



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:39 AM GMT

PDB ID : 3PGW
Title : Crystal structure of human U1 snRNP
Authors : Weber, G.; Trowitzsch, S.; Kastner, B.; Luehrmann, R.; Wahl, M.C.
Deposited on : 2010-11-02
Resolution : 4.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

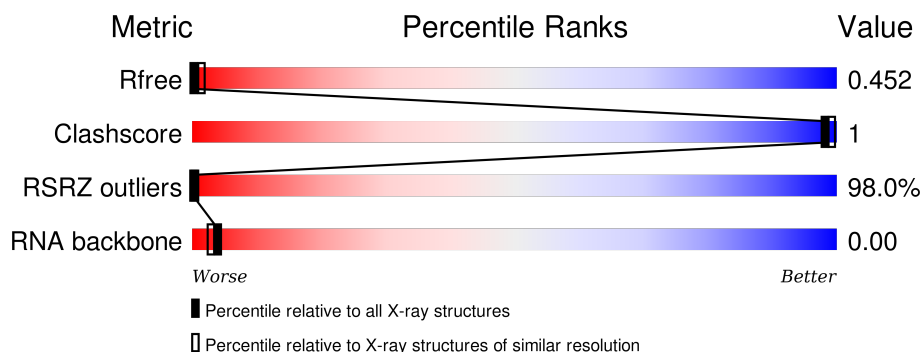
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---------------|-----------------------------|---|
| R_{free} | 91344 | 1067 (5.20-3.60) |
| Clashscore | 102246 | 1175 (5.20-3.60) |
| RSRZ outliers | 91569 | 1071 (5.20-3.60) |
| RNA backbone | 2183 | 1090 (6.00-2.80) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 1 | A | 282 | <div> <div>37%</div> <div>38%</div> <div>62%</div> </div> |
| 1 | P | 282 | <div> <div>38%</div> <div>40%</div> <div>60%</div> </div> |
| 2 | L | 437 | <div> <div>33%</div> <div>34%</div> <div>66%</div> </div> |
| 2 | S | 437 | <div> <div>33%</div> <div>34%</div> <div>66%</div> </div> |
| 3 | W | 126 | <div> <div>72%</div> <div>73%</div> <div>27%</div> </div> |
| 3 | Z | 126 | <div> <div>62%</div> <div>63%</div> <div>37%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 4 | B | 231 | |
| 4 | Q | 231 | |
| 5 | U | 119 | |
| 5 | X | 119 | |
| 6 | V | 118 | |
| 6 | Y | 118 | |
| 7 | F | 86 | |
| 7 | I | 86 | |
| 8 | E | 92 | |
| 8 | H | 92 | |
| 9 | G | 76 | |
| 9 | J | 76 | |
| 10 | N | 164 | |
| 10 | R | 164 | |
| 11 | D | 9 | |
| 11 | M | 9 | |

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 2058 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called U1-A.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|---------|---------|-------|
| 1 | A | 108 | Total | C | 0 | 0 | 108 |
| | | | 108 | 108 | | | |
| 1 | P | 113 | Total | C | 0 | 0 | 113 |
| | | | 113 | 113 | | | |

- Molecule 2 is a protein called U1-70K.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|---------|---------|-------|
| 2 | S | 150 | Total | C | 0 | 0 | 150 |
| | | | 150 | 150 | | | |
| 2 | L | 148 | Total | C | 0 | 0 | 148 |
| | | | 148 | 148 | | | |

- Molecule 3 is a protein called Sm-D3.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|---------|---------|-------|
| 3 | Z | 80 | Total | C | 0 | 0 | 80 |
| | | | 80 | 80 | | | |
| 3 | W | 92 | Total | C | 0 | 0 | 92 |
| | | | 92 | 92 | | | |

- Molecule 4 is a protein called Sm B.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|---------|---------|-------|
| 4 | B | 81 | Total | C | 0 | 0 | 81 |
| | | | 81 | 81 | | | |
| 4 | Q | 76 | Total | C | 0 | 0 | 76 |
| | | | 76 | 76 | | | |

- Molecule 5 is a protein called Sm-D1.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 5 | X | 85 | Total C 85 85 | 0 | 0 | 85 |
| 5 | U | 85 | Total C 85 85 | 0 | 0 | 85 |

- Molecule 6 is a protein called Sm-D2.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------------|---------|---------|-------|
| 6 | Y | 111 | Total C 111 111 | 7 | 0 | 111 |
| 6 | V | 103 | Total C 103 103 | 0 | 0 | 103 |

- Molecule 7 is a protein called Sm-F.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 7 | F | 85 | Total C 85 85 | 0 | 0 | 85 |
| 7 | I | 74 | Total C 74 74 | 0 | 0 | 74 |

- Molecule 8 is a protein called Sm-E.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 8 | E | 84 | Total C 84 84 | 0 | 0 | 84 |
| 8 | H | 89 | Total C 89 89 | 0 | 0 | 89 |

- Molecule 9 is a protein called Sm G.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 9 | G | 76 | Total C 76 76 | 0 | 0 | 76 |
| 9 | J | 76 | Total C 76 76 | 0 | 0 | 76 |

- Molecule 10 is a RNA chain called U1 snRNA.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------------|---------|---------|-------|
| 10 | R | 163 | Total P 163 163 | 0 | 0 | 163 |

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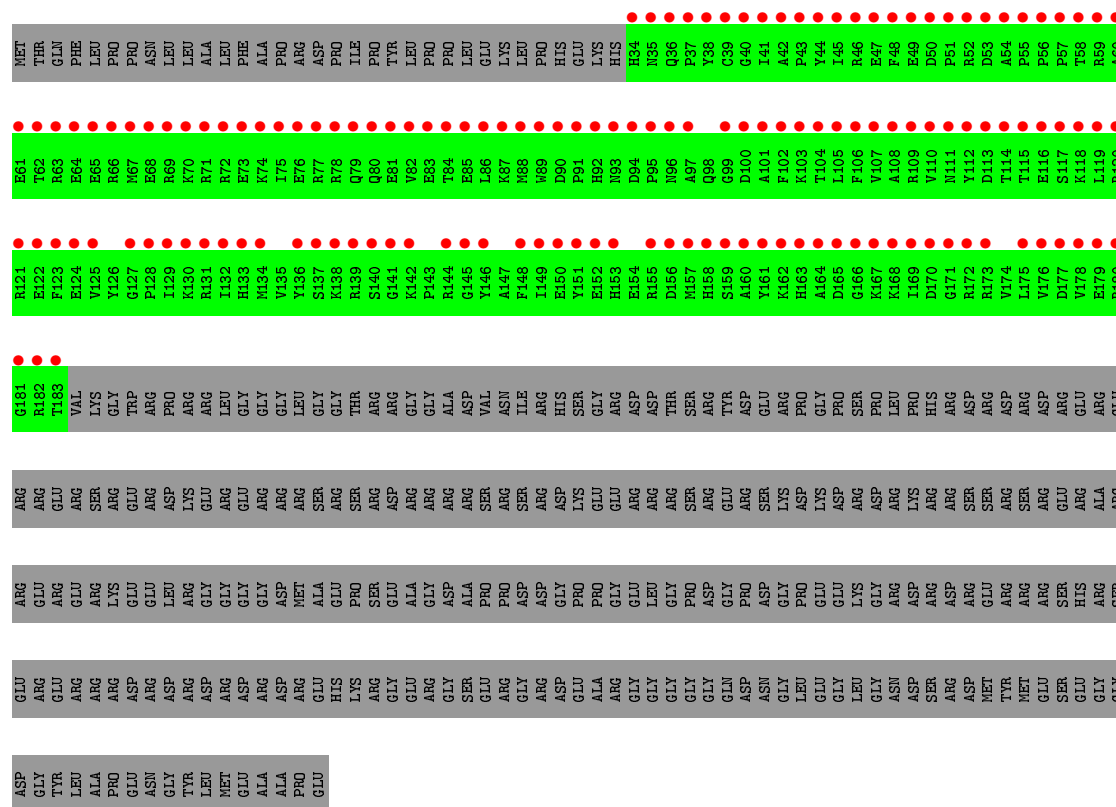
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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|---------|---------|-------|
| 10 | N | 163 | Total | P | 0 | 0 | 163 |
| | | | 163 | 163 | | | |

- Molecule 11 is a DNA chain called DNA 5'-D(*AP*GP*GP*TP*AP*AP*GP*TP*A)-3'.

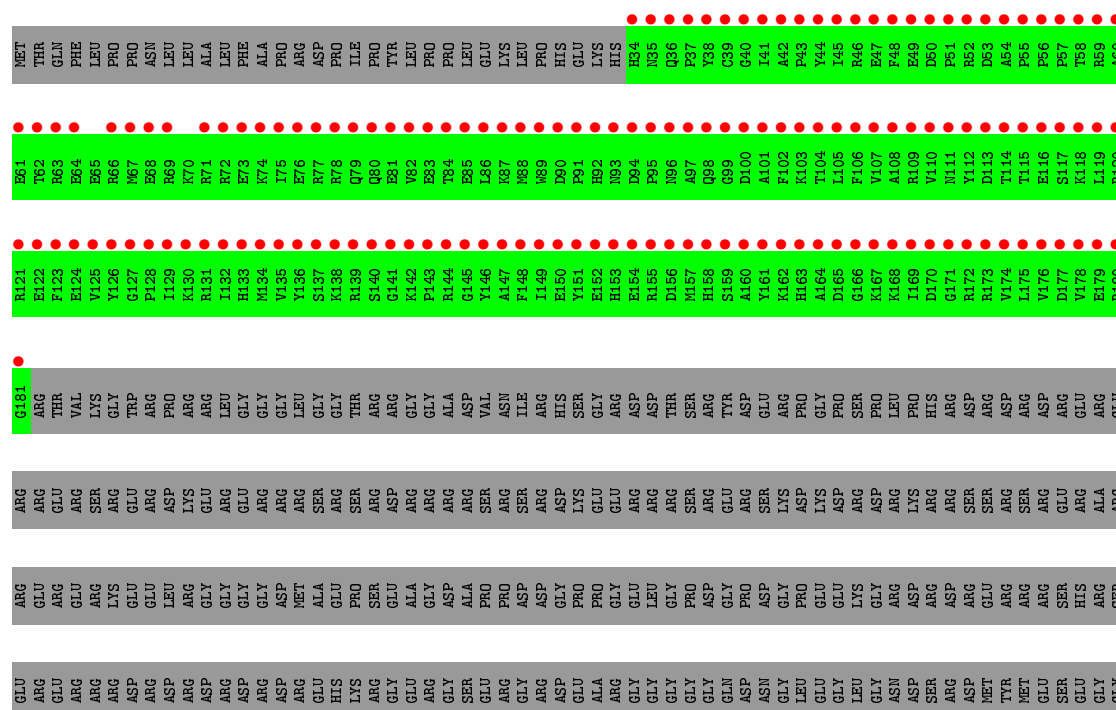
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|---|---------|---------|-------|
| 11 | D | 8 | Total | P | 0 | 0 | 8 |
| | | | 8 | 8 | | | |
| 11 | M | 8 | Total | P | 0 | 0 | 8 |
| | | | 8 | 8 | | | |

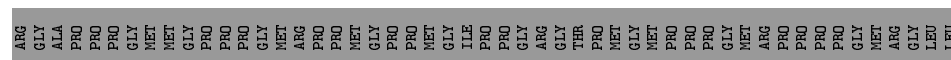
Chain S: 



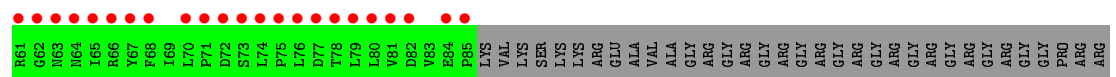
- Molecule 2: U1-70K

Chain L: 

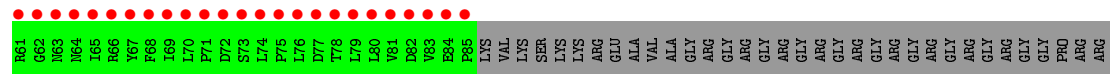


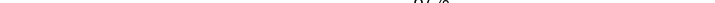


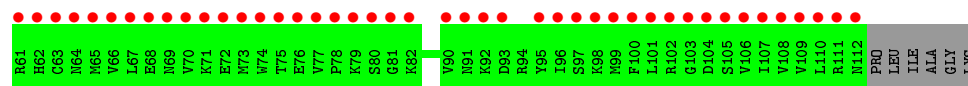
Chain X:  69% 71% 29%

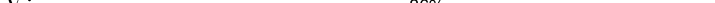


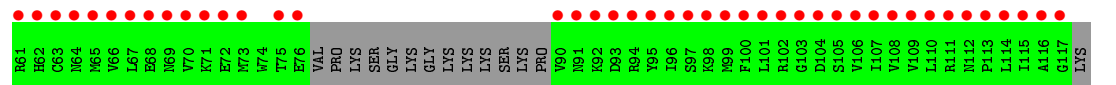
Chain U:  71% 29%

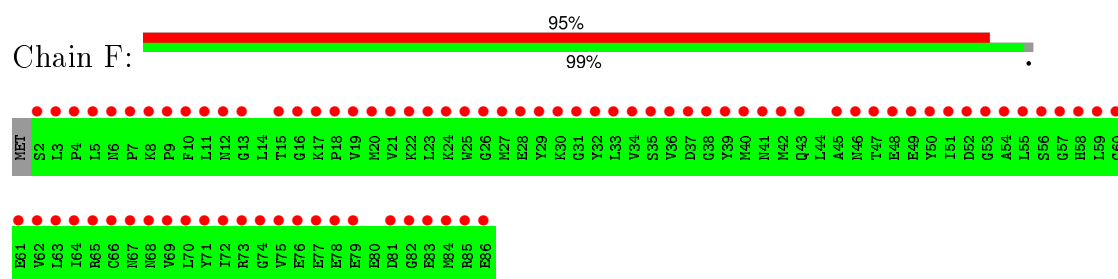


Chain Y:  87% 92% 6%

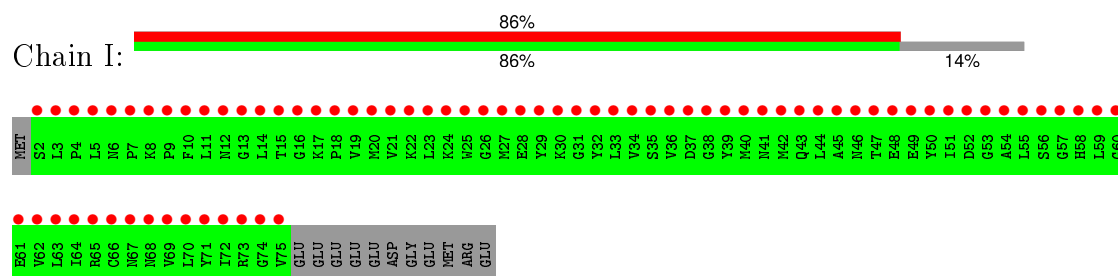


Chain V:  86% 86% 13%

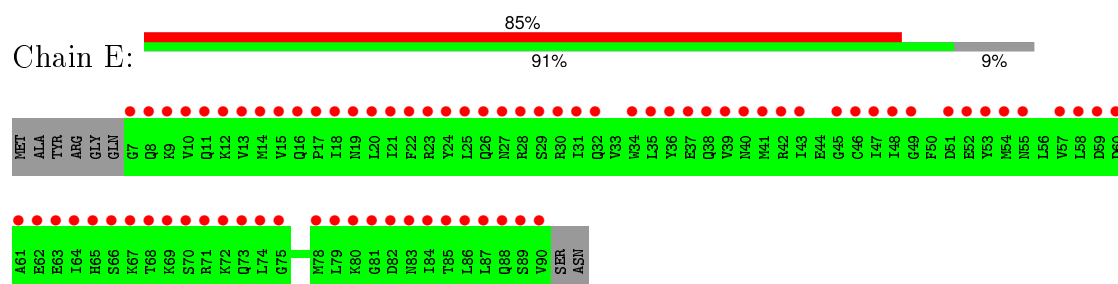


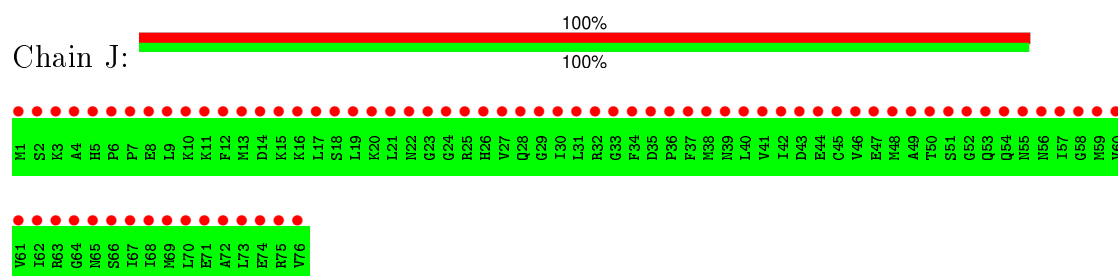


- Molecule 7: Sm-F

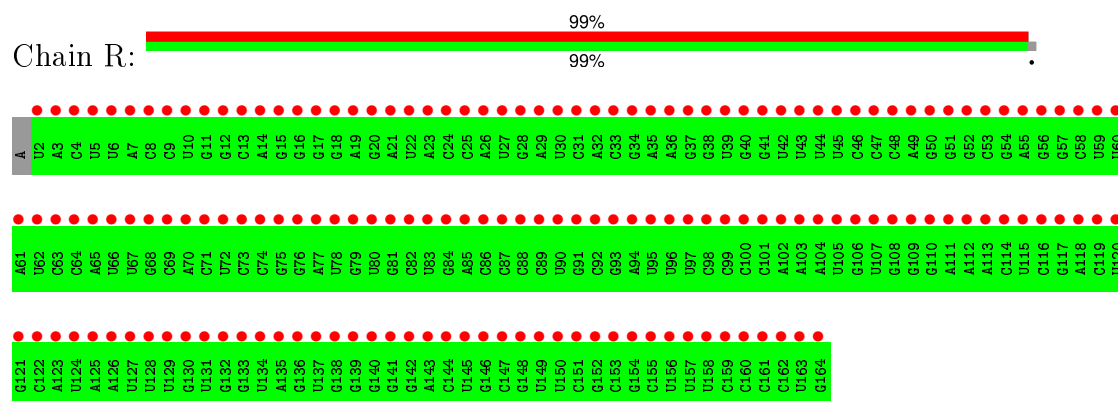


- Molecule 8: Sm-E

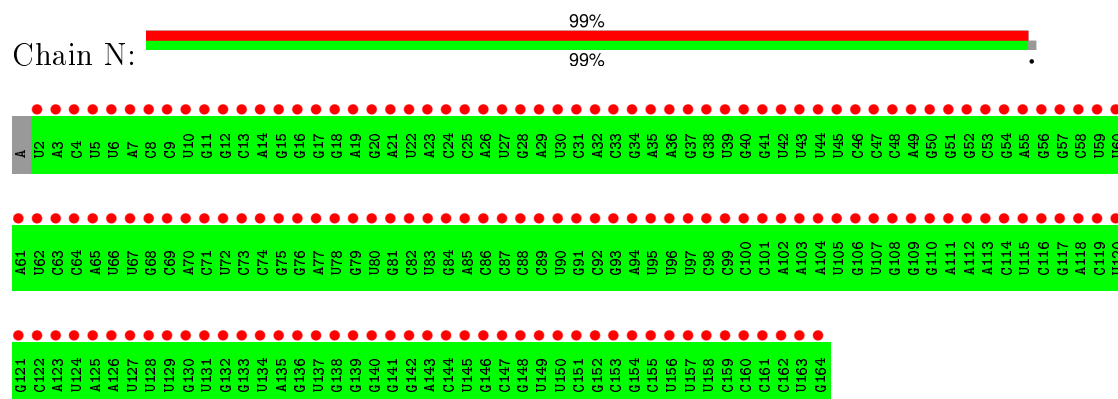




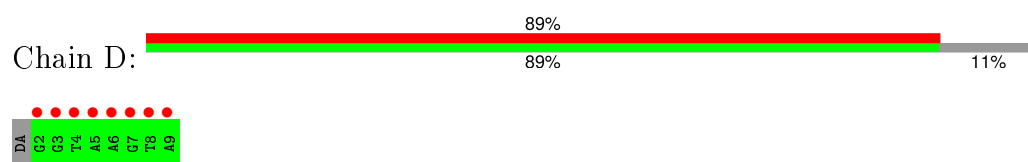
- Molecule 10: U1 snRNA



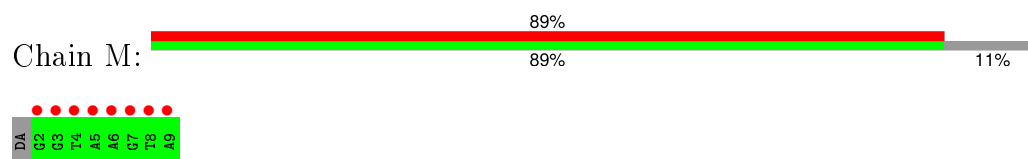
- Molecule 10: U1 snRNA



- Molecule 11: DNA 5'-D(*AP*GP*GP*TP*AP*AP*GP*TP*A)-3'



- Molecule 11: DNA 5'-D(*AP*GP*GP*TP*AP*AP*GP*TP*A)-3'



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | C 1 2 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 358.42Å 88.22Å 150.90Å 90.00° 111.88° 90.00° | Depositor |
| Resolution (Å) | 100.00 – 4.40 140.03 – 4.40 | Depositor EDS |
| % Data completeness (in resolution range) | (Not available) (100.00-4.40) 99.5 (140.03-4.40) | Depositor EDS |
| R_{merge} | (Not available) | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 2.43 (at 4.47Å) | Xtriage |
| Refinement program | PHENIX.REFINE, CNS 1.3 | Depositor |
| R, R_{free} | 0.299 , 0.348 0.434 , 0.452 | Depositor DCC |
| R_{free} test set | 1403 reflections (5.00%) | DCC |
| Wilson B-factor (Å ²) | 222.6 | Xtriage |
| Anisotropy | 0.203 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.54 , 0.8 | EDS |
| Estimated twinning fraction | 0.037 for -h-2*k,l | Xtriage |
| L-test for twinning ² | $\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$ | Xtriage |
| Outliers | 0 of 28079 reflections | Xtriage |
| F_o, F_c correlation | 0.70 | EDS |
| Total number of atoms | 2058 | wwPDB-VP |
| Average B, all atoms (Å ²) | 255.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 108 | 0 | 0 | 0 | 0 |
| 1 | P | 113 | 0 | 0 | 0 | 0 |
| 2 | L | 148 | 0 | 0 | 0 | 0 |
| 2 | S | 150 | 0 | 0 | 0 | 0 |
| 3 | W | 92 | 0 | 0 | 0 | 0 |
| 3 | Z | 80 | 0 | 0 | 0 | 0 |
| 4 | B | 81 | 0 | 0 | 0 | 0 |
| 4 | Q | 76 | 0 | 0 | 0 | 0 |
| 5 | U | 85 | 0 | 0 | 0 | 0 |
| 5 | X | 85 | 0 | 0 | 0 | 0 |
| 6 | V | 103 | 0 | 0 | 1 | 0 |
| 6 | Y | 111 | 0 | 0 | 1 | 0 |
| 7 | F | 85 | 0 | 0 | 0 | 0 |
| 7 | I | 74 | 0 | 0 | 0 | 0 |
| 8 | E | 84 | 0 | 0 | 0 | 0 |
| 8 | H | 89 | 0 | 0 | 0 | 0 |
| 9 | G | 76 | 0 | 0 | 0 | 0 |
| 9 | J | 76 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 10 | N | 163 | 0 | 0 | 0 | 0 |
| 10 | R | 163 | 0 | 0 | 0 | 0 |
| 11 | D | 8 | 0 | 0 | 0 | 0 |
| 11 | M | 8 | 0 | 0 | 0 | 0 |
| All | All | 2058 | 0 | 0 | 2 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (2) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|--------------|--------------|--------------------------|-------------------|
| 6:V:6:LYS:CA | 6:V:7:PRO:CA | 2.81 | 0.58 |
| 6:Y:6:LYS:CA | 6:Y:7:PRO:CA | 2.83 | 0.56 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|----------|-------------------|-----------------|
| 10 | N | 0/164 | - | - |
| 10 | R | 0/164 | - | - |
| All | All | 0/328 | - | - |

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 | |
|-----|-------|-----------------|--------|------------|-----------------------|--------------------|---|
| 1 | A | 108/282 (38%) | 10.63 | 104 (96%) | 00 | 135, 201, 306, 344 | 0 |
| 1 | P | 113/282 (40%) | 10.39 | 108 (95%) | 00 | 135, 202, 310, 344 | 0 |
| 2 | L | 148/437 (33%) | 12.20 | 146 (98%) | 00 | 189, 268, 352, 389 | 0 |
| 2 | S | 150/437 (34%) | 8.88 | 143 (95%) | 00 | 185, 269, 352, 390 | 0 |
| 3 | W | 92/126 (73%) | 11.00 | 91 (98%) | 00 | 153, 228, 354, 392 | 0 |
| 3 | Z | 80/126 (63%) | 11.04 | 78 (97%) | 00 | 152, 225, 260, 292 | 0 |
| 4 | B | 81/231 (35%) | 9.37 | 80 (98%) | 00 | 160, 250, 322, 350 | 0 |
| 4 | Q | 76/231 (32%) | 11.08 | 76 (100%) | 00 | 159, 232, 298, 350 | 0 |
| 5 | U | 85/119 (71%) | 9.82 | 85 (100%) | 00 | 151, 223, 260, 359 | 0 |
| 5 | X | 85/119 (71%) | 10.15 | 82 (96%) | 00 | 153, 222, 259, 363 | 0 |
| 6 | V | 103/118 (87%) | 10.71 | 102 (99%) | 00 | 149, 234, 295, 321 | 0 |
| 6 | Y | 104/118 (88%) | 10.12 | 103 (99%) | 00 | 150, 233, 300, 490 | 0 |
| 7 | F | 85/86 (98%) | 8.87 | 82 (96%) | 00 | 150, 224, 303, 373 | 0 |
| 7 | I | 74/86 (86%) | 9.88 | 74 (100%) | 00 | 151, 217, 265, 283 | 0 |
| 8 | E | 84/92 (91%) | 10.87 | 78 (92%) | 00 | 184, 243, 359, 423 | 0 |
| 8 | H | 89/92 (96%) | 9.97 | 85 (95%) | 00 | 181, 246, 362, 385 | 0 |
| 9 | G | 76/76 (100%) | 10.04 | 76 (100%) | 00 | 179, 237, 302, 315 | 0 |
| 9 | J | 76/76 (100%) | 9.19 | 76 (100%) | 00 | 180, 241, 307, 363 | 0 |
| 10 | N | 163/164 (99%) | 24.25 | 163 (100%) | 00 | 182, 295, 494, 557 | 0 |
| 10 | R | 163/164 (99%) | 24.32 | 163 (100%) | 00 | 183, 289, 494, 557 | 0 |
| 11 | D | 8/9 (88%) | 13.93 | 8 (100%) | 00 | 431, 501, 523, 526 | 0 |
| 11 | M | 8/9 (88%) | 13.11 | 8 (100%) | 00 | 431, 500, 522, 525 | 0 |
| All | All | 2051/3480 (58%) | 12.52 | 2011 (98%) | 00 | 135, 242, 379, 557 | 0 |

All (2011) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 10 | R | 41 | G | 65.1 |
| 10 | R | 34 | G | 61.3 |
| 10 | N | 52 | G | 57.5 |
| 10 | N | 70 | A | 55.5 |
| 10 | R | 84 | G | 53.4 |
| 10 | R | 133 | G | 52.9 |
| 10 | R | 39 | U | 51.1 |
| 10 | R | 129 | U | 49.8 |
| 10 | R | 115 | U | 49.7 |
| 10 | N | 71 | C | 48.3 |
| 10 | N | 57 | G | 47.4 |
| 10 | N | 56 | G | 47.3 |
| 10 | R | 75 | G | 46.3 |
| 10 | N | 13 | C | 45.6 |
| 10 | N | 124 | U | 45.5 |
| 10 | R | 71 | C | 45.3 |
| 10 | N | 29 | A | 44.5 |
| 10 | N | 45 | U | 44.5 |
| 10 | R | 78 | U | 44.1 |
| 10 | N | 72 | U | 43.9 |
| 10 | N | 49 | A | 43.1 |
| 10 | N | 129 | U | 43.0 |
| 10 | R | 66 | U | 42.8 |
| 10 | R | 161 | C | 42.5 |
| 10 | R | 50 | G | 42.2 |
| 10 | N | 17 | G | 42.1 |
| 10 | R | 40 | G | 42.1 |
| 10 | N | 51 | G | 41.5 |
| 10 | R | 83 | U | 40.6 |
| 10 | R | 38 | G | 39.8 |
| 10 | N | 91 | G | 39.7 |
| 10 | R | 47 | C | 39.5 |
| 10 | R | 159 | C | 39.4 |
| 10 | N | 48 | C | 39.2 |
| 10 | N | 27 | U | 39.1 |
| 10 | N | 123 | A | 39.0 |
| 10 | R | 81 | G | 38.8 |
| 10 | R | 42 | U | 38.7 |
| 10 | R | 89 | C | 38.6 |
| 10 | N | 69 | C | 38.1 |
| 10 | N | 23 | A | 37.6 |
| 10 | N | 66 | U | 37.5 |
| 10 | R | 63 | C | 37.4 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 10 | N | 118 | A | 37.2 |
| 10 | N | 38 | G | 37.1 |
| 10 | R | 96 | U | 36.8 |
| 10 | R | 64 | C | 36.7 |
| 10 | N | 161 | C | 36.7 |
| 10 | N | 139 | G | 36.7 |
| 10 | N | 32 | A | 36.2 |
| 10 | N | 159 | C | 36.2 |
| 10 | N | 40 | G | 36.1 |
| 10 | R | 123 | A | 36.1 |
| 10 | R | 46 | C | 35.7 |
| 10 | R | 69 | C | 35.6 |
| 10 | R | 122 | C | 35.5 |
| 10 | N | 89 | C | 35.4 |
| 10 | N | 47 | C | 34.8 |
| 10 | R | 20 | G | 34.5 |
| 10 | N | 22 | U | 34.1 |
| 10 | R | 146 | G | 33.8 |
| 10 | R | 27 | U | 33.8 |
| 10 | N | 107 | U | 33.7 |
| 10 | N | 78 | U | 33.7 |
| 10 | R | 111 | A | 33.6 |
| 10 | R | 70 | A | 33.4 |
| 10 | N | 127 | U | 33.2 |
| 10 | R | 132 | G | 33.1 |
| 10 | R | 91 | G | 33.1 |
| 10 | N | 114 | C | 33.1 |
| 10 | N | 58 | C | 33.0 |
| 8 | E | 81 | GLY | 33.0 |
| 10 | N | 80 | U | 32.9 |
| 10 | N | 108 | G | 32.6 |
| 10 | R | 59 | U | 32.4 |
| 10 | N | 130 | G | 32.4 |
| 10 | N | 59 | U | 32.2 |
| 10 | N | 136 | G | 32.2 |
| 7 | F | 20 | MET | 31.7 |
| 1 | A | 46 | SER | 31.5 |
| 10 | N | 115 | U | 31.3 |
| 10 | N | 63 | C | 31.3 |
| 10 | R | 142 | G | 31.2 |
| 10 | N | 121 | G | 30.9 |
| 10 | N | 111 | A | 30.9 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 10 | R | 51 | G | 30.7 |
| 2 | L | 149 | ILE | 30.6 |
| 10 | N | 54 | G | 30.6 |
| 10 | R | 17 | G | 30.3 |
| 10 | R | 49 | A | 30.3 |
| 10 | R | 158 | U | 30.1 |
| 10 | R | 92 | C | 30.1 |
| 9 | J | 56 | ASN | 30.0 |
| 10 | N | 81 | G | 29.8 |
| 10 | N | 65 | A | 29.8 |
| 10 | N | 117 | G | 29.5 |
| 10 | R | 60 | U | 29.4 |
| 10 | R | 162 | C | 29.1 |
| 10 | R | 94 | A | 29.0 |
| 10 | N | 43 | U | 29.0 |
| 10 | N | 68 | G | 29.0 |
| 10 | N | 41 | G | 28.9 |
| 10 | R | 26 | A | 28.8 |
| 10 | R | 52 | G | 28.8 |
| 10 | N | 101 | C | 28.7 |
| 10 | N | 112 | A | 28.7 |
| 10 | R | 100 | C | 28.7 |
| 10 | R | 12 | G | 28.5 |
| 10 | R | 48 | C | 28.4 |
| 10 | R | 18 | G | 28.4 |
| 10 | N | 26 | A | 28.4 |
| 10 | R | 116 | C | 28.2 |
| 3 | Z | 12 | GLU | 28.2 |
| 10 | N | 50 | G | 28.1 |
| 10 | N | 76 | G | 28.1 |
| 10 | N | 12 | G | 28.1 |
| 10 | N | 97 | U | 28.1 |
| 10 | N | 21 | A | 28.1 |
| 10 | R | 22 | U | 28.1 |
| 10 | N | 94 | A | 28.0 |
| 10 | R | 164 | G | 27.9 |
| 10 | N | 64 | C | 27.9 |
| 10 | N | 92 | C | 27.8 |
| 10 | R | 139 | G | 27.8 |
| 10 | N | 132 | G | 27.8 |
| 10 | R | 160 | C | 27.8 |
| 10 | N | 35 | A | 27.7 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 1 | P | 55 | ALA | 27.7 |
| 10 | N | 102 | A | 27.5 |
| 8 | E | 84 | ILE | 27.5 |
| 10 | R | 85 | A | 27.4 |
| 10 | R | 68 | G | 27.3 |
| 10 | N | 19 | A | 27.1 |
| 10 | R | 143 | A | 26.8 |
| 10 | R | 151 | C | 26.8 |
| 10 | R | 108 | G | 26.8 |
| 10 | R | 72 | U | 26.7 |
| 10 | N | 103 | A | 26.4 |
| 2 | S | 145 | GLY | 26.2 |
| 1 | A | 48 | SER | 26.2 |
| 10 | N | 150 | U | 26.0 |
| 10 | N | 85 | A | 26.0 |
| 10 | N | 96 | U | 25.8 |
| 10 | R | 136 | G | 25.8 |
| 10 | N | 93 | G | 25.7 |
| 10 | R | 118 | A | 25.7 |
| 1 | A | 78 | TYR | 25.6 |
| 10 | N | 110 | G | 25.5 |
| 6 | Y | 40 | THR | 25.5 |
| 10 | R | 145 | U | 25.4 |
| 10 | N | 30 | U | 25.3 |
| 10 | N | 83 | U | 25.3 |
| 3 | W | 11 | HIS | 25.3 |
| 9 | G | 39 | ASN | 25.3 |
| 10 | N | 120 | U | 25.3 |
| 4 | B | 34 | PHE | 25.1 |
| 1 | P | 27 | LYS | 25.0 |
| 10 | R | 56 | G | 24.9 |
| 10 | R | 125 | A | 24.9 |
| 10 | R | 140 | G | 24.8 |
| 1 | A | 19 | GLU | 24.7 |
| 10 | R | 163 | U | 24.7 |
| 10 | N | 154 | G | 24.6 |
| 10 | R | 101 | C | 24.6 |
| 10 | R | 88 | C | 24.4 |
| 10 | R | 90 | U | 24.4 |
| 10 | R | 14 | A | 24.4 |
| 6 | Y | 29 | LEU | 24.4 |
| 10 | R | 93 | G | 24.1 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 10 | R | 109 | G | 24.1 |
| 10 | N | 143 | A | 24.0 |
| 6 | Y | 21 | GLU | 24.0 |
| 1 | P | 66 | THR | 23.9 |
| 10 | R | 82 | C | 23.9 |
| 10 | R | 147 | C | 23.7 |
| 10 | N | 138 | G | 23.7 |
| 3 | Z | 66 | SER | 23.5 |
| 2 | L | 131 | ARG | 23.5 |
| 10 | R | 7 | A | 23.5 |
| 5 | U | 39 | HIS | 23.5 |
| 10 | R | 30 | U | 23.5 |
| 10 | N | 15 | G | 23.4 |
| 10 | R | 152 | G | 23.3 |
| 5 | U | 23 | THR | 23.2 |
| 10 | N | 86 | C | 23.1 |
| 10 | N | 141 | G | 23.1 |
| 5 | X | 72 | ASP | 23.0 |
| 10 | N | 122 | C | 23.0 |
| 10 | R | 5 | U | 22.9 |
| 10 | N | 116 | C | 22.9 |
| 10 | N | 55 | A | 22.9 |
| 10 | R | 155 | C | 22.9 |
| 8 | E | 59 | ASP | 22.8 |
| 10 | N | 157 | U | 22.8 |
| 10 | N | 46 | C | 22.7 |
| 10 | N | 104 | A | 22.7 |
| 7 | I | 41 | ASN | 22.7 |
| 10 | N | 25 | C | 22.7 |
| 10 | R | 9 | C | 22.7 |
| 6 | V | 91 | ASN | 22.7 |
| 6 | Y | 41 | GLN | 22.6 |
| 10 | R | 43 | U | 22.6 |
| 10 | N | 152 | G | 22.5 |
| 10 | N | 153 | C | 22.5 |
| 2 | L | 74 | LYS | 22.5 |
| 10 | N | 34 | G | 22.4 |
| 10 | N | 88 | C | 22.3 |
| 6 | V | 40 | THR | 22.3 |
| 10 | R | 144 | C | 22.3 |
| 10 | N | 11 | G | 22.3 |
| 10 | R | 19 | A | 22.3 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 10 | R | 8 | C | 22.2 |
| 10 | N | 28 | G | 22.2 |
| 2 | L | 160 | ALA | 22.2 |
| 10 | N | 42 | U | 22.1 |
| 10 | R | 16 | G | 22.1 |
| 2 | L | 108 | ALA | 22.1 |
| 10 | R | 11 | G | 22.1 |
| 10 | R | 44 | U | 22.0 |
| 10 | N | 98 | C | 22.0 |
| 10 | N | 156 | U | 22.0 |
| 10 | N | 61 | A | 22.0 |
| 10 | N | 148 | G | 21.9 |
| 10 | N | 100 | C | 21.9 |
| 8 | E | 48 | ILE | 21.8 |
| 2 | L | 122 | GLU | 21.8 |
| 2 | L | 78 | ARG | 21.8 |
| 1 | A | 18 | ASN | 21.8 |
| 5 | X | 47 | LEU | 21.8 |
| 10 | R | 4 | C | 21.6 |
| 2 | L | 150 | GLU | 21.6 |
| 8 | E | 31 | ILE | 21.5 |
| 2 | L | 153 | HIS | 21.5 |
| 1 | A | 55 | ALA | 21.3 |
| 10 | N | 131 | U | 21.3 |
| 10 | R | 113 | A | 21.2 |
| 1 | P | 57 | VAL | 21.2 |
| 10 | R | 121 | G | 21.2 |
| 10 | R | 76 | G | 21.1 |
| 1 | P | 51 | MET | 21.1 |
| 2 | L | 95 | PRO | 21.0 |
| 6 | V | 69 | ASN | 21.0 |
| 6 | V | 32 | LEU | 21.0 |
| 7 | I | 10 | PHE | 20.9 |
| 4 | B | 74 | GLY | 20.9 |
| 6 | V | 15 | GLU | 20.8 |
| 3 | Z | 65 | GLY | 20.8 |
| 7 | I | 31 | GLY | 20.7 |
| 8 | H | 54 | MET | 20.7 |
| 8 | H | 42 | ARG | 20.6 |
| 6 | Y | 45 | ASN | 20.6 |
| 4 | B | 24 | GLY | 20.6 |
| 6 | Y | 64 | ASN | 20.5 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 8 | E | 66 | SER | 20.5 |
| 10 | R | 110 | G | 20.5 |
| 10 | R | 103 | A | 20.5 |
| 10 | R | 106 | G | 20.5 |
| 3 | W | 81 | PRO | 20.4 |
| 10 | R | 98 | C | 20.4 |
| 10 | N | 4 | C | 20.3 |
| 2 | L | 168 | LYS | 20.2 |
| 6 | Y | 20 | GLU | 20.2 |
| 10 | N | 9 | C | 20.1 |
| 4 | Q | 10 | LEU | 20.1 |
| 6 | Y | 63 | CYS | 20.1 |
| 1 | P | 112 | LYS | 20.1 |
| 6 | V | 38 | ASN | 20.0 |
| 3 | Z | 72 | ILE | 20.0 |
| 10 | R | 74 | C | 19.9 |
| 2 | L | 83 | GLU | 19.9 |
| 10 | N | 105 | U | 19.8 |
| 4 | Q | 23 | ASP | 19.8 |
| 10 | N | 8 | C | 19.8 |
| 2 | L | 159 | SER | 19.8 |
| 10 | R | 114 | C | 19.7 |
| 10 | R | 15 | G | 19.7 |
| 10 | R | 23 | A | 19.7 |
| 8 | E | 55 | ASN | 19.6 |
| 3 | W | 34 | GLU | 19.6 |
| 10 | N | 137 | U | 19.6 |
| 2 | L | 146 | TYR | 19.5 |
| 8 | H | 22 | PHE | 19.5 |
| 3 | W | 62 | TYR | 19.5 |
| 3 | W | 12 | GLU | 19.5 |
| 8 | E | 79 | LEU | 19.5 |
| 7 | F | 60 | GLY | 19.5 |
| 5 | U | 9 | LYS | 19.5 |
| 3 | W | 16 | HIS | 19.4 |
| 10 | N | 144 | C | 19.4 |
| 10 | N | 75 | G | 19.3 |
| 7 | I | 71 | TYR | 19.3 |
| 6 | V | 68 | GLU | 19.3 |
| 2 | S | 93 | ASN | 19.3 |
| 10 | N | 62 | U | 19.3 |
| 4 | Q | 22 | GLN | 19.2 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 1 | A | 69 | LEU | 19.2 |
| 3 | Z | 67 | LYS | 19.2 |
| 11 | D | 3 | DG | 19.2 |
| 8 | H | 81 | GLY | 19.2 |
| 5 | X | 57 | THR | 19.1 |
| 10 | N | 33 | C | 19.1 |
| 3 | W | 59 | GLU | 19.1 |
| 10 | N | 160 | C | 19.1 |
| 3 | Z | 14 | GLU | 19.1 |
| 9 | J | 42 | ILE | 19.0 |
| 7 | F | 47 | THR | 19.0 |
| 10 | R | 130 | G | 18.9 |
| 2 | L | 75 | ILE | 18.9 |
| 10 | R | 97 | U | 18.9 |
| 2 | L | 99 | GLY | 18.9 |
| 1 | P | 14 | ILE | 18.9 |
| 3 | Z | 10 | LEU | 18.8 |
| 10 | R | 54 | G | 18.7 |
| 1 | A | 28 | LYS | 18.7 |
| 6 | V | 39 | ASN | 18.7 |
| 3 | W | 13 | ALA | 18.7 |
| 10 | R | 117 | G | 18.6 |
| 3 | Z | 74 | PRO | 18.5 |
| 3 | W | 40 | ASN | 18.5 |
| 10 | R | 148 | G | 18.5 |
| 1 | P | 111 | ARG | 18.4 |
| 6 | V | 14 | GLU | 18.3 |
| 10 | N | 60 | U | 18.3 |
| 9 | G | 64 | GLY | 18.3 |
| 4 | Q | 7 | SER | 18.2 |
| 11 | M | 7 | DG | 18.2 |
| 4 | Q | 89 | ASP | 18.2 |
| 5 | X | 56 | GLU | 18.2 |
| 9 | G | 61 | VAL | 18.1 |
| 10 | R | 21 | A | 18.1 |
| 2 | L | 121 | ARG | 18.1 |
| 8 | H | 14 | MET | 18.0 |
| 6 | Y | 44 | ILE | 18.0 |
| 8 | E | 68 | THR | 18.0 |
| 5 | U | 26 | HIS | 17.9 |
| 10 | R | 153 | C | 17.8 |
| 3 | W | 31 | LYS | 17.8 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 4 | Q | 15 | TYR | 17.8 |
| 4 | Q | 25 | ARG | 17.8 |
| 10 | R | 25 | C | 17.7 |
| 2 | L | 169 | ILE | 17.7 |
| 5 | X | 35 | SER | 17.7 |
| 8 | H | 21 | ILE | 17.6 |
| 11 | D | 2 | DG | 17.6 |
| 5 | X | 26 | HIS | 17.6 |
| 2 | S | 122 | GLU | 17.6 |
| 8 | H | 64 | ILE | 17.6 |
| 2 | L | 96 | ASN | 17.6 |
| 10 | N | 84 | G | 17.5 |
| 2 | L | 79 | GLN | 17.5 |
| 10 | R | 137 | U | 17.5 |
| 6 | V | 62 | HIS | 17.5 |
| 4 | Q | 40 | LEU | 17.5 |
| 9 | G | 5 | HIS | 17.5 |
| 1 | A | 68 | ALA | 17.5 |
| 1 | P | 49 | LEU | 17.5 |
| 4 | Q | 39 | ASN | 17.4 |
| 2 | S | 177 | ASP | 17.4 |
| 9 | G | 30 | ILE | 17.3 |
| 9 | J | 64 | GLY | 17.3 |
| 10 | R | 99 | C | 17.3 |
| 9 | J | 66 | SER | 17.3 |
| 10 | R | 86 | C | 17.3 |
| 2 | L | 165 | ASP | 17.2 |
| 10 | R | 58 | C | 17.2 |
| 2 | L | 101 | ALA | 17.1 |
| 8 | E | 54 | MET | 17.1 |
| 11 | M | 8 | DT | 17.1 |
| 6 | V | 49 | ASN | 17.1 |
| 3 | W | 17 | ILE | 17.0 |
| 4 | Q | 31 | PHE | 17.0 |
| 6 | V | 34 | GLN | 17.0 |
| 1 | A | 73 | GLN | 17.0 |
| 5 | X | 37 | ASN | 17.0 |
| 5 | U | 11 | SER | 17.0 |
| 10 | R | 157 | U | 17.0 |
| 9 | J | 70 | LEU | 17.0 |
| 5 | U | 72 | ASP | 17.0 |
| 1 | A | 66 | THR | 17.0 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | P | 24 | ASP | 16.9 |
| 6 | V | 57 | LYS | 16.9 |
| 7 | I | 25 | TRP | 16.9 |
| 7 | I | 69 | VAL | 16.9 |
| 6 | Y | 104 | ASP | 16.9 |
| 9 | G | 31 | LEU | 16.8 |
| 8 | E | 83 | ASN | 16.8 |
| 2 | S | 133 | HIS | 16.8 |
| 6 | Y | 30 | SER | 16.8 |
| 2 | L | 37 | PRO | 16.8 |
| 10 | R | 87 | C | 16.7 |
| 10 | R | 3 | A | 16.7 |
| 6 | V | 105 | SER | 16.7 |
| 7 | F | 71 | TYR | 16.7 |
| 10 | R | 37 | G | 16.7 |
| 3 | W | 73 | LEU | 16.7 |
| 10 | N | 36 | A | 16.7 |
| 10 | R | 127 | U | 16.6 |
| 10 | N | 7 | A | 16.6 |
| 3 | Z | 34 | GLU | 16.6 |
| 10 | R | 131 | U | 16.6 |
| 2 | L | 177 | ASP | 16.6 |
| 3 | Z | 24 | THR | 16.6 |
| 9 | G | 62 | ILE | 16.6 |
| 10 | R | 24 | C | 16.5 |
| 1 | A | 65 | ALA | 16.5 |
| 4 | Q | 74 | GLY | 16.5 |
| 9 | J | 69 | MET | 16.5 |
| 4 | B | 76 | ASN | 16.5 |
| 10 | N | 3 | A | 16.4 |
| 9 | G | 18 | SER | 16.4 |
| 5 | U | 27 | GLY | 16.4 |
| 8 | H | 63 | GLU | 16.4 |
| 6 | Y | 39 | ASN | 16.4 |
| 2 | S | 162 | LYS | 16.4 |
| 1 | A | 67 | ASN | 16.4 |
| 6 | Y | 25 | ASN | 16.4 |
| 3 | Z | 21 | GLU | 16.4 |
| 1 | A | 11 | THR | 16.3 |
| 2 | S | 94 | ASP | 16.3 |
| 7 | I | 29 | TYR | 16.3 |
| 8 | E | 13 | VAL | 16.3 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 5 | U | 5 | ARG | 16.3 |
| 4 | Q | 69 | LEU | 16.3 |
| 10 | R | 6 | U | 16.3 |
| 2 | S | 79 | GLN | 16.3 |
| 5 | X | 62 | GLY | 16.3 |
| 10 | N | 163 | U | 16.3 |
| 7 | F | 41 | ASN | 16.2 |
| 6 | V | 44 | ILE | 16.2 |
| 10 | N | 106 | G | 16.2 |
| 7 | I | 20 | MET | 16.2 |
| 4 | B | 11 | GLN | 16.1 |
| 4 | Q | 24 | GLY | 16.1 |
| 4 | B | 41 | ILE | 16.1 |
| 5 | U | 25 | VAL | 16.1 |
| 10 | R | 73 | C | 16.0 |
| 7 | F | 56 | SER | 16.0 |
| 7 | F | 17 | LYS | 16.0 |
| 2 | L | 76 | GLU | 16.0 |
| 1 | P | 40 | ILE | 16.0 |
| 10 | R | 77 | A | 16.0 |
| 3 | W | 10 | LEU | 16.0 |
| 5 | U | 17 | ILE | 16.0 |
| 2 | L | 154 | GLU | 15.9 |
| 9 | G | 44 | GLU | 15.9 |
| 5 | U | 60 | ILE | 15.9 |
| 2 | L | 104 | THR | 15.9 |
| 7 | I | 72 | ILE | 15.9 |
| 10 | N | 14 | A | 15.9 |
| 2 | L | 157 | MET | 15.9 |
| 4 | B | 7 | SER | 15.8 |
| 3 | Z | 57 | GLN | 15.8 |
| 6 | Y | 109 | VAL | 15.8 |
| 9 | G | 70 | LEU | 15.8 |
| 6 | V | 12 | THR | 15.8 |
| 10 | N | 155 | C | 15.8 |
| 6 | V | 35 | SER | 15.8 |
| 9 | J | 26 | HIS | 15.8 |
| 5 | X | 54 | GLN | 15.8 |
| 2 | S | 39 | CYS | 15.8 |
| 10 | R | 154 | G | 15.8 |
| 5 | X | 2 | LYS | 15.8 |
| 10 | N | 142 | G | 15.7 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 1 | P | 69 | LEU | 15.7 |
| 2 | L | 82 | VAL | 15.7 |
| 10 | N | 126 | A | 15.6 |
| 5 | X | 60 | ILE | 15.6 |
| 3 | W | 8 | LYS | 15.6 |
| 10 | R | 57 | G | 15.6 |
| 4 | B | 79 | SER | 15.6 |
| 4 | B | 23 | ASP | 15.6 |
| 5 | X | 5 | ARG | 15.6 |
| 1 | A | 94 | ILE | 15.6 |
| 10 | R | 107 | U | 15.5 |
| 8 | H | 35 | LEU | 15.5 |
| 3 | Z | 7 | ILE | 15.5 |
| 6 | Y | 62 | HIS | 15.5 |
| 10 | R | 62 | U | 15.5 |
| 3 | W | 35 | ALA | 15.5 |
| 3 | W | 90 | ASN | 15.5 |
| 6 | Y | 38 | ASN | 15.5 |
| 8 | E | 69 | LYS | 15.5 |
| 10 | R | 45 | U | 15.4 |
| 2 | L | 39 | CYS | 15.4 |
| 4 | Q | 11 | GLN | 15.4 |
| 1 | A | 45 | VAL | 15.4 |
| 8 | E | 63 | GLU | 15.4 |
| 3 | Z | 15 | GLY | 15.4 |
| 8 | H | 68 | THR | 15.4 |
| 9 | J | 61 | VAL | 15.3 |
| 3 | Z | 69 | ARG | 15.3 |
| 6 | V | 115 | ILE | 15.3 |
| 5 | U | 16 | THR | 15.3 |
| 2 | S | 43 | PRO | 15.3 |
| 2 | L | 151 | TYR | 15.3 |
| 8 | E | 36 | TYR | 15.3 |
| 1 | P | 58 | ILE | 15.3 |
| 1 | P | 29 | SER | 15.3 |
| 2 | L | 152 | GLU | 15.3 |
| 3 | W | 72 | ILE | 15.3 |
| 3 | Z | 70 | PHE | 15.3 |
| 3 | Z | 56 | ALA | 15.3 |
| 9 | J | 17 | LEU | 15.3 |
| 2 | L | 93 | ASN | 15.2 |
| 4 | Q | 83 | GLU | 15.2 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 6 | Y | 52 | LEU | 15.2 |
| 9 | J | 11 | LYS | 15.2 |
| 9 | G | 29 | GLY | 15.2 |
| 5 | U | 14 | THR | 15.2 |
| 2 | L | 88 | MET | 15.2 |
| 10 | N | 77 | A | 15.2 |
| 9 | J | 20 | LYS | 15.2 |
| 2 | L | 73 | GLU | 15.2 |
| 1 | P | 9 | ASN | 15.2 |
| 10 | N | 20 | G | 15.2 |
| 2 | L | 178 | VAL | 15.1 |
| 5 | U | 2 | LYS | 15.1 |
| 7 | I | 57 | GLY | 15.1 |
| 9 | G | 14 | ASP | 15.1 |
| 6 | V | 53 | LEU | 15.1 |
| 8 | E | 15 | VAL | 15.1 |
| 6 | V | 5 | ASN | 15.1 |
| 2 | L | 162 | LYS | 15.1 |
| 9 | J | 60 | VAL | 15.1 |
| 11 | M | 9 | DA | 15.1 |
| 1 | A | 87 | ALA | 15.1 |
| 1 | P | 23 | LYS | 15.1 |
| 2 | L | 143 | PRO | 15.0 |
| 2 | S | 114 | THR | 15.0 |
| 7 | I | 60 | GLY | 15.0 |
| 1 | A | 89 | THR | 15.0 |
| 8 | H | 77 | ILE | 15.0 |
| 9 | G | 45 | CYS | 15.0 |
| 2 | L | 170 | ASP | 15.0 |
| 2 | S | 56 | PRO | 15.0 |
| 5 | X | 73 | SER | 15.0 |
| 5 | X | 41 | LYS | 15.0 |
| 8 | H | 48 | ILE | 15.0 |
| 3 | W | 29 | ARG | 15.0 |
| 8 | H | 65 | HIS | 14.9 |
| 9 | J | 12 | PHE | 14.9 |
| 3 | W | 67 | LYS | 14.9 |
| 3 | Z | 78 | LYS | 14.9 |
| 2 | L | 173 | ARG | 14.9 |
| 1 | P | 26 | LEU | 14.9 |
| 7 | I | 56 | SER | 14.9 |
| 6 | Y | 65 | MET | 14.9 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | A | 102 | VAL | 14.9 |
| 6 | V | 43 | LEU | 14.9 |
| 10 | R | 28 | G | 14.9 |
| 10 | N | 74 | C | 14.9 |
| 11 | D | 5 | DA | 14.9 |
| 8 | E | 30 | ARG | 14.8 |
| 8 | H | 88 | GLN | 14.8 |
| 6 | V | 94 | ARG | 14.8 |
| 2 | S | 132 | ILE | 14.8 |
| 6 | V | 104 | ASP | 14.8 |
| 3 | W | 65 | GLY | 14.8 |
| 8 | H | 70 | SER | 14.8 |
| 1 | P | 45 | VAL | 14.7 |
| 6 | Y | 108 | VAL | 14.7 |
| 2 | L | 61 | GLU | 14.7 |
| 5 | U | 37 | ASN | 14.7 |
| 9 | G | 8 | GLU | 14.6 |
| 1 | P | 109 | GLU | 14.6 |
| 4 | Q | 32 | LYS | 14.6 |
| 2 | L | 133 | HIS | 14.6 |
| 7 | F | 24 | LYS | 14.6 |
| 10 | R | 32 | A | 14.6 |
| 3 | Z | 9 | VAL | 14.6 |
| 3 | W | 66 | SER | 14.6 |
| 2 | L | 77 | ARG | 14.6 |
| 4 | B | 28 | ILE | 14.6 |
| 1 | P | 8 | PRO | 14.5 |
| 2 | S | 117 | SER | 14.5 |
| 2 | S | 151 | TYR | 14.5 |
| 4 | Q | 33 | ALA | 14.5 |
| 8 | E | 53 | TYR | 14.5 |
| 2 | S | 106 | PHE | 14.5 |
| 10 | R | 150 | U | 14.5 |
| 8 | H | 71 | ARG | 14.5 |
| 11 | D | 9 | DA | 14.5 |
| 1 | P | 31 | TYR | 14.5 |
| 8 | H | 46 | CYS | 14.5 |
| 1 | P | 105 | ASP | 14.5 |
| 11 | M | 5 | DA | 14.5 |
| 3 | Z | 73 | LEU | 14.5 |
| 9 | G | 56 | ASN | 14.5 |
| 2 | L | 181 | GLY | 14.4 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 4 | B | 9 | MET | 14.4 |
| 10 | N | 128 | U | 14.4 |
| 2 | L | 36 | GLN | 14.4 |
| 7 | I | 68 | ASN | 14.4 |
| 7 | F | 66 | CYS | 14.4 |
| 5 | U | 46 | THR | 14.4 |
| 2 | L | 180 | ARG | 14.4 |
| 6 | Y | 103 | GLY | 14.4 |
| 9 | G | 3 | LYS | 14.4 |
| 10 | R | 95 | U | 14.4 |
| 8 | E | 23 | ARG | 14.4 |
| 10 | R | 102 | A | 14.4 |
| 9 | J | 32 | ARG | 14.3 |
| 10 | R | 138 | G | 14.3 |
| 1 | P | 13 | TYR | 14.3 |
| 5 | X | 16 | THR | 14.3 |
| 8 | E | 14 | MET | 14.3 |
| 1 | P | 79 | ASP | 14.3 |
| 2 | S | 37 | PRO | 14.3 |
| 10 | R | 53 | C | 14.3 |
| 9 | G | 27 | VAL | 14.3 |
| 2 | L | 129 | ILE | 14.3 |
| 8 | H | 31 | ILE | 14.3 |
| 1 | P | 61 | GLU | 14.3 |
| 2 | L | 97 | ALA | 14.3 |
| 5 | U | 40 | LEU | 14.2 |
| 5 | X | 77 | ASP | 14.2 |
| 7 | I | 47 | THR | 14.2 |
| 5 | U | 35 | SER | 14.2 |
| 3 | Z | 33 | ILE | 14.2 |
| 7 | F | 22 | LYS | 14.2 |
| 2 | S | 170 | ASP | 14.2 |
| 8 | E | 35 | LEU | 14.2 |
| 2 | L | 80 | GLN | 14.2 |
| 7 | F | 59 | LEU | 14.2 |
| 1 | P | 21 | ILE | 14.2 |
| 2 | L | 117 | SER | 14.2 |
| 4 | Q | 86 | PRO | 14.2 |
| 5 | X | 46 | THR | 14.2 |
| 10 | N | 16 | G | 14.1 |
| 7 | I | 73 | ARG | 14.1 |
| 1 | A | 26 | LEU | 14.1 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 2 | L | 144 | ARG | 14.1 |
| 5 | X | 25 | VAL | 14.1 |
| 2 | L | 58 | THR | 14.1 |
| 10 | N | 146 | G | 14.1 |
| 4 | Q | 84 | GLY | 14.1 |
| 3 | Z | 51 | ARG | 14.1 |
| 5 | X | 17 | ILE | 14.1 |
| 6 | V | 103 | GLY | 14.1 |
| 5 | U | 13 | GLU | 14.1 |
| 9 | J | 65 | ASN | 14.1 |
| 2 | L | 64 | GLU | 14.1 |
| 5 | U | 62 | GLY | 14.1 |
| 4 | Q | 19 | CYS | 14.1 |
| 1 | A | 23 | LYS | 14.1 |
| 3 | W | 80 | ALA | 14.0 |
| 4 | B | 81 | THR | 14.0 |
| 10 | N | 125 | A | 14.0 |
| 5 | X | 50 | ARG | 14.0 |
| 2 | L | 111 | ASN | 14.0 |
| 1 | A | 32 | ALA | 14.0 |
| 3 | W | 63 | ILE | 14.0 |
| 7 | F | 46 | ASN | 14.0 |
| 4 | Q | 81 | THR | 14.0 |
| 3 | W | 25 | GLY | 14.0 |
| 10 | R | 124 | U | 14.0 |
| 4 | B | 12 | HIS | 14.0 |
| 4 | B | 35 | ASP | 13.9 |
| 4 | Q | 30 | THR | 13.9 |
| 5 | X | 71 | PRO | 13.9 |
| 8 | H | 23 | ARG | 13.9 |
| 7 | F | 50 | TYR | 13.9 |
| 3 | W | 53 | GLY | 13.9 |
| 2 | L | 94 | ASP | 13.9 |
| 10 | N | 95 | U | 13.9 |
| 3 | Z | 8 | LYS | 13.9 |
| 6 | Y | 56 | VAL | 13.9 |
| 1 | P | 94 | ILE | 13.9 |
| 7 | I | 59 | LEU | 13.9 |
| 6 | V | 30 | SER | 13.9 |
| 1 | A | 15 | ASN | 13.9 |
| 5 | U | 7 | LEU | 13.9 |
| 3 | W | 33 | ILE | 13.9 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 4 | Q | 9 | MET | 13.8 |
| 10 | R | 80 | U | 13.8 |
| 8 | H | 53 | TYR | 13.8 |
| 5 | U | 57 | THR | 13.8 |
| 4 | Q | 75 | GLU | 13.8 |
| 10 | N | 44 | U | 13.8 |
| 2 | L | 145 | GLY | 13.8 |
| 1 | A | 92 | ASP | 13.8 |
| 2 | L | 114 | THR | 13.8 |
| 8 | H | 85 | THR | 13.8 |
| 6 | V | 106 | VAL | 13.7 |
| 3 | Z | 41 | CYS | 13.7 |
| 2 | L | 123 | PHE | 13.7 |
| 2 | L | 55 | PRO | 13.6 |
| 2 | L | 141 | GLY | 13.6 |
| 7 | I | 49 | GLU | 13.6 |
| 8 | H | 28 | ARG | 13.6 |
| 4 | Q | 77 | LEU | 13.6 |
| 2 | L | 137 | SER | 13.6 |
| 11 | M | 6 | DA | 13.6 |
| 3 | Z | 32 | LEU | 13.6 |
| 1 | A | 91 | SER | 13.6 |
| 3 | W | 44 | SER | 13.6 |
| 9 | G | 58 | GLY | 13.6 |
| 2 | L | 119 | LEU | 13.6 |
| 2 | L | 92 | HIS | 13.6 |
| 6 | Y | 18 | LYS | 13.6 |
| 6 | Y | 43 | LEU | 13.5 |
| 2 | S | 171 | GLY | 13.5 |
| 4 | B | 84 | GLY | 13.5 |
| 7 | I | 65 | ARG | 13.5 |
| 3 | W | 14 | GLU | 13.5 |
| 2 | S | 40 | GLY | 13.5 |
| 8 | E | 62 | GLU | 13.5 |
| 3 | W | 64 | ARG | 13.5 |
| 8 | H | 60 | ASP | 13.5 |
| 2 | S | 161 | TYR | 13.5 |
| 3 | W | 24 | THR | 13.5 |
| 7 | F | 63 | LEU | 13.5 |
| 8 | H | 40 | ASN | 13.4 |
| 1 | P | 67 | ASN | 13.4 |
| 3 | W | 23 | ASN | 13.4 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 6 | V | 111 | ARG | 13.4 |
| 2 | S | 101 | ALA | 13.4 |
| 4 | B | 69 | LEU | 13.4 |
| 1 | A | 64 | SER | 13.4 |
| 6 | Y | 72 | GLU | 13.4 |
| 8 | E | 49 | GLY | 13.4 |
| 5 | U | 24 | GLN | 13.4 |
| 1 | P | 92 | ASP | 13.4 |
| 8 | E | 41 | MET | 13.4 |
| 2 | L | 107 | VAL | 13.4 |
| 8 | H | 45 | GLY | 13.3 |
| 3 | W | 19 | THR | 13.3 |
| 2 | S | 103 | LYS | 13.3 |
| 3 | Z | 25 | GLY | 13.3 |
| 5 | X | 15 | VAL | 13.3 |
| 6 | V | 8 | LYS | 13.3 |
| 6 | V | 13 | PRO | 13.3 |
| 6 | V | 110 | LEU | 13.3 |
| 5 | X | 9 | LYS | 13.3 |
| 4 | Q | 37 | HIS | 13.3 |
| 9 | J | 34 | PHE | 13.3 |
| 5 | X | 70 | LEU | 13.3 |
| 8 | E | 43 | ILE | 13.3 |
| 6 | Y | 93 | ASP | 13.2 |
| 1 | A | 56 | PHE | 13.2 |
| 1 | P | 77 | PHE | 13.2 |
| 8 | H | 84 | ILE | 13.2 |
| 7 | I | 67 | ASN | 13.2 |
| 6 | V | 19 | ARG | 13.2 |
| 1 | A | 105 | ASP | 13.2 |
| 8 | H | 43 | ILE | 13.2 |
| 4 | Q | 82 | VAL | 13.2 |
| 9 | G | 2 | SER | 13.2 |
| 2 | S | 158 | HIS | 13.2 |
| 8 | E | 28 | ARG | 13.2 |
| 11 | M | 2 | DG | 13.2 |
| 3 | W | 30 | GLY | 13.1 |
| 7 | F | 40 | MET | 13.1 |
| 8 | E | 21 | ILE | 13.1 |
| 6 | Y | 54 | GLY | 13.1 |
| 8 | H | 69 | LYS | 13.1 |
| 8 | E | 37 | GLU | 13.1 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 3 | Z | 40 | ASN | 13.1 |
| 8 | H | 3 | TYR | 13.0 |
| 2 | L | 103 | LYS | 13.0 |
| 3 | W | 7 | ILE | 13.0 |
| 11 | D | 8 | DT | 13.0 |
| 1 | P | 60 | LYS | 13.0 |
| 1 | A | 40 | ILE | 13.0 |
| 7 | F | 25 | TRP | 13.0 |
| 9 | G | 60 | VAL | 13.0 |
| 8 | E | 29 | SER | 12.9 |
| 10 | R | 79 | G | 12.9 |
| 9 | G | 9 | LEU | 12.9 |
| 3 | W | 61 | VAL | 12.9 |
| 9 | G | 71 | GLU | 12.9 |
| 8 | E | 52 | GLU | 12.9 |
| 1 | A | 100 | THR | 12.9 |
| 8 | H | 24 | TYR | 12.9 |
| 2 | L | 171 | GLY | 12.9 |
| 1 | A | 76 | PRO | 12.9 |
| 5 | X | 29 | ILE | 12.9 |
| 1 | P | 78 | TYR | 12.8 |
| 2 | S | 42 | ALA | 12.8 |
| 2 | L | 132 | ILE | 12.8 |
| 2 | L | 110 | VAL | 12.8 |
| 2 | S | 167 | LYS | 12.8 |
| 8 | H | 83 | ASN | 12.8 |
| 2 | S | 160 | ALA | 12.8 |
| 4 | Q | 76 | ASN | 12.8 |
| 2 | L | 147 | ALA | 12.8 |
| 2 | S | 183 | THR | 12.8 |
| 9 | G | 22 | ASN | 12.8 |
| 3 | W | 89 | LYS | 12.7 |
| 8 | E | 47 | ILE | 12.7 |
| 3 | Z | 22 | THR | 12.7 |
| 10 | N | 79 | G | 12.7 |
| 2 | L | 84 | THR | 12.7 |
| 6 | Y | 32 | LEU | 12.7 |
| 6 | V | 52 | LEU | 12.7 |
| 1 | P | 50 | LYS | 12.7 |
| 5 | U | 73 | SER | 12.7 |
| 3 | Z | 79 | ASN | 12.7 |
| 9 | G | 43 | ASP | 12.7 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 6 | V | 33 | THR | 12.6 |
| 4 | Q | 29 | GLY | 12.6 |
| 5 | U | 55 | LEU | 12.6 |
| 3 | W | 57 | GLN | 12.6 |
| 10 | N | 24 | C | 12.6 |
| 9 | J | 38 | MET | 12.6 |
| 8 | H | 26 | GLN | 12.6 |
| 4 | B | 26 | ILE | 12.6 |
| 9 | J | 50 | THR | 12.6 |
| 4 | Q | 79 | SER | 12.6 |
| 7 | I | 63 | LEU | 12.6 |
| 8 | H | 29 | SER | 12.5 |
| 2 | L | 49 | GLU | 12.5 |
| 3 | Z | 64 | ARG | 12.5 |
| 7 | F | 68 | ASN | 12.5 |
| 6 | Y | 101 | LEU | 12.5 |
| 3 | W | 71 | LEU | 12.5 |
| 7 | I | 17 | LYS | 12.5 |
| 3 | Z | 30 | GLY | 12.5 |
| 6 | Y | 67 | LEU | 12.5 |
| 2 | L | 106 | PHE | 12.5 |
| 2 | L | 176 | VAL | 12.4 |
| 1 | A | 24 | ASP | 12.4 |
| 2 | L | 42 | ALA | 12.4 |
| 2 | L | 54 | ALA | 12.4 |
| 6 | Y | 35 | SER | 12.4 |
| 6 | Y | 76 | GLU | 12.4 |
| 4 | Q | 6 | SER | 12.4 |
| 9 | J | 28 | GLN | 12.4 |
| 8 | H | 52 | GLU | 12.4 |
| 10 | N | 113 | A | 12.4 |
| 8 | E | 12 | LYS | 12.3 |
| 6 | Y | 22 | GLU | 12.3 |
| 7 | F | 5 | LEU | 12.3 |
| 4 | B | 32 | LYS | 12.3 |
| 2 | S | 69 | ARG | 12.3 |
| 1 | P | 6 | THR | 12.3 |
| 6 | Y | 46 | CYS | 12.3 |
| 10 | N | 133 | G | 12.3 |
| 6 | Y | 58 | ALA | 12.3 |
| 2 | S | 76 | GLU | 12.3 |
| 2 | L | 116 | GLU | 12.2 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 2 | L | 102 | PHE | 12.2 |
| 8 | E | 38 | GLN | 12.2 |
| 7 | F | 30 | LYS | 12.2 |
| 5 | X | 3 | LEU | 12.2 |
| 1 | P | 65 | ALA | 12.2 |
| 3 | Z | 42 | GLN | 12.2 |
| 4 | B | 54 | LYS | 12.2 |
| 4 | Q | 52 | LYS | 12.2 |
| 1 | A | 104 | ARG | 12.1 |
| 5 | U | 75 | PRO | 12.1 |
| 8 | H | 79 | LEU | 12.1 |
| 8 | E | 80 | LYS | 12.1 |
| 5 | X | 79 | LEU | 12.1 |
| 10 | N | 87 | C | 12.1 |
| 8 | E | 87 | LEU | 12.1 |
| 1 | P | 104 | ARG | 12.1 |
| 1 | P | 11 | THR | 12.1 |
| 7 | I | 23 | LEU | 12.1 |
| 2 | L | 45 | ILE | 12.1 |
| 4 | B | 13 | ILE | 12.0 |
| 9 | J | 22 | ASN | 12.0 |
| 1 | P | 36 | GLN | 12.0 |
| 6 | V | 17 | GLN | 12.0 |
| 4 | B | 46 | ASP | 12.0 |
| 8 | H | 39 | VAL | 12.0 |
| 8 | H | 61 | ALA | 12.0 |
| 2 | S | 148 | PHE | 12.0 |
| 2 | L | 118 | LYS | 12.0 |
| 8 | H | 18 | ILE | 12.0 |
| 1 | P | 83 | ARG | 12.0 |
| 1 | A | 9 | ASN | 11.9 |
| 5 | U | 29 | ILE | 11.9 |
| 10 | R | 149 | U | 11.9 |
| 4 | Q | 35 | ASP | 11.9 |
| 2 | S | 84 | THR | 11.9 |
| 7 | I | 22 | LYS | 11.9 |
| 6 | V | 42 | VAL | 11.9 |
| 4 | B | 52 | LYS | 11.9 |
| 1 | A | 35 | SER | 11.9 |
| 8 | E | 72 | LYS | 11.9 |
| 5 | X | 61 | ARG | 11.9 |
| 8 | E | 42 | ARG | 11.8 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 3 | Z | 75 | ASP | 11.8 |
| 7 | F | 49 | GLU | 11.8 |
| 3 | W | 56 | ALA | 11.8 |
| 11 | D | 4 | DT | 11.8 |
| 1 | P | 91 | SER | 11.8 |
| 1 | P | 19 | GLU | 11.8 |
| 4 | Q | 78 | VAL | 11.8 |
| 3 | W | 92 | GLY | 11.8 |
| 6 | Y | 9 | SER | 11.8 |
| 7 | F | 35 | SER | 11.8 |
| 2 | L | 98 | GLN | 11.7 |
| 8 | H | 38 | GLN | 11.7 |
| 9 | J | 62 | ILE | 11.7 |
| 10 | R | 112 | A | 11.7 |
| 10 | R | 135 | A | 11.7 |
| 1 | P | 73 | GLN | 11.7 |
| 6 | Y | 33 | THR | 11.7 |
| 9 | J | 10 | LYS | 11.7 |
| 6 | Y | 100 | PHE | 11.7 |
| 6 | Y | 107 | ILE | 11.7 |
| 2 | S | 89 | TRP | 11.7 |
| 1 | P | 88 | LYS | 11.7 |
| 2 | S | 157 | MET | 11.6 |
| 8 | H | 87 | LEU | 11.6 |
| 1 | P | 68 | ALA | 11.6 |
| 2 | S | 163 | HIS | 11.6 |
| 7 | F | 4 | PRO | 11.6 |
| 1 | A | 109 | GLU | 11.6 |
| 1 | P | 90 | ASP | 11.6 |
| 2 | S | 68 | GLU | 11.6 |
| 2 | S | 92 | HIS | 11.6 |
| 6 | Y | 61 | ARG | 11.6 |
| 7 | F | 78 | GLU | 11.5 |
| 7 | I | 46 | ASN | 11.5 |
| 2 | L | 124 | GLU | 11.5 |
| 3 | Z | 83 | LEU | 11.5 |
| 7 | I | 55 | LEU | 11.5 |
| 2 | S | 113 | ASP | 11.5 |
| 2 | S | 99 | GLY | 11.5 |
| 1 | P | 93 | ILE | 11.5 |
| 1 | A | 30 | LEU | 11.5 |
| 10 | N | 6 | U | 11.5 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | P | 5 | GLU | 11.4 |
| 8 | E | 34 | TRP | 11.4 |
| 2 | S | 180 | ARG | 11.4 |
| 5 | X | 19 | LEU | 11.4 |
| 2 | S | 55 | PRO | 11.4 |
| 2 | L | 115 | THR | 11.4 |
| 2 | L | 172 | ARG | 11.4 |
| 10 | R | 105 | U | 11.4 |
| 6 | Y | 15 | GLU | 11.4 |
| 2 | L | 67 | MET | 11.4 |
| 3 | W | 39 | MET | 11.4 |
| 5 | X | 75 | PRO | 11.4 |
| 6 | V | 58 | ALA | 11.4 |
| 5 | U | 38 | THR | 11.4 |
| 5 | U | 56 | GLU | 11.3 |
| 8 | E | 65 | HIS | 11.3 |
| 1 | P | 76 | PRO | 11.3 |
| 4 | Q | 12 | HIS | 11.3 |
| 1 | P | 56 | PHE | 11.3 |
| 10 | R | 67 | U | 11.3 |
| 2 | S | 123 | PHE | 11.3 |
| 6 | V | 50 | LYS | 11.3 |
| 6 | V | 108 | VAL | 11.3 |
| 1 | P | 48 | SER | 11.3 |
| 9 | G | 50 | THR | 11.3 |
| 2 | S | 50 | ASP | 11.3 |
| 3 | Z | 26 | GLU | 11.3 |
| 1 | P | 15 | ASN | 11.3 |
| 8 | E | 39 | VAL | 11.3 |
| 8 | E | 58 | LEU | 11.3 |
| 2 | S | 36 | GLN | 11.3 |
| 10 | N | 18 | G | 11.2 |
| 1 | A | 77 | PHE | 11.2 |
| 9 | G | 68 | ILE | 11.2 |
| 9 | J | 27 | VAL | 11.2 |
| 5 | X | 21 | ASN | 11.2 |
| 6 | V | 109 | VAL | 11.2 |
| 8 | E | 32 | GLN | 11.2 |
| 8 | H | 15 | VAL | 11.2 |
| 2 | S | 95 | PRO | 11.2 |
| 4 | Q | 80 | MET | 11.2 |
| 8 | E | 19 | ASN | 11.2 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 7 | F | 79 | GLU | 11.2 |
| 4 | B | 30 | THR | 11.2 |
| 4 | Q | 42 | LEU | 11.1 |
| 1 | A | 42 | ASP | 11.1 |
| 7 | I | 11 | LEU | 11.1 |
| 7 | I | 21 | VAL | 11.1 |
| 2 | S | 121 | ARG | 11.1 |
| 1 | A | 88 | LYS | 11.1 |
| 1 | A | 59 | PHE | 11.1 |
| 2 | S | 130 | LYS | 11.1 |
| 11 | D | 6 | DA | 11.1 |
| 3 | W | 48 | VAL | 11.1 |
| 1 | A | 21 | ILE | 11.1 |
| 3 | Z | 17 | ILE | 11.0 |
| 4 | B | 6 | SER | 11.0 |
| 9 | J | 5 | HIS | 11.0 |
| 10 | R | 128 | U | 11.0 |
| 2 | S | 165 | ASP | 11.0 |
| 2 | L | 148 | PHE | 11.0 |
| 5 | X | 14 | THR | 11.0 |
| 1 | A | 34 | PHE | 11.0 |
| 1 | P | 70 | ARG | 11.0 |
| 5 | X | 7 | LEU | 11.0 |
| 1 | P | 87 | ALA | 11.0 |
| 5 | X | 28 | THR | 11.0 |
| 6 | V | 63 | CYS | 11.0 |
| 2 | S | 116 | GLU | 11.0 |
| 2 | L | 87 | LYS | 11.0 |
| 2 | L | 35 | ASN | 11.0 |
| 6 | V | 26 | THR | 10.9 |
| 5 | X | 81 | VAL | 10.9 |
| 3 | Z | 76 | MET | 10.9 |
| 3 | W | 74 | PRO | 10.9 |
| 1 | A | 54 | GLN | 10.9 |
| 6 | V | 46 | CYS | 10.9 |
| 2 | L | 167 | LYS | 10.9 |
| 2 | L | 166 | GLY | 10.9 |
| 6 | V | 98 | LYS | 10.9 |
| 5 | U | 54 | GLN | 10.9 |
| 2 | S | 166 | GLY | 10.9 |
| 10 | R | 33 | C | 10.8 |
| 8 | E | 85 | THR | 10.8 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 3 | W | 60 | GLN | 10.8 |
| 4 | B | 10 | LEU | 10.8 |
| 1 | P | 102 | VAL | 10.8 |
| 8 | H | 82 | ASP | 10.8 |
| 7 | I | 70 | LEU | 10.8 |
| 8 | E | 61 | ALA | 10.8 |
| 4 | Q | 68 | GLY | 10.8 |
| 2 | L | 81 | GLU | 10.8 |
| 9 | G | 17 | LEU | 10.8 |
| 5 | X | 31 | GLY | 10.8 |
| 10 | R | 36 | A | 10.8 |
| 2 | L | 174 | VAL | 10.8 |
| 10 | N | 31 | C | 10.8 |
| 9 | J | 36 | PRO | 10.8 |
| 6 | V | 45 | ASN | 10.8 |
| 6 | Y | 81 | GLY | 10.8 |
| 4 | B | 42 | LEU | 10.7 |
| 3 | Z | 48 | VAL | 10.7 |
| 5 | X | 24 | GLN | 10.7 |
| 9 | J | 44 | GLU | 10.7 |
| 3 | Z | 31 | LYS | 10.7 |
| 4 | B | 22 | GLN | 10.7 |
| 4 | B | 37 | HIS | 10.7 |
| 1 | P | 97 | MET | 10.7 |
| 1 | A | 90 | ASP | 10.7 |
| 10 | R | 126 | A | 10.7 |
| 1 | A | 20 | LYS | 10.7 |
| 2 | S | 59 | ARG | 10.7 |
| 5 | X | 13 | GLU | 10.6 |
| 3 | Z | 52 | ASP | 10.6 |
| 2 | S | 153 | HIS | 10.6 |
| 10 | N | 37 | G | 10.6 |
| 1 | P | 59 | PHE | 10.6 |
| 7 | F | 85 | ARG | 10.6 |
| 8 | H | 37 | GLU | 10.6 |
| 2 | L | 130 | LYS | 10.6 |
| 3 | Z | 82 | MET | 10.6 |
| 4 | B | 82 | VAL | 10.6 |
| 1 | P | 42 | ASP | 10.6 |
| 5 | U | 47 | LEU | 10.6 |
| 2 | S | 176 | VAL | 10.6 |
| 2 | S | 118 | LYS | 10.6 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 2 | S | 72 | ARG | 10.5 |
| 2 | S | 53 | ASP | 10.5 |
| 7 | F | 70 | LEU | 10.5 |
| 6 | V | 114 | LEU | 10.5 |
| 2 | S | 47 | GLU | 10.5 |
| 8 | H | 36 | TYR | 10.5 |
| 1 | A | 8 | PRO | 10.5 |
| 1 | A | 31 | TYR | 10.5 |
| 5 | X | 1 | MET | 10.5 |
| 10 | R | 141 | G | 10.5 |
| 2 | L | 43 | PRO | 10.5 |
| 7 | I | 13 | GLY | 10.5 |
| 7 | F | 29 | TYR | 10.5 |
| 1 | P | 35 | SER | 10.5 |
| 3 | W | 45 | ASN | 10.5 |
| 9 | G | 69 | MET | 10.5 |
| 2 | L | 89 | TRP | 10.4 |
| 6 | Y | 13 | PRO | 10.4 |
| 7 | F | 81 | ASP | 10.4 |
| 6 | Y | 23 | GLU | 10.4 |
| 1 | A | 75 | PHE | 10.4 |
| 4 | Q | 87 | PRO | 10.4 |
| 3 | W | 91 | GLN | 10.4 |
| 4 | B | 48 | PHE | 10.4 |
| 2 | S | 77 | ARG | 10.4 |
| 5 | U | 63 | ASN | 10.4 |
| 3 | W | 79 | ASN | 10.4 |
| 8 | E | 40 | ASN | 10.4 |
| 9 | J | 57 | ILE | 10.4 |
| 1 | A | 41 | LEU | 10.4 |
| 5 | X | 4 | VAL | 10.3 |
| 4 | Q | 18 | ARG | 10.3 |
| 6 | V | 70 | VAL | 10.3 |
| 2 | S | 73 | GLU | 10.3 |
| 10 | N | 90 | U | 10.3 |
| 6 | V | 41 | GLN | 10.3 |
| 1 | P | 34 | PHE | 10.3 |
| 9 | J | 21 | LEU | 10.3 |
| 5 | U | 68 | PHE | 10.3 |
| 4 | B | 19 | CYS | 10.3 |
| 2 | L | 105 | LEU | 10.3 |
| 3 | W | 70 | PHE | 10.3 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 4 | B | 31 | PHE | 10.3 |
| 6 | Y | 106 | VAL | 10.3 |
| 4 | Q | 45 | CYS | 10.2 |
| 9 | G | 4 | ALA | 10.2 |
| 4 | Q | 72 | LEU | 10.2 |
| 9 | J | 16 | LYS | 10.2 |
| 4 | Q | 51 | ILE | 10.2 |
| 8 | E | 70 | SER | 10.2 |
| 7 | F | 34 | VAL | 10.2 |
| 5 | U | 59 | SER | 10.2 |
| 4 | B | 75 | GLU | 10.2 |
| 1 | A | 110 | LYS | 10.2 |
| 1 | A | 61 | GLU | 10.2 |
| 5 | X | 49 | ASN | 10.2 |
| 1 | A | 70 | ARG | 10.2 |
| 2 | L | 71 | ARG | 10.2 |
| 4 | Q | 17 | MET | 10.2 |
| 6 | V | 71 | LYS | 10.2 |
| 9 | G | 32 | ARG | 10.2 |
| 3 | Z | 84 | LYS | 10.1 |
| 1 | P | 96 | LYS | 10.1 |
| 4 | B | 64 | LYS | 10.1 |
| 2 | L | 112 | TYR | 10.1 |
| 3 | W | 5 | VAL | 10.1 |
| 2 | S | 102 | PHE | 10.1 |
| 3 | Z | 11 | HIS | 10.1 |
| 9 | G | 33 | GLY | 10.1 |
| 6 | V | 31 | VAL | 10.1 |
| 10 | R | 156 | U | 10.1 |
| 6 | Y | 91 | ASN | 10.0 |
| 1 | P | 32 | ALA | 10.0 |
| 4 | B | 40 | LEU | 10.0 |
| 6 | V | 97 | SER | 10.0 |
| 10 | R | 65 | A | 10.0 |
| 6 | V | 29 | LEU | 10.0 |
| 9 | J | 74 | GLU | 10.0 |
| 2 | S | 146 | TYR | 10.0 |
| 2 | L | 85 | GLU | 10.0 |
| 3 | W | 38 | ASN | 10.0 |
| 7 | I | 28 | GLU | 10.0 |
| 5 | U | 33 | ASP | 10.0 |
| 7 | F | 67 | ASN | 10.0 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 2 | S | 58 | THR | 10.0 |
| 2 | L | 163 | HIS | 10.0 |
| 5 | U | 48 | LYS | 10.0 |
| 7 | I | 64 | ILE | 10.0 |
| 10 | N | 53 | C | 10.0 |
| 6 | Y | 110 | LEU | 9.9 |
| 6 | Y | 37 | LYS | 9.9 |
| 8 | E | 88 | GLN | 9.9 |
| 1 | A | 14 | ILE | 9.9 |
| 1 | A | 79 | ASP | 9.9 |
| 6 | V | 60 | ASP | 9.9 |
| 7 | I | 50 | TYR | 9.9 |
| 2 | S | 110 | VAL | 9.9 |
| 7 | I | 66 | CYS | 9.9 |
| 1 | P | 30 | LEU | 9.9 |
| 8 | E | 8 | GLN | 9.9 |
| 10 | N | 99 | C | 9.9 |
| 1 | P | 113 | PRO | 9.9 |
| 8 | E | 10 | VAL | 9.9 |
| 8 | H | 89 | SER | 9.9 |
| 5 | U | 31 | GLY | 9.9 |
| 4 | Q | 27 | PHE | 9.8 |
| 9 | G | 66 | SER | 9.8 |
| 7 | F | 53 | GLY | 9.8 |
| 2 | L | 113 | ASP | 9.8 |
| 1 | A | 22 | LYS | 9.8 |
| 2 | S | 51 | PRO | 9.8 |
| 6 | V | 64 | ASN | 9.8 |
| 8 | H | 11 | GLN | 9.8 |
| 1 | A | 72 | MET | 9.8 |
| 3 | Z | 81 | PRO | 9.8 |
| 9 | G | 47 | GLU | 9.8 |
| 10 | R | 104 | A | 9.8 |
| 9 | G | 28 | GLN | 9.8 |
| 5 | X | 55 | LEU | 9.8 |
| 2 | S | 125 | VAL | 9.8 |
| 9 | G | 21 | LEU | 9.8 |
| 9 | G | 59 | MET | 9.7 |
| 5 | X | 68 | PHE | 9.7 |
| 5 | U | 19 | LEU | 9.7 |
| 1 | A | 112 | LYS | 9.7 |
| 10 | R | 120 | U | 9.7 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 7 | I | 43 | GLN | 9.7 |
| 10 | R | 31 | C | 9.7 |
| 2 | L | 161 | TYR | 9.7 |
| 7 | F | 61 | GLU | 9.7 |
| 3 | Z | 37 | ASP | 9.7 |
| 6 | V | 51 | LYS | 9.6 |
| 6 | V | 4 | LEU | 9.6 |
| 6 | V | 9 | SER | 9.6 |
| 9 | J | 35 | ASP | 9.6 |
| 6 | V | 20 | GLU | 9.6 |
| 3 | W | 69 | ARG | 9.6 |
| 5 | U | 77 | ASP | 9.6 |
| 4 | B | 33 | ALA | 9.6 |
| 5 | U | 41 | LYS | 9.6 |
| 3 | W | 21 | GLU | 9.6 |
| 5 | U | 6 | PHE | 9.6 |
| 1 | A | 60 | LYS | 9.6 |
| 5 | U | 67 | TYR | 9.6 |
| 9 | G | 25 | ARG | 9.6 |
| 1 | P | 89 | THR | 9.5 |
| 4 | Q | 50 | LYS | 9.5 |
| 6 | Y | 42 | VAL | 9.5 |
| 3 | W | 43 | MET | 9.5 |
| 11 | M | 3 | DG | 9.5 |
| 8 | E | 22 | PHE | 9.5 |
| 4 | Q | 85 | PRO | 9.5 |
| 3 | Z | 61 | VAL | 9.5 |
| 2 | L | 40 | GLY | 9.5 |
| 2 | S | 181 | GLY | 9.5 |
| 6 | V | 65 | MET | 9.5 |
| 6 | Y | 111 | ARG | 9.5 |
| 6 | V | 61 | ARG | 9.5 |
| 8 | H | 75 | GLY | 9.5 |
| 2 | S | 63 | ARG | 9.5 |
| 9 | G | 36 | PRO | 9.4 |
| 10 | R | 29 | A | 9.4 |
| 6 | V | 72 | GLU | 9.4 |
| 2 | L | 100 | ASP | 9.4 |
| 5 | U | 4 | VAL | 9.4 |
| 6 | V | 55 | ARG | 9.4 |
| 6 | Y | 57 | LYS | 9.4 |
| 11 | D | 7 | DG | 9.4 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 7 | I | 14 | LEU | 9.4 |
| 5 | U | 66 | ARG | 9.4 |
| 1 | P | 103 | GLU | 9.4 |
| 2 | S | 111 | ASN | 9.4 |
| 4 | Q | 47 | GLU | 9.4 |
| 1 | A | 43 | ILE | 9.4 |
| 1 | A | 95 | ALA | 9.3 |
| 7 | I | 42 | MET | 9.3 |
| 3 | W | 75 | ASP | 9.3 |
| 2 | L | 155 | ARG | 9.3 |
| 2 | S | 115 | THR | 9.3 |
| 4 | Q | 41 | ILE | 9.3 |
| 3 | W | 32 | LEU | 9.3 |
| 1 | A | 29 | SER | 9.3 |
| 3 | W | 36 | GLU | 9.3 |
| 5 | X | 44 | LYS | 9.3 |
| 5 | X | 78 | THR | 9.3 |
| 7 | F | 55 | LEU | 9.3 |
| 10 | N | 67 | U | 9.3 |
| 7 | I | 39 | TYR | 9.2 |
| 10 | N | 109 | G | 9.2 |
| 2 | L | 56 | PRO | 9.2 |
| 6 | V | 59 | PHE | 9.2 |
| 6 | Y | 69 | ASN | 9.2 |
| 2 | S | 64 | GLU | 9.2 |
| 3 | W | 47 | THR | 9.2 |
| 4 | Q | 53 | PRO | 9.2 |
| 1 | P | 22 | LYS | 9.2 |
| 1 | A | 37 | PHE | 9.2 |
| 1 | P | 25 | GLU | 9.2 |
| 4 | B | 86 | PRO | 9.2 |
| 5 | U | 49 | ASN | 9.2 |
| 3 | W | 26 | GLU | 9.1 |
| 5 | X | 10 | LEU | 9.1 |
| 6 | Y | 48 | ASN | 9.1 |
| 9 | J | 4 | ALA | 9.1 |
| 1 | A | 16 | ASN | 9.1 |
| 10 | N | 10 | U | 9.1 |
| 4 | B | 25 | ARG | 9.1 |
| 9 | G | 53 | GLN | 9.1 |
| 6 | Y | 66 | VAL | 9.1 |
| 7 | I | 51 | ILE | 9.1 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 3 | W | 58 | LEU | 9.1 |
| 4 | Q | 38 | MET | 9.1 |
| 2 | S | 60 | ALA | 9.1 |
| 2 | L | 91 | PRO | 9.1 |
| 5 | X | 27 | GLY | 9.1 |
| 5 | X | 11 | SER | 9.1 |
| 1 | A | 97 | MET | 9.1 |
| 8 | E | 9 | LYS | 9.1 |
| 7 | F | 43 | GLN | 9.1 |
| 1 | A | 33 | ILE | 9.1 |
| 7 | F | 64 | ILE | 9.1 |
| 3 | W | 42 | GLN | 9.0 |
| 1 | P | 16 | ASN | 9.0 |
| 7 | F | 3 | LEU | 9.0 |
| 5 | U | 12 | HIS | 9.0 |
| 1 | P | 39 | GLN | 9.0 |
| 3 | W | 49 | THR | 9.0 |
| 5 | U | 30 | THR | 9.0 |
| 9 | G | 73 | LEU | 9.0 |
| 4 | Q | 70 | VAL | 9.0 |
| 9 | G | 67 | ILE | 9.0 |
| 9 | J | 18 | SER | 9.0 |
| 7 | F | 38 | GLY | 9.0 |
| 7 | F | 62 | VAL | 9.0 |
| 3 | Z | 13 | ALA | 9.0 |
| 6 | V | 95 | TYR | 9.0 |
| 6 | V | 54 | GLY | 9.0 |
| 8 | H | 47 | ILE | 9.0 |
| 2 | L | 134 | MET | 8.9 |
| 6 | Y | 98 | LYS | 8.9 |
| 8 | H | 80 | LYS | 8.9 |
| 2 | L | 86 | LEU | 8.9 |
| 1 | A | 93 | ILE | 8.9 |
| 6 | V | 23 | GLU | 8.9 |
| 2 | S | 182 | ARG | 8.9 |
| 2 | L | 142 | LYS | 8.9 |
| 1 | P | 75 | PHE | 8.9 |
| 6 | V | 27 | GLY | 8.9 |
| 1 | A | 80 | LYS | 8.9 |
| 7 | F | 82 | GLY | 8.9 |
| 2 | S | 80 | GLN | 8.9 |
| 3 | W | 18 | VAL | 8.9 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 2 | S | 34 | HIS | 8.9 |
| 5 | X | 45 | MET | 8.9 |
| 8 | E | 51 | ASP | 8.9 |
| 9 | J | 24 | GLY | 8.9 |
| 2 | L | 158 | HIS | 8.9 |
| 7 | F | 23 | LEU | 8.9 |
| 1 | A | 101 | PHE | 8.9 |
| 2 | L | 175 | LEU | 8.9 |
| 10 | N | 82 | C | 8.9 |
| 1 | A | 5 | GLU | 8.8 |
| 9 | G | 19 | LEU | 8.8 |
| 5 | X | 39 | HIS | 8.8 |
| 7 | F | 86 | GLU | 8.8 |
| 3 | Z | 38 | ASN | 8.8 |
| 9 | G | 74 | GLU | 8.8 |
| 1 | P | 86 | TYR | 8.8 |
| 10 | R | 10 | U | 8.8 |
| 2 | S | 149 | ILE | 8.8 |
| 8 | E | 67 | LYS | 8.8 |
| 9 | J | 49 | ALA | 8.8 |
| 1 | P | 43 | ILE | 8.8 |
| 1 | A | 51 | MET | 8.8 |
| 3 | W | 9 | VAL | 8.8 |
| 7 | F | 39 | TYR | 8.7 |
| 4 | Q | 26 | ILE | 8.7 |
| 8 | E | 78 | MET | 8.7 |
| 1 | A | 25 | GLU | 8.7 |
| 6 | V | 37 | LYS | 8.7 |
| 1 | A | 58 | ILE | 8.7 |
| 6 | Y | 47 | ARG | 8.7 |
| 2 | L | 164 | ALA | 8.7 |
| 4 | B | 80 | MET | 8.7 |
| 4 | Q | 34 | PHE | 8.7 |
| 6 | V | 75 | THR | 8.7 |
| 6 | V | 102 | ARG | 8.7 |
| 5 | X | 48 | LYS | 8.7 |
| 1 | A | 36 | GLN | 8.7 |
| 1 | A | 57 | VAL | 8.6 |
| 9 | G | 1 | MET | 8.6 |
| 3 | Z | 19 | THR | 8.6 |
| 3 | W | 93 | SER | 8.6 |
| 3 | Z | 71 | LEU | 8.6 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 3 | Z | 77 | LEU | 8.6 |
| 7 | I | 34 | VAL | 8.6 |
| 8 | H | 34 | TRP | 8.6 |
| 7 | I | 9 | PRO | 8.6 |
| 10 | N | 2 | U | 8.6 |
| 5 | X | 59 | SER | 8.6 |
| 5 | X | 42 | ALA | 8.6 |
| 9 | J | 9 | LEU | 8.6 |
| 7 | F | 33 | LEU | 8.6 |
| 9 | G | 11 | LYS | 8.6 |
| 9 | J | 75 | ARG | 8.6 |
| 5 | U | 43 | VAL | 8.5 |
| 2 | S | 91 | PRO | 8.5 |
| 3 | Z | 23 | ASN | 8.5 |
| 3 | Z | 63 | ILE | 8.5 |
| 2 | S | 97 | ALA | 8.5 |
| 10 | R | 13 | C | 8.5 |
| 2 | L | 90 | ASP | 8.5 |
| 2 | L | 156 | ASP | 8.5 |
| 6 | Y | 12 | THR | 8.4 |
| 6 | V | 67 | LEU | 8.4 |
| 2 | L | 41 | ILE | 8.4 |
| 10 | R | 55 | A | 8.4 |
| 5 | X | 18 | GLU | 8.4 |
| 4 | B | 36 | LYS | 8.4 |
| 2 | S | 71 | ARG | 8.4 |
| 2 | L | 51 | PRO | 8.4 |
| 4 | B | 38 | MET | 8.4 |
| 6 | V | 22 | GLU | 8.4 |
| 1 | A | 85 | GLN | 8.4 |
| 7 | F | 73 | ARG | 8.4 |
| 9 | G | 75 | ARG | 8.4 |
| 7 | I | 54 | ALA | 8.4 |
| 4 | B | 67 | LEU | 8.3 |
| 1 | A | 44 | LEU | 8.3 |
| 2 | S | 175 | LEU | 8.3 |
| 5 | X | 40 | LEU | 8.3 |
| 3 | Z | 6 | PRO | 8.3 |
| 1 | A | 50 | LYS | 8.3 |
| 2 | L | 63 | ARG | 8.3 |
| 9 | G | 63 | ARG | 8.3 |
| 3 | Z | 54 | ARG | 8.3 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 8 | E | 90 | VAL | 8.3 |
| 2 | L | 53 | ASP | 8.3 |
| 6 | Y | 49 | ASN | 8.3 |
| 3 | Z | 16 | HIS | 8.3 |
| 4 | B | 43 | CYS | 8.2 |
| 7 | I | 5 | LEU | 8.2 |
| 8 | H | 66 | SER | 8.2 |
| 2 | S | 178 | VAL | 8.2 |
| 4 | Q | 21 | LEU | 8.2 |
| 9 | G | 23 | GLY | 8.2 |
| 4 | B | 56 | SER | 8.2 |
| 6 | V | 90 | VAL | 8.2 |
| 2 | S | 45 | ILE | 8.2 |
| 9 | G | 57 | ILE | 8.2 |
| 9 | G | 10 | LYS | 8.2 |
| 5 | X | 38 | THR | 8.2 |
| 5 | X | 80 | LEU | 8.2 |
| 9 | J | 23 | GLY | 8.2 |
| 2 | S | 136 | TYR | 8.2 |
| 7 | I | 45 | ALA | 8.2 |
| 9 | G | 42 | ILE | 8.2 |
| 4 | B | 58 | GLN | 8.2 |
| 6 | V | 10 | GLU | 8.2 |
| 6 | V | 100 | PHE | 8.2 |
| 3 | Z | 60 | GLN | 8.2 |
| 5 | U | 58 | LEU | 8.2 |
| 9 | G | 49 | ALA | 8.2 |
| 6 | V | 76 | GLU | 8.2 |
| 5 | X | 6 | PHE | 8.2 |
| 8 | H | 7 | GLY | 8.1 |
| 2 | S | 66 | ARG | 8.1 |
| 3 | W | 15 | GLY | 8.1 |
| 6 | Y | 7 | PRO | 8.1 |
| 8 | H | 51 | ASP | 8.1 |
| 8 | E | 17 | PRO | 8.1 |
| 2 | S | 159 | SER | 8.1 |
| 6 | Y | 92 | LYS | 8.1 |
| 5 | U | 64 | ASN | 8.1 |
| 1 | P | 101 | PHE | 8.1 |
| 5 | U | 22 | GLY | 8.1 |
| 8 | E | 7 | GLY | 8.1 |
| 6 | Y | 16 | LEU | 8.1 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | P | 46 | SER | 8.1 |
| 1 | P | 99 | GLY | 8.0 |
| 2 | L | 52 | ARG | 8.0 |
| 5 | X | 34 | VAL | 8.0 |
| 4 | B | 18 | ARG | 8.0 |
| 7 | F | 26 | GLY | 8.0 |
| 6 | V | 107 | ILE | 8.0 |
| 1 | P | 44 | LEU | 8.0 |
| 2 | S | 46 | ARG | 8.0 |
| 7 | I | 40 | MET | 8.0 |
| 3 | W | 20 | CYS | 8.0 |
| 9 | G | 46 | VAL | 7.9 |
| 2 | S | 62 | THR | 7.9 |
| 6 | Y | 50 | LYS | 7.9 |
| 3 | Z | 55 | VAL | 7.9 |
| 10 | N | 135 | A | 7.9 |
| 5 | X | 33 | ASP | 7.9 |
| 4 | Q | 88 | LYS | 7.9 |
| 2 | S | 152 | GLU | 7.9 |
| 5 | U | 79 | LEU | 7.9 |
| 7 | I | 26 | GLY | 7.9 |
| 2 | S | 38 | TYR | 7.9 |
| 2 | S | 90 | ASP | 7.9 |
| 1 | P | 41 | LEU | 7.9 |
| 4 | B | 45 | CYS | 7.9 |
| 4 | Q | 67 | LEU | 7.9 |
| 3 | Z | 53 | GLY | 7.9 |
| 10 | N | 147 | C | 7.8 |
| 1 | P | 28 | LYS | 7.8 |
| 1 | P | 20 | LYS | 7.8 |
| 1 | A | 111 | ARG | 7.8 |
| 2 | L | 139 | ARG | 7.8 |
| 5 | X | 64 | ASN | 7.8 |
| 4 | B | 50 | LYS | 7.8 |
| 3 | W | 27 | VAL | 7.8 |
| 4 | B | 72 | LEU | 7.8 |
| 1 | P | 114 | LYS | 7.8 |
| 7 | F | 2 | SER | 7.8 |
| 2 | S | 83 | GLU | 7.8 |
| 10 | N | 140 | G | 7.8 |
| 8 | H | 6 | GLN | 7.8 |
| 2 | S | 88 | MET | 7.8 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 4 | Q | 71 | LEU | 7.8 |
| 5 | U | 71 | PRO | 7.8 |
| 7 | F | 16 | GLY | 7.8 |
| 9 | G | 52 | GLY | 7.8 |
| 2 | S | 134 | MET | 7.8 |
| 2 | L | 109 | ARG | 7.8 |
| 7 | F | 37 | ASP | 7.8 |
| 3 | W | 28 | TYR | 7.7 |
| 6 | Y | 97 | SER | 7.7 |
| 6 | Y | 105 | SER | 7.7 |
| 8 | E | 75 | GLY | 7.7 |
| 7 | I | 19 | VAL | 7.7 |
| 2 | L | 48 | PHE | 7.7 |
| 3 | Z | 80 | ALA | 7.7 |
| 6 | V | 48 | ASN | 7.7 |
| 5 | X | 30 | THR | 7.7 |
| 2 | L | 72 | ARG | 7.7 |
| 3 | Z | 27 | VAL | 7.7 |
| 4 | B | 71 | LEU | 7.7 |
| 10 | N | 145 | U | 7.7 |
| 7 | I | 61 | GLU | 7.7 |
| 6 | Y | 14 | GLU | 7.6 |
| 7 | F | 13 | GLY | 7.6 |
| 4 | Q | 28 | ILE | 7.6 |
| 4 | B | 83 | GLU | 7.6 |
| 5 | U | 65 | ILE | 7.6 |
| 2 | S | 128 | PRO | 7.6 |
| 5 | U | 85 | PRO | 7.6 |
| 8 | H | 50 | PHE | 7.6 |
| 2 | S | 87 | LYS | 7.6 |
| 5 | X | 76 | LEU | 7.6 |
| 1 | A | 6 | THR | 7.5 |
| 10 | N | 119 | C | 7.5 |
| 2 | L | 38 | TYR | 7.5 |
| 4 | B | 21 | LEU | 7.5 |
| 4 | Q | 73 | ARG | 7.5 |
| 9 | J | 73 | LEU | 7.5 |
| 9 | J | 46 | VAL | 7.5 |
| 4 | Q | 5 | LYS | 7.5 |
| 9 | J | 72 | ALA | 7.5 |
| 2 | S | 48 | PHE | 7.5 |
| 1 | P | 63 | SER | 7.5 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 7 | F | 74 | GLY | 7.5 |
| 1 | A | 84 | ILE | 7.5 |
| 6 | Y | 2 | SER | 7.5 |
| 7 | F | 51 | ILE | 7.5 |
| 7 | I | 35 | SER | 7.5 |
| 8 | H | 41 | MET | 7.5 |
| 5 | X | 66 | ARG | 7.5 |
| 6 | Y | 51 | LYS | 7.5 |
| 4 | B | 20 | ILE | 7.4 |
| 6 | Y | 36 | VAL | 7.4 |
| 6 | V | 113 | PRO | 7.4 |
| 8 | H | 19 | ASN | 7.4 |
| 5 | X | 82 | ASP | 7.4 |
| 3 | W | 78 | LYS | 7.4 |
| 5 | U | 10 | LEU | 7.4 |
| 2 | S | 169 | ILE | 7.4 |
| 1 | P | 74 | GLY | 7.4 |
| 1 | A | 83 | ARG | 7.4 |
| 2 | L | 125 | VAL | 7.4 |
| 6 | V | 101 | LEU | 7.4 |
| 4 | B | 53 | PRO | 7.4 |
| 6 | Y | 19 | ARG | 7.4 |
| 4 | B | 68 | GLY | 7.4 |
| 5 | U | 18 | GLU | 7.4 |
| 6 | Y | 5 | ASN | 7.4 |
| 3 | W | 50 | TYR | 7.4 |
| 6 | V | 2 | SER | 7.3 |
| 6 | Y | 53 | LEU | 7.3 |
| 9 | G | 76 | VAL | 7.3 |
| 7 | I | 15 | THR | 7.3 |
| 3 | W | 54 | ARG | 7.3 |
| 3 | W | 87 | LYS | 7.3 |
| 7 | F | 36 | VAL | 7.3 |
| 9 | G | 40 | LEU | 7.3 |
| 1 | P | 12 | ILE | 7.3 |
| 2 | L | 128 | PRO | 7.3 |
| 2 | L | 62 | THR | 7.3 |
| 6 | V | 99 | MET | 7.3 |
| 5 | X | 67 | TYR | 7.3 |
| 3 | W | 94 | GLY | 7.3 |
| 5 | U | 28 | THR | 7.3 |
| 1 | A | 27 | LYS | 7.2 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 7 | I | 8 | LYS | 7.2 |
| 3 | W | 22 | THR | 7.2 |
| 2 | S | 107 | VAL | 7.2 |
| 5 | U | 36 | MET | 7.2 |
| 1 | A | 52 | ARG | 7.2 |
| 6 | Y | 10 | GLU | 7.2 |
| 6 | V | 47 | ARG | 7.2 |
| 9 | J | 30 | ILE | 7.2 |
| 9 | J | 39 | ASN | 7.2 |
| 6 | V | 73 | MET | 7.2 |
| 8 | H | 13 | VAL | 7.2 |
| 7 | F | 48 | GLU | 7.2 |
| 9 | G | 13 | MET | 7.2 |
| 9 | G | 38 | MET | 7.2 |
| 2 | S | 173 | ARG | 7.1 |
| 3 | Z | 20 | CYS | 7.1 |
| 8 | H | 76 | ARG | 7.1 |
| 2 | L | 44 | TYR | 7.1 |
| 6 | V | 92 | LYS | 7.1 |
| 7 | I | 30 | LYS | 7.1 |
| 1 | A | 49 | LEU | 7.1 |
| 9 | J | 71 | GLU | 7.1 |
| 2 | L | 120 | ARG | 7.0 |
| 7 | F | 10 | PHE | 7.0 |
| 8 | H | 73 | GLN | 7.0 |
| 1 | A | 62 | VAL | 7.0 |
| 6 | Y | 31 | VAL | 7.0 |
| 3 | Z | 62 | TYR | 7.0 |
| 8 | H | 2 | ALA | 7.0 |
| 4 | Q | 66 | VAL | 7.0 |
| 7 | I | 33 | LEU | 7.0 |
| 3 | Z | 68 | ILE | 7.0 |
| 2 | L | 140 | SER | 6.9 |
| 6 | V | 96 | ILE | 6.9 |
| 2 | S | 100 | ASP | 6.9 |
| 5 | U | 34 | VAL | 6.9 |
| 2 | S | 44 | TYR | 6.9 |
| 9 | G | 12 | PHE | 6.9 |
| 3 | Z | 45 | ASN | 6.9 |
| 6 | Y | 90 | VAL | 6.9 |
| 9 | G | 26 | HIS | 6.9 |
| 4 | Q | 90 | THR | 6.9 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 6 | Y | 68 | GLU | 6.9 |
| 9 | G | 51 | SER | 6.9 |
| 7 | F | 54 | ALA | 6.8 |
| 3 | Z | 59 | GLU | 6.8 |
| 8 | E | 64 | ILE | 6.8 |
| 9 | J | 3 | LYS | 6.8 |
| 6 | Y | 96 | ILE | 6.7 |
| 4 | Q | 65 | ARG | 6.7 |
| 10 | N | 162 | C | 6.7 |
| 9 | J | 43 | ASP | 6.7 |
| 10 | R | 61 | A | 6.7 |
| 6 | V | 28 | PRO | 6.7 |
| 8 | H | 9 | LYS | 6.7 |
| 2 | S | 144 | ARG | 6.7 |
| 9 | J | 29 | GLY | 6.7 |
| 2 | L | 46 | ARG | 6.6 |
| 4 | B | 39 | ASN | 6.6 |
| 2 | L | 60 | ALA | 6.6 |
| 8 | E | 86 | LEU | 6.6 |
| 8 | H | 27 | ASN | 6.6 |
| 5 | U | 21 | ASN | 6.6 |
| 7 | I | 52 | ASP | 6.6 |
| 3 | W | 86 | MET | 6.6 |
| 4 | Q | 48 | PHE | 6.6 |
| 6 | Y | 95 | TYR | 6.6 |
| 2 | S | 78 | ARG | 6.6 |
| 7 | F | 31 | GLY | 6.6 |
| 5 | U | 74 | LEU | 6.6 |
| 2 | L | 126 | TYR | 6.6 |
| 3 | W | 6 | PRO | 6.5 |
| 4 | B | 29 | GLY | 6.5 |
| 4 | B | 59 | ALA | 6.5 |
| 6 | Y | 71 | LYS | 6.5 |
| 4 | B | 17 | MET | 6.5 |
| 4 | B | 8 | LYS | 6.5 |
| 1 | P | 107 | LYS | 6.5 |
| 7 | I | 24 | LYS | 6.5 |
| 1 | P | 10 | HIS | 6.4 |
| 5 | X | 23 | THR | 6.4 |
| 3 | W | 68 | ILE | 6.4 |
| 7 | F | 9 | PRO | 6.4 |
| 2 | S | 109 | ARG | 6.4 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 4 | Q | 46 | ASP | 6.4 |
| 7 | I | 18 | PRO | 6.4 |
| 3 | Z | 29 | ARG | 6.4 |
| 3 | Z | 47 | THR | 6.4 |
| 9 | J | 47 | GLU | 6.4 |
| 2 | S | 156 | ASP | 6.4 |
| 10 | N | 158 | U | 6.4 |
| 2 | S | 61 | GLU | 6.4 |
| 7 | F | 72 | ILE | 6.4 |
| 3 | W | 84 | LYS | 6.4 |
| 5 | X | 36 | MET | 6.3 |
| 3 | Z | 44 | SER | 6.3 |
| 4 | B | 47 | GLU | 6.3 |
| 1 | A | 39 | GLN | 6.3 |
| 6 | Y | 28 | PRO | 6.3 |
| 8 | E | 25 | LEU | 6.3 |
| 1 | P | 108 | ARG | 6.3 |
| 7 | I | 58 | HIS | 6.3 |
| 7 | I | 48 | GLU | 6.3 |
| 7 | F | 84 | MET | 6.3 |
| 1 | A | 7 | ARG | 6.3 |
| 4 | B | 62 | GLU | 6.3 |
| 7 | F | 19 | VAL | 6.3 |
| 9 | G | 65 | ASN | 6.3 |
| 10 | N | 134 | U | 6.3 |
| 7 | F | 28 | GLU | 6.2 |
| 2 | S | 120 | ARG | 6.2 |
| 9 | J | 37 | PHE | 6.2 |
| 2 | S | 35 | ASN | 6.2 |
| 9 | J | 67 | ILE | 6.2 |
| 7 | F | 15 | THR | 6.2 |
| 8 | E | 71 | ARG | 6.2 |
| 3 | Z | 49 | THR | 6.2 |
| 6 | Y | 79 | LYS | 6.2 |
| 6 | Y | 78 | PRO | 6.2 |
| 8 | H | 25 | LEU | 6.2 |
| 9 | J | 15 | LYS | 6.2 |
| 6 | Y | 55 | ARG | 6.2 |
| 4 | Q | 16 | ARG | 6.1 |
| 5 | X | 58 | LEU | 6.1 |
| 1 | P | 64 | SER | 6.1 |
| 7 | I | 38 | GLY | 6.1 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | P | 80 | LYS | 6.1 |
| 8 | H | 4 | ARG | 6.1 |
| 6 | Y | 99 | MET | 6.1 |
| 9 | G | 6 | PRO | 6.1 |
| 9 | J | 7 | PRO | 6.1 |
| 3 | W | 52 | ASP | 6.1 |
| 1 | P | 84 | ILE | 6.1 |
| 1 | P | 18 | ASN | 6.1 |
| 2 | S | 96 | ASN | 6.1 |
| 9 | J | 14 | ASP | 6.1 |
| 7 | I | 7 | PRO | 6.1 |
| 8 | H | 49 | GLY | 6.1 |
| 5 | U | 20 | LYS | 6.1 |
| 6 | V | 11 | MET | 6.1 |
| 8 | H | 55 | ASN | 6.1 |
| 3 | Z | 43 | MET | 6.1 |
| 1 | A | 108 | ARG | 6.0 |
| 10 | R | 119 | C | 6.0 |
| 3 | W | 37 | ASP | 6.0 |
| 9 | J | 33 | GLY | 6.0 |
| 6 | Y | 77 | VAL | 6.0 |
| 9 | J | 68 | ILE | 6.0 |
| 8 | E | 82 | ASP | 6.0 |
| 9 | G | 55 | ASN | 6.0 |
| 2 | S | 57 | PRO | 6.0 |
| 8 | H | 16 | GLN | 5.9 |
| 3 | W | 51 | ARG | 5.9 |
| 2 | S | 41 | ILE | 5.9 |
| 4 | B | 70 | VAL | 5.9 |
| 8 | H | 72 | LYS | 5.9 |
| 2 | S | 108 | ALA | 5.9 |
| 1 | P | 106 | ARG | 5.9 |
| 6 | Y | 82 | LYS | 5.9 |
| 2 | S | 49 | GLU | 5.9 |
| 2 | L | 69 | ARG | 5.9 |
| 7 | I | 3 | LEU | 5.8 |
| 5 | U | 61 | ARG | 5.8 |
| 7 | F | 7 | PRO | 5.8 |
| 2 | S | 139 | ARG | 5.8 |
| 2 | S | 138 | LYS | 5.8 |
| 6 | Y | 60 | ASP | 5.8 |
| 5 | U | 84 | GLU | 5.8 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 6 | Y | 17 | GLN | 5.7 |
| 1 | A | 106 | ARG | 5.7 |
| 5 | X | 85 | PRO | 5.7 |
| 8 | H | 30 | ARG | 5.7 |
| 5 | U | 78 | THR | 5.7 |
| 5 | U | 1 | MET | 5.7 |
| 9 | J | 58 | GLY | 5.7 |
| 7 | F | 69 | VAL | 5.7 |
| 1 | A | 81 | PRO | 5.7 |
| 3 | Z | 39 | MET | 5.7 |
| 8 | H | 86 | LEU | 5.7 |
| 1 | P | 54 | GLN | 5.7 |
| 1 | A | 74 | GLY | 5.7 |
| 2 | S | 52 | ARG | 5.6 |
| 7 | I | 2 | SER | 5.6 |
| 8 | E | 73 | GLN | 5.6 |
| 1 | P | 110 | LYS | 5.6 |
| 8 | E | 20 | LEU | 5.6 |
| 5 | U | 3 | LEU | 5.6 |
| 4 | B | 77 | LEU | 5.6 |
| 6 | Y | 73 | MET | 5.6 |
| 2 | S | 74 | LYS | 5.6 |
| 5 | U | 15 | VAL | 5.6 |
| 2 | L | 59 | ARG | 5.6 |
| 8 | E | 18 | ILE | 5.5 |
| 7 | I | 36 | VAL | 5.5 |
| 1 | A | 10 | HIS | 5.5 |
| 1 | P | 95 | ALA | 5.5 |
| 7 | I | 62 | VAL | 5.5 |
| 9 | J | 76 | VAL | 5.5 |
| 4 | B | 44 | ASP | 5.5 |
| 5 | X | 53 | VAL | 5.5 |
| 6 | V | 117 | GLY | 5.4 |
| 1 | P | 52 | ARG | 5.4 |
| 5 | U | 76 | LEU | 5.4 |
| 9 | J | 45 | CYS | 5.4 |
| 8 | E | 46 | CYS | 5.4 |
| 2 | S | 112 | TYR | 5.4 |
| 1 | A | 47 | ARG | 5.4 |
| 10 | R | 35 | A | 5.4 |
| 8 | H | 74 | LEU | 5.4 |
| 2 | L | 135 | VAL | 5.4 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 8 | E | 16 | GLN | 5.4 |
| 8 | H | 8 | GLN | 5.4 |
| 9 | J | 41 | VAL | 5.4 |
| 4 | B | 16 | ARG | 5.4 |
| 9 | J | 51 | SER | 5.4 |
| 7 | I | 75 | VAL | 5.4 |
| 6 | V | 18 | LYS | 5.4 |
| 9 | G | 24 | GLY | 5.3 |
| 10 | N | 5 | U | 5.3 |
| 3 | W | 4 | GLY | 5.3 |
| 2 | S | 179 | GLU | 5.3 |
| 9 | G | 72 | ALA | 5.3 |
| 4 | B | 61 | ARG | 5.3 |
| 7 | F | 6 | ASN | 5.3 |
| 8 | E | 24 | TYR | 5.3 |
| 2 | L | 68 | GLU | 5.3 |
| 2 | L | 138 | LYS | 5.3 |
| 6 | Y | 6 | LYS | 5.3 |
| 5 | U | 50 | ARG | 5.3 |
| 6 | Y | 102 | ARG | 5.3 |
| 1 | P | 85 | GLN | 5.3 |
| 6 | Y | 70 | VAL | 5.2 |
| 4 | B | 15 | TYR | 5.2 |
| 4 | B | 27 | PHE | 5.2 |
| 6 | V | 25 | ASN | 5.2 |
| 2 | S | 54 | ALA | 5.2 |
| 1 | P | 33 | ILE | 5.2 |
| 1 | A | 99 | GLY | 5.2 |
| 9 | G | 41 | VAL | 5.2 |
| 5 | X | 63 | ASN | 5.1 |
| 2 | S | 168 | LYS | 5.1 |
| 2 | S | 75 | ILE | 5.1 |
| 5 | U | 51 | GLU | 5.1 |
| 7 | F | 76 | GLU | 5.1 |
| 7 | I | 32 | TYR | 5.1 |
| 5 | X | 20 | LYS | 5.1 |
| 7 | F | 45 | ALA | 5.1 |
| 1 | P | 2 | ALA | 5.1 |
| 5 | U | 44 | LYS | 5.1 |
| 9 | G | 15 | LYS | 5.1 |
| 1 | P | 37 | PHE | 5.0 |
| 7 | F | 27 | MET | 5.0 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 9 | G | 48 | MET | 5.0 |
| 4 | Q | 13 | ILE | 5.0 |
| 8 | E | 26 | GLN | 5.0 |
| 7 | F | 77 | GLU | 5.0 |
| 9 | J | 63 | ARG | 4.9 |
| 9 | J | 2 | SER | 4.9 |
| 5 | U | 69 | ILE | 4.9 |
| 3 | W | 85 | SER | 4.9 |
| 5 | U | 53 | VAL | 4.9 |
| 2 | S | 85 | GLU | 4.9 |
| 3 | Z | 5 | VAL | 4.9 |
| 6 | V | 66 | VAL | 4.9 |
| 6 | Y | 59 | PHE | 4.9 |
| 9 | J | 6 | PRO | 4.9 |
| 4 | B | 66 | VAL | 4.9 |
| 8 | H | 57 | VAL | 4.9 |
| 10 | N | 151 | C | 4.8 |
| 10 | R | 2 | U | 4.8 |
| 6 | V | 93 | ASP | 4.8 |
| 8 | H | 62 | GLU | 4.8 |
| 1 | A | 12 | ILE | 4.8 |
| 7 | I | 74 | GLY | 4.8 |
| 2 | S | 82 | VAL | 4.8 |
| 9 | J | 31 | LEU | 4.8 |
| 5 | X | 52 | PRO | 4.8 |
| 2 | L | 34 | HIS | 4.8 |
| 3 | W | 55 | VAL | 4.7 |
| 8 | E | 74 | LEU | 4.7 |
| 1 | P | 47 | ARG | 4.7 |
| 1 | P | 7 | ARG | 4.7 |
| 8 | H | 59 | ASP | 4.7 |
| 6 | Y | 80 | SER | 4.7 |
| 2 | S | 137 | SER | 4.7 |
| 5 | X | 84 | GLU | 4.7 |
| 4 | B | 60 | GLU | 4.6 |
| 7 | F | 21 | VAL | 4.6 |
| 10 | N | 164 | G | 4.6 |
| 8 | H | 1 | MET | 4.6 |
| 1 | A | 13 | TYR | 4.6 |
| 9 | J | 19 | LEU | 4.5 |
| 4 | Q | 20 | ILE | 4.5 |
| 2 | S | 67 | MET | 4.5 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 6 | V | 21 | GLU | 4.5 |
| 9 | J | 1 | MET | 4.5 |
| 7 | I | 27 | MET | 4.5 |
| 2 | S | 141 | GLY | 4.5 |
| 4 | B | 55 | ASN | 4.5 |
| 4 | Q | 43 | CYS | 4.5 |
| 3 | W | 88 | ASN | 4.5 |
| 8 | E | 27 | ASN | 4.5 |
| 8 | H | 33 | VAL | 4.5 |
| 6 | Y | 24 | PHE | 4.4 |
| 5 | X | 8 | MET | 4.4 |
| 8 | E | 45 | GLY | 4.4 |
| 2 | L | 127 | GLY | 4.4 |
| 2 | S | 150 | GLU | 4.3 |
| 6 | Y | 34 | GLN | 4.3 |
| 9 | J | 55 | ASN | 4.3 |
| 2 | S | 172 | ARG | 4.3 |
| 3 | W | 3 | ILE | 4.2 |
| 8 | E | 11 | GLN | 4.2 |
| 6 | V | 112 | ASN | 4.2 |
| 3 | Z | 35 | ALA | 4.2 |
| 2 | S | 155 | ARG | 4.2 |
| 8 | H | 32 | GLN | 4.2 |
| 9 | J | 52 | GLY | 4.2 |
| 9 | J | 59 | MET | 4.2 |
| 7 | F | 58 | HIS | 4.2 |
| 7 | I | 6 | ASN | 4.2 |
| 6 | Y | 112 | ASN | 4.1 |
| 6 | V | 16 | LEU | 4.1 |
| 1 | A | 71 | SER | 4.1 |
| 9 | J | 25 | ARG | 4.1 |
| 4 | Q | 8 | LYS | 4.1 |
| 6 | V | 116 | ALA | 4.1 |
| 3 | W | 41 | CYS | 4.1 |
| 7 | I | 37 | ASP | 4.1 |
| 8 | H | 17 | PRO | 4.1 |
| 1 | P | 82 | MET | 4.1 |
| 4 | B | 63 | GLU | 4.0 |
| 2 | S | 127 | GLY | 4.0 |
| 2 | S | 164 | ALA | 4.0 |
| 1 | A | 53 | GLY | 4.0 |
| 6 | Y | 11 | MET | 4.0 |

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| Mol | Chain | Res | Type | RSRZ |
|------------|--------------|------------|-------------|-------------|
| 4 | Q | 14 | ASP | 4.0 |
| 5 | U | 52 | PRO | 4.0 |
| 1 | A | 107 | LYS | 4.0 |
| 5 | X | 65 | ILE | 4.0 |
| 4 | B | 51 | ILE | 3.9 |
| 1 | P | 72 | MET | 3.9 |
| 1 | A | 63 | SER | 3.9 |
| 2 | L | 136 | TYR | 3.9 |
| 5 | X | 43 | VAL | 3.9 |
| 8 | H | 5 | GLY | 3.9 |
| 5 | U | 8 | MET | 3.9 |
| 5 | U | 45 | MET | 3.9 |
| 7 | F | 57 | GLY | 3.9 |
| 8 | H | 20 | LEU | 3.9 |
| 4 | Q | 44 | ASP | 3.9 |
| 5 | X | 12 | HIS | 3.9 |
| 5 | U | 80 | LEU | 3.9 |
| 3 | Z | 58 | LEU | 3.8 |
| 7 | I | 12 | ASN | 3.8 |
| 7 | F | 52 | ASP | 3.8 |
| 10 | N | 149 | U | 3.8 |
| 11 | M | 4 | DT | 3.8 |
| 6 | V | 36 | VAL | 3.8 |
| 7 | I | 16 | GLY | 3.7 |
| 6 | V | 7 | PRO | 3.7 |
| 10 | N | 39 | U | 3.7 |
| 7 | I | 53 | GLY | 3.7 |
| 4 | B | 65 | ARG | 3.7 |
| 8 | E | 57 | VAL | 3.7 |
| 4 | B | 78 | VAL | 3.6 |
| 9 | G | 35 | ASP | 3.6 |
| 8 | H | 58 | LEU | 3.6 |
| 6 | V | 3 | LEU | 3.6 |
| 7 | F | 42 | MET | 3.6 |
| 1 | A | 86 | TYR | 3.6 |
| 7 | F | 8 | LYS | 3.6 |
| 3 | Z | 50 | TYR | 3.6 |
| 6 | V | 24 | PHE | 3.5 |
| 7 | F | 75 | VAL | 3.5 |
| 6 | Y | 8 | LYS | 3.5 |
| 6 | Y | 74 | TRP | 3.5 |
| 10 | R | 134 | U | 3.5 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | P | 62 | VAL | 3.5 |
| 2 | S | 70 | LYS | 3.5 |
| 1 | A | 103 | GLU | 3.4 |
| 4 | B | 73 | ARG | 3.4 |
| 9 | J | 13 | MET | 3.4 |
| 9 | J | 54 | GLN | 3.4 |
| 3 | Z | 18 | VAL | 3.4 |
| 8 | H | 67 | LYS | 3.3 |
| 2 | S | 129 | ILE | 3.3 |
| 2 | S | 140 | SER | 3.3 |
| 1 | P | 98 | LYS | 3.3 |
| 2 | S | 105 | LEU | 3.3 |
| 2 | L | 57 | PRO | 3.3 |
| 2 | S | 119 | LEU | 3.2 |
| 2 | L | 179 | GLU | 3.2 |
| 9 | J | 40 | LEU | 3.1 |
| 5 | U | 32 | VAL | 3.1 |
| 7 | F | 65 | ARG | 3.1 |
| 6 | Y | 75 | THR | 3.1 |
| 2 | S | 65 | GLU | 3.1 |
| 9 | J | 48 | MET | 3.1 |
| 9 | G | 34 | PHE | 3.1 |
| 8 | E | 60 | ASP | 3.1 |
| 3 | W | 76 | MET | 3.1 |
| 2 | S | 86 | LEU | 3.0 |
| 2 | S | 104 | THR | 3.0 |
| 9 | G | 20 | LYS | 3.0 |
| 8 | E | 89 | SER | 3.0 |
| 3 | Z | 46 | ILE | 3.0 |
| 10 | N | 73 | C | 3.0 |
| 4 | B | 14 | ASP | 2.9 |
| 5 | X | 74 | LEU | 2.9 |
| 2 | S | 81 | GLU | 2.9 |
| 5 | U | 42 | ALA | 2.9 |
| 4 | B | 85 | PRO | 2.8 |
| 6 | V | 56 | VAL | 2.8 |
| 6 | V | 6 | LYS | 2.8 |
| 7 | I | 44 | LEU | 2.8 |
| 2 | S | 124 | GLU | 2.8 |
| 7 | I | 4 | PRO | 2.8 |
| 1 | P | 81 | PRO | 2.8 |
| 7 | F | 12 | ASN | 2.7 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 5 | U | 70 | LEU | 2.7 |
| 6 | Y | 27 | GLY | 2.7 |
| 9 | G | 37 | PHE | 2.7 |
| 8 | H | 78 | MET | 2.7 |
| 4 | Q | 64 | LYS | 2.7 |
| 4 | Q | 36 | LYS | 2.7 |
| 5 | X | 32 | VAL | 2.7 |
| 7 | F | 83 | GLU | 2.6 |
| 1 | P | 100 | THR | 2.6 |
| 5 | X | 22 | GLY | 2.6 |
| 2 | L | 50 | ASP | 2.6 |
| 6 | Y | 26 | THR | 2.6 |
| 2 | L | 47 | GLU | 2.6 |
| 2 | L | 66 | ARG | 2.5 |
| 9 | J | 53 | GLN | 2.5 |
| 7 | F | 32 | TYR | 2.5 |
| 6 | Y | 3 | LEU | 2.5 |
| 5 | U | 83 | VAL | 2.5 |
| 3 | W | 46 | ILE | 2.5 |
| 5 | U | 82 | ASP | 2.5 |
| 1 | A | 96 | LYS | 2.4 |
| 7 | F | 18 | PRO | 2.4 |
| 9 | J | 8 | GLU | 2.4 |
| 2 | S | 142 | LYS | 2.3 |
| 9 | G | 16 | LYS | 2.3 |
| 9 | G | 7 | PRO | 2.3 |
| 6 | Y | 4 | LEU | 2.3 |
| 7 | F | 11 | LEU | 2.3 |
| 5 | U | 81 | VAL | 2.2 |
| 4 | B | 49 | ARG | 2.2 |
| 9 | G | 54 | GLN | 2.1 |
| 2 | S | 131 | ARG | 2.1 |
| 3 | W | 77 | LEU | 2.1 |
| 4 | Q | 49 | ARG | 2.1 |
| 1 | P | 53 | GLY | 2.0 |
| 3 | W | 82 | MET | 2.0 |

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.