | 207.22 |
| COSSX9_CRIGR | 4 | 142.94 | 4 | 12.43 | 241.15 | 4 | 12.43 | 239.6 | 4 | 12.43 | 269.15 | 4 | 12.43 | 4 | 481.84 | 207.22 |
| CD44_CRIGR | 2 | 95.26 | 2 | 16.88 | 220.06 | 2 | 18.6 | 155.35 | 2 | 18.6 | 132.71 | 2 | 16.88 | 2 | 211.19 | 140.44 |
| CIRBP_CRIGR | 7 | 32.47 | 4 | 16.88 | 361.09 | 7 | 31.49 | 230.98 | 6 | 29.55 | 386.43 | 4 | 16.88 | 4 | 211.19 | 140.44 |
| COPE_CRIGR | 2 | 10.15 | 2 | 10.15 | 33.28 | 2 | 10.15 | 27.54 | 12 | 27.92 | 434.05 | 11 | 27.92 | 10 | 379.54 | 269.54 |
| DPM1_CRIGR | 2 | 25.54 | 9 | 20.56 | 341.66 | 12 | 24.89 | 290.61 | 12 | 27.92 | 434.05 | 11 | 27.92 | 10 | 379.54 | 269.54 |
| EF1A1_CRIGR | 2 | 2.33 | 3 | 3.85 | 102.6 | 3 | 3.85 | 92.3 | 2 | 2.33 | 60.74 | 3 | 4.43 | 5 | 114.26 | 107.84 |
| EF2_CRIGR | 4 | 81.27072 | 4 | 15.73 | 157.71 | 5 | 28.86 | 66.81 | 5 | 24.88 | 137.06 | 6 | 25.87 | 8 | 325.8 | 149.98 |
| F7J0L2_CRIGR | 3 | 14.43 | 4 | 14.33 | 161.48 | 3 | 10.95 | 136.37 | 3 | 12.24 | 135.88 | 5 | 15.46 | 3 | 82.67 | 116.26 |
| F7J0L3_CRIGR | 4 | 13.04 | 4 | 14.33 | 161.48 | 3 | 10.95 | 136.37 | 3 | 12.24 | 135.88 | 5 | 15.46 | 3 | 82.67 | 116.26 |
| FXR1_CRIGR | 2 | 3.66 | 2 | 4.57 | 136.85 | 3 | 5.84 | 57.7 | 2 | 3.94 | 64.27 | 2 | 4.57 | 2 | 82.67 | 116.26 |
| FXR86_CRIGR | 4 | 7.41 | 2 | 4.57 | 136.85 | 3 | 5.84 | 57.7 | 2 | 3.94 | 64.27 | 2 | 4.57 | 2 | 82.67 | 116.26 |
| FXR93_CRIGR | 2 | 5.53 | 4 | 12.6 | 157.12 | 4 | 4.94 | 57.7 | 3 | 9.53 | 70.02 | 2 | 5.49 | 3 | 73.7 | 125.33 |
| FXR95_CRIGR | 2 | 9.53 | 4 | 12.6 | 157.12 | 4 | 4.94 | 57.7 | 3 | 9.53 | 70.02 | 2 | 5.49 | 3 | 73.7 | 125.33 |
| GGR10_CRIGR | 2 | 4.94 | 2 | 1.57 | 74.89 | 2 | 1.57 | 74.89 | 2 | 1.57 | 74.89 | 2 | 1.57 | 2 | 73.7 | 67.59 |
| GGRB1_CRIGR | 2 | 1.69 | 2 | 1.77 | 75.17 | 2 | 1.92 | 62.31 | 2 | 1.92 | 62.31 | 2 | 1.92 | 2 | 73.7 | 67.59 |
| GGRB9_CRIGR | 13 | 13.06 | 12 | 13.43 | 438.51 | 16 | 16.26 | 422.52 | 13 | 13.21 | 541.36 | 14 | 14.08 | 13 | 506.58 | 443.94 |
| GGRD7_CRIGR | 2 | 86.32 | 2 | 7.11 | 164.97 | 2 | 12.31 | 87.43 | 2 | 7.11 | 164.97 | 2 | 12.31 | 2 | 86.32 | 443.94 |
| GGRD8_CRIGR | 2 | 28.65 | 2 | 22.64 | 137.44 | 2 | 22.06 | 200.34 | 2 | 7.11 | 164.97 | 2 | 12.31 | 2 | 86.32 | 443.94 |
| GGRD9_CRIGR | 6 | 4.93 | 6 | 8.23 | 167.31 | 3 | 13.4 | 250.51 | 3 | 26.65 | 365.69 | 5 | 18.62 | 3 | 200.42 | 191.7 |
| GGRD9_CRIGR | 7 | 9.3 | 6 | 8.23 | 129.69 | 9 | 11.26 | 267.55 | 9 | 11.26 | 267.55 | 2 | 7.93 | 8 | 136.46 | 146.66 |
| GGRD9_CRIGR | 7 | 213.32 | 6 | 3.16 | 111.31 | 2 | 3.16 | 111.31 | 2 | 3.16 | 111.31 | 2 | 3.16 | 2 | 146.49 | 234.44 |
| GGRD9_CRIGR | 3 | 5.96 | 2 | 10 | 64.6 | 2 | 3.63 | 38.78 | 2 | 4.92 | 44.21 | 2 | 4.4 | 2 | 33.79 | 234.44 |
| GGRX2_CRIGR | 2 | 80.8 | 2 | 10 | 76.14 | 2 | 5.5 | 129.76 | 2 | 4.92 | 44.21 | 2 | 4.4 | 2 | 33.79 | 234.44 |
| GGS14_CRIGR | 2 | 16.49 | 2 | 13.23 | 266.81 | 7 | 15.96 | 215.79 | 2 | 15.96 | 65.83 | 2 | 15.96 | 2 | 15.96 | 265.68 |
| GGS61_CRIGR | 8 | 13.61 | 8 | 13.23 | 266.81 | 7 | 15.96 | 215.79 | 6 | 10.86 | 646.73 | 11 | 18.6 | 6 | 443.55 | 288.4 |
| GGS70_CRIGR | 2 | 243.46 | 2 | 1.38 | 46.28 | 2 | 1.92 | 79.23 | 2 | 1.92 | 79.23 | 2 | 1.92 | 2 | 443.55 | 288.4 |
| GGS82_CRIGR | 2 | 712.68 | 2 | 24.11 | 852.53 | 2 | 23.72 | 751.88 | 2 | 1.92 | 79.23 | 2 | 1.92 | 2 | 443.55 | 288.4 |
| GGS87_CRIGR | 2 | 424.54 | 7 | 16.77 | 703.19 | 3 | 15 | 68.68 | 3 | 8.67 | 100.9 | 5 | 23.72 | 5 | 1335.02 | 602.82 |
| GGS87_CRIGR | 8 | 18.43 | 7 | 16.77 | 703.19 | 3 | 15 | 68.68 | 10 | 21.45 | 564.9 | 11 | 22.96 | 10 | 541.24 | 602.82 |
| GGS87_CRIGR | 3 | 10.35 | 2 | 2.93 | 26.62 | 2 | 7.63 | 203.97 | 3 | 10.35 | 136.32 | 2 | 7.63 | 2 | 151.16 | 136.79 |
| GGS87_CRIGR | 4 | 175.71 | 4 | 14.71 | 217.02 | 2 | 7.63 | 203.97 | 3 | 10.35 | 136.32 | 2 | 7.63 | 2 | 151.16 | 136.79 |
| GGS87_CRIGR | 8 | 15.32 | 5 | 10.44 | 445.05 | 7 | 15.72 | 363.56 | 7 | 15.72 | 495.81 | 7 | 15.32 | 7 | 467.53 | 264 |
| GGS87_CRIGR | 2 | 2.33 | 2 | 2.73 | 116.62 | 2 | 3.33 | 168.44 | 3 | 3.64 | 160.94 | 2 | 3.76 | 2 | 139.68 | 38.43 |
| GGS88_CRIGR | 2 | 3.89 | 2 | 2.73 | 131.13 | 3 | 5.32 | 99.69 | 3 | 3.64 | 160.94 | 2 | 3.76 | 2 | 139.68 | 38.43 |
| GGS88_CRIGR | 2 | 68.13 | 2 | 32.11 | 530.9 | 17 | 29.46 | 587.29 | 19 | 29.96 | 560.55 | 18 | 29.33 | 17 | 630.12 | 102.01 |
| GGS88_CRIGR | 17 | 27.43 | 20 | 32.11 | 530.9 | 17 | 29.46 | 587.29 | 19 | 29.96 | 560.55 | 18 | 29.33 | 17 | 630.12 | 102.01 |
| GGS88_CRIGR | 2 | 616.38 | 2 | 10 | 76.14 | 2 | 5.5 | 129.76 | 2 | 4.92 | 44.21 | 2 | 4.4 | 2 | 33.79 | 234.44 |
| GGS88_CRIGR | 2 | 148.2 | 4 | 20 | 111.15 | 6 | 32.68 | 151.44 | 4 | 1.81 | 38.16 | 3 | 17.56 | 4 | 82.36 | 103.43 |
| GGS88_CRIGR | 4 | 312.77 | 4 | 20 | 238.49 | 3 | 24.35 | 213.85 | 3 | 15.65 | 256.91 | 3 | 15.65 | 3 | 247.26 | 207.53 |
| GGS88_CRIGR | 3 | 55.92 | 3 | 1.85 | 80.12 | 5 | 4.83 | 172.28 | 4 | 4.83 | 172.28 | 4 | 3.02 | 3 | 97.95 | 207.53 |
| GGS88_CRIGR | 3 | 77.26 | 2 | 5.16 | 97.68 | 4 | 10.68 | 117.22 | 5 | 14.69 | 210.76 | 5 | 14.69 | 5 | 210.76 | 97.95 |
| GGS88_CRIGR | 3 | 97.98 | 2 | 4.79 | 46.7 | 2 | 3.2 | 71.9 | 4 | 5.16 | 106.01 | 3 | 5.16 | 3 | 81.82 | 91.51 |
| GGS88_CRIGR | 3 | 97.98 | 2 | 4.79 | 46.7 | 2 | 3.2 | 71.9 | 4 | 5.16 | 106.01 | 3 | 5.16 | 3 | 81.82 | 91.51 |
| GGS88_CRIGR | 2 | 59.25 | 4 | 8.18 | 90.35 | 4 | 8.18 | 93.22044 | 3 | 6.7 | 155.64 | 2 | 8.18 | 2 | 137.19 | 58.11 |
| GGS88_CRIGR | 5 | 22.81 | 6 | 30.12 | 197.26 | 4 | 22.83 | 143.82 | 3 | 30.42 | 143.82 | 3 | 18.28 | 3 | 137.19 | 93.7 |
| GGS88_CRIGR | 3 | 55.96 | 4 | 10.12 | 135.92 | 4 | 13.99 | 129.19 | 6 | 30.42 | 143.82 | 3 | 18.28 | 3 | 137.19 | 93.7 |
| GGS88_CRIGR | 3 | 55.96 | 4 | 10.12 | 135.92 | 4 | 13.99 | 129.19 | 6 | 30.42 | 143.82 | 3 | 18.28 | 3 | 137.19 | 93.7 |
| GGS88_CRIGR | 16 | 49.48 | 17 | 49.48 | 477.19 | 16 | 48.8 | 466.77 | 17 | 51.89 | 773.8 | 16 | 51.89 | 16 | 773.8 | 115.17 |
| GGS88_CRIGR | 32 | 1083.21 | 31 | 15.63 | 860.67 | 2 | 20.23 | 125.13 | 41 | 20.75 | 1318.08 | 45 | 22.35 | 35 | 1522.99 | 541.83 |
| GGS88_CRIGR | 8 | 280.62 | 9 | 33.46 | 358.07 | 10 | 36.03 | 363.14 | 10 | 36.03 | 403.16 | 9 | 36.03 | 9 | 335.65 | 1165.86 |
| GGS88_CRIGR | 2 | 59.98 | 2 | 3.61 | 89.86 | 2 | 28.83 | 69.15 | 2 | 28.83 | 132.31 | 2 | 28.83 | 2 | 134.66 | 424.9 |
| GGS88_CRIGR | 5 | 11.11 | 4 | 10.88 | 333.44 | 3 | 7.64 | 364.43 | 4 | 11.11 | 250.69 | 4 | 10.88 | 5 | 396.18 | 107.55 |
| GGS88_CRIGR | 4 | 77.49 | 4 | 4.02 | 35.15 | 2 | 28.83 | 69.15 | 2 | 28.83 | 132.31 | 2 | 28.83 | 2 | 134.66 | 284.29 |
| GGS88_CRIGR | 6 | 4 | 4 | 4.02 | 35.15 | 2 | 28.83 | 69.15 | 2 | 28.83 | 132.31 | 2 | 28.83 | 2 | 134.66 | 284.29 |
| GGS88_CRIGR | 6 | 120.05 | 5 | 3.36 | 60 | 4 | 2.5 | 76.25 | 5 | 4.42 | 113.48 | 3 | 2.02 | 3 | 66.43 | 65.41 |
| GGS88_CRIGR | 6 | 6.33 | 5 | 5.46 | 393.86 | 6 | 3.59 | 82.01 | 7 | 7.26 | 402.13 | 4 | 7.26 | 4 | 451.96 | 272.74 |
| GGS88_CRIGR | 6 | 9.87 | 6 | 9.62 | 245.09 | 7 | 11.27 | 170.33 | 6 | 10.13 | 183.37 | 8 | 8.48 | 8 | 223.37 | 289.64 |
| GGS88_CRIGR | 4 | 147.15 | 4 | 12.37 | 143.5 | 3 | 7.58 | 86.58 | 3 | 9.34 | 80.82 | 4 | 12.37 | 4 | 114.14 | 175.95 |
| GGS88_CRIGR | 2 | 77.38 | 2 | 4.2 | 43.76 | 2 | 4.2 | 43.76 | 2 | 4.2 | 43.76 | 2 | 4.2 | 2 | 75.44 | 102.99 |
| GGS88_CRIGR | 2 | 43.76 | 2 | 5.48 | 43.76 | 3 | 5.48 | 43.76 | 2 | 4.02 | 44.53 | 2 | 4.02 | 2 | 44.53 | 102.99 |

Continued on Next Page...

Table S-7 – Continued

| Protein ID | Sequential 1 | | | Sequential 2 | | | Sequential 3 | | | Sequential 4 | | | Sequential 5 | | | Sequential 6 | | |
|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|
| | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) |
| GSGZB1_CRIGR | 2 | - | 12.03 | 3 | 139.68 | 1.94 | 2 | 6.68 | 98.1 | 6.68 | 49.43 | 2 | 2 | 6.68 | 2 | 49.43 | 6.68 | 72.29 |
| GSGZB3_CRIGR | 2 | 50.27 | 2.76 | 3 | 192.72 | 3.33 | 3 | 2.08 | 102.98 | 2.08 | 106.1 | 2 | 3 | 3.06 | 2 | 106.1 | 3.06 | 244.93 |
| GSGZD8_CRIGR | 4 | 7.96 | 5.19 | 4 | 59.22 | 7.96 | 4 | 2.78 | 61.82 | 2.78 | 61.82 | 4 | 4 | 3.07 | 4 | 61.82 | 3.07 | 47.59 |
| GSGZG5_CRIGR | 6 | 12.69 | 18.85 | 3 | 218.16 | 17.69 | 3 | 23.85 | 180.78 | 23.85 | 180.78 | 4 | 4 | 9.07 | 3 | 180.78 | 9.07 | 153.98 |
| GSGZH5_CRIGR | 6 | 13.13 | 8.39 | 8 | 176.24 | 14.11 | 9 | 19.3 | 389.16 | 19.3 | 389.16 | 7 | 7 | 15.03 | 8 | 389.16 | 15.03 | 279.76 |
| GSGZH6_CRIGR | 24 | 20.37 | 23.11 | 27 | 827.12 | 20.82 | 27 | 24.22 | 981.86 | 24.22 | 981.86 | 26 | 26 | 20.37 | 25 | 981.86 | 20.37 | 1056.95 |
| GSGZJ6_CRIGR | 3 | 7.76 | 7.76 | 4 | 116.75 | 13.55 | 5 | 12.99 | 123.19 | 12.99 | 123.19 | 2 | 2 | 5.37 | 2 | 123.19 | 5.37 | 269.64 |
| GSGZK6_CRIGR | 2 | 21.99 | 21.99 | 2 | 56.22 | 21.99 | 2 | 21.99 | 98.24 | 21.99 | 98.24 | 2 | 2 | 21.99 | 2 | 98.24 | 21.99 | 124.3 |
| GSGZQ4_CRIGR | 2 | 6.95 | 6.95 | 142.15 | 142.15 | 21.29 | 7 | 18.58 | 503.76 | 18.58 | 503.76 | 2 | 2 | 6.95 | 2 | 503.76 | 6.95 | 181.32 |
| GSGZU1_CRIGR | 9 | 30.27 | 25.68 | 265.11 | 265.11 | 6.39 | 4 | 138.15 | 186.65 | 6.39 | 186.65 | 6 | 6 | 16.28 | 6 | 186.65 | 16.28 | 296 |
| GSGZV9_CRIGR | 2 | 3.19 | 3.19 | 138.15 | 138.15 | 4.6 | 4 | 100.98 | 98.62 | 4.6 | 98.62 | 2 | 2 | 3.19 | 2 | 98.62 | 3.19 | 87.21 |
| GSGZV7_CRIGR | 4 | 3.81 | 2.66 | 75.11 | 75.11 | 11.38 | 2 | 1.58 | 97.29 | 11.38 | 97.29 | 4 | 4 | 4.32 | 4 | 97.29 | 4.32 | 92.17 |
| GSGZV7_CRIGR | 4 | 154.66 | 8.98 | 65.68 | 65.68 | 41.88 | 2 | 225.91 | 57.08 | 41.88 | 57.08 | 2 | 2 | 6.29 | 2 | 57.08 | 6.29 | 114.08 |
| GSGZV7_CRIGR | 4 | 44.38 | 473.2237 | 566.5942 | 566.5942 | 3.41 | 3 | 33.75 | 448.72 | 3.41 | 448.72 | 3 | 3 | 41.88 | 3 | 448.72 | 41.88 | 483 |
| GSH018_CRIGR | 4 | 9.83 | 212.54 | 43.29 | 43.29 | 2.47 | 2 | 2.47 | 75.99 | 2.47 | 75.99 | 3 | 3 | 3.12 | 3 | 75.99 | 3.12 | 51.05 |
| GSH037_CRIGR | 4 | 20.75 | 224.2974 | 370.26 | 370.26 | 9.83 | 4 | 9.83 | 198.21 | 9.83 | 198.21 | 5 | 5 | 11.22 | 5 | 198.21 | 11.22 | 192.84 |
| GSH042_CRIGR | 10 | 12.3 | 13.29 | 228.59 | 228.59 | 6.01 | 8 | 18.31 | 282.29 | 6.01 | 282.29 | 9 | 9 | 16.69 | 10 | 282.29 | 16.69 | 344.95 |
| GSH055_CRIGR | 3 | 5.34 | 318.54 | 90.09 | 90.09 | 12.3 | 3 | 10.11 | 147.78 | 12.3 | 147.78 | 3 | 3 | 12.3 | 3 | 147.78 | 12.3 | 160.13 |
| GSH054_CRIGR | 9 | 13.04 | 35.39 | 223.81 | 223.81 | 7.71 | 11 | 218.93 | 130.44 | 7.71 | 130.44 | 13 | 13 | 7.92 | 12 | 130.44 | 7.92 | 264.07 |
| GSH056_CRIGR | 2 | 7.71 | 8.92 | 59.98 | 59.98 | 7.23 | 2 | 15.22 | 152.46 | 7.23 | 152.46 | 2 | 2 | 15.22 | 2 | 152.46 | 15.22 | 74.16 |
| GSH056_CRIGR | 3 | 34.52 | 18.47 | 65.88 | 65.88 | 26.15 | 3 | 36.54 | 602.11 | 26.15 | 602.11 | 3 | 3 | 26.15 | 3 | 602.11 | 26.15 | 605.27 |
| GSH056_CRIGR | 2 | 27.52 | 26.15 | 333.95 | 333.95 | 7.96 | 5 | 7.96 | 89.98 | 7.96 | 89.98 | 5 | 5 | 8.12 | 6 | 89.98 | 8.12 | 92.26 |
| GSH060_CRIGR | 2 | 5.41 | 3.41 | 46.21 | 46.21 | 8.12 | 4 | 8.12 | 89.98 | 8.12 | 89.98 | 4 | 4 | 8.12 | 4 | 89.98 | 8.12 | 92.26 |
| GSH109_CRIGR | 2 | 18.11 | 3.71 | 85.61 | 85.61 | 16.14 | 2 | 16.14 | 82.75 | 16.14 | 82.75 | 2 | 2 | 8.83 | 2 | 82.75 | 8.83 | 122.43 |
| GSH125_CRIGR | 2 | 8.83 | 10.83 | 102.89 | 102.89 | 8.83 | 2 | 8.83 | 121.05 | 8.83 | 121.05 | 2 | 2 | 11.95 | 2 | 121.05 | 11.95 | 275.41 |
| GSH133_CRIGR | 3 | 11.95 | 15.26 | 76.77 | 76.77 | 15.26 | 4 | 15.26 | 120.11 | 15.26 | 120.11 | 4 | 4 | 15.26 | 4 | 120.11 | 15.26 | 108.48 |
| GSH151_CRIGR | 4 | 18.06 | 15.26 | 64.54 | 64.54 | 2.73 | 3 | 2.73 | 270.2 | 2.73 | 270.2 | 2 | 2 | 3.5 | 2 | 270.2 | 3.5 | 278.14 |
| GSH160_CRIGR | 4 | 5.46 | 12.78 | 141.43 | 141.43 | 20.78 | 5 | 20.78 | 155 | 20.78 | 155 | 5 | 5 | 26.41 | 7 | 155 | 26.41 | 288.76 |
| GSH162_CRIGR | 6 | 24.24 | 21.21 | 280.83 | 280.83 | 11.48 | 5 | 11.48 | 82.52 | 11.48 | 82.52 | 6 | 6 | 13.93 | 8 | 82.52 | 13.93 | 160.26 |
| GSH168_CRIGR | 3 | 13.86 | 253.6421 | 12.98 | 12.98 | 20.78 | 9 | 20.78 | 409.61 | 20.78 | 409.61 | 9 | 9 | 19.1 | 8 | 409.61 | 19.1 | 206.13 |
| GSH170_CRIGR | 10 | 21.78 | 20.44 | 561.07 | 561.07 | 18.59 | 7 | 18.59 | 109.76 | 18.59 | 109.76 | 5 | 5 | 6.24 | 2 | 109.76 | 6.24 | 84.63 |
| GSH177_CRIGR | 3 | 7.58 | 12.64 | 149.74 | 149.74 | 15.73 | 5 | 15.73 | 103.9 | 15.73 | 103.9 | 2 | 2 | 47.19 | 6 | 103.9 | 47.19 | 179.68 |
| GSH193_CRIGR | 3 | 16.56 | 142.6 | 113.78 | 113.78 | 10.6 | 2 | 10.6 | 103.9 | 10.6 | 103.9 | 7 | 7 | 47.19 | 6 | 103.9 | 47.19 | 179.68 |
| GSH194_CRIGR | 4 | 31.46 | 32.02 | 119.03 | 119.03 | 6.76 | 2 | 6.76 | 131.67 | 6.76 | 131.67 | 2 | 2 | 42.16 | 2 | 131.67 | 42.16 | 46.79 |
| GSH1A4_CRIGR | 5 | 50 | 45.1 | 288.92 | 288.92 | 45.59 | 9 | 45.59 | 307.65 | 45.59 | 307.65 | 8 | 8 | 42.16 | 8 | 307.65 | 42.16 | 323.77 |
| GSH1B3_CRIGR | 11 | 13.86 | 13.86 | 207.35 | 207.35 | 12.98 | 4 | 12.98 | 248.38 | 12.98 | 248.38 | 5 | 5 | 13.27 | 8 | 248.38 | 13.27 | 228.58 |
| GSH1F4_CRIGR | 3 | 21.47 | 26.38 | 133.35 | 133.35 | 25.15 | 4 | 25.15 | 148.71 | 25.15 | 148.71 | 6 | 6 | 30.06 | 6 | 148.71 | 30.06 | 151.64 |
| GSH1L7_CRIGR | 4 | 12.9 | 89.37 | 73.93 | 73.93 | 15.45 | 2 | 15.45 | 57.6 | 15.45 | 57.6 | 2 | 2 | 15.45 | 2 | 57.6 | 15.45 | 45.74 |
| GSH1M4_CRIGR | 2 | 20.82 | 187.4096 | 38.37 | 38.37 | 25.28 | 6 | 25.28 | 118.53 | 25.28 | 118.53 | 3 | 3 | 20.07 | 3 | 118.53 | 20.07 | 188.7 |
| GSH1M5_CRIGR | 5 | 6.5 | 78.92667 | 194.3 | 194.3 | 33.75 | 7 | 33.75 | 160.79 | 33.75 | 160.79 | 4 | 4 | 33.13 | 6 | 160.79 | 33.13 | 179.05 |
| GSH1R5_CRIGR | 2 | 33.75 | 237.99 | 131.12 | 131.12 | 26.57 | 6 | 26.57 | 150.84 | 26.57 | 150.84 | 5 | 5 | 26.57 | 6 | 150.84 | 26.57 | 158.28 |
| GSH1V1_CRIGR | 5 | 19.43 | 362.39 | 331.42 | 331.42 | 41.24 | 8 | 41.24 | 562.78 | 41.24 | 562.78 | 6 | 6 | 43.8 | 7 | 562.78 | 43.8 | 267.12 |
| GSH204_CRIGR | 7 | 14.24 | 225.36 | 11.15 | 11.15 | 14.13 | 6 | 14.13 | 346.19 | 14.13 | 346.19 | 7 | 7 | 18.21 | 6 | 346.19 | 18.21 | 312.09 |
| GSH239_CRIGR | 2 | 2.16 | 77.62 | 52.46 | 52.46 | 9.71 | 3 | 9.71 | 84.9 | 9.71 | 84.9 | 2 | 2 | 6.2 | 2 | 84.9 | 6.2 | 51.94 |
| GSH283_CRIGR | 4 | 4.75 | 110.86 | 81.76 | 81.76 | 11.78 | 4 | 11.78 | 105.57 | 11.78 | 105.57 | 3 | 3 | 2.57 | 3 | 105.57 | 2.57 | 51.94 |
| GSH286_CRIGR | 2 | 23.7 | 97.63 | 65.13 | 65.13 | 16.59 | 3 | 16.59 | 76.66 | 16.59 | 76.66 | 3 | 3 | 16.59 | 3 | 76.66 | 16.59 | 109.38 |
| GSH2E2_CRIGR | 4 | 6.49 | 73.7 | 68.51 | 68.51 | 12.41 | 2 | 12.41 | 92.94 | 12.41 | 92.94 | 3 | 3 | 3.83 | 3 | 92.94 | 3.83 | 49.0 |
| GSH2G5_CRIGR | 2 | 12.41 | 97.86 | 112.7254 | 112.7254 | 2.71 | 2 | 2.71 | 86.67 | 2.71 | 86.67 | 3 | 3 | 3.83 | 4 | 86.67 | 3.83 | 124.35 |
| GSH2H8_CRIGR | 3 | 5.11 | 53.43 | 135.62 | 135.62 | 6.77 | 4 | 6.77 | 143.31 | 6.77 | 143.31 | 2 | 2 | 3.8 | 2 | 143.31 | 3.8 | 105.25 |
| GSH2N6_CRIGR | 2 | 39.09 | 343.25 | 19.04 | 19.04 | 3.35 | 2 | 3.35 | 66.37 | 3.35 | 66.37 | 7 | 7 | 26.4 | 9 | 66.37 | 26.4 | 59.34 |
| GSH2P5_CRIGR | 9 | 43.65 | 614.16 | 40.48 | 40.48 | 25.38 | 6 | 25.38 | 389.69 | 25.38 | 389.69 | 2 | 2 | 31.73 | 9 | 389.69 | 31.73 | 277.81 |
| GSH2S5_CRIGR | 7 | 19.85 | 280.29 | 23.97 | 23.97 | 11.4 | 4 | 11.4 | 126.74 | 11.4 | 126.74 | 3 | 3 | 6.49 | 2 | 126.74 | 6.49 | 736.64 |
| GSH2T4_CRIGR | 2 | 6.32 | 113.31 | 36.11 | 36.11 | 19.74 | 5 | 19.74 | 116.54 | 19.74 | 116.54 | 6 | 6 | 22.11 | 6 | 116.54 | 22.11 | 153.19 |
| GSH2U6_CRIGR | 3 | 10.53 | 179.29 | 166.56 | 166.56 | 7.23 | 4 | 7.23 | 93.88 | 7.23 | 93.88 | 4 | 4 | 6.32 | 4 | 93.88 | 6.32 | 44.98 |
| GSH2W0_CRIGR | 3 | 10.95 | 76.7769 | 41.02 | 41.02 | 30.48 | 5 | 30.48 | 133.7788 | 30.48 | 133.7788 | 2 | 2 | 26.19 | 2 | 133.7788 | 26.19 | 137.03 |
| GSH2Z7_CRIGR | 2 | 27.37 | 3408.77 | 3181.02 | 3181.02 | 26.76 | 100 | 26.76 | 3001.26 | 26.76 | 3001.26 | 113 | 113 | 30.92 | 103 | 3001.26 | 30.92 | 3381.4 |
| GSH344_CRIGR | 102 | 27.37 | 3408.77 | 3181.02 | 3181.02 | 26.76 | 100 | 26.76 | 3001.26 | 26.76 | 3001.26 | 113 | 113 | 30.92 | 103 | 3001.26 | 30.92 | 3381.4 |
| GSH352_CRIGR | 102 | 27.37 | 3408.77 | 3181.02 | 3181.02 | 26.76 | 100 | 26.76 | 3001.26 | 26.76 | 3001.26 | 113 | 113 | 30.92 | 103 | 3001.26 | 30.92 | 3381.4 |

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Table S-7 – Continued

| Protein ID | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score |
|--------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|
| GSH354_CRIGR | - | - | - | - | - | - | 2 | 23.19 | 407.13 | 2 | 33.43 | 377.85 | 2 | 12.77 | 92.47 |
| GSH3C0_CRIGR | 2 | 1.79 | 40.43 | - | 2.03 | 52.3 | - | - | - | - | - | - | 2 | 2.27 | 58.03 |
| GSH3C3_CRIGR | 4 | 12.75 | 126.62 | 6 | 20.25 | 157.78 | 2 | 8.5 | 62.42 | 7 | 21.25 | 246.86 | 5 | 17.75 | 205.35 |
| GSH3E3_CRIGR | 2 | 4.06 | 96.19 | 6 | 13.25 | 199.19 | 3 | 9.36 | 126.51 | 3 | 11.13 | 89.69 | 3 | 8.48 | 99.49 |
| GSH3G9_CRIGR | 5 | 5.52 | 292.45 | 8 | 11.97 | 345.1 | 7 | 8.15 | 309.14 | 9 | 10.87 | 395.86 | 7 | 9.17 | 238.96 |
| GSH3J6_CRIGR | - | - | - | 5 | 10.93 | 88.88 | - | - | - | - | - | - | - | - | - |
| GSH3P1_CRIGR | 5 | 33.5 | 282.03 | 6 | 38.83 | 213.63 | 5 | 29.61 | 257.54 | 4 | 24.27 | 309.87 | 5 | 29.61 | 308.25 |
| GSH3P5_CRIGR | 5 | 8.61 | 175.76 | 6 | 10.15 | 109.02 | 4 | 8.1 | 289.76 | 4 | 8.1 | 191.47 | 4 | 7.84 | 115.1 |
| GSH3Q1_CRIGR | 16 | 42.16 | 1015.45 | 18 | 47.88 | 1091.27 | 14 | 38.35 | 928.59 | 17 | 47.03 | 756.1 | 20 | 51.69 | 790.25 |
| GSH3S0_CRIGR | 2 | 4.53 | 78.78 | 3 | 6.31 | 90.16 | 2 | 18.01 | 110.93 | 2 | 18.01 | 122.29 | 3 | 6.8 | 127.89 |
| GSH3V5_CRIGR | - | - | - | 4 | 9.8 | 99.17 | - | - | - | - | - | - | - | - | - |
| GSH3X1_CRIGR | 2 | 4.25 | 59.87 | 2 | 4.25 | 87.51 | 2 | 5.88 | 89.55 | 2 | 5.88 | 56.68 | 4 | 9.48 | 109.51 |
| GSH3Y2_CRIGR | 2 | 6.49 | 199.42 | 3 | 29.35 | 197.99 | 3 | 29.35 | 299.25 | 3 | 29.35 | 237.19 | 3 | 29.35 | 229.76 |
| GSH3Z5_CRIGR | 3 | 29.35 | 242.78 | 3 | 29.35 | 72.86 | 2 | 9.86 | 288.47 | 4 | 10.14 | 115.97 | 4 | 27.25 | 351.34 |
| GSH437_CRIGR | 3 | 19.71 | 201.82 | 4 | 26.67 | 72.86 | 2 | 9.86 | 64.28 | 2 | 10.14 | 107.61 | 2 | 2.5 | 63.29 |
| GSH445_CRIGR | - | - | - | 3 | 3.34 | 36.03 | - | - | - | 3 | 3.81 | 107.61 | 2 | 2.5 | 63.29 |
| GSH451_CRIGR | 6 | 13.68 | 345.52 | 3 | 6.76 | 81.51 | 5 | 12.5 | 302.38 | 6 | 15.54 | 371.34 | 6 | 15.54 | 565.21 |
| GSH487_CRIGR | 7 | 11.28 | 140.73 | 8 | 13.88 | 134.07 | 5 | 7.65 | 127.99 | 7 | 13.1 | 97.28 | 5 | 10.38 | 97.39 |
| GSH4D2_CRIGR | 2 | 2.64 | 56.47 | 2 | 2.64 | 56.47 | 2 | 2.64 | 64.49 | 2 | 2.64 | 64.49 | 2 | 2.64 | 111.53 |
| GSH4F5_CRIGR | 2 | 1.11 | 29.88 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH4H6_CRIGR | 3 | 8.39 | 93.88 | 4 | 11.11 | 106.63 | 5 | 15.65 | 129.57 | 3 | 8.39 | 160.92 | 3 | 8.39 | 73.61 |
| GSH4H1_CRIGR | 3 | 29.24 | 382.62 | 3 | 31.78 | 559.56 | 3 | 28.81 | 598.94 | 3 | 28.81 | 520.77 | 3 | 28.81 | 450.34 |
| GSH4L2_CRIGR | 2 | 21.89 | 213.92 | 2 | 19.23 | 270.92 | 2 | 21.89 | 170.18 | 2 | 23.02 | 69.35 | 2 | 2.5 | 63.29 |
| GSH4O0_CRIGR | 3 | 17.57 | 166.52 | 4 | 12.46 | 215.93 | 2 | 20.25 | 372.55 | 7 | 16.25 | 332.74 | 7 | 16.25 | 332.74 |
| GSH4V4_CRIGR | 4 | 15.26 | 140.73 | 3 | 11.84 | 107.99 | 5 | 20.25 | 122.31 | 5 | 20.25 | 172.37 | 2 | 8.48 | 77.76 |
| GSH4Z5_CRIGR | 5 | 7.48 | 193.06 | 6 | 9.19 | 281.27 | 7 | 10.04 | 273.62 | 8 | 11.75 | 232.92 | 7 | 7.8 | 149.34 |
| GSH515_CRIGR | 3 | 38.65 | 550.78 | 4 | 42.51 | 485.71 | 3 | 38.65 | 668.54 | 4 | 38.65 | 536.37 | 4 | 5.17 | 87.68 |
| GSH530_CRIGR | - | - | - | 2 | 5.17 | 35.31 | - | - | - | 2 | 5.17 | 30.68 | - | - | - |
| GSH533_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH559_CRIGR | 2 | 2.55 | 104.25 | 3 | 3.91 | 138.94 | 2 | 2.55 | 143.19 | - | - | - | 2 | 2.55 | 90.18 |
| GSH5A2_CRIGR | 2 | 26.32 | 44.63 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH5E5_CRIGR | 2 | 31.61 | 177.32 | 2 | 32.16 | 180.62 | 2 | 18.94 | 144.49 | 3 | 27.31 | 216.22 | 2 | 38.33 | 297.37 |
| GSH5H2_CRIGR | 4 | 31.61 | 177.32 | 4 | 31.61 | 165.85 | 2 | 16.77 | 161.43 | 2 | 16.77 | 154.98 | 3 | 23.23 | 189.32 |
| GSH5N5_CRIGR | 4 | 6.15 | 77.56 | 4 | 15.54 | 55.08 | 2 | 7.77 | 77.76 | 4 | 6.48 | 56.17 | 3 | 14.25 | 69.57 |
| GSH5U0_CRIGR | 2 | 6.15 | 77.56 | 4 | 12.09 | 92.07 | 3 | 5.93 | 78.31 | 2 | 5.93 | 78.31 | 2 | 6.15 | 69.57 |
| GSH5V0_CRIGR | 15 | 10.56 | 489.85 | 15 | 10.35 | 383.33 | 16 | 10.35 | 437.91 | 18 | 13.04 | 560.61 | 15 | 11.19 | 462.66 |
| GSH5W4_CRIGR | 4 | 25.71 | 410.43 | 4 | 25.71 | 276.34 | 4 | 25.71 | 512.8 | 6 | 51.43 | 32.86 | 6 | 32.86 | 317.41 |
| GSH5W5_CRIGR | 5 | 27.75 | 219.99 | 7 | 33.48 | 174.08 | 3 | 18.06 | 217.79 | 6 | 33.48 | 238.73 | 6 | 33.48 | 186.25 |
| GSH638_CRIGR | - | - | - | 3 | 7.11 | 182.96 | - | - | - | 3 | 7.59 | 160.82 | 3 | 12.13 | 98.3 |
| GSH656_CRIGR | 4 | 9.21 | 189.26 | 3 | 7.11 | 182.96 | 3 | 7.59 | 160.82 | 5 | 13.89 | 154.21 | 3 | 7.27 | 238.42 |
| GSH657_CRIGR | - | - | - | 2 | 9.29 | 100.54 | - | - | - | 2 | 13.04 | 104.87 | - | - | - |
| GSH6B1_CRIGR | 3 | 16.81 | 91.52 | 2 | 9.29 | 100.54 | 2 | 12.83 | 103.19 | 2 | 13.04 | 105.51 | 2 | 9.29 | 77.45 |
| GSH6E1_CRIGR | 5 | 26.56 | 180.35 | 4 | 21.56 | 262.14 | 3 | 4.18 | 63.35 | 3 | 18.75 | 121.09 | 3 | 18.75 | 111.74 |
| GSH6E2_CRIGR | - | - | - | 2 | 5.79 | 104.37 | - | - | - | 2 | 5.79 | 79.53 | - | - | - |
| GSH6H5_CRIGR | - | - | - | 2 | 5.79 | 104.37 | 2 | 11.84 | 123.66 | 2 | 2.91 | 66.08 | 2 | 2.91 | 51.73 |
| GSH6K1_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GSH6L0_CRIGR | 10 | 8.24 | 378.22 | 7 | 6.65 | 261.12 | 2 | 6.25 | 52.25 | 3 | 6.59 | 304 | 3 | 9.9 | 100.89 |
| GSH6L3_CRIGR | 2 | 4.93 | 30.19 | 7 | 5.62 | 386.88 | 3 | 2.08 | 137.25 | 8 | 6.59 | 304 | 6 | 4.52 | 437.56 |
| GSH6R2_CRIGR | 2 | 6.58 | 138.3 | 2 | 10.7 | 63.13 | 2 | 4.93 | 37.1 | 2 | 14.68 | 83.25 | 2 | 4.58 | 38.05 |
| GSH6T8_CRIGR | 3 | 6.58 | 138.3 | 8 | 9.07 | 170.13 | 4 | 5.08 | 38.86 | 3 | 3.08 | 84.23 | 3 | 14.68 | 38.05 |
| GSH6W0_CRIGR | 8 | 23.49 | 258.96 | 7 | 19.24 | 253.93 | 3 | 27.29 | 237.92 | 2 | 30.87 | 244.71 | 2 | 14.53 | 107.80 |
| GSH6X6_CRIGR | 2 | 1.03 | 82.56 | 2 | 1.03 | 82.56 | 9 | 27.29 | 237.92 | 10 | 30.87 | 244.71 | 8 | 24.16 | 227.22 |
| GSH6Y6_CRIGR | - | - | - | 2 | 7.53 | 41.82 | - | - | - | - | - | - | - | - | - |
| GSH746_CRIGR | 3 | 3.76 | 133.3 | 6 | 7.72 | 144.48 | 2 | 2.87 | 59.12 | 3 | 3.76 | 103.6 | 2 | 2.77 | 106.96 |
| GSH761_CRIGR | 3 | 2.05 | 30.16 | 3 | 3.33 | 62.97 | 5 | 4.48 | 43.48 | 3 | 5.82 | 71.65 | 2 | 2.82 | 89.68 |
| GSH777_CRIGR | 5 | 13.13 | 78.04 | 4 | 9.55 | 76.88 | 2 | 4.87 | 39.77 | 6 | 9.55 | 154.52 | 3 | 9.18 | 244.69 |
| GSH7A8_CRIGR | 9 | 11.07 | 457.85 | 8 | 9.93 | 426.28 | 9 | 11.07 | 373.34 | 9 | 11.35 | 376.26 | 7 | 9.18 | 244.69 |
| GSH7C7_CRIGR | - | - | - | 4 | 4.18 | 47.23 | - | - | - | 4 | 11.35 | 376.26 | - | - | - |
| GSH7D4_CRIGR | 9 | 19.12 | 143.84 | 6 | 19.78 | 244.26 | 3 | 4.08 | 42.76 | 5 | 18.46 | 145.87 | 7 | 15.82 | 203.18 |
| GSH7H4_CRIGR | 2 | 27.08 | 81.28 | 2 | 27.08 | 150.7 | 3 | 37.5 | 72.23 | 2 | 37.5 | 132.21 | 2 | 27.08 | 66.22 |
| GSH7H9_CRIGR | 2 | 12.21 | 133.01 | 3 | 22.14 | 226.05 | 5 | 30.15 | 327.86 | 3 | 21.76 | 307.86 | 4 | 25.95 | 358.48 |
| GSH7J2_CRIGR | - | - | - | 2 | 4.18 | 47.23 | - | - | - | 3 | 21.76 | 307.86 | - | - | - |
| GSH7K5_CRIGR | 2 | 4.99 | 79.67 | 2 | 4.07 | 122.86 | 2 | 10.35 | 255.2 | 4 | 12.01 | 226.47 | 6 | 12.57 | 100.35 |
| GSH7M8_CRIGR | 3 | 5.86 | 98.12 | 3 | 6.45 | 76.74 | 4 | 7.81 | 104.93 | 3 | 7.81 | 93.25 | 4 | 8.79 | 73.14 |
| GSH7R2_CRIGR | 2 | 10.04 | 52.63 | 2 | 10.04 | 80.68 | 3 | 8.1 | 59.65 | 2 | 10.48 | 134.38 | 2 | 10.48 | 28.75 |
| GSH7U0_CRIGR | 4 | 27.59 | 298.73 | 4 | 32.57 | 295.75 | 2 | 15.33 | 91.09 | 2 | 15.33 | 100.75 | 2 | 15.33 | 51.69 |
| GSH7U2_CRIGR | 3 | 3.33 | 70.05 | 3 | 3.33 | 40.77 | 2 | 2.11 | 74.5 | 6 | 7.87 | 156.71 | 2 | 2.92 | 114.6 |
| GSH7Y0_CRIGR | 27 | 26.72 | 676.59 | 23 | 24.26 | 664.49 | 22 | 23.04 | 703.92 | 24 | 24.84 | 716.25 | 27 | 27.04 | 735.88 |
| GSH7Z2_CRIGR | 2 | 14.57 | 133 | 4 | 31.16 | 148.21 | 4 | 40.2 | 157.51 | 6 | 40.2 | 217.72 | 3 | 20.6 | 123.83 |
| GSH830_CRIGR | - | - | - | 3 | 4.6 | 35.12 | - | - | - | 3 | 5.49 | 65.43 | - | - | - |

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Table S-7 – Continued

| Protein ID | Sequential 1 | | | Sequential 2 | | | Sequential 3 | | | Sequential 4 | | | Sequential 5 | | | Sequential 6 | | |
|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|
| | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) |
| GSHCW0_CRIGR | - | - | - | 2 | 91.9 | 2.59 | - | - | - | - | - | - | - | - | - | - | - | - |
| GSHCV1_CRIGR | - | - | 8.92 | 2 | 52.04 | 8.92 | 2 | 7.47 | 7.47 | 2 | 11.08 | 11.08 | 2 | 43.96 | 11.08 | 2 | 11.08 | 11.08 |
| GSHCW3_CRIGR | 2 | 39.91 | 15.75 | 2 | 426.64 | 16.54 | 2 | 21.26 | 21.26 | 2 | 17.13 | 17.13 | 2 | 206.11 | 17.13 | 2 | 17.13 | 17.13 |
| GSHCX7_CRIGR | 6 | 111.23 | 6.48 | 7 | 426.64 | 16.54 | 8 | 5.99 | 5.99 | 6 | 6.65 | 6.65 | 6 | 108.84 | 6.65 | 6 | 14.76 | 14.76 |
| GSHD22_CRIGR | - | - | 6.48 | 2 | 189.46 | 4.72 | 2 | 5.73 | 5.73 | 2 | 4.91 | 4.91 | 2 | 33.96 | 4.91 | 2 | 5.73 | 5.73 |
| GSHD44_CRIGR | 3 | 164.32 | 3.51 | 5 | 73.88 | 19.76 | 2 | 4.91 | 4.91 | 2 | 19.76 | 19.76 | 2 | 184.51 | 19.76 | 2 | 24.55 | 24.55 |
| GSHD63_CRIGR | - | - | 3.51 | 2 | 43 | 3.51 | 2 | 43 | 4.3 | 2 | 0.56 | 0.56 | 2 | 77.55 | 0.56 | 2 | 0.81 | 0.81 |
| GSHD93_CRIGR | - | - | 35.71 | 3 | 70.68 | 46.94 | 4 | 54.08 | 54.08 | 2 | 0.56 | 0.56 | 2 | 45.76 | 0.56 | 2 | 0.81 | 0.81 |
| GSHD94_CRIGR | 2 | 74.74 | 9.52 | 3 | 67.61 | 9.52 | 3 | 67.61 | 9.52 | 3 | 13.81 | 13.81 | 3 | 87.99 | 13.81 | 3 | 13.81 | 13.81 |
| GSHDA0_CRIGR | 3 | 86.23 | 3.47 | 3 | 99.85 | 3.47 | 3 | 99.85 | 3.47 | 3 | 3.47 | 3.47 | 3 | 83.47 | 3.47 | 3 | 3.47 | 3.47 |
| GSHDB3_CRIGR | 2 | 121.78 | - | 3 | 64.96 | 4.16 | 2 | 59.54 | 4.16 | 2 | 1.83 | 1.83 | 2 | 41.93 | 1.83 | 2 | 1.83 | 1.83 |
| GSHDD7_CRIGR | - | - | - | 2 | 48.3 | 2.36 | 2 | 48.3 | 2.36 | 2 | 10.08 | 10.08 | 2 | 59.27 | 10.08 | 2 | 6.05 | 6.05 |
| GSHDP3_CRIGR | - | - | - | 2 | 87.17 | 11.36 | 3 | 65.5 | 11.36 | 3 | 11.36 | 11.36 | 3 | 34.54 | 11.36 | 3 | 11.36 | 11.36 |
| GSHDK3_CRIGR | 3 | 99.48 | 25.38 | 6 | 374.17 | 25.38 | 6 | 374.17 | 25.38 | 6 | 25.38 | 25.38 | 6 | 325.19 | 25.38 | 6 | 25.38 | 25.38 |
| GSHDR8_CRIGR | 6 | 385.63 | 21.71 | 7 | 328.21 | 25.61 | 7 | 328.21 | 25.61 | 7 | 25.61 | 25.61 | 7 | 301.34 | 25.61 | 7 | 20 | 20 |
| GSHDT6_CRIGR | 4 | 159 | 8.75 | 4 | 86.19 | 9.09 | 4 | 6.69 | 6.69 | 4 | 6.69 | 6.69 | 4 | 101.41 | 6.69 | 4 | 6.17 | 6.17 |
| GSHES1_CRIGR | 2 | 62.38 | 6.53 | 2 | 176.19 | 9.13 | 3 | 180.99 | 9.13 | 3 | 6.53 | 6.53 | 3 | 106.66 | 6.53 | 3 | 6.53 | 6.53 |
| GSHES6_CRIGR | 2 | 131.51 | 22.35 | 2 | 68.46 | 7.09 | 2 | 68.46 | 7.09 | 2 | 7.09 | 7.09 | 2 | 106.66 | 7.09 | 2 | 4.10 | 4.10 |
| GSHEA9_CRIGR | - | - | 22.35 | 19 | 35.48 | 28.33 | 19 | 35.48 | 28.33 | 19 | 28.33 | 28.33 | 19 | 54.84 | 28.33 | 19 | 4.12 | 4.12 |
| GSHED4_CRIGR | 14 | 614.66 | 14.31 | 16 | 510.82 | 14.31 | 16 | 510.82 | 14.31 | 16 | 14.31 | 14.31 | 16 | 349.36 | 14.31 | 16 | 22.45 | 22.45 |
| GSHED5_CRIGR | 6 | 206.98 | 13.79 | 7 | 217.33 | 16.07 | 7 | 217.33 | 16.07 | 7 | 16.07 | 16.07 | 7 | 149.38 | 16.07 | 7 | 20.25 | 20.25 |
| GSHES3_CRIGR | 8 | 198.8 | 13.79 | 7 | 286.98 | 16.07 | 7 | 286.98 | 16.07 | 7 | 16.07 | 16.07 | 7 | 177.35 | 16.07 | 7 | 8.02 | 8.02 |
| GSHES6_CRIGR | - | - | 21.97 | 2 | 151.71 | 14.39 | 2 | 151.71 | 14.39 | 2 | 14.39 | 14.39 | 2 | 61.18 | 14.39 | 2 | - | - |
| GSHF02_CRIGR | 2 | 121.28 | 18.52 | 3 | 73.91 | 8.14 | 2 | 91.78 | 8.14 | 2 | 21.97 | 21.97 | 2 | 174.24 | 21.97 | 2 | - | - |
| GSHF04_CRIGR | 3 | 54.23 | - | 3 | 73.91 | - | 3 | 73.91 | - | 3 | - | - | 3 | 61.18 | - | 3 | - | - |
| GSHF06_CRIGR | 3 | 38.37 | - | 2 | 60.05 | - | 2 | 60.05 | - | 2 | - | - | 2 | 28.87 | - | 2 | 5.68 | 5.68 |
| GSHF08_CRIGR | 3 | 275.84 | 64.29 | 5 | 306.09 | 64.29 | 5 | 306.09 | 64.29 | 5 | 9.36 | 9.36 | 5 | 98.08 | 9.36 | 5 | 5.68 | 5.68 |
| GSHF09_CRIGR | 3 | 179.54 | 6.79 | 3 | 121.82 | 6.79 | 3 | 121.82 | 6.79 | 3 | 28.57 | 28.57 | 3 | 401.42 | 28.57 | 3 | 52.68 | 52.68 |
| GSHF10_CRIGR | 3 | 26.47 | 26.96 | 3 | 85.11 | 20.1 | 3 | 85.11 | 20.1 | 3 | 4.5 | 4.5 | 3 | 180.19 | 4.5 | 3 | 4.5 | 4.5 |
| GSHF14_CRIGR | 2 | 6.81 | 37.45 | 2 | 55.98 | 20.1 | 2 | 55.98 | 20.1 | 2 | 3.7 | 3.7 | 2 | 75.38 | 3.7 | 2 | 6.79 | 6.79 |
| GSHF16_CRIGR | 2 | 47.01 | 4.11 | 2 | 86.2 | 4.11 | 2 | 86.2 | 4.11 | 2 | 28.43 | 28.43 | 2 | 204.61 | 28.43 | 2 | 21.08 | 21.08 |
| GSHF17_CRIGR | 3 | 5.84 | 5.97 | 3 | 57.75 | 8.56 | 4 | 152.17 | 8.56 | 4 | - | - | 4 | 69.79 | 8.56 | 4 | 8.05 | 8.05 |
| GSHF18_CRIGR | 3 | 120.44 | 4.32 | 3 | 158.55 | 3.77 | 3 | 158.55 | 3.77 | 3 | 6.92 | 6.92 | 3 | 114.79 | 6.92 | 3 | 3.77 | 3.77 |
| GSHF19_CRIGR | 5 | 213.14 | 7.75 | 5 | 100.25 | 6.86 | 5 | 100.25 | 6.86 | 5 | 4.32 | 4.32 | 5 | 207.33 | 4.32 | 5 | 2.92 | 2.92 |
| GSHF23_CRIGR | 2 | 251.07 | 4.45 | 2 | 236.35 | 7.75 | 2 | 236.35 | 7.75 | 2 | 20 | 20 | 2 | 112.89 | 20 | 2 | 3.65 | 3.65 |
| GSHF28_CRIGR | 3 | 7.04 | 8.16 | 4 | 152.67 | 5.12 | 4 | 152.67 | 5.12 | 4 | 9.12 | 9.12 | 4 | 323.7 | 9.12 | 4 | 7.36 | 7.36 |
| GSHF26_CRIGR | - | - | - | 3 | 88.56 | 9.28 | 3 | 88.56 | 9.28 | 3 | 6.83 | 6.83 | 3 | 92.56 | 6.83 | 3 | 6.3 | 6.3 |
| GSHF28_CRIGR | - | - | - | 2 | 105.64 | 14.06 | 2 | 105.64 | 14.06 | 2 | 1.66 | 1.66 | 2 | 55.21 | 1.66 | 2 | 12.5 | 12.5 |
| GSHG3_CRIGR | 9 | 287.58 | 23.85 | 11 | 232.32 | 16.15 | 11 | 232.32 | 16.15 | 11 | 26.42 | 26.42 | 11 | 387.27 | 26.42 | 11 | 20.73 | 20.73 |
| GSHG5_CRIGR | 2 | 110.37 | 3.37 | 2 | 176.37 | 3.37 | 2 | 176.37 | 3.37 | 2 | 6.39 | 6.39 | 2 | 48.72 | 6.39 | 2 | 6.75 | 6.75 |
| GSHG3_CRIGR | 13 | 392.25 | 15.52 | 11 | 187.74 | 13.87 | 11 | 187.74 | 13.87 | 11 | 8.73 | 8.73 | 14 | 315.8346 | 8.73 | 14 | 20.76 | 20.76 |
| GSHG3_CRIGR | 8 | 5.99 | 4.35 | 6 | 128.89 | 6.24 | 9 | 202.03 | 6.24 | 2 | 8.95 | 8.95 | 8 | 28.54 | 8.95 | 8 | 5.35 | 5.35 |
| GSHG7_CRIGR | 3 | 176.22 | 8.28 | 4 | 273.83 | 8.28 | 4 | 273.83 | 8.28 | 4 | 5.88 | 5.88 | 4 | 436.54 | 5.88 | 4 | 8.28 | 8.28 |
| GSHG7_CRIGR | 2 | 6.14 | 8.11 | 3 | 86.66 | 8.11 | 3 | 86.66 | 8.11 | 3 | 10.31 | 10.31 | 3 | 40.51 | 10.31 | 3 | 4.12 | 4.12 |
| GSHG7_CRIGR | 4 | 81.52 | 10.33 | 3 | 69.96 | 12.05 | 3 | 69.96 | 12.05 | 3 | 7.13 | 7.13 | 3 | 53.22 | 7.13 | 3 | 2.6 | 2.6 |
| GSHG23_CRIGR | 8 | 215.57 | 3.91 | 8 | 294.5 | 3.16 | 8 | 294.5 | 3.16 | 8 | 10.87 | 10.87 | 8 | 48.38 | 10.87 | 8 | 4.8 | 4.8 |
| GSHH02_CRIGR | 6 | 235.84 | 5.85 | 7 | 354.76 | 8.36 | 7 | 354.76 | 8.36 | 7 | 2.99 | 2.99 | 7 | 177.45 | 2.99 | 7 | 7.7 | 7.7 |
| GSHH25_CRIGR | 2 | 5.71 | 5.71 | 2 | 38.13 | 5.71 | 2 | 38.13 | 5.71 | 2 | 9.61 | 9.61 | 2 | 308.16 | 9.61 | 2 | 3.2 | 3.2 |
| GSHH35_CRIGR | 5 | 172.01 | 36.54 | 4 | 80.44 | 24.04 | 4 | 80.44 | 24.04 | 4 | 6.36 | 6.36 | 4 | 308.16 | 6.36 | 4 | 10.45 | 10.45 |
| GSHH41_CRIGR | 2 | 189.51 | 6.45 | 2 | 122.28 | 6.45 | 2 | 122.28 | 6.45 | 2 | 36.54 | 36.54 | 2 | 133.39 | 36.54 | 2 | 4.53 | 4.53 |
| GSHH63_CRIGR | 4 | 23.1 | 6.42 | 3 | 235.39 | 6.42 | 3 | 235.39 | 6.42 | 3 | 8.43 | 8.43 | 3 | 163.85 | 8.43 | 3 | 3.62 | 3.62 |
| GSHH71_CRIGR | 4 | 475.31 | 27.96 | 8 | 468.66 | 25.23 | 8 | 468.66 | 25.23 | 8 | 8.43 | 8.43 | 8 | 466.55 | 25.23 | 8 | 6.92 | 6.92 |
| GSHH79_CRIGR | 4 | 5.66 | 5.66 | 4 | 45.27 | 6.17 | 4 | 45.27 | 6.17 | 4 | 3.34 | 3.34 | 4 | 148.52 | 3.34 | 4 | 5.66 | 5.66 |
| GSHHA3_CRIGR | 3 | 31.03 | 31.03 | 2 | 301.77 | 31.03 | 2 | 301.77 | 31.03 | 2 | 31.03 | 31.03 | 2 | 309.67 | 31.03 | 2 | 31.03 | 31.03 |
| GSHHE3_CRIGR | 3 | 7.02 | 9.22 | 4 | 89.44 | 8.8 | 4 | 89.44 | 8.8 | 4 | 9.22 | 9.22 | 4 | 113.8 | 9.22 | 4 | 10.45 | 10.45 |
| GSHHE4_CRIGR | - | - | - | 2 | 5.48 | 5.48 | 2 | 5.48 | 5.48 | 2 | 14.38 | 14.38 | 2 | 92.36 | 14.38 | 2 | 8.68 | 8.68 |
| GSHHJ3_CRIGR | 2 | 4.99 | 46.22 | 2 | 431.54 | 39.2 | 2 | 431.54 | 39.2 | 2 | 68.99 | 68.99 | 2 | 38.54 | 68.99 | 2 | 4.99 | 4.99 |
| GSHHK3_CRIGR | 6 | 425.72 | 86.48 | 5 | 1025.72 | 78.76 | 5 | 1025.72 | 78.76 | 5 | 39.2 | 39.2 | 5 | 441.59 | 78.76 | 5 | 40 | 40 |
| GSHHR9_CRIGR | 47 | 10893.8 | 4.03 | 7 | 70.33 | 8.26 | 43 | 897.21 | 8.26 | 48 | 86.7 | 86.7 | 43 | 9700.23 | 8.26 | 44 | 81.55 | 81.55 |
| GSHH28_CRIGR | - | - | - | 3 | 85 | 4.03 | 3 | 85 | 4.03 | 3 | 3.92 | 3.92 | 3 | 164.1 | 3.92 | 3 | 3.92 | 3.92 |
| GSHI57_CRIGR | 3 | 115.05 | 25.36 | 3 | 85.31 | 25.36 | 3 | 85.31 | 25.36 | 3 | 31.1 | 31.1 | 3 | 231.23 | 25.36 | 3 | 25.36 | 25.36 |
| GSHIC4_CRIGR | - | - | - | 2 | 7.57 | 7.57 | 2 | 7.57 | 7.57 | 2 | 7.24 | 7.24 | 2 | 30.5 | 7.24 | 2 | - | - |
| GSHIC5_CRIGR | 2 | 35.37 | 10.31 | 3 | 55.82 | 10.31 | 3 | 55.82 | 10.31 | 3 | - | - | 3 | - | - | 3 | - | - |

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Table S-7 – Continued

| Protein ID | Sequential 1 | | | Sequential 2 | | | Sequential 3 | | | Sequential 4 | | | Sequential 5 | | | Sequential 6 | | |
|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|
| | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) |
| GSHN02_CRIGR | 3 | 3.89 | 94.35 | 5 | 5.62 | 220.69 | 2 | 2.76 | 210.68 | - | 4.38 | 414.17 | - | 5.8 | 512.05 | - | - | - |
| GSHN14_CRIGR | 2 | 6.17 | 298.1 | 10 | 10.18 | 329.85 | 2 | 6.49 | 359.96 | 6 | 5.54 | 144.77 | 9 | 8.75 | 182.63 | 10 | 6.54 | 462.2 |
| GSHN37_CRIGR | 2 | 4.11 | 65.79 | 4 | 2.13 | 128.69 | - | 5.54 | 147.75 | - | - | - | 2 | 1.58 | 80.35 | 2 | 6.25 | 81.89 |
| GSHN40_CRIGR | - | - | - | 4 | 2.13 | 87 | - | - | - | - | 14.8 | 45.57 | 5 | 14.8 | 38.06 | 5 | 16.97 | 51.14 |
| GSHN65_CRIGR | - | - | - | 4 | 13.55 | 287.62 | 4 | 11.45 | 268.49 | 5 | 12.98 | 249.45 | 5 | 12.4 | 257.94 | 5 | 14.5 | 251.35 |
| GSHN77_CRIGR | 4 | 10.5 | 278.35 | 5 | 6.33 | 38.81 | 4 | 4.13 | 27.18 | 3 | 18.86 | 70.35 | - | - | - | - | - | - |
| GSHN88_CRIGR | 2 | 6.12 | 32.96 | 2 | 3.96 | 69.84 | 2 | 4.13 | 38.81 | 3 | 6.11 | 297.02 | 7 | 20.88 | 319.73 | 9 | 23.57 | 275.32 |
| GSHN92_CRIGR | 7 | 4.13 | 76.17 | 10 | 27.95 | 294.04 | 2 | 21.21 | 358.81 | 7 | 18.86 | 297.02 | 7 | 20.88 | 319.73 | 9 | 23.57 | 275.32 |
| GSHN16_CRIGR | 2 | 21.21 | 360.02 | 7 | 30.51 | 66.54 | 4 | 19.57 | 123.26 | 4 | 25.53 | 57.32 | 6 | 40 | 83.95 | 40 | 40 | 83.95 |
| GSHN44_CRIGR | 5 | 31.49 | 123.51 | 7 | 24.26 | 66.54 | 8 | 25.92 | 224.35 | 7 | 22.49 | 232.64 | 8 | 25.43 | 459.27 | 8 | 25.43 | 459.27 |
| GSHN96_CRIGR | 7 | 23.72 | 262.28 | 4 | 20.54 | 305.71 | 8 | 30.51 | 274.35 | 7 | 5.97 | 82.64 | 3 | 4.46 | 76.27 | 3 | 4.46 | 76.27 |
| GSHN22_CRIGR | 2 | 3.02 | 55.34 | 2 | 3.43 | 55.4 | 5 | 6.66 | 135.79 | 4 | 5.39 | 166.47 | 6 | 6.74 | 115.46 | 5 | 5.47 | 108.6 |
| GSHP24_CRIGR | 7 | 9.22 | 285.15 | 4 | 4.75 | 154.21 | 6 | 6.42 | 166.42 | 5 | 5.39 | 166.47 | 6 | 6.74 | 115.46 | 5 | 5.47 | 108.6 |
| GSHP44_CRIGR | 8 | 10.58 | 319.51 | 8 | 6.16 | 105.95 | 8 | 8 | 164.87 | 3 | 5.52 | 166.84 | 5 | 6.35 | 207.46 | 6 | 6.35 | 207.46 |
| GSHP69_CRIGR | 8 | 16.58 | 132.57 | 8 | 17.09 | 160.85 | 7 | 13.03 | 346.54 | 9 | 18.27 | 306 | 8 | 16.07 | 267.46 | 8 | 16.07 | 267.46 |
| GSHP71_CRIGR | 2 | 8.19 | 85.69 | 2 | 8.19 | 77.3 | 2 | 8.19 | 72.05 | 2 | 7.5 | 158.07 | 2 | 4.32 | 91.76 | 2 | 8.19 | 78.79 |
| GSHP75_CRIGR | 3 | 7.5 | 81.5 | 2 | 4.69 | 70.05 | 3 | 4.69 | 70.05 | 3 | 7.5 | 158.07 | 2 | 4.32 | 91.76 | 2 | 8.19 | 78.79 |
| GSHP80_CRIGR | 10 | 56.28 | 434.18 | 12 | 56.74 | 490.01 | 9 | 46.98 | 472.49 | 8 | 48.37 | 505.46 | 8 | 52.09 | 474.5 | 8 | 39.07 | 366.02 |
| GSHP82_CRIGR | 2 | 2.79 | 49.48 | - | - | - | 2 | 2.79 | 49.48 | - | - | - | 2 | 2.79 | 49.48 | - | - | - |
| GSHP92_CRIGR | 7 | 6.19 | 241.56 | 3 | 2.28 | 41.76 | 2 | 2.08 | 146.15 | 6 | 6.1 | 143.68 | 3 | 2.97 | 43.9 | 3 | 3.82 | 36.04 |
| GSHP96_CRIGR | 7 | 35.5 | 517.23 | 7 | 35.5 | 447.17 | 7 | 35.5 | 425.82 | 6 | 30.92 | 603.76 | 7 | 32.44 | 337.65 | 7 | 35.5 | 449 |
| GSHP25_CRIGR | 2 | 9.18 | 118.06 | - | - | - | 2 | 9.18 | 133.74 | - | 16.09 | 103.48 | 3 | 16.39 | 131.43 | 2 | 9.18 | 190.95 |
| GSHP26_CRIGR | 6 | 15.05 | 141.03 | 6 | 16.09 | 140.27 | 4 | 8.82 | 245.84 | 6 | 16.09 | 103.48 | 4 | 14.01 | 117.81 | 3 | 6.92 | 220.47 |
| GSHQ01_CRIGR | - | - | - | 3 | 10.62 | 83.93 | 3 | 10.62 | 111.15 | 2 | 14.09 | 306.63 | 2 | 7.74 | 165.69 | 2 | 7.74 | 188.32 |
| GSHQ32_CRIGR | - | - | - | 3 | 3.35 | 94.7 | 2 | 3.35 | 101.99 | 2 | 3.35 | 71.92 | 2 | 7.74 | 165.69 | 2 | 7.74 | 188.32 |
| GSHQ45_CRIGR | - | - | - | 2 | 3.08 | 36.26 | 2 | 3.08 | 36.26 | 2 | 3.35 | 71.92 | 2 | 3.35 | 71.92 | 2 | 3.35 | 91.78 |
| GSHQ69_CRIGR | - | - | - | 2 | 3.64 | 29.09 | 2 | 3.64 | 29.09 | 2 | 3.64 | 29.09 | 2 | 3.64 | 29.09 | 2 | 3.64 | 29.09 |
| GSHQ89_CRIGR | 2 | 8.3 | 112.82 | 2 | 8.3 | 90.2 | 2 | 8.3 | 90.2 | 2 | 8.3 | 104.24 | 2 | 8.3 | 96.44 | 2 | 8.3 | 82.9 |
| GSHQ97_CRIGR | 6 | 14.56 | 164.73 | 4 | 7.57 | 277.98 | 2 | 16.74 | 276.68 | 9 | 23.73 | 241.35 | 9 | 19.36 | 241.69 | 7 | 13.97 | 304.22 |
| GSHO03_CRIGR | 2 | 3.04 | 43.1 | 2 | 6.17 | 64.4 | 2 | 12.06 | 34.04 | 2 | 12.06 | 34.04 | 2 | 12.06 | 34.04 | 2 | 12.06 | 34.04 |
| GSHO04_CRIGR | 2 | 3.04 | 138.09 | 2 | 6.17 | 64.4 | 2 | 12.06 | 34.04 | 2 | 12.06 | 34.04 | 2 | 12.06 | 34.04 | 2 | 12.06 | 34.04 |
| GSHO16_CRIGR | 8 | 6.1 | 215.51 | 8 | 3.74 | 68.9 | 5 | 8.97 | 257.64 | 3 | 4.23 | 93.75 | 8 | 11.08 | 372.76 | 2 | 3.04 | 120.4 |
| GSHO17_CRIGR | 8 | 23.68 | 313.41 | 8 | 25.12 | 306.97 | 8 | 22.49 | 242.06 | 10 | 33.73 | 237.04 | 11 | 14.83 | 58.85 | 6 | 5.6 | 58.85 |
| GSHO09_CRIGR | 3 | 19.1 | 293.47 | 6 | 17.38 | 250.73 | 8 | 17.38 | 328.41 | 7 | 17.38 | 380.04 | 8 | 17.38 | 438.27 | 6 | 14.83 | 251.98 |
| GSHO87_CRIGR | 3 | 15.34 | 64.2 | 3 | 19.89 | 103.83 | 4 | 10.23 | 67.85 | 3 | 16.48 | 144.93 | 3 | 15.34 | 89.73 | 8 | 19.62 | 272.65 |
| GSHO89_CRIGR | 3 | 8.28 | 237.48 | 3 | 8.28 | 73.19 | 2 | 7.45 | 55.47 | 2 | 6.76 | 196.95 | 2 | 4.14 | 52.14 | 2 | 10.8 | 50.47 |
| GSHO11_CRIGR | 2 | 3.84 | 59.62 | 2 | 3.84 | 72.6 | 2 | 3.84 | 72.6 | 2 | 6.76 | 196.95 | 2 | 4.14 | 52.14 | 2 | 6.76 | 90.81 |
| GSHOX0_CRIGR | - | - | - | 2 | 16.76 | 128.9 | 2 | 16.76 | 128.9 | 2 | 16.76 | 128.9 | 2 | 16.76 | 128.9 | 2 | 16.76 | 128.9 |
| GSHOX5_CRIGR | 2 | 2.94 | 107.08 | 3 | 4.26 | 96.68 | 6 | 4.7 | 76.17 | 6 | 12.92 | 74.43 | 2 | 6.76 | 196.95 | 2 | 3.82 | 85.8 |
| GSHR09_CRIGR | 7 | 12.33 | 146.78 | 4 | 8.45 | 88.99 | 6 | 14.53 | 99.86 | 7 | 6.42 | 77.15 | 8 | 18.24 | 231.92 | 4 | 7.94 | 111.8 |
| GSHR65_CRIGR | 3 | 4.34 | 157.31 | 3 | 4.34 | 87.67 | 2 | 3.35 | 162.5 | 2 | 3.35 | 118.87 | 2 | 3.35 | 120.96 | 2 | 3.35 | 54.27 |
| GSHRCS_CRIGR | - | - | - | 2 | 3.34 | 136.77 | 2 | 3.15 | 112.2 | 2 | 3.15 | 86.15 | 2 | 2.52 | 151.47 | 2 | 2.52 | 155.7 |
| GSHRD0_CRIGR | 2 | 3.34 | 76.16 | 2 | 3.34 | 136.77 | 2 | 3.15 | 112.2 | 2 | 3.15 | 86.15 | 2 | 2.52 | 151.47 | 2 | 2.52 | 155.7 |
| GSHRE2_CRIGR | 3 | 3.5 | 162.06 | 2 | 3.43 | 39.08 | 4 | 4.8 | 192.37 | 3 | 3.15 | 86.15 | 3 | 5.38 | 121.05 | 3 | 5.38 | 114.7 |
| GSHRF8_CRIGR | 2 | 3.43 | 55.32 | 2 | 3.43 | 39.08 | 2 | 3.43 | 34.68 | 2 | 1.89 | 40.84 | 3 | 17.57 | 72.76 | 5 | 19.59 | 42 |
| GSHRH4_CRIGR | 2 | 12.16 | 50.25 | 2 | 13.18 | 32.78 | 4 | 16.22 | 96.76 | 2 | 2.36 | 51.42 | 2 | 2.01 | 44.16 | 4 | 3.72 | 44.3 |
| GSHRJ2_CRIGR | 4 | 4.25 | 64.4 | 3 | 2.78 | 32.78 | 3 | 3.07 | 33.04 | 2 | 2.36 | 51.42 | 3 | 3.65 | 96.76 | 3 | 5.26 | 87.74 |
| GSHRJ7_CRIGR | 4 | 5.26 | 81.83 | 4 | 5.15 | 55.12 | 3 | 3.07 | 33.04 | 2 | 2.36 | 51.42 | 3 | 3.65 | 96.76 | 3 | 5.26 | 87.74 |
| GSHRK4_CRIGR | 2 | 8.64 | 121.71 | 11 | 30.71 | 218.06 | 13 | 36.33 | 279.9 | 12 | 8.64 | 71.83 | 12 | 8.64 | 23.91 | 10 | 8.64 | 107.01 |
| GSHRM8_CRIGR | 9 | 26.22 | 616.16 | 8 | 49.7 | 544.31 | 8 | 49.67 | 589.28 | 10 | 27.15 | 204.13 | 18 | 40.82 | 204.13 | 18 | 40.82 | 435.79 |
| GSHRN0_CRIGR | 2 | 9.85 | 133.37 | 2 | 7.5 | 93.97 | 2 | 7.5 | 93.97 | 2 | 7.5 | 93.97 | 2 | 7.5 | 93.97 | 2 | 7.5 | 93.97 |
| GSHRS5_CRIGR | 3 | 9.85 | 133.37 | 3 | 16.58 | 137.92 | 2 | 7.16 | 119.45 | 2 | 7.16 | 119.45 | 2 | 7.16 | 119.45 | 2 | 7.16 | 119.45 |
| GSHRW8_CRIGR | 4 | 24.62 | 190.47 | 3 | 16.58 | 137.92 | 3 | 16.58 | 94.38 | 3 | 16.58 | 126.37 | 3 | 16.58 | 112.91 | 3 | 16.58 | 109.08 |
| GSHRY0_CRIGR | 3 | 13.72 | 53.11 | 4 | 18.58 | 49.23 | 3 | 16.58 | 94.38 | 3 | 4.26 | 33.28 | 3 | 3.72 | 55.42 | 2 | 7.08 | 34.01 |
| GSHS06_CRIGR | 3 | 15.51 | 28.27 | 2 | 14.79 | 108.91 | 4 | 21.52 | 121.06 | 3 | 13.72 | 55.42 | 3 | 13.72 | 55.42 | 2 | 7.08 | 34.01 |
| GSHS67_CRIGR | 3 | 15.51 | 28.27 | 2 | 14.79 | 108.91 | 4 | 21.52 | 121.06 | 3 | 13.72 | 55.42 | 3 | 13.72 | 55.42 | 2 | 7.08 | 34.01 |
| GSHS88_CRIGR | 6 | 8.8 | 92.37 | 7 | 12.77 | 279.1 | 8 | 13.2 | 142.13 | 7 | 10.19 | 209.85 | 8 | 14.38 | 278.24 | 7 | 10.52 | 178.82 |
| GSHSA2_CRIGR | 3 | 27.5 | 401.95 | 15 | 23.1 | 317.67 | 13 | 19.77 | 328.88 | 17 | 24.02 | 468.23 | 13 | 18.62 | 484.44 | 12 | 20 | 502.85 |
| GSHSC4_CRIGR | - | - | - | 15 | 23.1 | 317.67 | 13 | 19.77 | 328.88 | 17 | 24.02 | 468.23 | 13 | 18.62 | 484.44 | 12 | 20 | 502.85 |
| GSHSE5_CRIGR | - | - | - | 15 | 23.1 | 317.67 | 13 | 19.77 | 328.88 | 17 | 24.02 | 468.23 | 13 | 18.62 | 484.44 | 12 | 20 | 502.85 |
| GSHSH4_CRIGR | 5 | 38.18 | 385.77 | 4 | 30 | 548.41 | 4 | 32.73 | 546.84 | 5 | 35.45 | 641.09 | 4 | 34.55 | 877.34 | 2 | 18.18 | 136.85 |
| GSHSJ1_CRIGR | - | - | - | 4 | 30 | 548.41 | 4 | 32.73 | 546.84 | 5 | 35.45 | 641.09 | 4 | 34.55 | 877.34 | 2 | 18.18 | 136.85 |
| GSHSK4_CRIGR | - | - | - | 4 | 30 | 548.41 | 4 | 32.73 | 546.84 | 5 | 35.45 | 641.09 | 4 | 34.55 | 877.34 | 2 | 18.18 | 136.85 |
| GSHSM1_CRIGR | - | - | - | 4 | 30 | 548.41 | 4 | 32.73 | 546.84 | 5 | 35.45 | 641.09 | 4 | 34.55 | 877.34 | 2 | 18.18 | 136.85 |
| GSHSM8_CRIGR | 3 | 14.59 | 69.27 | 3 | 18.45 | 87.23 | 4 | 18.88 | 194.66 | 4 | 22.75 | 141.68 | 2 | 13.73 | 99.17 | 2 | 5.53 | 62.09 |
| GSHSX3_CRIGR | 5 | 17.96 | 205.69 | 5 | 17.96 | 195.63 | 5 | 20.82 | 191.23 | 4 | 22.75 | 141.68 | 2 | 13.73 | 99.17 | 2 | 5.53 | 62.09 |
| GSHSX7_CRIGR | 2 | 2.37 | 61.04 | 2 | 2.37 | 62.4 | 2 | 2.37 | 62.4 | 2 | 2.37 | 62.4 | 2 | 2.37 | 62.4 | 2 | 2.37 | 62.4 |
| GSHSY7_CRIGR | 2 | 8.03 | 63.57 | 2 | 12.26 | 56.85 | 2 | 7.4 | 53.75 | 3 | 12.26 | 67.84 | 3 | 12.26 | 102.67 | 2 | 8.03 | 74.22 |

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Table S-7 – Continued

| Protein ID | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score | Unique Peptides | Sequential Coverage (%) | Best Score |
|--------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|-----------------|-------------------------|------------|
| GHSZ4_CRIGR | 4 | 24.67 | 117.55 | 3 | 16.74 | 86.51 | 3 | 17.62 | 131.05 | 3 | 17.62 | 127.5 | 2 | 17.62 | 162.42 |
| GHSZ8_CRIGR | 2 | 7.29 | 102.78 | - | - | - | - | 7.29 | 80.59 | - | 7.29 | 80.59 | 2 | 7.29 | 64.25 |
| GHT18_CRIGR | - | - | - | 2 | 15.15 | 43.53 | 2 | 12.12 | 28.47 | - | 12.12 | 28.47 | - | - | - |
| GHT17_CRIGR | 2 | 1.84 | 110.35 | 5 | 4.95 | 193.33 | 2 | 2.08 | 181.68 | 3 | 2.71 | 149.86 | 4 | 3.83 | 94.96 |
| GHTD4_CRIGR | - | - | - | - | - | - | - | 10.2 | 42.91 | 2 | 10.2 | 47.42 | 3 | 17.86 | 63.56 |
| GHTE5_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 3.79 | 43.78 | 2 | 2.95 | 145.07 |
| GHTF6_CRIGR | - | - | - | - | - | - | - | - | - | 2 | 8.24 | 58.97 | - | - | - |
| GHTF7_CRIGR | 8 | 22.79 | 298.06 | 7 | 19.51 | 207.63 | 8 | 21.56 | 410.6 | 6 | 16.43 | 278.22 | 6 | 15.4 | 323.11 |
| GHTG4_CRIGR | - | - | - | - | - | - | - | 8.05 | 41.78 | - | 8.05 | 41.78 | - | - | - |
| GHTG6_CRIGR | - | - | - | 2 | 2.65 | 60.85 | - | - | - | - | - | - | - | - | - |
| GHTJ2_CRIGR | - | - | - | 2 | 13.77 | 387.85 | 2 | 7.34 | 33.19 | - | 7.34 | 33.19 | - | 9.04 | 31.08 |
| GHTL1_CRIGR | 9 | 16.8 | 514.83 | 7 | 13.97 | 89.36 | 11 | 19.93 | 775.99 | 6 | 12.77 | 270.93 | 8 | 13.97 | 338.82 |
| GHTM8_CRIGR | 2 | 13.97 | 76.88 | 2 | 13.97 | 89.36 | 2 | 13.97 | 97.59 | 6 | 13.97 | 97.59 | 3 | 13.97 | 74.14 |
| GHTN5_CRIGR | 2 | 1.29 | 84.62 | 2 | 1.29 | 29.66 | 2 | 1.29 | 46.1 | 2 | 1.29 | 106.58 | 2 | 1.29 | 42.81 |
| GHTW7_CRIGR | 9 | 19.43 | 193.48 | 8 | 18.67 | 247.71 | 9 | 21.14 | 291.29 | 5 | 11.81 | 430.58 | 7 | 15.62 | 405.26 |
| GHTU8_CRIGR | 4 | 21.32 | 169.4535 | 7 | 28.29 | 180.44 | 7 | 28.29 | 195.62 | 4 | 25.19 | 227.32 | 4 | 19.38 | 223.6 |
| GHTU7_CRIGR | 7 | 25.58 | 124.06 | 6 | 20.97 | 180.56 | 5 | 25.58 | 329.82 | 5 | 21.74 | 244.78 | 4 | 17.14 | 158.21 |
| GHTL2_CRIGR | 5 | 1.73 | 95.09 | 2 | 0.9 | 50.75 | 2 | 0.9 | 85.05 | 2 | 18.78 | 346.1 | 2 | 0.93 | 64.08 |
| GHTP4_CRIGR | 5 | 11.67 | 163.45 | 4 | 9.16 | 445.27 | 5 | 9.75 | 286.4 | 2 | 3.1 | 69.22 | 4 | 6.5 | 242.82 |
| GHTW2_CRIGR | 2 | 2.49 | 150.84 | 2 | 2.49 | 150.84 | 2 | 17.61 | 159.7 | 2 | 17.61 | 159.7 | 2 | 17.61 | 142.9 |
| GHTX2_CRIGR | 2 | 17.61 | 178.8 | 2 | 17.61 | 183.44 | 2 | 8.87 | 58.02 | 2 | 17.61 | 145.28 | 2 | 17.61 | 142.9 |
| GHTX8_CRIGR | 2 | 1.13 | 82.39 | 3 | 2.26 | 63.58 | 4 | 2.26 | 55.11 | 3 | 2.26 | 96.38 | 4 | 2.26 | 74.7 |
| GHTW34_CRIGR | 4 | 5.39 | 82.03 | 3 | 1.98 | 106.31 | 3 | 7.05 | 177.78 | 3 | 2.35 | 175.73 | 3 | 2.35 | 285.74 |
| GHTV48_CRIGR | 3 | 30.85 | 337.94 | 3 | 30.85 | 108.88 | 3 | 8.97 | 111.0 | 8 | 13.66 | 175.73 | 3 | 8.97 | 128.8 |
| GHTV8_CRIGR | 9 | 31.82 | 311.11 | 7 | 17.26 | 271.89 | 7 | 23.13 | 379.67 | 9 | 37.56 | 394.39 | 7 | 23.13 | 416.83 |
| GHTV80_CRIGR | 3 | 11.26 | 107.28 | 4 | 23.18 | 169.64 | 3 | 19.55 | 180.2 | 4 | 35.91 | 256.17 | 4 | 23.18 | 187.26 |
| GHTV83_CRIGR | 5 | 11.26 | 107.28 | 8 | 8.53 | 135.32 | 6 | 11.26 | 124.96 | 6 | 11.6 | 115.62 | 6 | 9.9 | 180.61 |
| GHTV87_CRIGR | 5 | 7.75 | 179.58 | 5 | 9.06 | 152.71 | 6 | 9.42 | 173.07 | 7 | 10.85 | 160.84 | 5 | 8.46 | 103.48 |
| GHTV88_CRIGR | 2 | 8.36 | 34.33 | 2 | 27.92 | 822.31 | 6 | 32.78 | 637.95 | 7 | 27.64 | 708.49 | 7 | 28.61 | 780.64 |
| GHTV83_CRIGR | 8 | 29.72 | 1106.56 | 26 | 50.63 | 5371.54 | 25 | 48.36 | 3868.58 | 25 | 51.35 | 5190.26 | 26 | 49.71 | 5229.56 |
| GHTV13_CRIGR | 2 | 6.5 | 155.37 | 3 | 11.45 | 75.5 | 4 | 11.45 | 74.7 | 3 | 19.53 | 127.43 | 3 | 10.44 | 57.04 |
| GHTV4_CRIGR | 3 | 14.14 | 104.62 | 5 | 18.18 | 191.42 | 2 | 17.2 | 59.06 | 2 | 17.2 | 92.47 | 2 | 17.2 | 92.47 |
| GHTV16_CRIGR | - | - | - | 5 | 16.61 | 180 | 8 | 24.1 | 230.51 | 6 | 20.2 | 296.67 | 8 | 27.04 | 429.25 |
| GHTV9_CRIGR | 7 | 21.17 | 418.07 | 5 | 17.59 | 445.62 | 4 | 22.69 | 129.22 | 5 | 30.56 | 110.99 | 4 | 23.15 | 106.38 |
| GHTV6_CRIGR | 3 | 17.59 | 77.42127 | 3 | 5.68 | 39.99 | 2 | 5.47 | 40.62 | - | - | - | 6 | 30.56 | 167.52 |
| GHTV89_CRIGR | 2 | 5.68 | 80.95936 | 2 | 5.68 | 39.99 | 2 | 5.47 | 40.62 | 2 | 5.05 | 31.73 | 2 | 5.68 | 34.92 |
| GHTW4_CRIGR | 2 | 8.97 | 83.64 | 3 | 14.1 | 55.06 | 2 | 10.26 | 38.29 | 2 | 8.97 | 50.84 | 2 | 8.97 | 92.1 |
| GHTX3_CRIGR | - | - | - | 2 | 26.57 | 196.3283 | 3 | 27.27 | 182.2994 | 2 | 27.27 | 217.08 | 2 | 19.35 | 51.96 |
| GHTX34_CRIGR | 3 | 27.27 | 210.0681 | 2 | 21.55 | 154.05 | 5 | 50.86 | 226.45 | 3 | 32.76 | 62.8 | 3 | 27.27 | 177.28 |
| GHTX40_CRIGR | 4 | 32.76 | 112.56 | 2 | 21.55 | 154.05 | 5 | 50.86 | 226.45 | 4 | 43.1 | 86.02 | 3 | 32.76 | 109.22 |
| GHTX69_CRIGR | 16 | 29.25 | 385.43 | 11 | 21.74 | 435.66 | 13 | 24.51 | 366.25 | 13 | 16.34 | 264.69 | 10 | 21.21 | 388.29 |
| GHTX3_CRIGR | 9 | 61.86 | 459.21 | 7 | 53.95 | 458.94 | 9 | 60.47 | 391.15 | 11 | 66.98 | 638.07 | 10 | 61.86 | 543.38 |
| GHTX2_CRIGR | 3 | 11.41 | 106.9 | 4 | 16.5 | 136.97 | 3 | 14.32 | 151.65 | 6 | 24.03 | 216.21 | 5 | 16.02 | 175.71 |
| GHTX6_CRIGR | - | - | - | 2 | 7.49 | 72.64 | 2 | 7.49 | 72.64 | 2 | 7.49 | 71.04 | 2 | 7.49 | 88.6 |
| GHTX9_CRIGR | 2 | 7.9 | 30.01 | 3 | 12.71 | 47.23 | 3 | 12.71 | 38.63 | 3 | 12.71 | 82.31 | 2 | 8.25 | 69.13 |
| GHTX0_CRIGR | 3 | 18.22 | 146.92 | 5 | 22.46 | 167.34 | 4 | 22.46 | 98.19 | 2 | 17.78 | 37.19 | 5 | 29.66 | 299.41 |
| GHTX2_CRIGR | 2 | 6.74 | 60.6 | 2 | 17.48 | 78.23 | 3 | 17.48 | 88.14 | 2 | 25.85 | 168.7 | 6 | 29.66 | 299.41 |
| GHTX40_CRIGR | - | - | - | 2 | 7.01 | 58.27 | - | - | - | 2 | 7.01 | 151.81 | 2 | 7.01 | 148.23 |
| GHTX8_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| GHTX9_CRIGR | - | - | - | 10 | 8.83 | 395.77 | - | - | - | - | - | - | - | - | - |
| GHTX99_CRIGR | 3 | 10.37 | 76.57 | 2 | 12.5 | 112.65 | 4 | 15.96 | 192.23 | 4 | 15.96 | 162.45 | 5 | 18.62 | 125.33 |
| GHTX93_CRIGR | 3 | 4.07 | 51.11 | 2 | 2.37 | 130.79 | 2 | 2.37 | 88.92 | 3 | 3.7 | 146.69 | 3 | 3.7 | 146.69 |
| GHTX7_CRIGR | 3 | 8.42 | 125.94 | 5 | 12.83 | 213.51 | 5 | 15.23 | 197.17 | 4 | 18.64 | 86.17 | 5 | 15.23 | 241.56 |
| GHTY61_CRIGR | - | - | - | - | - | - | - | 8.01 | 37.75 | - | 8.01 | 37.75 | - | - | - |
| GHTY7_CRIGR | 3 | 12.81 | 178.14 | 4 | 15.04 | 130.46 | 4 | 15.04 | 130.46 | 2 | 12.81 | 133.04 | 2 | 10.86 | 54.58 |
| GHTYH7_CRIGR | 7 | 42.11 | 221.7 | 5 | 29.82 | 218.3 | 6 | 35.96 | 197.53 | 6 | 35.96 | 197.53 | 6 | 35.96 | 197.53 |
| GHTY9_CRIGR | 3 | 17.41 | 53.75037 | 2 | 6.9 | 216.62 | 2 | 6.83 | 96.75 | 2 | 13.99 | 86.32 | 2 | 13.99 | 86.32 |
| GHTY0_CRIGR | - | - | - | - | - | - | - | 4.85 | 97 | - | 4.85 | 97 | - | - | - |
| GHTY9_CRIGR | 3 | 10.58 | 166.29 | 3 | 14.1 | 244.34 | 3 | 14.1 | 167.46 | 3 | 14.1 | 167.46 | 4 | 8.94 | 187.8 |
| GHTY5_CRIGR | 12 | 12.21 | 329.07 | 10 | 10.13 | 232.95 | 10 | 12.87 | 308.7 | 14 | 15.12 | 509.68 | 10 | 10.58 | 472.96 |
| GHTY7_CRIGR | 7 | 8.55 | 411.9 | 6 | 8.55 | 225.43 | 5 | 2.85 | 164.27 | 3 | 7.03 | 195.92 | 3 | 4.89 | 253.28 |
| GHTZ4_CRIGR | 2 | 22.13 | 119.55 | 2 | 35.25 | 153.15 | 2 | 23.77 | 155.03 | 3 | 35.25 | 265.9 | 3 | 35.25 | 307.94 |
| GHTZ6_CRIGR | 4 | 22.46 | 193.63 | 4 | 25.85 | 306.42 | 4 | 22.46 | 249.63 | 3 | 18.64 | 166.8 | 3 | 18.64 | 166.8 |
| GHTZ2_CRIGR | 7 | 21.31 | 233.22 | 6 | 17.01 | 242.51 | 7 | 22.43 | 324.09 | 4 | 11.21 | 282.46 | 3 | 14.95 | 455.61 |
| GHTZ5_CRIGR | 2 | 2.63 | 90.21 | 5 | 6.27 | 93.92 | 4 | 7.64 | 51.08 | 6 | 6.12 | 102.43 | 2 | 8.9 | 59.17 |
| GHTZ7_CRIGR | 2 | 2.89 | 59.47 | 2 | 2.96 | 37.42 | 2 | 2.96 | 37.42 | 2 | 2.81 | 62.53 | 2 | 2.81 | 59.17 |
| GHTZ4_CRIGR | 3 | 21.99 | 118.01 | 4 | 28.63 | 141.39 | 3 | 15.77 | 126.6421 | 4 | 20.75 | 188.76 | 2 | 20.75 | 218.51 |

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Table S-7 – Continued

| Protein ID | Sequential 1 Unique Peptides | Sequential 1 Coverage (%) | Best Score | Unique Peptides | Sequential 2 Coverage (%) | Best Score | Unique Peptides | Sequential 2 Coverage (%) | Best Score | Unique Peptides | Sequential 3 Coverage (%) | Best Score | Unique Peptides | Sequential 3 Coverage (%) | Best Score | Unique Peptides | Sequential 4 Coverage (%) | Best Score | Unique Peptides | Sequential 4 Coverage (%) | Best Score | Unique Peptides | Sequential 5 Coverage (%) | Best Score | Unique Peptides | Sequential 5 Coverage (%) | Best Score | Unique Peptides | Sequential 6 Coverage (%) | Best Score | | | |
|--------------|---------------------------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|-----------------|------------------------------|------------|---|-------|--------|
| G3HZG6_CRIGR | 3 | 6.09 | 124.81 | 2 | 5.04 | 56.69 | 4 | 7.24 | 74.07 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | | |
| G3HZM3_CRIGR | 2 | 6.84 | 72.56 | 4 | 4.34 | 115.78 | 5 | 5.86 | 164.69 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | | |
| G3HZU2_CRIGR | 5 | 5.56 | 122.18 | 4 | 4.34 | 28.57 | 5 | 22.56 | 119.13 | 5 | 4.95 | 207.75 | 5 | 4.95 | 97.21 | 4 | 4.34 | 211.44 | 4 | 4.34 | 211.44 | 5 | 5.86 | 196.39 | 5 | 5.86 | 196.39 | 5 | 5.86 | 196.39 | | | |
| G3HZW0_CRIGR | 4 | 28.57 | 102.49 | 4 | 28.57 | 948.7 | 3 | 44.85 | 737.58 | 3 | 37.57 | 97.21 | 3 | 37.57 | 1248.68 | 4 | 29.32 | 93.55 | 4 | 29.32 | 93.55 | 5 | 28.57 | 81.82 | 5 | 28.57 | 81.82 | 5 | 28.57 | 81.82 | | | |
| G3HZY1_CRIGR | 5 | 44.85 | 1088.81 | 5 | 44.85 | 57.73 | 5 | 5.02 | 97.8 | 5 | 5.41 | 59.54 | 5 | 5.41 | 59.54 | 4 | 43.38 | 1520.37 | 4 | 43.38 | 1520.37 | 5 | 43.38 | 1100.81 | 5 | 43.38 | 1100.81 | 5 | 43.38 | 1100.81 | | | |
| G3I003_CRIGR | 7 | 50.43 | 135.91 | 5 | 39.32 | 148.71 | 5 | 39.32 | 129.85 | 6 | 40.17 | 146.1 | 6 | 40.17 | 146.1 | 5 | 33.33 | 181.65 | 5 | 33.33 | 181.65 | 6 | 40.17 | 147.17 | 6 | 40.17 | 147.17 | 6 | 40.17 | 147.17 | | | |
| G3I004_CRIGR | 6 | 30.38 | 174.7379 | 4 | 14.56 | 157.12 | 4 | 11.69 | 172.15 | 5 | 18.99 | 138.85 | 5 | 18.99 | 138.85 | 4 | 14.56 | 163.46 | 4 | 14.56 | 163.46 | 4 | 14.56 | 163.46 | 4 | 14.56 | 163.46 | 4 | 14.56 | 163.46 | | | |
| G3I016_CRIGR | 7 | 24.69 | 229.08 | 5 | 11.69 | 59.7 | 3 | 16.95 | 180.13 | 3 | 9.45 | 79.62 | 3 | 9.45 | 79.62 | 2 | 7.96 | 87.61 | 2 | 7.96 | 87.61 | 4 | 16.46 | 163.46 | 4 | 16.46 | 163.46 | 4 | 16.46 | 163.46 | | | |
| G3I018_CRIGR | 3 | 12.71 | 78.73 | 3 | 16.95 | 222.72 | 7 | 15.94 | 180.13 | 7 | 28.75 | 292.22 | 7 | 28.75 | 292.22 | 7 | 31.87 | 242.71 | 7 | 31.87 | 242.71 | 6 | 28.44 | 211.15 | 6 | 28.44 | 211.15 | 6 | 28.44 | 211.15 | | | |
| G3I071_CRIGR | 5 | 30.33 | 493.37 | 3 | 22.13 | 368.03 | 3 | 22.13 | 391.44 | 3 | 22.13 | 368.03 | 3 | 22.13 | 368.03 | 3 | 16.95 | 110.46 | 3 | 16.95 | 110.46 | 3 | 16.95 | 90.86 | 3 | 16.95 | 90.86 | 3 | 16.95 | 90.86 | | | |
| G3I078_CRIGR | 2 | 6.92 | 137.43 | 2 | 6.92 | 108.5 | 2 | 6.92 | 89.1 | 2 | 6.92 | 89.1 | 2 | 6.92 | 89.1 | 2 | 6.92 | 87.14 | 2 | 6.92 | 87.14 | 2 | 6.92 | 348.59 | 2 | 6.92 | 348.59 | 2 | 6.92 | 348.59 | | | |
| G3I0C0_CRIGR | - | - | - | 2 | 37 | 161.51 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I0C6_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I0D8_CRIGR | 6 | 25.58 | 344.66 | 6 | 25.25 | 441.38 | 6 | 27.57 | 310.88 | 6 | 27.57 | 310.88 | 6 | 27.57 | 310.88 | 6 | 2.82 | 31.94 | 6 | 2.82 | 31.94 | 3 | 4.36 | 40.19 | 3 | 4.36 | 40.19 | 3 | 4.36 | 40.19 | | | |
| G3I0D9_CRIGR | 4 | 40 | 118.9902 | 3 | 33.91 | 102.83 | 3 | 26.96 | 182.4 | 3 | 26.96 | 182.4 | 3 | 26.96 | 182.4 | 3 | 20.87 | 132.74 | 3 | 20.87 | 132.74 | 6 | 25.58 | 258.17 | 6 | 25.58 | 258.17 | 6 | 25.58 | 258.17 | | | |
| G3I0E1_CRIGR | 4 | 7.14 | 348.26 | 3 | 5.54 | 189.96 | 5 | 8.25 | 169.74 | 5 | 8.25 | 169.74 | 5 | 8.25 | 169.74 | 5 | 8.25 | 321.48 | 5 | 8.25 | 321.48 | 2 | 20.87 | 149.53 | 2 | 20.87 | 149.53 | 2 | 20.87 | 149.53 | | | |
| G3I0X3_CRIGR | 2 | 8.61 | 70.09 | 3 | 13.11 | 69.37 | 3 | 13.11 | 177.17 | 3 | 13.11 | 177.17 | 3 | 13.11 | 177.17 | 3 | 13.11 | 63.65 | 3 | 13.11 | 63.65 | 3 | 5.3 | 111.41 | 3 | 5.3 | 111.41 | 3 | 5.3 | 111.41 | | | |
| G3I0Z2_CRIGR | 3 | 56.31 | 163.34 | 2 | 44.66 | 143.6 | 2 | 44.66 | 131.78 | 2 | 38.83 | 175.47 | 2 | 38.83 | 175.47 | 2 | 32.04 | 141.39 | 2 | 32.04 | 141.39 | 3 | 49.51 | 108.88 | 3 | 49.51 | 108.88 | 3 | 49.51 | 108.88 | | | |
| G3I100_CRIGR | - | - | - | 2 | 26.13 | 191.26 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I101_CRIGR | - | - | - | 2 | 6.9 | 36.3 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I112_CRIGR | 2 | 6.67 | 32.84 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I116_CRIGR | 2 | 7.1 | 40.1 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I129_CRIGR | 2 | 12.44 | 40.96 | 2 | 11.29 | 115.32 | 2 | 12.58 | 86.79 | 3 | 4.92 | 97.98 | 3 | 4.92 | 97.98 | 3 | 9.68 | 118.39 | 3 | 9.68 | 118.39 | 2 | 2.9 | 78.58 | 2 | 2.9 | 78.58 | 2 | 2.9 | 78.58 | | | |
| G3I187_CRIGR | 2 | 12.58 | 40.96 | 2 | 14.93 | 58.03 | 2 | 14.93 | 58.03 | 2 | 14.93 | 58.03 | 2 | 14.93 | 58.03 | 2 | 14.93 | 58.03 | 2 | 14.93 | 58.03 | 3 | 16.45 | 84.05 | 3 | 16.45 | 84.05 | 3 | 16.45 | 84.05 | | | |
| G3I196_CRIGR | 2 | 17.2 | 29.31 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I1H4_CRIGR | 13 | 30.29 | 1019.93 | 17 | 41.2 | 964.33 | 16 | 33.83 | 805.6 | 16 | 33.83 | 805.6 | 16 | 33.83 | 805.6 | 16 | 33.33 | 1138.28 | 16 | 33.33 | 1138.28 | 17 | 37.93 | 1088.02 | 17 | 37.93 | 1088.02 | 17 | 37.93 | 1088.02 | | | |
| G3I1I6_CRIGR | 3 | 2.76 | 156.17 | 3 | 2.76 | 91.31 | 3 | 2.05 | 67.86 | 3 | 3.68 | 87.94 | 3 | 3.68 | 87.94 | 3 | 3.68 | 87.94 | 3 | 3.68 | 87.94 | 4 | 3.26 | 82.14 | 4 | 3.26 | 82.14 | 4 | 3.26 | 82.14 | | | |
| G3I1N0_CRIGR | 2 | 11.26 | 103.39 | 2 | 11.26 | 103.39 | 2 | 7.85 | 141.23 | 2 | 7.85 | 141.23 | 2 | 7.85 | 141.23 | 2 | 7.85 | 128.73 | 2 | 7.85 | 128.73 | 2 | 11.26 | 148.28 | 2 | 11.26 | 148.28 | 2 | 11.26 | 148.28 | | | |
| G3I1X5_CRIGR | 2 | 14.29 | 141.49 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I220_CRIGR | 11 | 41.36 | 546.23 | 11 | 41.36 | 370.21 | 8 | 32.72 | 365.44 | 14 | 54.01 | 719.34 | 14 | 54.01 | 719.34 | 11 | 43.52 | 607.42 | 11 | 43.52 | 607.42 | 12 | 45.68 | 669.42 | 12 | 45.68 | 669.42 | 12 | 45.68 | 669.42 | | | |
| G3I278_CRIGR | 3 | 9.18 | 110.08 | 3 | 7.12 | 79.74 | 3 | 5.62 | 87.01 | 3 | 9.18 | 164.74 | 3 | 9.18 | 164.74 | 3 | 3.28 | 127.01 | 3 | 3.28 | 127.01 | 2 | 2.6 | 36.97 | 2 | 2.6 | 36.97 | 2 | 2.6 | 36.97 | | | |
| G3I2B6_CRIGR | 3 | 19.85 | 208.03 | 3 | 19.85 | 161.6 | 3 | 19.85 | 162.7 | 3 | 19.85 | 162.7 | 3 | 19.85 | 162.7 | 3 | 19.85 | 171.09 | 3 | 19.85 | 171.09 | 3 | 19.85 | 184.39 | 3 | 19.85 | 184.39 | 3 | 19.85 | 184.39 | | | |
| G3I2D3_CRIGR | 3 | 19.85 | 208.03 | 3 | 19.85 | 161.6 | 3 | 19.85 | 162.7 | 3 | 19.85 | 162.7 | 3 | 19.85 | 162.7 | 3 | 19.85 | 171.09 | 3 | 19.85 | 171.09 | 3 | 19.85 | 184.39 | 3 | 19.85 | 184.39 | 3 | 19.85 | 184.39 | | | |
| G3I2D8_CRIGR | 3 | 19.85 | 208.03 | 3 | 19.85 | 161.6 | 3 | 19.85 | 162.7 | 3 | 19.85 | 162.7 | 3 | 19.85 | 162.7 | 3 | 19.85 | 171.09 | 3 | 19.85 | 171.09 | 3 | 19.85 | 184.39 | 3 | 19.85 | 184.39 | 3 | 19.85 | 184.39 | | | |
| G3I2E9_CRIGR | 4 | 45.27 | 238.17 | 4 | 41.79 | 363.28 | 3 | 33.83 | 406.81 | 4 | 41.79 | 471.37 | 4 | 41.79 | 471.37 | 4 | 40.8 | 502.96 | 4 | 40.8 | 502.96 | 4 | 41.79 | 604.44 | 4 | 41.79 | 604.44 | 4 | 41.79 | 604.44 | | | |
| G3I2F2_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I2F5_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | | |
| G3I2F9_CRIGR | 16 | 37.97 | 1359.05 | 13 | 32.51 | 1017.95 | 16 | 32.51 | 1017.95 | 16 | 32.51 | 1017.95 | 16 | 32.51 | 1017.95 | 16 | 32.51 | 1131.75 | 16 | 32.51 | 1131.75 | 18 | 41.94 | 1193.61 | 18 | 41.94 | 1193.61 | 17 | 40.94 | 753.73 | | | |
| G3I2I9_CRIGR | 7 | 17.51 | 428.37 | 8 | 21.09 | 311.7 | 8 | 21.09 | 311.7 | 8 | 21.09 | 311.7 | 8 | 21.09 | 311.7 | 8 | 21.09 | 311.7 | 8 | 21.09 | 311.7 | 10 | 27.68 | 552.22 | 10 | 27.68 | 552.22 | 10 | 27.68 | 552.22 | | | |
| G3I2N0_CRIGR | 2 | 7.51 | 118.3638 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | 2 | 7.51 | 133.33 | | | |
| G3I2N1_CRIGR | 4 | 21.65 | 127.58 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 | 5 | 25.11 | 112.3 |
| G3I2N4_CRIGR | 4 | 20.69 | 237.86 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 | 2 | 11.04 | 135.92 |
| G3I2P6_CRIGR | 2 | 6.62 | 36.54 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 | 3 | 11.04 | 50.07 |
| G3I2S7_CRIGR | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | |
| G3I2X1_CRIGR | - | - | - | 2 | 6.8 | 39.1 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | |
| G3I2X8_CRIGR | 10 | 8.81 | 186.31 | 10 | 9.25 | 397.32 | 9 | 7.67 | 347.18 | 8 | 6.92 | 335.88 | 8 | 6.92 | 335.88 | 8 | 6.92 | 335.88 | 8 | 6.92 | 335.88 | 10 | 9.12 | 248.76 | 10 | 9.12 | 248.76 | 9 | 8.93 | 248.76 | | | |
| G3I306_CRIGR | 7 | 14 | 488.28 | 6 | 10.35 | 310.09 | 7 | 14.92 | 493.3 | 6 | 10.81 | 211.09 | 6 | 10.81 | 211.09 | 6 | 10.81 | 211.09 | 6 | 10.81 | 211.09 | 4 | 9.59 | 294.84 | 4 | 9.59 | 294.84 | 4 | 9.59 | 294.84 | | | |
| G3I | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Table S-7 – Continued

| Protein ID | Sequential 1 | | | Sequential 2 | | | Sequential 3 | | | Sequential 4 | | | Sequential 5 | | | Sequential 6 | | |
|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|-----------------|------------|--------------|
| | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) | Unique Peptides | Best Score | Coverage (%) |
| G319M1_CRIGR | 2 | 63.59 | 10 | - | - | - | - | - | - | - | - | - | - | - | 2 | 90.76 | 13.41 | 50.27 |
| G319S0_CRIGR | 5 | 511.8 | 29.19 | 441.54 | 29.19 | 29.19 | 573.17 | - | - | - | - | - | - | - | 2 | 418.39 | 26.34 | 1227.65 |
| G319W6_CRIGR | 4 | 541.43 | 3 | 329.69 | 61.11 | 61.11 | 435.91 | 35.4 | 35.4 | 6 | 397.87 | 6 | 397.87 | 5 | 472.17 | 29.19 | 472.17 | |
| G319X8_CRIGR | 3 | 92.18 | 3.24 | 122.87 | 1.64 | 1.64 | 91.55944 | 61.11 | 61.11 | 4 | 402.26 | 3 | 402.26 | 3 | 473.53 | 61.11 | 440.51 | |
| G319A9_CRIGR | 7 | 343.86 | 50.58 | 433.78 | 6 | 40.12 | 378.74 | 44.19 | 44.19 | 6 | 343.62 | 6 | 343.62 | 7 | 110.59 | 1.86 | 110.59 | |
| G319A0_CRIGR | - | - | - | - | - | - | - | 16.36 | 16.36 | 2 | 62.44 | 2 | 62.44 | 2 | 446.94 | 50.58 | 440.42 | |
| G31AS8_CRIGR | 5 | 125.39 | 7.17 | 151.07 | 8.82 | 8.82 | 235.68 | 11.66 | 11.66 | 4 | 235.68 | - | - | 2 | 16.36 | 16.36 | 30.15 | |
| G31AV4_CRIGR | 3 | 143.65 | 6.85 | 142.58 | 5 | 5.14 | 144.68 | 41.26 | 41.26 | 8 | 341.24 | 7 | 341.24 | 8 | 298.05 | 10.8 | 205.4 | |
| G31AY3_CRIGR | 4 | 114.55 | 4 | 142.58 | 5 | 5.14 | 144.68 | 7.72 | 7.72 | 5 | 261.95 | 5 | 261.95 | 5 | 321.91 | 19.18 | 266.95 | |
| G31B34_CRIGR | 2 | 95.81 | 1.6 | 95.81 | 2 | 1.6 | 95.81 | 8.14 | 8.14 | 3 | 72.6 | 3 | 72.6 | 3 | 61.48 | 5.14 | 52.91 | |
| G31B71_CRIGR | 4 | 260 | 7.35 | 152.09 | 8 | 8 | 191.02 | 5.03 | 5.03 | 6 | 187.54 | 7 | 187.54 | 6 | 109.2 | 14.45 | 185.36 | |
| G31BC6_CRIGR | 4 | 67.86 | 17.86 | 58.86 | 4 | 8.21 | 110.09 | 18.21 | 18.21 | 2 | 103.25 | 2 | 103.25 | 3 | 96.77 | 10.71 | 42.81 | |
| G31BF1_CRIGR | 4 | - | - | 108.01 | 4 | 24.46 | 125.58 | 24.46 | 24.46 | 2 | 103.25 | 2 | 103.25 | 2 | 263.72 | - | - | |
| G31B3_CRIGR | 7 | 395.31 | 22.05 | 446.23 | 5 | 20.99 | 68.34 | 33.93 | 33.93 | 2 | 68.34 | - | - | - | - | - | - | |
| G31B72_CRIGR | 18 | 608.02 | 11.33 | 512.36 | 21 | 14.67 | 438.5 | 27.51 | 27.51 | 6 | 396.03 | 7 | 396.03 | 9 | 450.02 | 28.04 | 464.73 | |
| G31B8_CRIGR | 3 | 170.7058 | 4.74 | 204.75 | 2 | 7.32 | 122.83 | 13.55 | 13.55 | 19 | 526.85 | 21 | 526.85 | 22 | 654.52 | 14.27 | 499.64 | |
| G31B91_CRIGR | - | - | - | 329.32 | 2 | 9.75 | 162.86 | 7.71 | 7.71 | 2 | 72.57 | 2 | 72.57 | 3 | 179 | 97.99 | 87.99 | |
| G31B7_CRIGR | 2 | 75.07 | 20.69 | 101.41 | 3 | 37.93 | 78.91 | 4.49 | 4.49 | 2 | 74.41 | 2 | 74.41 | 4 | 499.39 | 9.75 | 508.48 | |
| G31BZ1_CRIGR | 2 | 69.99 | 10.73 | - | 4 | - | 112.03 | 29.66 | 29.66 | 2 | 80.3 | 2 | 80.3 | 4 | 37.93 | 110.32 | - | |
| G31C54_CRIGR | - | - | - | - | - | - | - | 10.73 | 10.73 | 2 | 26.55 | 2 | 26.55 | 2 | 36.99 | - | - | |
| G31C73_CRIGR | - | - | - | - | - | - | - | 30.67 | 30.67 | 2 | 399.76 | 2 | 399.76 | 2 | 411.12 | - | - | |
| G31CB5_CRIGR | 3 | 82.41 | 5.95 | 125.43 | 3 | 4.03 | 89.32 | 6.76 | 6.76 | 2 | 124.95 | 2 | 124.95 | 2 | 183.04 | 6.76 | 64.84 | |
| G31CC2_CRIGR | 2 | 48.77 | 8.38 | 113.05 | 2 | 8.38 | 57.25 | 5.95 | 5.95 | 3 | 215.04 | 2 | 215.04 | 2 | 4.2 | 4.2 | 101.52 | |
| G31CG9_CRIGR | 2 | 2.69 | 21.52 | 108.52 | 2 | 2.69 | 83.65 | 8.63 | 8.63 | 3 | 123.64 | 3 | 123.64 | 3 | 10.66 | 10.66 | 87.48 | |
| G31CH9_CRIGR | 4 | 164.66 | 4.01 | 238.44 | 4 | 5.86 | 212.61 | 2.69 | 2.69 | 3 | 85.85 | 3 | 85.85 | 3 | 4.71 | 4.71 | 77.34 | |
| G31CK2_CRIGR | 3 | 106.51 | 4 | 153.83 | 4 | 5.86 | 122.67 | 20.2 | 20.2 | 5 | 189.94 | 5 | 189.94 | 5 | 23.51 | 23.51 | 284.58 | |
| G31CS0_CRIGR | 2 | 54.1067 | 3.16 | - | 2 | 1.8 | - | 4.32 | 4.32 | 3 | 118.97 | 3 | 118.97 | 3 | 125.2 | 4.01 | 109.55 | |
| G31D08_CRIGR | 14 | 675.81 | 42.45 | 420.87 | 15 | 46.52 | 54.4 | 4.12 | 4.12 | 3 | 115.17 | 3 | 115.17 | 3 | 491.96 | 4.12 | 119.69 | |
| G31DD4_CRIGR | 5 | 418.85 | 63.25 | 362.38 | 6 | 63.25 | 422.31 | 40.05 | 40.05 | 15 | 945.37 | 13 | 945.37 | 13 | 44.12 | 44.12 | 715.55 | |
| G31D8_CRIGR | - | - | - | - | - | - | - | 63.25 | 63.25 | 6 | 466.23 | 6 | 466.23 | 6 | 441.09 | 63.25 | 433.35 | |
| G31DL3_CRIGR | - | - | - | - | - | - | - | 20.44 | 20.44 | 2 | 113 | 2 | 113 | 2 | 2.95 | - | 71.39 | |
| G31DM2_CRIGR | 2 | 78.84 | 18.67 | 97.14 | 2 | 20.44 | 161.47 | 20.44 | 20.44 | 2 | 113 | 2 | 113 | 2 | 43.33 | - | - | |
| G31DS2_CRIGR | 2 | 106.89 | 14.16 | 179.84 | 3 | 18.88 | 87.88 | 23.49 | 23.49 | 2 | 187.15 | 2 | 187.15 | 2 | 178.97 | 10.73 | 125.49 | |
| G31DS7_CRIGR | 9 | 329.99 | 13.61 | 311.8 | 10 | 10.55 | 270.2 | 18.88 | 18.88 | 8 | 520.06 | 8 | 520.06 | 7 | 254.23 | 10.76 | 215.58 | |
| G31E4_CRIGR | 4 | 171.7 | 6.68 | 157.19 | 2 | 6.68 | 156.82 | 10.55 | 10.55 | 2 | 191.01 | 2 | 191.01 | 2 | 251.52 | 6.68 | 221.65 | |
| G31E25_CRIGR | 4 | 212.41 | 35.71 | 262.9704 | 4 | 27.86 | 210.27 | 11.5 | 11.5 | 3 | 51.47 | 3 | 51.47 | 3 | 184.34 | 28.57 | 243.37 | |
| G31EE4_CRIGR | 6 | 406.87 | 29.85 | 373.83 | 6 | 29.85 | 355.17 | 33.57 | 33.57 | 3 | 344.04 | 6 | 344.04 | 6 | 456.87 | 35.45 | 442.22 | |
| G31EE8_CRIGR | 7 | 150.38 | 3.81 | 150.38 | 6 | 4.8 | 281.81 | 35.45 | 35.45 | 6 | 354.5 | 6 | 354.5 | 6 | 148.98 | 35.45 | 422.22 | |
| G31EX2_CRIGR | 5 | 202.07 | 66.93 | 162.76 | 4 | 66.93 | 162.76 | 4.12 | 4.12 | 14 | 338.4 | 6 | 338.4 | 8 | 43.37 | 43.37 | 100.34 | |
| G31EY3_CRIGR | 4 | 197.89 | 22.45 | 271.24 | 3 | 14.52 | 206.84 | 15.48 | 15.48 | 2 | 238.32 | 2 | 238.32 | 3 | 148.98 | 4.36 | 154.44 | |
| G31F62_CRIGR | 27 | 931.83 | 23.34 | 531.4 | 23 | 19.16 | 276.98 | 23.34 | 23.34 | 2 | 166 | 2 | 166 | 2 | 198.77 | 10.32 | 204 | |
| G31F79_CRIGR | 12 | 368.7 | 10.03 | 412.77 | 14 | 11.11 | 703.22 | 34.39 | 34.39 | 2 | 253.47 | 2 | 253.47 | 2 | 263.27 | 26.32 | 234.16 | |
| G31F80_CRIGR | 19 | 557.52 | 18.91 | 420.26 | 17 | 18.49 | 691.66 | 19.88 | 19.88 | 21 | 643.58 | 20 | 643.58 | 20 | 471.39 | 16.48 | 608.28 | |
| G31FL3_CRIGR | 6 | 270.0831 | 18.91 | 234.78 | 5 | 14.71 | 258.44 | 25.68 | 25.68 | 13 | 541.62 | 14 | 541.62 | 14 | 399.06 | 22.13 | 461.94 | |
| G31FM4_CRIGR | 7 | 247.8 | 9.83 | 334.57 | 6 | 12.03 | 263.57 | 8.06 | 8.06 | 10 | 426.34 | 10 | 426.34 | 10 | 426.34 | 8.24 | 301.48 | |
| G31FV3_CRIGR | 3 | 95.61 | 5.97 | 263.91 | 3 | 5.97 | 168.2197 | 14.71 | 14.71 | 7 | 179.96 | 5 | 179.96 | 5 | 251.79 | 17.44 | 238.94 | |
| G31FZ0_CRIGR | 2 | 188.78 | 1.58 | 188.78 | 2 | 1.58 | 188.78 | 9.84 | 9.84 | 8 | 72.28 | 7 | 72.28 | 7 | 244.92 | 13.84 | 283.88 | |
| G31G05_CRIGR | 12 | 505.52 | 55.74 | 490.25 | 10 | 41.8 | 321.67 | 14.1 | 14.1 | 3 | 306.84 | 3 | 306.84 | 5 | 108.47 | 5.97 | 147.58 | |
| G31G20_CRIGR | 2 | 100.16 | 3.25 | 185.1 | 5 | 9.01 | 331.4 | 1.61 | 1.61 | 3 | 97.43 | 3 | 97.43 | 3 | 179.3 | 2.35 | 132.45 | |
| G31G78_CRIGR | 2 | 91.22 | 5.05 | 117.69 | 3 | 7.03 | 90.84 | 57.79 | 57.79 | 13 | 471.21 | 12 | 467.2 | 12 | 539.23 | 46.72 | 448.72 | |
| G31GG2_CRIGR | 3 | 63.17 | 20.46 | 41.28 | 2 | 10.42 | 41.28 | 8.64 | 8.64 | 7 | 246.53 | 7 | 246.53 | 7 | 230.31 | 3.25 | 101.48 | |
| G31G9_CRIGR | 3 | 459.18 | 39.22 | 399.83 | 3 | 39.22 | 406.48 | 7.03 | 7.03 | 3 | 76.8 | 3 | 76.8 | 3 | 70.3 | 7.03 | 76.17 | |
| G31G19_CRIGR | 7 | 259.47 | 10.77 | 138.26 | 3 | 3.48 | 79.16 | 6.36 | 6.36 | 2 | 104.8 | 2 | 104.8 | 2 | 110.83 | 4.3 | 43.7 | |
| G31G10_CRIGR | 3 | 145.24 | 10.88 | 84.59 | 2 | 10.88 | 84.59 | 14.29 | 14.29 | 4 | 60.96 | 2 | 60.96 | 2 | 150.62 | 3.64 | 82.92 | |
| G31G70_CRIGR | 3 | 145.24 | 10.88 | 84.59 | 2 | 10.88 | 84.59 | 39.71 | 39.71 | 3 | 670.24 | 3 | 670.24 | 3 | 568.04 | 16.6 | 581.4 | |
| G31H46_CRIGR | 2 | - | - | - | 2 | 20 | 30.45 | 17.65 | 17.65 | 2 | 157.58 | 2 | 157.58 | 2 | 58.87 | 7.65 | 101.52 | |
| G31H46_CRIGR | 2 | - | - | - | 2 | 17.5 | 127.29 | - | - | - | - | - | - | - | - | - | - | |

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