

## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 14, 2017 – 03:40 PM EDT

PDB ID : 5IJO  
EMDB ID: : EMD-8085  
Title : Alternative composite structure of the inner ring of the human nuclear pore complex (16 copies of Nup188, 16 copies of Nup205)  
Authors : Kosinski, J.; Mosalaganti, S.; von Appen, A.; Beck, M.  
Deposited on : unknown  
Resolution : 21.40 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

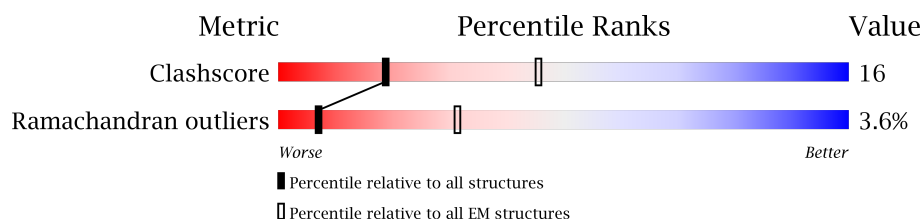
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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

**i**

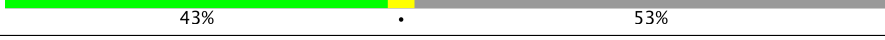
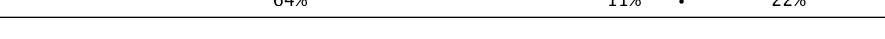
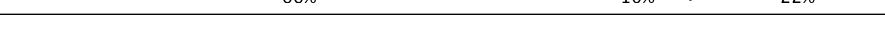

ELECTRON MICROSCOPY

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<br>(#Entries) | EM structures<br>(#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore            | 125131                      | 1336                        |
| Ramachandran outliers | 121729                      | 1120                        |

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$

| Mol | Chain | Length | Quality of chain   |
|-----|-------|--------|--|
| 1   | A     | 1391   |  |
| 1   | B     | 1391   |  |
| 1   | E     | 1391   |  |
| 1   | K     | 1391   |  |
| 1   | Q     | 1391   |  |
| 1   | W     | 1391   |  |
| 2   | C     | 819    |  |
| 2   | I     | 819    |  |
| 2   | O     | 819    |  |
| 2   | U     | 819    |  |
| 3   | D     | 2012   |  |

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| Mol | Chain | Length | Quality of chain   |
|-----|-------|--------|--|
| 3   | P     | 2012   |  46% . . 49%       |
| 4   | F     | 507    |  35% 16% 9% 5% 34% |
| 4   | L     | 507    |  35% 16% 9% 5% 34% |
| 4   | R     | 507    |  35% 16% 9% 5% 34% |
| 4   | X     | 507    |  36% 16% 9% 5% 34% |
| 5   | G     | 599    |  17% 7% . . 71%    |
| 5   | M     | 599    |  17% 7% . . 71%    |
| 5   | S     | 599    |  17% 7% . . 71%    |
| 5   | Y     | 599    |  17% 7% . . 71%    |
| 6   | H     | 522    |  18% 11% . . 68%   |
| 6   | N     | 522    |  18% 11% . . 68%   |
| 6   | T     | 522    |  18% 11% . . 68%   |
| 6   | Z     | 522    |  18% 11% . . 68% |
| 7   | J     | 1749   |  63% 7% . 28%    |
| 7   | V     | 1749   |  64% 7% . 28%    |

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 76526 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Nuclear pore complex protein Nup155.

| Mol | Chain | Residues | Atoms |      |      |      | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 1   | A     | 650      | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 3214  | 1914 | 650  | 650  |         |       |
| 1   | B     | 650      | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 3214  | 1914 | 650  | 650  |         |       |
| 1   | E     | 1083     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 5366  | 3200 | 1083 | 1083 |         |       |
| 1   | K     | 1083     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 5366  | 3200 | 1083 | 1083 |         |       |
| 1   | Q     | 1083     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 5366  | 3200 | 1083 | 1083 |         |       |
| 1   | W     | 1083     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 5366  | 3200 | 1083 | 1083 |         |       |

- Molecule 2 is a protein called Nuclear pore complex protein Nup93.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 2   | C     | 636      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 3152  | 1880 | 636 | 636 |         |       |
| 2   | I     | 636      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 3152  | 1880 | 636 | 636 |         |       |
| 2   | O     | 636      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 3152  | 1880 | 636 | 636 |         |       |
| 2   | U     | 636      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 3152  | 1880 | 636 | 636 |         |       |

- Molecule 3 is a protein called Nuclear pore complex protein Nup205.

| Mol | Chain | Residues | Atoms |      |      |      | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 3   | D     | 1028     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 5094  | 3038 | 1028 | 1028 |         |       |
| 3   | P     | 1028     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 5094  | 3038 | 1028 | 1028 |         |       |

- Molecule 4 is a protein called Nucleoporin p54.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 4   | F     | 335      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1658  | 988 | 335 | 335 |         |       |
| 4   | L     | 335      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1658  | 988 | 335 | 335 |         |       |
| 4   | R     | 335      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1658  | 988 | 335 | 335 |         |       |
| 4   | X     | 335      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1658  | 988 | 335 | 335 |         |       |

- Molecule 5 is a protein called Nucleoporin p58/p45.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 5   | G     | 171      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 853   | 511 | 171 | 171 |         |       |
| 5   | M     | 171      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 853   | 511 | 171 | 171 |         |       |
| 5   | S     | 171      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 853   | 511 | 171 | 171 |         |       |
| 5   | Y     | 171      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 853   | 511 | 171 | 171 |         |       |

- Molecule 6 is a protein called Nuclear pore glycoprotein p62.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 6   | H     | 169      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 842   | 504 | 169 | 169 |         |       |
| 6   | N     | 169      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 842   | 504 | 169 | 169 |         |       |
| 6   | T     | 169      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 842   | 504 | 169 | 169 |         |       |
| 6   | Z     | 169      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 842   | 504 | 169 | 169 |         |       |

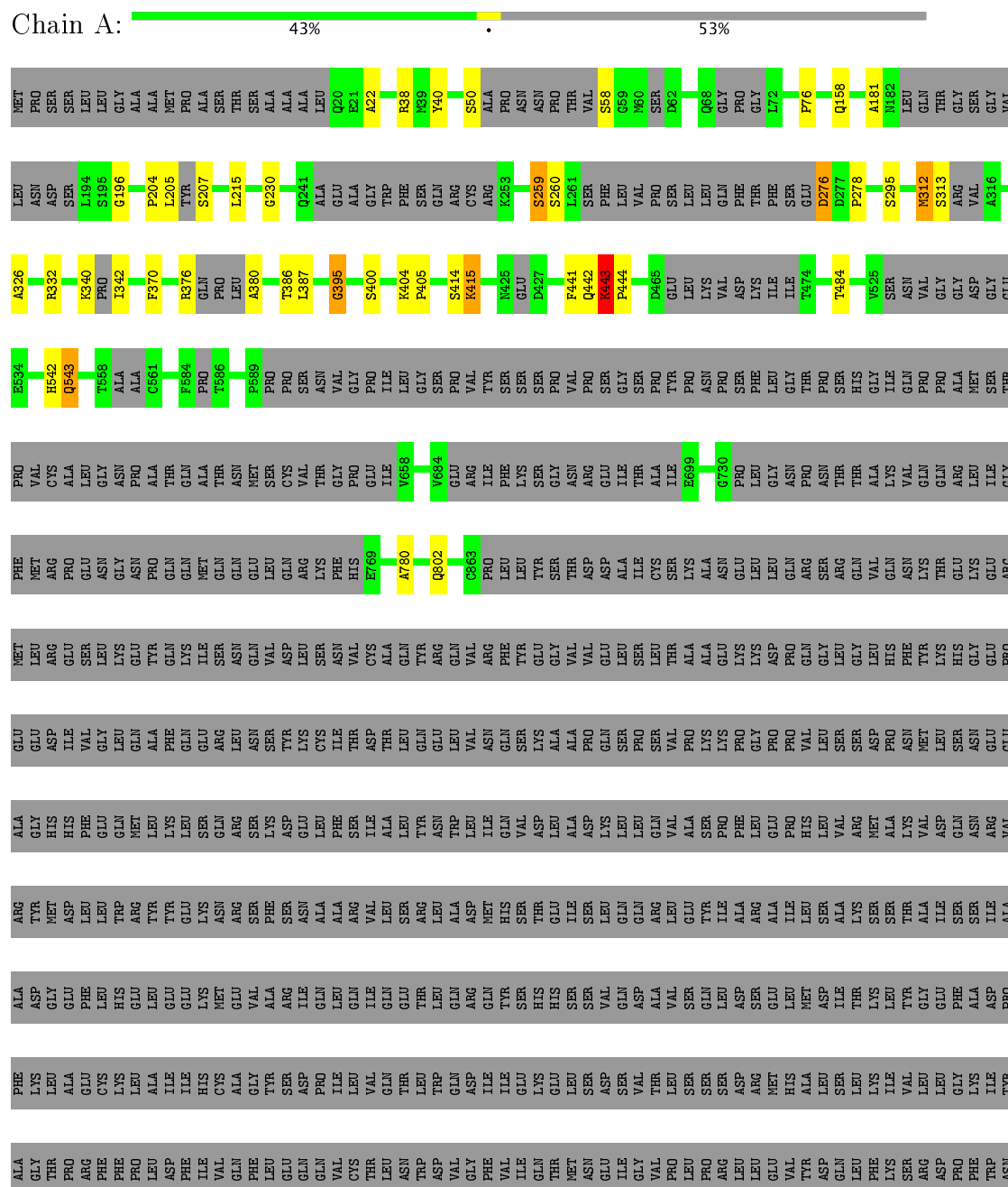
- Molecule 7 is a protein called Nucleoporin NUP188 homolog.

| Mol | Chain | Residues | Atoms |      |      |      | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 7   | J     | 1256     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 6213  | 3701 | 1256 | 1256 |         |       |
| 7   | V     | 1256     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 6213  | 3701 | 1256 | 1256 |         |       |

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Nuclear pore complex protein Nup155



ARG MET LYS LYS PRO PRO LEU HIS LEU LEU LEU ASP ASP ILE CYS HIS VAL LEU LEU LEU ILE ARG TYR VAL GLU ASN ASN SER SER GLN VAL VAL LEU LEU CYS ARG ARG ARG PHE THR ASN LEU LEU CYS GLU ARG ARG ARG ARG ARG THR ASN LEU LEU CYS GLU VAL VAL CYS GLY TYR LEU LEU VAL VAL GLN GLN SER SER MET SER SER VAL VAL VAL VAL GLN

ILE  
THR  
GLY  
ASN  
PHE  
LYS  
SER  
LEU  
GLN  
ALA  
LYS  
LEU  
GLU  
ARG  
LEU  
HIS

- Molecule 1: Nuclear pore complex protein Nup155

Chain B:  43% 1% 53%

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | PRO | SER | SER | SER | LEV | LEV | GLY | ALA | ALA | MET | PRO | ALA | ALA | ALA | ALA | ALA | ALA | LEV | Q20 | E21 | A22 | R38 | P39 | Y40 | S50 | ALA | ALA | ASN | ASN | ASN | PRO | THR | THR | VAL | S58 | G59 | P60 | SER | SER | D62 | L72 | GLY | GLY | P76 | Q158 | A181 | H82 | LEV | GLN | THR | THR | GLY | SER | GLY | GLY |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|

|     |     |     |     |      |      |      |      |      |     |      |      |      |      |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |     |     |      |
|-----|-----|-----|-----|------|------|------|------|------|-----|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|-----|-----|------|
| LEU | ASW | ASP | SER | L194 | S195 | G196 | P204 | L205 | TYR | S207 | L215 | G230 | Q241 | ALA | GLU | GLY | GLY | TRP | PHE | SER | SER | ARG | CYS | ARG | ARG | K253 | S259 | S260 | L261 | SER | PHE | PHE | LEU | LEU | GLN | VAL | VAL | PRO | SER | SER | LEU | LEU | GLU | D276 | D277 | P278 | S295 | M312 | S313 | ARG | VAL | A316 |
|-----|-----|-----|-----|------|------|------|------|------|-----|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|-----|-----|------|

|      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |     |     |     |     |     |     |      |      |      |     |     |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|
| A326 | R332 | K340 | P400 | I342 | N350 | S353 | F370 | R376 | G380 | T386 | L387 | C395 | S400 | K404 | P405 | S414 | K415 | M425 | G427 | H441 | K442 | K443 | P444 | D465 | G470 | LVS | VAL | ASP | LVS | IIE | IIE | T474 | T484 | V525 | ASR | VAL |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|

[illegible]

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |       |
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| MET | SER | THR | PRO | VAL | CYS | ALA | LEU | GLY | ASN | ASP | PRO | ALA | THR | GLN | ALA | THR | THR | MET | SER | CYS | VAL | THR | THR | GLY | PRO | GLU | ILE | V658 | V659 | V660 | V661 | V662 | V663 | V664 | V665 | V666 | V667 | V668 | V669 | V670 | V671 | V672 | V673 | V674 | V675 | V676 | V677 | V678 | V679 | V680 | V681 | V682 | V683 | V684 | V685 | V686 | V687 | V688 | V689 | V690 | V691 | V692 | V693 | V694 | V695 | V696 | V697 | V698 | V699 | V700 | V701 | V702 | V703 | V704 | V705 | V706 | V707 | V708 | V709 | V710 | V711 | V712 | V713 | V714 | V715 | V716 | V717 | V718 | V719 | V720 | V721 | V722 | V723 | V724 | V725 | V726 | V727 | V728 | V729 | V730 | V731 | V732 | V733 | V734 | V735 | V736 | V737 | V738 | V739 | V740 | V741 | V742 | V743 | V744 | V745 | V746 | V747 | V748 | V749 | V750 | V751 | V752 | V753 | V754 | V755 | V756 | V757 | V758 | V759 | V760 | V761 | V762 | V763 | V764 | V765 | V766 | V767 | V768 | V769 | V770 | V771 | V772 | V773 | V774 | V775 | V776 | V777 | V778 | V779 | V780 | V781 | V782 | V783 | V784 | V785 | V786 | V787 | V788 | V789 | V790 | V791 | V792 | V793 | V794 | V795 | V796 | V797 | V798 | V799 | V800 | V801 | V802 | V803 | V804 | V805 | V806 | V807 | V808 | V809 | V810 | V811 | V812 | V813 | V814 | V815 | V816 | V817 | V818 | V819 | V820 | V821 | V822 | V823 | V824 | V825 | V826 | V827 | V828 | V829 | V830 | V831 | V832 | V833 | V834 | V835 | V836 | V837 | V838 | V839 | V840 | V841 | V842 | V843 | V844 | V845 | V846 | V847 | V848 | V849 | V850 | V851 | V852 | V853 | V854 | V855 | V856 | V857 | V858 | V859 | V860 | V861 | V862 | V863 | V864 | V865 | V866 | V867 | V868 | V869 | V870 | V871 | V872 | V873 | V874 | V875 | V876 | V877 | V878 | V879 | V880 | V881 | V882 | V883 | V884 | V885 | V886 | V887 | V888 | V889 | V890 | V891 | V892 | V893 | V894 | V895 | V896 | V897 | V898 | V899 | V900 | V901 | V902 | V903 | V904 | V905 | V906 | V907 | V908 | V909 | V910 | V911 | V912 | V913 | V914 | V915 | V916 | V917 | V918 | V919 | V920 | V921 | V922 | V923 | V924 | V925 | V926 | V927 | V928 | V929 | V930 | V931 | V932 | V933 | V934 | V935 | V936 | V937 | V938 | V939 | V940 | V941 | V942 | V943 | V944 | V945 | V946 | V947 | V948 | V949 | V950 | V951 | V952 | V953 | V954 | V955 | V956 | V957 | V958 | V959 | V960 | V961 | V962 | V963 | V964 | V965 | V966 | V967 | V968 | V969 | V970 | V971 | V972 | V973 | V974 | V975 | V976 | V977 | V978 | V979 | V980 | V981 | V982 | V983 | V984 | V985 | V986 | V987 | V988 | V989 | V990 | V991 | V992 | V993 | V994 | V995 | V996 | V997 | V998 | V999 | V1000 |
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LYS GLU ARG ARG MET LEU ARG GLU SER SER LEU LEU GLU TYP GLN LYS ILE SER SER ASN ASN GLN VAL ASP LEU SER ASN VAL VAL CYS GLN ARG ARG ARG PHE PHE TYR TYR GLU GLY VAL VAL VAL VAL GLU LEU SER SER LEU THR ALA ALA ALA GLU GLU LYS LYS ASP ASP PRO PRO GLN GLY LEU GLY LEU HIS HIS PHE PHE TYR LYS

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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| GLY | GLU | PRO | GLU | GLU | ASP | ILE | VAL | GLY | GLN | ALA | PHE | GLN | GLU | GLN | ARG | LEU | ASN | SER | TYR | LYS | CYS | ILE | THR | ASP | THR | LEU | GLN | GLU | LEU | VAL | ASN | GLN | SER | GLN | LYS | ALA | ALA | ALA | PRO | PRO | GLN | GLN | SER | SER | PRO | SER | VAL | PRO | PRO | LYS | LYS | PRO | GLY | PRO | PRO | VAL | VAL | LEU | SER | SER | ASP | PRO | ASN | MET | LEU |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ASN GLU GLU GLU GLU GLY HIS HIS PHE GLU GLU GLN MET LEU LYS LYS LEU LEU SER SER GLN ARG ARG SER LYS ASP ASP GLU LEU LEU PHE PHE SER ILE ILE LEU LEU TYR TRP TRP LEU LEU ILE ILE GLN GLN VAL VAL ASP ASP LEU LEU LYS LYS ASP ASP ALA ALA VAL VAL GLN GLN LEU LEU LEU LEU LEU VAL VAL ARG ARG MET MET ALA ALA LYS LYS VAL VAL ASP ASP

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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| ASN | ARG | ARG | ARG | ARG | MET | ASP | LEU | TRP | ARG | TYR | TYR | GLY | ASN | ARG | SER | PHE | SER | ASN | ALA | ALA | ARG | VAL | LEU | SER | ARG | GLN | GLU | ILE | THR | GLU | GLU | TYR | ILE | ALA | ALA | ARG | ALA | ILE | SER | SER | THR | ALA | ILE |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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| SER | IIE | ALA | ALA | ASP | GLY | GLU | PHE | LEU | HIS | LEU | GLU | LEU | GLU | LYS | MET | GLI | VAL | ALA | ARG | ILE | GLN | LEU | GLN | IIE | GLN | GLN | THR | LEU | LEU | GLN | ARG | GLN | Tyr | SER | SER | HIS | HIS | SER | SER | VAL | VAL | GLN | ASP | ALA | VAL | VAL | SER | SER | GLN | LEU | LEU | ASP | SER | GLU | GLU | LEU | LYS | THR | IIE |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ALA ASP PRO PHE LYS LEU ALA GLU CYS LYS LEU ALA ILE ILE HIS HIS CYS CYS ALA GLY TYR SER ASP PRO PRO ILE LEU VAL VAL GLN THR LEU LEU TRP TRP GLN ASP ASP ASP ASP VAL THR LEU LEU SER SER SER SER ASP ARG MET HIS HIS ALA ALA LEU LEU SER LEU LEU ILE ILE VAL VAL LEU LEU

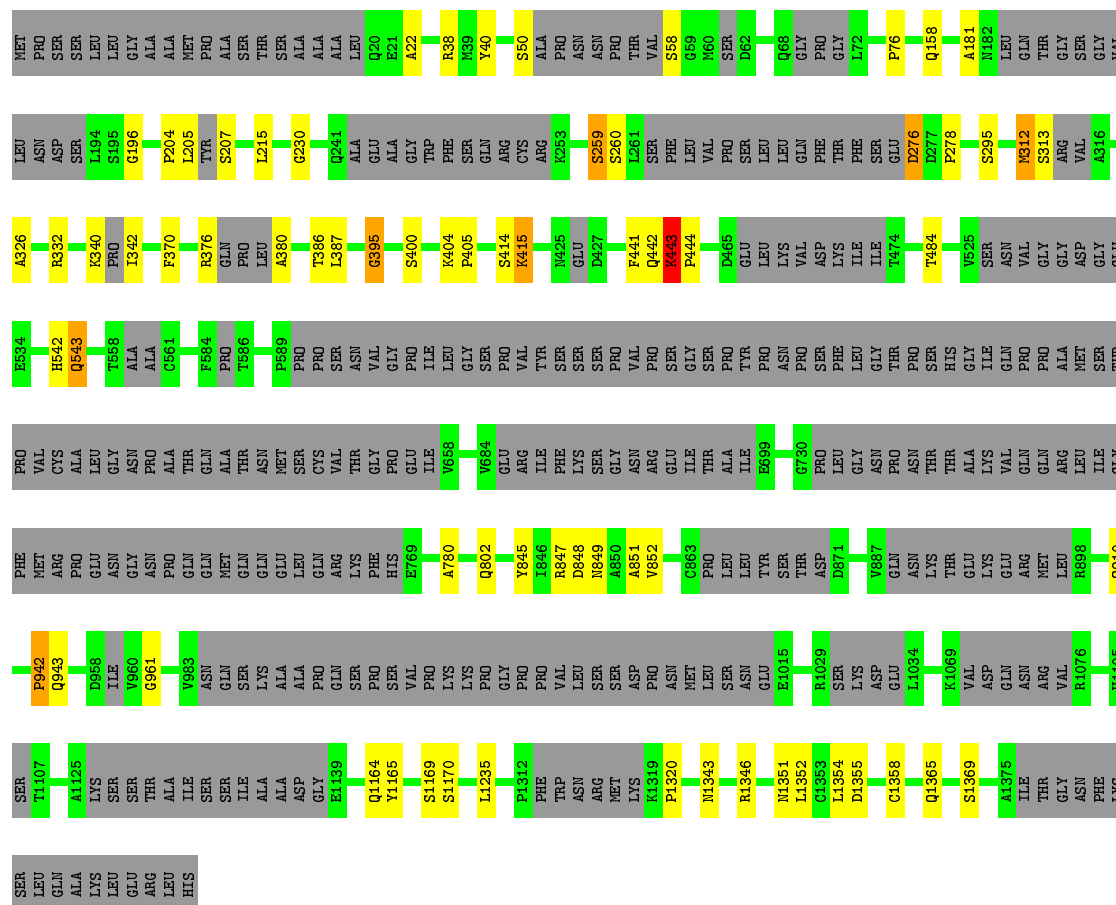
LYS ILE TYR ALA GLY THR PRO ARG PHE PHE PRO LEU ASP PHE ILE VAL GLN PHE LEU GLU GLN GLN GLN VAL CYS THR LEU ASN TRP ASP VAL GLY PHE VAL ILE GLN THR MET ASN GLU ILE GLY VAL PRO LEU PRO ARG LEU LEU VAL TYR ASP LEU PHE LYS SER ARG ASP

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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| PHE | TRP | ASN | ARG | MET | LYS | LYS | PRO | LEU | HIS | LEU | LEU | LEU | ASP | CYS | ILE | HIS | VAL | LEU | LEU | ILE | ARG | TYR | VAL | GLU | ASN | ASN | PRO | SER | SER | GLN | VAL | VAL | LEU | ASN | CYS | GLU | ARG | ARG | ARG | PHE | THR | ASN | CYS | LEU | LEU | LEU | ASP | ALA | VAL | CYS | GLY | TYR | LEU | VAL | GLU | LEU | GLN | SER | SER | SER | SER | VAL | ... |
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VAL GLN ALA ILE THR GLY ASN PHE LYS SER LEU GLN ALA LYS LEU GLU ARG LEU HIS

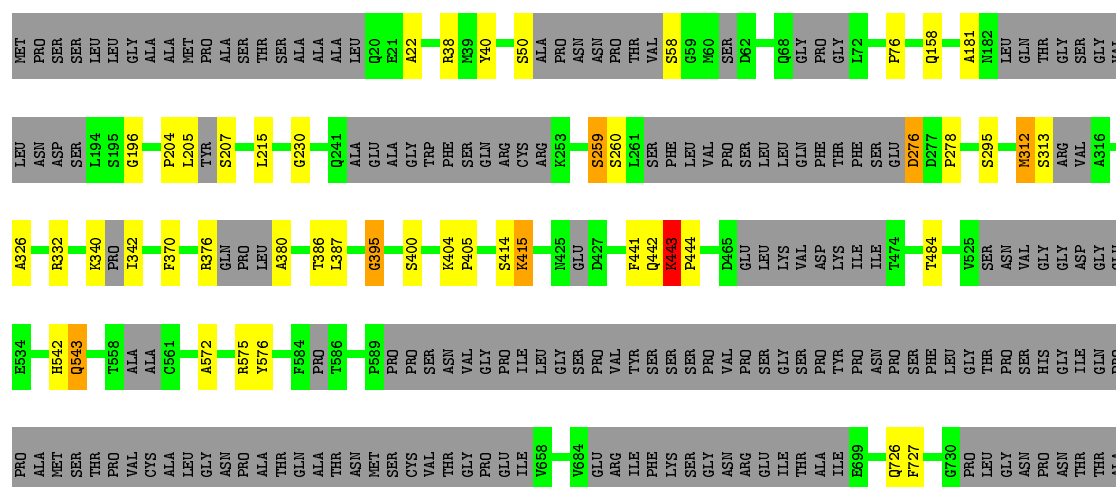
• Molecule 1: Nuclear pore complex protein Nup155

Chain E:  73% 22%

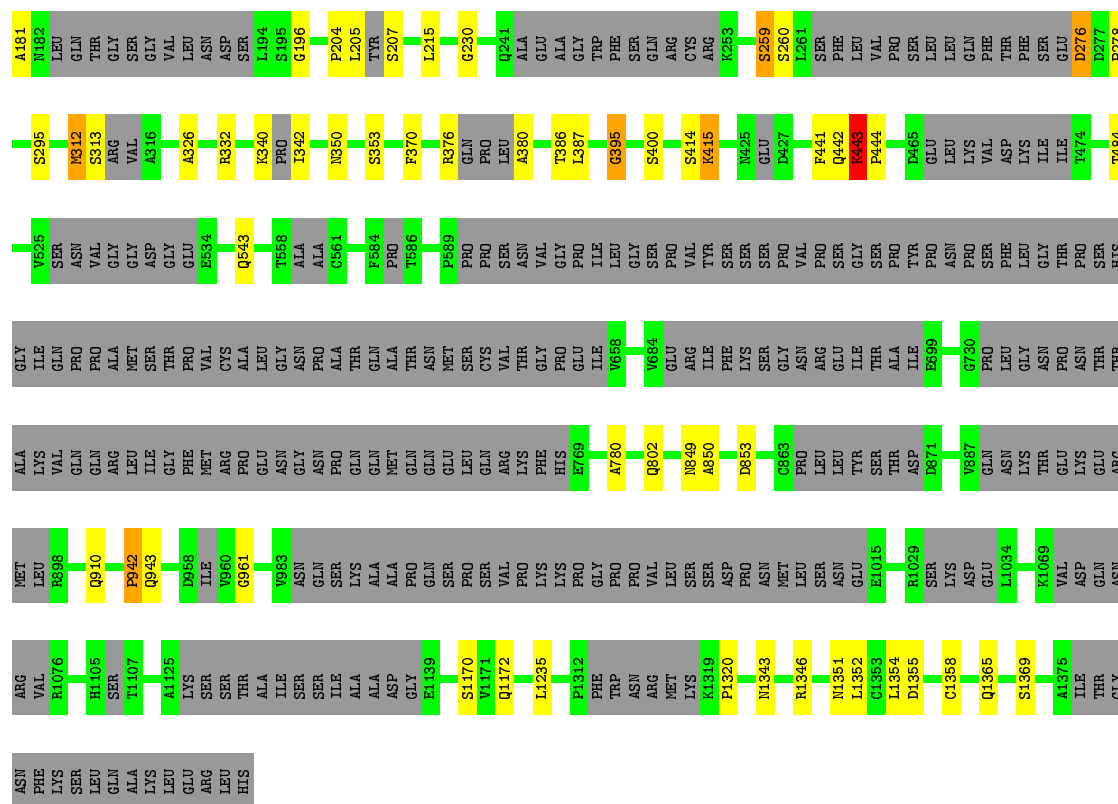


• Molecule 1: Nuclear pore complex protein Nup155

Chain K:  73% 5% 22%

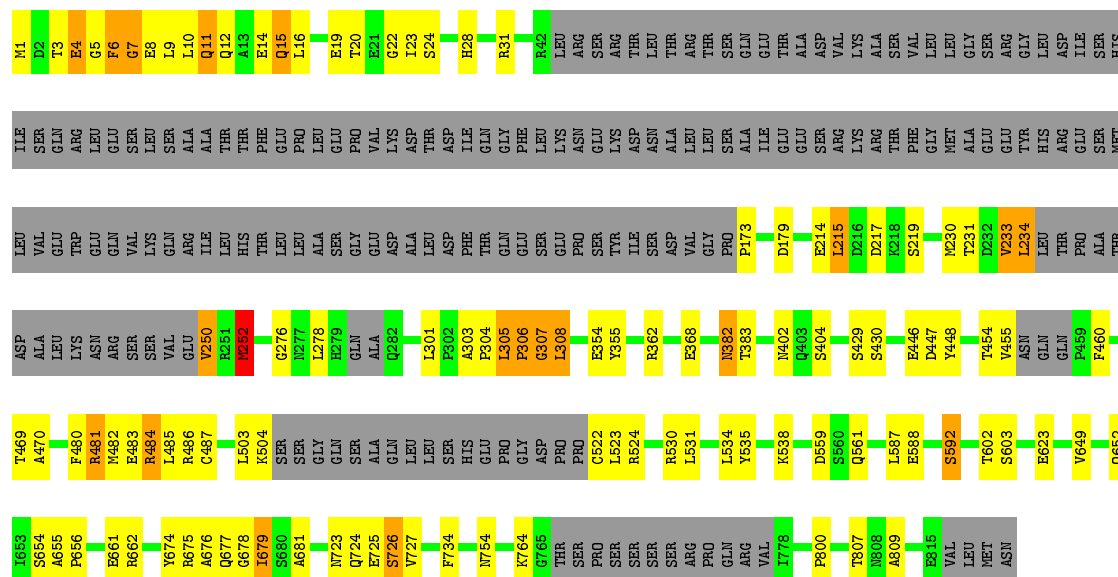






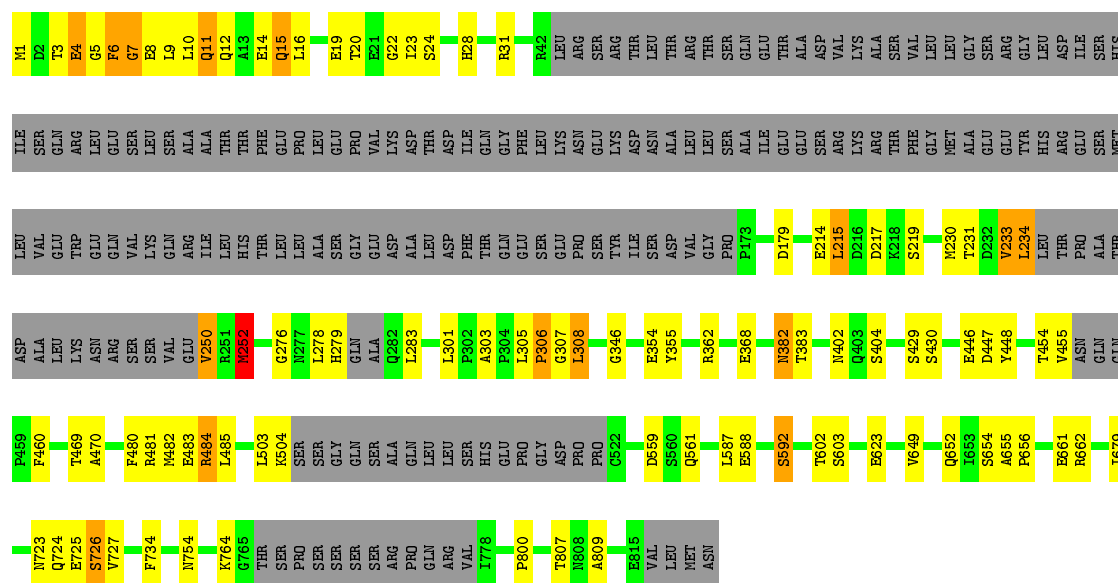
• Molecule 2: Nuclear pore complex protein Nup93

Chain C: 64% 11% 22%



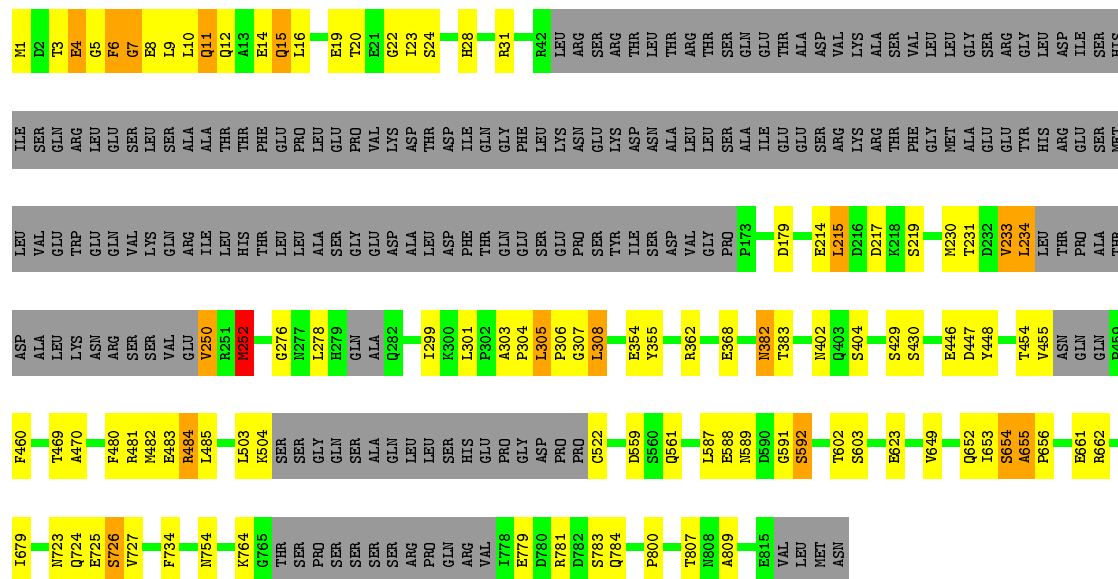
• Molecule 2: Nuclear pore complex protein Nup93

Chain I: 66% 10% 22%



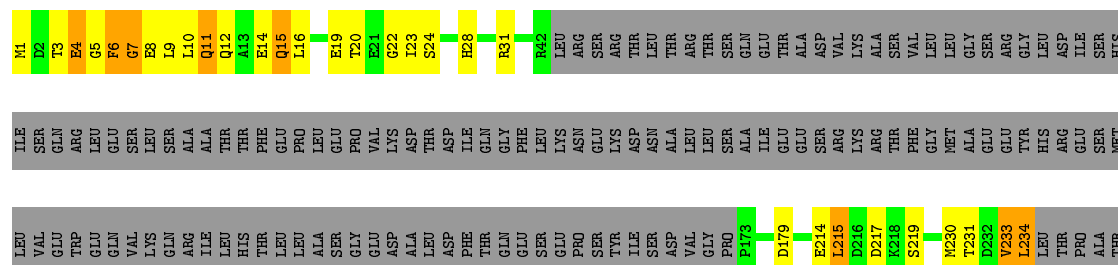
• Molecule 2: Nuclear pore complex protein Nup93

Chain O: 65% 10% 22%



• Molecule 2: Nuclear pore complex protein Nup93

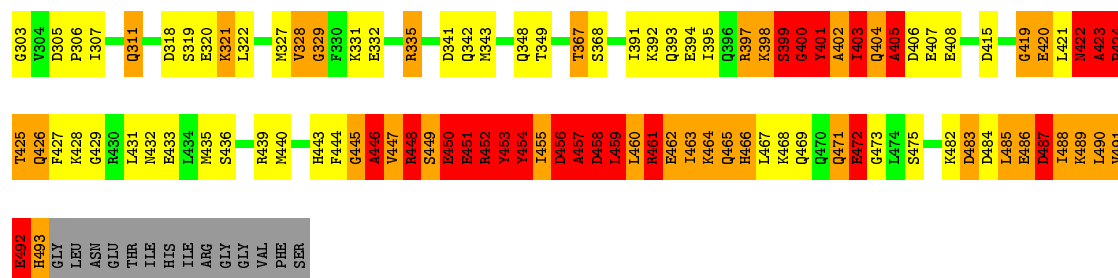
Chain U: 66% 10% 22%





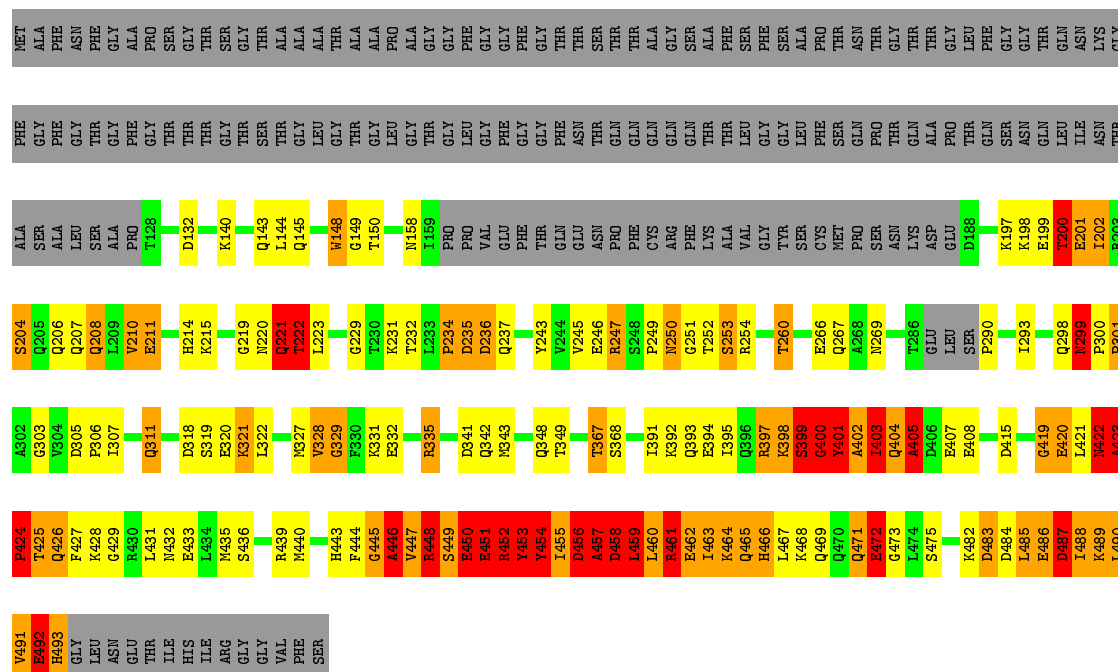
|     |       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  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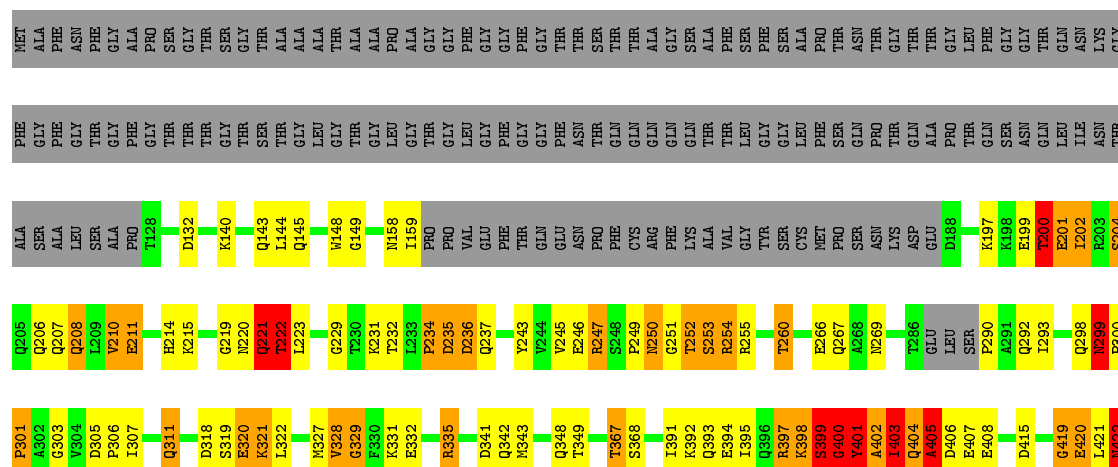
### • Molecule 4: Nucleoporin p54

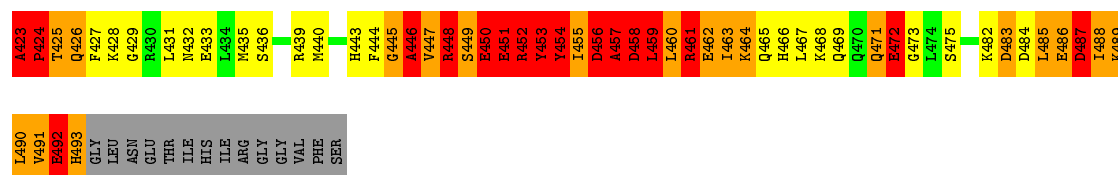
Chain L: 35% 16% 9% 5% 34%



### • Molecule 4: Nucleoporin p54

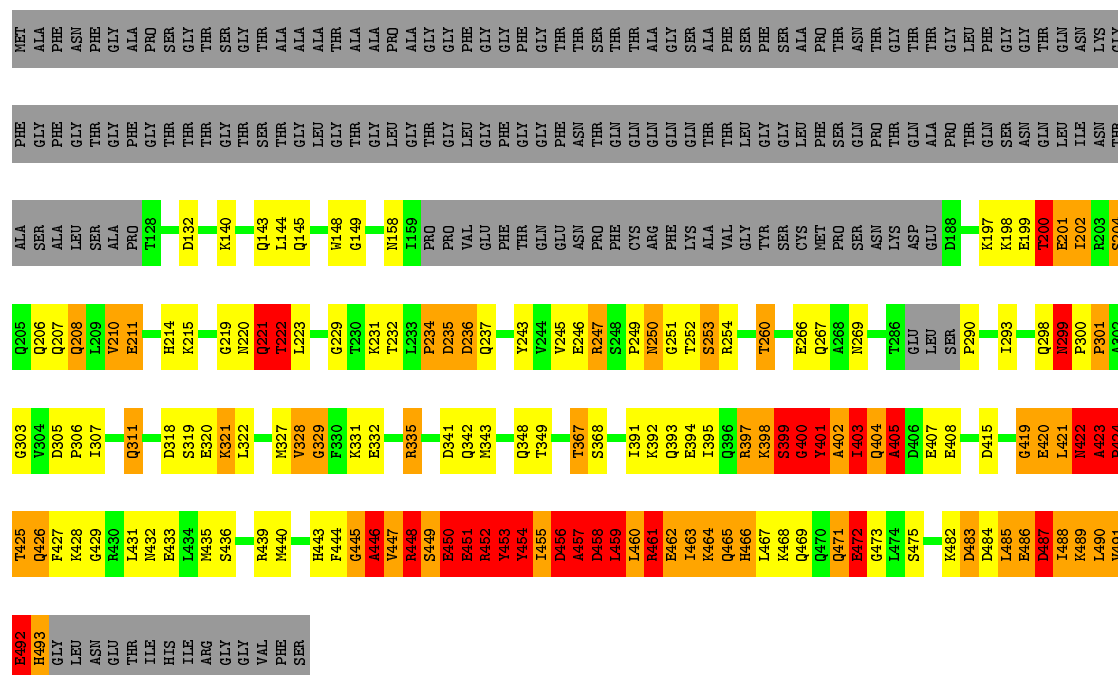
Chain R: 35% 16% 9% 5% 34%





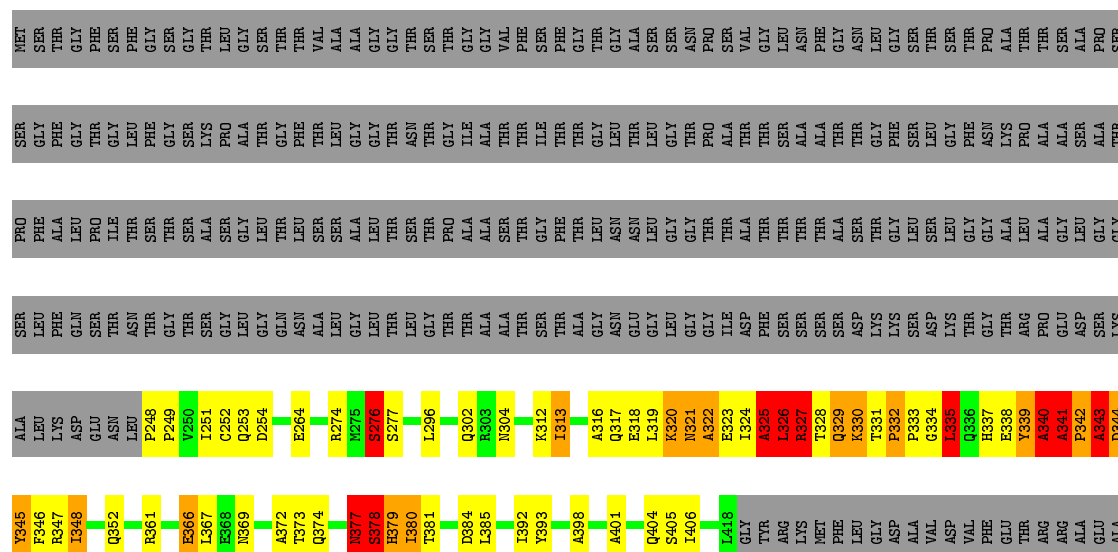
### • Molecule 4: Nucleoporin p54

Chain X:



### • Molecule 5: Nucleoporin p58/p45

Chain G:



ILE THR ALA SER ALA GLY LEU THR PHE GLY VAL SER ASN PRO ALA SER ALA GLY PHE GLY THR GLY GLY GLN LEU LEU GLN LEU LYS LYS PRO PRO ALA GLY ASN LYS ARG GLY LYS ARG

- Molecule 5: Nucleoporin p58/p45

Chain M:  17% 7% . . 71%

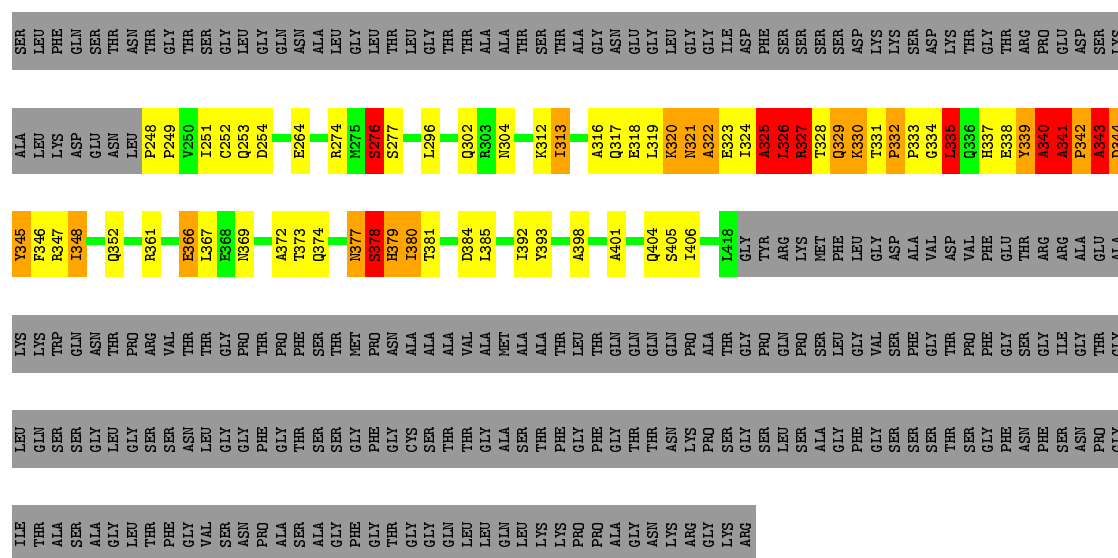
|      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Y345 | F346 | R347 | I348 | Q352 | R361 | E366 | L367 | E368 | N369 | A372 | Q374 | N377 | S378 | R379 | I380 | T391 | D884 | L386 | I392 | Y393 | A398 | A401 | Q404 | S405 | I406 | L418 | GLY | TYR | ARG | LYS | MET | PHE | LEU | GLY | ASP | ALA | VAL | ASP | VAL | PHE | GLU | THR | ARG | ARG | ALA | GLU |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ILE | THR | ALA | SER | ALA | GLY | LEU | THR | PHE | GLY | VAL | SER | ASN | PRO | ALA | SER | ALA | GLY | PHE | GLY | THR | GLY | GLY | GLN | LEU | LEU | GLN | LEU | LEU | LYS | LYS | PRO | PRO | ALA | GLY | ASN | LYS | ARG | GLY | LYS | ARG |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

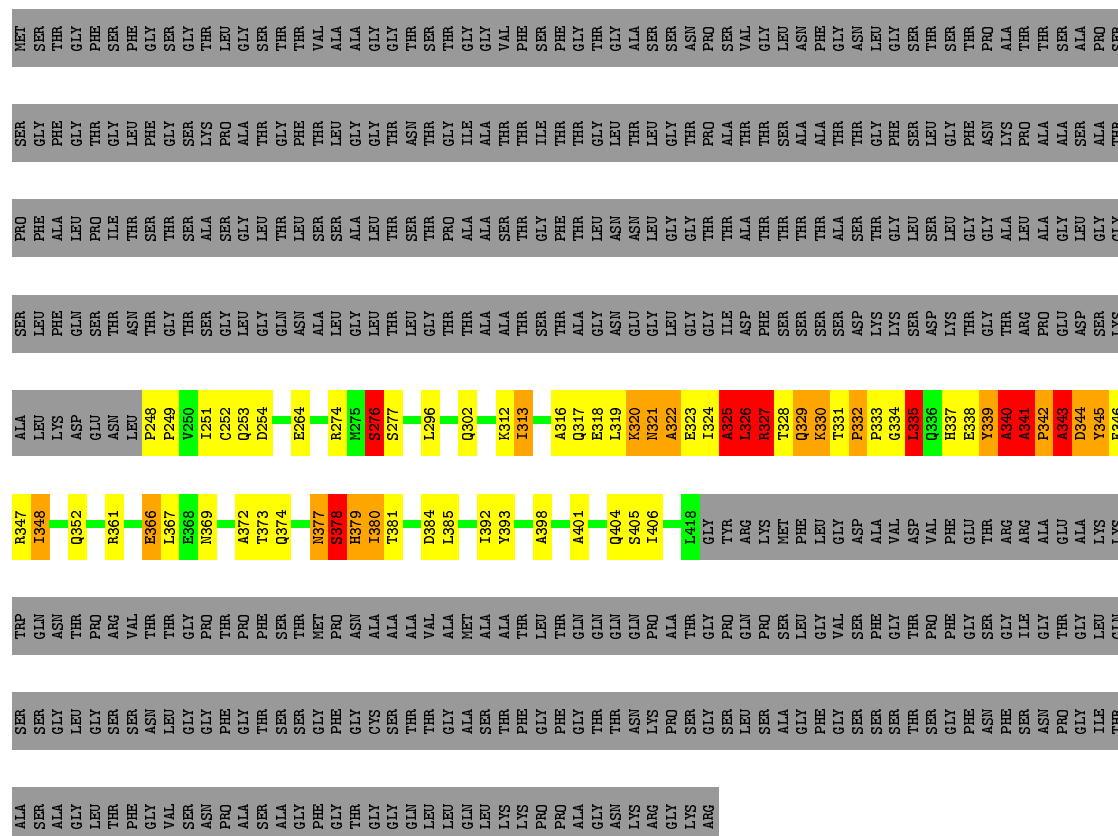
- Molecule 5: Nucleoporin p58/p45

Chain S:  17% 7% . . 71%

[illegible]

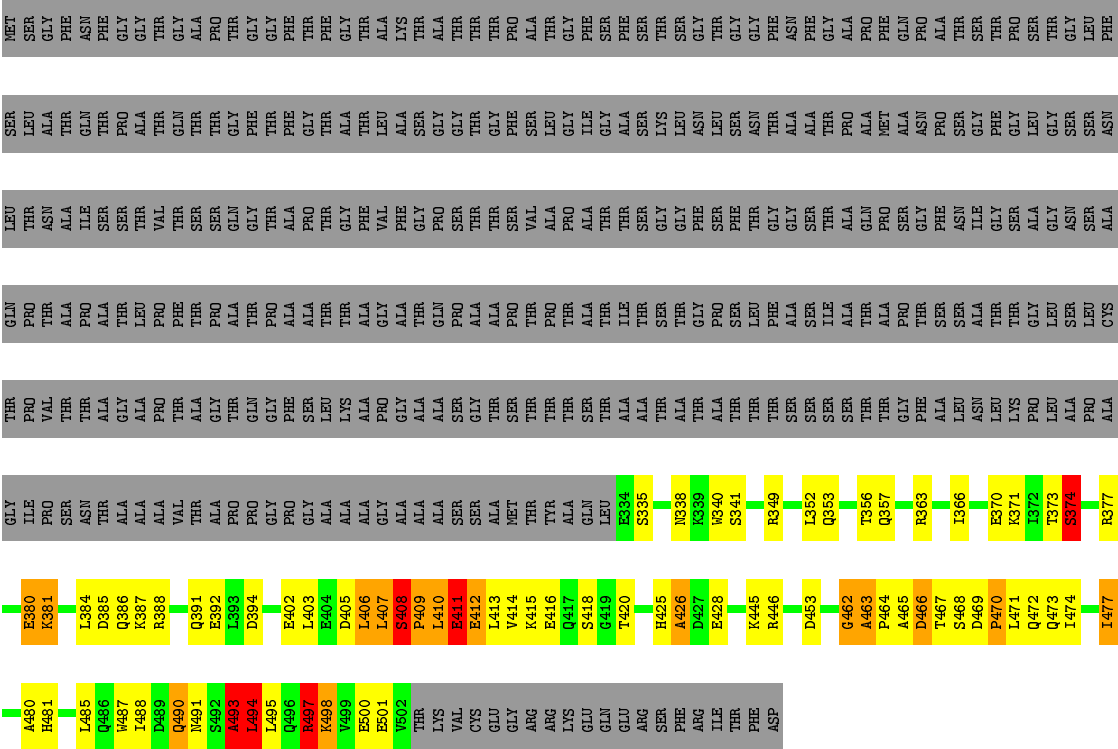


- Molecule 5: Nucleoporin p58/p45

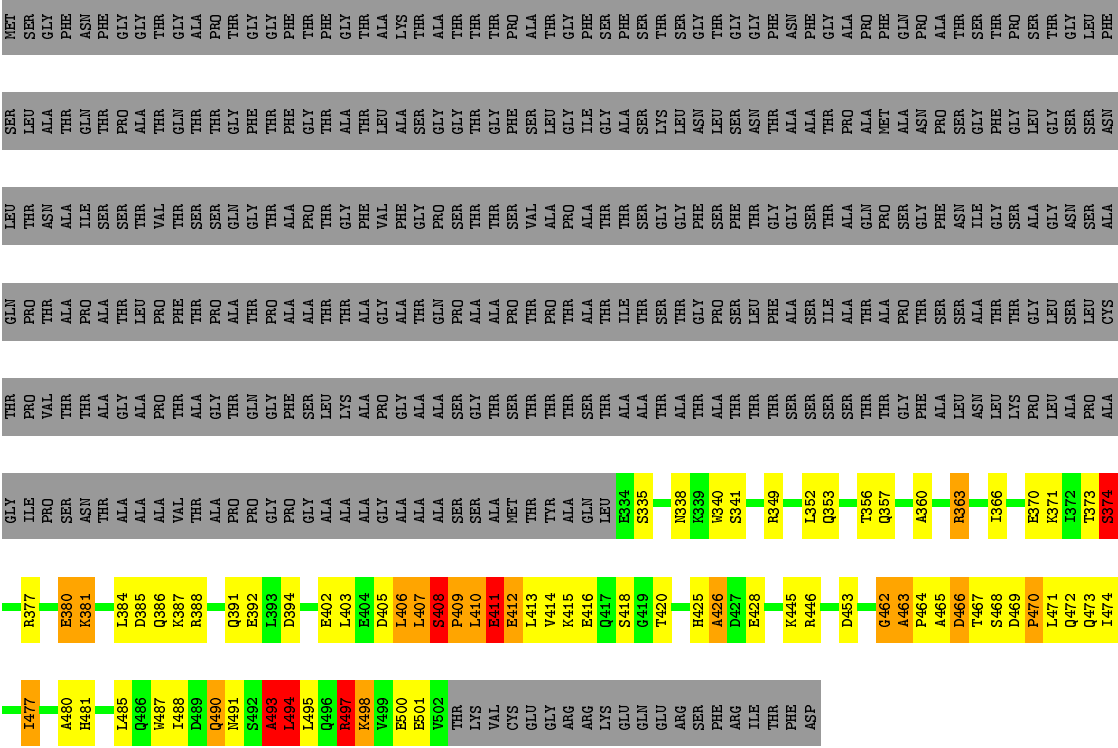


- Molecule 6: Nuclear pore glycoprotein p62

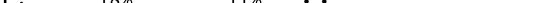


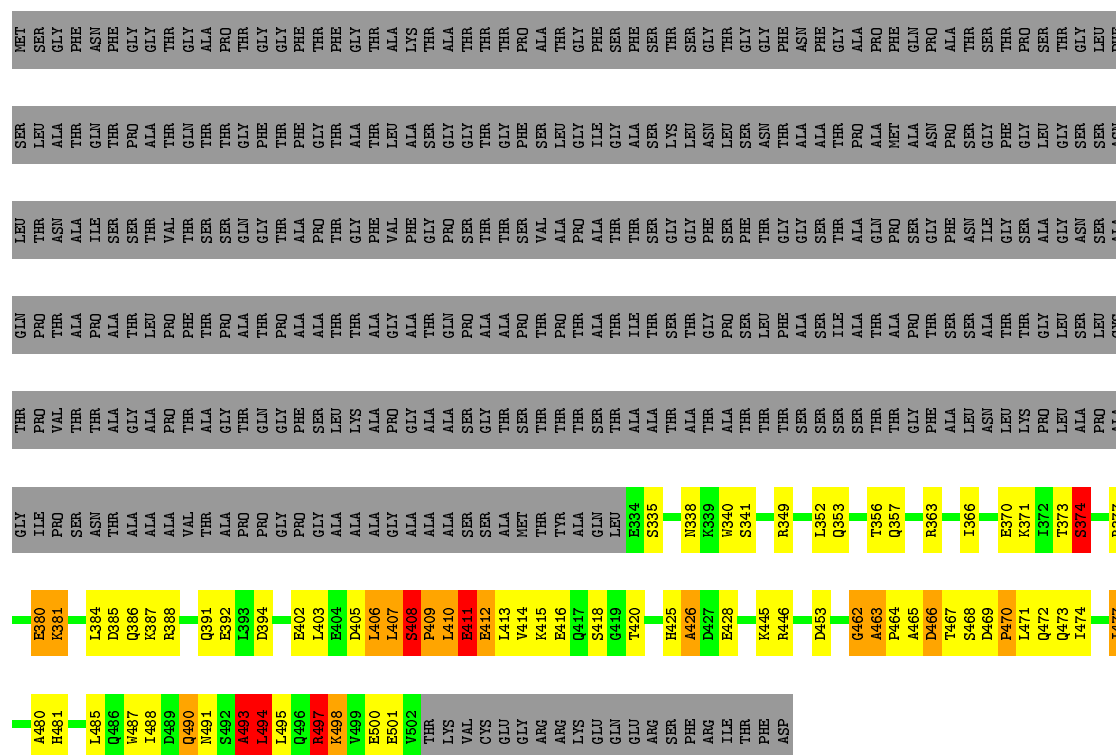


• Molecule 6: Nuclear pore glycoprotein p62



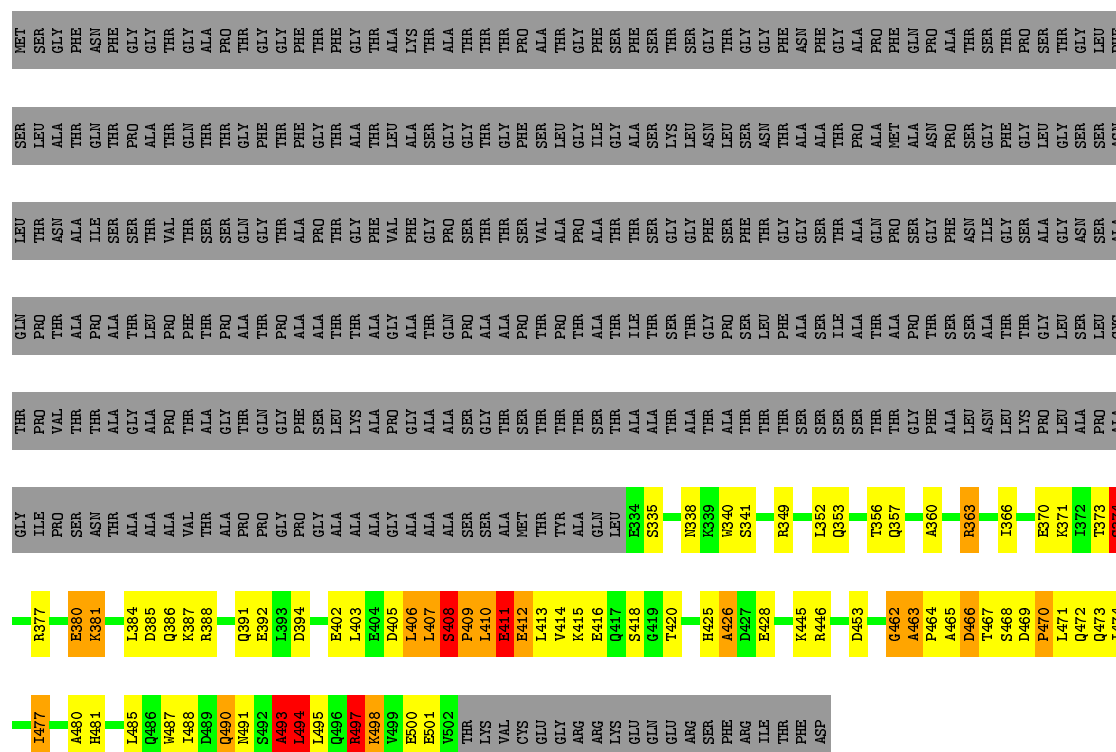
• Molecule 6: Nuclear pore glycoprotein p62

Chain T:  18% 11% . . 68%

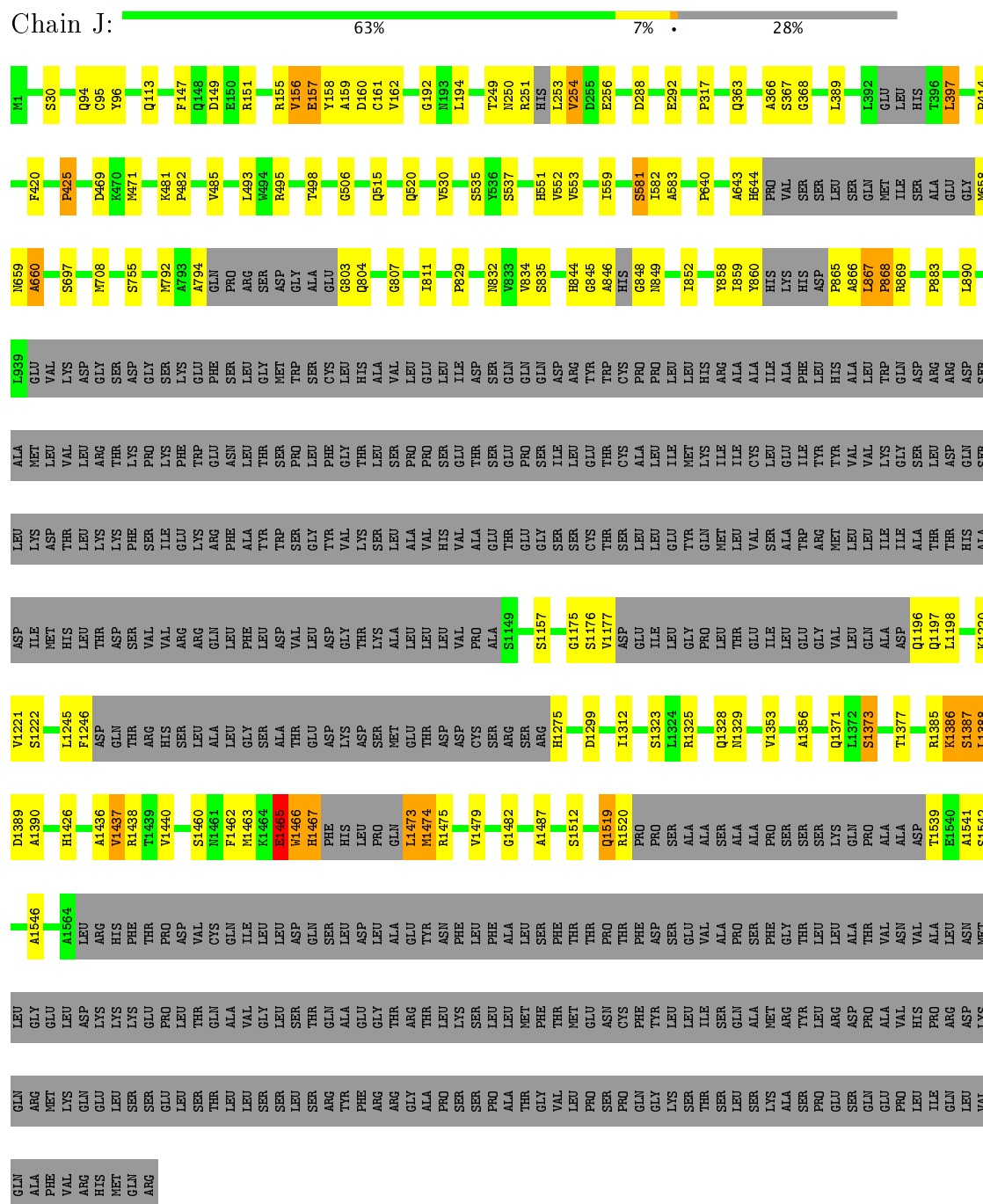


- Molecule 6: Nuclear pore glycoprotein p62

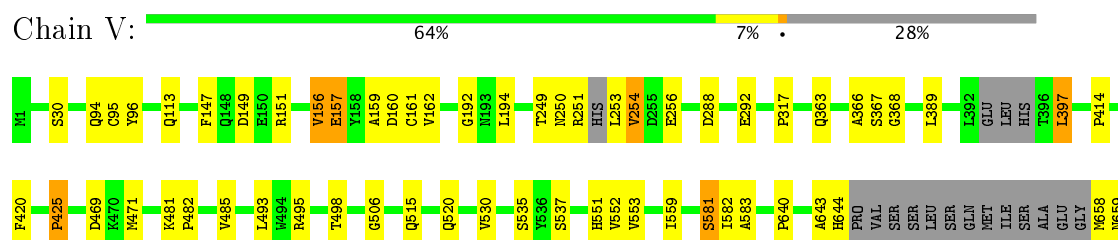
Chain Z:  18% 11% 2% 68%



- Molecule 7: Nucleoporin NUP188 homolog



- Molecule 7: Nucleoporin NUP188 homolog



[illegible]

## 4 Experimental information

| Property                             | Value                      | Source    |
|--------------------------------------|----------------------------|-----------|
| Reconstruction method                | SUBTOMOGRAM AVERAGING      | Depositor |
| Imposed symmetry                     | POINT, Not provided        | Depositor |
| Number of subtomograms used          | 8400                       | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF          | Depositor |
| CTF correction method                | PHASE FLIPPING ONLY        | Depositor |
| Microscope                           | FEI TITAN KRIOS            | Depositor |
| Voltage (kV)                         | 300                        | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 3                          | Depositor |
| Minimum defocus (nm)                 | Not provided               | Depositor |
| Maximum defocus (nm)                 | Not provided               | Depositor |
| Magnification                        | Not provided               | Depositor |
| Image detector                       | GATAN K2 QUANTUM (4k x 4k) | Depositor |

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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).

| Mol | Chain | Bond lengths |                   | Bond angles |                    |
|-----|-------|--------------|-------------------|-------------|--------------------|
|     |       | RMSZ         | $\# Z  > 2$       | RMSZ        | $\# Z  > 2$        |
| 1   | A     | 0.94         | 0/3195            | 1.25        | 10/4421 (0.2%)     |
| 1   | B     | 0.94         | 0/3195            | 1.25        | 10/4421 (0.2%)     |
| 1   | E     | 0.93         | 0/5338            | 1.17        | 10/7399 (0.1%)     |
| 1   | K     | 0.93         | 0/5338            | 1.18        | 10/7399 (0.1%)     |
| 1   | Q     | 0.93         | 0/5338            | 1.17        | 10/7399 (0.1%)     |
| 1   | W     | 0.93         | 0/5338            | 1.17        | 10/7399 (0.1%)     |
| 2   | C     | 1.13         | 13/3143 (0.4%)    | 1.44        | 45/4369 (1.0%)     |
| 2   | I     | 1.13         | 13/3143 (0.4%)    | 1.44        | 45/4369 (1.0%)     |
| 2   | O     | 1.13         | 13/3143 (0.4%)    | 1.44        | 45/4369 (1.0%)     |
| 2   | U     | 1.13         | 13/3143 (0.4%)    | 1.44        | 45/4369 (1.0%)     |
| 3   | D     | 1.22         | 38/5066 (0.8%)    | 1.74        | 122/7020 (1.7%)    |
| 3   | P     | 1.22         | 38/5066 (0.8%)    | 1.74        | 121/7020 (1.7%)    |
| 4   | F     | 4.14         | 197/1655 (11.9%)  | 4.03        | 272/2302 (11.8%)   |
| 4   | L     | 4.14         | 197/1655 (11.9%)  | 4.03        | 272/2302 (11.8%)   |
| 4   | R     | 4.14         | 197/1655 (11.9%)  | 4.03        | 272/2302 (11.8%)   |
| 4   | X     | 4.14         | 199/1655 (12.0%)  | 4.03        | 273/2302 (11.9%)   |
| 5   | G     | 3.95         | 84/852 (9.9%)     | 3.81        | 121/1190 (10.2%)   |
| 5   | M     | 3.95         | 84/852 (9.9%)     | 3.81        | 121/1190 (10.2%)   |
| 5   | S     | 3.95         | 84/852 (9.9%)     | 3.81        | 121/1190 (10.2%)   |
| 5   | Y     | 3.95         | 85/852 (10.0%)    | 3.81        | 120/1190 (10.1%)   |
| 6   | H     | 3.44         | 83/841 (9.9%)     | 3.10        | 110/1174 (9.4%)    |
| 6   | N     | 3.44         | 83/841 (9.9%)     | 3.10        | 110/1174 (9.4%)    |
| 6   | T     | 3.44         | 83/841 (9.9%)     | 3.09        | 109/1174 (9.3%)    |
| 6   | Z     | 3.44         | 83/841 (9.9%)     | 3.10        | 110/1174 (9.4%)    |
| 7   | J     | 0.92         | 0/6201            | 1.20        | 27/8622 (0.3%)     |
| 7   | V     | 0.92         | 0/6201            | 1.20        | 27/8622 (0.3%)     |
| All | All   | 1.89         | 1587/76240 (2.1%) | 2.00        | 2548/105862 (2.4%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | A     | 0                   | 1                   |
| 1   | B     | 0                   | 1                   |
| 1   | E     | 0                   | 1                   |
| 1   | K     | 0                   | 1                   |
| 1   | Q     | 0                   | 1                   |
| 1   | W     | 0                   | 1                   |
| 2   | C     | 1                   | 4                   |
| 2   | I     | 1                   | 4                   |
| 2   | O     | 1                   | 4                   |
| 2   | U     | 1                   | 4                   |
| 3   | D     | 0                   | 21                  |
| 3   | P     | 0                   | 20                  |
| 4   | F     | 10                  | 40                  |
| 4   | L     | 10                  | 40                  |
| 4   | R     | 10                  | 40                  |
| 4   | X     | 10                  | 40                  |
| 5   | G     | 9                   | 10                  |
| 5   | M     | 9                   | 10                  |
| 5   | S     | 9                   | 10                  |
| 5   | Y     | 9                   | 10                  |
| 6   | H     | 5                   | 5                   |
| 6   | N     | 5                   | 5                   |
| 6   | T     | 5                   | 4                   |
| 6   | Z     | 5                   | 5                   |
| 7   | J     | 0                   | 3                   |
| 7   | V     | 0                   | 3                   |
| All | All   | 100                 | 288                 |

The worst 5 of 1587 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 5   | S     | 380 | ILE  | N-CA  | 38.58 | 2.23        | 1.46     |
| 5   | M     | 380 | ILE  | N-CA  | 38.56 | 2.23        | 1.46     |
| 5   | G     | 380 | ILE  | N-CA  | 38.55 | 2.23        | 1.46     |
| 5   | Y     | 380 | ILE  | N-CA  | 38.48 | 2.23        | 1.46     |
| 5   | M     | 379 | HIS  | CA-C  | 37.09 | 2.49        | 1.52     |

The worst 5 of 2548 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|--------|-------------|----------|
| 4   | X     | 452 | ARG  | CA-C-N | -39.55 | 30.19       | 117.20   |
| 4   | F     | 452 | ARG  | CA-C-N | -39.54 | 30.20       | 117.20   |
| 4   | R     | 452 | ARG  | CA-C-N | -39.54 | 30.20       | 117.20   |

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| Mol | Chain | Res | Type | Atoms   | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|--------|-------------|----------|
| 4   | L     | 452 | ARG  | CA-C-N  | -39.53 | 30.24       | 117.20   |
| 5   | G     | 343 | ALA  | CB-CA-C | -36.23 | 55.76       | 110.10   |

5 of 100 chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|-----|------|------|
| 2   | C     | 11  | GLN  | CA   |
| 4   | F     | 200 | THR  | CA   |
| 4   | F     | 210 | VAL  | CA   |
| 4   | F     | 211 | GLU  | CA   |
| 4   | F     | 305 | ASP  | CA   |

5 of 288 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group     |
|-----|-------|-----|------|-----------|
| 1   | A     | 259 | SER  | Mainchain |
| 1   | B     | 259 | SER  | Mainchain |
| 2   | C     | 4   | GLU  | Mainchain |
| 2   | C     | 6   | PHE  | Mainchain |
| 2   | C     | 7   | GLY  | Mainchain |

## 5.2 Too-close contacts

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     | 3214  | 0        | 1424     | 23      | 0            |
| 1   | B     | 3214  | 0        | 1424     | 23      | 0            |
| 1   | E     | 5366  | 0        | 2364     | 58      | 0            |
| 1   | K     | 5366  | 0        | 2360     | 73      | 0            |
| 1   | Q     | 5366  | 0        | 2364     | 63      | 0            |
| 1   | W     | 5366  | 0        | 2364     | 56      | 0            |
| 2   | C     | 3152  | 0        | 1401     | 155     | 0            |
| 2   | I     | 3152  | 0        | 1406     | 30      | 0            |
| 2   | O     | 3152  | 0        | 1403     | 88      | 0            |
| 2   | U     | 3152  | 0        | 1406     | 30      | 0            |
| 3   | D     | 5094  | 0        | 2272     | 121     | 0            |
| 3   | P     | 5094  | 0        | 2273     | 77      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 4   | F     | 1658  | 0        | 715      | 168     | 0            |
| 4   | L     | 1658  | 0        | 715      | 169     | 0            |
| 4   | R     | 1658  | 0        | 714      | 169     | 0            |
| 4   | X     | 1658  | 0        | 715      | 168     | 0            |
| 5   | G     | 853   | 0        | 384      | 57      | 0            |
| 5   | M     | 853   | 0        | 384      | 55      | 0            |
| 5   | S     | 853   | 0        | 384      | 55      | 0            |
| 5   | Y     | 853   | 0        | 384      | 57      | 0            |
| 6   | H     | 842   | 0        | 365      | 36      | 0            |
| 6   | N     | 842   | 0        | 365      | 39      | 0            |
| 6   | T     | 842   | 0        | 365      | 38      | 0            |
| 6   | Z     | 842   | 0        | 365      | 38      | 0            |
| 7   | J     | 6213  | 0        | 2770     | 79      | 0            |
| 7   | V     | 6213  | 0        | 2770     | 78      | 0            |
| All | All   | 76526 | 0        | 33856    | 1791    | 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 16.

The worst 5 of 1791 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) |
|----------------|----------------|--------------------------|-------------------|
| 5:S:366:GLU:CB | 5:S:366:GLU:CA | 1.76                     | 1.64              |
| 4:F:451:GLU:CA | 4:F:451:GLU:CB | 1.77                     | 1.63              |
| 6:N:490:GLN:CA | 6:N:490:GLN:CB | 1.75                     | 1.62              |
| 4:F:454:TYR:CA | 4:F:454:TYR:CB | 1.77                     | 1.62              |
| 4:X:447:VAL:CA | 4:X:447:VAL:CB | 1.78                     | 1.62              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed          | Favoured    | Allowed  | Outliers | Percentiles |    |
|-----|-------|-------------------|-------------|----------|----------|-------------|----|
| 1   | A     | 612/1391 (44%)    | 562 (92%)   | 38 (6%)  | 12 (2%)  | 9           | 46 |
| 1   | B     | 612/1391 (44%)    | 562 (92%)   | 38 (6%)  | 12 (2%)  | 9           | 46 |
| 1   | E     | 1027/1391 (74%)   | 947 (92%)   | 58 (6%)  | 22 (2%)  | 8           | 45 |
| 1   | K     | 1027/1391 (74%)   | 947 (92%)   | 58 (6%)  | 22 (2%)  | 8           | 45 |
| 1   | Q     | 1027/1391 (74%)   | 947 (92%)   | 58 (6%)  | 22 (2%)  | 8           | 45 |
| 1   | W     | 1027/1391 (74%)   | 947 (92%)   | 58 (6%)  | 22 (2%)  | 8           | 45 |
| 2   | C     | 618/819 (76%)     | 516 (84%)   | 59 (10%) | 43 (7%)  | 1           | 19 |
| 2   | I     | 618/819 (76%)     | 516 (84%)   | 58 (9%)  | 44 (7%)  | 1           | 19 |
| 2   | O     | 618/819 (76%)     | 516 (84%)   | 59 (10%) | 43 (7%)  | 1           | 19 |
| 2   | U     | 618/819 (76%)     | 516 (84%)   | 59 (10%) | 43 (7%)  | 1           | 19 |
| 3   | D     | 972/2012 (48%)    | 899 (92%)   | 59 (6%)  | 14 (1%)  | 13          | 54 |
| 3   | P     | 972/2012 (48%)    | 899 (92%)   | 59 (6%)  | 14 (1%)  | 13          | 54 |
| 4   | F     | 329/507 (65%)     | 286 (87%)   | 21 (6%)  | 22 (7%)  | 1           | 21 |
| 4   | L     | 329/507 (65%)     | 286 (87%)   | 21 (6%)  | 22 (7%)  | 1           | 21 |
| 4   | R     | 329/507 (65%)     | 286 (87%)   | 21 (6%)  | 22 (7%)  | 1           | 21 |
| 4   | X     | 329/507 (65%)     | 286 (87%)   | 21 (6%)  | 22 (7%)  | 1           | 21 |
| 5   | G     | 169/599 (28%)     | 153 (90%)   | 10 (6%)  | 6 (4%)   | 4           | 33 |
| 5   | M     | 169/599 (28%)     | 153 (90%)   | 11 (6%)  | 5 (3%)   | 5           | 37 |
| 5   | S     | 169/599 (28%)     | 153 (90%)   | 11 (6%)  | 5 (3%)   | 5           | 37 |
| 5   | Y     | 169/599 (28%)     | 153 (90%)   | 11 (6%)  | 5 (3%)   | 5           | 37 |
| 6   | H     | 167/522 (32%)     | 152 (91%)   | 8 (5%)   | 7 (4%)   | 3           | 30 |
| 6   | N     | 167/522 (32%)     | 152 (91%)   | 8 (5%)   | 7 (4%)   | 3           | 30 |
| 6   | T     | 167/522 (32%)     | 152 (91%)   | 8 (5%)   | 7 (4%)   | 3           | 30 |
| 6   | Z     | 167/522 (32%)     | 152 (91%)   | 8 (5%)   | 7 (4%)   | 3           | 30 |
| 7   | J     | 1232/1749 (70%)   | 1111 (90%)  | 75 (6%)  | 46 (4%)  | 4           | 33 |
| 7   | V     | 1232/1749 (70%)   | 1111 (90%)  | 75 (6%)  | 46 (4%)  | 4           | 33 |
| All | All   | 14872/25656 (58%) | 13360 (90%) | 970 (6%) | 542 (4%) | 7           | 33 |

5 of 542 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 332 | ARG  |
| 1   | A     | 443 | LYS  |
| 1   | A     | 543 | GLN  |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 802 | GLN  |
| 1   | B     | 332 | ARG  |

### 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](#)

There are no RNA molecules in this entry.

## 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](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 4   | X     | 6                |
| 4   | R     | 6                |
| 4   | L     | 6                |
| 4   | F     | 6                |
| 5   | G     | 3                |

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| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 6   | H     | 3                |
| 2   | I     | 3                |
| 2   | C     | 3                |
| 6   | Z     | 3                |
| 6   | T     | 3                |
| 6   | N     | 3                |
| 2   | U     | 3                |
| 2   | O     | 3                |
| 5   | Y     | 3                |
| 5   | S     | 3                |
| 5   | M     | 3                |

The worst 5 of 60 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1     | C     | 483:GLU   | C      | 484:ARG   | N      | 4.02         |
| 1     | I     | 483:GLU   | C      | 484:ARG   | N      | 4.02         |
| 1     | O     | 483:GLU   | C      | 484:ARG   | N      | 4.02         |
| 1     | U     | 483:GLU   | C      | 484:ARG   | N      | 4.02         |
| 1     | C     | 447:ASP   | C      | 448:TYR   | N      | 3.63         |